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Preface

At the 5th International Oat Conference, held in Saskatoon, Canada, in 1996, it was agreed that the next conference would be held in New Zealand. Crop & Food Research generously agreed to host the event, and timed it to coincide with flowering of field-grown oat crops.

In hosting this oat conference, organizers considered whether oats were doomed to becoming an interesting food relic used in haggis, porridge, a few breakfast cereals and for a few horses or were they going to be an essential part of the food industry in the 21st century where taste, health, convenience and sustainable production drive the market? Oats are considered to have superior qualities for both food and feed consumption, yet in terms of world trade of cereal grains, oats have commodity and sometimes only novelty status. The health benefits of oats have only recently been acknowledged, as is its ability to grow in cold conditions. This latter attribute offers new opportunities for cool-winter environments as a green-feed crop for intensively farmed grazing animals, and as a dual purpose crop for resource-poor farmers. It is, therefore, timely to contemplate what oats have to offer at the beginning of the new millennium.

Keynote, invited speakers and presenters of poster papers were asked to address the conference theme "Why (eat) oats?" In this way, the conference organizers hoped to generate an informed debate on the current and potential prospects for oat production.

Richard Cross, Howard Bezar and Keith Armstrong
Local Organising Committee
November 2000

Acknowledgments

The 6th International Oat Conference gratefully acknowledges the generous sponsorship and support from the General Mills (USA), Quaker Oats (USA), the North American Oat Workers group and Bluebird Foods (NZ). Their sponsorship covered all aspects of the conference, enabling a full and generous programme to be made available to all delegates at reasonable cost. Hosted by Crop & Food Research, conference organizers were able to proceed using full Institute facilities at negligible financial cost to the conference.

The generous support and guidance of the International Organising Committee – Brian Rossnagle, Deon Stuthman, Robyn Mclean and John Oates – is gratefully acknowledged. The local organizing committee members were Richard Cross, Howard Bezar and Keith Armstrong who are responsible for the programme design and function, finance and sponsorship, special events and social activities, workshops, tours and accompanying persons programme. Helen Shrewsbury's efforts in conducting the conference secretariat, through Lincoln University, is especially acknowledged.

The local organizing committee also acknowledges the special efforts of Michael Lee-Richards, Virginia Humphrey-Taylor and Winna Harvey for their support in the regional food tasting session and buffet using oaten products; Justine Lee and Cass Boyd for computer services; and Damien Coup and Peter Thompson for transportation services.



WHY OATS?

Kenneth Frey — Distinguished Professor

Emeritus, Iowa State University, Ames, Iowa

When I was an oat breeder in the state of Iowa, USA for the period 1953 to 1993, so many producers ask me that question, that, at times, I had doubts about encouraging them to continue growing oats. Iowa, which has about 35 million acres of cropland, grew about 6 million acres of oats annually when I began as the oat breeder in 1953. The annual acreage of oats was down to 300 thousand acres when I retired in 1993. That gives a regression coefficient of a negative 140 thousand acres of oats per year. If I and the other oat researchers at Iowa State University were responsible for this regression, believe me, it was a dubious honor.

Well, to set the record straight, it was not our fault. As a matter of fact, during that 40-year period, oat cultivars developed by midwestern breeders were greatly improved for grain yield, agronomic traits, and grain quality. The real ogre, in terms of retaining oat growing, came about because of major changes in the agricultural production system that began about 1940. To understand these changes and the impact they had on the production of many crops, but especially oats, I will explain the situation in Iowa. The Iowa story with slight changes is analogous to what has caused the worldwide decline in oat production.

In pre World War II Iowa, a typical farm had 160 acres and rotational agriculture was used with a 3- or 4-year rotation, which typically would be corn-oats-meadow-meadow or corn-corn-oats-meadow. Rotational agriculture had a number of advantages, but the major one was that it distributed the labor of production quite evenly over the growing season, which in Iowa is/was April through October. (Note that oats never were a serious competitor with corn for pure grain production.) Oats were sown by mid-April when there was no other competing field work and oats were cut and threshed in mid to late July, after first-cut hay harvest and corn cultivation were complete, but before second-cut hay and corn harvest. Why oats and not another small grain? In Iowa, a spring small grain was required for the rotation because (a) most small grains of that era were not sufficiently winter-hardy for good winter survival and (b) corn, which was the preceding crop in the rotation, was not harvested early enough to give any small grain a good start in the fall. Unlike wheat and barley, spring oats were not seriously affected by scab disease, which also is a disease of corn that can destroy production and quality of grain. Oats also were a good feed for horses, which provided the power in Iowa agriculture. Thirty percent of the Iowa crop acreage was devoted to feeding horses. At that time only 5–10% of the oats produced were used for human food.

Starting about 1940, tractor power was substituted for horses, so a major use of oats as horse feed was lost. And as the tractors and other farm machinery grew in size, farm size also grew and a farmer no longer was concerned about using a variety of crops to distribute his labor over the growing season. So corn and oats, instead of being compatible partners on a farm, now were competitors in terms of grain production, and corn, for a number of reasons, won. Enter soybeans, which took the form of a cash crop. There was little demand for oats as just another grain crop, but there was a very large demand worldwide for a high-protein oilseed crop. Income wise, soybeans were a big winner over oats, so the oat acreage became the soybean acreage and then some.

This same scenario has played out in other parts of the world if one substitutes canola or wheat for soybeans, etc. No, neither you nor I are responsible for the demise of oats from importance in world agriculture. Changes in agriculture, and even more importantly, changes outside of agriculture, have dictated today's paradigm of world agriculture. As an example, there were less than two billion persons to feed in the 1940s and today there are six billion. You cannot expect to have a cool-temperate zone crop play a very big part in the feeding of this tripled population, especially when most of the population increase is coming in areas not adapted to oats. We must get real about the situation of oats in world agriculture. It will continue its role as a minor crop with a number of niches in world agriculture and in societal and industrial uses.

SO, WHY OATS?

There are a number of reasons for oats to be included in future world agriculture. The niches in which this crop can compete in agriculture are—

Niche I: Oats as a cool temperate-zone crop for food or feed grain—Several years ago, I was a visiting scientist for a summer at the Agricultural University of Norway in Aas, Norway. I traveled quite extensively in agricultural areas of Norway and I was quite surprised as to how much of the grain production in that country was devoted to oats. My colleagues at the university told me that small grain acreages (no corn is grown for grain in Norway) in Norway were divided about one-third to each of oats, barley, and wheat. Oats is a cool-season or cool-climate crop, and Norway and other areas of the world that have cool growing conditions represent a niche(s) where oats can compete well as a food and feed grain crop. In this niche, some of the oat grain is used as human food, but its primary use is as feed grain in livestock rations.

A specialized area of feed grain oats is the so-called “race horse market.” This market category includes oats fed to race, show, and pleasure horses, most of which are owned by affluent people—people who will pay any price for a commodity that is believed to be good for their special horses. In the Midwestern U.S., race horse oats are screened as a special fraction from ordinary bin-run oat grain. The bin-run oats are passed through grain-cleaning equipment where the plump primary grains are scalped off. This fraction, which has a high test weight and makes up 25% or less of the original grain lot becomes “race horse oats.” They sell for as much as five times the price of the bin-run oats from which they were screened. The remainder of the screened lot may be sold back into the commodity market or they may be used in formulated livestock feed.

Niche II: Oats as a forage crop for pasture, hay, or silage—In the southern U.S., a million or more acres of winter oats are used for fall and winter grazing for cattle. Also, as much as 50% of the oat acreage in Argentina and 25% of the acreage in Brazil are used for grazing. Winter in the areas when oats are grazed, has the cool-season conditions which are optimum for growing oats and sub-optimum for foliar diseases, which can be so devastating for oats. A small acreage of oats is used for hay or silage. A decade or so ago, the University of Wisconsin, USA devoted a portion of its oat breeding program to developing cultivars that produced high forage yields for use as silage. When used for silage, the oats are harvested when the grain is in the early to mid dough stage, which gives a good quality of silage with about 35% dry matter.

Niche III: Oat grain for breakfast cereal production—The use of oat groats to make rolled oat cereal goes back at least several centuries and was made famous as the ingredient for porridge which made Scotsmen so robust, vigorous, and virile. In the U.S., the trademark for Quaker Rolled Oats was filed 123 years ago, in 1877. I have a personal anecdote about rolled oat cereal which I have confided to only a few close friends and then only since I retired. For the first 17 years of my life, I lived on a farm in Michigan, USA, and every single morning of those 17 years, Sundays included, my mother served me rolled oat porridge for breakfast. Shortly after my 17th birthday, when I went off to university, I was so sick of rolled oats that I have never eaten rolled oat porridge since. The irony here is that for 45 years I made my living by being an oat breeder, and I could not relate this story because I would have been branded as a heretic. Grain used to make rolled oats traditionally has been purchased on the general grain commodities market. Only plump oat grain with high-test weight, good seed size, and low hull percentage was purchased for rolled oat milling. Actually, these mechanical traits had little to do with producing a good cereal product, but everything to do with milling characteristics and milling yield (pounds of rolled oats per 100 pounds of raw oats). Most oat groats have a relatively high protein content (12 to 16%) and oat grain protein has a high biological value when compared to wheat, rice, or corn, so rolled oats is a good protein source for humans. Millers stress low fat content in rolled oats, but this trait was controlled by discouraging the development and release of oat cultivars with more than 4% fat. The irony is that the compositional values of oat grain used for food and feed are about the same. Over the past 50 years, oat flour has become an important ingredient for cold breakfast cereals, but, as for rolled oats, the groats used for oat flour have no nutritional characteristics different from feed oats.

Niche IV: Oats with special groat or forage composition for specialty products—Composition of oat grain has been the subject of considerable research but little development. About three decades ago, the Quaker Oat Company supported research on elevating protein content of oat groats, and several oat cultivars with groat protein contents of 17–20% were released from breeding programs in the Midwestern U.S. These cultivars tended to produce lower than normal grain yield, and this was a “kiss of death” for them because millers did not pay a premium for their production. As mentioned in the discussion on rolled oats, millers have discouraged the release of oat cultivars with greater than 4.0% groat fat, so this is a case of controlled chemical composition. None of the other chemical constituents of oat groats have gone beyond the research stage. Germplasm lines of oats with 16–18% groat fat content have been produced via recurrent selection and some of these lines were used to develop high-fat lines by Svalof Company, but these lines have never occupied much acreage. Fatty acids can be manipulated genetically and some research has been done on anti-oxidants, such as the tocopherols and avenanthramides. A multi-station project to increase and lower β -glucan (soluble fiber) content of oats was initiated 12 years ago by Iowa, Minnesota, and Ag-Canada. Clinical nutrition studies have shown that high soluble fiber in human diets usually lowers cholesterol in the blood. Progress was made in elevating β -glucan content in germplasm lines to 7.0+% and lowering it to 3.0% via recurrent selection, but prior to the development of cultivars with modified β -glucan content, the project died for lack of funding.

Composition of oat forage has been researched very little. Typically, mature oat straw has about 3.0% protein, but analyses of straw of *Avena sterilis* has shown a range 3.0–12.0% in this species. Of course, oat straw is used as roughage feed only in emergencies. Probably, this range of protein percentages would not pervade in oat hay or oat silage because these two forms of oat forage include the grain.

SO, WHY OAT RESEARCH?

Well, the answer to that question is very simple—if research lapses on oats, their competitive advantages for the natural niches elaborated in the second section of this paper will gradually fade. If oat breeding ceases and breeding programs of crops with which oats compete in agriculture continue, oat productivity will, at best, plateau, whereas the productivity of its competitors will continue to gain. Yes, oats will continue to be grown for a time, but at higher and higher relative costs of production until they literally are driven from world agriculture. Or the price for products from oats will have to absorb the higher costs of production, which will result in a smaller and smaller demand and literally oats will be driven from production. The result is the same. Facetiously, I suggest that a possible exception to this scenario is “race horse oats.”

I would argue that a new paradigm is needed for global oat breeding. Future oat breeding needs to develop cultivars for niches that represent environments or uses where oats is equal to or has an advantage over competitor crops. In the past, some oat breeding has been done with a niche market in mind, but 95+% of the resources used for oat breeding have been devoted to increasing or stabilizing grain yield and breeding oats for niches, at best, has been sporadic and with few resources. In the first sentence of this paragraph, I used the term “global oat breeding”. As an experienced ex-oat breeder, I know that cultivars for local use, niches included, need to be developed locally. However, specialized germplasm for exploitation in locally developed cultivars does not need to be developed locally. It can be developed in a single location and exploited in cultivars in an oat breeding program anywhere in the world. Need an example—high-fat germplasm lines of oats developed in Iowa were used to produce high-fat cultivars in Sweden. This model has been used for half a century by the International Agricultural Research Centers (IARCs). And biotechnology is driving this germplasm development model to even greater extremes. The genetic construct that made “golden rice” possible was developed in a lab and greenhouse in Switzerland, hardly a natural area for rice production. If this trait, which provides a biosynthetic pathway for β -carotene production in rice, is compatible with the genome of elite rice cultivars, it can be used in cultivar development in national programs around the world.

With oats being the minor crop that it is, I do not foresee an IARC taking oats on as a “mandate” crop with the organization of a “global breeding program” for them. But, if the research and user segments of the oat industry want to organize a “global breeding program” that (a) supports cultivar development programs for niches where oats have an advantage, (b) provides for oat germplasm enrichment and enhancement done at various but mutually agreed upon sites, and (c) capitalizes on the methods of biotechnology and the potential of transformation, it can do so, albeit without a central research site like IRRI, CIMMYT, etc., via cooperation and coordination. I offer the suggestion that the natural body to organize a “global breeding program” for oats, if such a program is desired, is the International Oat Conference.

OATS: WORLD STATUS IN FOOD MARKETS

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FOREWORD

This paper is based on a global market study on oats commissioned by The Finnish Ministry of Agriculture and Forestry. The study was made in 1977-98 as a joint venture between Bio Business Consulting, Finland and Sparks Companies, Inc., Memphis, USA. The objectives of the study were to find out the major trends and opportunities in consumption, processing and production of oats in the world.

The study serves as a basis for further research and development work for Finnish oats, but hopefully benefits the world oat industry as well. As part of the study, over 100 interviews among the oat and food industries in Europe and nearly 50 interviews in the United States were conducted. Additionally, a questionnaire market research was carried out in Europe.

OATS PRODUCTION AND TRADE

The global oats production is about 30 million metric tonnes (MT), which is about 1,6 % of total world grain production. Share of oats from the total world grain production has been declining. Global oat consumption will continue to shift away from feed into food consumption as other feed grains take market share from oats in feed rations and human consumption increases.

The global oats trade is heavily dominated by the US as the largest importer and Canada as the largest exporter. Canada is expected to continue to be the primary source of oats for the US as well as market oats in Asia and Latin America. The exportable surplus of oats from the present EU has ranged between 100 and 800 thousand MT. The US market is expected to absorb only part of the forecasted EU oats surplus. Therefore new markets should be developed.

A price forecasting model was developed using Ordinary Least Square (OLS) Regression Analysis. According to the model, feed (corn) grain prices play a major role in oat price formation. This price formation mechanism is unfavourable to oats since it does not take oats' true value into account. Oats should be differentiated from feed grains.

CONSUMER TRENDS

Average age of population both in Western Europe and North America is growing. People are living longer and good health is important for elderly people. The role of food in the well-being of aging people will become more and more important. E.g. in USA there are 53 million health-conscious consumers. EU's 5th research framework programme will favor the development of health-promoting foods.

Health is becoming a major driving force in food marketing: Convenience and taste are viewed as the other important driving forces both in the US and EU. Also purity from residues and safety will be increasingly important. Importance of origin of the products will grow. Awareness of environmentally sound growing methods and vegetarianism are increasing.

US consumers are increasingly aware of the importance of fiber in the diet and consumption should increase. While there are a variety of food products that can increase dietary fiber intake, oat bran is one of the best known to consumers. Interview subjects indicated that there should be ample room for future growth in this area. Interviews emphasize the importance of low fat focus in the U. S. "healthy" food category. Obesity has become an issue in the U. S. and consumer interest in fat free foods has intensified. An oat product that is already perceived as healthy could have great promise as a low fat food.

Market segmentation will continue further. Consumer groups with identified specific dietary requirements will be the target segments in the future in the form of dietetic foods

DEVELOPMENT OF NOVEL TECHNOLOGIES

Novel processing technologies for oats have been developed recently in Finland, Sweden, USA, Canada and the UK. These use one or more of the following unit operations: wet milling, dry milling, solvent extraction and enzyme treatment. Commercial applications have recently been launched.

OATS FOOD MARKETS

Human consumption of oats is rather low with the US at 3,5 kg/ca and the EU at 1,5 kg/ca. Consumption is highest in Canada, USA, Scandinavia, UK, Ireland and Germany. The oats consumption consists of porridge, ready-to-eat (RTE) breakfast cereals (müsli, extruded cereals), biscuits, baby food, bakery products and snack bars.

Driving forces in the food market are positive for oats. Excellent eating quality combined with convenience and health aspects and backed with good marketing and promotion are the keys to success. Interest among European oat companies exists in joint marketing and advertising but it is difficult because of competitive situation.

In the USA, increases in the consumption of oats has lagged behind that of other grains such as wheat, rice, corn and durum as the growth of "ethnic" foods such as pizza, tortilla, pasta, and oriental food has been quite strong. Unlike other food products such as beef, milk, orange juice and raisins, oats have not had marketing campaigns aimed at boosting consumption.

FDA labeling of oat products is expected to eventually have a positive impact on consumption. It is recommended to US consumers that 35 grams of fiber is a "healthy" level of fiber consumption. US consumers eat only 11 grams of fiber, leaving plenty of room for consumption to reach an optimal level.

Japan consumes very little oats in food. As diets in Japan and other Asian countries become "westernized", there is an increasing need to add fiber to the diet. Additionally, Japan is a leading market in the development of functional foods.

Because of the large low income population in regions such as South America, Asia and Africa, there is potential to promote oats as a "complete" food that is both economical and nutritious.

ORGANICS MARKETS

The market for organic products in both Europe and North America has great promise. In Europe north of the Alps, the organic share of markets is 1-2 % and growing; forecasted market potential is 5 – 10 % depending on the country.

Oats is one of the easiest grains for organic production. Premium for organic oats and oat products is strongly affecting the market size. The higher the premium the smaller the market and vice versa. According to interviewed mills, premium for organic oats should be max 25 % and for organic consumer products 10 % for the market to grow considerably.

In the US organic products are 1-2 % of the market but are growing at a rate of 20% per year. Generally speaking, in both the EU and US large commercial firms have ignored the organic markets. Price premiums for organic grains in the US are high and have increased in recent years – prices are about 60% to 70% over normal base prices. Prices at the consumer level are two to three times conventional products.

FOOD AID PROGRAMS

Food aid is about 5 % of the food consumption in the developing countries (differs a lot between countries). Food aid is still mainly given in the form of grain (wheat, rice and corn). EU has donated about 1,755 million tons food aid annually in 1995 – 98, calculated as wheat. Previously oats and oat flakes were more used in food aid programs (until two years ago), presently wheat, rice and corn dominate.

Food Aid is an opportunity for oats. Oats would fit perfectly in the Food Aid programs for many reasons. Oats are “complete food” - oats contain almost all the nutrients what a human body needs. Oat flakes are easy to use on location; they can be used as such or cooked with water or milk powder. Oat flakes are known also in developing countries, especially in the British commonwealth countries.

Wheat flour is 50% cheaper/kg than oat flakes. Nutritional quality nor convenience have not been considered or favored. Information about the benefits of oats should be given both to aid givers and receivers - promotion is important.

OPPORTUNITIES BASED ON THE EUROPEAN MARKET SURVEY

A comprehensive written survey was conducted in Europe with focus in food use of oats. Over 500 questionnaires were sent to companies and R&D organizations representing various industry segments in Finland, UK, Germany and other European countries. 102 returned questionnaires were included in the analysis. Some of the critical findings were as follows:

Health properties are the most important R&D topic related to raw materials at the moment. Natural ingredients and fiber-enriched foods are regarded as most important nutrition-related consumer interests. Interest in fiber-enriched foods is highest in baby food and dairy sector.

Health promoting properties are the most important strength of oats. Other positive aspects are taste, quality properties and positive image. Image of oats is not strong enough. However, based on the properties of oats, it is possible to strengthen the image of oats with proper marketing. Negative aspects were mentioned clearly less frequently than positive aspects.

Many of the negative aspects are related to insufficient marketing. Therefore it is possible to change them to strengths with marketing related efforts.

Two thirds of the respondents will use oats in new products. New oat products will be launched in following product groups: health oriented foods, bakery products, biscuits, cookies, snack bars, breakfast cereals, prepared foods and baby foods. Nearly 1/3 of the respondents do not know enough about oats to give opinion about the future use of oats, reflecting an immediate need for active marketing of oats

Traditional oat ingredients (oat flour, flakes and bran), which are widely known and readily available, are ranked as the most interesting oat raw material types. β -glucan enriched fraction is a close second and clearly ahead of other novel oat ingredients.

A major conclusion from the market research is that there is a surprisingly strong interest and willingness to use oats in product development. Of the new product concepts, β -glucan attracted the highest interest.

CONCLUSIONS

The scenario for raw oat markets is not especially bright unless strong actions will be taken. Therefore it is necessary to develop new markets and applications in the magnitude of several hundred thousand tons. Various market development programs are required to succeed in this.

Another main conclusion of this analysis is that there are opportunities to develop oat-based businesses utilizing both traditional and novel technologies. Oats are an excellent and versatile raw material for various food applications. A major marketing effort should be initiated to support the recommended oat business developments.

RECOMMENDATIONS

- Plan and implement a major European marketing and lobbying campaign to increase the knowledge about oats and strengthen the positive image of oats.
- Inform EU commission about various aspects of oats, such as the new opportunities offered by oats and suitability and potential of oats in Food Aid programs.
- Promote and sell oat products into Food Aid programs. Develop suitable products for developing countries and Food Aid programs.
- Grow and market organic products. Manufacture organically grown agricultural products into value-added consumer products.
- Developed global oat convenience health food businesses based on the strengths of oats, supported by oat marketing programs.
- Create cooperation partnerships targeting new oat markets (such as South America, Asia).
- Initiate an EU research program covering basic health-related aspects of oats as well as the basic food chemistry and processing technology of oats.
- Develop oat-based consumer products with excellent eating quality and health properties.
- Intensify oat breeding programs.

INTERNATIONAL CO-OPERATION

Finland has initiated a coordinated cooperation and development program where different parties are partnering to reach common goals:

- strengthening of the competitive position
- development of new markets and applications for oats.

A concrete international oat technology and business development program should be started. It could include following topics:

- development of new and undisputed standards for oat soluble fiber and its functionality
- verification of β -glucan stability in consumer products during processing and distribution
- differentiate oats from commodity (insoluble) dietary fibers by building of a global brand for oat β -glucan using the above standards
- improvement of oat (lipids) stability
- obtaining approval of oats for coeliac patients.

NON DAIRY MILK PRODUCTS FROM OATS

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SUMMARY

Oat milk was developed as a base for the making of different milk-free dairy products. It is made from pure oats and water only without the use of additives such as emulsifiers and stabilisers. The flexible production process enables the manufacturing of products suitable for different end uses i.e. milk substitutes, yoghurts, creams and ice creams. The nutritional quality of the oat milk suits the need of humans very well, and its cholesterol lowering property has been confirmed in clinical studies. Oat milk products are a palatable, healthy alternative to traditional milk products for both milk intolerant and tolerant people alike.

BACKGROUND

Milk is one of the important foods of man, and is used as a healthy drink or as raw material for the production of dairy food such as yoghurt, cream, ice cream and more. Still, the ability of many humans to enjoy these products is limited for a number of reasons.

Lactose intolerance is the reduced ability of humans to digest milk sugar (lactose). Although most often described as intolerance, this is in fact the normal condition for most grown-up humans worldwide, making the ability to digest lactose the exception ('lactase persistence'). Low intestinal levels of lactase limits the amount of lactose in the diet that can be conveniently tolerated. Although complete avoidance of dietary lactose is not needed, about 10-15 g of lactose a day is often considered as a limit corresponding to an intake of 200 to 300 mL milk (Cummings, 1993). Higher amounts may create intestinal discomfort, a situation likely to negatively affect the attitude of the individual towards milk containing products in general.

Milk protein allergy affects about 2% of children 0-4 years of age and about 1 % of the population and put a strict limitation to the use of milk products for these categories. Total exclusion of milk protein containing products is a necessity. For such a family, soy-containing products is not a good alternative, since about 30% of the afflicted milk allergic children would then develop soy protein allergy (Rasmussen, *pers. com*).

Further, some religious concerns (i.e. 'Kosher food') limit the use of cow's milk based dairy products as a component in the diet.

Obviously, many humans cannot have products containing milk. This is an increasing problem both for individuals, families and catering establishments trying to meet the demands from a more integrated, international and travelling world, where food habits tend to spread and mingle with the local traditions. Facts thus suggest that there exist a potential market for a product category that can be appreciated as dairy products, but that is not made from milk.

Oats is an interesting candidate as raw material for such a non-dairy product line. Its nutrient composition is well suited for human needs. It has an attractive taste, and further, pure oats is now on the verge of being considered safe for individuals suffering from gluten intolerance.

Oat Milk Manufacture

In order to obtain milk like products from oats, we developed an industrial process to manufacture a palatable, liquefied oat base, eventually protected by patents (Lindahl et al. 1994). In short, the oat milk is made from oat flakes and fresh water, and includes a number of processing steps to transform the raw material into a suitable, palatable liquid to be consumed as such or used as a raw material for the manufacture of milk-free dairy products. Further refining (patent pending) utilising different combination of enzymes in the production process, allow the convenient production of products with different characteristics, i.e. sweetness, viscosity, fermentability, and emulsion stability.

It is possible to obtain a fermented oat milk with texture properties resembling that of traditional yoghurt. In fact, this oat milk yoghurt can be made without the use of additives such as stabilisers, if the inherent properties of the oat milk process are fully explored (patent pending). Oat milk suitable as the base for the manufacture of non-dairy cream and ice cream that minimizes the need of emulsifiers and stabilizers have also been developed (unpublished results). Also, it has been found that oat milk may substitute cow's milk when making pancakes, crepes and waffles with excellent results in ready-made long shelf-life batter's (patent pending procedure). The oat milk *per se* is appreciated as a non-dairy milk alternative in the health market (Anon, 1999).

Nutritional Aspects On Oat Milk

The major nutrients are protein, fat (lipids), carbohydrates and dietary fibre. Then there are vitamins (4 fat-soluble and 9 water-soluble vitamins), minerals and trace elements. It is a generally recognised fact among experts in human nutrition that no single food contains all essential nutrients in amounts sufficient for health. One who for example lives only on milk from cow will with time develop diseases. The same would be true for non dairy milk substitutes such as soy, rice or oat milk. So they all will have to be consumed together with other food.

This means that it is acceptable if milk/milk alternatives do not contain 'everything', nothing does. So on what grounds should we compare them? An approach that is logic to us, and that was a base for the development of oat milk, is to look at the major nutrients (protein, fat, carbohydrates, and dietary fibre). Other nutrients, the vitamins and the minerals and some fatty acids, are needed in much smaller amounts, and can, if deemed necessary, be conveniently added (they can be purchased in pure form) in the product during the manufacture to a small cost.

Composition of oat milk as compared to other milk substitutes:

The official nutrient recommendations in the Nordic countries express the need of the basic, major nutrients protein, fat, carbohydrates, as energy% of the diet, since they are all eventually used as an energy source in the body. This is a way to define the proportions of these basic nutrients that should be supplied by the food intake (Table 1). Notably, these figures are the same for males and females over the age of 3 years. Under this age, the

relative need of fat is higher. The Nordic figures are close to European recommendations and FDA's recommendation in the US, all obviously based on essentially the same state of scientific art. However, for protein, recommendation is 8-10% in the US, and somewhat higher, 10-15%, in the Nordic countries. In addition, the recommended value for dietary fibre intake is given in Table 1.

Figures for the relative contribution of energy from these macronutrients are also given in the table 1 for oats, soy, rice, milks thereof, and cow's milk (National Food Administration, 1988).

A comparison leads to the following conclusion: Oat milk (with added fat, or made from high fat variety Mathilda) is close to perfectly balanced with respect to the gross proportions of protein, fat and carbohydrates as compared to the need of humans over 3 years. Soy milk is too high in fat (44E% vs. recommended 30E%) and protein (32E% vs. 8-15E%), rice is too low in protein (2E% vs. 8-15E%) and fat. Cow's milk again is too high in protein (its made for rapidly growing calf's, not humans) and fat (however there are low fat milks on the market).

In addition, it should be observed that oat milk is the only milk/ milk substitute that gives the balanced amount of dietary fibre.

Table I: Basic nutrients (E%, energy contribution in percent) in non-dairy milks and corresponding raw materials compared to cow's milk and recommended intake for humans over 3 years of age.

Nutrient	Oats	Oat milk	Soy	Soy milk	Rice	Rice milk	Cow's milk	Rec, > 3 Years
Protein, E%	15	10	32	34	8	2	23	8-10 (10-15)
Lipid, E%	17 (30) ¹	33 ²	38	44	5	16 ³	47	30
Carbo- hydrates, E%	68	57	30	25	87	82	16	55-60
Dietary fibre(g/MJ)	7	4	8	0.5	6	0	0	3

¹Within parenthesis: variety Mathilda

²With added oil or with Mathilda as raw material in the oat milk manufacture

³With added oil (e.g. Rice Dream, Provamel)

The amino acid composition are well balanced in oats, soy and rice protein, and from this point of view they are all satisfactory. (National Food Administration, 1988).

Lipids should be rich in mono- and polyunsaturated fatty acids to fit recommendations for humans (<30% saturated fat) . Milk fat is not good from this point of view, soy fat and oat fat are good (National Food Administration, 1988).

In the nutritional world, much interest is now focused on antioxidants and other organic compounds that are not vitamins, but which may exert some physiological effect(s). Oats contains many interesting compounds in this area, suitable for more research in the area of oat consumption and human health (Dimberg et al., 1993, Collins, 1986).

Clinical Studies On Oat Milk

An increased level of cholesterol and LDL cholesterol in the blood is associated with an increased risk for developing coronary heart disease. Foods containing soluble fibres have been shown to decrease the blood cholesterol concentration. In particular the effect of oat products containing soluble beta-glucans has been focused by the the Food and Drug Agency in the US, and are now eligible for health claims (FDA 1997).

The oat milk was developed to retain the cholesterol lowering properties of oats through the manufacturing process. Its effects on blood lipid levels have been tested in three crossover studies.

In the first study, the oat milk made to contain insoluble fiber was compared with soy and cows milk (Önning et al. 1998). The oat milk was given to healthy subjects (n=24) during four weeks and the subjects then shifted over to either soy or cow's milk for four weeks. Blood lipids were measured in the end of the two diet periods. Compared to baseline, the oat milk decreased total cholesterol with 4% and LDL cholesterol with 9%. Also soy milk decreased the LDL cholesterol while cow's milk had no effect on total and LDL cholesterol. The oat milk was well accepted by the subjects. Thus, an intake of oat milk corresponding to 3.4-4.5 g beta-glucans per day positively affected the cholesterol levels in healthy subjects.

In the second study, a similar oat milk was compared with cow's milk in women with increased blood cholesterol levels (Wallmark et al., unpublished). The women (n=61) took oat milk or cow's milk for five weeks, followed by a two week wash-out period, and then the other drink for five weeks. Compared with cow's milk, the oat milk significantly reduced total and LDL cholesterol (3 %). In conclusion, an intake of oat milk corresponding to 3.4 g beta-glucan per day reduced the blood cholesterol levels in hypercholesterolemic women.

In the third study, and oat drink made without insoluble fibre was compared with a control drink (rice milk) in men with increased blood lipid levels in a double-blind cross over design (Önning et al. 1999). The drinks were flavoured with blackcurrant, so the subjects could not see or taste any difference. The men (n=52) took the oat milk or control milk for five weeks, followed by a five week wash out period, and then the other drink for five weeks. Compared with the rice drink, the oat milk gave significantly reduced total cholesterol (6%) and LDL cholesterol (6%) levels. Thus, an intake of oat milk corresponding to 3.8 g beta-glucans per day reduced the cholesterol levels significantly in hypercholesterolemic men.

From these studies, it is concluded that the oat milk is able to reduce total cholesterol and LDL cholesterol levels and can be used to improve the control of hyperlipidemia in people by dietary means.

It is well known that obesity is a major, increasing health problem with an enhanced risk of hyperlipidemia, cardiovascular disease and non-insulin-dependent diabetes mellitus. To improve associated metabolic disorders, weigh reduction is imperative. The most obvious way to achieve this is to modify the diet. The potential of oat milk as a base in a energy-restricted dietary regimen was evaluated on 32 subjects having a body mass index of 25-35 (slight to moderate overweight; Rytter et al, 1996). The 31 subjects who completed the study consumed for 23 weeks a diet including, as main meal once or twice a day, an oat milk based soup low in energy relative to nutrient content (high nutrient density).

The intake of energy decreased from 8.9 to 6.2 day from week 0 to week 22. The energy percentage from fat decreased from 35% to 30% and the intake of dietary fiber increased from 21 to 25 g/10 MJ. The average body weight decreased from 83 to 78 during the first 6 weeks, and the subject were then able to keep this reduced weight throughout the study. Blood lipids were significantly improved. It was concluded that the oat milk based regimen was well tolerated and appreciated by the subjects.

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PSYCHOLOGICAL FUNCTIONALITY OF FOOD CARBOHYDRATES: OATS AS FOOD FOR THOUGHT

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ABSTRACT

The brain depends almost exclusively on blood glucose for its energy. Although only 2 % of body weight, it uses 25 % of body glucose, is extremely vascular in taking 16 % of the blood supply of the body, and there is no barrier to glucose entry into the brain from the blood, all of which suggests that foods affecting blood glucose levels might also influence brain function. It has now been shown that despite homeostatic systems for keeping blood glucose levels within physiological bounds, normal variations in blood glucose levels can affect performances on tests of a number of psychological processes, such as abstract reasoning and memory.

The task of matching the glycaemic properties of foods with mental demands has barely begun. However, oats are likely to be a good material on which to base prototype products for enhanced psychological function because they have a relatively moderate effect on blood glucose, and the carbohydrate availability from them can be easily altered through food processing to furnish a range of products differing in glycaemic impact, and therefore probably in psychological impact. Testing the effects of oat products on psychological functions is possible under well controlled experimental conditions, but laboratory tests need to be validated as predictors of the effects of foods on the complex behaviours and under the conditions that are typical of the work-place.

INTRODUCTION

Although the brain evolved in a world of very different stimuli than today, the ability to rapidly and accurately process information is linked with success as much in modern society as it was during human evolution. In view of the importance of brain function, and therefore of brain nourishment, it is entirely appropriate to consider the possible psychological functionality of oat products, because there is growing evidence that carbohydrate-rich foods can affect psychological performance, and that oats have the right properties to create products for modulating brain function.

Blood Glucose Is The Brains Energy Source

The brain is intensely energy consuming

The intense neural activity involved in mediating between the environmental demands and patterns of adaptive response, and the need to keep the nervous system in an electrically polarised state so it is ready to respond immediately with nerve impulses, is reflected in the considerable metabolic investment there is in brain function:

- The brain is about 2% of body mass but –
- it is responsible for about 20% of the resting oxygen consumption of the body
- it accounts for about 25% of total body glucose utilization.

Blood glucose supplies almost all of the brains energy

Under normal (non-starvation) conditions glucose is almost the only source of energy used by the brain, and it is almost entirely oxidized to carbon dioxide and water (Magestretti, 1999). Furthermore, the brain stores only enough glycogen to act as a very short term glucose-supply buffer. It is therefore dependent on a steady supply of glucose and oxygen from the blood, and if blood glucose levels drop to less than about half their normal values severe brain dysfunction and death may result, as in insulin overdose.

To ensure that it is well supplied by with glucose and oxygen the brain is well endowed with blood vessels:

- it receives about 16% of the bodies blood supply,
- it receives ten times as much blood per unit mass as muscle tissue,

Coupled with extensive vascularity of the brain, and its large glucose requirements, is a very efficient active transport system to ensure a rapid supply of glucose from blood vessels to neural tissue. There is effectively no restriction on movement of glucose from the blood to the brain whereas admission of many other blood-borne substances is limited the blood-brain barrier, provided by cells surrounding the capillaries. Brain energy supplies are therefore quite rapidly affected by blood glucose levels and by systems that regulate them.

A number of homeostatic mechanisms including glycogenesis, fat synthesis and glucose excretion are involved in effectively keeping blood glucose levels to within a physiological band and eliminating extreme fluctuations. The buffering effect is not complete, however, as glucose outflows from the liver in response to carbohydrate inflows from the gut are able to temporarily exceed the rate at which the body stores and/or uses glucose. Therefore, fluctuations in blood glucose in response to meal carbohydrates occur within the physiological range, a phenomenon known as postprandial (post-meal) glycaemic response.

It is the ability of foods to change blood glucose levels within the physiological range and the effect of such changes on the functional capacity of the brain which offers the possibility of dietary modulation of behaviour via blood glucose responses to food.

Apart from being the fuel of the brain blood glucose may influence behaviour indirectly by favouring uptake of the amino acid tryptophan, a precursor of the neurotransmitter serotonin which has been linked to depression and resistance to stress, although whether or how it is causally involved within the complexity of the brain is not known. However, experiments on the tryptophan/carbohydrate effect in relation to mood and performance have given very mixed results (Bellisle *etal.*, 1998).

Normal Blood Glucose Variations Affect Brain Function

Psychological tests show food effects There is now definite although not extensive evidence that foods, dietary glucose, and blood glucose levels are able to influence behaviour. The findings are not all consistent, and they are still difficult to interpret because the influence of a large number of variables such as age, gender, reactivity to stimuli, personality, circadian rhythm, stress, timing of meals, task duration and so on have yet to

be fully defined. Humans are heterogeneous and complex, and the presence of confounding factors overlying subject variability makes them tricky to experiment with. For instance, a recent study found glucose to enhance performance of stress-prone but not non stress-prone individuals, and only on controllable but not non-controllable tasks (Markus et al., 1999).

A small number of the large range of available tests of psychological function have been used to measure the effects of carbohydrates on cognition. Tests of reaction time (simple and choice), memory (recall and recognition), perception, attention and arousal (vigilance and critical flicker fusion), reasoning and others have been used to study effects of foods on particular aspects of behaviour, and with the advent of computer-based versions of tests they may be administered with considerable control and accuracy. There has, however, been little done to identify tests that have appropriate item content and sensitivity, and define testing conditions that will model the effects of diet on skilled workplace performance. For instance, the effects of food may not become evident unless cognitive tests are sufficiently demanding (Kennedy and Scholey, 2000).

Research of most relevance to oats is that which has examined the relationship of meals, particularly breakfast, of dietary glucose, and of blood glucose levels to performance. The major findings are summarised immediately below.

Missing Breakfast Lowers Psychological Performance

Missing breakfast has been found to cause deterioration in some performances including reaction time, spatial memory and immediate word recall in adults. Breakfast generally leads to improvements in performance later in the morning (Kanarek, 1997). In children, memory, verbal fluency, and arithmetic problem solving were increased and error rate reduced by having breakfast, and the effect depended on the energy content of the breakfast (Wyon *et al.*, 1997), possibly as a result of effects on blood glucose.

The effects of food consumption at lunch time and in the evening seem to be different from in the morning (Bellisle *et al.*, 1998). Lunch usually impairs performance in mid afternoon, with decreases in reaction time, recall, and attention found in some studies. Results from evening meals are more mixed, but in the case of both lunch and evening meals the number of studies is small.

Glucose improves psychological performance

There have been more studies of the effects of glucose on performance and they have generally shown that performance is enhanced by glucose and is sensitive to blood glucose levels (Bellisle *et al.*, 1998).

In students the increase in memory as a result of eating breakfast correlated with blood glucose levels, and a decline in memory as a result of fasting could be reversed by a glucose-supplemented drink (Benton and Parker, 1998). Similarly, glucose improved memory in subjects who had fasted, but not in those who had eaten breakfast (Martin and Benton, 1999).

Application of a battery of tests to subjects has recently shown blood glucose to be related to cognitive functions in addition to memory (Donohoe and Benton, 1999). Scores on psychomotor performance (Porteus maze), verbal fluency, and abstract reasoning (Block design test, water jars test) were improved. Some of the differences in psychological function attributed to blood glucose in recent studies are summarised in Table 1. The differences represent improvements of about 20–30 % in performance, which, if translated into workplace productivity, or error and accident rates, could be quite substantial.

Reaction time has also been shown to be depressed by hypoglycaemia in several studies (Bellisle *et al.*, 1998).

The rate at which glucose is retrieved from the blood is related to enhanced performance, as subjects in whom blood glucose levels fell rapidly from an initial peak performed better on a memory task than subjects in whom blood glucose levels remained elevated (Donohoe and Benton, 1999). The authors interpreted this as showing that the ability of blood glucose to enhance performance depends on the individuals ability to utilise the glucose. Where glucose uptake into the brain is poor plasma glucose levels remain high and performance is not enhanced.

Uptake of blood glucose during particularly demanding cognitive tasks may be enhanced by greater blood flow, as heart rate increases during such tasks and, moreover, in subjects given glucose the increase in heart rate during the demanding cognitive task is greater than in those not receiving glucose (Kennedy and Scholey, 2000). The mechanisms underlying these phenomena are not yet known.

Oats Could Have A Role As Brain Food

Foods that enhance brain function may benefit any group that must deliver sustained skilled performance. Perhaps one of the most obvious groups, and one of the few for which effects of foods are already established is school children.

The effect of a food on blood glucose levels cannot, however, be determined from its content of available carbohydrate, because the impact on blood glucose depends on the rate at which carbohydrate is made available from the gut. Measures of functionality provide a better indication of the physiological effects of food carbohydrates that could be provided by food composition alone.

Food properties influence glycaemic responses

Product development for improved nutrition relies heavily on food composition data, but many of the nutritional effects of foods, including their impact on blood glucose levels, depend on food properties rather than on food composition (Monro, 2000). For instance, the effect of a food on blood glucose is the net result of a number of factors that determine the rate at which carbohydrate can be loaded into the blood.

The normal small intestine provides little restriction to the absorption of products from digestion of food carbohydrates, because, thanks its covering of villi, it has a real surface area of about 200 m² (Szepesi, 1996), and it is covered with a high density of wall-bound digestive and carbohydrate-transporting enzymes.

The discrepancy between the loading of glucose into the blood and the rate at which glucose can be removed from the blood by body cells determines the glycaemic response. Important factors affecting blood glucose loading from most starchy foods are (Ellis *et al.*, 1996):

- rate of starch digestion – is affected by access of digestive enzymes to a 1-4 and a 1-6 glucose bonds in starch so is influenced by food particle size, and starch conformation, gelatinisation and retrogradation.
- rate of movement of digested starch to gut wall – highly viscous intestinal contents will retard diffusion of digestion products to the gut wall and thus lower the glycaemic response to foods.

The effect of available carbohydrate in a food on blood glucose levels is expressed as its glycaemic index (Truswell, 1992) which is essentially the effect of the amount of food that provides 50 g of carbohydrate as a percentage of the effect of 50 g glucose. The GI values for a few foods is shown in Table 2 (Foster-Powel and Brand-Miller, 1995), to illustrate several things:

- The impact of food carbohydrate on blood glucose, as reflected in GI, differs quite markedly between foods,
- Porous foods based on finely milled grains, such as white bread, have higher GI values than those, such as whole grain bread, that contain coarsely milled grains,
- materials that are swallowed as solid lumps, such as pasta, tend to contain less rapidly digestible carbohydrate (lower GI) than porous products such as bread, into which digestive enzymes can easily penetrate,
- oat porridge has a relatively low impact on blood glucose compared with that in many other foods, possibly because of the particulate nature of porridge, but perhaps also because it contains β -glucan, which increases gut viscosity and thereby reduces the rate of diffusion of digestion products to the sites of absorption in the gut wall.

A moderate, sustained glycaemic response is best

Within the physiological range of blood glucose fluctuations, foods that produce a moderate increase in blood glucose levels are best for several reasons:

- homeostatic mechanisms are so well tuned that large rises in blood glucose are counteracted in healthy people,
- diets producing prolonged hyperglycaemia are considered unhealthy because of the widespread damage caused by glycation and other effects in the body,
- acute increase in blood glucose in response to starchy food is an indication that the starch has been rapidly digested, so its effects will often be short lived,
- the homeostasis that counteracts postprandial glycaemia may lead to an overshoot that causes reactive hypoglycaemia – a depression in blood glucose in reaction to the previous hyperglycaemic state.

Oats could have the right properties to improve mental performance

Oats have several properties that suggest that they may be used to make a range of foods with which to manage blood glucose and thus glucose-dependent modulation of brain function. Rolled oats, which are steamed and rolled, have a GI of 57.5, which is only about mid-range in the effect on blood glucose. Thus, by changing the degree of processing to which oats are subjected it should be possible to create range of products of lower and higher impact on blood glucose.

Figure 1 shows the effects of different forms of processing on the digestibility of starch in oats. The extent of milling from intact to kibbled to ground and rolled has a large effect, no doubt reflecting enzyme access to starch within grain particles. But on top of such comminution effects subsequent wet cooking considerably increases rapidly digested starch, probably reflecting increased digestibility of starch after gelatinisation. The results indicate that processing can have a considerable impact on glucose release and thus on blood glucose response, and that oats might be a good base from which to develop a range of psychomodulatory foods.

IMPLICATIONS

From the findings that:

- the brain has a continual dependence on a supply of glucose by the blood,
- brain function is sensitive to fluctuations in blood glucose levels,
- available carbohydrates in food can strongly influence blood glucose levels,
- availability of oat carbohydrates may be greatly affected by food processing,

it is reasonable to hypothesise that oats may be processed into a range of products of differing psychological functionality, and that it should be possible with appropriate tests of brain function to identify the food processes necessary to produce oat-based products for optimal performance.

Product evaluation will require good experimental control

Because a large number of steps intervening between a stimulus (independent variable) and a behavioural response (dependent variable), and between food intake and dietary modulation of behaviour, experiments aimed at testing the effects of foods on behaviour must control a large number of extraneous variables. Factors such as age, gender, personality and susceptibility to stress, the timing of meals before tasks (Vaisman *et al.*, 1996), and so on, need to be considered.

Tests of effects of foods on performance will need ecological validation

Laboratory tests of cognitive function usually focus on single components of the complex skills, yet skilled performance in the work place normally involves operation of all brain systems in a continually fluctuating pattern dictated by progress towards goals and environmental feed back. Tests reflecting combinations of cognitive processes, administered to reflect real time and effort demands in the work place, are required to establish the value of food products in performance enhancement.

Also, the implications for the work place of a given degree of performance change measured in the laboratory need to be clarified. For instance, how does a small change in test performance extrapolate to effects of a dietary pattern over an extended period of time on risk of a major accident.

Research aimed at defining the psychological functionality of food is in its infancy, partly because behaviour is not always easily amenable to tight experimental control, and also because there has traditionally been some disdain of behavioural and mood measures in food research. However, increasing understanding of the determinants of human reactions to differing situations is allowing identification of variables that need to be controlled to obtain interpretable results from experiments on the psychological functionality of foods.

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Table 1: Effects of blood glucose variables on performance of some psychological tests.

Test	Condition	Results	% change
<i>Water jars test:</i> Time to solve a series of maths problems; tests flexibility of approach ¹ .	Baseline blood glucose level. Low (< 4.1 mmol/l). High (> 4.9 mmol/l)	<u>Time:</u> 36 s 23 s	36 %
<i>Verbal fluency test:</i> Number of words starting with a given letter of the alphabet that can be recalled in 1 minute ¹ .	Drink containing 50 g glucose vs placebo. Placebo, before vs after. Glucose, before vs after.	<u>No. words:</u> 34.5 vs 34 37 vs 42.5	15 %
<i>Porteus maze test:</i> Time taken to solve maze ¹ .	Drink containing 50 g glucose vs placebo: <i>14 year old.</i> Placebo vs Glucose. <i>Adult.</i> Placebo vs Glucose.	Time to solve: 69 s vs 46 s 57 s vs 45 s	33 % 21 %
<i>Block design test:</i> Time taken to reproduce a number of complex designs with a set of given blocks ¹ .	Blood glucose after 50 g glucose drink. Falling (glucose use). Rising (slowly used).	<u>Time to solve:</u> 65 s 84 s	23%
<i>Porteus maze test:</i> Time taken to solve maze ¹ .	Blood glucose after 50 g glucose drink. Falling (glucose use). Rising (slowly used).	<u>Time to solve:</u> 37 s 53 s	30 %
<i>Brown-Petersen memory task:</i> Number of given trigrams recalled after counting backwards in threes from a given three digit number ² .	Drink containing 50 g glucose vs placebo: Placebo. Glucose.	Trigrams <u>recalled</u> 64 75	17 %
<i>Brown-Petersen memory task:</i> (see above ²)	Blood glucose changes after 50 g glucose drink. Falling (glucose use). Rising (slowly used).	Trigrams <u>recalled</u> 77 63	22 %

¹ (Donohoe and Benton, 1999)

² (Martin and Benton, 1999)

Table 2: Properties of starchy foods associated with their glycaemic indices.

Food	GI	State of food as swallowed
Porridge	61	Partially broken grains, soluble fibre.
Pearl barley boiled	25	Whole and partially crushed grains, soluble fibre.
Puffed wheat	80	Expanded and porous.
Rice bubbles	83	Expanded and porous.
Mixed grain bread	34	Whole and partially broken grains, dense structure.
French baguette	95	Very porous, finely milled flour
Macaroni	45	Non-porous chunks.
Puffed crispbread	87	Porous chunks.
Boiled potato	56	Lumpy
Instant potato	83	Finely divided.

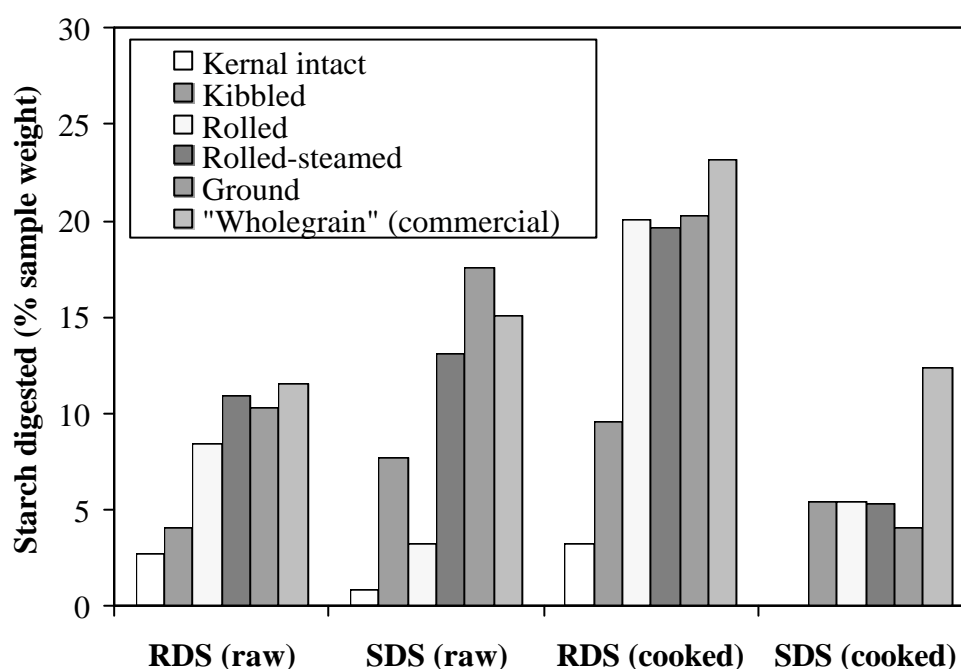


Figure 1: Effects of processing on starch digestion from oats in vitro: Rapidly digested starch (RDS; 20 min digestion) and slowly digested starch (SDS: 20 to 120 min digestion) in samples that were uncooked (raw) or cooked (5 g sample/30 ml water, 10 min, 100°C) after pretreatments shown in legend.

OATS IN FOOD – WHERE TO NEXT?

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New oat processing and fractionation industries are being seriously pursued in North America and the UK for both food and non-food applications. For the food industry, initiatives such as these, if successful, should help to revitalize the image and value of oats because even after rejuvenation in the late 1980's, oats have still largely been a commodity food or feed crop. There has been some differentiation of the oat grain into higher value food uses with the development of oat bran based food ingredients but more can be done. Cereal scientists can help the industry take advantage of the unique properties of oat carbohydrates, oils and proteins and to use these for imaginative new food products. Two examples discussed at this conference are dairy replacements and "brain food". It is my view that wide-spread use of the unique properties of oat starch in new foods would be facilitated by a food-grade oat fractionation industry.

OAT STARCH QUALITY AND RELATIONSHIPS TO OTHER QUALITY TRAITS

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ABSTRACT

Varietal variation in oat starch quality can greatly influence processing and food product performance. In this study, Rapid Viscosity Analysis (RVA) and Flour Swelling Volume (FSV) tests were used to reflect the starch properties of oat flour. The FSV technique is particularly useful for application in the selection of early generation lines from an oat breeding program. Results obtained showed a significant positive correlation between; RVA peak viscosity, final viscosity and measured FSV. Correlations of lesser magnitude were observed between groat oil, β -glucan contents and flour pasting characteristics. High relative mean values for RVA peak viscosity, final viscosity and flour swelling volume, with low pasting temperatures and short times to peak viscosity were observed in an oat cultivar currently accepted by Australian consumers.

INTRODUCTION

Starch quality is an important characteristic in oats that can determine the acceptability of a variety for use in processing for human consumption. It is important therefore that the starch quality of cultivars in an oat breeding program be measured to be able to select for this trait. Rapid Viscosity Analysis (RVA) and Flour Swelling Volume (FSV) tests that give information on gelatinisation and the extent of water uptake of starch, can be used to test flours for suitability for processing. The FSV test being relatively inexpensive and capable of a large throughput of samples is particularly useful for selection of early generation lines from an oat breeding program. It would be expected that oat starch that gelatinises at lower temperatures and takes up water quickly during processing to be an advantage to millers and the food manufacturers.

The main variation in the composition of oat starch is the amylose/ amylopectin ratio and chain length distribution of these fragments, with smaller variations in the amount of residual or bound lipids and protein (Hoover et al 1994). It has been reported that gelatinisation onset is strongly positively correlated with amylose content and starch lipid content (Hartunian-Sowa and White 1992). A positive correlation between the lipid content of groats and amylose content in the groat flour has also been reported (Morrison et al 1984).

An important step in oat processing is hydrothermal treatment, which involves roasting (kilning) and steaming of the dehulled grain to inactivate lipid degrading enzymes and to develop desirable flavours. It has been reported that these hydrothermal treatments influence oat starch properties by increasing the viscosity of oat flour slurries (Doehlert et al 1997). It is possible that hydrothermal treatment may influence the degree and nature of starch associations with other compounds such as lipids.

In this study the wholemeal starch quality of selected oat varieties grown in Western Australia over three seasons was measured after stabilising the groats with steam and heat to mimic industrial milling practices. Protein, lipid, β -glucan and fatty acid contents of the groats were measured to establish any relationships between these and the starch quality traits.

MATERIALS AND METHODS

Samples

Oat (*Avena sativa*) cultivars Mortlock, Pallinup, Coomallo, Toodyay, Hotham (Western Australian milling grade), and Dalyup, Needilup, Potoroo and Quoll (Western Australian feed grade), used in this study were grown in six sites throughout the Western Australian agricultural area in each of the 1997, 1998 and 1999 seasons. The cultivar Yarran was also included in the study, but only for the 1999 season. The samples were cleaned to remove free groats and foreign material, then dehulled using a Codema Laboratory Dehuller model LH 5095, (Minneapolis USA). After dehulling the samples were immediately steamed for 20 minutes and then kilned at 85°C for 3 hours. Samples were determined to be tyrosinase negative using Tyrosinase Qualitative Test (National oats Co., Cedar Rapids, IA, USA).

Laboratory Testing

1. **Moisture:** Determined using AACC method 44-15A.
2. **Rapid visco analysis:** Samples milled on a Retsch mill with a 0.5mm screen (Retsch Co., Germany) and viscograms developed on a Rapid Visco Analyser model RVA3D (Newport Scientific, Australia). Protocol: 4.0g flour (15% moisture) slurried with 25ml deionised water; stirring speed 960 rpm for 10 seconds followed by 115 rpm for rest of test; temperature 40°C 1 minute, 40 – 90°C in 4 minutes, 90°C for 8.5 minutes, 90 to 40°C in 4.5 minutes, 40°C for 4 minutes.
3. **Flour swelling volume:** Flour swelling volume of wholemeal flour (milled as in RVA test) slurry (0.45g dry flour in 12.5ml deionised water) determined using the method described by Crosbie et al (1992) and modified by Crosbie and Lambe (1993).
4. **Protein content:** Determined as dry basis by the Dumas combustion method using a Leco FP2000 instrument (Leco Corporation, Michigan, USA) after milling the samples on a Retsch mill with a 1.0mm screen.
5. **Oil content:** Determined on dried samples by nuclear magnetic resonance using a Newport Analyser (Newport Instruments Ltd, UK).
6. **Beta Glucan:** Determined as dry basis by flow injection analysis with calcofluor fluorescence using a Fiastar 5010 Analyser (Tecator Co., Sweden) after milling the samples on a Retsch mill with a 0.5mm screen.
7. **Fatty acid profile:** Wholegrain samples for fatty Acid composition analysis were milled using a Retsch mill with a 1.0mm screen. Methylation and extraction of the milled samples was carried out by heating with 2% methanolic sulphuric acid for 3 hours, followed by extraction with hexane. The extracted methyl esters analysed using a Hewlett Packard 5890 gas chromatograph (Hewlett-Packard Co. USA) equipped with a flame ionisation detector and a 16 metre Supelco Sil 88 capillary column.
8. **Data analysis:** Least significant differences of varietal data means were calculated using Genstat 5 software release 4.1 (Lawes Agricultural Trust).

RESULTS AND DISCUSSION

Flour Pasting and Swelling

The varietal means for the oat flour pasting characteristics and swelling volumes for the years 1997 – 1999 are presented in Table 1. Peak viscosity and FSV have higher values as a greater amount of water is absorbed by starch. There was a positive correlation between FSV and peak viscosity (Table 2), though of lower magnitude than that reported for wheat starch (Crosbie 1991). Final viscosity is the viscosity of the cooled sample slurry at the end of the RVA temperature program and higher values indicate the extent to which re-association has occurred between gelatinised starch chains. Other compounds present may complicate this process. Final viscosity shows a positive correlation to FSV and peak viscosity shown in Table 2. Peak time and pasting temperature reflect the temperature at which the starch granules swell and take up water. Shorter times and lower temperatures indicate a lower starch gelatinisation temperature.

Currently the Mortlock variety is generally preferred by Australian millers when processing oats for human consumption. Compared to other varieties included in this study Mortlock consistently had amongst the highest mean values for peak viscosity, final viscosity and flour swelling volume, with low pasting temperatures and short times to peak viscosity. Similar results for Mortlock have been reported from work conducted in Eastern Australia (Zhou et al 1999). It is likely that these starch properties have contributed to Mortlock's acceptance by consumers of oat based products, influencing the mouth feel and texture of cooked foods. In contrast the variety Yarran, reported to have poor cooking qualities, had amongst the lowest values for FSV, peak viscosity and final viscosity when tested in the 1999 season. If the assumptions regarding Mortlock are correct, the possession of these traits should contribute to selection of crossbreeds in breeding programs for milling class oats. Hotham and Coomallo were two varieties that had similar starch properties to Mortlock.

Table 1: Variety means for RVA pasting characteristics, FSV and chemical composition for the years 1997, 1998 and 1999, n=17.

Variety	Peak Viscosity	Final Viscosity	Peak Time (minutes)	Pasting Temp (°C)	FSV (mm)	Oil (%)	Protein (%)	b-glucan (%)
<i>Mortlock</i>	486	672	8.3	83	69.0	8.5	16.5	5.1
Hotham	486	613	8.9	88	63.3	9.6	15.8	4.7
Coomallo	463	669	8.6	82	63.7	9.2	15.3	4.9
Dalyup	442	607	8.9	86	58.7	9.1	15.6	5.0
Pallinup	439	635	9.1	87	59.0	9.4	15.5	5.4
Quoll	432	637	8.5	83	57.9	9.3	15.4	4.4
Toodyay	432	636	8.2	85	60.8	9.0	14.2	4.5
Potoroo	417	616	8.3	84	56.0	10.2	13.7	4.1
Needilup	408	631	7.6	83	61.6	10.4	14.7	4.6
LSD 5%	27	29	0.7	2.5	4.4	0.4	1.6	0.4

Note: Peak and final viscosity in RVA units; FSV in millimetres gel column height; oil, protein and β -glucan as percentage of groat, dry basis.

Table 2 Correlation table for RVA pasting characteristics, FSV and chemical analysis results for all samples 1997, 1998 and 1999.

Significance of correlation coefficient r at 5% level is 0.16, $n=153$.

	Peak Viscosity	Final Viscosity	Peak Time	Pasting Temp	FSV	oil	Protein	b-glucan	16:0	18:0	18:1	18:2	18:3
Final Viscosity	0.54												
Peak Time	0.30	-0.19											
Pasting Temp	-0.05	-0.31	0.39										
FSV	0.69	0.48	0.14	-0.07									
oil	-0.44	-0.26	-0.42	0.00	-0.32								
Protein	0.01	-0.07	0.44	0.18	0.04	-0.35							
b-glucan	0.26	0.38	0.16	0.01	0.17	-0.34	0.39						
16:0	-0.46	-0.30	-0.25	0.02	-0.31	0.86	-0.12	-0.31					
18:0	-0.27	-0.34	0.02	0.11	-0.22	0.45	-0.02	-0.17	0.61				
18:1	-0.32	-0.27	-0.43	0.00	-0.26	0.94	-0.49	-0.41	0.77	0.41			
18:2	-0.46	-0.11	-0.35	0.00	-0.30	0.79	-0.14	-0.09	0.60	0.19	0.57		
18:3	-0.20	0.10	0.07	-0.09	-0.09	0.23	0.50	0.12	0.39	0.03	0.03	0.37	
other	-0.44	-0.15	-0.31	-0.22	-0.37	0.71	0.00	-0.34	0.71	0.27	0.64	0.51	0.63

Note: Fatty acids calculated as grams/gram, fatty acid/ flour; 16:0 = palmitic acid, 18:0 = stearic acid, 18:1 = oleic acid, 18:2 = linoleic acid, 18:3 = linolenic acid, other = all other fatty acids measured.

RELATIONSHIPS BETWEEN STARCH CHARACTERISTICS AND OTHER COMPOUNDS PRESENT IN THE FLOUR

There were significant correlations between oil content and all flour pasting traits except pasting temperature (Table 2). Flours containing more oil had lower peak and final viscosity; shorter times to peak viscosity; reduced swelling volumes and no effect on pasting temperature. It appears that oil content did not influence gelatinisation temperature but was associated with less water uptake by the flour during gelatinisation. It should be emphasised that total groat oil content was reported in this study. Strong correlations for starch bound oil content and gelatinisation onset have been reported in the literature (Wang and White 1994). Positive correlations between starch bound oil and amylose content; and negative correlations between starch oil and swelling power were also reported by these authors. It is unclear whether oil content has a direct effect on the pasting properties of oat flour or it reflects other factors, such as the amylose/amylopectin ratio. The fatty acids composition of the oil was measured to determine if any were responsible for the apparent effect on flour pasting characteristics. However correlations between flour pasting characteristics and each of the three major fatty acids comprising approximately 95% of the oil; palmitic, oleic and linoleic, (Hall and Tarr 2000) were not significantly different to the correlations of that observed for oil. β -glucan content had a slight positive correlation with

peak viscosity, final viscosity and FSV with little effect on peak time and pasting temperature. As β -glucan is a water soluble, highly viscous gum, viscosity relationships would be expected. Protein content had little observed effect on flour pasting properties except for a positive correlation with peak time.

SEASONAL VARIATION OF MEAN VARIETAL FLOUR PASTING PROPERTIES AND OTHER FACTORS

The mean seasonal results for varieties of flour pasting and related traits are shown in Table 3. The relative ranking between varieties for these traits did not differ greatly between seasons indicating these traits are strongly influenced by genotype and so can be selected for in a breeding program. Table 3 also reports values for the variety Yarran that was included in this study for the 1999 season only. Yarran had been evaluated but rejected as a milling oat, it was reported to have a thin soupy texture and had a floury flavour when used to make porridge. It is significant that Yarran's mean peak viscosity, final viscosity and FSV were among the lowest of the varieties tested from the 1999 season. Yarran also had relatively high oil, protein contents and a low B-glucan content.

Table 3: Mean data for varieties across seasons. Highest and lowest values for each season highlighted in bold.

	Peak Viscosity			Final Viscosity			FSV			Oil			Protein			B-glucan		
	1997	1998	1999	1997	1998	1999	1997	1998	1999	1997	1998	1999	1997	1998	1999	1997	1998	1999
Mortlock	473	469	515	683	642	686	64.3	70.0	72.9	8.4	8.6	8.5	17.9	16.7	15.0	5.4	4.6	5.3
Hotham	448	464	542	604	582	648	57.0	64.2	68.7	9.5	9.7	9.6	17.5	15.8	14.0	4.9	4.1	4.9
Coomallo	446	460	480	662	644	692	58.7	69.3	64.9	9.2	9.3	9.2	16.9	15.8	13.5	5.1	4.5	4.9
Dalyup	440	423	460	634	576	609	55.8	56.7	62.9	9.2	9.0	9.1	17.3	15.5	14.2	5.4	4.7	4.9
Pallinup	433	416	464	648	598	652	57.1	59.4	60.4	9.4	9.6	9.1	17.3	16.0	13.4	5.8	4.7	5.5
Quoll	435	403	452	666	592	645	58.2	55.2	59.9	9.3	9.6	9.0	17.1	15.8	13.5	4.8	4.1	4.1
Toodyay	426	423	444	642	611	651	59.3	61.7	61.8	8.9	9.2	9.0	15.7	14.4	12.6	4.6	4.1	4.7
Potoroo	417	391	444	627	600	619	54.9	57.0	56.2	10.2	10.3	10.0	15.1	14.0	11.9	4.6	3.9	3.7
Needilup	404	387	430	642	604	642	58.6	62.9	63.5	10.5	10.6	10.2	16.5	15.0	12.8	4.8	4.2	4.9
Yarran			438			522			54.8			9.8			15.2			4.0

CONCLUSION

RVA and FSV methods were used to measure oat flour quality traits for selected oat varieties over three seasons. Oil content was negatively, and β -glucan content positively correlated to peak viscosity, final viscosity and swelling volume of the oat flour. The fatty acid composition of the oil and protein content had little observed relationship to starch quality traits as measured. The Mortlock variety currently accepted by consumers had consistently high values for the traits of peak viscosity, final viscosity and flour swelling volume. A variety reported as having poor cooking properties, had low values for these

traits. The measurement of these traits will be useful in identifying the acceptability of oat varieties for food processing. Hotham and Coomallo were two varieties that had similar starch properties as Mortlock, indicating these could find a similar level of acceptance by consumers.

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b-GLUCAN, THIAMINE AND SELENIUM CONTENTS IN OATS CULTIVATED IN FINLAND

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SUMMARY

b-Glucan content was studied in oat groats at 8-10 locations in official variety trials in 1997-99. The studied varieties were Belinda, Leila, Kolbu, Roope, Salo and Veli. Kolbu and Roope are yellow oats and other varieties are white oats. Average β -glucan content varied 4.8-5.2 % in different years. Significant difference in β -glucan content was found between the varieties. The average **thiamine** content was 7,1 mg/kg fresh wt in 1997 and 6,3 mg/kg fresh wt in 1998. The highest average thiamine concentrations were found in 1997 in Leila (7,3 mg/kg) and Roope (7,6 mg/kg). **Selenium** (Se) content was studied both in organic and conventional cultivation. The organic cultivation resulted in very low selenium contents, generally < 0,01 mg/kg dry wt. In conventional cultivation the average Se content was 0,059 mg/kg dry wt in 1997 and 0,018 mg/kg dry wt in 1998. The warm and dry summer 1997 resulted significantly higher Se contents compared to rainy and cold summer 1998.

INTRODUCTION

The quality of Nordic oats is recognised as the best in the world. The principal asset of Finnish oats is its light colour and high quality. Finland's farming conditions are also favourable to the production of pure oats. The main use of oats has been as feed, and the use of oats in food products has remained quite minimal. Due to its excellent quality, Finnish oats are exported as a food and feed to the U.S.A. as well as within the EU region. In addition, the significance of oats as a specific health product is growing. Especially the published health claims in the U.S.A. have increased the value of oats as a functional foodstuff or food product.

The Ministry of Agriculture and Forestry in Finland started three years ago a national oats programme including ten different projects for the improvement of competitive capability of Finnish oats and oat products in domestic and foreign markets. Research focusing on the chemical composition of Finnish oats called "Logistic information system for quality of Finnish oats" is one of these projects. This project has three main aims: 1) To study the basic quality of various oat varieties cultivated in Finland. The aim is to find those varieties, conditions of cultivation and farming techniques which produce the best nutritional and technological quality adaptable for various industry applications. Corresponding factors are examined also with organically grown oats; 2) By monitoring the oat-related conditions for cultivation, the aim is to control the possible risk factors such as mycotoxins and cadmium to ensure the safety of food and feed and 3) On the basis of the cultivation and chemical quality data as well as the weather information accumulated within this research, the I

ogistic information system for quality of Finnish oats shall be developed. This information system is going to promote industry and commerce in the selection of oat material for their fixed applications. In addition, the farmers will use the data to improve their procedures concerning oat-farming.

In the present study following chemical compounds has been analysed: nitrogen, ash, mineral elements, crude fat, fatty acids, β -glucan, phytic acid, starch, vitamins, lignans, heavy metals and mycotoxins. In this paper results of β -glucan, thiamine and selenium contents in oats cultivated in Finland are presented.

MATERIALS AND METHODS

Samples

Samples of oats were collected after harvest from official and agronomy trials conducted by the Agricultural Research Centre of Finland in 1997-1999. The official variety trials conducted at 8-10 locations were managed according to standard protocol. There were two types of agronomy trials. The first included comparison of oat cultivars grown in conventional and organic farming systems at six locations, and the second had six nitrogen rates (0, 40, 80, 120 and 160 kg N/ha) with four oat cultivars at two locations. After harvest grains were immediately dried with warm air in flat bed grain drier to the moisture content below 14 percent. The total number of oat samples analysed were 141, 150 and 125 in 1997, 1998 and 1999 respectively.

Analytical methods

The oat grains were sorted by a 2.0 mm sieve and hulled by a laboratory hulling machine BT 459 using air pressure. Oat groats were milled by Falling Number hammer mill using 1.0 mm sieve. β -Glucan contents of milled oat groats were analysed using the enzymic method of McCleary (McCleary & Glennie-Holmes 1985, McCleary & Codd 1991). Thiamine was determined by high performance liquid chromatographic method (Hägg 1994) and selenium by graphite furnace atomic absorption spectrometry after wet digestion and extraction into MIBK (Kumpulainen et al. 1983).

RESULTS AND DISCUSSION

β -Glucan content

β -Glucan content of oats was studied in official variety trials in the years 1997-99 at 8-10 locations representing the total oat cultivation area in Finland. Oat varieties analysed were most popular cultivars and new varieties at the national list of cultivars in Finland: The varieties were Belinda, Kolbu, Leila, Roope, Salo and Veli. The hull of the grains of Kolbu and Roope is yellow and Belinda, Leila, Salo and Veli are white oats.

There was variation in the β -glucan content between the trial locations, but the variation was not regular between the locations. Only small differences were found in the average β -glucan content between the years. The highest average β -glucan content (5.18 %) was found in 1997, which was a warm and rather dry summer in Finland. The average β -glucan content of the year 1998 (4.95 %) was only a little lower than that of 1997. The year 1998 was very rainy and rather cool. The lowest average β -glucan content (4.84 %) was found in 1999, which was very dry and hot summer in Finland.

In previous researches it has been found, that high temperature of growing period increases (Saastamoinen et al. 1992, Miller et al. 1993, Saastamoinen 1995) and high precipitation decreases β -glucan content of oats (Miller et al. 1993). In the present study such effects were not found.

Significant differences were found in β -glucan content between the varieties. Roope, Leila and Belinda had higher β -glucan content than other varieties. Kolbu had the lowest β -glucan content. The relative order of the varieties was quite the same in all three years. Kolbu had the lowest β -glucan content in every year. Roope had the highest average β -glucan content in the years 1997 and 1998 and Leila had the highest average β -glucan content in 1999 (Fig 1).

It seems that the β -glucan content of oat groats in Finland is only slightly depended on the cultivation year. The most significant factor effecting on β -glucan content seems to be variety. Significant, regular and not year dependent differences are found between the varieties in β -glucan content. The best way to get high β -glucan oat is to cultivate the best varieties.

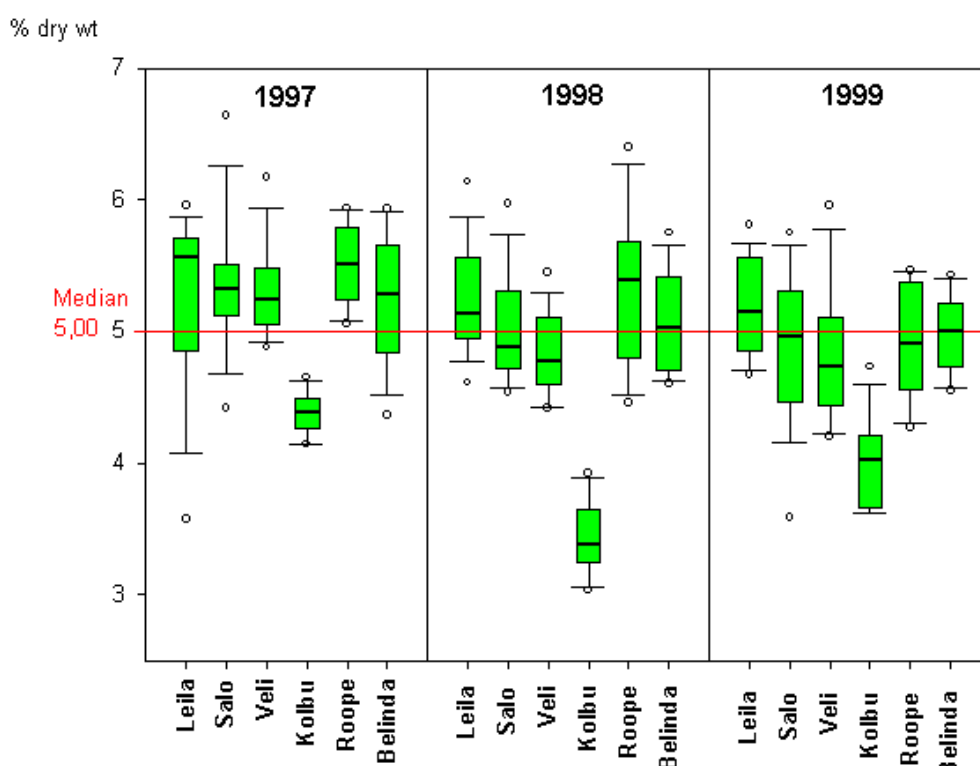


Fig 1: β -Glucan content of different oat cultivars grown in Finland in 1997-99.

Thiamine content

Cereals and cereal products are the most important source of thiamine. Over 40 % of the dietary intake of thiamine comes from cereals and cereal products. In Finland thiamine was added into the wheat flours until the autumn of 1993. It was finished as unprofitable at the same time when the addition of iron was finished. As a consequence the dietary intake of thiamine from food has decreased considerably.

The results in this study showed that oats is very good source of thiamine. The average content of thiamine in various oat varieties in official variety trials in 1997 and in 1998 was 7,1 mg/kg fresh wt and 6,3 mg/kg fresh wt, respectively. The highest average thiamine concentrations were found in the year 1997 in Leila (7,3 mg/kg fresh wt) and Roope (7,6 mg/kg fresh wt) varieties. In the year 1998 the average thiamine concentrations were about 10 % lower. The summer of 1997 was very warm and dry in Finland, but the summer of 1998 was totally different than the previous year being cold and rainy. The lower thiamine content in 1998 was likely caused by higher nitrogen losses due cold and wet soil conditions. Thiamine molecule contains four nitrogen atoms. In conclusion, the results showed that there is some difference in thiamine contents between various oats varieties but the effect of weather conditions and the type of soil on thiamine contents are even bigger (Fig 2).

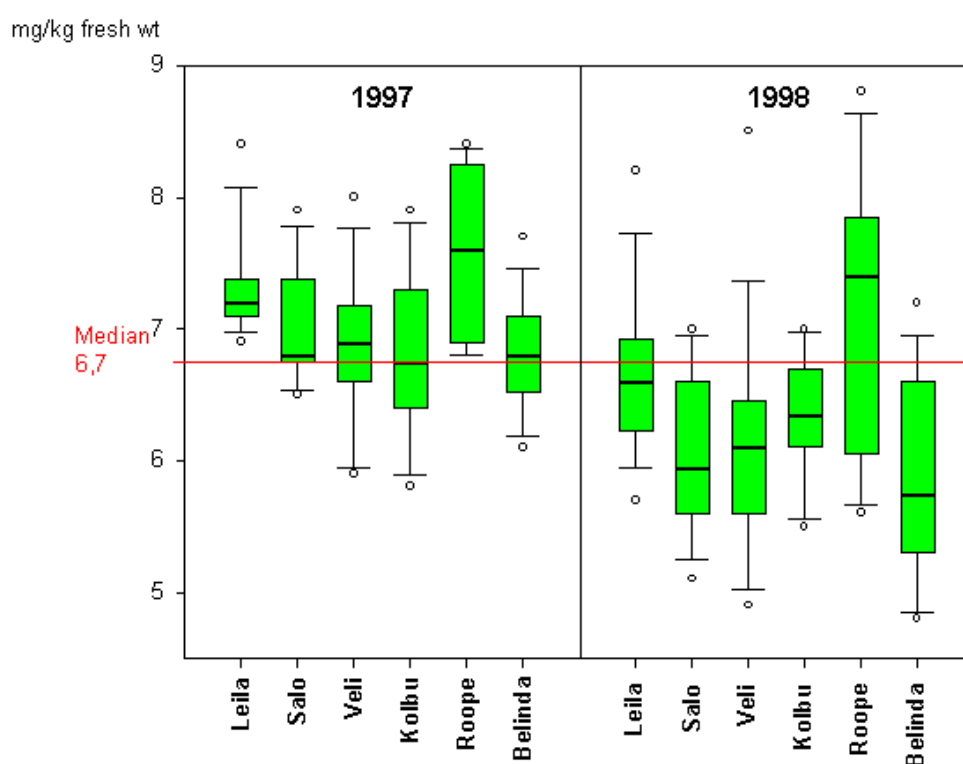


Fig 2: Thiamine content of different oat cultivars grown in Finland in 1997-98.

Selenium content

Selenium (Se) content of oat was studied at 6 locations in organic cultivation trials in the years 1997-98. Oat varieties Veli and Puhti were grown both organic and conventional methods except in one location where only organic cultivation was carried out.

Finland is one of the low selenium regions in the world. In order to raise the selenium content of domestic agricultural products the inorganic fertilisers have been supplemented with selenium since 1984. The supplementation level is now 10 mg Se/kg. However, the Se supplementation does not reach the organically grown products. In the present study the organic cultivation resulted in very low selenium contents, generally < 0,01 mg/kg dry wt. Only in two most southern locations Se concentrations in organic cultivation were slightly higher. The warm and dry summer 1997 resulted in significantly higher Se contents

compared to rainy and cold summer 1998 (Table 1). In conventional cultivation the average Se content was 0,059 mg/kg dry wt in 1997 and 0,018 mg/kg dry wt in 1998. Se content tends to be higher in the clay soils whereas organic and coarse mineral soils contain less Se (Sippola 1979).

Table 1: Selenium content (mg/kg dry wt) of conventionally and organically cultivated oat in Finland in 1997-98.

Trial location	1997										
	Jokioinen		Mietoinen		Laukaa		Partal a	Ylistaro		Ruukki	
Cultivar	A	B	A	B	A	B	B	A	B	A	B
Veli	32	15	65	20	180	< 10	< 10	25	< 10	25	< 10
Puhti	26	12	41	15	160	< 10	< 10	20	< 10	18	< 10
Average	29	13	53	17	170	< 10	< 10	23	< 10	22	< 10
1998											
Veli	18	33	< 10	< 10	27	< 10	< 10	14	< 10	33	< 10
Puhti	20	24	< 10	< 10	15	< 10	< 10	11	< 10	33	< 10
Average	19	29	< 10	< 10	21	< 10	< 10	12	< 10	33	< 10

A = conventional, B = organic

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DEVELOPMENT OF A FERMENTED, YOGHURT-LIKE, PRODUCT BASED ON OATS

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An oat-base product, Adavena[®], completely derived from oats and water by a patented enzymatic process (Lindahl et al., 1997) was used in the developing of a new kind of non-dairy yoghurt-like product. One application of this oat-base is as a non-dairy milk substitute, Mill Milk[™] that has been found to have high acceptance and also cholesterol lowering effect (Önning et al., 1998, 1999). The low consumption of products from oats is mainly due to the lack of acceptable and suitable food products containing soluble fibers in appropriate levels (Salovaara et al., 1991).

Here we present the use of a tailor made oat-base as the main substrate for yoghurt cultures and the development of a yoghurt-like product with high sensory acceptance.

MATERIALS AND METHODS

Adavena[®] M40 oatbase concentrate (20 % dry matter), was provided by Ceba AB, Sweden. Two commercial yoghurt cultures V2 and ABT were used. V2 is a 1:1 mixture of *Lactobacillus delbrueckii* subsp. *bulgaricus* and *Streptococcus salivarius* subsp. *thermophilus* (Visby Tønder, Denmark). ABT is a mixture of *L. acidophilus*, *S. salivarius* subsp. *thermophilus* and *Bifidobacterium* ssp. (Chr. Hansen A/S, Denmark). Fermentations were performed at 43 °C for 16 h. Additives such as xanthan gum (Monsanto, Switzerland), different flavour components, e.g. strawberry or mixed black berries (Hafi AB, Sweden) and vegetable fat, Akoblend NS (Karlshamns AB, Sweden) were added to the final products. The yoghurt control was obtained from Skånemejerier, Sweden. Danone, France provided the fermented non-dairy product (Sevea[®]). The contents of fat, maltose, lactic acid and β -glucans were measured after fermentation.

Viscosity (Bohlin Visco 88 BV, cylinder C30, 1208 s⁻¹, Bohlin Reologi, Sweden), texture (Instron 4442, Instron Ltd, Buckinghamshire, UK), water activity (Rotronic instrument, Rotronic AG, Germany) and colour (Minolta Colour Instrument CR-310) were also parameters measured in the final products. Finally, a sensory evaluation using intensity scales was performed using a panellist consisting of 13 persons.

RESULTS AND DISCUSSION

Viscosity, texture pH, titratable acidity, maltose and β -glucan were measured in the M40 substrate after fermentation using two different starter cultures and dry matters of the concentrate (Table 1.)

Table 1. Viscosity, texture, pH, titratable acidity, β -glucan and maltose content after fermentation for 16 h of the M40 substrate with two different dry matters (16 and 18 %) in comparison to a yoghurt control

Starter Culture	Dry matter (%)	*Viscosity (mPas)	†Texture (cm)	‡pH	Titratable acidity (%)	Maltose (%)	β -glucan (%)
ABT	16	78	1.7	3.9	0.5	0.5	0.6
ABT	18	83	1.5	4.0	0.5	0.5	0.6
V2	16	43	1.7	4.4	0.3	6.2	0.6
V2	18	67	1.8	4.5	0.2	6.3	0.6
Yoghurt	14	42	1.8	4.0	1.0	---	---

*Viscosity measured after 2 minutes of shear thinning using a shear rate of $1\,207\text{ s}^{-1}$ at $10\text{ }^{\circ}\text{C}$ values are the mean of three measurements.

†Texture measured at $10\text{ }^{\circ}\text{C}$ using a speed of 100 cm/min values are the mean of three measurements.

‡pH measured after 16 h of fermentation, the initial pH was 7.4.

The ABT culture gave a lower final pH in the M40 substrate in comparison when using the V2 culture. A higher dry matter resulted in higher final viscosity for all products. The higher dry matter gave only a small effect on the buffer capacity of the substrate. After fermentation the contents of β -glucans were 0.6% for all products. When adding fat to the product (1.0%) both mouth feel and consistency were improved and the product was smoother and gave a more acceptable appearance. However, the consistency in these products appeared not to be as thick and creamy and had also a more compact structure in comparison to the yoghurt control. Products with a dry matter of 16%, 0.3% xanthan gum and 1.0% fat were selected for the sensory evaluation. The a_w values for these products were 0.98. The products were less white (L value) than the yoghurt control, but appeared to have the same lightness as the commercial non-dairy product (Table 2). The products were also less green (a value) than the control samples. The colour component that showed most similarities between the products tested was the yellow/blue (b value).

Table 2. L , a and b values for the fermented products in comparison with a commercial non dairy product (Sevea®) and a yoghurt control

Product	L	a	B
V2	74.8 _(0.02)	-0.5 _(0.01)	18.9 _(0.70)
ABT	75.4 _(0.02)	-0.5 _(0.01)	9.4 _(0.02)
Sevea®	77.8 _(0.00)	-0.4 _(0.01)	15.6 _(0.00)
Yoghurt	92.0 _(0.09)	-3.6 _(0.02)	12.0 _(0.03)

The values shown are the means of 3 determinations. The figures in parenthesis are the standard deviations.

Table 3. Flavour and acceptability profiles of two plain and four flavoured products based on the M40 substrate using intensity scales

Sample	Appearance	Consistency	Mouth	Sweetness Feel	Acidity	Oat flavour	Overall acceptability
V2*	3.5 _(2.1)	3.9 _(1.8)	3.7 _(2.1)	2.8 _(1.8)	1.7 _(1.8)	5.5 _(2.2)	3.5 _(1.8)
V2* ^{a)}	4.6 _(2.1)	3.3 _(1.8)	4.5 _(1.8)	5.7 _(1.8)	2.4 _(1.9)	4.9 _(2.8)	4.6 _(1.1)
V2* ^{b)}	3.8 _(0.4)	4.8 _(1.5)	5.0 _(1.0)	6.0 _(1.0)	1.6 _(0.9)	2.2 _(2.6)	5.2 _(1.6)
ABT†	4.1 _(1.9)	2.7 _(1.4)	3.9 _(1.9)	1.9 _(1.4)	4.6 _(2.6)	5.5 _(2.5)	2.8 _(2.2)
ABT† ^{a)}	5.3 _(1.9)	3.1 _(1.4)	4.0 _(2.4)	4.6 _(1.4)	2.9 _(2.6)	4.8 _(2.5)	4.4 _(2.2)
ABT† ^{b)}	5.2 _(1.8)	4.8 _(2.4)	5.4 _(1.9)	5.4 _(0.9)	2.6 _(2.3)	2.6 _(2.7)	5.2 _(1.6)
Sevea®‡	2.8 _(1.8)	4.3 _(2.0)	3.7 _(1.9)	5.0 _(2.7)	1.8 _(1.7)	4.3 _(1.9)	3.1 _(1.6)
Sevea®‡ ^{c)}	6.1 _(1.3)	6.1 _(1.9)	6.3 _(1.9)	5.8 _(2.0)	3.2 _(1.5)	1.3 _(1.8)	5.6 _(1.8)
Yoghurt§ ^{a)}	6.6 _(1.5)	4.7 _(1.3)	6.1 _(1.7)	5.6 _(1.7)	4.3 _(2.0)	0.9 _(1.7)	6.0 _(1.9)

The intensity scales were done using 9-cm lines. Figures are mean values ($N = 13$) of distances marked by panellists from 0 (no perception) to 9 (highest value of perception).

The figures in parenthesis are the standard deviations.

*M40 fermented with *S. thermophilus* and *L. bulgaricus* (V2).

†M 40 fermented with *S. thermophilus*, *L. acidophilus* and *Bifidobacterium* spp. (ABT).

‡Commercial fermented non-dairy product.

§Commercial yoghurt.

^{a)} Product flavoured with mixed black berries.

^{b)} Product flavoured with strawberries.

^{c)} Product flavoured with black currant.

In the intensity evaluation six fermented products, both plain and flavoured with strawberry or mixed black berries were used. In addition, flavoured yoghurt and two commercial fermented non-dairy products were included in the test (Table 3).

The panellists gave a higher score to the flavoured products in comparison to the unflavoured products. Oat flavour was found to be less apparent in flavoured products. The flavoured product fermented with ABT culture was considered to have the best appearance of the oat-based products.

Notable was the panellists' remark on the yoghurt control to have oat flavour; thus oat flavour should be considered as a general off flavour in the product not necessarily coming from oats. It was generally considered that appearance, overall acceptability, consistency and sweetness increased by adding strawberry jam to the products and that oat flavour was not appreciated by the panellists.

SUMMARY AND CONCLUSIONS

The fermented oat-based yoghurt-like product developed in this study was had an appearance and taste that was shown to be acceptable. Fermentation with yoghurt bacteria led to both acid and aroma development and consumption of carbohydrates. As oat is a palatable cereal there was no negative off flavours that needed to be masked. The fermentation process showed to have small effects on the β -glucan content in the products. This study shows a new possibility to make an acceptable fermented product mainly based on oats that can be suggested as an alternative to similar products based on other raw materials. A deeper nutritional and physiological investigation of the product and its effects ought to be conducted.

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OATS FOR FEED - A UK PERSPECTIVE

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INTRODUCTION

The aim of this paper is to identify recent developments in the UK, from the standpoint of working as a crop developer within the supply chain of raw materials to the feed industry. It would be difficult to present a paper on oats in a world context since the value of oats for feed will depend heavily on local circumstances such as the influence of variety and environment on nutritional value and on different countries' agricultural and feed industries and the availability of other raw materials.

Oats were the traditional feed on farms for many centuries, once the motive power of farms, and a grain recognised as having valuable characteristics such as good quality protein and a higher oil content than other cereals. In the UK oats can be easily grown, and the resultant grain is safe in terms of giving few digestive problems and possibly even having health benefits. There are a number of areas where high oat diets can lead to product quality benefits. On the negative side, oats have varying levels of fibre of poor nutritional value which degrades the overall digestibility of the oat, as well as other potentially anti-nutritional components such as beta-glucans and phytates.

UK OAT CONSUMPTION

The UK oat production for 1999/2000 season was 580,000t of which 260,000t was utilized for human food, and 214,000t as animal feed. Of this 33,000t was compounded and the balance fed on farm. This compares extremely unfavorable with UK wheat usage as animal feed of 5.3Mt and barley at 3.9Mt

The decline in oat production has been accelerated with the UK's accession to the European Union (EU), which encouraged the production of wheat and barley [Figure 1]. However oats can compete effectively in agronomic terms and now are competitive with barley in terms of yield. [Figure 2].

In my view, there are a number of reasons for the poor usage of oats in animal feed.

- Poor feed performance. Many livestock producers regard oats as being 'poor' feed for stock. This is a view also shared by compounders. However there is limited utilisation of oats as animal feed, either in equine rations, or for specific applications, e.g. pig weaner feeds, which utilise naked or processed oats.
- Lack of continuity of supply. In order to attract feed compounders' interest, there must be a plentiful supply of oats to ensure year round supply. This has become more important since most UK mills now operate on minimum holding bin capacity.

- Price volatility. The oat price has been highly variable depending on the seasonal quality and quantity, and this can be exacerbated by the export of oats to the Southern EU countries.
- Handling difficulties. The flow characteristics of oats can lead to bridging in bins, and conveying difficulties.
- Lack of current nutritional data. There is little independent verifiable nutritional data available, which forces feed formulators to take a very conservative view of the nutritional profile. This in turn then reduces the relative value in the feed ration thereby making oats uncompetitive against other cereal crops.
- Poor image. This perception is made worse by the consumers' misconception that modern oats are similar to the varieties of twenty years ago, and that generally the oat crop is 'poor' grain grown on poor land.

THE BENEFIT OF OATS IN FEED RATIONS

However there is good evidence to suggest that the feed industry should take a renewed interest in modern oat varieties:

- Nutrient density. Oats are particularly suitable for monogastric diets, with a high PUFA content in the oil and a quality amino acid profile. As the protein in oats is globulin based, the amino acid profile remains constant as total protein increases - unlike wheat or barley where the quality degrades with increasing protein content.
- Value-added benefits. Oats are high in antioxidants which may have an effect on animal well-being and benefit humans through higher antioxidant levels in meat, egg or milk products. Whilst β -glucan is perceived to have an antinutritional effect, there is evidence to suggest that limited amounts may be beneficial in improving gut digestion. There is also some evidence to support the use of oat hulls in monogastric diets in order to increase the beneficial xylanolytic bacteria, thereby improving cellulose digestion.
- Agronomic competitiveness. Oats have out-yielded barley for five out of the last six years in England and Wales.
- Environmentally benign. Under the UK's intensive production systems, oats require reduced rates of fertiliser, herbicides and fungicides when compared to wheat or barley.
- Non-GM material. The advent of BSE in the UK has made the public very sceptical of scientists' claims to the beneficial effect of new technology such as genetically modified varieties. There is now strong pressure to move meat production away from soya with its attendant GM contamination to homegrown 'wholesome' crops. The consumer perceives oats as having a traditional and 'safe' image.

BREEDING ADVANCES

Advances in the breeding of winter oats mainly from IGER in the UK have supported the opportunities for increased utilisation.

Increased yield. The average yield of oats has improved faster than that of barley.

Improved agronomic characteristics. Varieties have improved resistance to lodging, and better disease resistance against crown rust and mildew.

Thin-husked varieties. The use of oats as an animal feed has been restricted by the hull reducing overall energy values and digestibility. Breeding advances have now reduced the thickness of the husk in certain varieties, and improved their overall digestibility. The new variety Millennium from IGER has a thin-husk, with a published kernel content of 77.6 compared to Gerald at 73.7 and correspondingly higher digestibility and metabolisable energy.

Naked oats. Naked oats have been commercialised in the UK for 10 years and have a high quality nutritional profile. They have not been exploited for general animal feed use other than in high value rations because of limited availability, and their relatively high production cost due to the lower yield when compared to conventional varieties.

Dwarf stiffed strawed varieties. New varieties similar in height to barley will help the farmer process crops as efficiently as wheat or barley.

Higher oil lines. Breeding advances may allow the oil content to be raised from 10 to 16%. It is currently unknown what effect this would have on the nutrient profile, but this may lead to new feed opportunities for particular animals.

AGRONOMIC ADVANCES

The breeding advances have been further enhanced by improvements in agronomic techniques:

- Increased yield manipulation. It is known that the yield of oats can be significantly improved with the use of increased nitrogen applications and correct timing. The advent of dwarf varieties allows the grower to use increased levels of nitrogen more effectively, without the fear of the crop lodging.
- Improved protein content. Similar techniques can be used to increase grain protein content.
- Improved disease resistance. The advent of the strobilurin family of fungicides has improved disease control which has had the effect of potentially increasing yield by up to 10% as well as preventing head diseases which affect grain discolouration.

THE POTENTIAL FOR NEW MARKETS FOR THE UK OAT CROP

The competitiveness of the UK poultry industry depends largely on the cost of poultry food as it represents approximately 70% of farm costs. The UK feed industry has specific difficulties, when compared to the rest of Europe, as legislation prevents the use of animal products within the rations, and the climate is unsuitable for the production of corn. There are further disadvantages when compared to global competitors, as soya must be imported resulting in a higher cost due to freight etc, and UK cereal prices are likely to be higher than the world price due to the EU's cereal support mechanisms.

There is therefore an opportunity for homegrown cereal based crops such as naked oats as an alternative raw material which is nutritionally valuable to poultry diets. Naked oats are also better suited to production in the UK's maritime climate than either the rest of Europe or most parts of the world. From the feed formulator's perspective there are additional benefits such as the inclusion of naked oats in the ration increases the value of locally grown canola relative to imported soya.

THE NEED FOR ADDITIONAL RESEARCH

The question may be asked as to why if such an opportunity exists it has not been previously exploited. The main barrier has been a lack of confidence by the growers to produce the volumes required for the feed industry to establish the crop as a serious feed alternative, and a lack of confidence by the compounder who perceived themselves as vulnerable to the continuity and quality of supply. These barriers can be overcome if focused research is undertaken to demonstrate the economic competitiveness of the crop to the grower, and the true nutritional advantages to the compounder.

AFENO

A research project has therefore been proposed under the UK Ministry of Agriculture, Fisheries, and Food [MAFF] Sustainable Livestock Scheme with the title 'AFENO - Avian Feed Efficiency from Naked Oats', which sets out to answer the fundamental question as to why do monogastrics perform better on oat diets than the feed formulations suggest they should.

This three-year project has four objectives:

- To develop agronomic techniques to maximise naked oat production both in terms of yield and grain quality utilising both conventional and dwarf naked oats.
- To investigate all aspects of animal nutrition including the use of enzymes to improve nutrient availability.
- To investigate effects on meat quality with the increasing substitution of oats in the diet.
- To investigate the feasibility of a short-chain production contract.

It has financial support from all areas of expertise:

- MAFF. MAFF interest includes increasing the area of oats under production, and the reduction of the UK's reliance on imported protein sources.
- Bernard Matthews plc. Bernard Matthews are a leading turkey producer and meat processor growing 17 million turkeys annually, and feeding 600,000t compounds.
- Sun Valley Poultry Ltd. Sun Valley are a subsidiary of Cargill plc and produce approximately 500m birds annually for further processing feeding 300,000t of compounds.
- British United Turkeys Ltd. More than half the turkeys produced in the world come from this company's breeding stock, including all of New Zealand's turkeys.
- Semundo Ltd. A leading crop developer in the UK with a specific interest in oats, marketing the majority of the UK leading oat varieties.
- Superioat Co. Ltd. The Superioat Co. has commercialised naked oats through a contracted production system for the last ten years and now wishes to expand.

- HGCA. The statutory farmer levy body which supports research and development to enhance UK agriculture.
- British Poultry Meat Federation. BPMF is the industry body, which identified the opportunity for naked oats within their sector.

The research will be undertaken at three centres:

- ADAS Consulting Ltd. ADAS will undertake the agronomy trials within AFENO.
- The Roslin Institute, which is a leading research facility with expertise in monogastrics, will investigate all the nutritional aspect.
- The University of Bristol will assess meat quality.

The research has been divided into eight objectives:

Objective I: To determine agronomic effects on yield and grain nutrient content

The effects of agronomic practice on maximizing yield and grain quality will be examined using coordinated multi-site replicated field trials carried out over 2 crop years by both ADAS and Semundo Ltd.

Objective II: Grain nutritional analysis

Nutrient analysis will be performed on the grain resulting from the agronomic trials. All samples will be analyzed for crude protein, starch and oil contents. A subset of samples will be analyzed for more detailed nutritional composition, including amino acids, fibre, beta-glucan, fatty acids, phytate and ash contents. This data will be related to the variations determined in the current commercial crop from data supplied by the Superioat Co. Ltd.

Objective III: Nutritional value of grain to poultry

Metabolisable energy concentration of naked oats when fed to broilers and turkeys. Much of the initial research will be based on the precision-feeding assays for energy metabolisability (TME) and nutrient digestibility developed at the Roslin Institute. An exception to this will be the use of a self-feeding assay to determine the effects of enzyme treatment on raw materials. The latter is usually employed to generate AME (apparent metabolisable energy) values but the results can be adjusted to TME (true metabolisable energy) using the same "glucose controls" as for the precision-feeding assay. Adiabatic bomb calorimetry will be used for measuring energy content of feedstuff and excreta samples. Nitrogen concentrations will be measured in the gas phase following oxidation of samples in an automated analyser.

Amino acid digestibilities from naked oats in broilers and turkeys. This research will be based on nutritional balance trials, incorporating the feeding of oat-containing diets precisely analyzed for amino acid contents. Amino acid analysis will be performed by ion exchange chromatography. Amino acid digestibilities will be measured at ileal and faecal levels, using titanium dioxide as an indigestible marker.

Fat and fatty acid digestibilities from naked oats in broilers, layers and turkeys. Fat (ether extract) will be determined by solvent extraction in an automated Soxhlet-type apparatus. Fatty acid composition of raw materials, feeds and droppings will be measured by GLC (gas-liquid chromatography).

Objective IV: Factors limiting or enhancing nutrient utilisation

Effects of exogenous enzymes (proprietary feed enzymes) on energy metabolisability and nutrient digestibilities in naked oats. Proprietary feed enzymes are thought to exert most of their effect by decreasing digesta viscosity and allowing more rapid diffusion of nutrients from the lumen to the absorptive surfaces of the gut. The major soluble fibre constituents in oats are the beta-glucans. The effects of identified exogenous enzymes on digestion and absorption of energy, protein, amino acids, fat and fatty acids will be measured.

Comparison of digesta viscosities with diets based on naked oats and other cereals; effect of enzymes. The biological measurements under Objective III will be related to digesta viscosity by physical measurement of viscosity, using a Brooke's viscometer. Sample birds will be killed by anaesthetic overdose, to avoid disturbing the intestinal contents. The ileal contents will be isolated for viscosity measurements.

Comparison of ME and relative digestibility of increased hull content in naked oats. There is some evidence to support the inclusion of oat hulls in monogastrics diets, but this in turn reduces energy available. Naked oats with increasing hull content from 0 to 15% will be assessed for digestibility and energy values.

Objective V: Prediction of metabolisable energy value

All samples of naked oats used for metabolisability and digestibility measurements will also be analyzed for crude protein, fat, starch, sugars, fibre, ash and moisture contents and for physical characteristics such as water-extract viscosity. These measurements will be used to construct models predicting ME. Different models will be assessed for predictive ability.

Objective VI: Characteristics of meat in relation to an oat-containing diet

Fatty acid composition will be measured. Sensory attributes of cooked meat (flavour, tenderness, juiciness) will be assessed by taste panel techniques. Susceptibility to oxidation will be assessed by measurement of thiobarbituric-acid-reactive substances. Comparison will be made between the naked oat diets and conventional cereal diets on both fresh and hung birds.

Objective VII: Commercial growth trials

British United Turkeys Ltd.: Breeder trials will measure food consumption and body weights during the birds' life. During lay, data will be collected on settable eggs, unsettable eggs, true fertility, dead germs, hatchability of fertile, and hatch of set. A subjective assessment will be made on poult quality and on 7-day liveability. Potential problems have been identified with muscle integrity in fast growing turkeys, and investigations will assess the value of the high antioxidant level in oats in combatting this when compared to standard wheat diets. This will involve measuring creatine kinase in the blood of a sample of birds on each diet at several ages and supporting the findings with histological work.

Sun Valley Foods Ltd.: Trials utilising the results from the Roslin Institute will assess the effect of different dietary treatments on the performance of Cobb birds using increasing levels of naked oats replacing wheat.

Bernard Matthews plc: Utilising information from Roslin Institute, trials based on day-old stag turkeys will investigate the effect of stepped inclusions of naked oats. Growth rate, FCR and mortality will be recorded, as well as factory deboning yields. Qualitative assessments on bird welfare including feather pecking will be undertaken during the trial.

Objective VIII: The construction of a production and processing blueprint for naked oats

The feasibility of an industry lead production contract will be assessed which demonstrates the commercial viability of naked oats to the cereal grower as a break crop, the feed and poultry industries as a raw material and the consumer in improved nutrient composition, sensory qualities and storage life.

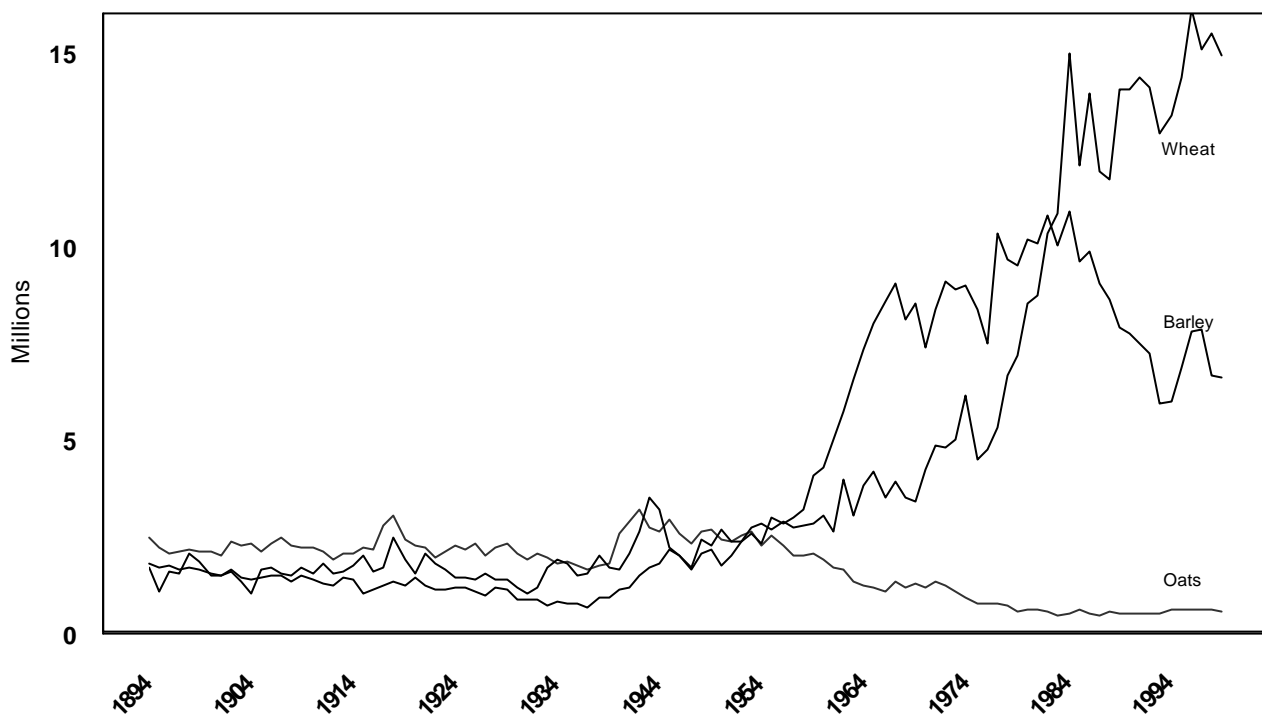
A successful outcome of this project would generate the production and processing of approximately 600,000t of naked oats annually. It is also felt that as poultry constitute an important model species group, success in poultry nutrition may encourage uptake by other sectors of the livestock industries, particularly pigs.

CONCLUSION

The advent of thin-husked varieties, naked oats, and higher oil lines together with improved agronomic techniques, has created a window of opportunity to exploit oats' known benefits in animal feeds. Initially research will focus on monogastrics, where there is considerable consumer interest, but it is intended to build from this platform to exploit other unique characteristics of oats, unavailable in other cereals.

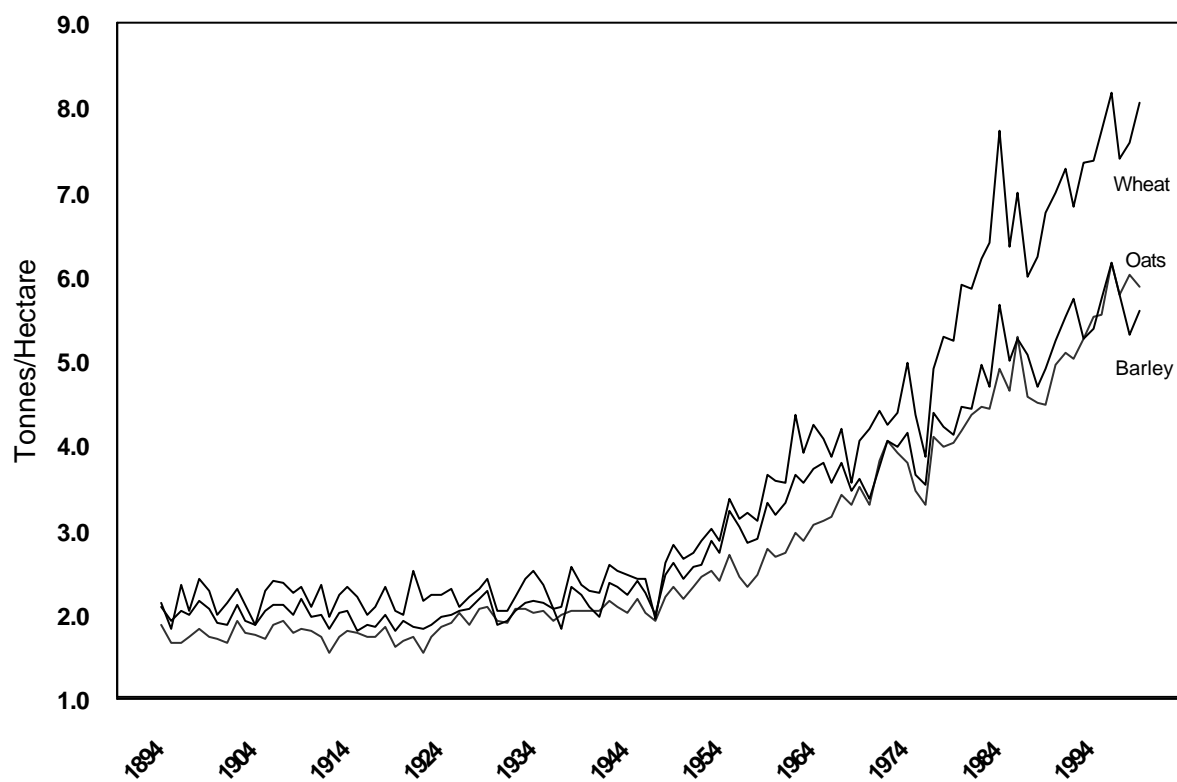
The modern oat crop is competitive in the farmers' rotation, but further expansion is restricted by the lack of new markets. The current research programme into the use of oats as animal feed could increase consumption from the current 214,000t to 1Mt annually. An increase of this magnitude, coupled with a smaller increment in human food use, would restore UK oat production to the 1980 levels of 1.5mt per year and prevent the oat crop from becoming marginalised with little interest from growers or compounders.

**Figure 1: UK Cereal Production
1894 to 1999**



Source: HGCA UK.

**Figure 2: UK Average Cereal Yields
1894 to 1999**



OATS FOR DAIRYING

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ABSTRACT

Oats can contribute to dairy cow nutrition as a grazed forage, silage or grain. They provide palatable forage for non-lactating cows in winter or cows in early lactation. Unfortunately, their full DM yield potential cannot be obtained without compromising nutritive value. Yield is also affected by multiple grazing. Oats silage can provide the winter component of a double cropping system with maize silage. This system can potentially yield 30-35 t DM/ha per annum. Oat grain has a lower energy density than other grains, however, its higher effective fibre and N content make it a useful component of dairy rations.

INTRODUCTION

Oats differ from wheat, barley, and rye in that they have a panicle type inflorescence and do not equal wheat for nutritional value for humans. However, they remain a valuable feed for farm animals and have some unique characteristics that make them valuable in cropping systems. They can be grown in the winter in the warm temperate zone, and make good companion seedlings for ryegrass and legumes. They mature early enough in spring to allow double cropping, make the best hay of the cereals and will grow on acid soils, producing high yields where barley and wheat would fail (Mills, 2000).

This paper examines the attributes of oats as a grazed forage, silage and grain as a feed for dairy cows. It is compared with other forages and grains that may fulfil a similar role. Its role in both current and future New Zealand dairy systems is discussed.

Greenfeed Oats

Oats as a species have low tolerance for multiple cutting or grazing. However, they can generate a large amount of herbage in late autumn and winter for a single grazing in late winter-early spring.

Oats for grazing should not be allowed to progress past Feekes scale 8, which is equivalent to about 6 t DM/ha (Table 1). Past this stage absolute amount of leaf may remain constant but there is rapid development of stem and sheath causing a decreased leaf : stem ratio. At 3 t DM/ha oat leaf has 80% digestible dry matter (DDM) 12 megajoules metabolisable energy (MJME/kgDM), falling to 70% DDM (10.5 MJME/kg DM) at 6 t DM/ha; crude protein falls from 20% at 3 t DM/ha to 15% at 6 t DM/ha. These levels indicate a forage that is suitable for increasing the condition score of dry cows, or providing a supplement for pasture fed cows in early lactation.

Table 1. Oat yield and composition at different growth stages (from Hughes and Haslemore, 1981).

Feekes scale	Growth stage	DM Yield (t/ha)	Digestible DM (%)	Crude Protein (%)	Digestible DM (t/ha)	Crude Protein (t/ha)
2	Leafy	0.2	80	33.0	0.16	0.07
4		0.8	80	31.2	0.64	0.25
6	Stem growth	2.5	80	21.9	2.0	0.55
8		5.5	72	15.6	4.0	0.86
9	Boot	8.0	60	10.9	4.8	0.87
10	Ear emergence	11.0	55	7.5	6.0	0.83
11	Flower head	12.2	50	6.2	6.1	0.76

Theoretically, grazing utilisation of a 6 t DM/ha crop could approach 80-90%. However, high utilisation by lactating cows will reduce overall diet quality. A compromise would involve approximately 50% utilisation by lactating cows to allow selection of high quality leaf, followed by dry cows to consume the lower quality residual. At such a high herbage mass it is important that grazing occurs only in dry weather to avoid high trampling losses.

Table 2 shows that oats have the ability to out yield Tama ryegrass from sowing to first cut but oats produce less than Tama in subsequent regrowth periods when cut a total of three or five times. However, total production when cut 3 or 5 times was the same for both species. The potential herbage production of both oats and Tama ryegrass is substantially affected by harvesting on either three or five occasions compared with a single harvest.

Table 2. Effect of cutting frequency on dry matter production (t/ha) of oats and Tama ryegrass (from Stephen, McDonald and Kelson, 1978).

Date of first Cut	No of cuts	First cut		Total	
		Oats	Tama	Oats	Tama
27 August	5	1.9	1.0	4.4	4.4
29 October	3	9.8	8.8	10.5	9.9
16 December	1	16.1	13.5	16.1	13.5

Work by Taylor et al (1976) in the 1970's showed that neither Mapua oats nor Tama ryegrass produced more than 1 t DM/ha 20 weeks after a mid-April sowing in South Island sites of Timaru, Invermay and Gore. In contrast Mapua oats had produced 6-11 t DM/ha and Tama ryegrass 4-8 t DM/ha at Palmerston North, Rukuhia and Kaikohe in the North Island. Recent work at Lincoln, Canterbury has shown that a new forage oat "Stampede" sown in early March is able to produce 5.0-6.4 t DM/ha by early July (de Ruiter et al., 2000).

Nitrate toxicity

Although nitrate is often implicated in poisoning, it is the nitrite ion that is more toxic. Plants which contain from 1 to 1.5% potassium nitrate on a DM basis may cause acute intoxication in ruminants but generally unless other factors are involved which predispose to toxicity, animals may consume such fodder without ill effect. Oats, and the other cereals, have been implicated in nitrate poisonings (O'Hara and Fraser, 1975). The highest concentration of nitrate is found in the stem and stalk of the plant, rather than leaves, and usually some environmental conditions predominate at the time of an outbreak of toxicity to have enhanced the nitrate levels in the plants. These factors include high concentrations of nitrate in the soil and/or a deficiency of certain nutrients (sulphur or molybdenum), low light intensity and drought.

Nitrate is broken down to nitrite, through microbial action in the rumen and then to ammonia. If the level of nitrate is too high or the conditions for metabolism to ammonia are not optimal, nitrite will accumulate and be absorbed into the blood. This reduces the ability of the body to transport oxygen. Ruminants can tolerate high levels of nitrate if the intake is spread over the whole day and if the diet is otherwise high in readily available carbohydrates to support microbial activity. Care must therefore be taken to ensure gradual introduction of the feed when feeding fresh forages, high in nitrates, to ruminants. Care must also be taken when ensiling. Forages high in nitrates are more difficult to ensile than low nitrate forages.

OAT SILAGE

Forage is the key resource for milk production and it accounts for up to 65% of feed for dairy cattle world-wide. Therefore, the quality of forage is an important determinant of cattle performance (Kennelly et al., 2000). Dairy producers have traditionally conserved surplus grass as the forage source for periods of reduced feed availability. Grass does not produce high yields, however, during the cold months of the winter and early spring, and in recent years the increased use of maize silage as an energy supplement has prompted consideration of alternative break crops. Dairy producers overseas generally consider lucerne to be the forage of choice in conjunction with maize silage for supplemented animals due to high yields under cutting regimes and its high crude protein and reasonable energy concentration. However, climatic conditions in the winter limit the yield of lucerne. Cereals planted in the autumn can be grown in a wide range of climatic and soil conditions. Furthermore, because cereals are annual crops, they are not subject to winter kill (Kennelly et al., 2000) and can produce up to 8 t DM/ha between the time of maize harvesting and sowing of the new crop. Thus, the interest in whole crop cereals in a double cropping arrangement with maize silage has gained considerable interest.

Composition of cereal forages

Fibre content is an important measure of forage quality. Lactating dairy cows require a minimum amount of effective fibre in the diet to stimulate rumination, salivation, maintain a healthy rumen and thereby maximise dry matter intake (DMI) (NRC, 1989). However, fibre is negatively correlated with DMI and too much in the diet can reduce DMI through increased rumen fill (Mertens, 1985; NRC, 1989). The review of fibre by NRC (1989) suggest maximum production of 4% fat corrected milk when NDF (Neutral Detergent Fibre) and ADF (Acid Detergent Fibre) were between 24-26% and 17-21% respectively, although a minimum NDF of 28% was recommended for cows during the first 3 weeks of lactation. Recent work in New Zealand has shown these recommendations to be inappropriate for

high quality grass only diets due to the fermentable nature of the fibre in grass and the lower critical rumen pH for fibre digestion on a grass diet (Kolver, 2000). These inconsistencies indicate that fibre requirements, and supply, may be better described by the term “effective fibre” (eNDF), which also takes into account the nature of fibre in feeds. Minimum NDF and ADF values for grass-fed cows are 35% and 17%, respectively. Above minimum fibre requirements, intake is negatively correlated to NDF and eNDF. Table 3 shows the chemical composition of barley, lucerne, oats, wheat and maize silages (Burgess et al., 1973; Kolver, 2000).

Table 3. Chemical composition of cereal grain and lucerne silages.

	Barley	Lucerne	Maize	Oats	
	Wheat				
ME (MJ/kg DM)	9.8	9.5	10.3	10.5	10.5
Soluble Carbohydrates (%)	19.9	16.7	35.1	16.1	16.1
Starch (%) ¹	100	45	100	100	100
Crude Protein (%)	11.9	20.0	8.0	13.0	13.0
Soluble Protein (%) ²	70	54	48	67	67
NDF (%)	57	51	49	59	59
ADF (%)	36.7	42.2	29.7	40.0	32.8

¹ Starch as a percentage of soluble carbohydrate

² Soluble protein as a percentage of total crude protein

The protein concentration of lucerne silage is higher than that of the cereal grain silages. However, of the high yielding cereal grain silages the protein concentration of oats and wheat are higher than for barley or maize with similar energy concentrations. Therefore when oat silage is used as an energy supplement a protein deficiency is less likely to occur than for maize silage. However, the higher NDF concentration of oat silage compared with lucerne or maize will probably reduce the intake capacity of the cow for these forages. This is supported by Khorasani et al. (1993) who reported that cows fed silage with high NDF content (oat and triticale) had a lower DMI than cows fed silage with lower NDF (lucerne and barley). Based on NDF concentration the qualities of the cereal grain silages were ranked in the decreasing order of barley, triticale, and oats (Khorasani et al., 1993).

Stage of maturity at harvest significantly affects the DM yield and crude protein and fibre concentrations of cereal forages (Kennelly et al., 2000, Table 1). Tradeoffs between total DM yield, ME concentration and crude protein content must be considered when using oats for silage. The use of silage for milk production must consider stage of lactation; if used for non-lactating cows the level of liveweight gain must be considered. In addition, the feeds used to complement oat silage must be taken into account.

Data from Table 1 show that to produce a silage of 72% DDM (10.5 MJME/kg DM) and crude protein of 15.6% requires silage to be cut at Feekes scale 8. The silage can be used at any stage of lactation as a supplement to pasture without a detrimental effect on intake or milk yield. However, total yield will be 5.5 t DM/ha, only 45% of potential DM yield, or 65% of potential DDM yield, but crude protein and leaf yield will be nearly maximal.

If silage is cut at Feekes scale 9 it will be 60% DDM (9 MJME/kg DM) and 11% crude protein. This silage is only of sufficient quality to be used in late lactation perhaps to allow pasture to be saved for winter. It could also be used as a maintenance ration of 6-7 kg DM/cow/day for non-lactating cows. It has insufficient crude protein to support milk

production if fed in conjunction with poor quality summer pasture. Total yield will be 8 t DM/ha, only 66% of potential DM yield, or 79% of potential DDM yield and crude protein yield will be maximal.

If silage is cut at Feekes scale 11 it will be 50% DDM (7.5 MJME/kg DM) and 6.2% crude protein. Although potential DM yield is maximised there is insufficient energy and crude protein to support milk production. It is not of sufficient quality to feed to dry cows during the last month of gestation. It could be used as a fibre supplement in situations where large amounts of starch supplements are being fed. At best this material could be used as a maintenance forage for dry cows.

Production responses to cereal forage

If supplements are supplied during periods of adequate grass production high rates of substitution occur. Substitution occurs where cows replace grazed grass in their diet with an alternative feed. Substitution may be high when forage supplements are employed (84-102%; Phillips, 1988) and total energy intake can in fact decrease because of very high substitution rates of a less energy dense feed for grass. Grazing times have been found to decrease by 43 minutes/day for each kg of silage DM consumed (Mayne et al., unpublished; cited by Stockdale et al., 1997). This decreased grazing time is greater than that reported by Leaver (1986) for starch supplements (23 min/kg concentrates) and hence the difference in substitution between different supplement types. Substitution increases as quantity of supplement fed increases (Stockdale et al., 1997) but decreases with increased frequency of feeding (Agnew et al., 1996).

Although New Zealand's climate allows the production of large quantities of grass and legumes, there are times of the year when both quantity and quality of feed are lacking. Research at DRC in recent years has shown significant responses to supplements (70-90g MS/kg DM of supplement), during these periods, if used to increase lactation length (Penno et al., 1996).

A number of production studies have been conducted at the University of Alberta to evaluate cereal forage quality (Kennelly et al., 2000). In general, DMI of cows fed lucerne and barley silages was higher than for cows fed oat silages. However, the effect of silage type on DMI was less pronounced in mid-lactation (DMI was reduced by 0.38 kg/d per 1% increase in NDF) than in early lactation (DMI was reduced by 0.94 kg/d per 1% increase in NDF). No difference in milk production was observed between the three forage diets when fed in mid lactation. This is an important consideration for New Zealand farmers considering that most forage supplements are fed to cows during mid and late lactation in an attempt to increase days in milk.

Burgess et al. (1973) also reported that cows had a lower DMI when fed oat silage compared with barley or wheat silage. However, milk production responses were similar on all three forage diets. Maize silage was used more efficiently for milk production. Blood urea nitrogen was higher in cows receiving oat silage which indicated that the diet had a higher crude protein

content. Similar milk protein concentrations were measured from cows fed oat, barley, and wheat silage, but milk fat percentage was lower on wheat silage diets compared to barley or oat silage diets. The lower milk fat concentration in cows fed wheat silage may be a reflection of the substantially lower ADF concentrations in wheat silage.

OAT GRAIN

Oat grain can be successfully used as a sole supplement for lactating cows grazing pasture, or as a component in a concentrate dairy meal. However, oats offer few nutritional advantages for ruminants over alternative grains such as maize, barley and wheat. Usage will therefore depend on availability and price relative to alternatives. When grass quality is high and available in sufficient quantities, substitution for starch-based energy feeds (e.g. cereal grains) can exceed 50% (Stakelum et al., 1988; Faverdin et al., 1991). As a result, improvements in energy intake and subsequent milk production are small. When supplements constitute less than 30% of the cow's daily intake, energy is most likely to be first limiting milk production, as high quality grazed grass can fulfil the remaining nutritional needs (Kolver, 2000). As the energy density of cereal grains is generally higher than forage supplements and substitution rates are lower, cereal grains are the energy supplement of choice. Historically, in the North Island of New Zealand the high price of cereal grain supplements and the low milk price has made their use uneconomical. Growing cereals on farm and taking them into grain stage similarly has not been an option as the loss in energy yield/hectare is substantially greater than the advantage of higher energy density in the cereal grain. For example, yields of 25 tonnes of maize silage (10.5 MJ ME/kg DM) in the Waikato are now a reasonably common event in autumn (T. Deane, pers com.). If this crop was carried through to grain stage, yields in excess of 12 tonnes are unlikely (13 MJ ME/kg DM).

Dairy production in the South Island has access to reasonably priced cereal grains, and is a rapidly growing sector of the NZ Dairy Industry. It is expected that starch supplements will be increasingly used there in the future. Access to these energy supplements is allowing higher milk yields per cow and per hectare to be achieved.

Composition of cereal grains

The composition of oat grain relative to maize, wheat and barley is presented in Table 4. On the basis of ME, oats have traditionally been regarded as being inferior to other grains as an energy supplement for dairy cows (Moran, 1986). However, relative to the other cereals, oats has a higher concentration of crude protein (CP), neutral detergent fibre (NDF) and effective fibre (eNDF). These factors may improve the value of oats as a supplement for dairy cows, depending on the nutrient content of other feeds in the diet.

Table 4. Comparative nutrient composition of oats and other grains (NRC, 1989; Kolver 2000).

	Barley	Oats	Maize	Wheat
ME (MJ/kg DM)	13.7	12.5	13.1	14.5
Crude Protein (CP) (%)	11.0	13.0	8.0	11.3
Undegradable Protein (%)	27	17	52	24
Soluble CP (%)	31	27	12	23
NDF(%)	21	31	9	14
eNDF (%NDF)	34	34	5	3
Soluble Carbohydrate (SC) (%)	61.4	47.5	75.1	70.2
Starch (%SC)	90	90	99	90
Fat (%)	2	4.9	4.3	1.9
Ash (%)	2.8	3.6	1.6	2.6
Ca (%)	0.06	0.1	0.02	0.07
P (%)	0.44	0.41	0.31	0.36
Mg (%)	0.18	0.15	0.12	0.13
K (%)	0.57	0.53	0.4	0.46
S (%)	0.17	0.19	0.12	0.16
Na (%)	0.03	0.01	0.03	0.01
Cl (%)	0.18	0.11	0.05	0.08
DCAD (mEq/kgDM)	+2	-10	+26	0

The source of the dietary starch and the processing of the cereal grain can have a substantial effect on the incidence of lactic acidosis. Although lactic acidosis can be reduced by slowly introducing the starch source to allow sufficient time for the ruminal micro-organisms to become adapted to the lactic acid challenge, the rate at which ruminal pH declines can also be influenced by the degree of grain processing and rate of starch digestion. Whole grains, due to less surface area being exposed, are fermented more slowly than processed grains. Cereal grains have varying starch degradation rates due to different chemical compositions which cause a range of lactic acid and propionate production. Table 5 shows the effect of barley, maize, oats and wheat grains on ruminal pH and on the production of acetate and propionate in sheep. Oat diets result in a higher ruminal pH, and the reduction in ruminal pH as a result of processing is not as great for oats compared with other grains. Oat diets also result in a higher acetate to propionate ratio and this is likely related to the higher NDF and eNDF content of oats. Acetate and propionate are used as an energy source with similar efficiency by the cow, except when the animal is in a ketotic state (Orskov, 1986).

Table 5. Effects of different cereal grains on ruminal pH and acetate and propionate production (Orskov, 1986).

Cereal	Form	Ruminal pH	Acetate (%)	Propionate (%)	Acetate: Propionate Ratio
Barley	Whole	6.4	52.5	30.1	1.74
Barley	Ground	5.4	45.0	45.3	1.00
Maize	Whole	6.1	47.2	38.7	1.22
Maize	Ground	5.2	41.3	43.2	0.96
Oats	Whole	6.7	65.0	18.6	2.86
Oats	Ground	6.1	53.2	37.5	1.42
Wheat	Whole	5.9	52.3	32.2	1.62
Wheat	Ground	5.0	34.2	42.6	0.80
SE		0.14	2.4	3.2	

Comparisons of animal performance on cereal grain diets have produced mixed results. Moran (1986) reported a higher yield of fat corrected milk (FCM) for cows fed oats (27.6 kg/cow/day) than cows fed barley (24.6 kg/cow/day) and wheat (24.9 kg/cow/day), even though intake of digestible organic matter was lower. Cows fed oats had higher milk fat (1.18 kg/cow/day) and lower protein (0.78 kg/cow/day) than cows fed wheat (1.01 and 0.89 kg/cow/day) or barley (1.03 and 0.80 kg/cow/day) respectively (Moran, 1986). These changes in milk composition were reflections of changes in rumen fermentation. Rumen pH was 6.98, 6.88, and 6.69 for cows fed oats, barley, and wheat, respectively, while the ratio of acetic + butyric to propionic acid was 4.17, 3.84, and 3.24, respectively (Moran, unpublished as cited in Moran, 1986). This higher ratio of acetic plus butyric: propionate is more conducive to a high milk fat concentration (Roche and Dalley, 1996). It is important to note, however, that rumen pH values reported in this experiment were extraordinarily high for animals receiving 60% of their diet as cereal grain. These differences are likely a result of the higher NDF content of oat grain compared to barley or wheat (Kolver, 2000).

Others have reported no difference in milk production between cereal grains (Tommervik and Waldern, 1969; Jeffery et al., 1976 as cited by Kennelly et al., 2000). However, in the work of Tommervik and Waldern (1969), the grains were given in pelleted form. The grinding of the cereal grain prior to pelleting will more than likely have increased the rate of ruminal degradation and utilisation of starch and reduced the natural advantage of oats over other cereals.

As supplement inclusion increases beyond 30% of the diet consideration must be given to dietary factors other than energy and fibre, such as protein. Recent dry summers in New Zealand have led to situations where low protein grass and higher than normal use of low protein-energy supplements has induced dietary protein deficiencies. Macdonald et al. (1998) found a significant increase in milk production through supplementation of protein in these situations. Consequently, there is increased interest in energy supplements which contain a reasonable protein content. Oats have a higher crude protein content than other cereals commonly used, and may avoid the need for expensive protein supplements during periods where crude protein content of the diet is marginal. One kg of oats provides 130 g of crude protein whereas 1.2 kg barley, 1.6 kg maize and 1.15 kg wheat would be required to provide the same amount.

The higher protein and NDF content of oats is offset by a somewhat lower energy content than for maize, wheat and barley. The nutritive value of oats is dependent to a large extent on the proportion of kernel to hull. Hull can vary from 23 to 35% (McDonald et al., 1981), which is a greater and more variable range than barley (10 to 14%). The large variation in the hull content of the oat grain explains the variability in energy concentration between oat samples. This is supported by the work of Jeffery et al. (1976; as cited by Kennelly et al., 2000) who found no difference in milk production between cereal grains when inclusion rate was low (3 kg/day). Oat grain therefore needs to be 9% less expensive than barley, 14% less expensive than wheat and 5% less expensive than maize grain to be the gain of choice from an economic perspective. However, as inclusion rate of cereal grain increases above 32% of the diet, the use of oat grains may have greater advantages because of the high fibre and protein contents (Gomez, 1975).

Conventional New Zealand Dairy System

A conventional dairy system relies almost solely on pasture and pasture silage to feed dairy cows. Up to 100 kg N/ha per annum is used to boost winter and spring pasture growth. All replacement stock are grazed off farm. The place of a summer crop in this system was evaluated by Clark et al. (1996). Many of the same considerations refer to winter crops such as oats. To be profitable a winter crop needs to produce enough extra feed above what would have been produced by the resident pasture, at a cost that is competitive with other options. Where pastures need major renovation an option of turnips-oats-turnips followed by autumn pasture sowing spreads the costs across several crops. However, where satisfactory pasture is cultivated to sow oats several important constraints exist. Firstly, farmers rarely sow >6% of their effective farm area in crops because on high-stocked farms larger proportions may reduce the area available for cows in late lactation, and increase the grazing pressure on the rest of the farm in early winter. Secondly, a cropping option exposes the farmer to two risks, the risk of crop failure and the risk of the resown pasture failing. Thirdly, oats offer the flexibility of grazing at different times during the winter but early or frequent grazing will lead to reduced total DM yield. Conversely, achievement of high yields will coincide with peak pasture growth rates and decreased forage quality and utilisation.

Intensive New Zealand Dairy Farming

In the last decade many New Zealand dairy farmers have intensified their conventional pasture-based system (van der Poel, 1996). Common features of this intensification include: the grazing off of non-lactating cows as well as replacement stock, increased stocking rate and earlier, more compact calving. Maize silage is the most common bought-in forage with some addition of protein supplements e.g. brewer's grains. These farmers require an inexpensive energy feed. Oats can act as a complementary crop to maize. New Zealand work (Hughes, 1985; Thom & Gillespie, 1987) have shown that a maize silage-oat silage system could produce 25-35 t DM/ha per annum. The silages produced from this double cropping would complement a pasture-based diet for cows producing 300-400 kg milk solids (MS) per annum.

Mitchell (1974) suggested the use of such a double crop system coupled with a high protein feed such as lucerne to increase per ha productivity of New Zealand dairy farming. The high costs of cropping and the low price New Zealand farmers receive for milk has meant that the theoretical advantages of this system have never been tested in practice.

Breeding

Successful breeding involves the introduction of a new variety with better production characteristics. However, what is deemed advantageous for one species of livestock may not be so for others. For example, the main advantage of oats as a supplement for dairy cows is the higher concentration of NDF in the grain. This advantageous characteristic for dairy cows is a disadvantage for pigs as the increased NDF results in reduced energy intake and lower production. Therefore animal species and management systems need to be considered when evaluating cereal grain diets. Selection has largely been driven on agronomic characteristics with little or no emphasis on the impact of these selection criteria on the nutritional value to the end user, the animal. It may well be that it is unrealistic to expect cereals to be bred for all classes of livestock (as well as humans) as the characteristics required will differ depending on what is being fed (Kennelly, et al., 2000).

The breeding of cultivars that respond better to multiple grazing and earlier sowing should allow oats to be competitive with other short-term winter feeds such as brassicas and annual ryegrass.

CONCLUSIONS

Oats can contribute to dairy cow nutrition as a grazed forage, silage or grain. They have the advantage of high yield potential from autumn sowings and complement maize in a double cropping silage system. They are a flexible crop that allow different harvesting options depending on current feed supply. Their disadvantages include a lack of cultivars developed specifically for grazing and lower yield if grazed early or often. Nitrate levels can cause animal death under some circumstances. The lower, and more variable energy content of oat grain compared to maize and barley means that oats will be discounted as a component in high concentrate dairy rations.

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COMPARATIVE GROWTH AND NUTRITIONAL QUALITY OF OAT HERBAGE

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ABSTRACT

Oats (*Avena sativa* L.) sown in autumn or spring provide suitable pasture supplements for grazing animals. These were compared with wheat, barley and triticale alternatives over two seasons. The objective was to determine growth responses to temperature and radiation and to utilise the differences in biomass and nutritive quality (protein, soluble carbohydrate, NDF, OM digestibility and ME) to discriminate between breeder's lines and commercial standards. Thermal time accumulation provided opportunities for initial cultivar selection when related to biomass and there were differences among cultivars in radiation use efficiency. Season had a stronger influence on nutritive value than cultivar selection. Optimum use for grazing or silage was best managed by appropriate choice of harvest time depending the end use.

INTRODUCTION

Oats and other cereals are a good source of biomass, protein and fibre supplements for dairy, beef and sheep production in New Zealand, (Eagles et al., 1979; Hughes and Haslemore, 1984). Use of cereals for grazing and silage is not new (Burgess et al., 1972), however the introduction of cultivars with improved yield and disease resistance (de Ruiter et al., 2000) has caused renewed interest. There has been a recent increased demand for high quality cereal herbage produced on contract for dairy farmers in Canterbury. Cereals provide flexible animal feed options (Jermyn et al., 1993) when utilized for silage (single cut-spring sown) or for multiple light grazing (autumn-sown). The latter, with good spring regrowth after grazing, may also be considered for silage. The increased use of forage cereals in the Canterbury region has provided opportunities for pasture renovation and alternative feeding strategies when there is an increased requirement for protein or fibre. Cereals may also provide a balanced protein/carbohydrate diet that compliments the nutritional and production pattern of ryegrass.

Cereals are well adapted to produce high amounts of biomass at most times of the year in the cool temperate environment. The pattern of production may be dependent on the efficiency of utilisation of resources during periods of active growth. Factors such as biomass yield, seed yield, harvest index, canopy development and light capture, radiation use efficiency (RUE), water use efficiency and environmental effects on nutritional composition will determine the suitability of cultivar selections, (Bruckner and Raymer, 1990). Simple models using combinations of thermal time and radiation explain a significant amount of the yield variation of autumn oats grown in New Zealand (Hughes et

al., 1984). Deviations from generalised growth responses provide the best opportunity for screening the identifying potentially useful germplasm. Development of improved methods for predicting biomass increase and quality changes during development are important in the process of selection as it is not possible to rigorously screen for all characters important in the production system.

The objective of the study was to derive patterns of leaf development, biomass and herbage quality and to related these variables to environmental determinants. In addition, it was proposed to use these relationships to assist with cultivar selection on the basis of yield and quality, and therefore determine optimum times for grazing (autumn-sown) or silage (spring-sown) production.

MATERIALS AND METHODS

Four (two spring and two autumn) trials were sown at Lincoln, New Zealand (Lat. 43°39'S; Long. 173°30'E) on a Templeton silt loam (Typic Ustochrept, USDA soil taxonomy).

Autumn-sown (AS) trials

Trials in each of two years (1999 and 2000) were sown as randomised complete block designs with three replications. Triticale lines were included for comparison with the oat selections (Table 1). Sowing was on 4 March and 1 March, respectively. The site was managed for non-limited production and did not require irrigation. In both years, 200 kg/ha of Cropmaster20 was applied during pre-plant cultivation, and weeds were controlled with 3L/ha of MCPA at the 4th leaf stage.

Spring trials

Two spring trials, each with six entries (Table 1) were sown on 27 August and 2 November 1999 respectively in randomized complete block designs with three replicates. Sowing rates were adjusted for seed viability and kernel weight for target plant populations of 250 plants per m².

The early spring trial (ES) required 3 irrigations of 25 mm each on 27/10, 18/11 and 20/12. Cropmaster20 (200 kg/ha) was applied pre-planting, and two applications of nitrogen was applied during growth (150 kg and 100 kg urea on 2 September and 3 November, respectively). Trimec (3.5 L/ha)/Cougar 0.75 L/ha herbicide. Puma S (0.75 L/ha) was applied on 20 October to control annual grasses. In the late-spring (LS) sowing, 50 kg N/ha urea and 200 kg/ha of 15% potassic super was applied pre-sowing and 50 kg N/ha urea was applied on 24 December. Trimec (3.5 L/ha) was applied on 7 December for weed control and the trial was irrigated on 1 Dec (50 mm).

Measurements

Leaf area was determined at two-weekly intervals using a Licor LAI-2000 canopy analyser until canopy closure and thereafter by destructive harvest and leaf area measurement using a digital image analysis system. Radiation intercepted by the crops was measured weekly using a ceptometer (Delta-T SF80) during the period from emergence to canopy closure.

Two 0.1 m² quadrats were cut at ground level and combined for biomass determination at 4-day intervals from flowering until grain maturity in the spring trials. Dry matter (%) of the whole crop was determined by drying for 24 hours at 80°C. Additional samples were taken

for production/loss of leaf weight and leaf area by sub sampling 15 stems and separating leaf fractions that were green or senesced. Leaf area was determined using a dry weight correction following calibration for specific leaf area using a Delta-T image analysis system. In addition, twenty representative stems were sampled randomly, frozen then freeze-dried for quality analysis (total soluble carbohydrate, protein, neutral detergent fibre (NDF), acid detergent fibre (ADF), organic matter digestibility (OMD) and metabolisable energy (ME)) by NIR analysis (feedTECH, Grasslands). Samples were ground to pass a 1 mm screen.

Herbage in the autumn trial in both years was sampled for dry matter (DM) yield accumulation and for herbage quality at three-week intervals beginning 1 May. Sampling for biomass, production/loss of leaf area and quality as described for the spring trials. However, determination of crop dry matter percent, leaf area development (by destructive sampling) and pattern of senescence of successive leaves (leaf area and leaf dry weight) on the main stem culms were determined only for the penultimate and final harvest of the trial in year 2.

Table 1. Cereal cultivar/entries in spring and autumn trials at Lincoln.

Species	Spring trial entries		Autumn trial entries	
	Early sowing	Late sowing	Year 1	Year 2
<i>Avena sativa</i> L.	Hokonui ¹	Hokonui	Hokonui	Hokonui
<i>Avena sativa</i> L.	Stampede ¹	Stampede	Stampede	Stampede
<i>Triticum aestivum</i> L.	Sapphire	Sapphire	--	--
<i>Hordeum vulgare</i> L.	Omaka	Omaka	Omaka	--
<i>Hordeum vulgare</i> L.	1828.100	1828.100	--	--
<i>Triticum</i> (x <i>Triticosecale</i>)	4723.4	4723.4	--	4723.4
<i>Triticum</i> (x <i>Triticosecale</i>)	--	--	Aranui	--
<i>Triticum</i> (x <i>Triticosecale</i>)	--	--	17 ITSN 144	--
<i>Triticum</i> (x <i>Triticosecale</i>)	--	--	--	Doubletake
<i>Avena sativa</i> L.	--	--	CDA103	CDA103
<i>Avena sativa</i> L.	--	--	Makuru	--
<i>Avena sativa</i> L.	--	--	Caravelle	--
<i>Avena sativa</i> L.	--	--	Gartons	--
<i>Avena sativa</i> L.	--	--	93 CDA	--
<i>Avena sativa</i> L.	--	--	501.0.2	--
<i>Avena sativa</i> L.	--	--	501.0.3	--
<i>Avena sativa</i> L.	--	--	476.0.4	--
<i>Avena sativa</i> L.	--	--	--	Longford
<i>Avena sativa</i> L.	--	--	--	CROA51
<i>Avena sativa</i> L.	--	--	--	CROA45
<i>Avena sativa</i> L.	--	--	--	MN94112
<i>Avena strigosa</i> L.	--	--	--	NZ-SAIA

¹ herbicide damage

Weather records

A mobile Campbell CR10 weather station was located adjacent to the trial site. Air temperature at screen (1.2 m) height was averaged from hourly mean measurements and daily observations reported as true means. Total short wave radiation flux (MJ/m²/day) was recorded using a LICOR pyranometer.

RESULTS AND DISCUSSION

Crop development

All cultivars (except Omaka barley) in the autumn trials remained vegetative through the sampling period. Omaka was the only cultivar that produced ears at the time of the final harvest, however there was no grain development. In contrast, the spring-sown crops all progressed rapidly through to flowering and grain development (Table 2).

Table 2. Developmental observations cultivars in autumn and spring trials.

Trial	Canopy closure		Anthesis	
	Days after emergence	Degree days after emergence	Days after emergence	Degree days after emergence
<u>Autumn sowing (AS)</u> (Year 2)	53.5 (6.2) ¹	636 (51.7)	--	--
<u>Early spring sowing (ES)</u> (Year 1)	49 (-)	599 (-)	78 (9.4)	1044 (80.4)
<u>Late spring sowing (LS)</u> (Year 1)	39 (1.0)	519 (12.4)	57 (27.9)	898 (103.8)

¹ Values in parentheses are standard errors.

Temperature and biomass production

There were significant differences ($P < 0.05$) in biomass production between cultivars in all harvests of autumn and spring-sown crops. The pattern of biomass increase for two oat cultivars is shown in Figure 1A. Biomass accumulation in calendar days from emergence was not linear. However, the response to thermal time accumulation (base 0°C) was near linear ($r^2 > 0.94$) for all cultivars and sowing times. Mean biomass production efficiency was more than double in spring (1.74 t/ha/100°Cd) compared with autumn sowing (0.57 and 0.71 t/ha/100°Cd for years 1 and 2). This calculation was determined on different groups of cultivars, however this would not account for the differences in temperature-related production efficiency. The base temperature was possibly underestimated for biomass production and for crop development. It was noted that the thermal time accumulations for emergence to canopy closure and emergence to anthesis were also shorter in the late sowing compared with early spring sowing (Table 2). In addition, cultivars common to both autumn and spring trials (Stampede and 4723.4) also showed improved growth response to thermal time in the warmer conditions.

Light interception and biomass production

Interception efficiency (E_i) of light by crop canopies explained by the Lambert-Beer law

(Monteith, 1977) and evaluated as $E_i = 1 - e^{-kL}$, where E_i is 1-fractional transmittance, L is the leaf area index and k is the extinction coefficient. Calculated values of the k were 0.56 for both AS and LS trials. This compares with values of 0.44 and 0.45 reported by Thorne et al., 1988 and Gales, 1985. Values ranging between 0.54 and 0.80 (Green, 1987) were found for wheat, depending on N nutrition. N fertiliser has also been shown to exert little influence on the optical properties of foliage and therefore differences in k result from differences in canopy structure (Green, 1987).

Yield potential is limited by the amount of solar radiation intercepted over the growth duration. The total seasonal radiation intercepted is dependent on the plant canopy structure (interceptance by leaves) and the crop growth duration. In the case of autumn sown cereals, the former is possibly more important when making selections for improved performance from the range of breeding material. Early canopy closure will confer improved potential for biomass accumulation. Crops may be sown at higher densities to advance the timing of canopy closure. However, lodging of the crops may occur especially in high fertility situations or during irrigation/rainfall. Following canopy closure, biomass production continues at rates determined by the level of canopy light interception and is reduced by the decline in leaf area through senescence and leaf death.

There were significant differences between the cultivars in the respective patterns of light interception. The range in duration to 50% interception for the respective AS, ES and LS trials was 16, 4, and 3 days. Full cover (95 % interception) occurred over a 16, 3 and 8-day period beginning 47, 49 and 38 days after plant emergence, respectively.

A comparison of autumn-sown Hokonui and Stampede oats showed that the biomass increase (Fig. 1A) occurred along with a rapid decline in leaf to stem ratio (Fig 1B). Stem growth occurred at a faster rate than the expansion and development of leaf area (Fig. 1C). Changes in leaf and stem fractions has consequences for the quality of herbage. The pattern of leaf:stem ratio in pre-anthesis period of autumn crops was quite different from that of the post-anthesis harvest period of spring crops. This also contributes to the generally low nutritive value of plants growing through the summer. The effects on crop quality will be considered later.

Leaf area

Leaf area index (LS trial) development followed a characteristic exponential increase in response to biomass increase ($r^2=0.84$). In this trial, observations were made beyond the point of canopy closure and were discontinued at anthesis. In the AS trial, leaf area index was linearly related to biomass up to 3.5 t/ha in the period before canopy closure ($r^2=0.96$). Leaf area index development (before canopy closure) is therefore a potentially useful tool for rapidly screening selections with good early growth. The relationship was less well defined after canopy closure ($r^2=0.65$) and therefore late screening for LAI was not practical. However, plants with long leaf area duration are likely to have high nutritive value.

Leaf longevity, leaf size and leaf area duration are possible plant characteristics that could be exploited to identify potential high performing forage selections. The pattern of green leaf area on main stem culms in the AS trial was similar for the oat cultivars Stampede, CDA103 and NZ-SAIA at the 4 July harvest. More than 70% of the green leaf area was on leaves 2 and 3, and 15% on the partially expanded first and fully expanded 4th leaves. The oat *A. strigosa* cv. NZ-SAIA had much smaller leaves with less than half the culm leaf area of the other cultivars and a dry weight distribution pattern that was similar to Doubletake triticale. The capacity for culms to maintain high green leaf area on lower leaves (cultivars

CROA45, Longford, MN94112, and Stampede) in the canopy is also dependent on the culm density. Cultivars with larger upper (2nd and 3^d) leaves (Stampede, CROA45, CDA103 and MN94112) also produced highest biomass.

RADIATION USE EFFICIENCY (RUE)

For most arable crops, published data has shown strong linear relationships between the amount of radiation intercepted and the biomass produced with efficiency rarely exceeding 1.40g/MJ in unstressed crops (Gallagher and Biscoe, 1978; Green, 1987). Water deficit is known to reduce the efficiency (Gallagher et al., 1983) as well as reducing interceptance. Relationships between biomass production and intercepted radiation were linear for the duration of crop however the autumn-sown crops had a lower mean RUE (1.11 g biomass/MJ total radiation) compared with spring-sown crops (1.28 g/MJ). These data were derived using least squares regression for individual cultivar responses of successive above ground biomass harvests against accumulated intercepted radiation during the growth period. Reduced efficiency during periods of cooler temperatures may occur when the base temperature is below the minimum to sustain growth.

There were apparent differences in RUE in both autumn (emergence to final harvest) and spring trials (emergence to anthesis) that could explain differences between cultivars for total biomass accumulation. The oat cultivar, Stampede was the best performing entry in all trials with RUE of 1.21 and 1.23 in respective AS and LS trials. Stampede together with MN94112 were on average 8% more efficient than other cultivars in the AS trial (Year 2), while in the LS trial, Stampede was 21% more efficient than the mean for all species.

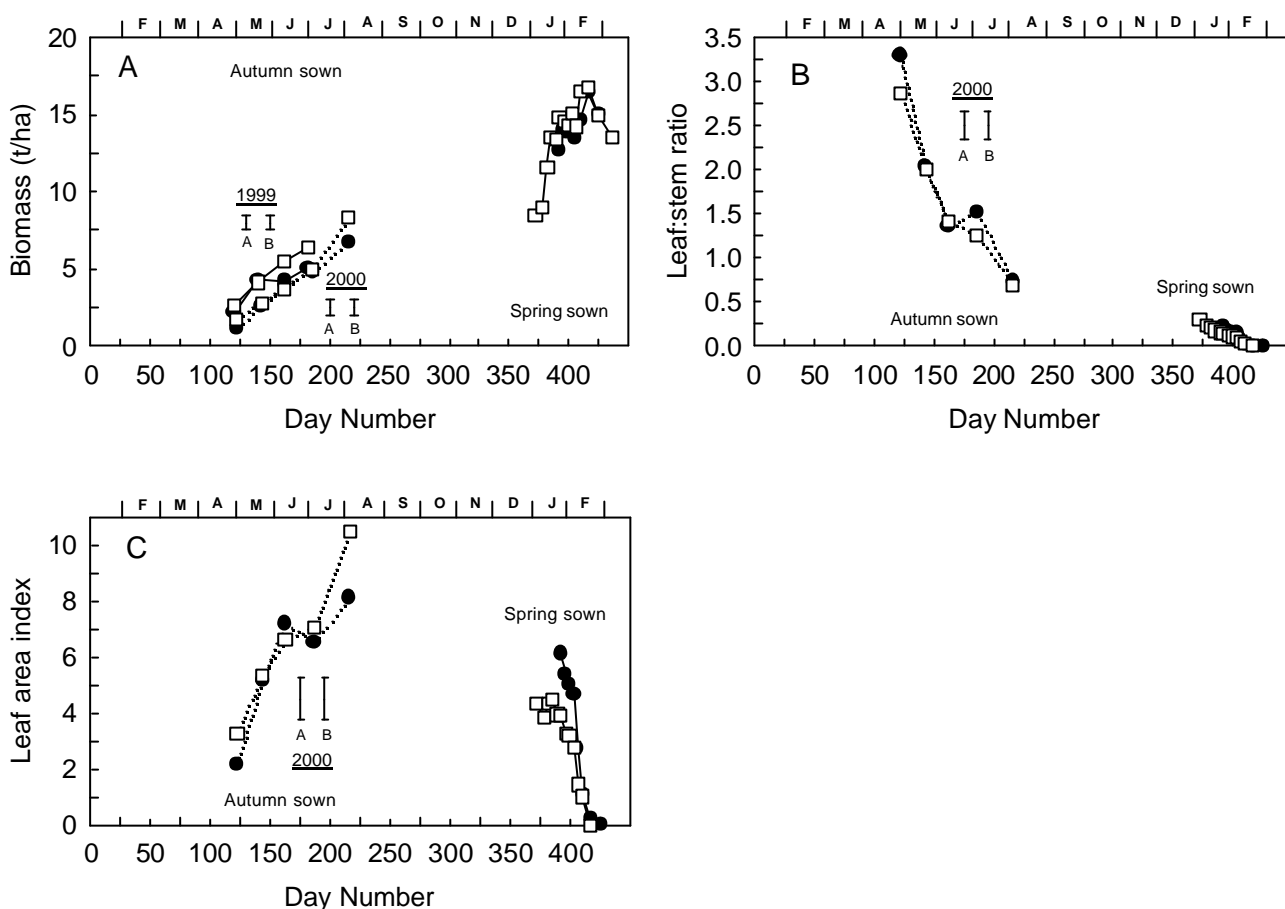


Figure 1. Progression of biomass (A), leaf stem: ratio (B) and leaf area index (C) for autumn and spring-sown Hokonui (·) and Stampede (□) in year 1 (—) and year 2 (···). Error bars (A) are for comparing cultivar \times harvest means, except when comparing means within the same harvest time (B).

Crop quality

Autumn sowing: Protein content of the harvestable biomass of Hokonui and Stampede declined progressively from a high near 30% at the first harvest to around 10% by the beginning of August (Table 3 and Fig. 2A). Total cell wall constituents (NDF) were relatively consistent (37-45%) over the harvest period (May-August). While the biomass yield increased and protein content declined during this time there was a steady increase in the concentration of total soluble carbohydrate from a low of 6.2% (Hokonui) and 7.3 % (Stampede), to around 16% at the time of final harvest (Fig. 2B). In addition, the organic matter digestibility and metabolisable energy was progressively lower as the crop matured. Utilisation of this material for grazing will ultimately depend on the seasonal requirements for feed, however these results show there are strong shifts in quality that need to be balanced against the requirement for high yield.

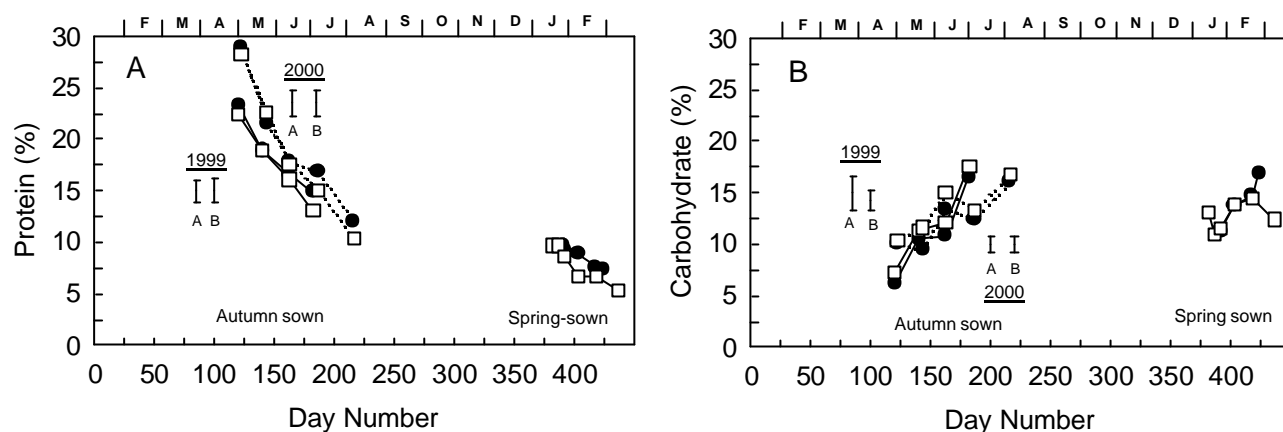


Figure 2. Protein (A) and carbohydrate (B) composition of autumn and spring-sown oat cultivars, Hokonui (·) and Stampede (9). Refer to Fig. 1 for details of symbols and error bars.

Table 3. Changes in quality of autumn sown herbage of Hokonui and Stampede oats for early (E) and late (L) harvests sampled on 1 May and 1 August, respectively.

Variable	Harvest	Year 1		Year 2	
		Hokonui	Stampede	Hokonui	Stampede
<u>Protein (%)</u>	E	23.3	22.4	28.9	28.3
	L	14.9	13.1	16.8	15.1
¹ LSD (a), P<0.05			2.13		2.56
LSD (b), P<0.05			2.36		2.64
<u>NDF (%)</u>	E	45.0	43.7	34.7	34.7
	L	40.6	41.4	44.4	44.6
LSD (a), P<0.05			5.51		2.60
LSD (b), P<0.05			1.93		3.10
<u>Soluble Carbohydrate (%)</u>	E	6.2	7.3	10.1	10.3
	L	16.5	17.6	12.4	13.3
LSD (a), P<0.05			3.31		1.68
LSD (b), P<0.05			1.82		1.67
<u>OMD (%)</u>	E	76.4	75.7	84.9	84.5
	L	76.0	76.2	76.4	74.4

Variable	Harvest	Year 1		Year 2	
		Hokonui	Stampede	Hokonui	Stampede
LSD (a), $P<0.05$			2.23		2.27
LSD (b), $P<0.05$			2.36		2.88
<u>ME (MJ/kg)</u>	E	10.5	1.9	10.4	11.7
	L	10.8	10.7	10.9	10.5
LSD (a), $P<0.05$			0.37		0.33
LSD (b), $P<0.05$			0.33		0.36

¹ Least significant difference for comparing cultivar x harvest means within year (a), $df=30$; except when comparing means within the same level of harvest (b), $df=30$.

Two cultivars only (Hokonui and Stampede) were included in analyses to examine year and harvest date effects on herbage quality. There was little difference in protein content, OMD or ME when comparing cultivars, however fibre levels (NDF, $P=0.01$; ADF, $P=0.006$) were reduced and carbohydrate levels increased ($P<0.001$) in Stampede when compared with the commercial standard (Hokonui). There were significant year x harvest interactions for all quality variables. Between-year differences in quality invariably had greater influence than the cultivar effects. For example, mean OMD on May 1 (H1) was significantly higher in year 2 (84%) than in year 1 (76%). Protein content was higher in year 2 than year 1 for all harvest dates. Fibre content was initially higher in year 1 (H1) but lower as the crops matured. The opposite pattern occurred for carbohydrate content. Levels were initially lower for the immature crop in year 1 than in year 2 but this was reversed in the mature herbage.

Table 4. Comparative quality of selected oat and triticale (Doubletake) cultivars in year 2 (autumn sowing).

Harvest/Cultivar	Protein (%)	NDF (%)	Carbohydrate (%)	OMD (%)	ME (MJ/kg)
<u>Harvest 1 (1 May)</u>					
Stampede	28.3	34.7	10.3	84.5	11.7
NZ-SAIA	30.7	35.0	9.3	85.0	12.0
MN94112	26.5	35.9	11.1	85.0	11.8
Doubletake	27.0	29.1	13.1	83.8	11.5
<u>Harvest 3 (10 June)</u>					
Stampede	17.6	40.7	15.1	80.8	11.4
NZ-SAIA	18.1	45.1	12.8	78.9	11.1
MN94112	17.5	44.5	12.8	79.4	12.1
Doubletake	18.0	40.6	12.0	74.6	10.4
<u>Harvest 5 (3 August)</u>					
Stampede	10.4	47.4	16.7	73.6	10.6
NZ-SAIA	10.9	57.7	13.7	67.0	9.8
MN94112	9.4	50.4	16.5	72.7	10.6
Doubletake	11.2	48.1	14.4	68.6	9.9
^a LSD (P<0.05)	(1), 2.11	2.55	1.72	3.63	0.51
LSD (P<0.05)	(2), 2.15	2.27	1.52	3.23	0.44

^a Least significant difference for comparing cultivar x harvest means within year (1), except when comparing means within the same level of harvest (2).

In year 2, quality was determined for six entries (Hokonui, Stampede, NZ-SAIA, MN94112, Doubletake and 4723.4) at three developmental stages (Table 4). Cultivar differences were significant ($P<0.001$) for all quality variables. Therefore, there are opportunities for improving the genetic base by selecting new and improved cultivars and also for managing cultivars for the appropriate level of quality required for grazing.

Spring sowing: Herbage quality of biomass from summer growth was significantly lower than material used for grazing in the winter period. Direct comparison between autumn-sown and spring-sown material is not valid given the crops were at different developmental

stages, grew in widely different environmental conditions and were intended for differing end uses. After flowering, mean protein content (mean of all cultivars) fell below 10% and declined to 6-7% at final harvest. Soluble carbohydrate (12-16 %) and NDF (53-61 %) of oats (Hokonui and Stampede) were 43% lower and 28% higher, respectively when compared with wheat and barley entries. The low carbohydrate was a direct consequence of the low harvest index (0.39-0.41) of oats, and the NDF content was higher and indicative of the coarse stem material in these cultivars. Likewise, protein content of oats was lower (6.3 vs 8.0%) and metabolisable energy lower (8.4 vs. 9.7 MJ/kg) than means for wheat and barley entries. These data were for final harvest samples taken at dry matter contents in excess of requirements for direct cut silage. Quality of herbage for ensiling would be improved if harvested at the appropriate time (~38% DM) (K. Bolsen, pers. comm.) when there is a significant amount of green leaf present. Harvesting of spring material (with higher digestibility and protein content) for silage after wilting been recommended as early as the boot stage, but the gain in yield and energy content from grain carbohydrate is compromised.

CONCLUSIONS

Determination of the scale of cultivar differences in yield and quality to environmental factors has assisted with the selection of improved material for grazing and silage. Cultivar choice should be made with consideration for the timing of production, best developmental stage for utilisation, and the quality specifications required by the grazing situation. Further definition of the comparative yield and quality differences among cultivars will ensure the best use of oats and other cereals from both farming system and nutritional perspectives.

Autumn-sown crops have high nutritive value early in growth. Optimum utilisation will include consideration of the increased yields achieved by delaying harvest. Irrespective of sowing time, there is a need to balance the requirements for increased yield and declining quality with crop maturation. Deviations on the pattern of growth responses to thermal time suggested that temperature-driven growth patterns may be used as a first step toward selection of lines with high forage potential. Variation in yield could also be accounted for by differences in light interception because of differences in canopy development or establishment. Differences in RUE were observed that could explain, for example, the improved biomass potential of Stampede, a newly released oat suited to autumn sowing. In spring-sown crops for silage, regular monitoring of yield and quality is required during the grain filling period. During this time there are rapid changes in moisture content and green leaf fractions. Further work is required to define the criteria for best use of biomass before the loss of nutritive value nearing crop maturity.

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THE IMPORTANCE OF OATS IN RESOURCE-POOR ENVIRONMENTS

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ABSTRACT

The impact of introduced western oat cultivars, used as livestock fodder, on people living in resource-poor areas of Asia over the past two decades has been remarkable. In Nepal and other areas along the Himalayas, greenfeed oats have helped significantly to alleviate starvation and improve nutrition. This success of this has stimulated the belief that even more can and should be done to help up-date these cultivars and bring new adapted oats and other improved greenfeeds to resource-poor regions throughout the world.

Key words: Oats, Asia, China, Nepal, Pakistan, Himalayas, greenfeed, impoverished regions, resource-poor environments, fodder oat network, forage crops in undeveloped, difficult and cool climatic regions.

INTRODUCTION

Resource-poor areas where oats have potential for poverty alleviation include lowland as well as highland areas stretching all the way from latitude 48° South (Chile and Argentina) to more than 60° North (the former Soviet Union). This includes many areas inhabited by poor minority groups living within larger ethnic majorities in Central and South America, the Horn of Africa, Nepal, Bhutan, Myanmar, Thailand, Indonesia, Cambodia, Laos, Vietnam, the Balkans, Central Asian Republics, South and North Korea for example.

Oats are or have the potential to become an important crop for improving the well being of millions of impoverished people dependent on livestock, who have either been passed by, or fall outside the main stream of international humanitarian aid or other development support. Oats have been shown to have great importance in countries that have been at war for many years, such as Afghanistan, and also in Bosnia and other trouble spots around the world, as well as emerging market economies including China and large areas of the former Soviet Union where they are used directly and/or crossed with local materials including local landraces (still in need of collection, documentation and preservation). More can and should be done to help up-date these cultivars and bring adapted oats and other improved greenfeeds to impoverished regions throughout the world.

Oats originating from New Zealand, Canada and Europe and introduced into Asia over the past 20 years continue to play a highly significant and strategically important role in feeding livestock across a wide range of ecologies, especially within the poorer regions of countries bordering the Himalayas, where they are used either as greenfeed or oaten hay. Considerable genotype by environment interaction has been noted across latitude/altitude/seasonal sequences, with some cultivars producing significantly better than others in certain areas / management regimes. So far, this is poorly documented and has only been modestly exploited due to limited local resources and lack of a regionally co-ordinated approach. Besides historic materials, more recently bred oat cultivars and previously discarded crosses never tested in these areas may have an important role to play in humanitarian relief, poverty alleviation and development throughout the developing world. This is, provided, they can be properly introduced and systematically evaluated, tested, multiplied, maintained, and disseminated / sold/traded. The same applies to legume companion crops such as vetches, peas and clovers.

This paper presents a case study from Nepal covering such materials, dating back to the 1950s, re-enforced with examples from Pakistan, Afghanistan and China, highlighting the need for and advantages of developing a co-ordinated international fodder oat network targeting resource-poor environments.

NEPAL

The increasing population in Nepal (presently more than 20 million inhabitants) has put severe pressure on domestic food production, arable land, forest resources and the environment in general. There has been and still is an on-going massive human migration from the hills to lowland areas, and from rural villages to the cities which has been precipitated by a combination of factors including long-term global climate changes, accelerated population growth, fragmentation of individual family land holdings and accelerated deforestation and degradation of arable and grazing land resources (Table 1).

There has been widespread drying up of natural streams, springs and seepage areas at all

altitudes combined with increased flooding, erosion and local climatic changes causing substantial areas of formerly cultivated land to be abandoned. This has been accentuated by the closure of borders with Tibet during the mid 1980s, which broke traditional co-habitation and summer migratory trading and grazing patterns, putting extreme year-round-pressure on already fragile high altitude grazing lands and catchment areas feeding some of the largest and most densely populated river systems in the world. Increased tourism as an alternative income source to traditional farming / livestock management has also put additional pressure on fuel wood supplies in these areas (Rajbhandari and Shah, 1981; DFAMS, 1986; MPFS, 1988 LMP, 1990).

Table 1. Thirty-year trends in human and animal population, and forest coverage in Nepal¹.

Decade	Human Population (‘000)	Animal Population (‘000 head)	Forest Area (‘000 ha)
1960s ²	9413	-	6500
1980s	15023	8226	6000
1990s	18600	8783	5500

¹Archives, His Majesty's Government of Nepal.

²Feudal system, pre land reform.

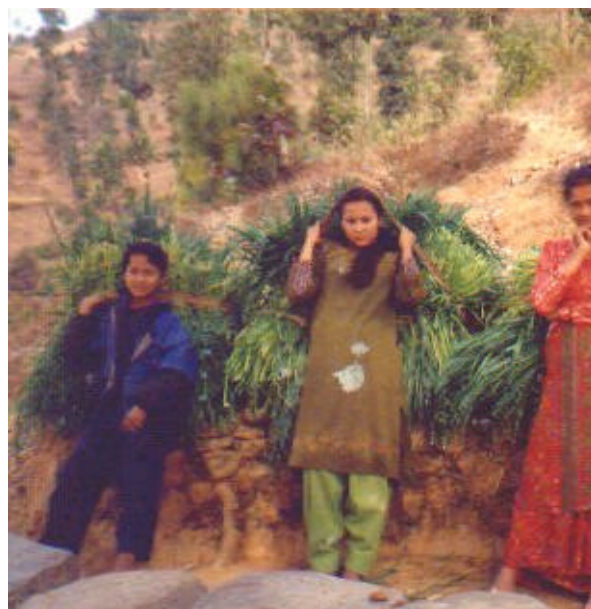
The average area of arable land farmed by a family has dropped from more than one hectare during the 1960s to less than 0.25 ha per family today. Many rural households (almost half) now have less than 0.18 ha, from which they can barely meet half of their staple food requirements. This is forcing impoverished families to become increasingly dependent on the government as well as communal forests and rangeland (FAO, 1992; Pariyar, 1992; HLFFDP, 1996). Other mountainland countries in the region are suffering the same pressures.

ROLE OF FODDER OATS IN NEPAL'S DEVELOPMENT STRATEGY

Resolving livestock forage and fodder constraints have dominated Nepal's development strategies for almost fifty years. During the pioneering 1950 - 60s era, rangelands were targeted for producing more milk and cheese from yaks and yak hybrids. With increasing environmental pressure, this changed to focus more on zero grazing / cut and carry systems targeting environmental conservation and sustainable land management covering a wider range of livestock classes and types, many and varied ecologies, and an increasingly diverse selection of fodder crops (including fodder legumes, oats and trees). Increased importance was given to this during the 1990s, as the widespread extent and seriousness of Nepal's ecological crisis began to emerge, particularly in the medium elevation (700 to 2,500m) and the high hill areas (above 2,500m).



Malaria control, plus forest clearing in lowland plain (Terai) areas of Nepal (below 500m) bordering India during the 1970s and 80s opened up new arable land for families from the adjacent middle regions, and the high hill areas (bordering Tibet). Dairying became popular in these lowland Terai areas where greenfeed oats quickly developed as a major source of winter and spring fodder (Photo 1). Building on this, fodder oat technology was then very successfully re-introduced into mid (400 to 2,500m) and high hills (above 2,500m) during the 1990s (Photos 2 and 3). Degraded forest and other government lands were leased to local families (1 ha / family, for 40 years, renewable) for re-development in conjunction with their traditional holdings, using legume-based rotations incorporating compulsory zero grazing / stall feeding and improved milk animals, especially buffalo (IFAD, 1990; Pariyar, 1996; Pariyar, Munakarmi, Shrestha and Mishra, 1999).



Photos 2 and 3. Greenfeed oats were successfully re-introduced into the mid and high hills and carry systems for stall feed and tethering animals, to spell degraded land and allow it to regenerate.

Protecting mid- and high altitude degraded land (400 to 2,500 and above 2,500m, respectively) from grazing animals by using stall feeding and tethering¹ as part of traditional rotations, allowed rapid regeneration of the indigenous vegetation and naturalised exotic species in economically viable ways under leasehold forestry. Within a three to five years, depending on altitude, degraded lands could again be producing more than 1 t/ha of dry hay (Paudel and Tiwari, 1992; HLFFDP progress reports 1998/99).

NEW ZEALAND BACKGROUND

Forage crop varieties sent from New Zealand to Nepal have played a significant role over the past 40 years for improving livestock nutrition and alleviating poverty. Fodder oats have been especially successful for zero grazing / stall-feeding which is environmentally friendly and normally practiced across a wide range of altitudes and ecologies from 400 to higher than 2,500m covering tropical / sub-tropical, temperate and continental climates. Very often, farmers have travelled for up to five days each way on foot to procure seed (Photo 4) to begin their own village multiplication and production programmes (Photo 5).



Photos 4 and 5. Farmers from remote areas often travel ten days on foot to collect and carry back fresh oat seed needed to establish and maintain their village seed multiplication programmes.

New Zealand's involvement with fodder improvement in Nepal started during the 1950s with the successful introduction and dissemination of Grasslands Huia white clover (Trifolium repens) in temperate zones 1,200 m and above, followed with Grasslands Maku lotus (Lotus pedunculatus in warm temperate and temperate transition zones 1,200 to 1,800m). Whero field pea (Pisum sativum) at all altitudes and various NZ ryegrass, clover and fescue cultivars (1,200m and above). Plus a range of fodder oat cultivars able to be grown successfully at all altitudes ranging from tropical / sub-tropical winters in lowland areas through to high alpine summers above 2,500m, usually mixed cropped with one of several vetches (Vicia sativa, or Vicia faba), field pea (Pisum sativum) or grass pea (Pisum lethyris) depending on altitude. NZ DSIR (now NZ CFRI) has been the major

¹ Made possible by introducing fodder oats on to adjacent arable land, mixed cropped with legumes.

supplier of research samples / quantities of these seeds (donated), combined with commercial importations made by the Food and Agricultural Organisation of the United Nations, Asian Development Bank and various other projects. Supporting research and extension has been provided by the Nepal Agricultural Research Centre and HMG Ministry of Agriculture as implementing partners.

The greenfeed oat types sent (Table 2) focused on rapid early growth and a good yield of herbage under the cool, low fertility conditions comparable to those often experienced during the Canterbury, New Zealand winters. G.M. Wright, at Lincoln, bred most of the NZ cultivars sent. The lines designated Can/NZ were derived from crosses made in Canada but selected for New Zealand conditions by M. McEwan at Palmerston North, as part of a collaborative agreement.

Table 2. Origin of Oat Cultivars sent to Nepal from New Zealand in the mid-1980s.

Cultivar / Line	Origin	Maturity	Breeding History	Characteristics in New Zealand
32302	NZ	Med	Ohau/Lyon	Med-tall, broad leaved, cold tolerant
346/2	NZ	Med	Goodland/Omihi//293	Med-tall, broad leaved, Good DM yield.
83 Inc 19G3	Can/NZ	Med	Unknown	Good biomass Broad leaves.
Amuri	NZ	Med	3mf/VR Algerian	Good winter greenfeed cultivar. Short straw. Tolerant to BYDV
Awapuni	Can/NZ	Med	Unknown	Good crown rust & BYDV res. Not cold tolerant. Good grain yield.
Canadian	Can/NZ	Med/Late	Unknown	Broad leaved. Very high DM yield. Good grain yield.
Caraville	France	Med	Unknown	Black hulled. Not cold tolerant. Used for greenfeed in NZ.
Charisma	NZ	Med	Firecracker/Oreti	Good utility oat. Cold tolerant.
Kent	UK	Med	Unknown	----
Swan	Aust	Early / Med	Unknown	Narrow leaves. Not cold tolerant.
Makuru	N.Z.	Med	Forward/Milford	Main NZ milling/utility oat from its release as Mapua in 1953 until 1990's.
Taiko	NZ	Med	Complex cross Based on Onward	Main NZ black oat used for chaffing. Broad leaves. Med-short straw.

ACHIEVEMENTS

Donated and purchased oat materials from New Zealand were first multiplied and then tested and evaluated across a range of altitudes / ecologies during the 1980s and 90s, from 400 to above 2,500m under a series of on-farm, farmer managed, and research station trials, plots and socio-economic surveys. These were variously supervised by technicians from the Nepal Agricultural Research Centre, HMG Ministry of Agriculture, and FAO and Asian Development Bank Projects. Representative examples of data generated from mid altitude zones (400 to 2,500m) / dairy pockets are given below (including Table 3; Pariyar et.al., 1999) and discussed. Green fodder and/or oaten hay produced from these cultivars were usually chopped by hand and fed mixed with other crop residues such as dried grass, wheat and maize straw. Resulting animal wastes mixed with livestock bedding materials were returned to the land as farmyard manure according to established farmer practices / customs. The basal fertilizer application was 5t/ha of farmyard manure. Fertiliser treatment was either 15:50:0 kg/ha of NPK or zero. There were significant differences between the overall performance of cultivars at two of the three sites, and at all three sites for fertilizer treatments (Table 3), suggesting significant differences in agro-ecological adaptation. Across-site comparisons were not made. These data could not be properly compared with other data on record, due to limited computer and other resources for detailed field research and data analysis. International assistance is needed urgently.

Concurrently (1996-98), a series of on-farm crop-cut surveys was made of farmer-planted and -managed crops involving more than 1000 families farming between 400 and 2,500m above sea level in four districts of central Nepal (Makawanpur, Kavre, Sindhupalchowk and Ramechhap), using one or more of these cultivars of fodder oats grown as a single crop and/or mixed cropped with vetch, grass pea or fodder pea. Trials were replicated across farmers within and across altitude sequences, with and without fertilizer chemical fertiliser (40:60:0 kg/ha NPK) using a split plot design applied over normal farmer basal application rates of farm-yard manure / forest litter (10 t/ha). Activities were organised and implemented jointly by Nepal Agricultural Research Council (Pasture and Fodder Research Division) and the Hill Leasehold Forestry and Forage Development Project (HLFFDP Progress Reports, 1998/99).

Table 3. Performance (green weight t/ha) of different cultivars of oat, with and without fertilizer applied in farmer's fields within dairying areas of Rupendehi, Kaski and Illam (Nepal, during 1996-98.

District / Altitude Zone	Rupendehi ()						Kaski ()						Illam ()					
Year	1996		1997		1998		1996		1997		1998		1996		1997		1998	
Fertilizer/ Cultivar	F	NF	F	NF	F	NF	F	NF	F	NF	F	NF	F	NF	F	NF	F	NF
Caraville	32.8	22.7	33.5	28.0	22.0	18.3	24.0	15.3	19.5	14.0	29.5	15.0	32.9	23.7	17.7	15.0	26.3	18.0
83INC 19G3	29.3	22.3	31.5	33.0	17.7	18.3	29.3	20.3	15.7	11.0	26.5	15.0	39.3	25.3	14.3	10.0	24.6	17.0
Canadian	36.3	24.7	29.2	27.0	16.8	13.7	30.0	21.3	17.8	14.0	27.5	16.0	35.0	24.0	17.7	14.0	26.0	19.0
Awapuni	40.3	22.7	29.8	26.0	29.0	13.3	25.3	18.3	15.0	10.0	26.5	13.0	29.7	21.0	13.5	8.0	23.3	16.7
Charisma	29.3	24.6	30.5	28.0	28.3	19.3	24.7	16.0	19.6	16.0	24.5	19.0	31.3	21.0	7.8	6.0	18.7	14.0
Taiko	40.3	30.6	29.3	24.0	16.0	15.5	33.9	23.7	17.5	11.0	28.0	16.5	35.3	24.0	15.7	12.5	22.7	17.0
Kent	31.0	29.0	28.8	32.0	27.0	20.0	27.0	20.9	17.0	9.0	28.5	16.0	39.7	26.0	18.8	14.0	21.3	14.7
Swan	36.0	30.4	28.0	26.0	26.0	15.0	25.9	16.9	19.0	13.0	20.5	13.0	33.7	22.7	16.1	10.0	25.0	19.1
F-test																		
Cultivar	**						*						NS					
Fertilizer	***						***						***					
CV%	3.54						4.25						5.58					
Lsd at 0.05	1.15						0.96						1.4					
Note: Fertilizer Treatment - (F) 5 t/ha farm yard manure plus 15:50:0 NPK (NF) Zero																		

Key findings were that:

In many, but not all instances, more recently bred cultivars out-produced older ones.

Oat/vetch combinations produced on average 25 t/ha of green material compared with 21 t/ha from oat plus pea mixtures and 20 t/ha from pure oat stands within the 400 to 800 m band.

Significantly higher yields (up to three times these quantities) were produced within the 900 to 2,500m band compared with lower altitude zones, possibly reflecting better agro-ecological adaptation, but also higher in-coming radiation levels along the margins of the monsoon rain belt, above and/or beyond the foot hill temperature inversion layers typified by many months of low-lying fog bordering the adjacent plains of Nepal (Terai zone) and India.

Using oat/vetch mixtures increased milk production by 30 litres per animal per month on average, compared with traditional practices. At the same time, the demand for purchased concentrates was reduced by 30 kg / month and milk production was extended by an extra eight weeks. This translated into an additional net profit of 1,538 Ruppees per month (USD 22) under conditions where on average, the total cash income of families was USD 264.

Not all milk was sold; additional production increased family dietary quality substantially over traditional practices, especially important for the young and the aged. (Milk and milk products are valued dietary constituents in this culture.) Fodder oat, vetch and pea seed was also produced for family use, bartering and for sale, represented an additional advantage.

Compared with wheat and barley, the traditional sources of arable green fodder, fodder oats provided multiple cuts, yielded more, and are of higher nutritional value. Furthermore, they proved more flexible for specialised uses in local management systems where time-isolation was needed to produce commercial maize seed, high-value vegetable crops and other seed crops. A major reason for this was that the standing oat crop could be harvested progressively, releasing land earlier than normal for follow-up crops or relay cropping. Late in the season, any remaining standing crop could be cut at the farmer's discretion and dried as oaten hay, just as the monsoon was starting. This coincided with optimum soil moisture for land cultivation and the planting of the next crop. This also allowed small areas or peripheral lines on terraces to be saved for seed for the next season's crop. Managerial flexibility introduced in this way often made the difference between success and failure, good or bad summer crops, especially at the marginal higher altitudes on the fringes of the monsoon belt, where irrigation was not possible, or restricted.

N and P fertiliser gave substantially higher yields than using FYM alone, especially on seriously depleted soils which had been monocropped for many years with wheat / maize / rice. However, increased usage of chemical fertilizer could not realistically be justified in many instances for economic as well as logistical reasons since most inputs had to be carried on people's backs along narrow foot tracks, often across steep terrain. Nepal has no indigenous commercial sources of artificial nitrogen or other inorganic fertilizers, is seriously short of foreign exchange, and farmers lack seasonal credit. Soils are mostly pre-weathered, heavily leached and seriously deficient in phosphate. Fertilizer usage is often limited to areas within one- to one and a half days walking distance of road heads, where it can be purchased and back loaded with porters carrying out milk / milk products. Beyond this, it was not economic to transport chemical fertilizer for use on fodder oats.

More detailed analysis although needed, was not possible due to limited computer and other research resources including formal international linkages.

PAKISTAN AND AFGHANISTAN

Western fodder oat cultivars from Canada, Australia, New Zealand and Europe form the basis of Pakistan's fodder oat improvement programme which, dates back to the British era and includes materials (comparable to those supplied to Nepal) donated by NZ DSIR / NZ

CFRI in 1979 then up-dated during the mid 1980's both directly with NARC (National Agricultural Research Centre) which has the national mandate in oats, and through the FAO Across Border Agricultural Assistance Programme for Afghanistan. These materials were augmented by commercial importations made under the WB for Azad Kashmir during the late 1970s and the FAO Afghan Programme during the 1980s which, arranged for these materials to be further multiplied in the private sector in Pakistan under Government supervision (Seed Certification).

Fodder oats from these sources have been grown and used routinely by resource-poor farmers, commercial dairy units and the army in Pakistan in lowland as well as hill areas for 20 years, as green fodder (and some oat hay), and in Afghanistan by returning refugees, internally displaced persons and local residents since the mid 1980s. Depending on altitude and where they fitted into the rotation, they have usually been mix cropped with a range of locally adapted clovers, vetches, alfalfas, medics or brassicas, to improve traditional fodder yields in terms of quantity, quality and seasonal availability, grown as an alternative to barley, wheat or one of the forementioned fodder crops grown by itself.

Oats are especially important on the plains during the cooler autumn, winter and spring months and in the mountains during autumn, spring and early summer. Reported yields of green fodder and dry matter are generally higher than in the lowlands and mid hills of Nepal (up to three times using comparable varieties which include locally bred / selected materials of western origin), due mainly to better inherent soil fertility combined with the widespread use of chemical fertilizer and higher in-coming radiation (less fog and cloud cover).

In Afghanistan, oats have proved to be invaluable for feeding animals, especially those in milk, not able to use traditional grazing lands because of landmines. They were also of great importance where traditional cropping routines had been disrupted by war. Often the age-old irrigation systems had either been destroyed or had fallen into disrepair. Families were without their menfolk, impoverished and displaced. Available and safe cropping area had been diminished, the population was at the mercy of unreliable and highly seasonal rainfall and seldom able to harvest their grain crops. Under these circumstances, the people were even more dependent on livestock and fodder for their survival and very vulnerable to the vagaries of war.

CHINA

China has a long history in selecting and using local oat landraces, and in modern times, especially the last twenty years, breeding and testing improved cultivars incorporating materials from the same western sources as those successfully introduced into Nepal and Pakistan. Oats are now the main source of winter and spring forage in the higher and colder regions, especially Xinjiang, Inner Mongolia, Qinghai, Gansu, Heilongjiang, Jilin, Tibet and Shanxi Provinces. They are grown on more than 35% of the available arable land of northern Inner Mongolia and over 15% of the arable area of Gannan, Dixi, and the Linxia prefectures of Gansu. Grain yields vary from 2.4 to 3.2 t/ha in the better environments but, less at higher altitudes (3000m). Green weight yields range from 40 to 80t/ha. In Gannan at an altitude of 3500m the highest recorded yield was 12t/ha greenweight.

CONCLUSIONS

Modern oat cultivars are not reaching millions of needy people in resource-poor environments, particularly in populations with minority groups, and in areas of the world

where the people survive in difficult environments. Landraces and inferior cultivars bred and released decades ago continue to be grown. New and improved material, although available internationally, cannot be easily or legally introduced or circulated, because of the absence of proper mechanisms, financing and networks, especially in small nations and/or minority areas which lack resources to develop their own breeding programmes.

There is an urgent need to launch and develop a globally co-ordinated forage and fodder oat programme for resource-poor regions of the world, to up-date and disperse suitable, modern oat cultivars through the CGIAR and other networks, along comparable lines to those which have been in place and operating globally since the late 1970s, for wheat, barley, maize, pulses, selected vegetables and other cash crops. Serious consideration should be given to bulking up and systematically evaluating past fodder oat crosses derived in New Zealand, Canada and Europe with good re-growth potential, never advanced due to poor seed yield characteristics, because some of them will undoubtedly have substantial application in developing countries / ecologies where seed yield is secondary to green fodder production for resource-poor farmers. Care should be taken while doing this to replicate tests / evaluations properly across altitude / latitude / planting date / management sequences at national, regional and international levels using well known, internationally recognised and established cultivars as standards, besides locally recommended cultivars and farmer choices.

Plant breeding alone will not be enough. A hands-on, multi-disciplinary, integrated approach is needed including, livestock improvement, small-scale direct seeding equipment and other appropriate mechanisation and seed supply systems. The organisation should involve representatives of the countries in need, plus the international community working with oats and other greenfeed crops. ILRI (International Livestock Research Institute), we feel would be an ideal international focal point for the proposed initiative (network), to be established and managed in co-operation with other international and national agencies, etc. throughout the world with the combined objectives of:

- Attracting donor funding (in cash and/or kind).
- Successfully linking the network with recognised United Nations and other educational and technical organisations, agencies and institutions mandated to work within targeted areas for humanitarian relief, rehabilitation and development.
- Suitably endowing the network with a portfolio of oat breeding materials, guidelines and finished cultivars keeping in mind that plant variety rights would probably have to be negotiated by the network as an integral part of releasing them to needy countries, through the network.

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(www.semec.ws/wintersteiger.htm), Hege Maschinen on-line™ (www.semec.ws/hege.htm), Svalov Weibull (www.swseed.ca) and the New Zealand Crop and Food Research Institute (www.crop.cri.nz) confirm their willingness to support this initiative.

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AMINO ACID AND PROTEIN ANALYSES IN THE KERNEL OF NAKED OAT CULTIVARS

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ABSTRACT

A study was made on the protein- and amino acid contents and their relationships in oat cvs Obraztsov chiflik-4 (hulled and kernel), Mina, Adam, Rhiannon, Tibor, Caesar, 83106110 and 83106111 (locals from VIR) and 89106245 (a local from Austria). The protein was correlated only with cystine - $r=0,57^*$. Around 40 significant correlation coefficients among the amino acids were established. A correlation with only one amino acid was found for lysine - with glycine and isoleucine - with histidine. The multiple linear correlation analysis showed that arginine was the most powerful, participating in 6 equations. Although the year differences in the protein content among cultivars were great, they equalized when considered over a long period (8 years) of cultivation. The amino acid distribution remained stable. The environmental conditions proved to have less influence on cvs Mina, Rhiannon and the two locals from VIR. High-yielding mutant lines, containing up to 25% protein and 7% lysine, were identified.

The naked oat is a comparatively new crop, still hardly making its way into practice. This is due to a lot of reasons, the most important of which is, unfortunately, its low production efficiency. Therefore, the interest to this crop could be increased only in regions where the price of its application focuses on the qualitative traits of the grain, on the one hand, and satisfies the producers, on the other. In 1994, it was developed the first and still the only Bulgarian naked oat cultivar Mina. It is medium early, productive, with a grain of healthy appearance due to its low susceptibility to *A. alternata* and *A. tenuissima*. In favourable years, with sufficient precipitation during vegetation, its absolute yield reached 520 kg/dka. Under such conditions, the yields of hulled oat cultivars were around 800 kg/dka, or by 35% higher than those of the naked ones (Antonova et al., 1995).

The versatile use of oat in human- and animal nutrition, based mainly on its valuable biochemical properties, including the balanced amino acid composition, is a good reason for its being initially used as a substitute for more expensive products, as well as in medicinal preparations (Frej 1973, Georgieva et al., 1995, Valentine 1990). This predetermines the current necessity for investigations on the amino acid composition of proteins in the kernel, and their interrelationships, as well.

MATERIAL AND METHODS

Mean seed samples, obtained from a competitive varietal test in the Institute for Introduction and Plant Genetic Resources "K.Malkov", were used for the study. The content of amino acids was monitored for 4 consecutive years, and only that of protein and lysine - for 8 years. The following cultivars were studied: 1. Obratzov chiflik-4 (hulled); 2. Obratzov chiflik-4 - kernel, Bulgaria and the naked oats; 3. Mina - Bulgaria; 4. Adam - Ceska; 5. Rhiannon - UK; 6. Tibor - Canada; 7. Caesar - Germany; 8. 88106110 and 9. 88106111 locals from VIR; 10. 89106245, local from Austria; 11. Mina - hulled grains; 12. Mina - kernel of hulled grains. The selection of cultivars was made according to their significance for breeding. The same cultivation technology was applied in the separate years.

The amino acid content was determined holographically by means of an AAA-881 amino-analyzer, on Nx6,25 by the Kjeldahl method. The amino acids are marked in the following way: x1 - lysine, x2 - histidine, x3 - arginine, x4 - aspartic acid, x5 - threonine, x6 - serine, x7 - glutamic acid, x8 - proline, x9 - glycine, x10 - alanine, x11 - half cystine, x12 - valine, x13 - methionine, x14 - isoleucine, x15 - leucine, x16 - tyrosine, x17 - phenylalanine, x19 - sum of essential-, x20 - sum of sulfur-containing-, and x21 - sum of aromatic amino acids and γ -protein.

The correlation analysis was conducted by the methods of Dewey R.D. (1959) and Gary M.N. (1979), and the multiple correlation analysis after Drajer N. & G.Smith (1973) - by the step-wise regression method.

RESULTS AND DISCUSSION

The mean values of amino acids in the cultivars studied, with some insignificant exceptions, almost did not differ from those reported by other authors (Peterson, 1976; Robbins et al., 1971; Welch, 1995).

Table 1. Amino acid composition

Amino acid	Mean	Range
1.Lysine	4,08±0,02	0,23
2.Histidine	2,49±0,04	0,57
3.Arginine	7,27±0,05	0,6
4.Aspartrtic acid	8,65±0,06	0,72
5.Threonine	3,76±0,03	0,29
6.Serine	5,19±0,04	0,49
7.Glutamic acid	22,1 ±0,15	1,93
8.Proline	5,29±0,05	0,57
9.Glycine	4,05±0,02	0,31
10.Alanine	4,64-±0,03	0,47
11Half cystine	2,57±0,06	0,69
12.Methionine	1,50±0,05	0,62
13.Valine	5,01±0,02	0,26
14.Isoleucine	3,69±0,02	0,26
15.Leucine	8,42±0,07	0,81
16.Tyrosine	3,85±0,03	0,32
17.Phenylalanine	5,62±0,06	0,64
18.Protein	19,23±0,53	6,51
19.Σ of ess.am.	38,51-+0,1	1,26

With these initial data, we conducted correlation and regression analyses and established that valine, tyrosine and phenylalanine did not correlate with any of the amino acids. A correlation with only one amino acid was established for lysine - with glycine, isoleucine - with histidine, and the only protein relation with cystine. The total number of significant correlation coefficients among the amino acids was around 40. The most frequent correlation was found for alanine - with a total of 11 amino acids.

The following regression equations were developed:

$$x_1 = 3,01 + 0,27x_6 \quad D=0,22$$

$$x_2 = 3,01 - 0,78x_{10} + 0,84x_{14} \quad D=0,75$$

$$x_3 = 0,30 + 0,66x_4 + 0,74x_5 - 0,91x_6 + 0,61x_8 \quad D=0,85$$

$$x_4 = -0,66 + 0,73x_3 + 1,06x_5 \quad D=0,86$$

$$x_5 = -0,40 + 0,35x_{10} + 0,29x_4 - 0,06x_7 + 0,39x_{14} \quad D=0,92$$

$$x_6 = 1,30 + 0,90x_{10} - 0,01x_7 \quad D=0,90$$

$$x_7 = 3,10 + 1,65x_3 + 1,31x_8 \quad D=0,68$$

$$x_8 = 0,20 + 0,60x_{15} \quad D=0,60$$

$$x_9 = 9,41 - 0,24x_7 \quad D=0,32$$

$$x_{10} = 0,90 + 0,21x_3 + 0,51x_6 - 0,31x_{12} \quad D=0,94$$

$$x_{11} = 8,04 - 1,45x_5 \quad D=0,61$$

$$x_{12} = 6,66 - 0,61x_{15} \quad D=0,72$$

$$x_{14} = 2,44 + 0,22x_{17} \quad D=0,26$$

$$x_{15} = 6,71 + 0,55x_8 - 0,82x_{12} \quad D=0,81$$

$$x_{16} = -1,19 + 0,06x_2 - 0,03x_3 + 0,05x_{19} + 0,91x_{21} - 1,0x_{17} \quad D=0,99$$

$$x_{17} = -1,22 + 0,06x_2 - 0,03x_3 + 0,05x_{19} + 0,91x_{21} - 0,99x_{16} \quad D=0,99 \text{ or}$$

$$x_{17} = -0,60 + 0,05x_2 - 0,04x_3 - 0,02x_9 + 0,04x_{19} + 0,93x_{21} - 1,0x_{16} \quad D=0,99$$

$$x_{19} = 31,78 + 1,45x_{17} - 0,35x_9 \quad D=0,77$$

$$x_{21} = -0,90 + 1x_{17} + 0,03x_{17} + 0,99x_{16} + 0,05x_9 \quad D=0,99$$

A different number of independent variables - from 1 to 6, were involved in the equations developed. Unlike the protein, a significant relationship existed among the amino acids. On the basis of the 8-year investigation on the protein- and lysine variation in 8 naked oat cultivars, the average protein content for the period was found to be between 20 and 21%, that of lysine - from 3% (891106245) to 4,2% (Mina), i.e., under equal other conditions for a longer period of time, the differences in the grain protein content between the genotypes equalized, irrespective of the fact that these differences between the separate years were significantly greater. The environmental conditions had less effect on the protein of cvs Mina, Rhiannon and the two locals from VIR. The data for lysine almost confirmed those for protein; only for number 89106245 the negative difference was significant at 1% level of significance. Small differences among cultivars, grown under equal conditions, in terms of their protein and lysine contents, were reported also by Welch (1995). The distribution of the other amino acids in the grain, in result of their genetically determined stability, remained unchanged, which was confirmed with cv. Mina (Peterson, 1976).

As amino acids, with their balanced and constant composition, are the main qualitative index for the protein value of oats, the protein quality is the main reason for oat importance in human and animal nutrition (Georgieva et al., 1997; Penkov, 1997; Penkov et al., 1999). A protein-amino acid relationship was reported by Campell (1996), Robbins et al. (1971), and Welch (1995). In our experiment, the protein was in a moderately significant correlation only with cystine - $r=0,57^*$. We also attributed this fact to the lack of significant differences in the growing conditions, and the genetic determination of cultivars which was not expressed to the extent of being able to affect the relationships between protein content and amino acids. Although the cultivars differed in the level of their protein content by about 30%, under conditions where moisture was not a limiting factor, it did not correlate with the amino acids. Therefore, in the breeding for increased protein content, due to the stable composition of amino acids, there is no risk of deteriorating their balance. Probably, under more intensive conditions, with increased N and P fertilizer application and other factors, an increased protein content could be observed, but the differences in its quality could be related to quantitative changes in the protein fractions (Welch, 1995).

In the course of work, mutant naked oat lines were identified, in which the negative grain yield/protein content correlation was overcome to a different extent. Some lines showed also an increased lysine content (Table 2).

The overcoming of the breeding press toward improvement of grain quality should not be taken as a compromise with other useful objectives (McFerson and Frey, 1992; Schipper and Frey, 1992). The management of the breeding process could be based only when genetic resources of independent genes, encoding high protein quality, are found.

Table 2. Promising naked oat lines

Line number	Grain yield	Protein	Lysine
	%	%	%
1. 18/20/58/1	103	116	100
2. 110/21	106	118	100
3. 110/48	109	111	102
4. 18/20/60/12	111	114	100
5. 115/44	115	109	100
6. 110/46	119	123	107
7. 115/50	119	116	100
8. 120/20	121	102	105
9. 115/14/2	124	124	107
10. 7x5/39/3	137	104	107
11. 7x15/46/11	138	125	90

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EFFECT OF MANURE-N ON NUTRITIONAL VALUE AND DIGESTIBILITY OF ORGANIC GROWN OATS IN DENMARK

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SUMMARY

In Denmark, field trials were performed in 1997, 1998 and 1999 in order to investigate the effect of liquid manure nitrogen (0-120 kg / ha) on both quantitative (yield) and qualitative (nutritional value and digestibility) parameters of two hulled and three naked organically grown oat varieties.

The results indicate that the organically grown naked oat varieties performed as well as the hulled varieties but that nutritional value and digestibility is less influenced by the nitrogen application than by seasonal variation. In addition, the measured quality parameters show that the naked oat varieties investigated are superior to hulled oats, but at the cost of lower grain yield.

INTRODUCTION

In Denmark, conventionally husked oats has not been grown for feed in pig, poultry and livestock production because of the high hull content, which lowers digestibility and the overall nutritive value. Therefore, naked oats is becoming a potential new crop for use in organic farming. Here, the hull content is approx. 5% as compared to 25-30% in conventional husked oats.

The primary agronomic drawback for naked oat compared with hulled varieties lies in the resulting lower yield, which is unacceptable for conventional farming practices due to economic constraints. Organic farmers on the other hand have to know the history of the feed, need to produce the feed on the farm, and may use naked oats to replace soybean as protein source in feed formulations.

In organic farming systems, the availability of nitrogen is limited, and in organic pig farms in Denmark typically supplied as liquid manure. In addition, sound rotation practices for disease control is an important aspect of organic farming and oats has a different disease pattern compared to wheat and barley and are able to break the disease pattern of the field.

The aim of the present study was to investigate both the quantitative (yield) and qualitative (nutritional value and digestibility) repercussions of nitrogen applied as liquid manure to organically grown oats.

MATERIALS AND METHODS

Field experiments were established in 1997, 1998 and 1999 at the Research Centre Flakkebjerg (55°19'00"N 11°24'00"E) of the Danish Institute of Agricultural Sciences on a sandy loam soil which contains approximately 14% clay (< 2 µm), 24% silt (2-63 µm), 60% sand (63-200 µm) and 2% organic matter. The five oat varieties in the trial were the conventional varieties *Floriant* and *Rise* and the naked varieties *Rhianon*, *Salomon* and *Bullion*. Nitrogen equivalent to 0, 40, 80 and 120 kg / hectare was injected as liquid manure in the soil between rows immediately after sowing. The trial was sown in blocks with four replications of each variety/nitrogen combination. After yield determination (t/ha, 85% DM) and correction to 15% moisture content, grain samples were taken from each plot for analysis. The chemical grain analysis was done on dry matter basis without further preparation or dehulling. The following parameters were detected: ash (AOAC, 1990) and crude fibre content (Tecator, 1978); enzymatic prediction of the digestibility of organic matter in feedstuffs and feed mixtures for pigs by *in vitro* analysis (EFOS, Boisen, & Fernandez, 1992). Insoluble and soluble dietary fibre were determined by a rapid enzymatic assay and protein calculated as 5.7 x total N analysed by the Dumas combustion technique (Hansen, 1989). Gross energy was measured according to (LECO, 1987), fat as ether extract (Arbejdsmetoder 1958; Stoldt, W. 1952.) and starch content detected by standard spectroscopic methods (Åman and Hesselman; 1984). Statistical treatment of the resulting data included analysis of variance (ANOVA) followed by Duncan's means comparisons test.

RESULTS AND DISCUSSION

Results of the quantitative parameters grain yield, test weight and thousand-kernel weight (TKW) are shown in Table 1. The low mean grain yield of only 3.3 t / ha in the 1997 harvest was due to a significant grain loss following a late harvest. The grain yield of 1998 and 1999 was more than 5.0 t / ha and was due to better harvest conditions. All three varieties of naked oat yielded significantly less grain than the conventional oats (Table 1). Conventional oats had a significantly lower test weight and higher TKW than the naked oat varieties. Up to 80 kg N / ha increased the yield significantly whereas the TKW decreased with increasing N fertilization.

Results of the seasonal influences, variety as well as applied N-amounts on the quality parameters are shown in Table 2. Significant seasonal variation influenced all measured parameters, but not as much as the variance between cultivars. The naked oat varieties showed a significantly increased digestibility of organic matter (EFOS) and higher protein, fat, starch, soluble fibre and energy content compared with hulled oats, where, by contrast, the content of insoluble and crude fibre and total ash decreased. Increased N application resulted in both significant increases of protein and energy contents and decreases in fat and starch content. The amounts of (in)soluble and crude fibre were unaffected as was the digestibility of organic matter (Table 2).

In summary, the results indicate that the quality parameters analysed were less influenced by the N application than by seasonal variation. In addition, the quality of the naked oat varieties under investigation was found to be superior to those of common hulled oats but at the cost of lower grain yield. Based on these results both common and naked oats seem to be well adapted for organic feed production with limited access to nitrogen fertilizer-use.

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Table 1. Mean grain yield, test weight and thousand kernel weight (TKW) in response to year, variety and N application as liquid manure. Means followed by the same small letter are not significantly different at $P \leq 0.005$ as determined by Duncan's multiple range test.

	Yield		Test weight TKW	
	t/ha		g/l	g
Year				
1997	2.48	c	625.6 b	22.46 b
1998	5.32	a	662.1 a	14.39 c
1999	5.05	b	570.7 c	24.92 a
LSD	0.25		6.8	0.51
Variety				
Florian ¹	5.04	b	565.0 c	22.31 b
Rise ¹	6.54	a	485.1 d	29.38 a
Rhianon ²	3.66	c	614.9 b	17.80 e
Salomon ²	3.96	c	658.2 a	20.53 c
Bullion ²	3.94	c	664.8 a	19.50 d
LSD	0.35		9.6	0.72
N in liquid manure (kg / ha)				
0	3.65	c	616.6 b	20.97 a
40	4.22	b	627.8 a	20.86 a
80	4.57	a	618.8 b	20.40 ab
120	4.67	a	614.3 b	20.15 b
LSD	0.29		7.8	0.58

LSD: P=0.005 level

¹Hulled varieties; ²naked varieties

Table 2. Mean grain content of protein, ether extract fat, insoluble and soluble fibre, crude fibre and total ash, EFOS (enzymatic prediction of the digestibility of organic matter) and energy. Means followed by the same small letter are not significantly different at $P \leq 0.005$ as determined by Duncan's multiple range test.

	Protein (N*5.7)	Ether extract fat	Starch	Insoluble fibre	Soluble fibre	Crude fibre	Total ash	EFOS	Energy
	g 100g ⁻¹ dm								gkal/g
Year									
1997	13.22 a	7.6383 a	56.819 b	11.403 b	3.9153 b	3.6740 b	2.0902 b	90.461 a	4824.71 a
1998	11.80 b	7.2898 b	59.010 a	12.367 ab	3.6654 c	3.8230 b	2.2057 b	89.568 a	4723.21 c
1999	12.04 b	6.6105 c	58.696 a	13.630 a	4.4203 a	4.6177 a	2.5413 a	88.148 b	4771.28 b
LSD	0.33	0.2627	1.021	1.396	0.1965	0.5047	0.1390	1.298	18.96
Variety									
Floriant ¹	9.87 d	5.5154 d	50.209 d	24.292 a	3.4428 d	9.0215 a	2.5241 a	76.414 c	4683.01 c
Rise ¹	10.47 c	5.3750 d	52.687 c	24.119 a	3.7688 c	9.2019 a	2.6694 a	76.706 c	4699.38 c
Rhianon ²	12.82 b	8.3698 a	59.868 b	9.515 b	3.8425 bc	2.8056 b	2.1244 b	92.410 b	4825.04 a
Salomon ²	13.45 a	7.6866 b	59.675 b	8.752 bc	4.5177 a	2.3500 bc	2.2192 b	93.882 ab	4796.12 b
Bullion ²	13.35 a	7.1996 c	62.189 a	7.259 c	4.0987 b	1.8751 c	2.2000 b	94.919 a	4783.90 b
LSD	0.47	0.3706	1.442	1.972	0.2775	0.7129	0.1964	1.832	26.78
N in liquid manure (kg/ha)									
0	11.62 c	7.3204 a	59.313 a	11.733 a	3.9375 ab	3.8625 a	2.225 ab	89.870 a	4767.96 bc
40	11.61 c	7.1196 ab	58.492 a	12.851 a	3.8502 a	4.2546 a	2.3331 ab	88.714 a	4752.63 c
80	12.80 b	7.2611 ab	58.661 a	11.969 a	4.0944 b	3.8552 a	2.1925 b	89.945 a	4790.77 a
120	13.67 a	7.0106 b	56.176 b	13.333 a	4.1289 b	4.1883 a	2.3689 a	88.100 a	4782.14 ab
LSD	0.38	0.3033	1.179	1.612	0.2269	0.5828	0.1606	1.500	21.90

LSD: P=0.005 level

¹Hulled varieties; ²naked varieties

RISK PERCEPTION AND RISK COMMUNICATION ABOUT FOOD – SOME REASONS WHY PEOPLE MAY NOT EAT OATS

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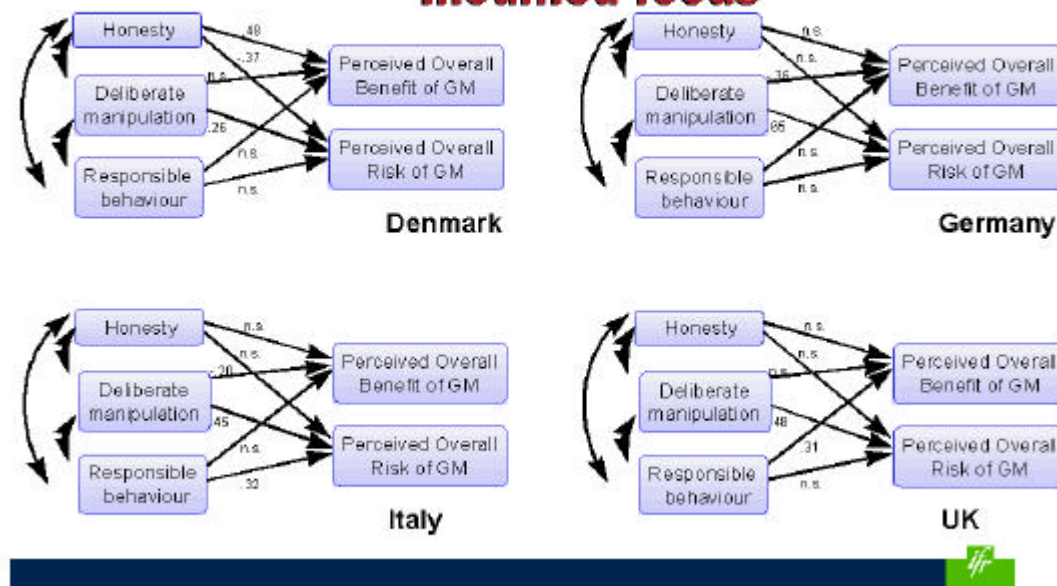
The public have become increasingly concerned about the risks associated with food. Public concern about genetically modified foods, BSE, emerging pathogens such as E-Coli 0157, and increasingly complex information about appropriate nutrition all indicate that effective risk communication with consumers is important and necessary.

Many different psychological factors influence public risk perceptions. Involuntary, unknown and unnatural hazards are feared more than those which people choose to take, which are understood and known to those exposed and science, and which are believed to be natural in origin. These include, for example, ethical concerns, trust and distrust (in scientific institutions, risk regulators and information providers) and perceptions of social exclusion from risk management processes. These all represent important determinants of how individual members of the public will respond to information about particular food related hazards, effects which are, of course, dependent on hazard type and perceived characteristics associated with individual hazards. All these factors may be important reasons why people do not consume particular nutritious foods such as oats – this will be discussed in depth in this presentation.

The way in which people respond to different risks is socially constructed. That is, it is those psychological elements, which guide people's responses to a particular hazard rather than the technical risk estimates traditionally provided by experts. Research conducted by Paul Slovic and his co-workers has consistently demonstrated that factors such as whether a risk is perceived to be involuntary, potentially catastrophic, or uncontrolled will increase public risk perceptions (1).

Both perceptions of risk and benefit associated with specific hazards must be understood if public responses to different food risks are to be assessed in an accurate way. Differences in perceptions of risk and benefit may exist between different countries, and between different individuals within countries. National and international differences in risk perceptions must be understood if the development and application of emerging technologies is to be harmonised in a world where trade and communication is increasingly global. What is acceptable to one demographic or cultural group may not be acceptable to another (figure 1).

Figure 1 Cross-cultural differences in consumer attitudes to genetically modified foods



People are unlikely to tolerate food risks if they do not perceive that there is a benefit associated with them - there appears to be an inverse relationship between risk and benefit (2, 3). Finally, for the risks of a technology to be acceptable to the public, the benefits from a technology must be perceived to accrue to people exposed to the risks, or to the environment, (4) and not to industry.

It is also important to remember that simply providing information about technical risk estimates is unlikely to influence the way that people think about potential hazards. In particular, risk information which does not address all the concerns of the people to whom it is directed, and which does not take account of the social context in which the information is embedded, may be discounted the person receiving the information (5).

Public negativity and resistance to the nuclear industry in Europe and North America has been well documented, and is paralleled by increased public concern about emerging technologies in general (6). Industrial and government concern about a similar level of public resistance being associated with emerging technologies such as genetic modification of foods, cloning of animals (and, recently, human embryos and cloning) has resulted in a communications industry growing in parallel with the industrial expansion linked to the technology in the agro-food sector. Much of this communication work has utilised the deficit model adopted historically by the public understanding of science movement - that if the public only understood the science, they would accept an emerging technology and its applications - and that the way forward for science policy was to "educate" the public in order to generate acceptance (of, for example, genetically modified foods). This "deficit" model does not take into account the role that trust in institutions and information sources may be in determining public responses to risk

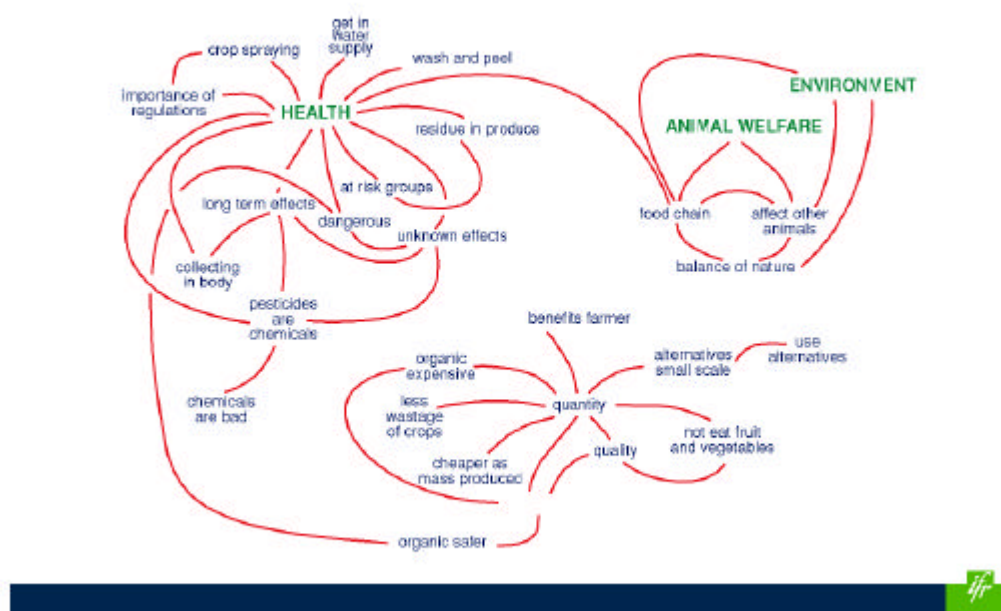
communication. There are also likely to be large individual differences in people's beliefs and information needs, and these should be understood and information adapted and targeted to suit these different information requirements.

Two major dimensions have emerged as being important in determining trust - that of "competence", the expertise held by the communicator and the extent to which they are able to pass on information about a particular subject area, and "honesty", the extent to which a communicator will be truthful in communication of information (7). Trust appears to be linked to perceptions of accuracy, knowledge and concern with public welfare. Distrust is associated with perceptions of deliberate distortion of information, being biased, and having been proven wrong in the past. Sources which are perceived to be over-accountable, or protecting a vested interest, are unlikely to be trusted (8).

Trust in information source is unlikely to be very influential for potential hazards where people already hold very extreme attitudes about a particular hazard. Under these circumstances, people are more likely to assess the information with which they are presented, to see if it aligns with the view that they already hold - if it does not, they change their opinion about the information source rather than change their attitudes. It is likely that this distrust might spread such that all information disseminated by the source about other hazards is subsequently distrusted (9).

However, source characteristics may influence the direction of attitude change in situations where people have not developed very strong views about a particular issue (10). Persuasive language has been found to increase the extent to which people use in depth "central" information processing to interpret information, which is more likely to result in attitude changes to align with the information content. A similar effect is observed if the personal relevance of information is increased, or if trust in the information source providing the information is very high. Central processing is less likely to occur if the information is low in persuasive content and personal relevance, and attributed to a distrusted source. Research using this model has shown that trust in information source is influential in determining how people respond to risk-benefit communication. However, source effects are very hazard dependent, particularly if people perceive that they have very little personal control over exposure to the risks. In the case of hazards where people perceive a high level of "optimistic bias" (where people perceive that they are at less risk than a comparable or typical member of society from a particular hazard) the effect of information source are very much reduced (11). This is very much the case for risk communication about microbiological hazards, or nutritional risks such as mineral deficiency or over-nutrition of calories or minerals. It is also important to understand what people are really worried about when thinking about food-related risks, and developing communication which focuses on these concerns, rather than assuming people simply want technical risk information (figure 2).

Figure 2 Pesticide residues in food



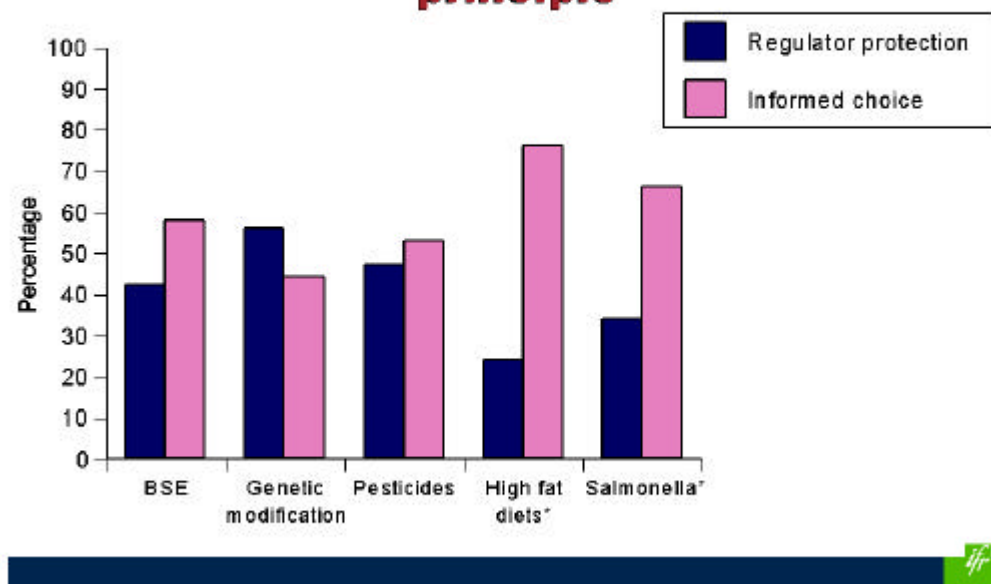
Individual differences in risk perception might relate to regional, ethnic, socio-economic or gender distinctions, and have important implications for risk communication practice. One of the most consistent findings in the risk perception literature regarding demographic differences in risk perception is the well-established difference in risk perception between men and women. In general, women tend to perceive more risk from a hazard than men. Research in the UK has demonstrated that women express greater personal perceived risk from technological and food-related hazards compared to men and, when general risk was considered, women perceived greater risk from ALL of the hazards relative to men. Women also rated all the hazards as being more important priorities for government risk mitigation efforts, and wanted greater public involvement in the risk management process independent of hazard type. Women tended not to trust the government as much as did men to take appropriate actions to reduce the risks associated with of the different hazards. Similarly, personal risk for all of the hazards tended to be perceived as greater by Afro-Caribbeans, whereas Asians expressed similar high levels of perceived personal risk from poor nutrition, radon and outdoor pollution. Afro-Caribbeans expressed greatest desire for the government to reduce the risks associated with all of the hazards, and wanted greater public involvement in risk management decisions.

Finally, members of the top two socio-economic groups tended to perceive less personal and general risk from the hazards compared to respondents in the lower socio-economic groups. Comparing affluent and poorer respondents yielded a similar pattern of results. In particular, poorer individuals were more concerned about the cloning of animals, and genetic engineering of human beings. Poorer people expressed the greatest preference for the government to reduce all risks, whereas richer people rated risk mitigation as a less important priority for the government. Similarly, more affluent individuals rated public involvement in risk management decisions as being less important than less well off individuals (12).

One interpretation is that the wealthy already perceive that they have high levels of involvement with technological risk management and decision-making through social inclusion and influence. Similar effects were observed for men, members of culturally dominant cultural groups, and those in more professional jobs, where it is likely that they had more autonomy and perceived greater personal involvement in decision-making processes. It is poorer people, women, and members of ethnic minorities who perceive that they are excluded, and would prefer greater involvement in risk management decisions, particularly decisions associated with technological hazards. It is important to ensure that these individuals are fairly represented and included in risk management decision-making, particularly public participation exercises and consultations. Social inclusion is also likely to improve trust in government and, by implication, the regulatory framework associated with risks. Increasing transparency in risk management processes, and the need to improve public trust in those processes, is likely to involve increased public participation in risk management itself. Many different types of public participation methodology have been identified in the literature (13).

It is also important to understand public preferences for different regulatory approaches. In Europe, food regulation tends to take more account of process considerations, and utilizes the precautionary principal as a basis for decision-making. American approaches are much more driven by the perspective that foods should be regulated on a case-by-case basis. Research in the UK has shown that British consumers much prefer informed choice over precaution for lifestyle type food hazards (inappropriate nutrition for optimal health, for example), and the only food hazard where there is a preference for precaution is that of genetically modified foods (Figure 3).

Figure 3 Consumer preference for informed choice versus precautionary principle



Effective communication about good nutrition is another priority if the current government targets for a reduction in cancer rates are to be attained. In particular, it is important to identify and quantify public barriers to healthful eating, clarify individual differences to enable more effective targeting of interventions, and produce recommendations for

facilitating dietary change. Similar approaches might be used to promote effective dietary change associated with, for example, management of type II diabetes.

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BIOGRAPHICAL NOTE

Dr. Lynn Frewer graduated from the University of Bristol in Psychology (B.Sc.), followed by an M.Sc. in Ergonomics from University College London and a Ph.D. in Applied Psychology from the University of Leeds. Lynn is currently Head of the Consumer Sciences Section at the Institute of Food Research in the UK. Her current research interests include the psychology of risk perceptions and attitudes, the influence of the media on risk perception, public reactions to genetic modification, the impact of trust on the

effectiveness of risk communication, and developing methodologies for fostering public participation in strategic development of food technologies.

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COMPARATIVE GENOMICS FOR OAT IMPROVEMENT

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ABSTRACT

Genomic research emphasizes comparison of genes and genomes across species and genera using sequence and map-based tools that utilize evolutionary continuities among organisms at both the structural and functional levels. Elucidation of gene and genome structure-function relationships is based in comparative genomics and evolutionary genetics is the underlying organizational principle. Comparative genetics research and is critical for future improvement of species with large complex genomes or less research support. Trait dissection, integration of information about metabolic pathways, gene expression, and chromosome location facilitate the rational selection of candidate genes. Allelic diversity experiments can be designed to facilitate the identification of superior alleles for genes of economic importance so that they can be assembled in superior crop varieties.

INTRODUCTION

What methods and technologies should be considered when developing strategies for oat improvement? Certainly, all the traditional aspects such as inheritance of key traits, ploidy, reproductive biology, and genetic variation in the primary gene pool are important but if we are to incorporate marker-assisted selection and/or transformation, there are a few additional considerations. Availability of a saturated molecular marker map, marker polymorphism, linkage relationships between markers and genes controlling important traits, as well as funding for the increased cost of using these technologies must also be taken into account.

In recent years, we have collaborated with other research groups to construct molecular marker maps for cultivated oat (O'Donoghue, et al. 1994) and diploid relatives (O'Donoghue, et al. 1992), comparative maps for oat, triticeae, rice and maize (Van Deynze, et al. 1995a, b) and QTL maps for cultivated oat (Siripoonwiwat et al. 1996). Given the volume of research on oat, one might assume that the tools and information are now available to implement marker - assisted selection for oat improvement. However, considering the complexity of key traits and genome structure of oat as well as waning interest from industry, currently it seems that efficient marker - assisted selection strategies for oat are not at hand. Also, the complexity of oat genetics suggests that transformation may be a better biotechnological approach for improving cultivated oat. Never-the-less, EST databases, functional genomics, and comparative sequence analysis have substantially altered our research strategies so that informatics approaches and strategies such as direct allele selection (Sorrells and Wilson, 1997) are becoming feasible for oat as well as other crops that are challenged by limited funding and genomic complexity. Candidate gene analysis combined with large scale allele discovery and characterization may allow more efficient characterization of genetic control of traits versus conventional QTL mapping. Comparative sequence analysis allows us to transfer information about genes among species and allele characterization provides the within species information for application of

marker – assisted selection as well as better transformation strategies. Our crop improvement strategy is to utilize comparative genetics to identify the genes controlling traits of interest and then assess within species allelic diversity so that the best alleles can be identified and assembled in superior genotypes.

Comparative Genomics: Comparative genomics is a broad field of research with the general goal of estimating similarity at some level of organization. The patterns of relationships discovered can lead to new knowledge, hypotheses, and predictions about those species. The evolution of comparative genetics research from the whole plant level to the DNA level has synergistically expanded our knowledge of genome structure and function due to the complementarity of research among scientists working on different species. There has been a rapidly growing interest in comparative genomics over the past couple of years for several reasons, three of which are discussed below.

Industrialization of Crop Improvement: The rapid industrialization of crop improvement that we are witnessing today is based on 1) intellectual and material property rights, 2) the efficiencies gained through consolidation of high cost operations, and 3) the vertical integration of operations to produce unique plant products. This revolution is having a dramatic impact on relationships between public and private researchers and is forcing universities to reassess their research and teaching missions. Public researchers must reorient their programs to reduce overlap with industrial research on major crops. At the same time, minor crops are being ignored. There is now a greater demand than ever for plant breeders trained in modern breeding methods but fewer university plant breeders training them.

Changing Technologies, Methods and Goals: There has been a greatly increased emphasis on the use of model species for genomics research, largely due to the ability to make rapid advances in the discovery of genes and their function. Parallel to the increased research on model species comparative genetics has expanded to encompass new methods and a greater range of species. New technologies and methods are being discovered daily that are changing the way we think about crop improvement. Gene discovery and transformation technologies facilitate the introduction of novel genotypes. New marker systems as well as genes producing unique traits that are now accessible through transformation are becoming available. Finally, the scenario of large scale gene discovery through QTL and candidate gene analysis followed by determination of gene function and assessment of allelic value is approaching reality. Improved information transfer technologies are becoming critical for oat.

Integration of Information from Disparate Sources: Online databases (e.g. Graingenes: <http://probe.nalusda.gov:8300/cgi-bin/browse/graingenes>) are making information more available, especially for germplasm, genes, and maps, and they are presenting the information in novel ways that facilitate interpretation and utilization. One of the most exciting prospects is the integration of information about genes, metabolic pathways, and agronomic phenotypes. Most metabolic pathways have been elucidated using microorganisms and model species; however, much of the information is applicable to a broad range of species. The Kyoto Encyclopedia of Genes and Genomes (KEGG: <http://www.genome.ad.jp/kegg/kegg.html>) has an impressive array of genomic information for microbes that is linked to metabolic pathways,

regulatory pathways, and molecular assemblies. New visualization tools for cross-species analyses are needed to facilitate the transfer of information to crop species via comparative genetics. Ultimately, linking gene to phenotype is our goal.

Figure 1 illustrates the integration of various sources of information that allow us to identify the genes controlling a trait of interest and eventually understand their function. Given a trait of interest, we first need to know how many important genes control the trait and where they are located in the genome. QTL mapping is still the most common approach to acquiring that information; although, analysis of various kinds of mutants is beginning to contribute to that knowledge base. Once we know the approximate location of the genes, we next want to learn their function. If we know something about the metabolic pathway that might be involved we can intelligently select a subset of candidate genes that have been previously located to that region of the genome. These may be cloned and characterized genes or ESTs that have been assigned a putative function. We can gain supporting evidence for the candidate genes if information about gene expression can be obtained regarding tissue or developmental specificity. Finally, once there is ample evidence for the role of a particular gene, the final but most important step is to characterize allelic variation in the gene. It is critical that superior alleles be identified for variety improvement; however, locus x environment and locus x locus interactions are likely to complicate this process.

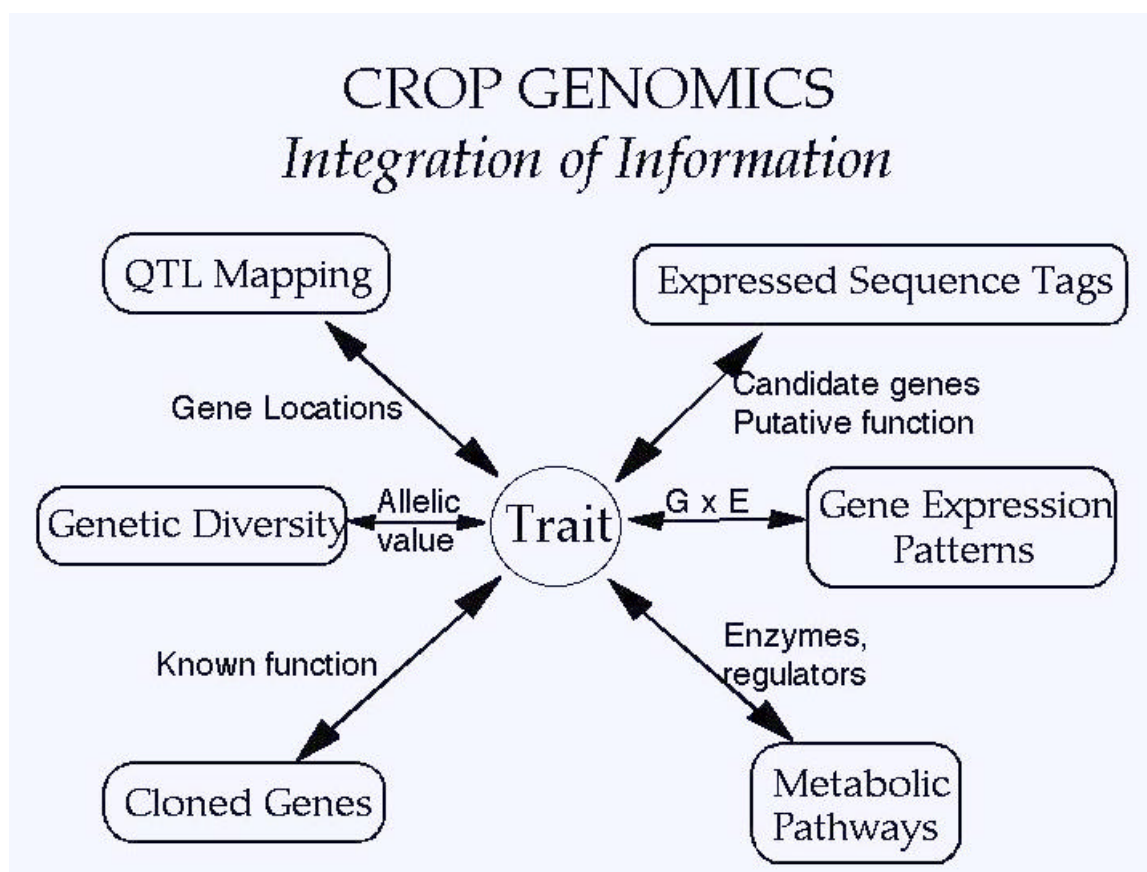


Figure 1. Integration of information can lead to gene discovery and characterization for trait improvement.

Goals of Comparative Genetics

There are three primary goals of comparative genomics research. The first is to transfer and build on information from model species and simpler organisms. Second, comparative genetics is used to integrate information on gene location and expression across species and disciplines. The third goal is to ensure that minor crops benefit from the information generated. It is important to note that the primary beneficiaries of comparative genetics are the genomically challenged, the economically disadvantaged, and the technologically deficient crop species and the transfer of genetic information is vital to the survival of those crops. Oat is clearly genomically challenged with a genome size 40 times larger than rice and a high percentage of repeated DNA and being a minor crop, oat is likely to benefit greatly by the genomic information being generated for rice, maize, wheat, and barley.

Classification of Genes and Proteins: The universal system of classification of living organisms introduced by Linnaeus effectively organized the complexity of biological relationships. This provided scientists with a valuable framework for the study of plant evolution and genetic relationships that has been adapted to other fields of study. Systematists have evaluated variation in a wide range of different traits from obscure plant structures to biochemical pathways to establish evolutionary relationships within and among species. This paradigm has been extended to genes and proteins, and their families, subfamilies and superfamilies to create a molecular taxonomy (e.g. Henikoff et al., 1997). Ancestral duplications and rearrangements of genes or parts of genes has lead to a complex evolution of gene family relationships and genome structure. The understanding of how these complex patterns of gene evolution resulted in the diversity of living organisms we see today will be among our most important scientific accomplishments.

Comparative genetics will continue to evolve as new technologies, methods, and information become available. Current and future research will emphasize comparisons of genes and genomes across species and genera using sequence and map-based tools that will utilize evolutionary continuities among organisms at both the structural and functional levels. Genomic research is rapidly evolving from a descriptive science to predictive science where we can predict gene or protein function and either modify or reverse engineer those genes for transfer into elite varieties.

Benefits of Comparative Mapping

Recent advances in molecular genetics have enabled a more complete understanding of the genomic structures of the grasses including oat, the triticeae, rice, and maize. This has encouraged researchers to expand their vision of what might be possible if we examine species further out on the evolutionary tree. Comparative maps allow transfer of information from species with small diploid genomes, such as rice, to species with more complex genomic structures (increased repetitive DNA, polyploidy) and less economic support. Because of the size and complexity of the genomes, it is scientifically inappropriate to sequence the entire genomes of wheat, rye, oat, or barley. However, alternative strategies involving identification of gene-rich regions of the Triticeae genome and comparison of the genome structure and genetic colinearity with rice, maize, sorghum, and other species provide oat researchers with the knowledge and tools necessary for genetic parity with simpler genomes.

Gramineae Maps: Crop species of the Poaceae display a remarkable level of genetic similarity despite their evolutionary divergence 65 million years ago (Bennetzen and Freeling, 1993; Paterson et al., 1995). Molecular markers have been used to develop comparative chromosome maps for several members of the Gramineae and these have been used to study genes of agronomic importance across species (for review see Snape and Laurie, 1998). Large segments of the genomes of maize, sorghum, rice, wheat, and barley conserve gene content and order (Ahn and Tanksley, 1993; Ahn et al., 1993; Gale and Devos, 1998; Hulbert et al., 1990; Kurata et al., 1994; Van Deynze et al., 1995a,b,c), although the correspondence has been modified by chromosome duplications, inversions, and translocations. For the domesticated grasses, the conserved linkage blocks and their relationships with rice linkage groups provides the insight into the basic organization of the ancestral grass genome (Moore et al., 1995; Wilson et al., 1999). Wilson et al. (1999) described a higher resolution rice/maize comparative map that details more than 20 arrangements. In comparative mapping studies involving maize, the tetraploid nature of the genome is readily apparent. Rearrangements between rice and maize include telosomic fusions, intrachromosomal inversions, and non-reciprocal translocations. These rearrangements and the homoeologies with related species lead us to propose that the maize genome progenitor was probably composed of 8 chromosomes rather than the 5 or 10 chromosomes proposed earlier (Wilson et al., 1999).

Future Genomics Research – Where is it leading us?

Comparative genomics research falls into 3 major categories: 1) gene sequence and genome structural relationships for integrating genomic information across species, 2) characterization of the function of all genes that affect agronomic performance and quality, and 3) bioinformatics - integration, visualization, and analysis of complex data.

The large volumes of information from genome sequencing and gene expression studies now require far more sophisticated computational tools for display, analysis and integration.

Genome-Wide Expressed Gene Sequencing: Although there are undoubtedly fascinating mysteries locked up in the ubiquitous repeated DNA sequences of large genome species (LGSs), for the near future, the primary focus will be on coding regions. Expressed sequence tag (EST) analysis was first proposed in 1991 by Craig Venter's group at The Institute for Genomic Research (TIGR) for efficiently sampling a genome for information about genes that could be used to search existing databases (Adams et al., 1991). By searching online databases for similar genes with known function, one can determine if a specific gene (or gene motif) has been found in the same or other organisms and if its function has been determined. These ESTs can also be useful for further laboratory work in gene expression, mapping, and direct alteration of the organism. Sequences may be rare or absent either because they were not expressed under the conditions in which the organisms were grown for library construction or because they were not expressed in the tissues sampled at the particular stage of development. Several strategies have been devised to minimize re-sequencing these commonly-expressed genes and specific groups of genes can be targeted with techniques that induce differential gene expression. This indicates that whole genome sequencing and EST data are to a large extent complementary and both are essential.

EST databases are being screened for simple sequence repeats that may be useful for mapping and for various kinds of motifs that allow classification of gene sequences. For the long term, EST information will be a critical resource for crop improvement and will be used extensively for locating genes, understanding changing patterns of gene expression, and biotechnological modifications of traits.

Comparative Mapping by Sequence Matching: Southern hybridization using anchor probes has been the method of choice for evaluation of relationships among species and genera especially for comparative mapping (Van Deynze et al., 1998). This is because other molecular methods such as PCR-based fragment amplification may be an all or none reaction (dominant), may amplify non-orthologous loci, or inadequately sample sequence variation because of the specificity of the primers. New methods of enhancing and scaling comparative map information are needed that take advantage of existing information in the literature and genome databases. One approach is to sequence previously mapped probes or generate new ESTs for the LGS and map them in the LGS. These sequences can be cross-referenced by sequence matching using BLAST searches against the model species either before or after mapping. The information generated can be used to develop high density comparative maps for genetic linkage and physical distance between genes as well as evolutionary information about the genes and their phenotypes in the two species. The utility of this approach is assessed below.

Automated sequence comparisons based on sequence alignments are among the most popular queries in biological research. GenBank (<http://www.ncbi.nlm.nih.gov>) now has over 2 million ESTs and 2 billion DNA bases in the database. Lazo et al. (1998) reported on DNA sequence analyses and graphical displays of wheat, oat, and barley cDNA clones some of which were mapped in rice, maize, oat, sugarcane, and Triticeae species. In their BLAST searches a large number of oat and barley cDNA sequences matched rice EST sequences which had mapped by the Rice Genome Program in Japan. Recently, we compared the rice chromosome locations of the oat and barley cDNAs that matched the mapped rice ESTs according to our BLAST searches (Sorrells et al., 1999) (Table 2). Nine of our oat or barley probes were both mapped in rice by Southern analysis and matched a rice EST that was mapped by Southern analysis. Out of those 9 matches, 5 of the rice chromosome locations were similar or identical for the cDNA and the EST while the other 4 mapped to different chromosomes. I then used our comparative maps for maize, barley and wheat to predict the map location of those clones as well as other oat and barley cDNA-probed loci in rice. Six matching rice ESTs were available for maize and 18 were available for barley and wheat. In maize 4 out of 6 matched the predicted location and for wheat/barley, 12 out of 18 matched the predicted location. These results suggest that it is possible to identify homologous sequences and their map location by comparing anonymous cDNA sequences. Furthermore, it may be possible to resolve gene order relationships in gene rich regions. Most importantly, sequence matching can supplement the costly data provided by Southern analysis and greatly enhance the resolution of comparative maps required for information transfer between species.

Two primary limitations to using sequence matching are that 1) different genes are known to evolve at different rates and 2) the accuracy and sensitivity of the sequence comparisons decline in more distantly related species. Intragenomic duplications may be resolvable by comparing adjacent markers.

Table 2. Rice, maize, wheat, and barley chromosome map locations for anonymous barley and oat cDNA probes versus map locations for rice ESTs with similar DNA sequences. (NM = not mapped)

RGP, Japan	BLAST	Probed	Seq/Probe	Probed	Seq/Probe	Probed	Seq/Probe		
Sequence	Chr Loc of	Score	Probe	Chr Loc	Matched?	Chr Loc	Matched?	Chr Loc	Matched?
EST	RiceEST	Best	Name	Rice	Rice/Rice	Maize	Rice/Maize	W/B	Rice/W/B
S1524	3	265	CDO1373	3	Match	NM		5	Match
C0985	9	396	BCD981	9	Match	NM		5	Match
C1479	5	185	CDO89*	5	Match	6	Match	1	Match
C0488	10	676	BCD1449	10	Match	NM		1	Match
R1891	11	134	BCD1095	11	Match	NM		2	No
S2287	2	399	CDO215	1	No	NM		NM	
S11679	12	280	CDO215	1	No	NM		NM	
C0016	10	387	CDO20*	3	No	1S,9	No	4	No
R1811	3	592	BCD98*	8	No	1	No	1,7	No
C0713	1	323	CDO344*	12	No	3	Match	NM	
S2072	3	130	CDO586	NM		1,9	Match	NM	
C0632	9	1109	BCD9	NM		7	Match	5	Match
C0009A	1	395	BCD1380	NM		NM		NM	Match
R2167	1	898	BCD1495	NM		NM		3	Match
R0106	1	346	BCD1823*	NM		NM		3,6	Match
C0854	1	365	BCD809	NM		NM		3	Match
C0037	2	963	CDO1428	NM		NM		6	Match
R0738	4	413	BCD445	NM		NM		2	Match
Lox		144	BCD1802	NM		NM		5	Match
Lox		?	BCD873	NM		NM		4,5	Match
R0886	1	194	BCD1930	NM		NM		1,7	No
C0106	2	469	CDO370	NM		NM		2	No
R0476B	5	898	BCD1495	NM		NM		6	No
Waxy	6	143	BCD1802	NM		NM		5	No

Quantitative Trait Locus Mapping: Even with detailed comparative maps, the potential application of new molecular technologies, especially for LGSs will not be realized unless there is adequate oat - specific data that identifies the genes controlling quantitative traits.

A quantitative trait locus (QTL) is the chromosomal location of a gene that affects a trait that is measured on a quantitative scale. Examples of quantitative traits include plant height, grain yield and grain quality. These traits are typically affected by more than one gene, and also by the environment. Thus, mapping QTL is not as simple as mapping a

single gene that affects a qualitative trait (such as flower color). A saturated linkage map allows the detection of all loci affecting a quantitative trait within a specific population and set of environments. A major objective for QTL detection is to manipulate the underlying determinants in an applied breeding program. Paterson et al. (1991) and Dudley (1993) have provided excellent overviews of the potential applications of these techniques to breeding. Some traits can be broken down into components that together determine the overall phenotype of a complex trait, and this is referred to as trait dissection. (Hayes et al., 1993). Trait dissection can help identify QTL determinants; e.g., shattering resistance as a determinant of yield.

Comparative QTL analysis has shown that convergent domestication of the grasses has resulted from selection for a few important genes for traits such as non-shattering, short plant height, optimum flowering time and others. Studies that combine QTL results from different populations grown in different environments can be used to construct consensus QTL maps. Such maps can then be related across species using anchor loci that have been previously mapped. This approach combined with trait dissection can be utilized in candidate gene analysis.

Candidate Gene Analysis: As the genomic maps become more densely populated with gene sequences of known function and expression, candidate gene analysis becomes more efficient and may eventually replace other methods of gene discovery but it does not eliminate the need for phenotypic data. A candidate gene is a gene that is associated with variation in a trait and believed to be involved with the development or physiology of the trait. Candidate gene analysis has the goal of finding genes responsible for genetic variation in traits of interest. Candidate genes are often sequenced genes of known or suspected function and may belong to biochemical or regulatory pathway (Rothchild and Soller, 1997). Genetic dissection of complex traits refers to QTL analysis of components of a trait and can lead to candidate gene hypotheses and can be helpful in understanding the effects of genes on a trait and their interactions. Often the components will have a higher heritability and be less affected by the environment. Candidate gene analysis is complementary to QTL analysis as it provides different kinds of genetic information, often over a broader range of germplasm. Because there may be large numbers of genes located in the region of a QTL, the odds of identifying the gene that actually controls the trait appear to be quite low; however, a number of factors can increase the odds of success, especially as the number of genes sequenced increases.

The methodology begins with choosing candidate genes based on biological system or QTL mapping information. Next a technique is chosen for amplifying part or all of the gene using consensus or degenerate primers. Once the gene has been amplified and sequenced for a few genotypes, polymorphisms are identified in the candidate genes' sequences or restriction sites. It is not critical at this point that these polymorphisms be responsible for the phenotypic variation because only the association is tested. Eventually, an understanding of the relationship between variation in the gene product and phenotype will be necessary for proving gene identity and especially important for predicting and constructing uniquely useful genes. The final step is to analyze the association between allele and phenotype. Candidate gene analysis is another useful tool in our long term goal of large-scale gene discovery and characterization. Alleles can then be identified and assessed for their usefulness or desirability.

Large Scale Allele Discovery and Characterization: Core germplasm collections are a vital component for an allele detection and characterization project. For identification of alleles, at least part of the sequence of the target gene must be known and the portion of the gene

being analyzed is critical. New sequencing technologies such as pyro-sequencing and denaturing high performance liquid chromatography (Oefner and Underhill, 1998) are drastically reducing the cost of detecting DNA sequence variation. Three important considerations for assessing the utility of this approach include copy number of the gene, some knowledge of the DNA and amino acid sequences for designing universal primers (for the species involved), and information about the protein structure and function is helpful to target specific parts of the gene that are likely (or known) to have a phenotypic effect. Allele characterization is complicated by gene duplication, insertion/deletion events, and polyploidy. The choice of technology(ies) used will be dependent on cost per sequence sample, knowledge of the relationship between protein structure and function, and complexity of the genetic control of the trait.

CONCLUSIONS

Genomic research has emphasized structural aspects in recent years; however, the focus will rapidly shift to determining the functional role of genes and the mechanisms of evolutionary change that have resulted in the diversity of living organisms we see today. Methods for genome-wide gene expression studies are developing rapidly and will lead to enhanced understanding of protein structure-function relationships that are necessary for predicting gene function and for rationally engineering genes. Bioinformatics will play an increasingly important role in the integration of information from different species and sources through the use of novel approaches to analysis and visualization of complex data. Structural genomic research linking genes and genomes across species benefits all species but is especially important for species with large genomes and for crops of less economic importance. Breeding progress depends on i) discovery and generation of genetic variation for agronomic traits and ii) accurate selection of rare genotypes that possess new or improved attributes due to superior combinations of alleles at multiple loci. Consequently, efficient methods are needed for identifying and evaluating allelic effects on a large scale so that desirable alleles can be assembled in superior varieties. This can be facilitated by integration of genetic information across species, identification of superior alleles, and by focusing on the most important genes and traits for the species of interest.

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OAT BIOTECHNOLOGY – WHERE TO NEXT?

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INTRODUCTION

What are the opportunities and requirements for oat biotechnology at the beginning of this millennium? How can we best utilize the power of comparative genomics? What bioinformatics tools should we be aware of? What technological developments should we watch, and what technologies do we need to develop ourselves? Why even bother with oat?

In this discussion, I will try to address these questions, emphasizing the challenges and opportunities that are unique to oat. However broadly one defines “biotechnology”, it is clear that oat research needs to progress on all technical and scientific fronts in order that oat remain a viable and competitive commodity. I have tried to address individual topics, but the interrelatedness of these topics necessitates some cross-referencing and overlap. The final topics, “comparative genomics” and “bioinformatics”, are unifying themes. I have deliberately avoided the topic of transformation, primarily because I have no expertise in this area. Despite current uncertainties about public acceptance of novel traits introduced by transformation, this is an enormous omission which readers must factor in as they see fit.

MOLECULAR MAPPING

The production of a complete molecular marker map in hexaploid oat has been a recalcitrant challenge, but it is an effort that must continue. A high-quality structural map is an essential tool for applied genomics, and an organizational pivot for genomic research.

The development of a hexaploid map in the Kanota x Ogle population (O'Donoghue, et al., 1995) was a major landmark in oat genomic research. This map provides an important point of reference upon which further research is being built. Minor updates to the structure of this map are in press (Kianian, et al., 2000), and a Kanota x Ogle map enhanced by the addition of AFLP loci was described by Jin, et al. (2000). A more complete Kanota x Ogle map is being prepared by the author and collaborators, and several maps in additional populations are also in preparation, including Terra x Marion (from AAFC, Ottawa. See Tinker, et al., 1998), Kanota x Marion (University of Minnesota) and Ogle x TAM 0-301 (USDA-ARS Idaho and Iowa State University). While this information is adding significantly to our ability to dissect specific genomic regions, our hexaploid oat maps still form a fragmented and incomplete picture, and no map has been capable of resolving 21 linkage groups.

What are the problems with mapping in oat, and how shall we overcome them? Many difficulties are due to polyploidy, as summarized by Sorrells (1992). In addition to the presence of homeologous loci, oat has accumulated and maintained frequent duplications of loci or chromosome segments. This is indicated by the presence of more than three loci for many RFLP probes (e.g., O'Donoghue, et al., 1995). Since duplications and

rearrangements may have arisen before, during, or after polyploidization, the co-linearity of markers between hexaploid and diploid oat is fragmented. Thus, while diploid species have provided useful comparative information, we cannot use diploids to fully deduce genome organization in hexaploid oat. There is also evidence for chromosomal rearrangements between different hexaploid cultivars, even within the same species (e.g. Fedak, et al., 1999), so even the most complete maps may have peculiarities to the germplasm in which they were produced.

While structural complexity adds challenge to the work, fragmentation of current maps may be due primarily to a combination of a large genome size and the limited size of mapping populations. Most mapping in the Kanota x Ogle population has been performed on a set of 71 RI lines. Simulations by the author (unpublished) were performed using a hypothetical RI oat population and a set of random markers on an idealized 21 x 170 cM oat genome. Simulated data was used to estimate maps for 750 randomly-placed markers. Repeated tests of this experiment with new sets of random data usually gave results in which the estimated map was fragmented into 35 to 45 linkage groups. Increasing the number of markers provided some improvement, but better results were obtained by doubling the population size.

Some efforts in progress will help to remedy the above problems. Progress in assignment of linkage groups to physical chromosomes (Kianian, et al., 1997) is continuing (Ron Philips, personal communication), and maps in new populations are under development. However, comparison among maps, and recognition of allelic marker loci continues to be a challenge which must be overcome in order to produce a consensus map. If and when a consensus map becomes a reality, there will still be a need for interactive exploration of specific genomic regions based on all available information. Bioinformatics tools to address this challenge are discussed later.

Whether efforts should be concentrated on new populations, or on standard reference populations is debatable. The use of new populations brings new opportunities to map additional genes and QTLs, whereas the existence of a large, well characterized oat reference population would greatly facilitate collaborative efforts. I hope the current conference will provide opportunities to discuss this badly-needed resource.

Molecular Markers

Strengths and weaknesses of different types of molecular markers greatly influence the way in which they contribute to further map development and genomic applications. Unfortunately, no marker is ideal for all purposes, so continued efforts are needed to generate and map several flavours of molecular marker:

Markers for comparative mapping

Applications in comparative mapping favour the use of conserved cDNA clones that are common to maps in other grasses (Van Deynze, et al., 1998). Efforts to increase the representation of anchor loci on the Kanota x Ogle map have been made by Mark Sorrells and others, and are being developed further in forthcoming versions of the map. Anchor clones have also been used extensively to develop a forthcoming map in Ogle x Tam 0-301 (Mike Lee, personal communication). The concept of anchor loci may need to be expanded as finer structural maps become available in model species such as rice, corn, and wheat. This would allow more detailed analysis of ancestral chromosome fragments.

Markers for candidate loci

By mapping molecular markers based on cDNA sequences of characterized genes, we increase the opportunities for discovery of genes responsible for mapped genetic factors, including QTLs. This is referred to as a candidate gene approach. The mapping of candidate genes will be an ideal opportunity to link “traditional” genomics with new areas of functional genomics. The cDNA clones for many anchor loci (discussed above) have now been sequenced and assigned a tentative function; thus we already have some potential candidate loci on our oat maps. However, large scale application of this approach would require mapping of many additional cDNA-based markers. Efficient high-throughput use of this strategy may require innovative use of new technologies such as microarrays and single nucleotide polymorphisms (SNPs). Since this will be a priority in many other species, oat researchers may be able to adopt the resulting technological advances.

Markers for better oat maps

Anchor loci and candidate loci are not necessarily the best markers for improving the map of hexaploid oat. In order to resolve differences among maps and extend maps into new populations, the ideal marker is highly polymorphic, multi-allelic, and unique to one chromosomal location. One such marker is based on simple sequence repeats (SSR) or “microsatellites”. A library of SSR-enriched clones has been developed by Graham Scoles and distributed to some colleagues (personal communication). While these markers are ideal for continued map development, they are somewhat expensive to develop. The international oat community needs to find ways to encourage the development and sharing of a large toolbox of microsatellite markers.

Markers for selection

The above markers are useful for generating information. However, for use in germplasm improvement, there is an ongoing need to develop markers for large-scale automated scoring. Markers based on SSRs can be scored using an automated sequencing apparatus, and there seem to be good long-term possibilities for the use of microarrays to characterize loci based on SNPs. However, most current breeding programs require markers that can be scored using affordable technologies. Currently, this means PCR-based markers scored using agarose gels. Such markers can be developed for specific target loci, and are commonly referred to as “sequence characterized amplified regions” (SCARs). A presentation at this conference describes the ongoing development of a toolbox of SCARs (Molnar, et al., this issue).

QUANTITATIVE TRAIT ANALYSIS AND MARKER ASSISTED SELECTION

Several studies have reported on the analysis of QTLs in oat (Siripoonwiwat, et al., 1996; Holland, et al., 1997; De Koeyer, et al., 1998; Kianian, et al., 1999). The Kanota x Ogle population has been useful for the analysis of QTLs because a map has been available for several years, and because the RI population has been distributed to numerous researchers. Notably, one of these studies has led to the discovery that the candidate locus “ACCase” may be responsible for a major QTL effect on groat oil (Kianian, 1999). Another study shows that some loci affecting tolerance of BYD virus may be conserved between different germplasms (Jin, et al., 1998). While studies of major QTL may lead to additional hypotheses regarding candidate loci, there is limited potential in Kanota x Ogle for the detection of additional QTLs applicable to marker assisted selection. This is due partially to the segregation of major genes affecting heading date and vernalization response (Holland, et al., 1997). These genes essentially fragment the population into

subsets, limiting the sensitivity for detecting minor QTLs in an appropriate genetic background. There are also fundamental limits to the number of QTLs that can segregate in a given cross, and to our ability to detect those QTLs within a single population.

Additional QTL studies in new populations, such as Tibor x Marion (Dekoeper, et al., 1998), are needed to reveal locations of more QTLs affecting agronomic and quality traits. However, the cost of developing new large scale QTL mapping studies is prohibitive for applications that seek to utilize information directly in germplasm enhancement. For the discovery of new alleles at existing loci, or for rapid detection of major loci, other strategies are required. Detection of major QTLs using bulked segregate analysis (BSA; Michelmore, et al., 1991) has been used to examine the presence and location of groat oil QTLs in new germplasm (Tinker, et al., 1999).

Discovery of QTLs depends heavily on well-characterized germplasm and good phenotypic observations. Because this is the realm of the breeder, and because breeders are primary clients for the results, strategies are needed to integrate the discovery of QTLs with existing breeding programs. Breeders need to continue to be alert to opportunities presented by unique populations. When possible, un-selected RI populations with interesting characteristics should be documented and preserved. Above all, information about these resources needs to be communicated. The need for a formal information and distribution system that is conducive to sharing experimental germplasm has been mentioned by at least one breeder (Brian Rossnagel, personal communication). Is it time to make this happen?

CYTOGENETICS

I cannot do justice to this topic due to lack of experience. However, it seems that this is an area of research which deserves special emphasis in oat. It is also an area in which technological advances could play a major role. As mentioned, the size and complexity of the oat genome has hindered the development of well characterized linkage maps. The progress of understanding and using the oat genome would be greatly enhanced if we could simply "paint" locations of genes or ancestral chromosome fragments using a toolbox of fluorescent probes. Fluorescent *in situ* hybridization has been used effectively in oat to study genome structure (Chen and Armstrong 1994; Jellen, et al., 1997; Linares, et al., 2000). Methods for genome, chromosome, or gene painting have been developed for use in other crops such as soybean (Shi, et al., 1996) and rice (Fukui and Ohmido 2000) and are well established for use in human or mouse (Henegariu, et al., 1999; Liyanage, et al., 1996). Will there be a time when *in situ* hybridization techniques are mature enough that we can use them routinely in our oat genomics efforts?

FUNCTIONAL GENOMICS AND PROTEOMICS

New directions in genomics research require large scale investments in infrastructure and extensive multi-disciplinary collaboration. In order to facilitate this within public and academic research communities, many countries have set up major genomics initiatives. I am not aware of any of these initiatives that specifically involves oat. However, it is highly likely that oat will benefit in many indirect ways from these initiatives, including access to infrastructure, new technical expertise, and new information from model species. As an example, approximately 500 expressed sequence tags (ESTs) for oat cDNAs are now publicly available through efforts by Mark Sorrells, and through the genomics infrastructure at USDA, Albany, CA (see <http://wheat.pw.usda.gov/NSF/>). In Agriculture and Agri-Food

Canada, we have established functional genomics initiatives in wheat, corn, brassica, and soybean. The current emphasis is to develop cDNA libraries and EST sets that are enriched for genes associated with disease resistance and stress. Microarrays are being used to generate hypotheses regarding transcription-based expression. Additional species such as rye, oat, and barley may be utilized for comparative purposes.

Where will this lead? It seems likely that great advances will be made within the next decade in functional genomics and proteomics of model species. Through complete genome sequencing, detailed structural analysis, and large scale expression studies, the model plants *Arabidopsis* and rice will be closest to having detailed genomic information that is both predictive and exploitable. Species such as corn, soybean, and wheat will have large databases to permit rapid transfer of knowledge. Oat is unlikely to be in this position, but smaller-scale strategic efforts can produce rapid results. For example, Cheng, et al., (1999, 2000) used sequence information from cloned disease resistance genes in other species to extract analogous genes from oat, and showed that some of these mapped to locations known to contain clusters of crown and stem rust resistance loci. The protein division of Genbank currently contains 176 polypeptides from oat (<http://www.ncbi.nlm.nih.gov/Web/Genbank/index.html>). We will probably see this number expand dramatically as tools to generate this information mature and become available to oat researchers. Knowledge of important pathways and representative genes from model grasses will enable efficient targeting of oat alleles without the benefit of a large pre-built genome database. Superficially, this information is useful on two levels: (1) the targeting of DNA polymorphism in oat for application in candidate gene analysis, and (2) direct prediction of protein polymorphism and/or alteration of protein structure. In reality, most progress will probably be made through combined approaches, relying on the foundations that we build now.

COMPARATIVE GENOMICS

This subject has been discussed in detail in a keynote address (Sorrells, this issue), and alluded to throughout this paper. Thus, we have convincing arguments that comparative genomics is of particular importance in oat. As a minor and “genomically challenged” crop species, oat is positioned to receive a net benefit from studies in comparative genomics. However, the benefits of comparative genomics will be maximized if certain pre-requisites are fully realized. Most importantly, we need a common reference map and population, accessible to all oat researchers, which is well-populated with comparative anchor loci. Finally, some fundamental questions need to be answered; for example, is it possible to use microarrays from wheat, barley, or corn for expression studies in oat? Perhaps we need to emphasize the differences as much as the similarities. As we know, oat has unique qualities and attributes that make it worthwhile to grow and eat. What are the causes of these differences? Can we design experiments to specifically target these differences?

BIOINFORMATICS

The face of biological research is changing. It is no longer adequate to make isolated discoveries. New discoveries usually find meaning and application only in the context of a diverse and rapidly growing body of information. The primary literature is often inadequate for building the context of a biological discovery. Most researchers now accept that they must acquire and use the skills and tools of bioinformatics.

Bioinformatics is a mixed stand of opportunity. Some tools are very mature – international gene databases, for example. Others tools are less mature, but serve as temporary fixes or prototypes while more complete and integrated solutions are developed. Many of the tools available for use in oat biotechnology fit the latter category.

Other than Genbank, the Graingenes database is the most complete and universal database containing genomic information on oat. Graingenes is based on the ACeDB data format, which is capable of evolving to accept new types of data. As such, it should be the ideal warehouse for all research in oat biotechnology. Currently, Graingenes has some limitations which hinder its utility: it is difficult to link directly to genome databases of other grass species (corn and rice), it is difficult for a novice to build useful queries, it can be slow – particularly when accessed through a web-based format, it is not as complete as it could be (little information is available on germplasm and QTLs), and there is no system for users to submit and maintain their own records. Graingenes developers and curators are aware of these limitations, and database capabilities are continually evolving. The UK CropNet has implemented a special interface tool called CORBA to enable queries to be performed across different ACeDB databases. There has been some discussion of moving to different formats, including a relational database format such as that being developed by the *Arabidopsis* group (<http://www.arabidopsis.org/>). Such a resource is essential as genome sequencing projects move toward a complete sequence, but probably not essential for species such as oat which may never benefit from a complete genome sequencing project. Of more concern is the need for tools to integrate comparative genomic studies among grasses. Research in this area is being conducted at the USDA-ARS Center for Bioinformatics and Comparative Genomics, Cornell University (<http://ars-genome.cornell.edu/>) and at the National Centre for Genomics Research (<http://www.ncgr.org/research/cgmt/>).

Occasionally, special tools are needed for management of “in-house” or collaborative projects. Figures 1-3 (below) depict some of the tools developed and used by the author in applied genomics research. None of these tools provide complete vertical or horizontal data management. However, they serve our current needs, and can be considered as prototypes for features that may be built into future systems of data management.

CONCLUSIONS

Due to rapid advances in genomics of model crop species, the future holds many opportunities for discovery and applications in oat biotechnology. To fully realize these opportunities, we need to continue building some basic tools, including molecular markers and linkage maps. We need to ensure that we do general genomic research which will provide information about similarities as well as differences between the oat genome and other grass species. We need to make sure we can access basic genomics infrastructure, technologies, and bioinformatics tools. Finally, we need to create common resources which are available to the entire oat research community. Because we are a small

community with close links between breeding and basic research, and because we are not burdened by major, direct corporate interests, the international oat community should be a leader in the sharing of unique resources such as experimental germplasm.

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FIGURE CAPTIONS

Figure 1. Dramatization of an oat mapping resource managed by M5 software (Tinker 1999). Raw data is managed using a Microsoft Access relational database. The M5 software reads text files exported from the database and generates a set of static web pages such as those shown in this illustration. We have found these pages to be a useful in-house resource for sharing data and developing projects. Pages are uploaded to a secure web server for sharing with external collaborators. In this illustration, the user has started with a home page (top left) and navigated to one of a dozen oat maps under development. The map page (lower left) contains an entire map in tabular format, which can be scrolled or searched for key-words. Each marker connects to a link-page showing other maps and loci mapped using the same probe (top right). Inferences about QTL locations are shown as small thumbnails, which link to further information about how the inference was made (lower right).

Figure 2. Gmaps: a new program for navigating and displaying comparative linkage maps (N. Tinker, unpublished). Data for maps, linkage groups, markers, probes, and mapping populations are read into computer memory from disk. The user can select one or two linkage groups from any set of maps for instantaneous view. Red lines show markers that are named identically, and blue lines show markers which appear to be based on the same probe. Solid lines are used when both markers are identified as “framework”, and dotted lines are used when one or more markers are identified as “placed”. We currently use this software to explore chromosome regions of interest, and to compare new vs. old versions of maps that are under development. The Gmaps software is undergoing further development to allow the display of common markers based on clones with similar sequence. When released, it is hoped that this software will fill a niche for users requiring a quick exploratory tool as well as a means to generate publication-quality comparative maps.

Figure 3. A query from an EST database developed in Microsoft Access at ECORC, AAFC, Ottawa. This database is shared by approximately 30 genomics researchers and technicians at AAFC in Ottawa. With minimal training, users are able to design their own queries to mine information from this database. We have found this to be an advantage over web-based (server-side) queries where designers with advanced computer skills must anticipate user needs. The disadvantage of this database platform is that it is not easily implemented across the internet. For our purpose, this is not a major concern since most data will also be submitted to mature public databases. The example in this figure shows a query to identify oat and rye ESTs belonging to a specific similarity group. The top panel shows the design of the query: the user has chosen desired fields from three related tables, and specified selection criteria. The second panel shows the results of the query: seven oat or rye sequences belong to similarity group 4181, and each has sequence homology to a protein called “Elongation Factor 1-Alpha”. The lower panel shows an additional query which extracts SwissProt annotation for the highest ranking BLAST hit. Oat is not currently part of our sequencing projects, so records have been imported from publicly available oat sequences contributed by Cornell university. The clone called “cdo1359” has been mapped in Kanota x Ogle to linkage group 14 by O'Donoughue, et al., (1995). The rye sequences shown in this query have been submitted to Genbank by ECORC researchers.

Quaker Map Database - Netscape

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Bookmarks Location: nt.NCR.AGR.CA/quaker/maps/maps.htm What's Related

WebMail Contact People Yellow Pages Download Channels RealPlayer

Quaker Map Database

- Home page: <http://res.agr.ca/prc/quaker/index.htm>
- QTL Summary Page
- crude graphical maps
- Raw Data - [Mapmaker format](#)
- Raw Data - [QMendel format](#)
- Raw Data - [MOTL format](#)
- Raw Data - ["Wallpaper" style](#)
- HTML Maps:
 - [tm](#) --- Terra x Marion Hexaploid Oat Map
 - [tmredo](#) --- Terra x Marion Hexaploid Oat Map
 - [tmex](#) --- Linkage map for Terra x Marion extended population in hexaploid oat
 - [tmold](#) --- Terra x Marion Hexaploid Oat Map
 - [ko](#) --- Kanota/Ogle Hexaploid Oat Map

Placement criteria: Minimum Chi Sq. = 7.0

Linkage Group: TM1(KO33)

(changed)
Total cM: 31

cM	Framework Map	Placed markers (informative recombination fraction is shown in brackets)
0	(seq)* cdo836B	(10/98) {-----} = 6 cM (12/95) {---X---} (4/96) * seq (3/71) {---X---} (6/71) * ACG (8/53) {-----X-----} (6/53)
6	(seq)* cdo1255	(22/98) {-----} = 14 cM
20	(seq)* cdo497X	(9/99) {-----} = 5 cM (8/95) {---X---} (4/96) * acol17 (4/99) {---X---} (9/100) * aco2 (9/94) {---X---} (2/94) * acor16 (7/85) {---X---} (3/86) * acor21 (9/99) {---X---} (4/100) * umun (10/91) {---X---} (15/92) * ACG (4/63) {---X---} (4/63) * ACG (14/83) {---X---} (9/84) * ACG (11/90) {---X---} (4/91) * AG (6/46) {---X---} (4/46) * A (8/35) {---X---} (2/45) * A (6/45) {---X---} (2/45) * A (5/87) {---X---} (6/87) * acol13
25	(seq)* cdo1321B	(8/83) {-----} = 5 cM (4/82) {---X---} (6/72) * acol1 (3/100) {---X---} (6/84) (seq)* acol1 (10/73) {---X---} (9/61) * A (7/70) {---X---} (6/59) * A (2/31) {---X---} (0/25) * ACA * C (5/87) {---X---} (7/76) * ACC (3/47) {---X---} (3/42) * AGG (6/39) {---X---} (5/30) * A (4/92) {---X---} (6/78) * ACA
31	* ACC_CAC140	

Go to [top of this map](#)

Document: Done

QTL Inference "hgt_tm_b"

Anchor	acor160
trait	hgt
QTL Name	hgt_tm_b
Trait	Plant Height
Updated	27-Apr-00
Contact	De Koeper
General description	QTL Tibor/Marion affecting plant height (QTL x E - whole, covered)
Evidence (Whole)	
Evidence (Covered)	
Evidence (Naked)	
Effect (Whole)	
Effect (Covered)	
Effect (Naked)	
QTL x E (Whole)	TS=21.4, p<0.0001
QTL x E (Covered)	TS=25.1, p=0.001
QTL x E (Naked)	

Project: Quaker Map Database
Home Page: <http://res.agr.ca/prc/quaker/index.htm>
Email: linkema@em.agr.ca
Generated by: [Multiple Molecular Marker Map Manager \(M5\)](#) Version: 31 December 1999
Creation date: 9/6/00

map]

Clone	N	H%	T%	D%	Caution	match	info needed
cdo1255	111	3	41		No	yes	

map]

P	Clone	N	H%	T%	D%	Caution	match	info needed
	cdo1255	111	3	41		No	yes	

map]

s TM group

1

map]

Enzyme	AFLP	part1	part2	Filters	Likely Group	Chisq	D
					G	1.19	N

Figure 2

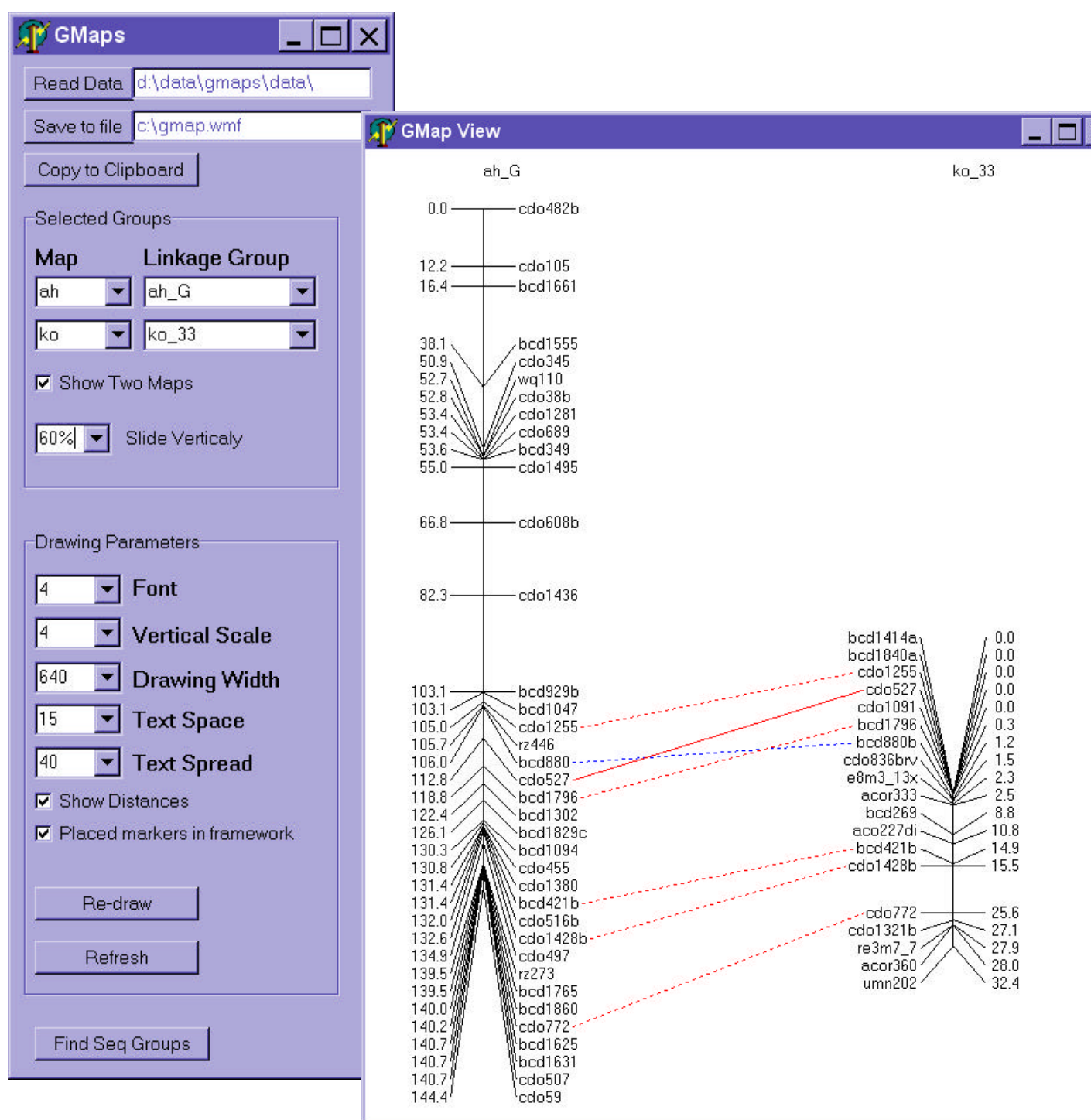


Figure 2

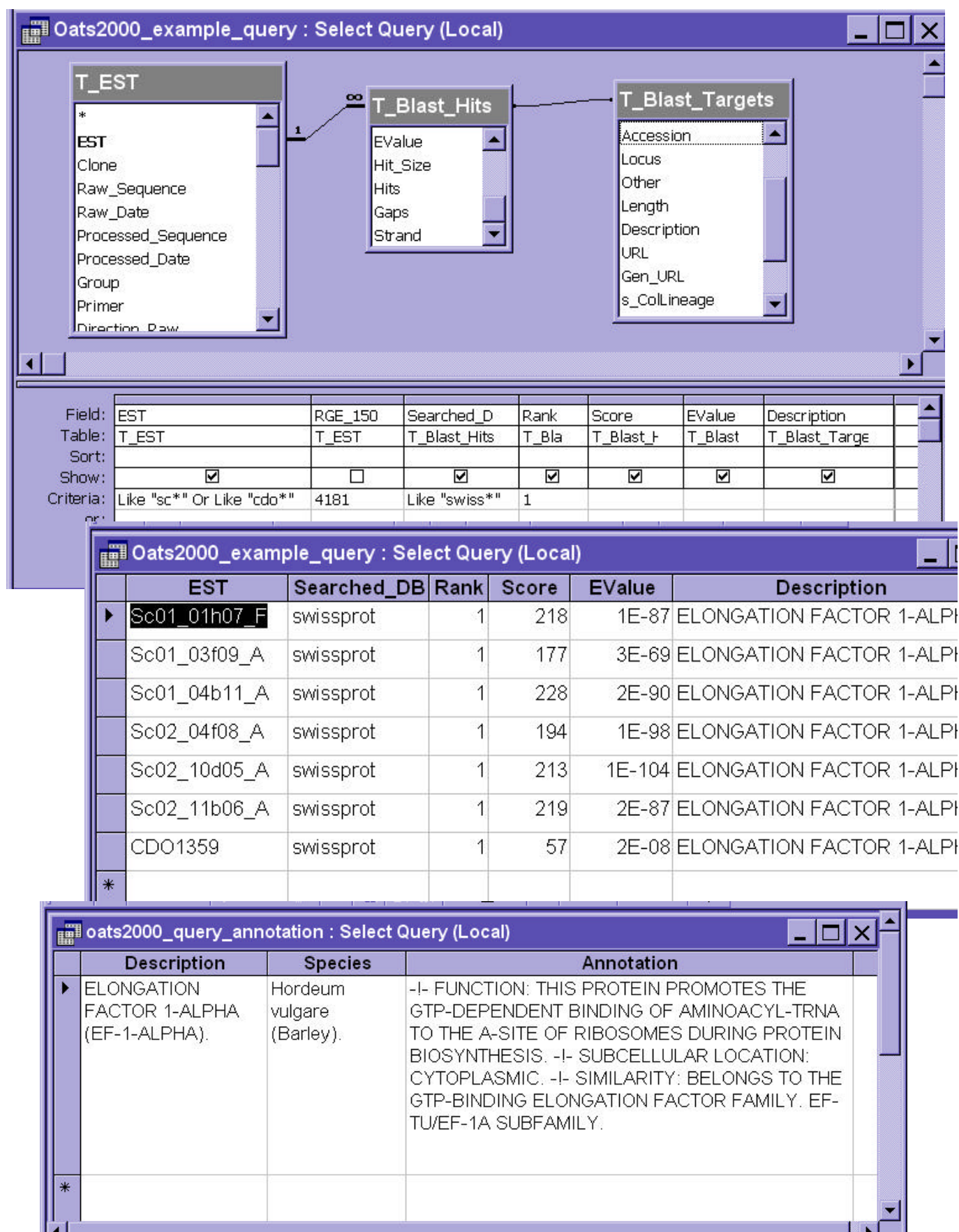


Figure 3.

QUANTITATIVE TRAIT LOCI (QTLs) FOR PARTIAL RESISTANCE TO CROWN RUST IN OATS

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ABSTRACT

To identify QTLs in oat (*Avena sativa*) associated with adult-plant partial resistance to the crown rust pathogen (*Puccinia coronata* f. sp. *avenae*), a population of 158 F₆-derived recombinant inbreds from a cross of an identified partial-resistance line MN841801-1 by a susceptible cultivar selection Noble-2 was mapped with 112 RFLP loci. A linkage map was constructed into 17 linkage groups and 23 unlinked loci. Three partial resistance QTLs were identified in field tests and explained about 27% of phenotypic variance. Two of these QTLs were also identified in greenhouse tests. The consistency of identification of these QTLs across three field environments and two greenhouse environments suggests that markers associated with them may be useful in marker-assisted selection for partial resistance to crown rust in oat breeding.

INTRODUCTION

In oats the demonstrated ability of the crown rust pathogen to rapidly overcome high level race-specific host resistance has led to a strong interest in breeding oats with partial, race-nonspecific resistance with expectations that the resistance will be more durable. Such partial resistance often is expressed only in adult plants and under multigenic control, thus making selection and breeding for it complex. Molecular marker analyses of test populations to characterize QTLs contributing to partial resistance and to identify markers associated with these QTLs should facilitate breeding for the traits using marker-assisted selection. A molecular marker linkage map for hexaploid cultivated oat has been developed in the cross Kanota x Ogle and consists of more than 700 restriction fragment length polymorphism (RFLP) markers supplemented with amplified fragment length polymorphism (AFLP) and other markers (O'Donoghue et al. 1995; Kianian et al. 2000a; Groh et al. 2000). QTLs have been characterized in this and related populations for several traits including barley yellow dwarf virus resistance (Jin et al. 1998), oil content (Kianian et al. 1999), β -glucan content (Kianian et al. 2000b), and several agronomic traits (Siripoonwiwat et al. 1996; Holland et al. 1997). The purpose of this report is to describe identification of QTLs and associated RFLP markers for partial crown rust resistance in the oat line MN841801 crossed with the susceptible cultivar Noble.

MATERIAL AND METHODS

Plant populations

A population of 158 F_6 -derived recombinant inbred lines (RILs) from a cross between 'MN841801-1' and 'Noble-2' was developed by single seed descent. The two parents are single-plant selections from the partial resistance line MN841801 and from the rust susceptible cultivar Noble. MN841801 is susceptible to most rust isolates in seedling tests but has retained adult plant partial resistance through many years of field testing in a buckthorn nursery.

Disease resistance evaluation

Adult plant resistance was evaluated in two greenhouse environments and three field environments. For greenhouse tests a 10 cm length segment of the first leaf below the flag leaf of a plant at floral emergence stage was spray inoculated with a spore suspension aliquot of rust isolate 93MNB236. This isolate was chosen from among five isolates tested based on its high virulence to both parents in seedling tests. Beginning at about 12 days post-inoculation, pustule number was counted at 2-day intervals for 5 dates. After the last reading, the leaf was harvested and a digital image made which was used to estimate a percentage of pustule area (PPA) as a function of the area of the inoculated leaf segment. This leaf area measurement was used with the previous pustule number count to calculate pustule number per cm^2 (PN) and the 2-day interval counts to calculate a Area Under Disease Progress Curve (AUDPC). Three environments were used for field tests, two years at St. Paul and one year at Rosemount, Minnesota. Plants at St. Paul were spray inoculated at heading with a bulk mixture of rust isolates collected from a buckthorn nursery. Rust development at Rosemount was from natural infection. Percentage of pustule area on the flag leaf was estimated on 2 to 3 dates and the PPA values used to calculate AUDPC values.

Molecular marker linkage map

Two hundred forty-two RFLP markers previously mapped in Kanota x Ogle (Kianian et al. 2000a) were selected to provide optimal map coverage and together with seven resistance gene analogs (RGAs) from barley were tested for polymorphisms between MN841801-1 and Noble-2. A total of 112 scorable polymorphisms were used to construct a linkage map for MN841801-1 x Noble-2. DNA extractions and RFLP analyses were as described in Kianian et al., 1999.

QTL data analysis

Data were analyzed by single marker regression and by interval mapping using the software package MQTL (Tinker and Mather, 1995). One marker with the highest R^2 value from each QTL was chosen for multiple regression to estimate the proportion of phenotypic variance explained by all the QTLs identified. Disease data from greenhouse (pustule number, AUDPC, and percent pustule area) and field (percent pustule area and AUDPC) tests were analyzed separately.

RESULTS AND DISCUSSION

Disease evaluation

The disease rating values for the population were normally distributed with no progeny line consistently being more resistant than the MN841801-1 parent. Only a few lines were more susceptible than the Noble-2 parent. Correlations of the various disease parameters analyzed were higher between the three field environments (0.42 to 0.56) and between the two greenhouse environments (0.44-0.49), $P < .0001$ for all, than between field and greenhouse environments (0.19-0.41), $P < .05$. Because of the diversity of environments and inoculums, QTL data from greenhouse tests were analyzed separately from those of field tests.

Linkage map construction

Based on 112 RFLP loci analyzed in 158 RILs of MN841801-1 x Noble-2, 17 linkage groups were formed and 23 loci remained unlinked.

QTL detection

Three crown rust partial resistance QTLs, termed PRQ1, PRQ2, and PRQ3, were identified in field tests and together explained about 27% of the phenotypic variance for analyses based on either percent pustule area or AUDPC. These QTLs were located on linkage groups C, P, and N, which putatively correspond to linkage groups 17, 36, and 22 of the Kanota x Ogle map based on the respective associated markers, CDO1467, UMN23, and UMN360. Two of these QTLs (PR1 and PR2) were also identified in greenhouse tests and together explained 0.26 to 0.39 of the phenotypic variance observed there, depending on the rust parameter analyzed. All resistance alleles were contributed by the MN841801-1 parent.

Current efforts

This population is being screened and mapped with AFLPs to provide more extensive map coverage of the large hexaploid oat genome and to find possible additional QTLs and markers more tightly linked to the identified QTLs. More user-friendly PCR-type markers are being tested or developed for these QTLs for use in marker-assisted selection. Also, we crossed MN841801-1 by two Minnesota breeding lines, MN94112 (now cv. Richard) and MN95102, and F7 progeny lines of these crosses were scored for rust resistance in field tests this summer. Markers associated with QTLs identified in MN841801 x Noble will be tested on these two populations to determine if the same crown rust partial resistance QTLs can be detected in these two crosses as were found in the original mapping cross.

ACKNOWLEDGMENT

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QTL ANALYSIS AND MAP UPDATE FOR THE OAT CROSS 'OGLE' X 'TAM O-301'

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SUMMARY

Detailed molecular genetic maps of crop species have enabled the detection of quantitative trait loci (QTL)- molecular marker associations. These associations they have identified candidate markers for marker-assisted-selection (MAS) procedures. Our objectives were to use new mapping information to determine QTL-marker associations, and to add more amplified fragment length polymorphism (AFLP) markers to the new 'Ogle' x 'TAM-O301' map. The parents, recombinant inbred lines, and two check cultivars were evaluated for seven agronomic and two seed quality traits in four environments (two years x two locations). Significant QTL-marker associations were found and these were compared with results of a previous study. This information will be useful to oat breeders and geneticists who are improving oat.

INTRODUCTION

Common cultivated oat (*Avena sativa* L.; *A. byzantina* C. Koch) is an allohexaploid ($2n=6x=42$) with three distinct sub-genomes: A, C, and D (Rajhathy and Thomas, 1974). Among cereal grains, oat has several unique properties such as elevated oil and protein concentration of the seed (Schrinkel, 1986). Although the breeding and genetics of oat has not received as much attention as other major cereal crops, the modern tools of molecular biology have enabled the development of molecular maps for diploid oat (O'Donoghue et al., 1992; Rayapati et al., 1994) and hexaploid oat (O'Donoghue et al., 1995). The oat mapping effort has led to a study

to find associations between quantitative trait loci (QTL) and marker loci (Siripoonwiwat, et al., 1996). They reported on QTL for several agronomic traits for cultivated oat and emphasized the need to further study oat QTL-marker associations with other crosses in additional environments.

The objectives of this study were to further assess oat QTL-marker relationships using a newly constructed hexaploid 'Ogle' x 'TAM O-301' (OT) oat map (Portyanko et al., 1999) and to add more amplified fragment length polymorphism (AFLP) markers to the new map. The results will be compared to a previous oat QTL study and the information will be used to design specialized marker-assisted selection procedures for oat, a unique cereal grain.

MATERIALS AND METHODS

Plant Materials and Experimental Design The mapping population consisted of 136 F₂-derived F₆ recombinant inbred (RI) oat lines developed by single seed descent (SSD) from the cross of Ogle and TAM O-301. The population was grown in 1998 and 1999 at Aberdeen and Tetonia, Idaho, USA. The Aberdeen location represents an irrigated valley site, while the Tetonia location is typical of a high elevation non-irrigated environment.

The experimental design was a twelve by twelve lattice with two blocks. Each environment (location x year) contained the RI lines, parents, and two each of adapted checks 'Monida' and 'Ajay' in 144 1.22 m X 2.44 m four-row plots in each block. The seeding rate was 48 grams per plot (140 kg/h) at both locations. All 136 recombinant inbred lines were used in the analyses. The cultivated hexaploid oat RFLP linkage map developed by Portyanko et al. (1999) was utilized in this study. A framework map of 280 DNA markers providing good linkage map coverage was used in the QTL analyses.

AFLP Analysis The protocol for the AFLP procedure follows that given in Hoffman et al. (2000) with the following exceptions: DNA was isolated from plants at the three-leaf stage using the chloroform extraction procedure of Doyle and Doyle (1980); the *Eco*RI primers with an infrared dye instead of ³³P-dATP. The final amplification products were run in a 7% w/v Long Ranger® polyacrylamide gel inside a LiCor 4200L automated DNA sequencer. Primer pairs were selected based upon the number of polymorphisms and strength of amplification observed in a preliminary screening procedure. Polymorphisms were scored visually from a digitally produced image generated by the Base ImagIR® program.

Evaluation of Field Traits Days to heading was estimated as the time from planting until approximately 50 per cent of the panicles in a plot completely emerged from their respective leaf sheaths. After the plants reached maturity, plant height was measured to the top of the canopy. At maturity, lodging was scored on a 0 to 100 percentage basis with zero equating to no lodging while 100 was severe lodging. Tertiary seeds were counted from five randomly chosen panicle tops from each plot. The number found was the score given. Plot damage prevented the scoring of tertiaries at the Aberdeen location. Grain yields were obtained by machine harvest of the two internal rows at Aberdeen and all four rows at Tetonia. The seed was dried in a greenhouse and weighed on an electronic balance and recorded as grams per plot. Test weight was obtained from one sample of each plot experimental unit using a 0.946L container.

Quality Analyses

Fourteen grams of seed from each plot was initially dehulled with a barley de-awner and hand-picked until seven grams of clean, unbroken groats was obtained for quality analyses. Groat oil and protein concentration was determined on a dry weight basis. These analyses were conducted at the USDA-ARS Cereal Crops Research Unit in Madison, Wisconsin, with the near-infrared transmittance (NIT) technique.

Data Analyses

Phenotypic data for all traits, except tertiary development, were initially analyzed using analysis of variance (ANOVA) and correlation (CORR-Pearson) procedures (SAS institute, 1995). A Windows™ compatible version of the MQTL program (Tinker et al., 1995) was used to infer QTL associations with marker intervals. The SIM (simple interval mapping) procedure was used. A walk speed of 5cM and 1000 permutations were used in the SIM analysis to find significant ($\alpha = 0.05$) associations.

RESULTS

The tables and figures showing the results were too lengthy to be presented here and will be presented on the poster. A brief summary of the results follows. Genotypic effects for all traits were significant as were location effects. Year effects were not significant for the traits analyzed at the time of this writing. Thus, a second analysis was conducted as to location over years. Transgressive segregation was observed for each trait in all four location x year environments.

At Aberdeen, heading date was negatively correlated with test weight and groat oil concentration, while groat protein concentration was positively correlated with groat oil concentration and test weight. Plant height was correlated with lodging percentage. Similar relationships were determined for the Tetonia location except that heading date and groat protein concentration were negatively correlated. Also, at Tetonia, seed yield was positively correlated with test weight, yet negatively correlated with groat oil and protein concentration.. Test weight was negatively correlated with groat protein concentration at Tetonia.

Significant associations between QTL and marker intervals were found. All QTL were found in both locations except for test weight. One significant association was found for groat protein concentration, test weight, lodging, and tertiary seed development at both locations. Two associations each were identified for heading date, and groat oil concentration. Three were found for seed yield and plant height. A small cluster of QTL was identified on Ogle x TAM O-301 Linkage Group 1 (OT LG1) and consisted of plant height, lodging, and test weight.

The newly added AFLP markers were distributed throughout the established framework markers and some mapped into sizable gaps. Some clustering of AFLP markers was noted.

DISCUSSION

Eleven significant QTLs were identified for the nine quantitative traits reported here. Paterson et al. (1991) demonstrated that correlated traits tend to map to the same region or marker. Siripoonwiwat et al. (1996) also found this trend in their oat QTL study. We found this to be the case for the correlated traits plant height and lodging which displayed peaks on OT LG 1, but not for traits correlated to heading date as found by Siripoonwiwat et al. (1996). The two studies did overlap in the use of the Aberdeen location, but different mapping populations were used in the two experiments.

Based on some common markers, this study and that of Siripoonwiwat et al. (1996) apparently identified some of the same QTLs such as that for plant height (OT LG 1; 'Kanota' x Ogle (KO) LG 24_26_34) and groat oil concentration (OT LG13; KO LG 11_41). It is possible that this study may have identified some new QTLs, such as for seed yield and groat protein concentration. This supports the suggestion in Siripoonwiwat et al. (1994) that further QTL studies are needed to identify all (or most) of the QTLs for a given trait.

We are collecting and analyzing data from additional environments (locations x years) and these will be added for the final report of this study. In addition, Dr. David Peterson is analyzing the entries from this experiment for levels of certain antioxidants. The information found from this experiment and others like it will be useful for oat breeders and geneticists in designing selection schemes and experiments for the genetic enhancement of oat.

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SCAR MARKERS LINKED TO THE PC68 RESISTANCE ALLELE ARE AN EFFECTIVE TOOL FOR SELECTION

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ABSTRACT

Crown rust resistance is an important characteristic for oat varieties developed in many areas of Canada and the United States. Marker-assisted selection (MAS) with two sequence characterized amplified region (SCAR) markers linked to the Pc68 crown rust resistance gene was successfully utilized to identify oat lines containing Pc68 resistance in four oat populations. Each of these markers can be used as either a dominant or co-dominant marker, depending on the alleles present in the population of interest. Research is ongoing to improve the efficiency of MAS using these markers.

INTRODUCTION

Effective crown rust (*Puccinia coronata* Corda. F. sp. *avenae* Eriks. & E. Henn.) resistance genes provide yield and quality stability in oat (*Avena sativa* L.) growing regions where this disease is prevalent. Pc68 is a gene that has been incorporated into cultivated oat from the wild species, *A. sterilis* (Wong et al., 1983), and has been utilized extensively in Canadian oat breeding programs. Several important cultivars possess this resistance gene, including AC Assiniboia and AC Medallion developed at the Cereal Research Centre (CRC) in Manitoba and AC Aylmer and AC Francis developed at the Eastern Cereal and Oilseed Research Centre (ECORC) in Ontario. The Pc68 gene resides in a genomic region also containing the stem rust (*P. graminis* Pers. F. sp. *avenae* Eriks. & E. Henn.) resistance genes, Pg3 and Pg9 (O'Donoghue et al., 1996). Randomly Amplified Polymorphic DNA (RAPD) markers linked to Pc68, Pg3, and Pg9 have been identified (Penner et al., 1993b; Penner et al., 1993a; O'Donoghue et al., 1996). SCAR markers were successfully developed based on the RAPD markers linked to Pg3 and Pg9 (Orr et al., 1998). The objective of this study was to evaluate the effectiveness of the Pg3 and Pg9 SCAR markers for selection of oat lines possessing the Pc68 resistance allele.

MATERIALS AND METHODS

Plant Material

Four populations were evaluated in this study and are designated A-D. These included: 189 F2 plants from AC Assiniboia x MAS4-112 (A), where MAS4 is a cross between AC Antoine and OA 971-8, two Terra x Marion progeny; 85 F3 families from Pc68 x Pc94 (B); 189 F3 families from the complex cross AC Antoine *3 / AC Goslin // OA971-8 *3 / AC Medallion (C), where only progeny from OA971-8 *3 / AC Medallion homozygous for Pc68 were used for crossing; and F6 plants from AC Aylmer x AC Goslin (D). For population D, only lines with the marker allele linked to resistance were evaluated for crown rust reaction.

Rust Screening

Crown rust evaluation took place in greenhouses at ECORC or CRC. Race CR241 was used to test for Pc68 resistance in populations A, C, and D and race CR223 was used to screen population B, due to the presence of Pc94. For populations A and D, the whorls of tillers of individual plants were needle inoculated with urediniospores suspended in a very dilute Tween 20 solution. Twelve or more one-week old seedlings from F3 families of populations C and D were spray inoculated with urediniospores suspended in light mineral oil. Inoculated seedlings were placed in a dew chamber overnight and then returned to the greenhouse. Crown rust reactions were scored 10-12 days after inoculation. Plants and families were categorized as resistant, susceptible, or segregating.

PCR Analysis

Genomic DNA was extracted from leaf discs using the methods described by Edwards et al. (1991) or using leaf squashes onto DNA collection cards (Gentra Systems, Minneapolis, MN). SCAR markers were developed based on amplified fragments linked to Pg3 and Pg9 obtained using the RAPD primer UBC195 (Orr et al., 1998). Standard PCR analysis protocols were used to amplify DNA fragments. Both Pg3 and Pg9 SCAR markers can be used as a dominant or co-dominant marker, depending on the alleles present in the parents. For the co-dominant marker system, digestion with *RsaI* is required to differentiate between the resistant (0.3 kb) and susceptible (0.2 kb) alleles. The Pg9 SCAR was tested in population A, C, and D, and the Pg3 SCAR was used in population B. For population A, these markers are dominant and amplified products were run on 1.5% agarose gels. In populations B, C, and D, post-amplification restriction was required and PCR products were separated on 5% agarose gels. All three alleles were segregating in population C. Images of ethidium bromide stained gels were captured using a Kodak Digital Science 1D version 3.5 digital image analysis system.

RESULTS AND DISCUSSION

Each of the parents with the Pc68 resistance allele (AC Assiniboia, Pc68, AC Aylmer, and AC Medallion) produced the PCR product (0.3 kb) associated with this allele using either Pg3 or Pg9 SCAR markers. Segregation of Pc68 resistance fit the expected ratios of 3:1, 1:2:1, and 1:2:1 for populations A - C ($p = 0.90, 0.18, \text{ and } 0.88$, respectively) based on Chi-square tests. The marker alleles fit the segregation ratios 3:1 (dominant), 1:2:1 (co-dominant), and 22:2:1:7 (dominant and co-dominant) for populations A - C ($p=0.24, 0.40, \text{ and } 0.60$, respectively). The complex segregation of the marker alleles in population C

reflects the presence of the amplified products linked to the resistant allele from AC Medallion, the susceptible allele from AC Goslin, and a “null” susceptible allele present in AC Antoine and OA971-8. The plants or families within each population were classified according to marker genotype and crown rust reaction in Table 1.

There was a good association between marker genotype and presence of the Pc68 resistance allele. The accuracy of predicting rust reaction from the presence of the marker allele linked to the resistance allele in the resistant class of plants or families ranged between 0.92 to 0.97 for the four populations (Table 1). In the susceptible class, the accuracy was between 0.80 and 1.00. The lowest estimate was obtained using the dominant marker system on individual F2 plant data from population A. An explanation for the lower association in this population may relate to the difficulties associated with dominant PCR-markers and the inability to distinguish “null” alleles from failed PCR reactions. For this reason, we have a preference to use and develop PCR markers with constitutive / background bands or with co-dominant inheritance.

Based on the results of this study, marker assisted selection in oat has the potential to augment conventional phenotypic selection. MAS for simply inherited crown rust resistance has the greatest potential in locations or environments with infrequent or inconsistent rust infestations or to pyramid more than one effective resistance gene into a single line. The co-dominant SCAR markers also allows identification of homozygous lines within a population with a reduced need for progeny testing. The marker system described in this paper is now routinely utilized in the oat breeding program at ECORC as pre-selection tool in early generations. Research is continuing to improve the MAS system by: incorporating additional PCR markers associated with other disease resistance genes, quality and agronomic traits; developing and refining rapid DNA extraction protocols; and working towards an automated, high-throughput MAS laboratory.

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Table 1. Association of SCAR marker alleles and reaction of individual plants or families to race CR223 or CR241 of Puccinia coronata in four oat populations.

Pop.	Gen.	SCAR	Rust Reaction	Marker Genotype†					
				AA	A_	AB	BB	B_	Null
A	F2 Plant	Pg9	R_	-	130	-	-	-	11
			S	-	4	-	-	-	43
			Accuracy‡	-	0.97	-	-	-	0.80
B	F3 Family	Pg3	R	24	-	2	0	-	-
			Seg.	2	-	33	0	-	-
			S	0	-	1	23	-	-
			Accuracy	0.92		0.92	1.00		
C	F3 Family	Pg9	R	-	52	0	-	0	0
			Seg.	-	81	9	-	0	2
			S	-	5	0	-	6	34
			Accuracy		0.96	1.00		1.00	0.94
D	F6 Plant	Pg9	R_	105	-	-	-	-	-
			S	5	-	-	-	-	-
			Accuracy	0.95	-	-	-	-	-

† A is the amplified product (0.3 kb) associated with the Pc68 resistance allele; B is the amplified product (0.2 kb) associated with the Pc68 susceptibility allele; “null” is no amplified product associated with the Pc68 susceptibility allele.

‡ Accuracy of predicting rust reaction from marker genotype within marker class.

COMPARISON OF MICROSATELLITE AND RFLP- DERIVED PCR MARKERS

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ABSTRACT

Two sources were evaluated for the production of polymerase chain reaction (PCR) markers in oats. First, nucleotide sequences of 306 randomly selected clones from an oat microsatellite-enriched genomic library were determined. Fifty of the 68 primer pairs designed were functional, of which 32 (64%) were polymorphic among 13 *Avena* species and 14 (28%) were polymorphic between Kanota and Ogle. Second, primers were designed from the sequences of six cDNA RFLP probes. Primer pairs from all 6 cDNA clones were polymorphic among the 13 *Avena* species and three were polymorphic between 'Kanota' and 'Ogle'. Thirty-five loci were placed on the hexaploid oat RFLP map.

INTRODUCTION

Cultivated oat (*Avena sativa* and *A. byzantina*) is an important cereal crop. It is a self-pollinating allohexaploid with a large genome. Breeders and geneticists are increasingly using molecular markers in oat and other plant species to study genome structure, genetic relationships, and manipulate genes. Microsatellites or simple sequenced repeats (SSRs) have emerged as an important source of ubiquitous genetic markers for many eukaryotic genomes (Wang et al., 1994). Microsatellites are tandemly repeated stretches of 2 to 8 base pairs that can vary extensively in the number of repeats and have been reported to be highly informative, locus-specific markers in cereals including barley (Saghai Maroof et al., 1994), rice (Wu and Tanksley, 1993), and wheat (Roder et al., 1998). The analysis of microsatellites is based on polymerase chain reaction (PCR), which is much easier to perform than RFLP analysis and is highly amenable to automation. The reproducibility of microsatellites is such that they can be efficiently used by different research laboratories (via published primer sequences) to produce consistent data.

The objectives of the present study were to (i) isolate and characterize microsatellite markers in oat (ii) compare the levels of polymorphism of SSR and RFLP-based PCR markers, and (iii) map microsatellites on a molecular linkage map of hexaploid oat (O'Donoghue et al., 1995).

MATERIALS AND METHODS

Plant materials

Thirteen oat cultivars ('Clintland 64', 'IL86-5698', 'IL86-6404', 'Golden', 'Gopher', 'Pennuda', 'Hazel', 'Don', 'Coast Black', 'Ogle', 'Kanota', 'Terra', and 'Newdak') and 10 accessions/plant introductions representing 13 *Avena* species (*A. byzantina*, *A. fatua*, *A. abyssinica*, *A. barbata*, *A. maroccana*, *A. vaviloviana*, *A. wiestii*, *A. brevis*, *A. eriantha*, *A. longiglumis*, *A. nuda*, and *A. strigosa*) were used to investigate the polymorphism detected by microsatellites. Genomic DNAs were extracted from the above oat lines and 71 RILs of a cross of 'Kanota' × 'Ogle' mapping population (O'Donoghue et al., 1995) by the CTAB method.

Library construction and microsatellite retrieval

Microsatellite-enriched libraries were constructed as described by Prochazka (1996) using genomic DNA from oat cv. 'Clintland 64'. Plasmid DNAs were extracted using Qiagen Plasmid Mini Kits. DNA of 30 clones containing GAA repeats were provided by G. Scoles (University of Saskatchewan). Insert sequences were determined using Applied Biosystems model 377 sequencers.

Primer design and evaluation

Primers flanking cloned microsatellites sequences were designed using PRIMER3 (Rozen and Skaletsky, 1997) and synthesized by GIBCO BRL. A second set of primers were designed from the sequences of RFLP probes BCD1882, BCD1950, BCD1407, CDO1158, CDO270, and CDO669 that are linked to loci for barley yellow dwarf virus tolerance (BYDV; Jin et al., 2000). For the RFLP-derived primers that did not produce polymorphic bands directly, the PCR products were cloned and sequenced from the 'Clintland64' and 'IL85-5698' parental lines as described above.

PCR amplifications were performed in 20 µl containing 30 ng of template DNA, 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 0.2 mM of each dNTP, 2.5 mM MgCl₂, 0.1 unit Taq DNA polymerase, 1.5 pmole ³³P-labeled forward primer and 1.5 pmole of unlabelled reverse primer. PCR was performed using one of the following two PCR conditions (i) one cycle of 94°C, 1 min; followed by 25-30 cycles at 94°C, 1 min; 58°C, 1 min; 72°C, 1 min with a final elongation step of 72°C for 5 min; (ii) a 'touchdown' PCR consisting of 14 cycles at 94°C, 1 min; 65°C, 1 min; and 72°C, 1 min. Annealing temperatures were decreased 0.7°C/cycle to 55°C. PCR continued for 30 additional cycles at 94°C, 1 min; 55°C, 1 min; and 72°C, 1 min with a final elongation step of 72°C for 5 min. PCR products were analyzed on 6% denaturing polyacrylamide gels and detected with x-ray films.

Linkage analysis

Linkage analysis and map construction were performed using MAPMAKER version 3.0 (Lander et al., 1987) and a 'Kanota' × 'Ogle' data set (Siripoonwiwat et al., 1996). Markers were grouped with a log-likelihood of the odds (LOD) score of 3.0 and maximum recombination level of 0.30. Map distances were calculated as previously described (Jin et al., 2000).

RESULTS

Characterization of microsatellite clones

Of the 306 cloned inserts sequenced, 250 (82%) were unique and contained microsatellite repeats. One hundred fifty-five (62%) clones had perfect repeats. Three types of dinucleotide repeats (AC/TG, AT/TA and AG/TC) were identified in this study. AG/TC repeats were the most prevalent followed by AC/TG and AT/TA repeats. Repeat length ranged from 2 to 69 for dinucleotide repeats and from 3 to 60 for trinucleotide repeats. In about 30% of the clones, sequence flanking the repeats was not of sufficient length or complexity to design specific primers. Primer pairs were designed from 68 unique microsatellite flanking sequences.

Out of the 68 pairs of primers, 50 (74%) gave amplification products of the expected sizes at Tms ranging from 55 to 60°C. The sizes of the products varied from 102-341 bp with an average size of 198 bp. These 50 primer pairs were used to detect polymorphisms among 13 *Avena* species and 13 different oat cultivars. Among the 13 *Avena* species, 32 (64%) of the primer pairs were polymorphic. Primer pairs produced from one to six bands representing up to five loci and up to seven alleles with an average of 2.9 alleles per locus. In contrast, most of the primers were monomorphic for the oat cultivars 'Clintland64', 'IL86-5698', 'IL86-6404', 'Golden', 'Gopher', 'Pennuda', 'Hazel', 'Don', and 'Newdak'. Only 14 (28%) of the primers showed polymorphisms among cultivars 'Kanota', 'Ogle', 'Coast Black', and 'Terra'.

All but one of the primer pairs that were designed from RFLP probe sequences amplified multiple loci with two to four alleles per locus. Primer pairs from all six of the RFLP probes were polymorphic among the 13 *Avena* species and three (p1882, p270, and p1158) were polymorphic between Kanota and Ogle. Only p270 was directly polymorphic between 'Clintland64' and 'IL86-5698'. Even though the sequences of the amplified fragments from 'Clintland64' and 'IL86-5698' were very similar, about 94% identical, it was possible to identify differences in restriction sites in the two parents for bands produced by primers p1407 (*Mbol*) and p1950 (*Msel*).

Linkage analysis

The segregation of all 17 (14 microsatellite and 3 RFLP) primers that showed polymorphism between 'Kanota' and 'Ogle' was evaluated in the 'Kanota' × 'Ogle' mapping population. Thirty eight polymorphic bands were scored and assigned to 19 linkage groups. Twelve markers were mapped to unique positions; 23 assigned to intervals; and three were unlinked.

Most of the markers mapped at LOD score values greater than 6.0. Markers AM112, AM75A, AM98A mapped at the same positions as RFLP markers on linkage groups 17, 37, and 15. RFLP-derived markers p1882-1, p1882-2, p270-1 and p270-2 mapped either very close to (distance less than 5 cM) or at the same position as the corresponding RFLP markers. In the 'Clintland 64' × 'IL86-5698' population, p270 mapped to a position corresponding to p270-1 in the 'Kanota' × 'Ogle' population and p1950 was unlinked.

DISCUSSION

A set of 250 microsatellite-containing clones was isolated from an enriched library constructed from 'Clintland 64' genomic DNA. A high percentage of clones (65%) contained AG/TC, CA/GT, or AT/TA dinucleotide repeats, which is similar to earlier reports of microsatellites in wheat (Bryan et al., 1997) and rice (Panaud et al., 1995). As previously reported for barley, wheat, and rice (Liu et al., 1996; Ma et al., 1996; Panaud et al., 1996), (AG) repeats were more common than (AC) in our study. (AT) repeats usually represent the most common type of repeat in plants (Powell et al., 1996; Wang et al., 1994), but in this study the frequency was lower than that of (AG) and (AC). This may be because (AT) repeats are palindromic and therefore may not have been efficiently enriched during the capture process.

Primer pairs could be designed from 71% of the unique microsatellite clone sequences. Most of the primer pairs designed (74%) yielded functional microsatellite markers. Similar success rates were reported for sorghum (Brown et al., 1996) and wheat (Roder et al., 1998).

Of the functional primer pairs, 64% (32 out of 50) detected polymorphisms among 13 *Avena* species. Only 28% of the functional primer pairs detected intraspecific polymorphisms, which is similar to AFLPs (Jin et al., 2000), but less than that of RFLPs on the same material (O'Donoghue et al., 1995). The low level of polymorphism observed with the microsatellites could be because of the small sample size.

No clear relationship between total repeat length and degree of polymorphism was observed in this study. Longer repeats, like (AC)₃₅, were monomorphic whereas, shorter repeats, like (AC)₉, were polymorphic. This is in contrast to results for wheat (Bryan et al., 1997) where the degree of polymorphism increased with the total length of the repeat. The average number of alleles per locus of 2.9 observed in our study is comparable to the value for wheat (Bryan et al., 1997; 3.5).

The PCR markers derived from sequences of RFLP markers (e.g., p1882-2, p1882-1, p270-1, and p270-1) often mapped to the same or similar positions as the corresponding RFLP markers within and among mapping populations. In these studies, we were able to use sequence information from the amplified bands to identify RFLPs within monomorphic fragments. It should also be possible to use this type of sequence information to develop nucleotide polymorphism markers (SNPs), like molecular beacons (Tyagi and Kramer, 1996), for use in marker-assisted selection for BYDV tolerance loci. In this study, microsatellites were no more polymorphic than other markers. Since multiple SNPs could be detected even within the coding regions of genes and the techniques for the development of SNPs and microsatellites are similar, it may be possible to identify more informative SNP markers than microsatellites from the same level of analysis.

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FACTORS INFLUENCING T-DNA TRANSFER IN OATS

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ABSTRACT

A protocol for *Agrobacterium*-mediated transformation of oats was determined following the study of the effect of various factors affecting T-DNA transfer to oat tissue. Highest transformation efficiencies were obtained when tissues were co-cultivated with *Agrobacterium* for long periods in absence of acetosyringone and on a low salt medium for the first 3d. Wounding the tissue prior to inoculation with *Agrobacterium* and vacuum infiltration also increased transformation efficiency. Although GUS expression was observed 4 weeks after inoculation of embryo, embryo axis, embryogenic callus and leaf base, no plants regenerated following selection on PPT.

INTRODUCTION

While genetic transformation of oat by particle bombardment is now well established, it often results in integration of high copy number of transgenes, transgene rearrangements and co-integration of separately transferred genes (Leggett *et al.*, 2000; Pawlowski and Somers, 1996; Pawlowski and Somers, 1998). Plant transformation via *Agrobacterium tumefaciens* can however result in simpler integration patterns and in the independent segregation of co-transferred genes. While the number of reports of *Agrobacterium*-mediated transformation of rice (Zhang *et al.*, 1997), barley (Wu *et al.*, 1998), wheat (Cheng *et al.*, 1997) and maize (Ishida *et al.*, 1996) is increasing, so far, transformation of oat by this method has not been reported. We describe here the observation of GUS expression in oat tissue transformed with the *gus* gene via *A. tumefaciens* and propose a transformation protocol based on the study of variables affecting transformation efficiency.

MATERIAL AND METHODS

Excised mature embryos, embryo axes, 6 weeks-old mature embryo-derived embryogenic callus and seedling leaf bases of *Avena sativa* cv. Melys or Bullion were inoculated with *Agrobacterium tumefaciens* ($OD_{600} < 1$) in MS2 (MS salts, 30 g/l sucrose, 2 mg/l 2,4-D, pH5.2) or $\frac{1}{10}$ MS2 (as MS2 with $\frac{1}{10}$ MS salts) as stated in the text. Co-cultivation was carried out on solidified MS2 and/or $\frac{1}{10}$ MS2. Acetosyringone (AS) was used at 200 μ M unless otherwise stated. Media used for callus induction were MS2.TA (MS salts, 20 g/l sucrose, 150 mg/l asparagine, 0.5 mg/l thiamine, 2 mg/l 2,4-D, 0.3% gelrite, pH5.8) for embryos and L3 (Gless *et al.*, 1998) for leaf bases, both supplemented with 150 mg/l Timentin. Selection and regeneration were carried out on MS2 (pH5.6) and MSK medium (MS salts, 30 g/l sucrose, 0.2 mg/l kinetin, 0.8% agar, pH 5.6) respectively, both supplemented with 150 mg/l Timentin and 3 mg/l PPT.

Agrobacterium strains AGL1 and LBA4404 carrying binary plasmids based on the pSoup/pGreen system (Hellens *et al.*, 2000) were used for transformation. The T-DNA containing the *bar* and *gus* genes, both controlled by the maize *Ubi1* promoter, was carried by the pGreen vector renamed pAL156. Two pSoup vectors carrying a *virG* gene were used (*virG*^{WT} on pAL166 and *virG*⁵⁴² on pAL155).

RESULTS

Development of GUS expression in transformed tissues

No transient expression was observed immediately after co-cultivation in initial transformation experiments carried out using various *Agrobacterium* strains, oat explants and experimental procedures. However GUS expression could be detected four weeks after co-cultivation, in tissue that had been cultured on non-selective medium. Therefore the effect of various variables on transformation efficiency, as described in the next section, was determined as the number of GUS expressing foci detected 4 weeks after transformation.

Study of the effect of variables on transformation efficiency and determination of a transformation protocol

Because zygotic embryos are readily available, whole embryos or embryo axes were used as explants to test the effect of different variables on transformation efficiency, and to select and regenerate plants. Due to the destructive nature of the GUS assay, and in order to increase the chances of recovering transformed plants, transformation efficiency was determined on the non-embryogenic tissue that had developed from the embryos or embryo axes, while the embryogenic tissues were cultured on selection medium. Transformation efficiency was calculated as the mean number of GUS expressing foci/explant.

Effect of co-cultivation period. The length of the co-cultivation period significantly affected the transformation efficiency, with almost no GUS foci being detected four weeks after transformation in experiments in which explants were co-cultivated for 3 days or less. Highest transformation efficiencies were detected following a 9-day co-cultivation period (Fig1). Other experiments confirmed that long co-cultivation times (6-10d) were necessary for T-DNA transfer to oat cells (data not shown).

Effect of salt concentration. When the salt concentration in the MS inoculation and co-cultivation media was decreased tenfold, the number of GUS foci on embryo axes four weeks after transformation with AGL1/pAL155/pAL156 was increased 22 fold (av. 31 foci/explant). However $\frac{1}{10}$ MS2 medium had an adverse effect on embryogenesis from embryo axis which produced less and smaller embryogenic calli than embryo axes co-cultivated on full strength MS2 medium. The effect of reducing the time the tissues were incubated on $\frac{1}{10}$ MS2 during co-cultivation on the transformation efficiency was therefore investigated. Results showed that a minimum of 3d on $\frac{1}{10}$ MS2 medium during a 7d co-cultivation was necessary to observe a significant increase (6.6-fold) in transformation efficiency compared to a 7d co-cultivation on MS2 medium (Fig2). In addition, the embryo axes produced embryogenic calli which resembled those produced by the embryo axes co-cultivated on MS2 medium in both number and quality. Therefore a 3d-cocultivation on $\frac{1}{10}$ MS2 followed by a 4d-cocultivation on MS2 was optimal for efficient T-DNA transfer without loss of embryogenic potential of embryo axes.

Effect of acetosyringone. The effect of the concentration of the *vir* gene inducer AS was tested on embryos of cv. Bullion with AGL1/pAL155/pAL156 on MS2 medium for 9d, either in the absence of AS or with 200 or 400 μ M AS. GUS expression four weeks after transformation was 10-fold higher in tissues that had been transformed in the absence of AS (av. 7.8 foci/explant) than in tissues transformed in the presence of 200 μ M AS (Fig3A), even though *Agrobacterium* had not been pre-induced. Increasing the AS concentration to 400 μ M resulted in a 7-fold decrease in GUS expression. The development of calli was also adversely affected by 400 μ M AS, and to a lesser extent by 200 μ M AS. The effect of omission of AS in the inoculation and co-cultivation media ($1/10$ MS2) on the transformation efficiency of embryo axes was further investigated using a preinduced *Agrobacterium* strain. Omission of AS from the co-cultivation medium alone had no effect on transformation efficiency (Fig3B), however omission of AS from both media induced a 2.3-fold increase in efficiency compared to when AS was present in both media.

Effect of cell damage. Treatments destined to favour *Agrobacterium* attachment onto oat cells were tested. Although transformation conditions in these experiments were not optimal (full strength MS, 200 μ M AS), and resulted in low GUS expression (<0.9 foci/explant), wounding the tissue by particle bombardment and vacuum infiltration were shown to increase transformation efficiency, while plasmolysing the explants on $1/10$ MS2 supplemented with 0.2 M mannitol + 0.2 M sorbitol only slightly increased transformation efficiency (data not shown).

These studies have led to the outline of a protocol for *Agrobacterium* transformation of oat, in which the *Agrobacterium* were pre-induced with 200 μ M AS in MG/L medium, centrifuged, and resuspended in inoculation medium ($1/10$ MS2) at $OD_{600} < 1$. Explants were immersing in this suspension for 2-3h (inoculation), rinsed in $1/10$ MS2 medium and blotted on sterile filter paper. Co-cultivation was carried out on solid $1/10$ MS2 medium for 3d and then on MS2 medium for a further 3-4d. Explants were then transferred to callus induction (MS2.TA) medium supplemented with Timentin to inhibit *Agrobacterium* growth and transferred to selection medium (MS2) containing PPT, 2-4 weeks after co-cultivation, depending on the explants used for transformation.

Potential of different oat explants for transformation

Four oat explants (embryo, embryo axis, callus and leaf base) were tested for their potential for transformation by *Agrobacterium* using the above protocol with *Agrobacterium* strain AGL1/pSoup/pAL156. Five weeks after inoculation, and callus growth in the absence of PPT, transformation efficiencies for embryogenic callus and leaf base were very similar (1.9 and 1.62 GUS foci/explant, respectively). In addition some of the somatic embryos produced from leaf base callus, also showed strong GUS expression. The number of GUS foci/explant were comparable for embryo and embryo axes explants (23.9 and 21, respectively) and much higher than the GUS expression observed in embryogenic callus or leaf base explants.

Selection of transformed tissue

Tissues from all experiments were transferred to selection medium containing PPT. Five weeks after the start of selection the GUS expression detected in embryogenic callus (derived from inoculated callus, embryo or embryo axis) was limited to small spots, but no large clusters of transformed cells originating from the division of an initial transformant, or

GUS expressing somatic embryos were observed. Surviving calli turned green when transferred to regeneration medium and shoots were induced. However, no plants regenerated on 3 mg/l PPT, no GUS expression was detected in these regenerating calli and the transgenes could not be detected by Southern blot analysis.

DISCUSSION

We present here a report of the occurrence of T-DNA transfer into oat cells, the identification of factors that affect transformation, and we propose a protocol for *Agrobacterium*-mediated transformation of oat. The long co-cultivations (6 to 10d) required for T-DNA transfer into oat cells correlates with reports of long co-cultivations in other cereals (Guo *et al.*, 1998; Li *et al.*, 1992; Wu *et al.*, 1998; Zhang *et al.*, 1997). This is in contrast with the short, 2 to 3d co-cultivation usually needed for transformation of dicots and suggests that T-DNA transfer might be slower in monocots. The salt content of the media had the most dramatic effect on transformation efficiency, as was found in wheat by Cheng *et al.* (1997). However in oat, limiting culture on $\frac{1}{10}$ MS2, to a maximum of 3 d, was necessary to avoid adversely affecting somatic embryogenesis. Unexpectedly we found that both T-DNA transfer and the growth of oat tissue were negatively affected by prolonged co-cultivations in the presence of AS. The highest level of GUS expression was obtained when *Agrobacterium* was pre-induced before centrifugation, and inoculation and co-cultivation were done in the absence of AS. Moreover efficient T-DNA transfer was observed when *Agrobacterium* was not induced at all, suggesting that oat tissue alone is able to induce *vir* genes, which is in accordance with the work of Usami *et al.* (1988). Similarly, Wu *et al.* (1998) reported that addition of AS in co-cultivation did not influence the development of transient or stable expression in barley. The absence of GUS expressing somatic embryos or large GUS expressing cell cluster after five weeks selection on PPT, and the lack of transformed plants was surprising and suggests that the *bar* gene was not expressed in these tissues. Non-expression of a complete *bar* gene sequences could be due to silencing or to malfunction of the construct itself. Alternatively, the gene sequence integrated in the genome could be incomplete. The protocol reported here using embryo or embryo axis as explant provides a good system to study additional factors that could further increase transformation rates. In spite of the difficulties encountered, we believe that oat will soon join the list of cereal crops transformable via *Agrobacterium*.

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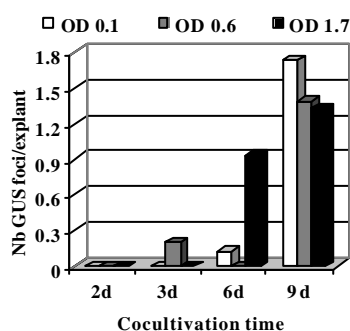


Fig. 1. Effect of cocultivation time on transformation efficiency.

GUS expression was determined 4 weeks after transformation of mature

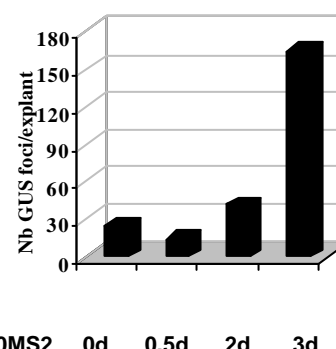
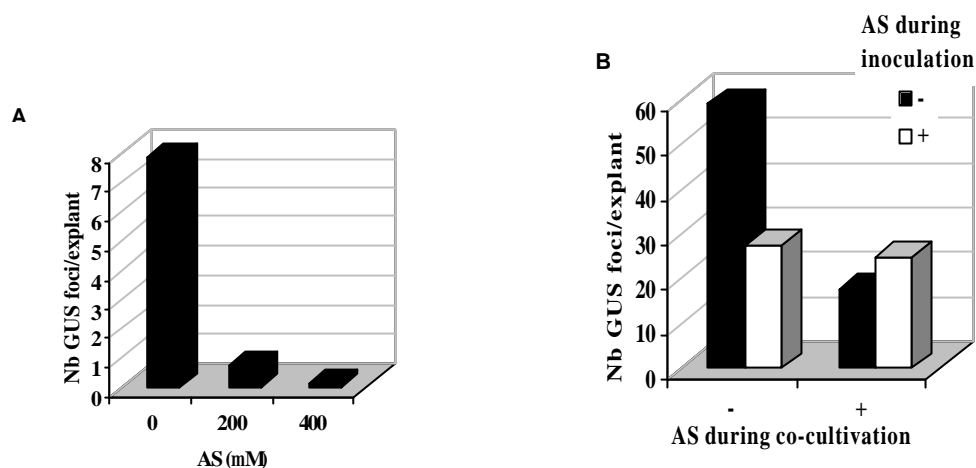


Fig. 2. Effect of low salt concentration on transformation efficiency.

GUS expression was determined 4 weeks after transformation of embryo axes of cv



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Fig. 3. Effect of acetosyringone on transformation efficiency.

GUS expression was determined 4 weeks after transformation of embryo cv. Bullion (A) and embryos axes cv. Melys (B) with AGL1/pAL155/pAL156. A, effect of the presence or absence of AS during both inoculation and cocultivation (MS2); B, effect of the presence or absence of AS during inoculation and/or co-cultivation ($1/10$ MS2).

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DEVELOPMENT OF PCR BASED MARKERS FOR MOLECULAR MARKER ASSISTED BREEDING

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ABSTRACT

Within the ECORC oat development program, a total of 44 PCR based markers are currently under development and study for molecular Marker Assisted Selection (MAS). The data for the entire collection has been reviewed with regard to several parameters important to the design of MAS in oats. This poster summarizes the behaviour of these markers including the average percent polymorphism and the percent of PCR based markers mapping to the target loci.

INTRODUCTION

Our research group is developing and testing MAS (Marker Assisted Selection) in oats. MAS breeding is an attractive breeding alternative for traits that are genetically complex or that are difficult or expensive to monitor conventionally, such as certain pathology and quality traits. MAS is based on establishing the genetic linkage between the gene or QTL (quantitative trait locus) of breeding interest and a neighbouring molecular genetic marker and then monitoring this molecular marker "tag" in lieu of the gene or QTL itself. To be practical, MAS requires "user-friendly" PCR (Polymerase Chain Reaction) based markers as tags. However, the existing molecular recombination maps of oats were largely developed using robust but labourious RFLP (Restriction Fragment Length Polymorphism) markers which are not PCR based, supplemented with RAPD (Randomly Amplified Polymorphic DNA) or AFLP (Amplified Fragment Length Polymorphism) markers. Both RAPD and AFLP markers are PCR based and contribute significantly to mapping, but may be inappropriate for MAS. Current initiatives are populating the oat map with suitable PCR based markers. Estimating the size of the oat genome as 3,000 cM, this would require a minimum of 300 such markers, and likely twice that number, to achieve uniform 10cM density coverage. A promising strategy is the random mapping of microsatellite or SSR (Simple Sequence Repeat) markers as undertaken by G. Scoles and collaborators.

Our short term goal was to initiate MAS studies at ECORC as soon as a few loci of interest were identified and mapped. These earliest available loci were for crown and stem rust resistance and QTL for certain agronomic and quality traits. To explore MAS with these loci required targeted development of suitable PCR based markers (Orr et al 1998; conference poster by De Koeyer et al, SCAR Markers Linked to the Pc68 Resistance Allele Are An Effective Tool for Selection). The major strategy was to develop convenient PCR based markers, especially SCAR (Sequence Characterized Amplified Region) markers, from flanking RAPD and RFLP markers. Our "toolbox" currently holds forty-four PCR based markers. While still a small number for rigorous statistical analysis, certain trends are emerging which may help to guide similar initiatives.

MATERIALS AND METHODS

For converting RAPD markers, the polymorphic RAPD band was excised from an agarose gel and sequenced. New larger PCR primers of 20 to 25 bp were designed, usually including the 10 bp RAPD primer binding site at each end of the original RAPD fragment. These first generation SCAR primers were tested and optimized under a series of PCR reaction conditions in an effort to duplicate the original polymorphism and simultaneously produce a much simpler banding pattern than the original multi-band RAPD pattern. To facilitate this, several variants of the first generation SCAR primers were also designed and tested in parallel, and in pair-wise combinations of all forward with all reverse primers. To convert an RFLP marker, the plant DNA insert in the bacterial plasmid used for the original RFLP mapping was purified and sequenced. In our original approach, several potential forward and reverse SCAR primers were designed based on standard rules. Recently, additional strategies based on a deeper study of a probe's DNA sequence, or comparison to homologous or orthologous genes from a database, have been employed to guide primer design. These RFLP derived SCAR primers were tested as described above for RAPD derived primers. When SCAR primer(s) gave equal size band(s) on the genotypes of interest, then post-amplification restriction with up to 17 restriction enzymes was done to search for a useable polymorphism in DNA sequence.

To validate linkage of new SCAR markers with the target locus, each was screened for polymorphism against mapping parents or appropriate Near Isogenic Lines. If monomorphic, post-amplification restriction was tested. Where polymorphic, SCARs were mapped. To establish applicability, new SCARs were screened for polymorphism on AC Aylmer and AC Goslin, the parents of our first MAS study, and on a broad selection of breeding germplasm.

RESULTS AND DISCUSSION

A total of 44 PCR based markers, which include 41 SCARs plus 3 barley SSRs, have been developed or evaluated for MAS in oats. The present report summarizes the results and identifies trends that will prove useful in making PCR based markers more readily available.

Polymorphism of PCR Based Markers

Percent polymorphism is a critical parameter at both the development and implementation stages for PCR based markers. At the development stage, new markers must be validated by confirming their linkage to the target trait through mapping on a polymorphic population. At the implementation stage, the validated marker must be polymorphic on the parents of the MAS cross. Further, to be a broadly applicable tool for MAS, the marker should have a high level of polymorphism across diverse germplasm. Percent polymorphism data has been determined for a number of germplasm comparisons.

The most complete reference map for oats is based on the Kanota x Ogle (K x O) cross (Groh et al, 1998). Polymorphism of PCR based markers on K x O was 39 % (14 polymorphic markers of 36 tested). This is within the range of 17, 48, 53 and 63 % observed for RFLP probes from four different cDNA libraries during the original K x O mapping (O'Donoghue et al 1995). As K x O is an *A. byzantina* cv Kanota x *A. sativa* cv Ogle cross, it is expected to be more polymorphic than the typical intraspecific cross encountered in MAS. This is an advantage for mapping and validating newly designed markers. A more typical intraspecific cross is Terra x Marion, the cross that we have used to develop an extensive map (Tinker et al 1998b) for QTL analysis in elite germplasm (De Koeijer et al 1998). Percent polymorphism was 19 % (6 of 32 SCARs polymorphic), only

half that of K x O. However, two of the five SCARs that could be mapped in T x M, could not be mapped in K x O, so that access to multiple mapping population is an advantage. In a comparison of fairly narrow Ontario germplasm, a percent polymorphism of 7% (1/14) was observed for the AC Aylmer x AC Goslin cross. The weighted average for the two intraspecific crosses is 15% (7/46). Of monomorphic SCARs, post amplification restriction digestion revealed new polymorphisms for 2 of 7 SCARs tested on K x O, for 0 of 4 on T x M and for 3 of 5 on AC Aylmer x AC Goslin. For the combined data, the percent of monomorphic SCARs which revealed polymorphism after restriction digestion was 31% (5 of 16 tested).

In complementary studies to assess cross applicability, validated SCARs, with or without a specific post-amplification restriction step as required, were surveyed across a broad set of breeding lines. SCARs for which two alleles were detected had frequencies for the minor allele of 15% (13 of 88 lines had minor allele), 18% (15/85), 17% (14/82), 18% (9/50), 22% (4/18), 11% (2/18) and 18% (2/11). The weighted average is 17% (59/352). A few SCARs for which more than two alleles were detected had greater polymorphism.

These results suggest that approximately 60% of typical newly designed SCARs can be mapped in K x O either directly (39%) or following post amplification restriction digestion (19% = .31x61%). A significant portion of the remainder can be mapped in additional less polymorphic intraspecific mapping populations. Validation of linkage to the target locus can then occur through mapping or comparative mapping. Application of a validated SCAR under a single set of reaction conditions will detect the minor allele in 15 to 20% of breeding germplasm. For efficient MAS, options include: the development of multiple independent PCR based markers at important loci; re-evaluation of post-amplification restriction to reveal useful polymorphism between the MAS parents; selection of alternate polymorphic MAS parents.

Probability of SCAR Linking to Target Trait

The final step in developing a PCR based marker for a specific locus is to confirm that the resultant marker in fact maps to the target locus, rather than elsewhere in the oat's complex and polyploid genome. Three of ten SCARs mapped to their target locus in K x O and 3 of 5 in T x M. The weighted average is 40% (6 of 15). On closer inspection, 5 of 10 SCARs derived from RAPD markers and 1 of 5 SCARs derived from RFLP markers mapped to their target loci. These are very small numbers, however SCAR primers derived from RAPD primers often contain the RAPD primer sequence within them and may capture the original mapped RAPD polymorphism. In contrast, RFLP probes often reveal polymorphisms that flank the sequence of the actual probe insert and a SCAR derived from the insert actually reveals a new polymorphism. In addition, matching the size of the SCAR band to the size of the diagnostic RAPD band, can guide the SCAR development to the correct homeolog in a polyploid like oats.

Oat QTLs can occur at homeologous loci (Tinker et al 1998). Therefore, SCARs that mapped to homeologous loci rather than to their intended locus may be of interest for MAS. Of seven SCARs in K x O and two in T x M that did not map to their intended locus, at least two have mapped to homeologous or duplicated regions within a rearranged genome based on flanking markers.

The results suggest that PCR based markers, especially with post amplification restriction, have average percent polymorphism appropriate for MAS. Multiple independent PCR based markers per locus would be recommended.

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USING MOLECULAR MAPPING TO ACCESS AND UNDERSTAND VALUABLE TRAITS IN WILD RELATIVES OF OATS

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ABSTRACT

Wild relatives of crop species are a rich source of valuable traits from which currently only a small fraction have been exploited for crop improvement. One of the fundamental problems of crop improvement is how to successfully access genetic variation from such wild species. This is particularly important to the transfer of valuable, novel genes from wild relatives belonging to the secondary or tertiary gene pools to polyploid food crops. In this project, diploid and hexaploid relatives of the cultivated oat are being assessed for a wide range of agronomic characters. We are also producing a genetic map at the diploid level using parents possessing characteristics of added value to industry and agriculture. Moreover, molecular markers identified in this project will not only enable precise transfer of beneficial genes from wild diploid relatives to hexaploid cultivated oats but also assist in the development of novel designer tetraploid oats containing specific combinations of genes as required by specific end-users. Identification of markers to undesirable traits will make possible selection against the simultaneous transfer of adversely linked genes such as shedding grain base, awns and hairy lemmas, which have in the past often reduced the potential of such introgressions in plant breeding programmes. The use of markers should also overcome the previously insurmountable difficulties involved in the breeding of complex traits; the inability to identify individual genes, the masking effects of environment (e.g. soil fertility) and the presence of linked undesirable genes. Molecular markers will then be used to identify recombinants with maximum desirable loci and minimum undesirable loci from the diploid species. An increased understanding of the molecular genetic basis of grain composition will provide tools that will enable the production of premium value grain designed to meet the specific needs of the end user.

RESULTS AND DISCUSSION

Wild diploid relatives of cultivated polyploid crops possess many beneficial characters which are currently difficult to exploit. One of the fundamental problems of crop improvement is how to successfully access genetic variation from such wild species. This is particularly important to the transfer of valuable, novel genes from wild relatives belonging to the secondary or tertiary gene pools to polyploid food crops. In this project, diploid and hexaploid relatives of the cultivated oat are being assessed for a wide range of agronomic characters. We are also producing a genetic map at the diploid level using parents possessing characteristics of added value to industry and agriculture. Moreover, molecular markers identified in this project will not only enable precise transfer of beneficial genes from wild diploid relatives to hexaploid cultivated oats but also assist in the development of novel designer tetraploid oats containing specific combinations of genes as required by specific end-users. Identification of markers to undesirable traits will make possible selection against the simultaneous transfer of adversely linked genes such as shedding

grain base, awns and hairy lemmas, which have in the past often reduced the potential of such introgressions in plant breeding programmes. The use of markers should also overcome the previously insurmountable difficulties involved in the breeding of complex traits; the inability to identify individual genes, the masking effects of environment (e.g. soil fertility) and the presence of linked undesirable genes. Molecular markers will then be used to identify recombinants with maximum desirable loci and minimum undesirable loci from the diploid species. Wild relatives of crop species are a rich source of valuable traits from which currently only a small fraction have been exploited for crop improvement.

The grain composition of oats (*Avena sativa* L.) is critical for its utilisation for food, agricultural and industrial purposes. An increased understanding of the molecular genetic basis of grain composition will provide tools that will enable the production of premium value grain designed to meet the specific needs of the end user. The major storage products found in the oat grain are protein, starch, oil and β -glucan; the highest value fraction being β -glucan, the major endospermic cell wall polysaccharide. However, the genetic variation for β -glucan content in cultivated hexaploid oats is small and this limits progress to improvement from within the existing primary gene pool. Cultivated oats is a hexaploid ($2n = 6x = 42$) comprising three genomes: A, C, and D. We have conducted a survey of diploid *Avena* accessions which revealed that they possess a wide range of seed characteristics, in particular the type and concentration of β -glucans and other storage compounds. Of particular interest, one accession of the wild diploid *A. atlantica* (an A-genome species) had a particularly high β -glucan content in the grain.

The two parental lines chosen for mapping show contrasting performance for a wide range of traits (Table I). 2 reciprocal mapping populations have been developed from single F_1 plants from crosses between these parents. The subsequent F_2 populations produced segregate for these traits (Table I). The frequency distribution of each trait was approximately normal across the 200 F_2 plants assessed for each population. Transgressive segregation was apparent for a number of traits. DNA has been extracted from the F_2 leaf tissue and from the parental lines and is currently being screened for marker polymorphism using both microsatellite and RFLP markers. Further traits are being assessed in the progeny including detailed analysis of seed and panicle characteristics and grain composition. This cross also segregates for the domestication syndrome and the abscission types of the grain have been evaluated.

Table 1 Variation for a range of traits between the 2 mapping family parents and in the F_2 progeny developed from a cross between them.

Trait	<i>A. atlantica</i>	<i>A. strigosa</i>	Mapping progeny		
	mean	mean	mean	min	max
No. of tillers (juvenile stage)	31.5	10.5	16.8	8.0	27.0
No. of productive tillers at harvest	7.2	11.8	9.8	4.0	17.0
Days to flowering (primary stem)	77.3	85.1	80.8	70.0	102.0
Rate of flowering (first 4 tillers)	12.9	2.6	8.1	3.0	16.0
No. of nodes (main stem)	3.0	7.4	4.9	3.0	8.0
Mean internode length (main stem)	53.1	24.7	38.7	27.9	58.7
Panicle length (cm)	41.0	19.6	38.6	26.5	53.0
Straw dry weight (g per plant)	11.8	17.7	18.4	7.4	27.0
Straw length (m)	1.6	1.6	1.8	1.3	2.4

The disadvantage of using a wild relative such as *Avena atlantica* as a source of beneficial characters in that it has low yield, tall straw and agriculturally undesirable non-domesticated traits such as small seeds and spikelet shedding is apparent. However it also possesses a number of desirable traits and it will be possible using the approach described to not only understand the genetic control of those traits but how they are linked on the chromosomes and the involvement of the parental pedigree. Markers developed from this work will enable the precise selection both for desirable traits such as high β -glucan content and against undesirable traits associated with the non-domesticated type with the end result of increasing the marketable quality of the oat crop.

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INTERNATIONAL NAKED OAT - UK TRIALS

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A series of trials to evaluate the UK performance and adaptability of a range of internationally sourced spring naked oats were initiated in 1993. Since then, and with a widening interest in the crop, the trials have now been extended to include a number of European sites.

BACKGROUND

In the early 1990's it was felt that the naked oat offered considerable potential for development and commercialisation and on this premise a trial was initiated to evaluate the performance and adaptability of a number of international naked oat lines.

RESULTS

This dedicated and replicated trial series covering sites throughout the UK recorded yield, disease resistance, lodging, protein and oil content, degree of nakedness, groat discolouration, groat hairiness and hectolitre weight. The varieties in trial emanate from organisations in Canada, USA, Czech Republic, and New Zealand. (Formerly lines from Finland and Norway proved unadaptable). The contribution of varieties to the trials is gratefully acknowledged. Results are summarised below.

INTERNATIONAL NAKED OAT TRIALS – 1999 SUMMARY						
Varieties	Relative Yield % control	Height (Cms)	Maturity 1= late 9=early	Lodging %	Protein %	Oil %
Bullion (c) 5.8t/ha	100	117	6.5	40	12.8	5.6
UK Variety Range	84-103	108-117	3.5-6.0	0 - 75	10.2-14.4	5.5-8.7
USA I Range	64 - 102	106 - 16	2.5 - 7.0	0 - 40	12.7-17.9	4.5-9.0
USA II Range	71 - 76	109-112	5.5-6.5	0-100	14.8-15.4	4.9-5.3
New Zealand Range	76-101	88-113	2.5-6.5	0-50	10.5-15.4	4.6-7.5
Czech Republic	83	123	4.5	95	13	6.5

Source: IGER Report of 1999 International Oat Series

The 2000 trial series has been extended to include trial sites in Finland, Norway, Sweden and Germany where the proportion of spring oats grown is much higher than that in the UK. Yield and agronomic results for the 2000 trials for one site are shown below, the complete agronomic and quality results are eagerly awaited.

Varieties	Relative Yield %	Heading Date (June)	Height (cm)	Brackling (%)
Bullion Control 7.3 t/ha	100	17	107	13
UK	93-109	17-20	100-108	5-18
Norway	74	18	124	6
Finland	86	18	119	18
USA	60-92	13-20	106-116	0-8
Germany	88	17	116	8
Poland	82-93	12-18	112-116	2-3
New Zealand	80-96	14-25	108-112	0-5
Canada	84	20	129	0

Source: IGER 2000 report in preparation - data from Aberystwyth only

In order to protect individual confidentiality the results are shown as a range.

DISCUSSION

Yield performance has generally been promising where naked oats have given yields some 20% less than would be achieved with husked varieties. A wide maturity range was noted with two lines, one from both New Zealand and USA being markedly later than all others in 1999. Lodging is a significant factor and a marked improvement has been noted in the new types being included in these trials. With regard to protein, lines approaching 18% were recorded and this is particularly interesting in respect to improving the grain quality. High oil lines were recorded in both the UK and one of the US series.

From the initial 2000 results some high yielding lines have been identified.

With the trials now being extended to other European countries, it is expected the results will provide interesting comparisons between performance and protein contents.

The collaborators of this project are keen to extend an invitation to participate to any breeder with bona fide naked oat lines which they may wish to be included in this series. Individual trial results will be available to participants. These trials are sponsored by Semundo and the Superioat Company and co-ordinated by IGER.

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EUROPEAN OAT BREEDING PERSPECTIVES

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INTRODUCTION

Geographically, Europe is similar in size to the inhabited areas of North America, but its border and language barriers make an understanding of European activities in many subjects nigh impossible. It is with much trepidation therefore, that we agreed to make a presentation on Oat Breeding in Europe.

The Russian Federation remains the largest oat producer but production in the last two years has almost halved. Declines in production in Ukraine and Belarus have pushed these countries into 6th and 12th highest producers compared to 3^d and 7th in 1994 (Valentine 1996). Production has more or less stabilised in Poland, Germany, Finland, Sweden and the UK. Notably, production in Spain has more than doubled to a level broadly similar to that of the UK (Table 1). The oat area in Spain (409,500ha in 1999) is over four times larger than that of the UK (92,000ha), with average yields in 1999 reported as 1.3t/ha compared to 5.9t/ha in the UK (Anon, 2000).

SURVEY OF EUROPEAN BREEDERS

Unfortunately, very few European oat breeders attend international conferences. In order to obtain some facts regarding the breeding opportunities in Europe, we decided to undertake a survey of breeders. A short questionnaire was designed, bearing in mind that lengthy forms were unlikely to be completed. We sent out 22 questionnaires to breeders in 12 countries. Ten replies - a 45% response - were received from UK (2), Germany, Austria, Sweden, Norway, Finland, Latvia, Poland and Czech Republic. A full list is given in the Acknowledgements.

Main uses of Oats

Nine of the ten respondents indicated that the main use of oats was for animal feed. The UK is notable in that 49% of the oat crop was used for human consumption and only 39% for animal feed. As expected, seed accounted for the small portion of usage but no respondent reported non-food industrial use. Sweden and Finland export significant quantities of oats.

Breeding Method

Pedigree selection was the main (75-100%) breeding method in 8 cases. One breeder (Norway) used bulk breeding (progenies bulked in early generations). Seven breeders used a pedigree bulk method to a greater (e.g. Sweden, Finland and Austria) or lesser extent (e.g. Norway, Latvia, Poland and Czech Republic). This commonly involves multiplication in bulk until the F3 generation. In contrast, Boreal Plant Breeding in Finland select in F2 and F3 and again in F5 or F6.

Small amounts of effort were devoted to back crossing (IGER UK, Sweden, Latvia and Czech Republic) and to introgression from wild spaces (IGER, Sweden, Finland and Czech Republic). IGER devoted a small amount of effort into recurrent selection (to produce radically earlier, higher yielding spring oats), accelerated breeding methods, namely accelerated pedigree selection and mutagenesis. Finland devoted a small amount of effort into single seed descent. No programme used marker-assisted selection or transformation in breeding.

Size of Programme

Five breeding programmes reported making 50-100 crosses. The programmes in Poland and Finland reported making 100-150 crosses. Breeding work in each of these programmes was carried out by one or two persons. One programme (Sweden) made 200 crosses carried out by four persons, while two (IGER, Czech Republic) made 250 crosses being carried out by three and eight persons respectively. The actual number of persons involved should be treated with caution as it depends on whether less skilled staff or research workers have been included.

Breeding Objectives

Most programmes, except for the UK, solely bred husked spring oats with white or yellow grains. Exceptions were IGER and Monsanto in the UK (mainly winter oats), Norway and Austria (small effort in black oats) and IGER, Finland, Poland and Czech Republic which also bred naked oats.

All respondents ranked yield as the most important breeding objective for growers although two breeders ranked standing power as equally important, or as in the case of Finland, ranked standing power and earliness as equally as important. Six of the other respondents ranked standing power the second most important objective for growers. For the two organisations breeding winter oats, winter hardiness was the third most important objective; otherwise the remaining objectives were earliness followed by disease resistance.

For breeding objectives for food use, kernel content was generally rated most important, with kernel discolouration recognised as equally important or even more important by two respondents. Though we know specific weight to be a poor indicator of quality between varieties, most breeders (except IGER) gave a high ranking to this characteristic. One breeder (Norway) abstained on the basis of not breeding oats for food use.

For breeding objectives for feed use, kernel content was ranked first or second by seven out of eight respondents. The naked character was ranked equalled first and second by IGER and Poland respectively. Not unnaturally, others not involved in oat breeding gave naked oats a very much lower ranking. There was generally poor consensus as to what constituted a high quality feed oat.

Nature of Funding

Only one of the surveyed breeding programmes (Latvia) was wholly funded by the public sector. Others were either wholly commercially funded, or in addition as in the UK, Swedish, Finnish and Polish programmes, had attracted farmer co-operation, levy or public funds.

We would consider that the partnership between the Ministry of Agriculture, Fisheries and Food, the Home-Grown Cereals Authority and Semundo Ltd, with underpinning research funded by the Biotechnology and Biological Sciences Research Council, has been particularly successful in maintaining breeding programmes at IGER which are responsive

to the needs of growers and industry. As part of continual dialogue with industry, IGER and its partners held a meeting with diverse end-users in August 2000 which demonstrated clear interest and direction in the genetic improvement of oats in terms of its role in sustainable agricultural systems, new and existing uses of oats for human consumption and naked oats for animal feed.

We would also regard the Svalöf Weibull AB breeding programme as another successful funding model. Formed by the merger of two world-famous establishments (Svalöf AB, owned by the Swedish government and farmers, and the privately owned W.Weibull AB), Svalöf Weibull AB is now 60% owned by SLR (The Swedish Farmer's Supply & Crop Marketing Association) and 40% by BASF. Svalöf Weibull also has a 15% stake in BASF Plant Science.

ACHIEVEMENTS OF BREEDING

In this Section we will rely on our own experience rather than the survey to outline some of the recent achievements of breeding in Europe.

In the UK, advances in the last decade (e.g. the release in 1993 of the short straw winter oat i.e. Gerald) have made oat growing more profitable and easier. Winter oats are also grown in France. The black-grained oat Fringante (bred at INRA in 1980) is still by far the most widely-grown variety there despite the much higher yield of recently released varieties such as the black-grained Caleche (Serasem). In the European spring oat crop, important varieties include Jumbo and Lutz (Nordsaat), Flamingslord (Lochow-Petkus), Expander and Explorer (Saatzucht Edelhof) and Revisor (Firlbeck) in Germany and Austria; the black-grained oat Auteil (Serasem) and the white-grained oat Chantilly (Serasem) in France; Freja, Stork and Belinda (Svalof-Weibull) in Sweden; Veli (Boreal) in Finland; Dragon and Jawor (Danko) from Akt, Bajka and Slawko from Strzelce Plant Breeding in Poland and Auron, Ardo and Abel (Selgen) in Czech Republic. In the most northerly parts of Norway, Sweden and Finland, specific varieties are required that will mature in their very short growing season. Roope and Aarre are two recent varieties produced in Finland by Boreal Plant Breeding. Varieties such as Barra widely grown in Ireland (Svalof-Weibull) and Prevision (breeder not known) in Spain are autumn-sown but lack winter-hardiness or vernalisation requirements.

As far as high quality is concerned, naked oats are a well established crop in the UK at an interesting stage of development in relation to poultry feed markets (see paper by Maunsell). A third generation of naked oats since commercialisation in 1999 includes the winter naked oat Grafton, the dwarf Icon and the spring oat Bullion which incidentally has also done well in Western Canada. As a result of the release of the naked variety Akt in Poland in 1997, naked oats occupied 16% of seed production in 1999. The grain is used for poultry feeding.

In Sweden the high oil variety Matilda, containing 100g/kg DM oil, has found a valuable role in feeding to horses.

Another notable quality achievement has been the release of the winter oat Millennium from the IGER programme. This variety combines very large grains with thin husks conferring high milling quality and high potential feeding value.

The release of the new thin-husked varieties Birgitta and Vendela by Svalöf Weibull AB will be of great interest to the millers.

CONCLUSIONS

It is apparent from the survey and our background knowledge of breeding in Europe that oats are an under-invested crop in Europe. The number of crosses made by oat programmes is much smaller than the number of crosses that would be made in wheat or barley programmes. Oat programmes have not yet been able to tap into molecular biological techniques such as new technologies particularly marker-assisted selection. On the positive side, medium sized oat breeding programmes that have brought in additional funding from commercial industry, farmers, levies or government may be able to have more distant horizons in relation to meeting the needs of industry and to the use of alternative breeding methods to produce radical changes.

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Table 1 - Oat Production in Europe (Top twelve countries in descending order)

	Production ('000t)				
	1995	1996	1997	1998	1999
Russian Fed	8562	8346	9387	4662	4400
Poland	1494	1581	1630	1460	1446
Germany	1420	1606	1599	1279	1347
Finland	1097	1261	1243	975	1215
Sweden	947	1200	1274	1136	1093
Ukraine	1116	731	1062	777	759
France	601	622	568	658	550
UK	617	589	577	587	540
Spain	231	664	520	698	530
Norway	353	385	359	381	396
Romania	404	290	325	362	389
Belarus	638	706	829	501	375
Europe (excluding former USSR)	8790	9886	9880	9272	9235
N C America	7002	5247	6706	6009	6456
World	35734	33678	25598	30913	25508

Source: FAOSTAT Database, 25 August 2000

GLOBAL AND MEGA-REGIONAL BREEDING PERSPECTIVES: NORTH AMERICA

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INTRODUCTION

Oat breeders in North America focus on the enhancement or improvement of several critical traits important to oat production and utilization. In the United States, consideration of disease resistance is the most critical aspect of oat germplasm enhancement and cultivar development, with crown rust resistance receiving special attention, and barley yellow dwarf virus resistance or tolerance, stem rust resistance, and smut resistance also being important. Other characteristics of obvious importance include grain and forage yield, lodging and shattering resistance, test weight, oat groat content, protein content, oil content, soluble fiber content (as measured by beta-glucan content), grain color, short straw, and insect resistance. However, the most critical issue relative to oat improvement is the marked decline in oat acreage over time, especially in the United States, and the gradual decline in oat research effort in both the public and private sector in North America.

OAT PRODUCTION IN THE UNITED STATES, CANADA, AND MEXICO

The USDA – National Agricultural Statistics Service (NASS) has published oat acreage statistics for the United States since 1866. The U.S. acreage first reached 30 million acres in 1895; coincidentally the date of the first entry of an oat accession in what is now the USDA-ARS National Small Grains Collection. Over the years in the late 1800s and early 1900s, the U.S. acreage maintained or gradually increased, reaching a peak of 47.5 million acres in 1955. A steady decline in oat acreage has occurred in the U.S. since 1955 to a point where only 4.5 million acres were planted in 2000. Wheat acreage in the U.S. in 1955 was 58.2 million acres and in the same year 16.3 million acres of barley were planted. Today about 4.7 million more acres of wheat are planted in the U.S. vs. 1955; however, barley has declined to 5.7 million acres, and now exceeds the U.S. oat acreage. Perhaps as somewhat of a surprise, corn acreage in the U.S. today is about the same as in 1955 when 80.9 million acres were planted vs. the 79.6 million acres planted in 2000. Another point to ponder is that since 1955, oat yields reported by the USDA-NASS have increased by about 56% whereas wheat yields have increased 116%, barley yields 113%, and corn yields 217%.

The USDA–NASS also publishes oat acreage statistics for Canada, Mexico, and other nations. During the past twenty years the oat acreage in North America has declined from about 6.6 million hectares to the current 2.8 million hectares. The harvested area in Canada and Mexico has been relatively constant during the past 20 years, with most of the decline in North America attributable to the decline in oat plantings in the United States. (See Table 1.)

Based on statistics published by Statcom, Ltd., during the past seven years the planted acreage of oats in Canada has been relatively constant, with the 2000 planted acreage

being slightly higher than the 1994 acreage. There appears to be a slight tendency toward a decline in acreage in eastern Canada and an increase in acreage in western Canada. In any case, in 2000 over 93% of the planted oat acreage in Canada was reported in the western provinces of Alberta, British Columbia, Manitoba, and Saskatchewan. Brian Rossnagel indicates that with Canadian freight/transportation changes, the oat acreage in western Canada has shifted from being grown primarily in Alberta and Saskatchewan to primarily Saskatchewan and Manitoba, with Saskatchewan being the major oat production province in Canada during the past 7 to 10 years (B. Rossnagel, 2000, personal communication).

<i>Table 1. Oat harvested area (1,000 hectares), 1978-1997.</i>				
Year	North America	Canada	United States	Mexico
1978	6553	1829	4614	110
1979	5548	1541	3917	90
1980	5086	1515	3501	70
1981	5446	1561	3810	75
1982	5833	1612	4151	70
1983	5171	1400	3671	100
1984	4809	1406	3303	100
1985	4662	1263	3309	90
1986	4163	1287	2776	100
1987	4150	1263	2787	100
1988	3710	1371	2239	100
1989	4603	1708	2785	110
1990	3665	1154	2406	105
1991	2887	842	1945	100
1992	3157	1238	1819	100
1993	2980	1341	1539	100
1994	3213	1490	1623	100
1995	2502	1203	1199	100
1996	2871	1684	1087	100
1997	2778	1500	1178	100

In the U.S. the top oat producing states of Iowa, Minnesota, North Dakota, South Dakota, and Wisconsin planted just over 2 million acres of oats in 2000 according to the USDA-NASS. Texas planted 600,000 acres in 2000, but much of the Texas oat crop is grazed and not harvested for grain. In contrast, the five Midwest states planted 5.6 million acres in 1990 and 7.3 million acres in 1980. The five western states of California, Idaho, Montana,

Oregon, and Washington planted 540,000 acres in 2000, 750,000 acres in 1990, and 832,000 acres in 1980. These statistics indicate that in 2000 the five major Midwest states planted 36% of the 1980 acreage and the five western states planted 65% of the 1980 acreage. The Idaho acreage is small, but nevertheless Idaho is unique among these states in that the 80,000 acres planted in 2000 is an increase over the 62,000 acres planted in 1980 and the 60,000 acres planted in 1990.

OAT BREEDING PERSPECTIVES

I do not know what new directions researchers need to take, but I am certain that something different needs to be done, or the net result will be that we will have collectively presided over the demise of a major crop in North America. We may, however, merely be observing the natural course of events where crop selection and crop production respond to market demand and efficiency of production, i.e., demand has declined markedly in North America and perhaps oats can be produced most efficiently in western Canada, with production in other areas of North America attributable to grower or other local needs and/or specialty markets. Perhaps we need only to acknowledge reality and move forward with breeding and research addressing obvious and immediate needs of the crop.

On a more positive note, the major strength of the oat research community has been the dedication of a relatively small group of researchers that have a history of working closely together, including an effective exchange of germplasm and other cooperation and collaboration. The Quaker Oats Company has also been a vital force in oat research and oat improvement in North America, providing leadership and guidance as well as financial support of oat research. The American Oat Workers Conference (AOWC), the AOWC Crop Germplasm Committee, the National Oat Improvement Committee, and the NOIC Legislative Subcommittee have also played an important role in the support of oat research in the U.S. and North America.

An example of cooperation in the U.S. is the National Oat Germplasm Enhancement program, coordinated by ARS and currently involving oat researchers in several states. The AOWC Oat Crop Germplasm Committee (CGC) has identified specific enhancement objectives including development of germplasm with improved genetic potential for yield or production efficiency through the introgression of genes from wild species and through recurrent selection programs that accumulate genes from cultivated species; development of germplasm with improved lodging resistance through the introgression of genes for stiff straw and reduced plant height; incorporation of genes for maximum protein content in desirable cultivated germplasm; determination of the diversity available for critical dietary fiber components in cultivated and wild germplasm combined with a program to incorporate optimum fiber quality and quantity in germplasm; and incorporation of genes for high groat oil content or modified fatty-acid composition from cultivated and wild species into gene pools for developing special purpose oat or other small grains cultivars. Special attention is given to value-added or other unique traits, looking toward new or innovative crop uses, and more effective utilization of germplasm resources in the development of a more sustainable agriculture and increased global competitiveness. In addition, germplasm enhancement is directed toward reduction of environmental impacts of agriculture, and improvement of animal and human nutrition. A portion of the research conducted by the enhancement project is performed by ARS at Aberdeen, Idaho; Madison, Wisconsin; and other locations, with work by ARS staff outside the Management Unit partially supported by fund transfers to the cooperating ARS research unit. Research performed by university researchers are partially supported under terms of Specific Cooperative Agreements,

principally with Iowa State University, Purdue University, North Carolina State University, North Dakota State University, the University of Illinois, and the University of Minnesota. The project accomplishments mirror the several diverse objectives of the effort. Recently reported research accomplishments include the identification of high yielding oat lines at Iowa State University from cooperative field evaluations in Iowa, Idaho, and Norway; identification of agronomically superior oat lines with multiple crown rust resistance genes including Pc-91, at North Dakota State University; the release of oat germplasm lines at the University of Illinois that are highly tolerant to BYDV infection as well as a set of near-isogenic lines that differ in response to BYDV infection; development of advanced oat lines with partial resistance to crown rust (slow rusting) and excellent resistance to BYDV at Purdue University; incorporation of crown rust resistance in the form of slow rusting into elite oat germplasm at the University of Minnesota; and the development of superior hullless and hulled oat lines suitable for release in North Carolina and Idaho. Results from this research project contribute to the development of disease resistant oat cultivars, with improved grain quality or value-added traits, needed to maintain crop diversity in this country and to assure significant domestic oat supplies.

Involvement of the ARS staff at Aberdeen in the enhancement project is based on the USDA declaration that the enhancement of germplasm pools of important field crops is a national responsibility of ARS. Oats is one of the major cereal grains and much in need of germplasm enhancement for future improvement of its yield and value as food and feed. Oats are recognized as being unique among cereal grains in several respects, especially for nutritional properties and diverse utilization of the crop. The protein content of oats is the highest among the cereal grains and the quality of the protein is also recognized as superior to other cereal grains for many purposes. Soluble dietary fiber (or beta-glucan) found in oats has proved effective in reducing serum cholesterol levels and providing other health benefits. The protein utilization efficiency of oats is about 76% that of casein which compare to wheat at 60% and corn at 48%. The oil content of oats, which is distributed evenly in the kernel, is 1.8 times greater than that of corn or millet and 3.5 times (or more) greater than that of barley. The favorable ratio of polyunsaturated to saturated fatty acids in oat oil is desirable for maintaining normal blood cholesterol. In other research related to oat quality, crosses have been made between high oil oat lines and adapted oat cultivars and lines with the expectation of deriving high oil lines with good agronomic characteristics. High oil lines are desirable for feed because of the high-energy value associated with this trait. ARS researchers are also examining anti-oxidant levels in oats because of the importance of various anti-oxidant compounds as anti-cancer agents. Preliminary findings show a three-fold difference in anti-oxidant levels among varieties indicating the potential for developing higher levels in new varieties. The maximum anti-oxidant levels found to date are in the oat cultivar 'Ajay'.

GERMPLASM EVALUATION AND UTILIZATION

New value added traits are sometimes developed as the result of technologies such as mutant production, as in the case of low phytic acid grains developed by Dr. Victor Raboy, USDA-ARS, Aberdeen, Idaho. Often, however, the desired traits can be found directly in the naturally occurring diversity of the crop or its wild relatives. The ARS National Small Grains Collection (NSGC) exists to provide a way to preserve the genetic diversity of our small grains crops. National Small Grains Germplasm Research Facility (NSGGRF) staff at Aberdeen, Idaho coordinate the systematic evaluation of accessions in the NSGC. Descriptors appropriate for each of the principal small grains crop species - wheat, barley, oats, and rice - have been established in collaboration with the appropriate Crop Germplasm Committees. Dr. David M. Peterson and staff at the ARS Cereal Crops Research Unit, Madison, Wisconsin, conduct evaluations of oat accessions for beta-glucan, protein, and oil. These important quality evaluations focus on a diversity of NSGC and other oat germplasm. Beta-glucan and protein data have been obtained for over 5,000 NSGC oat accessions to date. In addition, oat entries grown in the Uniform Midseason Oat Nursery, the Uniform Early Oat Nursery, the Uniform Northwestern States Oat Nursery, and other cultivars or advanced lines grown in various trials at Aberdeen and Tetonia, Idaho since 1988 have been submitted for beta-glucan and protein evaluations. Evaluations of oil content have also been conducted in recent years. Selected oat descriptors with data entered in the GRIN system are summarized in Table 2.

The NSGC oat collection includes over 21,000 accessions representing 18 *Avena* species. This collection is an invaluable resource for disease and insect resistance and for the improvement of yield, quality, and other characteristics in oats. Numerous examples of benefits from using accessions in the collection in breeding programs can be cited, especially involving disease and insect resistance. In addition to evaluation activities referred to above, the primary ongoing NSGC activities involve the acquisition, maintenance, and distribution of small grains germplasm. During the years 1990-2000, 1824 new accessions have been assigned PI numbers and added to the NSGC. During that same time period, over 30,000 samples of *Avena* accessions have been distributed by NSGC staff. Although the latter is a large number, during the same time period over 95,000 *Hordeum* distributions have been completed. The number of accession requested for oat research and breeding may in part reflect the personnel and resources committed to oat research in North America and elsewhere.

Table 2. USDA-ARS National Small Grains Collection oat evaluation data on GRIN for selected descriptors.

Descriptor	Location	No. Accessions
Beta-Glucan	Madison, WI & Aberdeen, ID	5,382
BYDV	Urbana, IL	8,551
Crown Rust (264A)	Ames, IA	10,391
Crown Rust (264B)	Ames, IA	10,397
Crown Rust (Pc59)	Ames, IA	1,859
Growth Habit	Aberdeen, ID	10,856
Lemma Color	Aberdeen, ID	8,292
Oil/Lipids	Urbana, IL	4,448
Panicle Type	Aberdeen, ID	8,383
Plant Height	Aberdeen, ID; Mesa & Maricopa, AZ	8,280
Protein	Madison, WI & Aberdeen, ID	5,381
Straw Lodging	Aberdeen, ID; Mesa & Maricopa, AZ	8,372
Smut	St. Paul, MN	4,233
Test Weight	Aberdeen, ID	6,504
Yield	Aberdeen, ID	6,527

Despite the resource limitations, the 1824 new PI assignments include over 30 new oat cultivars developed in the United States plus new varieties from Canada, Mexico, and other countries. Breeders continue vigorous cultivar development programs as evidenced by the participation in regional oat performance nurseries. In the past year alone in regional nurseries such as the Uniform Midseason Oat Performance Nursery, the Uniform Early Oat Performance Nursery, the Uniform Winter Oat Yield Nursery, the Uniform Northwestern States Oat Nursery, and the Cooperative Naked Oat Test, all grown in the U.S., over 130 advanced lines or new cultivars were tested. These entries originated in 16 states (Arkansas, Florida, Idaho, Illinois, Indiana, Iowa, Louisiana, Minnesota, Missouri, North Carolina, North Dakota, Pennsylvania, South Carolina, South Dakota, & Texas) and two Canadian provinces (Ontario & Saskatchewan). The pedigrees of these new entries include a diversity of oat germplasm.

Oat breeders have an excellent record of germplasm exchange, but a challenge currently exists in North America related to Karnal bunt disease that seriously impedes germplasm exchange. Karnal bunt (incited by *Tilletia indica*), a fungal disease of wheat and triticale previously restricted mainly to India, Mexico, Afghanistan, and Pakistan, was identified in the southwestern United States in March 1996. The disease has the potential to have significant negative impact on yield and grain quality of wheat, but the major immediate domestic impact relates to the effect of quarantines imposed on the affected areas of the United States and the resulting disruptions in export shipments and movement of grain and seed stocks within the United States. Major negative impacts on the national and international movement of wheat and other small grains seed stocks have also resulted from the disease. Small grains researchers and other interested parties have attempted to address the issue, but progress has seemingly been minimal and germplasm exchange, especially from the U.S. to Canada is being negatively impacted.

NEW OPPORTUNITIES IN CULTIVAR DEVELOPMENT AND UTILIZATION

Hulless oats have long been known, but breeder and commercial interest has increased significantly in recent years. The Cooperative Naked Oat Test, coordinated by H.G. Marshall, is one of the largest regional trials in the U.S today, indicating the level of breeder interest in hulless oats. The author receives numerous requests for germplasm and/or information concerning hulless oat germplasm, the frequency far exceeding requests involving other oat germplasm. The first hulless oat accession in the NSGC, CI 16, recorded about 1895, with the hulless oat cultivars 'Provena' and 'Lamont' entering the NSGC in 1996 and being among the most recent hulless accessions. In the interim, a number of hulless cultivars has been included in the NSGC, including for example, from Canada 'Liberty' (1919), 'Brighton' (1942), and 'Terra' (1977), and from the U.S., 'Shadeland' (1920), 'Nakota' (1931), 'James' (1948), and 'Pennuda' (1988). Hulless oats offer the potential of increased feed value, value-added products, specialty food markets, and reduced shipping and storage requirements. Challenges or negative aspects of hulless oat development and utilization include yield considerations, expression of the hulless character, germ damage, shattering resistance, itch factor, lodging resistance, and disease resistance.

Two hulless oat cultivars, Lamont and Provena, were formally released by ARS and the Idaho Agricultural Experiment Station in 2000. Lamont offers the option of a well-adapted oat with high yield potential for producers interested in hulless oat production and marketing in Idaho and other western states. Lamont is expected to compete favorably with existing spring oat varieties, especially hulless oat varieties, in nonirrigated or dryland environments in Idaho and other western states, with the high yield potential, good shattering resistance, and satisfactory lodging resistance of Lamont being of importance to many growers. Although Lamont is probably too tall for many irrigated growers, it has produced excellent yields with little lodging in short season environments such as Tetonia, Idaho under moderate irrigation. Provena offers the option of a well adapted, short-strawed oat for producers interested in hulless oat production and marketing in Idaho and other western states. Provena is expected to compete favorably with existing spring oat varieties, especially hulless oat varieties, in irrigated and higher rainfall dryland environments in Idaho and other western states, with the short straw and good lodging and shattering resistance of Provena combined with good expression of the hulless trait and other satisfactory or superior traits being of importance, especially in irrigated environments. Producers need to be aware that at harvest the groats or grains of hulless

oat varieties typically have a high frequency of exposed trichomes or hairs and that these trichomes are probably largely responsible for hullless oats being very itchy during harvest and handling operations. Hullless oats reportedly also have a greater tendency toward plugging some handling equipment.

The potential exists to develop exciting new markets for hullless oats based on a new cooperative ARS/University of Idaho project designed to conduct a coordinated research program to concurrently 1) develop genetically enhanced barley and oats as feed sources for aquaculture, 2) develop genetically enhanced rainbow trout to effectively utilize these feed sources, and 3) evaluate strains or stocks of rainbow trout and other fish species for adaptation to diets containing grains and grain products, including evaluation of enzymes involved in carbohydrate digestion in trout, and characterization of the nutritional value of enhanced barley and oat germplasm. The project is designed to achieve objectives through the improved characterization and use of the NSGC accessions and special genetic stocks, molecular genetic marker development and testing for marker-trait associations, mutant isolation, and genetic transformation, recognizing that effective exploitation of genetic diversity almost always requires introgression of new traits into enhanced germplasm.

In addition to addressing the needs of grain producers, this research may provide the aquaculture industry with alternatives to limited and hence expensive fish meal and other protein sources currently used in the aquaculture production. A series of eight barley and oat entries were selected for evaluation in trout feeding trials at the University of Idaho Fish Culture Experiment Station at Hagerman, Idaho, including two-rowed barleys that represent a range in protein content, hullless vs. hulled, and waxy vs. normal starch as well as hullless oat samples from two environments, with a modest range in protein content. Results from these preliminary trials reported by R.W. Hardy indicated that among the grains tested, hullless oats were highest in apparent digestibility coefficients for dry matter, energy, and protein, determined *in vivo* using rainbow trout as the test fish. These trials complement earlier trials involving low phytic acid grains and bring a new dimension to rainbow trout feeding trials since few, if any, grains of this type have been evaluated to date, thus providing the promise of alternative sources of feed stocks for use in aquaculture.

GROWER AND MARKET VIEWS

The author informally reviewed topics such as the decline in oat acreage, oat marketing, crop and variety choice, sustainability of oats as a crop, and other oat related issues with a number of producers, seedsmen, elevator operators, and researchers, all with an interest in oats. The number one issue that concerns all of these individuals is the lack of established markets for oats in the U.S. Growers indicated that local elevators typically do not purchase oats. One individual observed that the infrastructure for marketing oats in the U.S. essentially no longer exists. Another individual indicated that transportation issues also impact marketing of oats.

Seedsmen and farmers alike see advantages or the need for the exclusive or restricted release of publicly developed cultivars, indicating that under the present circumstances individuals that invest in developing markets for specific cultivars see their efforts being for naught as competitors respond to developing demand and market the cultivars or the produce from these cultivars at prices that preclude acceptable profit margins. Frequently independent and relatively small seed companies market oat cultivars.

Growers feel compelled to locate markets before planting oats. At least one grower suggested that perhaps growers need to develop marketing cooperatives, for example for marketing hullless oats to assure profitability. All growers are interested in yield as well as characteristics such as test weight, lodging resistance, shattering resistance, tillering capacity, options for double cropping for forage, and short straw for irrigated production, especially under wheel lines.

Researchers need to focus more on nutritional aspects of oat improvement, involving nutritionists in the evaluation of oat germplasm. Protein content, lysine content, and fat content are thought to be especially important to the dairy industry. Several individuals indicated that we need to develop or capitalize on specialty markets, with the horse trade, especially racehorses and show horses being mentioned. In addition to dairy and horse interests, some see the potential for marketing to swine and poultry producers. We need to develop or define advantages for oats over corn in terms of nutrition and create a situation where oats are of more value to the ultimate consumer, and hence worth more money than corn. At least in some areas of the West, a good market exists for oat hay and the need to focus more attention on oats for forage production is indicated.

Finally, perhaps we also need to address the disparity between the potential yield of oats and the yields reported by producers. During the past 20 years under irrigation at Aberdeen, Idaho, the highest yielding entries in regional nurseries, i.e., the Uniform Northwestern States Oat Nursery, the Uniform Midseason Oat Performance Nursery, and the Uniform Early Oat Performance Nursery, have averaged, respectively, 233.0 bu/A, 200.8 bu/A, and 196.7 bu/A whereas the 1998 average commercial oat yield in Idaho was 75.0 bu/A and the average for the U.S. was 60.4 bu/A. Oregon reported the highest average yield among oat producing states with 110.0 bu/A. The yields at Aberdeen are from a very favorable environment, but it seems likely that the yields obtained by producers are frequently well below the potential of current cultivars.

In summary, the U.S. oat acreage has probably declined to a marked degree due to the lack of established markets. We need to do the best we can in addressing traditional areas of oat improvement while also developing an expanded focus on the nutritional properties of oats for both grain and forage production; developing cultivars specifically designed for hay or forage production; addressing specialty markets; and giving consideration to the utilization of exclusive releases of publicly developed cultivars.

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GLOBAL AND MEGA – REGIONAL BREEDING PERSPECTIVES : LATIN AMERICA

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ABSTRACT

Oats is an important crop in several countries of South America. Besides the grain used by the industry, oats have been used as forage, cover crop for no-till systems, as a grain for horses and dairy cattle. There is four major macro-environments : Chile,Argentina – Uruguay , South Brazil and the more tropical area of Brazil under 24 degree South, that present large differences on soil fertility,diseases and in adaptation. The breeding effort of oat in Latin America has been long and its concentrated in 7 major breeding programs (3 in Brazil, one in Uruguay, 2 in Argentina and one in Chile),with new varieties been released with specific adaptation to each environment.

INTRODUCTION

Oats is cultivated in South America, in Brazil, Uruguay, Argentina and Chile, as important crop, for forage production during the winter months, cover crop for posterior no-till planting or harvested the grain for livestock feeding and milling industries (Table 1). Brazil grows more than 2 million hectares of oat, but that 80 % is of black oats (*Avena strigosa*) used as cover crop in no-till systems or forage, and around 200 000 hectares harvested as a grain. In Uruguay the area sown with oats is around 260.000 hectares,most for forage or grazing, and the area harvest for grain is near 36 000 hectares (Rebufo,1997). In Argentina almost all oat planted is for grazing (more than 2,0 million of hectares) and some are left for harvest (300 000 hectares), but lately oats has been grown for grain production only, with excellent results. In Chile, near 60 000 hectares are grown for grain production (Beratto Medina,1997). The yield obtained depends on the environment, and if the oats was grazed or not, but in general they are higher in Chile, than Argentina and Brazil. Also in the more tropical area of Brazil the yields are more variable and there is significant differences among years and the interaction genotype x year (Federizzi et al, 1993)is always significant. Good farmers can produce until 8 ton/hectare in Chile, 6 ton/hectare in Argentina e 4 ton/hectare in Brazil, what reflects the major differences in the macro environments. Area grown with oats is increasing in South America the amount of grain with good milling yield and quality produced can be increased very rapidly .

MACRO-ENVIRONMENTS

There is four major macro-environments in South America, that are diverse with respect the end use of the crop, soil fertility and composition, amount of rainfall, average temperatures, day length, air moisture and length of season. Chile represent the most different environment, Argentina and Uruguay are similar and Brazil has two contrasting environments.

1.Chile

The Chilean environment is an excellent area for cropping and about 8 % of the area for grain production is devoted to oats, around 80% of the oat crop is harvested for grain. Oat in Chile is grown between the parallels 37 and 43 of latitude South, with soils with high fertility, mild temperatures, long days and with long season . Oats can be seeded in may or mid-august and it is harvested in January or February. Because air moisture is low, diseases are not problem and yields are generally high and the oat grain has excellent quality and milling yield. In some years low rainfall in November/December may reduce yield and grain quality. Because the competition with wheat and barley the area grown with oats is limited. The better farmers can obtain yields over 8 ton per hectares.

2.Argentina - Uruguay

This is a large area grown with oats and it is located between the parallels 32 and 36 of latitude South, soils with high fertility, adequate rainfall, mild temperatures, long days and long season. Oats is seeded as pasture in the beginning of the fall and is most of the times grazed and than harvested as a grain in the summer. When farmers grows oats with the only purpose of grain production, it is planted in June-July and it is harvested in January. There is several frost during the season and late ones may cause damage to oats. More than 3 million hectares are grown with oats and the area can be superior, once oats can compete well in yield with wheat and barley. Better farmers can harvest 6 ton per hectare of grain, with excellent quality. The major problems related the crop are stem rust and crown rust. Since 1993, stem rust has been endemic early in the season (May) or in November and December with severe damage on yields and grain quality.

3.South Brazil

Brazil has two major areas for oat production . This region is located between the parallels 24 to 32 degree of latitude South, with soil of average fertility with the presence of high levels of aluminum in the soil, and it is possible to grown two crops a year, one of winter (generally a small grain) and a summer crop, corn or soybean. Oat is grown as forage, soil cover and for grain production. As forage it is planted in the end of summer early fall and it is grazed in the winter months. For grain, it is planted in June and harvested in early to middle November, when the summer crop is planted. Most of the farmers are using no till planting and in this crop system oats represents an important source of biomass, protecting the soil and decreasing the need for herbicide in the subsequent crop. In this area, rainfall is over 1600 mm a year, and the air moisture usually is very high during most of season, days are short and the season is less than 150 days long. Diseases are endemic, specially crown rust, with several different and virulent races occurring most years and with high probability of rainy days during the harvest time. Because that, yields are variable among years and there is a larger interaction genotype x year. Best farmers can harvested 4 ton per hectares of grain. In this area black oats a diploid (*Avena strigosa*) is grown in more than 2 million hectares as soil cover or forage.

4. Brazil sub-tropical

This area posted between the parallels 24 and 20 of latitude South, is a new area where oats have been grown with relative success. Soil are of middle fertility, without aluminum, temperature are higher and short days, with the season of less than 120 days, yields are variable with the main differences among years. Oats is planted in march and harvested in August, usually with low air moisture and no rain what makes the grain harvested of excellent quality. Major problem is crown rust, low rainfall and in some years of more severe winter can occurs frost damage.

MAJOR OAT BREEDING PROGRAM IN SOUTH AMERICA

Breeding oat is a old activity in South America, it started with the first experimental station in the area by INIA in Uruguay, INTA in Argentina and Secretaria de Agricultura do Estado do Rio Grande do Sul in Brazil, and INIA in Chile (Boerger, 1943, Beratto Medina, 1994 ; Federizzi et al., 1999). In modern times, since 1974 to present, all breeding effort in South America was based in the project `Breeding oat cultivars suitable for production in developing countries` or Quaker Oat International Nursery (QOIN) that provided intense introduction of new genetic material in South America and elsewhere (Forsberg and Shands, 1986 ; McDaniel, 1997). Currently there is seven major oat breeding programs in activity in South America, there is minor breeding effort by private companies in Brazil and Argentina, but they had very little contribution with new varieties in the recent past.

1. INIA- Carrilanca (Chile)

This program started in 1965 at Experimental Station of Carrilanca (INIA – Instituto Nacional de Investigaciones Agropecuarias) and it covers the Chilean environment with several varieties released . The main objectives are :

- introduction and development of oat varieties with high yield potential
- improve the milling yield and chemical composition of oat grain
- introduce resistance to main diseases
- improve the agronomic type of the oat plant (agronomic type, resistance to lodging, short plant height)

2. INTA -Chacara Experimental of Barrow (Argentina)

This is one of oldest oat breeding program in South America, and until recently 1990 the major goal was to release oat variety for double-purpose, production of forage a after harvest the grain. The main objectives are (Wehrhahne and Carbajo, 1997) :

- develop new cultivars with higher yield potential (forage and/or grain)
- increase the adaptability to different regions
- improve grain quality
- increase resistance to crown and stem rust
- increase tolerance to frost damage
- improve tolerance to aphids.

The program relay in the introductions of material from the QOIN, and recently released two new varieties more suitable for grain production.

3.INTA – Experimental Station of Bordenave (Argentina)

This Experimental Station was created in 1927 and the first experiments with oats were reported in 1934. All varieties released in this program were for double purpose (production of forage and grain) the most successful variety was introduced in 1969 and it was the cultivar Suregrain that occupied more than 90 % of the area grown with oats in the 80's (Tomaso and Bucar, 1994). The main objectives are :

- improve the production of forage and grain
- increase the resistance to crown and stem rust

All varieties released so far by the program are more suitable for forage production

4.INIA – LA ESTANZUELA (URUGUAY)

This is an oat breeding program that started very early in this century. Because, oat historically has been a multipurpose crop in Uruguay, specially producing forage for fall and winter, most varieties are old and they have these characteristic, new varieties released recently are better producer of grain. (Rebuffo,1997). The main objectives are :

- develop new varieties with more forage and grain production
- develop cultivars with different morphological characteristics
- increase resistance to crown and stem rust
- increase tolerance to BYDV

The last three programs,INTA –BARROW, INTA-BORDENAVE,INIA-LA ESTANZUELA cover the macro-environment 2.

5.UPF – University of Passo Fundo (Brazil)

This program started in 1977, and it is located in the Agronomy School at Passo Fundo in the State of Rio Grande do Sul, and it has been very successful in releasing varieties with excellent yield potential and grain quality. In the beginning, the program relayed exclusively in the germoplasm introduced by the QOIN, but in the 90's the crosses made in the program were of more importance . It has six varieties that are recommended for all regions of oat production. The main objectives of the program are :

- develop varieties with high yield potential and adaptation to Brazilian environments
- create new varieties with better grain quality
- increase the tolerance to crown and stem rust
- resistance to BYDV
- tolerance to aluminum

6.UFRGS – University Federal of Rio Grande do Sul (Brazil)

The program at UFRGS started in 1974 and it is located at Porto Alegre in the Agronomy School. The primary goals in the University was of training students in plant breeding at under and graduate levels and do basic research with small grains. Because of the needs for new oat varieties the program since late 80's was devoted more to oats and now it is exclusively devoted to oat breeding. Nine varieties from the program are currently in use by farmers. One main characteristic of the program it is the genetic studies most of them done by graduate students. The main objectives are :

- develop oat germoplasm with higher yield and grain quality with adaptations to sub-tropical environments
- modify the oat plant from a producer of forage to a true grain producer (better agronomic type), with short plant height and resistance to lodging
- create varieties with early cycle
- increase resistance to crown and stem rust, use of partial resistance to crown rust
- increase resistance to leaf spots (caused by *Pyrenophora avenae*)
- do genetic studies with traits of importance oats

7.FAPA – Fundação Agrária de Pesquisa Agropecuaria (Paraná, Brazil)

In 1986, the Cooperative Agraria Mista Entre Rios located in the state Paraná started a oat breeding program. The Cooperative is the major supplier of the Quaker Brasil and the breeding objectives are :

- to develop oat varieties with higher grain yield and grain quality
- to select germoplasm with higher tolerance to frost damage and with local adaptation
- to increase the level of resistance to crown and stem rust

The Brazilian oat breeding programs at UPF and UFRGS they cover the two last macro environment, even if they both are located in environment 3.

PERSPECTIVES

All major breeding program in South America in the recent past and for the next future will depend on the exchange of germoplasm that was carried out by the Quaker Oat International Nursery, with the Universities of Texas A& M, Wisconsin, Florida e Minnesota. All varieties released are from or derived from material that was brought by the QOIN program. Because the environmental conditions, more pressure for releasing new varieties are imposed by Brazilian and Argentinean farmers in the programs located in these countries. In Brazil and Chile, where the main purpose of grow oats is grain for the milling industries, the new varieties released by the breeding programs replaced all old varieties. In contrast, in Argentina e Uruguay where oats is grown for producing forage the main varieties in use by the farmers are very old. In Chile new varieties have been released with excellent yield as shown in Table 1, and excellent quality and milling yield. Average yield in the statistics of each country are not informative (with exception of Chile) because the average includes the area that was grazed or used as cover crop. Good farmers have consistently obtained high yield in Argentina and Brazil (Fig.1). Studies of gains in grain yield due to breeding in Chile indicate that the new varieties were responsible for 54.7% of total gain (Berato – Medina, 1997) In Brazil, gain in grain yield were 28 kg/há/year or 1.1% in the last 15 years (Pacheco et al, 1997 and Federizzi et al, 1999), with advances in milling

yield from 50% in 1980 to 68% in 1999, due to the strong selection pressure on test weight and uniformity of the grains. However, bigger modifications were obtained with the agronomic type, decreasing the plant height and total cycle (from emergence to maturation). Breeding program of South America have been successful in releasing new varieties with the traits needed by farmers (Table 2), and varieties from the region are very good sources for aluminum tolerance (Floss et al,1999; Sanches-Chacon et al,1997), good grain filling in warmer environments, resistance to stem and crown rust (Cruz et al,1999) and agronomic type (Federizzi et al,1999).

Because the pressure imposed by diseases mainly crown and stem rust, varieties have a very short life in the farmers field and they need to be substituted, so the program in the region should be very dynamic, and exchange of germoplasm is fundamental. New oat breeders have been added in the programs, and a new effort was launched in 1998 ` South American Oat Integrated Program `joining all breeders of the region. Biotechnology is been placed in the Brazilian programs, molecular markers are been obtained for several different traits and oat transformation is in it infancy (Cavichioli-Lamb et al,2000).

Farmers are adapting very fast the no-till system (more than 10 million of hectares), specially in Brazil and Argentina, and oats are an important component in the crop rotation used. The possibility of the increasing the area grown with oat is real and it is limited only by the oat grain market.

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Table 1. Area cultivated and grain yield of oats in different countries of South America.

Year	Argentina		Brazil		Chile	
	Area (000 ha)	Yield (t/ha)	Area (000 ha)	Yield (t/ha)	Area (000 ha)	Yield (t/ha)
95	1980	1.0	172*	0.9	55*	2.2
96	2000	1.3	172	1.3	85	3.8
97	1900	1.1	220	1.5	74	3.3
98	1900	1.1	250	1.0	61	2.3
99	2000	1.1	280	1.5	60	3.0

* Only for grain production.

Table 2. Oat varieties recently released in South America.

Variety	Country	Institution	Source of germoplasm	Use
Tucana	Uruguay	INIA	QOIN	Forrage / Grain
Polaris	"	"	QOIN	"
Maxima	Argentina	INTA	QOIN	Forrage
Maja	"	"	QOIN	Grain
Calen	"	"	QOIN	"
Pilar	"	"	QOIN	Forrage
UFRGS 16	"	UFRGS	QOIN	Grain
Urano	Chile	INIA	QOIN	"
Neptuno	"	"	Hibr.	"
UPF 18	Brazil	UPF	Hibr.	Grain / Forrage
UPF 19	"	UPF	QOIN	Grain
UFRGS 19	"	UFRGS	Hibr.	"
URS 20	"	UFRGS	Hibr.	"
URS 21	"	UFRGS	QOIN	"

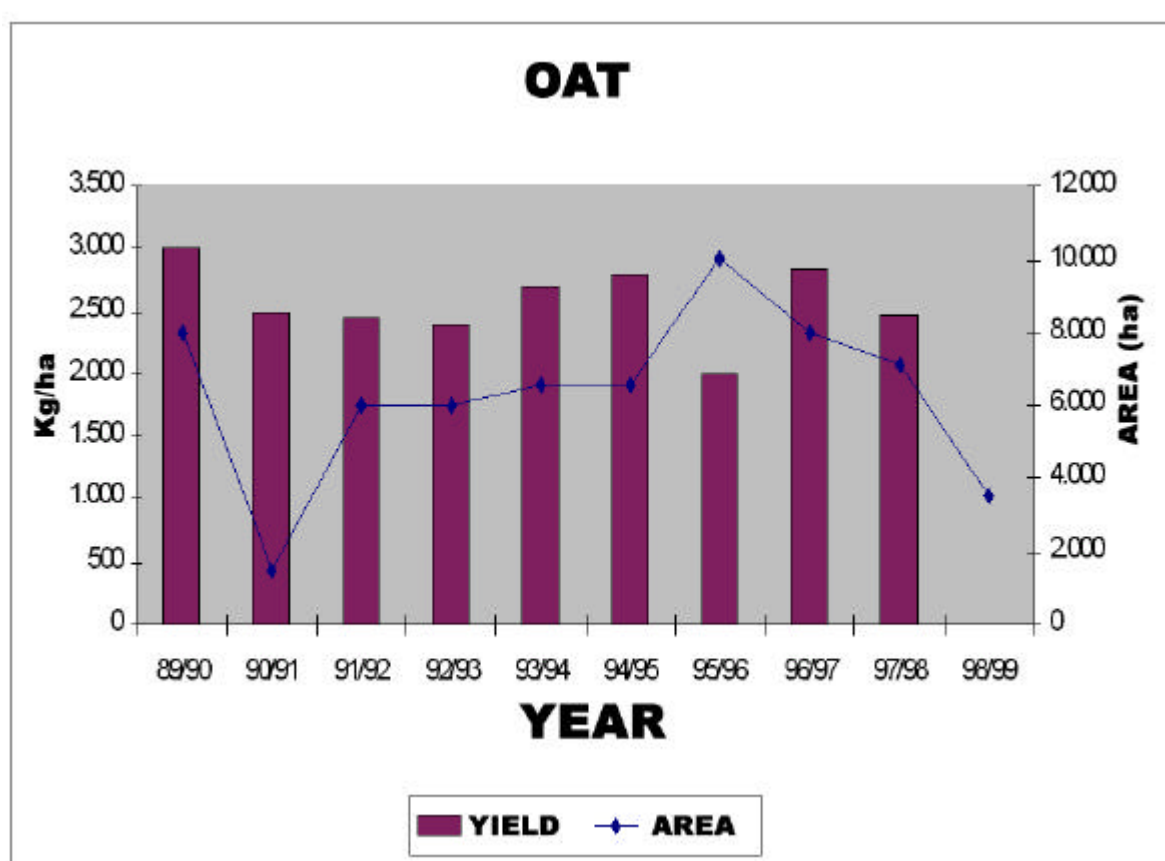


Figure 1. Area (há) and grain yield of oats grown in different years in the Cooperative Agraria Mista Entre Rios,Paraná, Brazil.

REGIONAL BREEDING PERSPECTIVES – AUSTRALASIA

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INTRODUCTION

Now is a time of considerable change in breeding programs generally throughout Australasia, and oat breeding is no exception. We are facing changes in research funding arrangements, breeding directions and priorities, changing market and end user quality requirements, and the integration of new breeding technologies into our programs.

It is also a time of exciting new prospects and opportunities to be seized by breeding programs. We have the opportunity to use new tools, such as marker technology, genetic engineering, doubled haploids, and others to improve our breeding programs and our ability to select superior lines. It is also a time in Australasia when we are starting to make significant advances in defining oat quality through our collaborations with end users and exporters.

PRODUCTION

Oats are a multi-use crop in both Australia and New Zealand. In New Zealand oats are used for milling, feed and forage. Fig. 1 shows where oat production occurs. All milling oats are grown in Southland and Otago, on the South Island, to service mills in Gore and Dunedin. Feed oats are grown in Canterbury with very little production in the North Island, due to leaf rust (*Puccinia coronata* f. sp. *Avenae* Eriks. & Henn.) problems, but also it is more difficult for oats to compete economically for land use. Most forage oats are grown in the North Island, though there is increasing use of forage oats in the South Island as more sheep farms change over to dairying.

Oats are used for milling, animal feed, forage, silage, and hay in Australia. There are also dual-purpose oats that are grazed early by stock that are removed before stem elongation allowing the crop to recover and produce grain for harvest. Oat production mainly occurs in the southern agricultural areas, with an area of grazing oats in sub tropical Queensland (Fig. 2).

Australia produces approximately 1.6 m. tonnes of oat grain each year with New South Wales and Western Australia the major producers (Fig. 3). South Australia and Victoria combined production is similar to the major producers. Hay is a major oaten product in Australia. It is used on farm as a fodder reserve, in the animal feed industry, and is exported to mainly Asian markets. Each year 1.2 m tonnes of hay are produced, with Western Australia and South Australia being the major producers (Fig. 4).

Exports of oaten hay have increased each year since the early 1990's. South Australia and Western Australia exported 148,000 and 147,000 tonnes, respectively, in 1999. Total exports of cereal hay and straw, of which oaten hay predominates, was almost 400,000 tonnes in 1999. There is potential for further growth in exports.

Of the oat grain produced about 200,000 tonnes are exported, with Western Australia being the major exporter. The balance is used by the domestic milling and feed industries, with a significant proportion of the crop maintained on-farm for stock feed.

BREEDING PROGRAMS

There are oat breeding programs based at Christchurch, Toowoomba, Temora, Adelaide and Perth (Fig. 5). The barley breeding program in Tasmania also does some oat improvement. These programs all exist within government departments of agriculture. Private industry involvement in oat breeding is limited with Heritage Seeds, Pacific Seeds, Pioneer Hi-bred and the University of Queensland mainly being involved in screening lines from other sources for suitability for forage production, focussed mainly in Queensland. The National Cereal Rust Control Program (NCRCP) is managed by the University of Sydney, and based at Camden.

NEW ZEALAND - CHRISTCHURCH

The New Zealand effort in oat breeding is centered in Christchurch, and has focussed on milling oats. The program has been very successful and approximately 95 % of oat production for forage and milling in New Zealand uses Crop and Food Research cultivars.

The diseases the program focuses on are leaf rust and barley yellow dwarf virus (BYDV) in all regions and includes septoria blotch (*Phaeosphaeria avenaria* (G.F.Weber) D. Eriksson) in Southland. Leaf rust and BYDV resistances are particularly important for forage oats in the North Island, where forage oat production is most concentrated.

In future the New Zealand breeding effort will be more closely aligned with the food science programs and will concentrate on new food uses for the oat crop. The program will also increase its efforts in developing forage cultivars to meet the expanding demands of the dairy industry. Currently in the South Island there is a shift from sheep farming to the dairy industry with increasing demand for adapted forage cultivars.

Stem rust (*Puccinia graminis* Pers. f. sp. *avenae* Eriks. & Henn.) is a future threat and resistance is likely to be added to the program aims. Though it is not yet seen as a problem in commercial crops, stem rust has been occurring more frequently in breeding nurseries.

QUEENSLAND - TOOWOOMBA

Oats are widely grown as the main winter forage crop in Queensland due to its ability to produce good quality feed when most pastures are dormant. Oats are relied on to produce feed from late autumn through to early summer. Suitable cultivars incorporate the ability to grow rapidly, tiller and remain vegetative for a longer period. A major problem for the industry is leaf rust. Leaf rust lowers feed quality, and hastens maturity thereby limiting forage production. The experience to date with single gene resistances has not been positive due to the frequent shifts in virulence of rust races. Cultivars with new genes for resistance only remain effective for 1 – 3 years.

The oat breeding program aims to develop cultivars combining leaf rust resistance and improved forage yield and quality. As well as producing cultivars suitable for grazing the program also plans to produce cultivars suitable for hay production. Cultivars for grain production are not a priority as only limited grain production occurs in Queensland, with stem rust a major limiting factor. The major focus of the program is to develop cultivars with more durable forms of resistance to leaf rust, and the approach chosen is to “pyramid” resistance genes. Molecular markers are being used to select lines with multiple resistance genes, and these are then advanced for assessment of their forage yield.

NEW SOUTH WALES – TEMORA

The NSW oat breeding program has concentrated mainly on dual purpose oats (grazing and grain) with a lesser emphasis on grain oats. While NSW is often the largest oat producing state in Australia, only a small quantity of the crop is either milled or exported, the crop being largely used on farm. This has resulted in very poor oat grain prices.

In the absence of a contract to produce milling oats, farmers in NSW consider oats non-competitive with other higher value crops such as canola or wheat, unless they can be used to provide grazing to livestock throughout autumn and winter. As a result the area of oats sown in NSW fluctuates widely with the profitability of livestock enterprises. Dual purpose oats are sown in early autumn and grazed through to early winter when cold temperatures limit pasture growth. As temperatures increase and alternative pastures become available stock are removed from the oats and the crop is allowed to develop for grain production and harvest. In 1996 it was estimated that 50 % of the oat crop in this region was sown with dual purpose oat cultivars. In 2000 it is likely the proportion of the crop sown to dual purpose oats has increased significantly. Major disease problems faced are stem and leaf rusts and BYDV. As a result of the poor disease resistance currently available in oat cultivars there has been a shift away from oats as a dual purpose crop in longer season areas towards dual purpose early sown winter wheat and triticale. Better grain prices and disease resistance to both the rusts and BYDV result in better returns to producers.

The Temora program has recently lost GRDC (Grains Research and Development Corporation) funding. The reduction in resources will result in a significant change in program direction. The program will now focus on dual purpose oats and will cease all work on milling oats, relying on the Adelaide and Perth breeding programs for milling cultivars. In future emphasis will be placed on selection for winter growth habit, disease resistance and grain quality parameters important in animal production. This will include metabolisable energy and digestibility if resources are available.

NEW SOUTH WALES – CAMDEN

The University of Sydney is responsible for the National Cereal Rust Control Program (NCRCP). The major crop of interest is wheat, but limited resources are available to oat breeders. Each year the NCRCP conducts a survey of races of stem and leaf rusts prevalent in Australia, receiving samples of rust on oats and wild oats from collectors across the country. Results of the survey are published each year giving guidance to breeders in their decisions regarding use of rust resistance genes.

The NCRCP also provides a screening service to breeding programs. Glasshouse and field screening for both stem and leaf are conducted each year with results, and in some cases resistant selections, being returned to the originating breeding program. This service is of particular value to the Perth based program as rust epidemics for screening are not reliable in Western Australia.

The Camden program is also investigating alternatives to single gene resistance to the rusts, and has an interest in screening related wild species for possible new sources of resistance.

A more recent service offered to oat breeders is screening for resistance to BYDV. This work has been developed in partnership with the Temora based program. The Perth, Adelaide and Temora programs each year submit breeding lines for screening and selection. GRDC has ceased funding of this program as from July 2000 necessitating the curtailment of this service in December 2000.

SOUTH AUSTRALIA - ADELAIDE

The South Australian program is based in Adelaide at an integrated university / state agriculture department facility and is able to take advantage of interactions with a broad range of disciplines co-located at the Waite Precinct. Funding for the program comes from state government, GRDC, the Rural Industries Research and Development Corporation (RIRDC) and the Uncle Tobys Company.

The program aims to develop improved husked and naked grain oat cultivars with enhanced milling and feed quality, improved disease resistance, and increased yield potential for the diverse agro-ecological zones in south east Australia. The program also aims to provide growers and industry with improved oat cultivars for hay end use. There is a growing export hay industry in South Australia and Victoria that rely on improved hay cultivars. Hay is also an important fodder reserve. These cultivars should be of high quality so first grade hay can be reliably produced, and economic losses due to down grading can be avoided.

For both grain and hay cultivars the program aims to improve resistance to stem and leaf rusts, cereal cyst nematode (*Heterodera avenae* Wollenweber), stem nematode (*Ditylenchus dipsaci* (Kuhn) Filipjev), root lesion nematode (*Pratylenchus neglectus* (Rensch) Filipjev & Schuurmans Stekhoven and *P. thornei* Sher & Allen), BYDV, and bacterial blight (*Pseudomonas syringae* pv. *coronaficiens* (Elliot) Young, Dye & Wilkie and *Pseudomonas syringae* pv. *striafaciens* (Elliot) Starr & Burkholder). These diseases are seen as major factors limiting yield and quality for both grain and hay production. For the nematode diseases both resistance and tolerance are required. Routine screening programs are in place for the nematode diseases. Breeding lines are evaluated with specific pathotypes for resistance to stem and leaf rusts and BYDV in cooperation with the University of Sydney NCRCP. The oat breeding group is also able to take advantage of regular natural epidemics in field trials to assess breeding lines.

Quality is an important component in the breeding program. The South Australian program focuses on both domestic and export quality requirements. A cooperative research program with the Uncle Tobys Company, a major domestic miller and end user, ensures new oat cultivars meet their end-use specifications. This interaction is important in defining quality for specific end uses. Both analytical and sensory characters of advanced breeding lines have been assessed since 1997. Although South Australia and Victoria are not the major exports of grain in Australia, there are a few small export markets as well as great potential when the North American market opens. Physical characters assessed include hectolitre weight, screenings, 1000 kernel weight, groat yield, colour, and grain size uniformity. Chemical characters assessed are protein, oil, β -glucan, and metabolisable energy for potential feed cultivars. Near Infra-red Reflectance (NIR) calibrations to predict moisture, protein, oil, and groat percent have been used since 1996. Breeding lines are assessed from F_4 seed to cultivar release. Digital imaging was incorporated into the program as a potentially useful assessment tool for physical quality, such as seed size, uniformity, and colour in 1999. It will be integrated as a routine assessment tool with the 2000 harvest.

Quality characters are also important in the development of hay cultivars. Traits such as digestibility, palatability, stem diameter, hay colour, neutral detergent fibre (NDF), water soluble carbohydrate, and shear energy are among the quality characters assessed for the most advanced breeding lines.

The South Australian program is involved in co-operative programs to improve the efficiency of the oat by maize doubled haploid methodology, and to develop molecular markers for cereal cyst nematode resistance and tolerance, stem nematode tolerance, and quality characters. The oat doubled haploid project is lead by Dr. Phil Davies, SARDI, in cooperation with Dr. Taing Aung, Agriculture & Agri-Food Canada, Winnipeg, Canada. In a recent experiment, over 8,000 florets from 5 different oat cultivars were pollinated with maize. The proportion of florets producing caryopses was 52% with 7% of caryopses containing an embryo. The overall proportion of embryos per floret pollinated was 3.8%. This frequency of haploid production is greater than any reported in the literature and experiments are currently underway to further improve the efficiency of haploid production. The doubled haploid technology will be used to develop mapping populations, and to create homozygous lines for selected elite crosses. The molecular markers research is in cooperation with Dr. Kevin Williams, the CRC for Molecular Plant Breeding. A Mortlock x Potoroo population is currently being analysed. In future doubled haploid technology will be used to develop mapping populations, and to create homozygous lines for selected elite crosses. A major benefit seen from developing and using molecular markers is the ability

to pyramid disease resistance genes with improved milling quality. Other technology to be explored is the use of transformation as a means of introducing effective stem rust resistance into oats.

Future targets for the breeding program reflects industry plans and directions. A major goal will be optimising end use quality tailored to consumer preference. This will require sensory evaluations to identify consumer preferences, and to build these preferences into new cultivars. Industry also is looking for cultivars with better milling yield, higher protein and β -glucan content with low oil content. The feed industry is looking for higher oil content cultivars. Improved hay quality is essential to the growth of the export hay market. Identification of characters that improve palatability or preference is a priority for hay quality improvement.

WESTERN AUSTRALIA - PERTH

Both Agriculture Western Australia (state department) and GRDC, a major funding partner, are currently reviewing the Western Australian oat breeding program. The result of this is likely to be some redirection of the program. The program has always focussed on grain oats for milling and feed quality for the south west region of Australia, though has released a few cultivars suitable for hay production. The program has been very successful with 95 % of oats in the south western region being Agriculture Western Australia bred cultivars. Likely future directions are a decrease in work on feed oat cultivars and a component of the program is likely to be redirected to develop cultivars suitable for the export hay industry.

There are major environment, soil type, and disease pressure differences between the western and southern regions of Australia. Hence there are two breeding programs to service these diverse regions. Western Australia's focus is on export rather than domestic markets due to the low population and lack of extensive domestic manufacturing. As a result of this Western Australia is the largest Australian exporter of both grain oats and oaten hay. This focus is reflected in the industry partnerships the program has developed. Major partners are Agracorp, Australia's largest grain oat exporter, and Quaker Oats Australia which has an export focus.

Milling quality has always been a key focus of the program. During the recent five year project we have had funding from GRDC to employ a cereal chemist (Maurice Hall) in the program to improve and widen our quality testing methodology, and to improve our understanding of what makes a good milling quality oat. Characters of importance include hectolitre weight, sievings, grain weight, grain and groat colour, groat per cent, protein, oil and β -glucan content. The program has been able to develop robust NIR calibrations for whole grain groat per cent and moisture, protein, and oil content. The time saved through using NIR techniques has meant we can select earlier for important quality traits, currently on F₄ seed.

Milling yield has also been looked at in more detail. For advanced lines milling yield was assessed by measuring the proportion of free groats, sievings, groat per cent, groat breakage loss during dehulling (soft groats) and ease of dehulling. The program is working with Quaker Oats Australia to develop this testing methodology to better reflect oat performance in a commercial mill, compared with a simple laboratory dehulling test. Work is also starting using DIA to measure grain size uniformity, another trait important to millers. Other work is reported in poster papers presented at this conference.

Through a joint Agriculture Western Australian – Quaker Oats Australia quality working group the program aims to better understand milling oat quality so oat cultivars can be better targeted to specific end products. Additional important traits have been identified by the working group, the most challenging being aroma and taste of end products. The program is also working with Agracorp to identify quality characteristics important to their customers to better target cultivar development.

Quality is also an important consideration for developing hay cultivars. The limited work to date has focussed on stem thickness, protein content, digestibility and metabolisable energy. Testing for other traits such as shear energy, soluble carbohydrate, fibre content, palatability and hay colour will have to be implemented.

Diseases considered important in Western Australia include stem and leaf rusts, BYDV and septoria avenae blotch, with bacterial blight of more minor importance. Disease resistance has not been a strong point of the breeding program, though this is changing with increased frequency of epidemics of diseases such as leaf rust. Screening of lines for resistance/tolerance to stem and leaf rusts and BYDV is done through the NCRCP, supplemented with local data from natural infection in field trials. A specific nursery is set up each year to screen lines for resistance to septoria avenae blotch.

The Western Australian program works closely with oat agronomist Glenn McDonald. This collaboration aims to provide growers with production packages for new oat cultivars, and to improve grower awareness and adoption of agronomic practices to improve both yield and quality of milling oats.

Similarly to South Australia the program is working on increasing reliability and frequency of doubled haploid production using the maize crossing method. This work is being lead by Sue Broughton. The aim is to speed up the breeding process for selected elite crosses. Molecular marker technology is seen to have a place both in the doubled haploid and more traditional breeding strategies, and a Coomallo x Vasse cross has been made to create a population to develop markers for various milling quality traits and BYDV resistance.

THE FUTURE

PRODUCTION

Grain oat production is likely to continue to decline due to economic factors. Return from oats is less than alternative crops. Another major concern to growers is price stability. Oat prices are more volatile than alternative enterprises, as seen by some dramatic price drops in recent years. The decline of the wool industry in Australia has also contributed to this instability as growers try to sell more grain off-farm.

Oat production is likely to be more concentrated in areas where oats have a natural advantage over other crop species. Oats have advantages in waterlogging and frost tolerances, and are more tolerant of acid soils, particularly where aluminium toxicity occurs. Oats also fill an important role in forage production due to their ability to continue growth in cold conditions.

Production of oats for export hay in southern Australia is likely to increase. Though more risky than grain production greater returns can be achieved from hay production, and new markets are still being developed. Markets have also been developed for second grade hay, and this has decreased some of the risks associated with hay production. With the development of herbicide resistant weed species hay also offers a useful non selective strategy for weed control with the crop and weeds being cut before seed set.

Oats are an important break crop to control CCN and take-all in South Australian and Victorian rotations, particularly in the low rainfall areas where there are few feasible rotation crops.

In the north eastern parts of Australia oat production is limited by the lack of sources of effective resistance to stem and leaf rusts due to the rapid evolution of virulence by the pathogens. New approaches to develop more stable and durable forms of resistance are essential given the failure of single gene resistant cultivars. Perhaps transformation will offer some future hope.

Quality assurance will rapidly be a required element of production for growers and others in the production chain.

MARKETING

World demand for oats is currently viewed as static and Australia will continue in attempts to improve market share at the expense of our competitors. Any increase in world demand for oats will have to come from the development of new and novel end uses for oats, in either the food or industrial sectors.

We will see more specific matching of cultivars to end uses for both domestic and export markets. Associated with this will be the advent of identity preserved, single cultivar exports to premium markets.

Australia looks forward to a positive resolution of quarantine issues with the USA that will allow us to export oats to this important market.

PLANT BREEDING

We will see an increase in the current public investment – private good debate regarding government investment in all public plant breeding programs. This is likely to lead to governments further reducing their investment in plant breeding.

Partly as a result of the above there is likely to be a change to closer industry relationships with breeding programs, including a direct funding and research management role by marketers and end uses to protect the future of their raw inputs.

In Australia we may see less collaboration between breeding programs. The momentum for this will come from two directions. The first is support for competitive breeding programs by some organisations in Australia. The second factor involves private investors in the breeding program and their need to protect their intellectual property investment. Given the small size of the oat industry and low levels of research investment available this will be detrimental to the industry. Unfortunately with less collaboration it would be more difficult to develop costly enabling technology, such as molecular markers, doubled haploids, and transformation, and to pursue shared goals through national and international collaboration.

In future we need to integrate new technologies, such as molecular markers, into our breeding programs in the most cost effective and efficient manner.

Through interaction with industry breeding programs are likely to have clearer, better defined quality goals for different end uses. Through plant breeders knowledge of oat germplasm available we may be able to assist industry to develop new end uses for oats.

The future success for all our breeding programs is dependent on retaining access to international germplasm. Germplasm exchange between breeding programs and international nurseries are essential, and better characterisation and documentation of germplasm held in various germplasm banks will enable better utilization of existing germplasm resources.

Interaction with agronomists to produce cultivar “production packages” will be important to maximise the advantages of new cultivars, and to ensure growers are able to meet end user quality specifications.

An essential requirement for future successful breeding programs is plant breeders. Currently in Australasia we have an aging population of plant breeders across all crops, and little succession planning by breeding organisations. It is essential that investment be made in training new plant breeders, ensuring they have the necessary breadth of knowledge to succeed. All of us, even those not based in an educational organisation, have a responsibility to assist in the training of the next generation of plant breeders.

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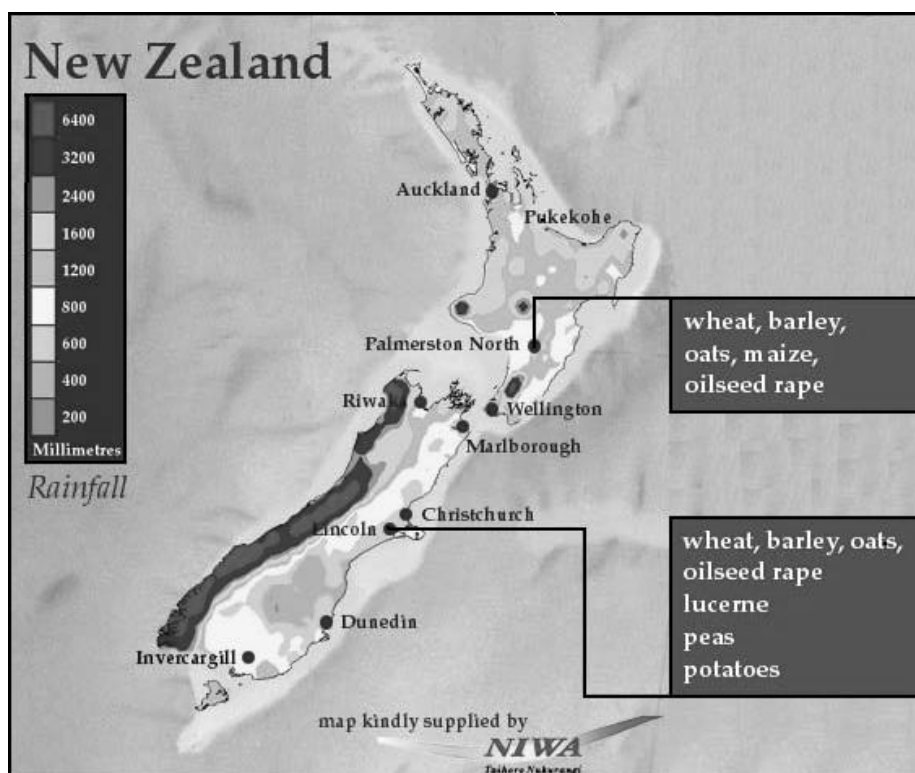


Fig. 1. Location of oat production in New Zealand.

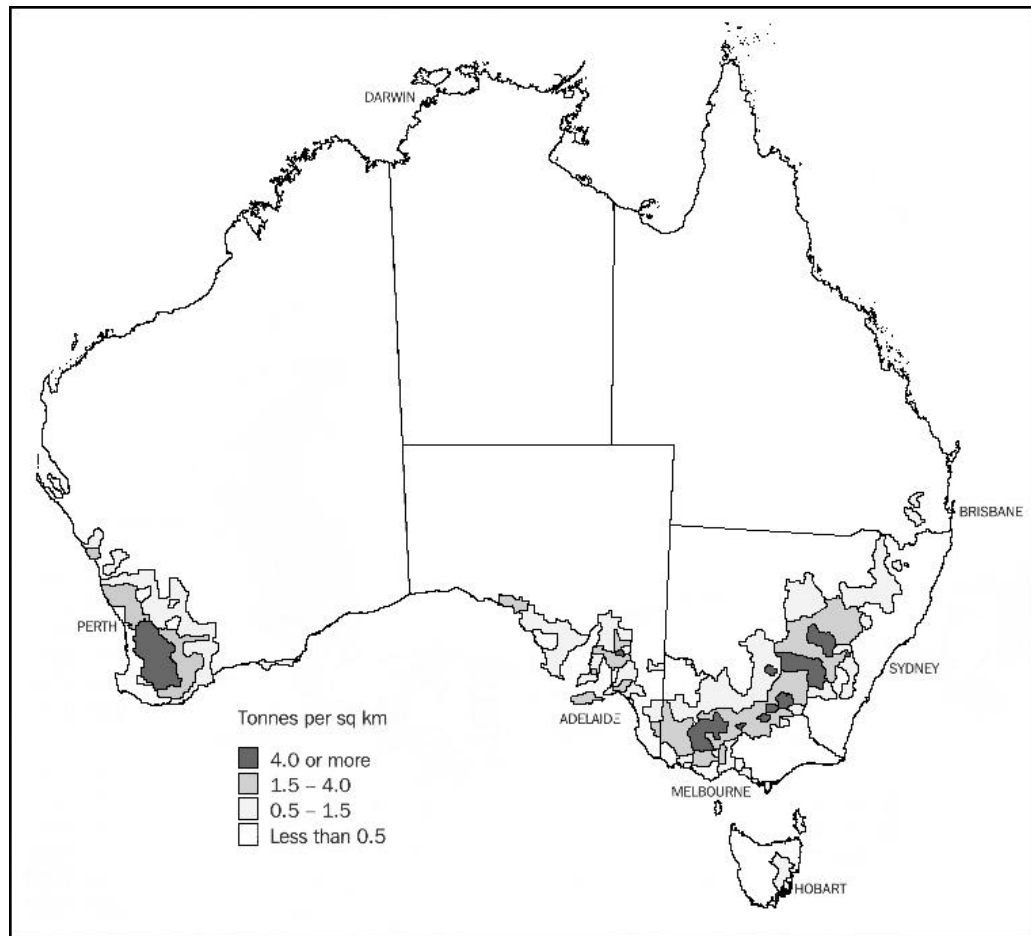


Fig. 2. Location of oat production in Australia (Australian Bureau of Statistics).

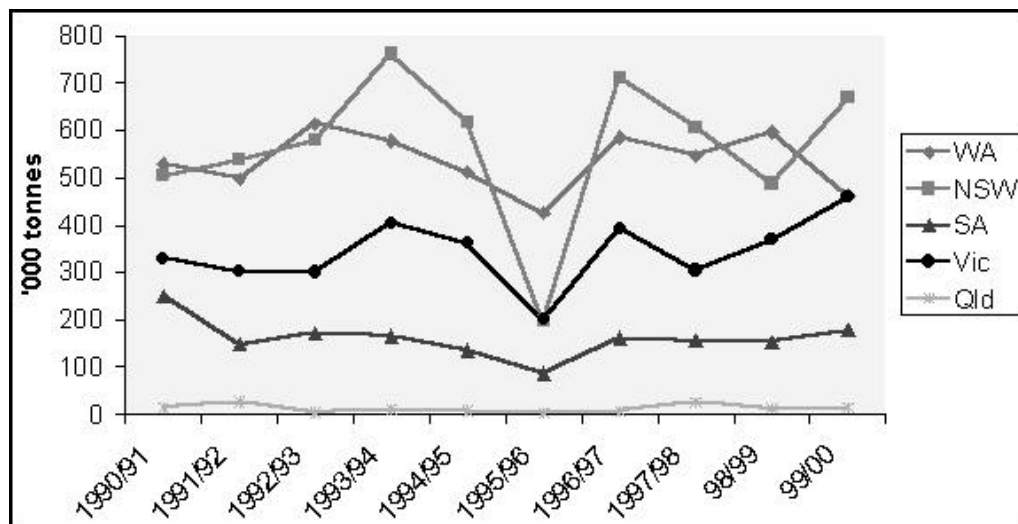


Fig. 3. Oat grain production by state in Australia in the past 10 years (Data from Australian Bureau of Statistics).

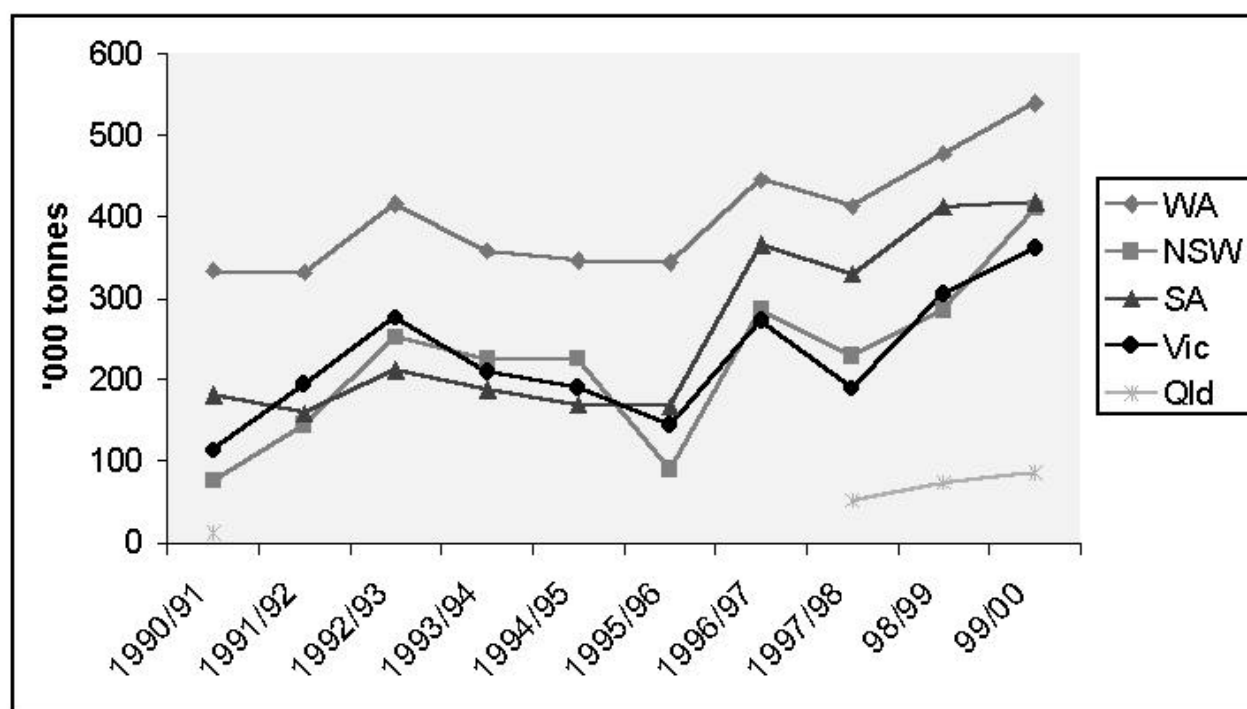


Fig. 4. Oat hay production by state in Australia in the past 10 years (Data from Australian Bureau of Statistics).

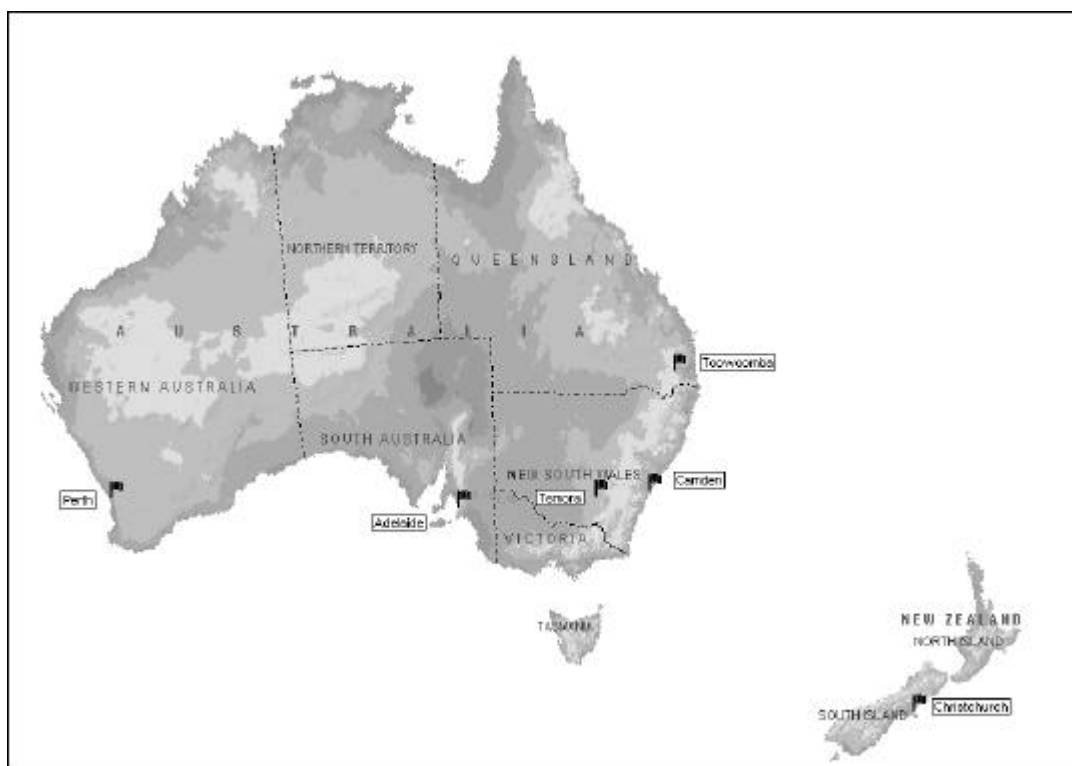


Fig. 5. Location of breeding programs in Australasia.

WHOLE GRAIN NIR PREDICTIONS TO IMPROVE OAT QUALITY

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ABSTRACT

Improving milling and feed quality is an important breeding priority in the SARDI Oat Breeding Program. NIR was used to develop whole grain calibrations that predict protein, oil, and groat percent. Reliable calibrations were developed and are being used for routine evaluation in the breeding program. NIR predicted quality values were analysed from single replicate seed samples and unreplicated trials to determine consistency of the measurements between years. The breeding lines were highly correlated with years and trials for protein, oil, and groat percent. Thus identification of superior quality breeding lines is effective using NIR predicted quality measurements.

INTRODUCTION

The development of oat varieties adapted to southeastern Australia with improved milling and feed quality is needed to maintain current oat production and to expand into new markets.

In order to meet the growing demand for specific chemical quality characters in milling and feed oat varieties, a rapid, non-destructive evaluation, such as whole grain near infrared reflectance (NIR), was required to assess moisture, protein, oil, and groat percent (Williams, 1975. Tkachuk, 1987) The technique allows assessment of a large sample numbers earlier in the breeding program.

Once the calibrations were developed, seed was evaluated from F3 headhills, stage 1 and 2 unreplicated yield trials, and stage 3 and 4 replicated yield trials. Promotion of breeding lines was based on yield, quality, and disease resistance. However, the variability of the predicted values for protein, oil, and groat due to differences in sampling and year effects was not known.

Aims of the study were to develop whole grain NIR calibrations to predict moisture, protein, oil, and groat percent in both early and late generation breeding lines and to determine the stability of the quality measurements for breeding lines between years.

MATERIALS AND METHODS

Near infrared whole grain calibrations were developed using a set of 90 oat samples from 20 sites across South Australia and Victoria in 1996 and 303 oat samples from 20 sites in 1997. A Perten DA7000 NIR instrument was used to assess the 200 g samples. Duplicate chemical testing was performed on these samples sets. GRAMS plus/IQ[®] software was used to develop the calibrations to predict protein, oil, and groat percent.

A single replicate of grain was obtained from several sites in 1996, 1997, and 1998 for protein, oil, and groat percent measurements using NIR calibrations (Table 1). Entries in

the Stage 2 (S2) trials were F₅ and F₆ lines, entries in the Stage 3 (S3) trials were F₆ and F₇, and entries in the Stage 4 (S4) trials were F₇ to F₁₀. The total data set consisted of 1149 unique dwarf and tall breeding lines arranged in three arrays over three years. The data sets were arranged into three arrays to improve data handling. The arrays followed the progression of lines through each stage of the breeding program. Array 1 consisted of 575 lines from 32 trials composed from 1996 S2 trials, 1997 S3 trials, and 1998 S4 trials. Array 2 consisted of 441 lines from 17 trials including 1997 S2 and 1998 S3 trials and array 3 consisted of 192 lines from 26 trials including 1996 S3 and 1997 S4 trials.

Table 1. Year, trial type, location, and entry number for grain samples used in the year effect analysis. Arrows indicate array relationships.

1996			1997			1998		
Trial type	No. of sites	No. of entries	Trial type	No. of sites	No. of entries	Trial type	No. of sites	No. of entries
S2-Tall	2	377	S2-Tall	4	288			
S2-Dwarf	2	104	S2-Dwarf	4	138			
S3-Tall	3	77	S3-Tall	5	84	S3-Tall	5	84
S3-Dwarf	3	87	S3-Dwarf	6	96	S3-Dwarf	4	52
			S4-Tall and Dwarf	20	29	S4-Tall and Dwarf	17	30

A model was developed to determine the oil, protein and groat percent of lines in each trial. A trial is the combination of year, site, and stage (S2, S3, or S4) and type is a factor representing two height classes, dwarf and tall.

A reasonable model for these data can be expressed as the linear combination of the effects from each trial, the effects from the types as well as all possible sources of variation. The model formulation may be written

Protein, oil or groat percent = trial/type + line + line.array + line.array.year.

Table 2 gives an explanation of each term in the above model.

Table 2. Terms used to model oil, protein and groat percent from numerous breeding lines over three arrays and up to 3 years of trials within each array.

Model Term	Fixed (F) or Random (R)	
trial	F	Fixed effects due to each individual trial
type.trial	F	Effects due to type within each trial
line	R	Variation due to line
line.array	R	Variation due to lines within each array
line.array.year	R	Variation due to lines within each year within each array
error	R	Random error

There exists a certain amount of variation for each variable protein, oil, and groat in each trial and year. For example the values for protein vary from 7.1 to 16.1%, values for oil vary from 3.4 to 8.5%, and groat values vary from 56.9 to 79.8% in the calibration set (Table 3). This variation is a combination of the four random components shown in Table 2. The random component associated with line is an estimate of the variation for the genotypes in the trials. After allowing for this we can find the variation due to each of the three arrays and the variation due to the three years. All remaining variation can be thought of as random noise. Our third error term, line.array.year, is structured to allow for possible

correlations between years within each array. This correlation structure was used to determine the stability of the quality measurements between years.

RESULTS AND DISCUSSION

Whole kernel oat calibrations to predict protein, oil, and groat percent were developed in the SARDI Oat Breeding Program. Table 3 shows the sample range, standard error of prediction (SE), and the coefficient of multiple determination (R^2) for the calibration set grown in 1996 and 1997. The high R^2 value and the low SE relative to the sample value range shows the whole grain NIR calibrations reliably predicted protein, oil, and groat percent in the 1996, 1997, and 1998 trials. However, it was not known if the predicted quality measures remained consistent for breeding material over years.

Table 3. Oat prediction sample set from 1996 and 1997.

	Protein %	Oil %	Groat %
R^2	.92	.90	.81
SE	.52	.38	2.0
Range	7.1-16.6	3.4-8.5	56.9-79.8
Sample no.	393	393	393

Variety and breeding line values for the predicted characters, protein, oil, and groat percent, were highly correlated with other years and trials within the arrays. Tables 4, 5, and 6 show pairwise correlations between each year/trial combination. These correlations show good estimates of the relationships between line effects of each trial. Since they are all quite high we can conclude that the effects for each of the quality measurements are similar regardless of the year and stage.

Although genotype trends were similar among arrays and years, the spread of oil values were different in each trial and over years. The variance of protein values remained similar between arrays, but varied in the trials between years. The variance of groat values was not influenced by array or year, resulting in a similar spread of values in all trials and years.

Table 4. Correlation matrix for array and year for NIR predicted oil content.

	96-S2	97-S3	98-S4	97-S2	97-S4
96-S2		.95	.95		
97-S3			.99		
98-S4					
97-S2					
98-S3				.94	
96-S3					.89

Table 5. Correlation matrix for array and year for NIR predicted protein content.

	96-S2	97-S3	98-S4	97-S2	97-S4
96-S2		.73	.74		
97-S3			.98		
98-S4					
97-S2					
98-S3				.86	
96-S3					.98

Table 6. Correlation matrix for array and year for NIR predicted groat percent.

	96-S2	97-S3	98-S4	97-S2	97-S4
96-S2		.99	.97		
97-S3			.97		
98-S4					
97-S2					
98-S3				.92	
96-S3					.99

CONCLUSION

Whole grain NIR calibrations has been used to predict protein, oil, and groat percent as a routine method in the SARDI Oat Breeding Program since 1996. Evaluation begins for samples harvested from F₃ headhills when sufficient seed is available and continues through stage 1 to stage 4 yield trials. Although seed samples represent a single replicate, strong correlations for varieties with years and trials indicate the quality data for breeding lines is consistent from year to year and in the different trials. Thus NIR predicted values for protein, oil, and groat percent can be used to effectively select superior quality genotypes in F₄ and later generations using data from a single year and multiple sites.

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Tertiary Kernel Impact on Oat Kernels and Production

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ABSTRACT

Oat (*Avena sativa* L.) panicles are divided into spikelets, which have a somewhat variable number of kernels. Commonly there are only two kernels, but three and even four can be present. In most cases the primary kernel is bigger than the secondary one, and both are bigger than the tertiary kernel (TK). Not much attention was given to TKs until a few years. Some plant breeders believe that a high TK frequency might have been indirectly selected when selecting for high yield and/or high test weight (TW). These TKs may contribute to higher yields (more sinks) and may allow better packing of seeds inside the TW cup, giving higher TW results. This becomes a problem as the industry needs uniform grain for more efficient milling yield. It is unknown how the presence of TKs influence the oat plant development and the size and shape of the other oat kernels. Near Isogenic Lines (NILs) were used to compare agronomic and physical characteristics of oat lines with high and low TK frequencies. There is significant GxE interaction, causing TW to vary differently across environments. For the physical evaluations a detailed digital image analysis (DIA) experiment was conducted. Oat kernels vary significantly for size and shape across kernel type, position in the panicle and presence or absence of TK in the spikelet. Other DIA results will be discussed.

OAT BREEDING AT INRAT, TUNISIA

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ABSTRACT

Oat (*Avena sativa* L.) is the dominant fodder crop in Tunisia. It is grown mainly for hay and silage. Research activities on oat started as early as 1913. The oat breeding program began in mid 70's by the introduction of germplasm leading to the release of four varieties. To date, the breeding program has been revived; its objective is to develop superior varieties with high forage yield potential and good level of tolerance to the prevailing foliar diseases. Ninety-five oat pure-lines, obtained from the Quaker Oat Nursery, have been evaluated. After two cycles of selection, the best lines were evaluated in replicated trials in the oat growing regions. However, greater improvements need to be achieved in order to produce enough silage and oaten hay that will sustain livestock production.

INTRODUCTION

Oat (*Avena sativa* L.) is the most important livestock feed and one of the components of crop rotations in Tunisia's rainfed farming systems. It is widely grown and used either as a fodder or as a cash crop (sold as hay). Oat, cut for hay represent over 60% of the winter forage cultivated area. A large proportion of oaten hay is produced in the North and sold to livestock owners in the central and southern part of the country. Sown areas of oat mixed with vetch and oat alone have changed. During the past five seasons, out of the 174,000 hectares of oats grown, it is estimated that only 30% were sown with oat/vetch mixture, while 70% were cultivated with pure oat of which an average of 10% were harvested for seed (D.G.P.A. Ministry of Agriculture, 1999).

In Tunisia, research on oats began since the establishment of the Botanical Service (renamed later, INRAT) in 1913. Boeuf, 1914, reported oat evaluation tests to determine the grain and forage potential of 29 introduced lines. The first selected oat variety was described and released by the Tunisia Botanical and Agronomic Service (Seguela and Jacquard, 1953). Until recently, the number of varieties used is limited to two: Creme (*Avena bysantina* Koch.), the red local variety which became susceptible to lodging and crown rust and Avon (*A. sativa* L.), introduced since 1962, early maturing type and susceptible to the major foliar diseases.

The two major diseases that affect oats are crown rust (CR) and barley yellow dwarf virus (BYDV). Their severity varies with seasons and often cause significant losses. Therefore, resistance to these diseases is an important criterion of selection in Tunisia for improving oat productivity. In 1990, a serious epidemic of crown rust caused by *Puccinia coronata* f. sp. *Avenae*, occurred on the introduced Australian Swan variety causing yield losses of around 30% (Anonymous, 1990). The same phenomenon was observed in spring 1995 following the cultivation of Mortlock.

In recent years, four varieties (e.g., Fretissa, El-Alia, Meliane and Mejerda) were developed at the Tunisia's National Agronomic Research Institute (INRAT) and were registered (Chakroun et Maamouri, 1998), nevertheless, they do not have wide adaptation for growing in all oat cultivation areas.

Variety selection is one of the most important decisions a farmer must make. Oat growers in Tunisia often produce low yields when they grow varieties non adapted to their region and conditions.

A new oat breeding and selection program has recommenced aiming to develop varieties with varying maturity duration, tolerance to diseases, high performance and good adaptation. The intended multiple use of oats and the evolution of sown oat-vetch mixture in favour to oat alone suggests a broadening of the genetic base of the actively used oat pool. Our short term breeding strategy is to select varieties from the Quaker Oats International Nursery (QOIN), which is designed to breed oats for developing countries.

The objective of this work is to present the status of the oat breeding program at INRAT, Tunisia.

METHODS

In 1975, an oat breeding program was initiated at the Cereal Genetic Laboratory of INRAT with the screening and evaluation of hundreds of lines for forage/grain productivity under subhumid conditions. These lines were received from Dr H. Shands of University of Wisconsin; (Maamouri et al., 1988, Rondia et al., 1985). Strong selection pressure was applied for foliar disease tolerance and high forage and grain yield potential. Within 10 years, 11 genotypes/lines were identified with foliar disease tolerance, and differing height and maturity level, and forage and grain yield potential. However, available information related to their performance was limited. These lines were: Av. 3, Av. 14, Av. 72, Av. 77, Av. 81, Av. 86, Av. 88, Av. 89, Av. 90, Av. 93, and Av. 95. The following limited cultivation of these lines can be attributed to the lack of a good extension program and the failure of establishing a seed multiplication strategy.

Meanwhile, an oat variety testing program was conducted with the objective of determining the relative performance of commercially available varieties mainly from Australia. Dolphin, Swan, Bulban, Winjardie, Mortlock and Potoroo were found very susceptible under Tunisia's environments mainly to CR.

In 1993, the oat breeding initiatives were turned over to the Forage Production Laboratory and were integrated in the priority forage species improvement project. An agronomic evaluation study was conducted to confirm previous results obtained on these oat lines. Based on their relative performance in variety trials replicated over locations and years (1994 to 1996), the better genotypes were described and registered. The best genotypes are Av. 3, Av. 14, Av. 77 and Av. 89; which were named Fretissa, El-Alia, Meliane and Mejerda, respectively.

In 1996, Ninety-five pure-lines of oat obtained from Dr. McDaniel, Texas A&M University, Quaker Oat International Nursery and the two Tunisian varieties (Fretissa and El-Alia) used as local checks (systematically after every 10 lines) were evaluated. Seed from each pure-line and a check were planted in plots of 2 m rows with 0.4 m spacing between rows at the "Fretissa" experimental station, near Mateur, northern Tunisia, during 1996-97 cropping season. Standard agronomic practices were adopted and irrigation was provided as needed. Visual rating (1-9) where 1=excellent and 9=poor have been used to evaluate

vigour and disease tolerance. Data on number of tillers/plant, number of leaves of the main shoot, days to maturity, plant height, straw diameter, grain yield and 1000 seed weight were recorded. Analysis of variance was performed on the traits studied. Based on their adjusted mean, 21% of the lines were identified and used for evaluation at multiple locations at three sites during 1997-98 season. Taking into account three selection criteria (dry matter forage yield, earliness and tolerance to diseases), 10 lines were identified for additional cycle of selection. Screening has been continued on multi-location basis.

RESULTS AND DISCUSSION

Performance of the selected oat varieties

At present, the four new varieties are cultivated by farmers. Variety, plant height, maturity, straw strength, disease reaction to CR and BYDV, and 1000 seed weight are presented in Table 1. Dry matter (DM) yield (% Avon), grain yield and use are reported in table 2.

Table 1. Plant height, maturity, straw strength, disease reaction to CR and BYDV, and 1000 seed weight of 4 released varieties.

Variety	Plant height	Maturity	Straw Strength	Disease Reaction to CR	BYDV	1000 Seed Weight (g)
Fretissa	medium	early	Excellent	R	R	42
El-Alia	very tall	late	thin	MR	R	17
Meliane	tall	medium	Excellent	R	S	40
Mejerda	very tall	Late	thin	MR	R	30

R: resistant; MR: moderately resistant, S: susceptible

Table 2. DM yield (% Avon) and grain yield of 4 oat varieties registered.

Variety	DM Yield % Avon	Grain Qx/ha	Use
Fretissa	148	32	silage
El-Alia	160	15	hay
Meliane	159	41	silage
Mejerda	149	20	hay

Seed Multiplication

In collaboration with National Agricultural Development Organisations and the National Seed Inspection Service, the Forage Production Laboratory at INRAT is engaged in the establishment of an efficient oat seed production sector. In 1994, the multiplication of the four newly released oat varieties following the generation systems was started. This work was carried out with the Office of Livestock and Pasture (OEP) at the Fretissa production farm. Over a hundred tons of certified oat seed was produced. Government and private seed organisations are now involved in the production, processing, marketing and distribution to Tunisian farmers of adequate quantities and good quality seed of the improved oat varieties. This is under direct supervision of the National Seed Inspection Service. Oat variety multiplication is carried out through a formal agreement between INRAT and the seed production companies.

Evaluation of the QOIN lines

The evaluation of disease tolerance showed that 19 lines are susceptible to oat diseases and thus were eliminated. Lines 4, 28, 40, 43, 44, 45, 46, 47, 48 and 67 were susceptible to CR, lines 79, 83, 84 and 86 were susceptible to the BYDV, and lines 85, 87, 88, 89 and 90 were very susceptible to SR. Significant differences were found for days to maturity, number of leaves on the main tiller and 1000 seed weight.

Genetic variability of this collection for several agronomic traits suggested that twelve lines produced greater dry matter than the control varieties: Fretissa and El-Alia. Lines 3, 14, 15, 20, 24, 25, 70, 78 and 91 would be suitable for forage crops, lines 9 and 82 would be useful for both forage and seed production, whereas line 56 is recommended for grain production (Table 1). Further investigations are needed to validate the relative performance of these identified lines using multilocation testing for most forage and seed yielding ability and to ensure that the newly selected lines have wide adaptation.

The oat breeding work targeted to different areas is at varying stages of progress. For the sub-humid region, the issue of variety choice has been addressed with the four newly released varieties. They have the potential to produce high forage quality and good grain yield. The semi-arid environments program seeks to select adapted early types with resistance to foliar diseases and high yield.

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INFLUENCE OF KERNEL SIZE ON TEST WEIGHT IN OATS

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Test weight (TW), a measure of weight per volume, is used as a physical quality measurement for cereal grain by the cereal processing industry. Plump kernels are desirable for milling and, assuming their density is similar to that of thin kernels, they should weight more. Seed weight has also been found to be inversely related to infection of diseases such as crown rust. For these reasons the oat processing industry buys oats based on TW, and encourages plant breeders to select for high TW. However there is a contradiction associated with industry requirements for high TW because a less uniform grain size lot, having a mix of big and smaller kernels may have a higher TW than a very uniform size lot, other factors being equal. This happens because the mix of kernel sizes allows for better seed "packing" per volume. This becomes a problem as the industry needs uniform grain for more efficient milling yield. Ten varieties were used to measure TW across different seed shapes and sizes. Seed samples were sieved with three sieves of different widths, and digital image analysis (DIA) was used to profile seed size and shape. Significant genotype*sieve interactions were observed, especially when sieving did not create TW differentials for some varieties. The variety Richard had two distinctive widths for primary and secondary kernels, maximizing sieving differences and showing higher TW for the smaller kernel sample.

ANALYSIS OF KERNEL SIZE UNIFORMITY IN OATS

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ABSTRACT

Oats are routinely separated by size prior to milling because dehulling occurs most efficiently with uniformly sized kernels. Oats that divide into uniformly proportioned size fractions are more desirable for milling. Here, we report our investigations into approaches to the analysis of uniformity. We compared kernel length analysis by digital image analysis with physical separation of kernels by width. Separation by width appeared to give a better fractionation by kernel mass because kernel length among genotypes had poor correlation with kernel mass. Uniformity products are introduced to quantify uniformity of distributions among three size fractions.

INTRODUCTION

Oat kernel size has an inherent non-uniform nature because of the multi-floret nature of the oat spikelet. The primary floret generally produces oat kernels that are larger than the secondary or tertiary kernels, although primary kernels generally have lower groat percentage than the secondary kernels. As a result of multi-floret spikelet, oat kernel size distributions are frequently of a multi-modal nature.

In commercial oat mills, oat dehullers, whether they be stone or impact dehullers, function most efficiently with uniformly sized oats (Ganssmann and Vorwerck, 1995). Oats are routinely separated by size, prior to dehulling to optimize dehulling (Deane and Commers, 1986). Oats that would divide into equally proportioned size fractions would accommodate the milling process most effectively. Yet, little work has been done to characterize this property of oats. This study was initiated to develop effective approaches to size uniformity analysis and to provide preliminary indications of genotypic variation in oat kernel size uniformity.

MATERIALS AND METHODS

Twelve genotypes of oats (*Avena sativa* L., cultivars AC Assiniboia, AC Medallion, Gem, Jerry, Jud, Marion, Milton, and Youngs, and breeding lines ND910569, ND910592, ND910779, and ND911048) were grown in replicated plots at three locations (Carrington, Edgeley, and Prosper) in North Dakota, USA during the 1997 growing season.

Oat kernel size was evaluated by digital image analysis (DIA) using the protocols described by Doehlert et al. (1999). Data on individual oat kernel length and width were downloaded onto a spreadsheet computer program where numbers of kernels in large, medium and small length classes were determined by sorting the data lists. Large oats were defined as being longer than 9.5 mm. Medium oats were 8.7 to 9.5 mm, and small oats were less than 8.7 mm long.

Oats were also fractionated physically into different size classes by sequential sieving with slotted sieves. Oats held back by 3.18-mm slots were considered oversized and were discarded. Oats held back by 2.58-mm slots were removed and considered to be large, oats held back by 2.38 mm slots were removed and considered to be medium sized, and oats held back by 1.98 mm slots were considered small. Oats passing through the 1.98 mm sieve were considered undersized and were discarded. The mass of each size fraction was recorded and calculated as a proportion of the total mass.

Uniformity Products (UP) were calculated as the product of the percent large, medium and small kernels as separated either by length or by width. Test weight, and mean kernel mass were calculated according to Doehlert et al. (1999).

Data were subjected to analysis of variance, where location was considered random and genotype was considered fixed using the Stastitix (Analytical Software, Tallahassee, FL, USA) software package. Least significant differences (LSD) were also calculated with the Stastitix package. Correlations matrixes were calculated (also using the Stastitix software package) for each location individually and pooled according to Steel et al. (1997).

RESULTS

Size distributions of oats as determined by sequential sieving on slotted sieves are shown in Table 1. Larger oats, such as AC Assiniboia, AC Medallion, Youngs, and ND910779, appeared to have more uniform distributions by this test because of a greater amount of kernels in the large class, which were virtually absent in the smaller oats, such as Jerry, Jud, and Milton.

Table 1. Size distributions and width uniformity products of oat cultivars when separated physically by width using slotted sieves.

Genotype	Mean oat mass	Large (2.58-3.18 mm)	Medium (2.38-2.58 mm)	Small (1.98-2.38 mm)	Width Uniformity Product
	mg/kernel	% of total mass			
AC Assiniboia	38.6	22.8	38.8	35.2	28490
AC Medallion	36.1	25.8	32.0	37.9	29874
Gem	33.7	10.2	34.5	49.1	15734
Jerry	30.7	3.7	14.7	72.9	4206
Jud	29.8	2.4	5.8	69.4	1285
Marion	32.4	3.8	13.7	66.5	3646
Milton	26.9	1.4	2.8	77.4	317
Youngs	39.6	9.4	39.5	47.0	16962
ND910569	33.3	6.0	19.6	61.2	7788
ND910592	31.0	6.9	18.8	58.6	6448
ND910779	39.4	39.0	30.0	26.3	30190
ND911048	30.4	12.3	35.8	47.1	19048
LSD (0.05) ¹	1.9	6.1	9.3	9.8	6004

¹LSD = Least significant difference ($\alpha = 0.05$).

Distributions of kernel length among genotypes (Table 2) differed considerably from the distributions according to width. Many relatively small oats by mass and width, were longer than the plumper, heavier genotypes. Jud and Marion were two genotypes that appeared small, judged by mass and width, but were large when judged by length.

We developed the UP as a measure of uniformity. Being the product of the percentages of large, medium and small kernels, the largest possible product would be 37,037, if all portions were equal. The UP values approaching this value were more representative of oat samples with more uniformly distributed kernel sizes. UP values derived for width and length distributions (Tables 1, 2) indicated major differences in uniformity among genotypes, depending on whether width or length was the decisive factor. For example, Jerry, Jud, and Milton had low uniformity products as determined by width, but had high products based on length.

Kernel length, width, and UP values were correlated with several oat quality parameters. The kernel width and the width UP were highly correlated with mean oat kernel mass, as well as mean groat mass. Kernel length was negatively correlated with test weight (data not shown).

DISCUSSION

The UP allows the rapid quantitative comparison of uniformity of distributions of oat kernel size, based on the industrial need for uniformly sized milling streams into dehulling machines (Ganssmann and Vorwerck 1995). The results presented here indicated that genotypes differ significantly in uniformity of length and width, and that a genotype with a high level of length uniformity may exhibit a low level of width uniformity (Table 3). The results presented here suggest that if the goal of sizing oats prior to dehulling is to generate batches of kernels with less variation in kernel mass, then separation by width would be more effective. We found a strong correlation between kernel mass and kernel width, and no such correlation for kernel length. Many oat genotypes with light kernels are just as long, if not longer than oats with heavy kernels (Tables 1, 2).

Table 2. Size distributions of twelve genotypes of oats as separated by length.

Genotype	Mean Kernel length	Less than 8.7 mm	Between 8.7-9.5 mm	Greater than 9.5 mm	Length Uniformity Product
	mm	% of total number			
AC Assiniboia	10.0	23.7	15.3	61.0	21667
AC Medallion	9.6	35.3	14.5	50.1	24640
Gem	9.7	28.4	19.6	52.0	27557
Jerry	9.0	49.0	20.8	30.2	28058
Jud	9.8	29.8	16.8	53.4	25706
Marion	11.0	11.8	10.8	77.3	10274
Milton	9.6	39.5	20.5	40.0	30136
Youngs	10.1	23.8	14.7	61.5	20121
ND910569	9.1	39.1	22.2	38.8	30200
ND910592	9.7	37.1	18.7	44.3	28167
ND910779	9.5	27.5	17.0	54.9	25074
ND911048	9.3	35.6	18.7	45.8	26043
LSD(0.05) ¹	0.3	7.5	3.9	8.1	5254

¹LSD = Least significant difference.

It is important to point out that values of width derived from digital image analysis are not analogous to the widths indicated by sequential sieving analysis. When images for DIA are recorded, the kernels lay with their creases down, so that their true width can be measured. When shaken in slotted sieves, kernels are actually separated according to their height, which is about 60% of the width.

It is also important to note here that the analyses by width quantify fraction sizes by mass, whereas fractionation by length (as determined by DIA) quantifies by kernel number. Quantification by kernel number gives more weight to small kernels, which would be a smaller proportion if expressed as mass.

Obviously, distributions into the different size classes are dependent on size definitions for each class. The ranges used here were selected in part arbitrarily, partially from literature reports (Deane and Commers 1986, Ganssmann and Vorwerck 1995), and partially from the availability of sieve slot sizes. However, no matter what ranges are used, clear genotypic differences would be apparent, and results derived from sieve separation would differ markedly from length separation.

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RELATIONSHIPS BETWEEN OAT QUALITY TRAITS AND MILLING YIELD

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ABSTRACT

Oat samples from selected varieties and sites throughout Western Australia were tested for the following milling parameters over the 1997 to 1999 seasons; milling yield, percentage broken kernels, ease of dehulling and groat percent. The sample set was also tested for other quality traits such as protein, oil, B-glucan; and physical traits using Single Kernel Characterisation System (SKCS) and Digital Imaging apparatus (DIA). Milling quality traits were more influenced by genotype than environment in this study. Trends in milling quality rankings between varieties were largely consistent over the three years of the study. The data indicated the variety Coomallo as having a milling yield consistently 2 - 3 percent higher than the current Australian industry preferred variety Mortlock. Groat percent had the largest single influence on milling yield with these two traits having a close, linear relationship. The mean breadth and standard deviation of width of wholegrain samples were found to be negatively correlated with groat percentage and milling yield, indicating the ratio of primary to secondary grain to be an important factor in oat milling quality.

INTRODUCTION

Milling yield in oats can be defined as the weight of sound, undamaged groats obtained after dehulling a given quantity of oats. It is a measurement that gives oat millers an indication of the economic value of an oat variety. Previous workers in this field have expressed milling yield either as a ratio (Root 1979) or as a percentage (Humphries et al. 1994). The desirable higher milling yields have high values expressed as a percentage but inversely, low values when expressed as a ratio.

The exact definition of milling yield as reported also varies in the literature. For example, Humphries et al (1994) reported milling yield values as being the groat percentage of a sample corrected for foreign material and moisture content before drying. Doehlert et al (1997) reported milling yield as the mass of whole groats recovered after hand cleaning to remove broken groats and dehulled grains, as a percentage of the initial mass of whole oats.

Strong positive correlations between milling yield, test weight and groat percentage have been reported in the literature (Root 1979). Other work has focussed on groat breakage during dehulling. Rosnagel (1999) concluded that while low groat breakage was effected by environment, genetic differences had more significance. Linear relationships between kernel size and breakage during dehulling, with larger kernels suffering more breakage have been reported (Symons and Fulcher 1988). Positive correlations of groat breakage

with groat weight, proportion of grains undehulled and negative correlations for groat breakage with moisture, beta-glucan and groat hardness have been reported (Doehlert and McMullen 1999). A strong relationship of low breakage with high fat and with smaller thinner grain and a lesser relationship of high B-glucan content with low breakage was reported by Rossnagel (1999).

In this study milling yield has been defined as the percentage by weight of undamaged groats obtained from a standard dehulling procedure. Other trait measurements associated with milling yield performance are; percentage unhulled (ease of dehulling), groat breakage, groat percentage and percentage milling loss (groat percent - milling yield). Undehulled grains remaining after dehulling are treated as a milling loss. Oat grains that are harder to dehull will require a more vigorous dehulling procedure, thus resulting in a higher proportion of broken groats. To determine the extent groat hardness contributes to groat breakage, the groat hardness of samples was measured using SKCS. Digital imaging of wholegrain was performed on the 1997 and 1998 samples in the set to determine any relationship with wholegrain shape and size with milling performance.

MATERIALS AND METHODS

Samples

Oat (*Avena sativa*) cultivars Mortlock, Pallinup, Coomallo, Toodyay, Hotham (Western Australian milling grade), and Dalyup, Needilup, Potoroo and Quoll (Western Australian feed grade), used in this study were grown in six sites throughout the Western Australian agricultural area in each of the 1997, 1998 and 1999 seasons. The samples were cleaned to remove free groats and foreign material before further testing.

The milling yield/ efficiency data was obtained using a Codema Laboratory Dehuller model LH 5095, (Minneapolis USA). Duplicate, accurately weighed ca 50g samples were dehulled for 2 minutes with an air pressure of 80psi. Broken groats and undehulled grain were separated from the dehulled groats using screens and hand sorting. All 3 fractions were then accurately weighed.

Milling and other traits were determined per sample as follows:

Laboratory Testing

1. **Percentage Milling Yield:** Weight of undamaged groats divided by weight of initial sample multiplied by 100.
2. **Percentage Broken Groats:** Weight of damaged groats divided by the sum of weights of broken and undamaged groats multiplied by 100.
3. **Percentage Undehulled Grains:** Weight of undehulled grains divided by weight of initial sample multiplied by 100.

4. **Groat Percentage:** Sum weight of broken groats and undamaged groats divided by the total obtained by the weight of the initial sample reduced by the weight of dehulled grains multiplied by 100.
5. **Milling Loss:** Percentage groat minus milling yield.
6. **Groat Hardness:** SKCS 4100 measurements of mean hardness index were carried out on 300 grains according to RACI Cereal Chemistry Division Official Method No.12.01.
7. **Protein content:** Determined as dry basis by the Dumas combustion method using a Leco FP2000 instrument (Leco Corporation, Michigan, USA) after milling the samples on a Retsch mill with a 1.0mm screen (Retsch Co., Germany).
8. **Oil content:** Determined on dried wholegrain samples by nuclear magnetic resonance using a Newport Analyser (Newport Instruments Ltd, UK).
9. **Beta Glucan:** Determined as dry basis by flow injection analysis using a Fiastar 5010 Analyser (Tecator Co., Sweden) after milling the samples on a Retsch mill with a 0.5mm screen.
10. **Moisture:** Measured using a conductance moisture meter (Marconi Instruments Ltd, UK).
11. **Digital imaging:** Performed on the 1997 and 1998 samples at the South Australian Research and Development Institute (SARDI) using a Panasonic CCD camera (Model GP-KR222E) with Fujinon 16mm lens and VideoPro 32, version 4 software (Leading Edge Pty Ltd., Marion, SA).
12. **Data Analysis:** Least significant differences of means for milling and other data were calculated using Genstat 5 software release 4.1 (Lawes Agricultural Trust).

RESULTS AND DISCUSSION

Milling Results

Milling quality traits were observed in this study to be effected by both genotype and growing environment, however the greater effects were shown by genotype. The mean milling yields for variety varied from an average of 72.2% for Coomallo to 63.9% for Dalyup (Table 1). The varietal rankings for milling yield were very consistent from year to year over the course of this study with only small changes in relative ranking between varieties on a seasonal basis which can be seen clearly in Figure 2. The current industry preferred variety Mortlock was overall ranked 5th of the varieties tested, yielding on average 2.8% less than Coomallo. As expected groat% was the single greatest factor influencing milling yield, a positive correlation ($r = 0.86$) being observed (Table 2). This close, linear relationship can be seen clearly in Figure 1. Milling yield was negatively correlated with percentage grain unde-hulled and percentage groat breakage, (these two traits contribute to the percentage milling loss trait). The feed grade varieties Needilup and Dalyup proved comparatively hard to dehull which contributed to their low yield. Among the milling grade varieties, Mortlock was the hardest to dehull thus contributing to its low milling yield ranking in this sub-group. The varieties having the lowest groat breakage were Dalyup, Hotham and Pallinup. This low breakage, combined with their ease of dehulling enabled Pallinup and Hotham to have the lowest milling loss of the varieties tested in this study.

The equilibrium moisture level of the oat samples being dehulled in this study reduced the amount of groat breakage but also increased the amount of grains unde-hulled and so had no significant effect on milling loss, (results not included in Table 1). This result replicates in part work done by Doeblert (1997) who indicated a moisture level of approximately 9% as being ideal for reducing milling loss in oat dehulling.

Table 1: Variety means for milling results, SKCS data, oil, protein and B-glucan contents for samples grown in the years 1997 – 1999, ($n = 17$).

Variety	Milling Data					SKCS Data			OIL	Protein	B-glucan
	Yield	Milling loss	Broken kernels	Unhulled grain	Groat%	Weight	Diameter	Hardness			
Coomallo	72.2	2.1	2.6	0.2	74.3	27.9	1.6	-60.5	6.9	11.4	4.9
Pallinup	70.9	1.6	1.6	0.6	72.5	29.1	1.6	-53.1	6.8	11.2	5.4
Hotham	70.7	1.7	1.7	0.6	72.4	27.7	1.5	-60.8	6.9	11.4	4.7
Toodyay	70.0	2.4	2.8	0.5	72.4	28.2	1.5	-67.5	6.5	10.3	4.6
Mortlock	69.4	2.6	2.4	1.2	71.9	28.9	1.6	-64.6	6.1	11.9	5.1
Potoroo	67.5	2.0	2.3	0.5	69.5	26.8	1.5	-63.8	7.1	9.5	4.1
Quoll	67.5	2.6	2.9	0.8	70.1	27.6	1.5	-65.0	6.5	10.7	4.4
Needilup	64.1	3.0	1.8	2.7	67.1	25.8	1.5	-57.3	7.0	9.9	4.6
Dalyup	63.7	3.5	1.2	4.0	67.2	27.1	1.5	-59.5	6.1	10.5	5.0
LSD 5%	2.0	1.1	1.3	1.2	1.8	2.0	0.1	6.3	0.2	1.0	0.4

(All milling data expressed as percentage. SKCS data for groats; weight in milligrams, diameter in millimetres and hardness as calibrated hardness index for wheat. Oil and protein as percentage of wholegrain, dry basis. B-glucan as percentage of groat weight, dry basis.)

Milling Results and SKCS Data

The hardness index measurement reported in Table 1 is based on interpretation of the SKCS 4100 crush force profiles for wheat. Calibration on an arbitrary scale of 0-100 is accomplished by the use of a set of US National Institute of Standards and Technology Reference Materials. Crush force profiles for oats reported by Osborne and Kotwal (1999) show that the peak force occurs earlier in time than for wheat. This explains why the values for oats are negative on the wheat calibration scale. The smaller negative values reflect an increase in groat hardness.

The average groat hardness values measured by SKCS for varieties ranged from –67.5 for Toodyay to –54.2 for Pallinup. This compares with previous work on North American genotypes that showed a range of –42.2 to –32.6 (Doehlert 1999). Groat hardness was negatively correlated with groat breakage, kernel weight and diameter (Table 2). Samples with larger groats tended to be softer which may explain in part why they were more likely to be damaged during dehulling. Despite have higher milling loss, samples with larger groats were positively correlated with groat percentage and consequently with milling yield.

Milling and Grain Composition Data

Oil and protein content were not observed to have significant associations with milling traits except for a slight negative correlation between protein and milling loss. Beta-glucan correlated negatively with percentage broken groats and milling loss; and positively with groat hardness and milling yield. These correlations were very minor however.

Table 2: Correlation table of Milling, SKCS, protein, oil, and b-glucan for individual samples in the years 1997 – 1999, ($n = 153$).

Significance of correlation coefficient r at 5% level is 0.16.

	Broken kernels	Unhulled grain	Groat%	Yield	Milling loss	Weight	Diameter	Hardness	Oil	Protein
Unhulled grain	0.00									
Groat%	0.24	-0.46								
Yield	-0.19	-0.71	0.86							
Milling loss	0.75	0.67	-0.08	-0.59						
Weight	0.35	-0.07	0.49	0.27	0.24					
Diameter	0.31	-0.10	0.52	0.33	0.18	0.91				
Hardness	-0.43	0.08	-0.26	-0.07	-0.27	-0.55	-0.37			
%OIL	0.13	-0.11	0.17	0.12	0.03	0.14	0.19	-0.01		
Protein	-0.18	-0.15	0.01	0.13	-0.23	-0.18	-0.23	0.10	-0.56	
B-glucan	-0.24	-0.07	0.09	0.18	-0.21	-0.09	-0.07	0.18	-0.33	0.43

Table 3 Correlation table of Milling and Digital Imaging Data for individual wholegrain samples in the years 1997 and 1998, ($n = 99$).

Significance of correlation coefficient r at 5% level is 0.20.

	Area	StDev Area	Length	Breadth	stdev width	Round-ness	Plump-ness	Square-ness	Broken kernels	Undehulled grain	groat%	Yield
StDev Area	0.77											
Length	0.81	0.59										
Breadth	0.78	0.69	0.29									
Stdev width	0.38	0.61	0.02	0.66								
Round-ness	0.25	0.13	0.76	-0.39	-0.37							
Plump-ness	0.12	-0.01	0.67	-0.52	-0.47	0.98						
Square-ness	0.92	0.83	0.83	0.72	0.44	0.34	0.18					
Broken kernels	-0.31	-0.36	-0.39	-0.11	-0.12	-0.32	-0.26	-0.38				
Undehulled grain	0.18	0.19	0.07	0.32	0.21	-0.12	-0.18	0.31	-0.13			
groat%	-0.22	-0.32	-0.05	-0.38	-0.60	0.17	0.23	-0.31	0.10	-0.43		
Yield	-0.13	-0.20	0.06	-0.37	-0.50	0.28	0.33	-0.23	-0.20	-0.67	0.89	
Milling Loss	-0.08	-0.12	-0.22	0.16	0.05	-0.31	-0.32	-0.03	0.61	0.71	-0.23	-0.64

Milling and Digital Imaging Data

Digital imaging of wholegrain was performed on the 1997 and 1998 samples in the set to determine any relationship with wholegrain shape and size with milling performance. Correlations with milling properties are shown in Table 3.

The percentage of broken groats after dehulling was observed to be slightly but significantly negatively correlated with larger, plumper, “squarer” grain and with the length of the grain. The percentage of grain undeulled was positively, though slightly correlated with wider and “squarer” grain. Groat percent and therefore milling yield was observed to have a relatively strong negative correlation with the standard deviation of width of wholegrain, while a lesser negative correlation was observed with mean breadth. It is likely that the relative proportions of primary, secondary and tertiary grains in each sample are responsible for this observation. The smaller secondary grains have been reported to have higher groat percentages than primary grains (Atkins 1943).

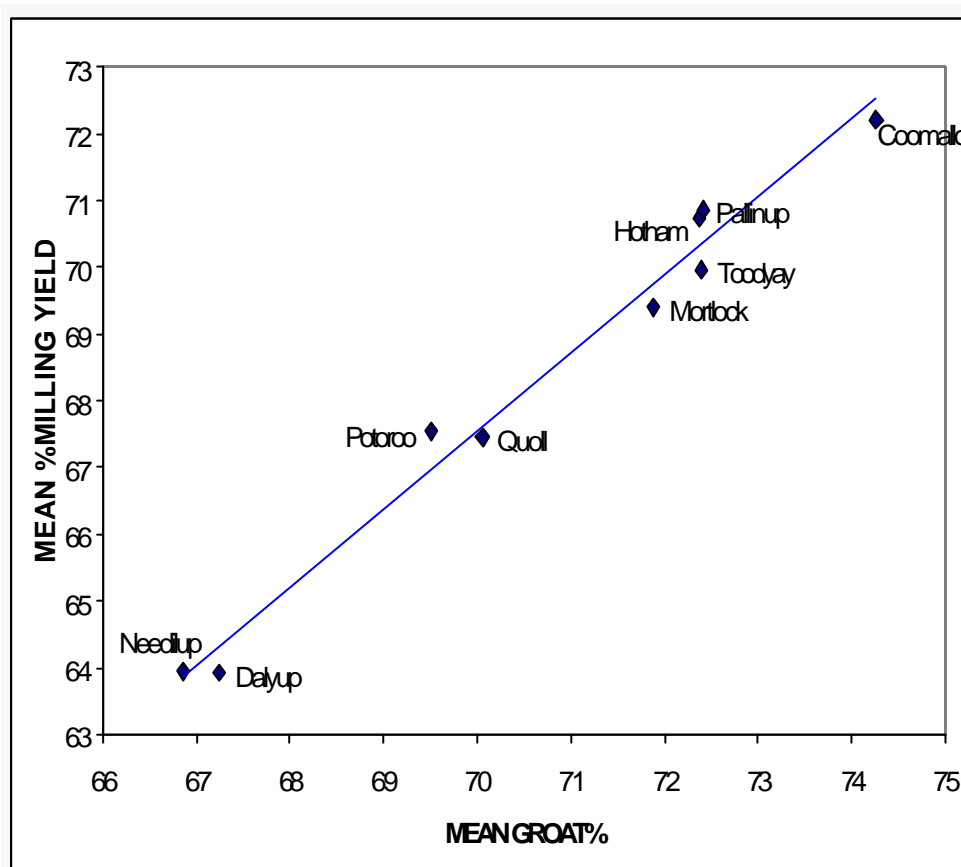


Figure 1: Mean groat percent plotted against mean percentage milling yield for varieties for the seasons 1997 - 1999.

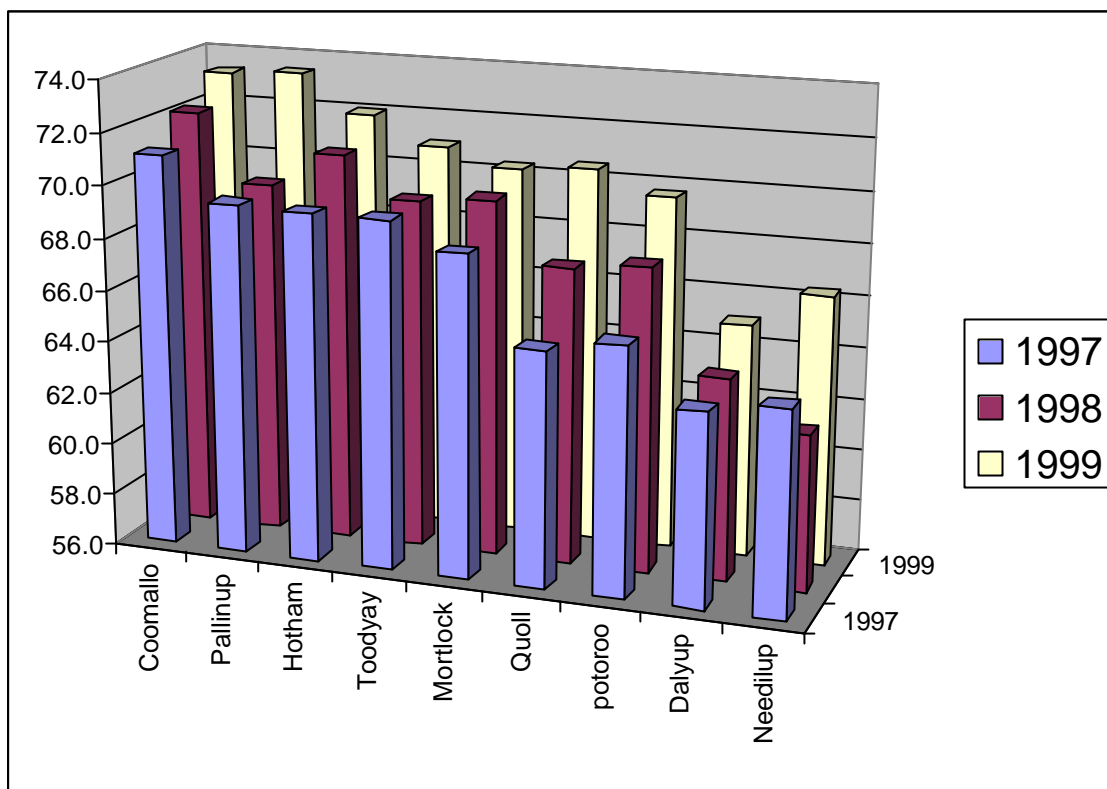


Figure 2: Histogram plot of seasonal mean milling yield for varieties for the years 1997, 1998 and 1999

CONCLUSION

All oat milling quality traits measured, the most important being milling yield were more influenced by genotype than environment in this study. The single greatest factor determining milling yield is groat percentage, which is a highly heritable trait. Hence breeding for increased milling yields in oats will largely depend on improved groat content, with smaller but significant contributions coming from varieties being easier to dehull and having less brittle groats. Groat hardness as measured by SKCS and β -glucan content were found to be significant factors contributing to the extent of groat breakage. The mean breadth and standard deviation of width of wholegrain samples was found to be negatively correlated with groat percentage and milling yield, indicating the ratio of primary to secondary grain to be an important factor in oat milling quality. Rankings in milling yield between varieties and the related traits; groat percent, ease of dehulling, groat breakage and milling loss were found to vary little from season to season indicating these traits are likely to be heritable, and thus able to be improved through plant breeding.

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SELECTION INDICES IN FORAGE OAT (*Avena sativa* L.)

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ABSTRACT

Selection indices were constructed and their efficiency assessed in terms of expected genetic advance using 30 genotypes of forage oat. Six characters viz., plant height, number of tillers and number of leaves per plant, growth rate (g/day/plot), dry matter and green fodder yield (kg/plot) were selected for the formulation of selection indices for green fodder yield. Efficacy of indices over direct selection in terms of relative selection efficiency ranged from 14.9 to 667.5%, the highest efficiency being for the index score involving all the six traits. The efficiency of indices increased with increasing number of characters. The index score revealed 567.5% higher efficiency over straight selection based on green fodder yield it self.

Key words: *Avena sativa*, Oat forage, selection indices, genetic advance, selection efficiency.

INTRODUCTION

Oat (*Avena sativa* L.) is an important cereal fodder grown during winter season. During the recent years it is catching up in a big way to supplement the high dry matter content and quality in mixtures with berseem clover and lucerne. With the advent of intensified dairy industry in India especially with the crossbred livestock, the oat fodder is gaining significance and attracting the attention of forage breeders for the genetic improvement of this crop. Selection indices provide the means for making use of correlated characters for higher efficiency in selection for characters of low heritability like yield (Smith, 1936). But all the characters are of not equal value, for this purpose and in the absence of any objective criterion for choice of characters, several indices (with varying combination of characters) need to be evaluated to find out the most efficient index. This study was undertaken to construct selection indices and assess their efficiency over direct selection for green fodder yield in oats.

MATERIALS AND METHODS

Thirty genotypes of oat (*Avena sativa* L.) were evaluated in randomized complete block design with three replications during winter 1998-99. Each plot consisted of four rows, 3 in long and spaced 40 cm apart. Plant-to-plant distance was maintained 10 cm by thinning. Five plants taken at random from each plot at 50 per cent heading stage, were used for recording observations. However, for days to 50 per cent heading, green fodder yield, dry matter yield and growth rate data were recorded on plot basis. Data recorded on six characters viz., plant height (cm), number of tillers per plant number of leaves per plant, growth rate (g/day/plot), green fodder yield (kg/plot) and dry matter yield (kg/plot) were selected on the basis of variability and correlation studies and Used to formulate selection indices. Genetic advance was calculated assuming 5% selection intensity by method

suggested by Robinson *et al.* (1951). Relative efficiency of selection was computed with that of straight selection for green fodder yield alone where its value was taken to be 100.

RESULTS AND DISCUSSION

Five characters namely, number of tiller per plant (X2), number of leaves per plant (X3), dry matter yield per plot (X4) growth rate (X5) and plant height (X6) which exhibited maximum direct and indirect effects on green fodder field were selected for construction of suitable selection indices. Besides these characters green fodder yield per plot (XI) was also included as an independent variable. When the six characters were considered individually, the maximum expected genetic advance (8.74) was observed for growth rate (Table 1). It is apparent from the results that the index involving all the six characters exhibited the highest relative efficiency of 667.5% whereas, the minimum relative efficiency (14.9%) was indicated by the index having single trait viz., number of tiller per plant. The single variable indices except number of leaves per plant and growth rate (g/day/plot) showed lower relative efficiency when compared with independent variable index i.e., green fodder yield *per se*. For the selection index involving two variable combination the maximum expected genetic advance (11.4) and relative selection efficiency (291.5%) was observed for the discriminant function comprising green fodder yield and growth rate. Among the three variable indices, the traits comprising green fodder yield with number of leaves per plant and growth rate recorded still higher genetic advance (18.21) and relative selection efficiency (465.7%).. Among the four variable selection indices when green fodder yield with number of tillers per plant, number of leaves per plant and dry matter yield were taken together, the genetic advance and relative efficiency further increased to 20.25 and 517.9% respectively. The index with five variables involving green fodder yield along with number of tillers and leaves per plant, growth rate and plant height exhibited the much higher genetic advance (25.87) with the maximum relative efficiency (661.6%) over straight selection for green fodder yield only. This result supports previous report of Choubey and Gupta (1986) from a path analysis study in forage oat.

The validity of the predicted superiority of indices over direct selection or of any one index over others depends on the precision of estimates of variance and covariance (which formed the basis of index construction here), through there was no objective criterion to judge the reliability of these estimates (Brim *et al.*, 1959). However, selection indices have specific applicability to the particular set of material for realizing the expected superiority.

In the present study, selection indices based on multiple characters resulted in increased efficiencies. This indicated the usefulness of multi trait selection for yield over selection based only on a single trait. The highest values of both genetic advance (26.1) and relative efficiency (667.5%) were obtained when all the six characters were considered simultaneously. Thus, plant height, number of tillers and number of leaves per plant, growth rate, dry matter yield and green fodder yield per plot are the traits needed for index construction and may be used for simultaneous improvement of these characters in forage oats.

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Table 1. Selection index, expected genetic advance and relative selection efficiency in forage oat

Selection index	Discriminant function selection efficiency	Expected genetic advance	Relative
X,	7.66	3.91	100.00
X2	4.68	1.60	14.92
X3	15.89	4.69	119.94
X4	3.40	0.79	20.20
X5	16.98	8.74	223.52
X6	87.79	1.53	39.13
XI + X2	7.66+4.68	3.27	83.63
XI + X3	7.66+15.89	7.17	183.37
XI + X4	7.66+3.40	2.29	58.56
X, + X5	7.66+64.98	11.40	291.56
XI + X6	7.66+87.79	6.32	161.63
X1 +X2 +X3	7.66+4.68+ 15.89	9.04	231.20
XI+X2 +XI	7.66 + 4.68 + 3.40	3.97	101.53
X, + X2 +X5	7.66 + 4.68 + 64.98	14.42	368.80
XI + X2 + X6	7.66 + 4.68 + 87.79	8.59	219.69
XI + X3 + X4	7.66 + 15.89 + 3.40	7.88	201.53
XI + X3 + X5	7.66 + 15.89 + 64.98	18.21	465.72
XI + X3 + X6	7.66 + 15.89 + 87.79	12.52	320.20
XI + XI + X5	7.66 + 3.40 + 64.98	12.18	311.51
XI + X4 + X6	7.66 + 3.40 + 87.79	7.02	179.53
XI + X5 + X6	7.66 + 64.98 + 87.79	18.29	467.77
XI + X2 + X3 + X4	7.66 + 4.68 + 15.89 + 3.40	9.74	249.10
XI + X2 + X3 + X5	7.66 + 4.68 + 15.89 + 64.98	20.25	517.90
XI + X2 + XI + X6	7.66 + 4.68 + 15.89 + 87.79	14.42	368.80
XI + X2 + X4 + X5	7.66 + 4.68 + 3.40 + 64.98	15.22	389.26
XI + X2 + X4 + X6	7.66 + 4.68 + 3.40 + 87.79	9.26	236.83
XI + X2 + X5 + X6	7.66 + 4.68 + 64.98 + 87.79	19.59	501.02
XI + X2 + X3 + X4 + X5	7.66 + 4.68 + 15.89 + 3.40 + 64.98	20.89	534.53
X1 + X2 + X3 + X4 + X6	7.66 + 4.68 + 15.89 + 3.40 + 87.79	15.11	386.44
XI + X2 + X3 + X5 + X6	7.66 + 4.68 + 15.89 + 64.98 + 87.79	25.87	661.64
XI + X2 + X3 + X4+ X5 + X6	7.66 + 4.68 + 15.89 + 3.40 + 64.98 + 87.79	26.10	667.52

X, - Green fodder yield (kg/plot); X2 - Number of tillers per plant; X3 - Number of leaves per plant;

X4 - Dry matter yield (kg/plot); X5 - Growth rate (g/day/plot); X6 - Plant height (cm)

OAT BREEDING FOR FOOD AND FEED IN HUNGARY

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The growing area of oats settled in Hungary on about 50 thousand hectares in the past 10 years. Nowadays the average yields are hardly behind those in Western Europe thanks to the excellent, well-adaptable varieties, although mainly wheat, maize and barley are grown on the better soils of the Carpathian Basin.

Oat breeding has been conducted almost exclusively at our institution, the Cereal Research Non-Profit Company in Hungary, although foreign varieties are introduced by several other companies as well. The following foreign oat varieties introduced into Hungary are worth mentioning: *Salvador* and *Tikal* (from Germany), *Eberhard* and *Expander* (from Austria), *Kwant* and *Komes* (from Poland).

The spring oat variety *GK Pillangó* (registered in 1989) is the leading one among the 10 commercially grown oat varieties, and it is grown nearly on the half of the domestic growing area. It can be widely grown because it is highly adaptable, and therefore it can perform well both under the more extensive and dry low-land conditions and under the more intensive and moist conditions of the western region of Hungary near the Alps - where even the soils are better. The oat variety *GK Iringó* (registered in 1998) originates from the crossing of the above oat variety and two other genotypes. It has got all the positive features of *GK Pillangó*, moreover, *GK Iringó* is not susceptible to smut (*Ustilago avenae* Rostr.), it has got good field resistance to crown rust (*Puccinia coronata*), and to red leaf BYVD (*Oat Newsletter*, Vol. 44., 1998).

In the last decade the utilisation of oats changed somewhat. Previously it was used almost exclusively for feeding horses. Nowadays its role in pig-breeding and keeping poultry is increasing. Its good nutritive value is utilised in various grain mixtures and its straw is an excellent fodder for ruminants. There are more than 200 officially registered horse-breeding in Hungary, with 10 heads of horses in the average. Fortunately, the exploitation of the oats as green fodder is rising as well. For this purpose one of our promising winter oat experimental varieties is used mixed with Hungarian velch (*Vicia pannonica* Cr.) or with field pea (*Pisum arvense* L.). This is an excellent fodder for dairy cows.

A special oat variety has been bred for human consumption, the naked oat variety *GK Zalán* (*Avena nuda* L.). It was registered in 1993. It is highly advantageous because it has got very high protein content (ca. 20%) and amino acid content. It can be processed by energy saving methods because it need not be hulled (the glumes need not be removed mechanically). Although it is grown on a relatively small area, ca. 2,000 ha, its seed is demanded more and more, even in the neighbouring countries. It is very significant in our opinion, that this variety is apt to be grown as a bio- or eco-product, free from any chemicals or chemical residues. Its great advantage is the earliness and the excellent drought resistance.

There is only one flake factory in our country (even it is supplied with an old equipment from the no longer existing East Germany), the capacity of which is not able to satisfy the domestic demand any longer, and therefore mainly finished products are imported.

ASSESSMENT OF YIELD CRITERIA IN OAT LINES OF QUAKER NURSERY

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Although oat (*Avena sativa* L.) is one of the oldest small grain cereals for food and feed in the world, the use of oat as food has recently raised. This trend has increased number of research on oat due to its emerging importance. In this study, one hundred and thirty five oat lines of Quaker Nursery were compared to local check, a land race, for their agronomic characters. The material was sown in the forth week of October 2000 at Urkutlu experiment location (37° 19' N, 30° 17' E and 850 m from sea level) in the West Mediterranean region of Turkey. Oats is generally sown in early spring and harvested after May in Turkey. Plots arranged in one row of 2 m length with inter- and intra-row spacing of 30 and 10 cm (20 grains sown for each plot), respectively. Fertilizers were applied at a rate of 18 kg per ha nitrogen and 46 kg per ha prior to planting. Number of surviving plants per row, plant height (cm), number of tillers, spikelets per panicle, number of grain per spikelet, number of total grain per panicle, biological yield (g), single plant yield (g), 1000-grain weight (g), harvest index (%) and cold tolerance (%) were recorded in each line. From the preliminary researc, some lines of Quaker nursery has perrformed better than local check for single plant yield, spikelets per panicle and number of grain per spikelet.

Average of surviving plants (7.87 and 7.13); number of tillers (3.42 and 3.38); spikelets per panicle (18.4 and 17.2); plant height (62.0 and 56.6 cm); biological yield (40.0 and 52.5 g/plot); number of grain per spikelet (2.66 and 2.75); number of total grain (330 and 420 per plot); single plant yield (1.42 and 1.08 g); 1000-grain yield (39.06 and 19.9 g); harvest index (29.5 and 13.6 %) and cold tolerance (39.4 and 35.7 %) were calculated for each genotype in the breeding lines and check, respectively.

INTERNATIONAL COLLABORATIVE NURSERY

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Today's oat research and breeding efforts globally are being impacted by a number of factors. Most oat production areas are being reduced in size and thus are becoming increasingly regionalized and even localized. This fact and others has resulted in a decrease in public support for most oat research funded at public institutions. As a result there are fewer oat researchers in all relevant disciplines and most of those remaining are not working on oats exclusively. Although there are few private companies doing oat breeding, ownership of intellectual property by public institutions/organizations, and the potential revenue stream that might result from exercising those ownership rights have become increasingly of more interest to public institutions. All of these factors and others have marginalized many long-standing oat improvement efforts.

Within this new "climate", it is essential that the effectiveness of all available oat research resources be maximized by optimizing each individual research program, and by connecting each program to as many others as possible for interaction and support. Regarding program connections, the existence of this meeting and the five meetings that have preceded it are a great step forward in connecting oat researchers around the planet. I want to publicly commend the group that produced the proposal that created the International Oat Conference (IOC), and in turn, these meetings. I also want to salute all of the members of the organizing committees who have planned each of the meetings. Equally important, the existence of the Quaker International Oat Nursery (QION), funded mainly by the Quaker Oats Co. for nearly 25 years, has been a great asset for sharing germ plasm among some members of the oat breeding community. Although the QION began mainly as a South American enterprise, it has been spreading in recent years, both in terms of germ plasm contributors and in terms of people and locations receiving seed of the nursery.

Another dimension of the interaction among oat researchers, and especially the sharing of each others' germ plasm, is the Oat Breeders Code of Ethics. I anticipate that the Code will have been adopted at the IOC business meeting earlier this week. By defining what is considered to be intellectual property and establishing the rights accorded such ownership, the Code sets standards for the exchange of germ plasm in all levels of development. It is flexible enough to accommodate the various policies that have been created by the public and private employers of oat breeders, and researchers in general. However it should be remembered that, as with all such codes, they are only effective to the extent that the people involved operate in a manner consistent with the intent of the provisions of the Code.

The idea for the International Parent Germ Plasm Exchange was born in a conversation that Dr. R. A. Forsberg and I had while we were travelling in Argentina as part of the "Quaker Team" that was reviewing the QION at the locations growing it in 1995. Briefly what we wanted to do was to accumulate as many as possible of the Uniform Performance Nurseries that were being grown in countries that have significant oat acreage. These Nurseries contain the elite advanced breeding lines of most of the significant oat improvement programs in the world. As most of you know, a selected subset of these lines are actually released to the public as new varieties. The remainder may well be equally, if

not more so, useful as parents in crosses that produce segregating populations from which breeders make selections to produce the next round of varietal candidates.

Another component of this Parent Exchange proposal started when the Minnesota program started using New Zealand as an off-season nursery site in the early 1990's. Other programs had been doing so quite successfully since as early as the mid 1970's. New Zealand has many advantages for those of us in the Northern Hemisphere, including better weather than we would have at home. The Crop and Food (C&F) organization actually has an International Nursery section that is well suited to assist others who want to grow an off-season field nursery. Thus, many of the seed shipping logistics are already at least partially in place.

Following the IOC meeting in Saskatoon in 1996 where I made a skeleton proposal for the Parent Exchange, I sent the proposal to the more than 50 oat breeders for which I had email addresses or fax numbers. I received only positive responses from every party contacted at that time, and subsequently as well. The rules for participating are only two: abide by the Oat Breeders Code of Ethics, and contribute either germ plasm or make some other in-kind contribution to the Exchange. I make the contact to receive permission of the owner of the lines in each Nursery and the Nursery coordinator has kindly shipped the seed to the C&F people for grow out and seed increase. We now include Nursery materials from Canada, the USA, Australia and South America. More nurseries would be most welcome. All lines included thus far are part of the demo plots here this year in conjunction with this meeting.

Immediately after the harvest of Nursery materials grown in Palmerston North, the seed is sent to South America, Canada, Norway and the USA for further distribution and secondary grow-outs. We welcome other locations for these grow-outs. Our intent is to have other breeders visit the site(s) nearest to them to observe the material first hand, thereby reducing travel costs and giving breeders the best opportunity to determine the usefulness of germ plasm from other programs. One of the grow-out sites will be Aberdeen, ID, where the entries will also be added to the USDA World Oat Collection.

Future plans include further development of the efforts already undertaken to obtain maximum participation by everyone working on oat improvement anywhere. Locations with grow-outs will be encouraged to record the standard traits and to monitor disease reactions at their site. We are already using material from the Exchange as parents in winter X spring three-way crosses for the Quaker International Oat Nursery. Thus, those of you who will be growing the QION will already be benefiting from access to the new germ plasm.

PLANT VARIETY PROTECTION – TIME FOR COMMON SENSE

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ABSTRACT

It is argued that because of its confused nature a 1998 attack on the plant variety protection system in Australia has little if any validity. A subsequent call by the CGIAR for a moratorium on the granting of intellectual property rights on designated germplasm in its collections appears to have been a hasty overreaction taken without full consideration of the facts. So that oat and other breeders can continue to have confidence in an ongoing, effective and balanced system of plant variety protection, a common sense appraisal of such attacks is needed to quickly expose any invalid claims as such.

OAT BREEDING AND PLANT VARIETY PROTECTION

In the brochure promoting this Conference the question is asked: “Are oats going to be an essential part of the 21st century food industry where taste, health, convenience and sustainable production drive the market?” This points to a most worthwhile goal.

If the goal is to be achieved there will need to be considerable plant breeding efforts. Plant breeding is expensive; funding it will be difficult if there is no way of recouping the costs. Plant variety protection, by giving breeders exclusive control over the commercialisation of their new varieties for a specified number of years, gives breeders the chance to recoup breeding costs, and possibly even make a profit.

More and more countries accept that an effective national plant variety protection law is a must if they are to provide an incentive for investment in research and development in plant improvement. The great majority of countries having plant variety protection laws follow the model of UPOV, the international plant variety protection organisation.

Recent Attack On Plant Variety Protection

There has long been some opposition to plant variety protection. Plant variety protection has been accused of leading to genetic erosion, of opening the door to domination of the seeds industry by multinationals, and so on. It is not my intention to reopen old debates. Rather I intend to discuss a recent attack on plant variety protection, an attack targeted at Australia that led to international repercussions.

In 1998 claims were made on the Internet that over 120 varieties were the subject of invalid applications or grants for plant breeders' rights in Australia. These claims came from two organisations, RAFI (Rural Advancement Foundation International) and HSCA (Heritage Seed Curators Association of Australia). Most of the varieties concerned had been developed from material coming from international gene banks, had originated from discoveries, or were based upon selections from existing varieties or populations.

The claims on the Internet were quickly followed by reaction from the CGIAR (Consultative Group on International Agricultural Research), the organisation which oversees the operation of the international gene banks. The CGIAR appeared to accept the RAFI claims at face value; in February 1998 its Chairman called a moratorium on the granting of intellectual property rights on designated plant germplasm held in CGIAR collections. "Designated germplasm" refers to plant accessions which the CGIAR Centres have placed under the auspices of the FAO and held in trust for the benefit of the international community, in particular developing countries. They are subject to terms and conditions contained in agreements signed between the Centres and FAO in 1994. Designated germplasm includes material ranging from farmers' varieties, landraces and wild species to modern varieties.

The moratorium was of concern for plant breeders. Many rely upon international exchanges of plant genetic resources for use in breeding programmes and are concerned about any barriers that may hinder reasonable exchanges.

The call for the moratorium and its terms was also of concern to UPOV because it misrepresented the role and functioning of the UPOV system. It was likely to mislead governments and individuals about the nature and effects of the UPOV system at a time when many countries were introducing or preparing laws on plant variety protection.

What Was The Nature Of The Attack On Plant Variety Protection

Restrictive interpretation of "plant breeding"

RAFI and HSCA take a very narrow interpretation of "plant breeding". In their view apparently, the only varieties which should be regarded as having been bred and which should be eligible for plant variety protection are those coming from a deliberate crossing of selected parents. They imply that varieties developed from discoveries or natural mutations, or from selection from existing varieties or populations, are not "bred varieties" and should not be eligible for protection.

This is too narrow a view. It overlooks the reality that many highly useful varieties are developed from discoveries, or selection from existing varieties or populations, using legitimate procedures which may involve much time, cost and plant breeding expertise.

UPOV clearly allows the protection of such varieties. The 1991 UPOV Convention defines "breeder"; this definition includes any person who "discovered and developed a variety". In March this year UPOV discussed the question again. The conclusion was that while such varieties may not be bred varieties in the sense of coming from a controlled cross-breeding programme, they are valid forms of plant improvement which should be eligible for protection.

Confusion arising from concerns over genetic loss and indigenous farmer's rights

Was RAFI motivated by concerns over genetic loss and indigenous farmers' rights? If so there is no basis to suggest that UPOV systems contribute to such problems.

- It is accepted that there is no conflict between the UPOV Convention and the International Undertaking on Plant Genetic Resources. This was recognised in Resolution 4/89 adopted by the FAO Conference in 1989.
- There is no contradiction or conflict between the UPOV Convention and the Convention on Biological Diversity. Indeed, effective intellectual protection is not only in harmony with the Convention on Biological Diversity but may be invaluable in the achieving of its goals.

Confusion between plant variety rights and patents

In the RAFI claims there seemed to be confusion of plant variety protection with (industrial) patents. Patents, like plant variety protection, are a form of intellectual property rights and create incentives for research and development. Patents have certain features which in some circumstances plant breeders may be able and wish to take advantage of. However apart from superficial similarities plant variety protection and patenting are separate and quite different systems. It is unhelpful to confuse one with the other.

How do patents differ from plant variety protection? There are significant differences. Some are shown in the table.

	Patent	Plant variety protection
Object of protection	Invention	Plant variety
Ease of making application	Needs patent specialist	Breeder can do it
Conditions for protection	novelty (not disclosed to public) industrial applicability inventive step enabling disclosure	novelty (commercial) distinctness uniformity stability denomination
Scope of protection	Determined by claims of patent	Stipulated in legislation
Use of protected variety for breeding other varieties	May require authorisation of breeder	Does not require authorisation of breeder

The distinction between plant variety protection and patents is unfortunately blurred in some countries.

- In the USA vegetatively-propagated plants are protected by what are known as plant patents. These are not patents at all but a form of plant variety protection. In this presentation when I refer to patents I mean industrial patents and exclude US plant patents.
- In Australia, in the plant breeders rights system, there is a complication over the concept of invention. In order to introduce the original law on plant breeders rights the Federal Government had to work within the complicated constitutional arrangements between the Federation and the States. It apparently claimed authority to legislate for plant variety

protection under its right under the Australian Constitution to issue patents. This makes Australia an easy target for groups such as RAFI which can challenge the validity of any Australian plant breeder's right by asking whether the variety concerned is an invention. This is a question which normally has no relevance to plant variety protection.

How Valid Are The Rafi Claims

I understand that the Australian PBR Office does not accept the validity of the claims made in Australia.

Because some of the listed varieties are also protected in NZ I have become involved in discussions with the HSCA. No good reason has been presented by HSCA to show that any NZ plant variety right has been issued incorrectly.

Was There Good Reason For The Cgiar Moratorium

It seems that the CGIAR accepted the RAFI claims at face value and that its call for a moratorium was a hasty overreaction made without full consideration of the facts.

UPOV has pointed out that the call for the moratorium implied it is possible to secure intellectual property rights for material that is in the public domain held in CGIAR collections. Under the UPOV system this is not possible. If someone is to secure protection, under the UPOV system:

- that person must be the breeder of the variety.
- the variety must be new (in the sense that it has not been sold before certain time limits).
- the variety must be distinguishable from any other variety.
- the variety must be uniform.

Any application for protection for designated germplasm would fail because one or more of these conditions would not be met.

What if an authority made a mistake by granting protection for such material? It would have to correct the mistake by annulling the grant as soon as it became aware of the true facts.

CONCLUSION

A balanced common-sense appraisal indicates that there is little if any validity in the claims by RAFI and HSCA and that the CGIAR's call for a moratorium was hasty and unnecessary. It is important that common sense prevails in the future. If there are future criticisms of the UPOV system it is important that valid concerns are acted upon, but any invalid claims exposed as such. Plant breeding is of a long-term nature. It is important that there be an effective, balanced and ongoing system of plant variety protection, such as that of UPOV, in which breeders and their financial backers can have confidence.

PRACTICAL CONSIDERATIONS OF COLLABORATION

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ABSTRACT

The practical considerations for successful germplasm exchange rely upon good communication of actual exchange, recognising differing country requirements for quarantine issues and respecting conditions surrounding ownership.

Good field plot techniques among differing research environments require timeliness of sowing; allowance for differing field plot design; consideration of differing growing conditions for daylength, vernalisation, plant maturity, plant types and other edaphic conditions such as alkaline or acid soils; bird control; evaluations for and where required, protection against pests and diseases; special evaluations for disease "hot spots".

Dispatch of germplasm is facilitated by systematic orientation of packaged accessions, accompanying field book listing accessions in packaged order. Type of packaging will influence recipient's ability for rapid turnover for sowing, including identification and labeling of individual packets. Because some nurseries are not suited to all types, harvesting of well formed, clean, sound and dry seed sometimes is not possible, but the consequences of harvesting immature seeds or seeds with high moisture content will lead to subsequent sowing problems, and possibly embryo death by some seed treatment regimes.

Quarantine is an issue for most countries. Some countries are quite restrictive, and conditions for importation changing. For New Zealand, recent changes include the requirement for field inspections prior to harvest to be free of disease, as well as the more commonly accepted requirement for standard phytosanitary certificate.

Different countries have differing laws concerning ownership of varieties. Many subscribe to the UPOV convention, but each country may have issues particular to that country, for example, provisions for "farm saved seed". Some countries may have other forms of patent, or no varietal protection at all. Participation in an international collaborative nursery transcends these differing country property laws, but acknowledgement of these differences must be made. A general agreement covering all nursery accessions is ideal, but in practice, difficult to achieve. Allowances need to be made, recognising differing levels of cultivar development, and allowance for individual contractual arrangements for germplasm exchange.

CHROMOSOME 5C AND THE DOMESTICATION OF HEXAPLOID OAT

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ABSTRACT

The oat genomes are replete with cytogenetic landmarks. We have identified a knob at the telomere of chromosome 5CL that cosegregates with alleles conferring wild traits in a BC₂F₂ population of *A. magna*. Linkage analysis confirms the map order [*Knob* – *Ba* – *A* – *Lc*] – *Lp*. We are also screening for linked AFLP markers. The 5CL knob was found in *A. sterilis*, *A. hybrida*, approximately 50% of *A. fatua*, and allotetraploid *A. magna*, *A. murphyi*, and *A. insularis* accessions. The knob was absent in accessions of *A. byzantina*, *A. sativa*, *A. sativa* var. *nuda*, and the wild, floret-shattering taxon *A. occidentalis*.

INTRODUCTION

Ladizinsky (1995) produced BC₁-derived lines of tetraploid *A. magna* carrying the domestication syndrome characters from hexaploid *A. sativa* cultivars. The purpose of this study was to determine if domesticated *A. magna* having larger seed and higher seed protein than domesticated *A. sativa* could be developed as a crop in its own right. The domestication characters are controlled by alleles at four loci: basal articulation (*Ba*), awnedness (*A*), lemma color (*Lc*), and lemma pubescence (*Lp*). The four genes showed linkage in a BC₁F₂ *A. magna* population, with a consensus gene order of [*Ba* – (1.4) – *A* – (13.6) – *Lc* – (8.0) – *Lp*]. Ladizinsky then proceeded with the second backcross between domesticated parent Ba 13-13 and wild parent #169, eventually deriving a BC₂F₂ population of 118 individuals segregating for the domestication traits.

The C-banding technique is useful for identifying individual oat chromosomes and for studying evolutionary changes in the oat genomes. Jellen et al. (1993a) reported variation among seven hexaploid oat accessions (*Avena byzantina*, *A. fatua*, *A. sativa*, *A. sterilis*) for C-banding patterns near the telomere of the long arm of chromosome 5C. Jellen et al. (1993b and 1988) reported that this chromosome was absent in cultivated nullisomics exhibiting fatuoid characteristics (Hacker and Riley, 1965). In addition, Jellen and Ladizinsky (2000) observed that wild allotetraploid *A. insularis*, *A. magna*, and *A. murphyi* had a prominent telomeric knob on the long arm of the apparent homologue to chromosome 5C. However, we observed that the 5CL knob ubiquitous in other *A. magna* accessions was notably absent in the BC₁-derived domesticated *A. magna* line Ba 13-13. The objective of this study was to study inheritance, identify linked AFLP markers (Jin et al., 1998; Yu and Wise, 2000), and pinpoint the chromosomal location of genes controlling domestication syndrome traits in domesticated *A. magna*.

MATERIALS AND METHODS

Plants from the segregating BC₂F₂ population described above were grown in the greenhouse and scored for prominence of the awn, lemma pubescence (scale of 1-5), shattering versus non-shattering spikelet, and dark versus light lemma color. Three or four F₃ progeny from 64 F₂'s were screened using C-banding for zero/one/two copies of the 5CL telomeric knob (Fig. 1). In addition, DNA was harvested from F₂'s or from five bulked F₃'s for AFLP analysis according to Doyle et al. (1990). Amplified fragment length polymorphisms (AFLPs) were generated using standard protocols from Life Technologies and Vos et al. (1995). Bulks of five F₂'s for each domestication character were screened using 20 primer combinations. Two primer combinations, yielding a total of nine polymorphic bands, were selected for screening on the segregating F₂ population: E(*Eco*RI-ACG)/J(*Mse*I-CAC) and E/O (*Mse*I-CTG). The C-banding technique was performed by the protocol of Jellen et al. (1993a) using liquid Giemsa stain (Sigma, St. Louis) instead of Wright's stain powder. Map orders were calculated using MAPMAKER 3.0 (Whitehead Institute).

In addition to the *A. magna* Ba13-13 x 169 segregating population, over 300 tetraploid and hexaploid oat accessions and cultivars (not listed) were examined using C-banding and scored for presence or absence of the 5CL knob.

RESULTS AND DISCUSSION

The 5CL knob was able to be reliably scored using C-banding (Fig. 1) and linkage analysis revealed it to be linked to genes controlling the four domestication traits, with [*Knob* – *Ba* – *A* – *Lc*] forming a linked cluster and *Lp* approximately 40 centimorgans distant. Using *Knob* as the terminal anchor of the linkage group, two of the best gene orders determined by Mapmaker were *Knob* – 4.5 cM – *A* – 7.0 – *Lc* – 14.3 – *Ba* – (44.1) – *Lp* (log-likelihood of –150.40) and *Knob* – 11.3 – *Ba* – 12.0 – *A* – 9.3 – *Lc* – (44.2) – *Lp* (log-likelihood of –160.70). However, we are uncertain about our scoring and positioning of *Lp*, since expression of this character was affected by an unlinked modifier that only permitted identification of 17 glabrous, homozygous recessive F₂ plants, which falls well below the expected 1:3 ratio for a single dominant gene. The domestication syndrome genes are clearly located on the distal portion of the long arm of chromosome 5C. It is interesting to note the apparent high degree of homology conserved on chromosome 5C between *A. sativa*, the hexaploid source of the domestication genes, and tetraploid *A. magna*, as evidenced by recombination in the second backcross as well as in the BC₁F₁ (Ladizinsky, 1995). This is somewhat surprising due to the high degree of chromosomal rearrangement in the *Avena* genus evidenced by intra- and interspecific hybrid pairing studies (Ladizinsky, 1970; McMullen et al., 1982; Singh and Kolb, 1991), C-banding (Jellen and Ladizinsky, 2000), genomic *in situ* hybridization (Chen and Armstrong, 1994; Jellen et al., 1994), and molecular mapping studies (O'Donoghue et al., 1995; Van Deynze et al., 1995).

Initial linkage analysis of the two AFLP primer combinations, E/O and E/J, prescreened on small numbers of 40-50 F₂ plants bulked for recessive domestication characters, failed to detect linkage, either with each other or with the domestication syndrome-*Knob* gene cluster. Of these nine potential markers, five segregated in the expected 3:1 pattern for dominant Mendelian markers. We are continuing analysis of bulked F₃ plants using these potential molecular markers. We are also raising 6-10 F₃ plants from each line in order to genetically characterize, and more accurately score, *Lp* in the population.

We observed the 5CL knob in the majority of accessions of *A. sterilis*, *A. hybrida*, approximately 50% of *A. fatua*, and allotetraploid *A. magna*, *A. murphyi*, and *A. insularis*. The knob was absent in accessions of *A. byzantina*, *A. sativa*, *A. sativa* var. *nuda*, and the wild, floret-shattering taxon *A. occidentalis*.

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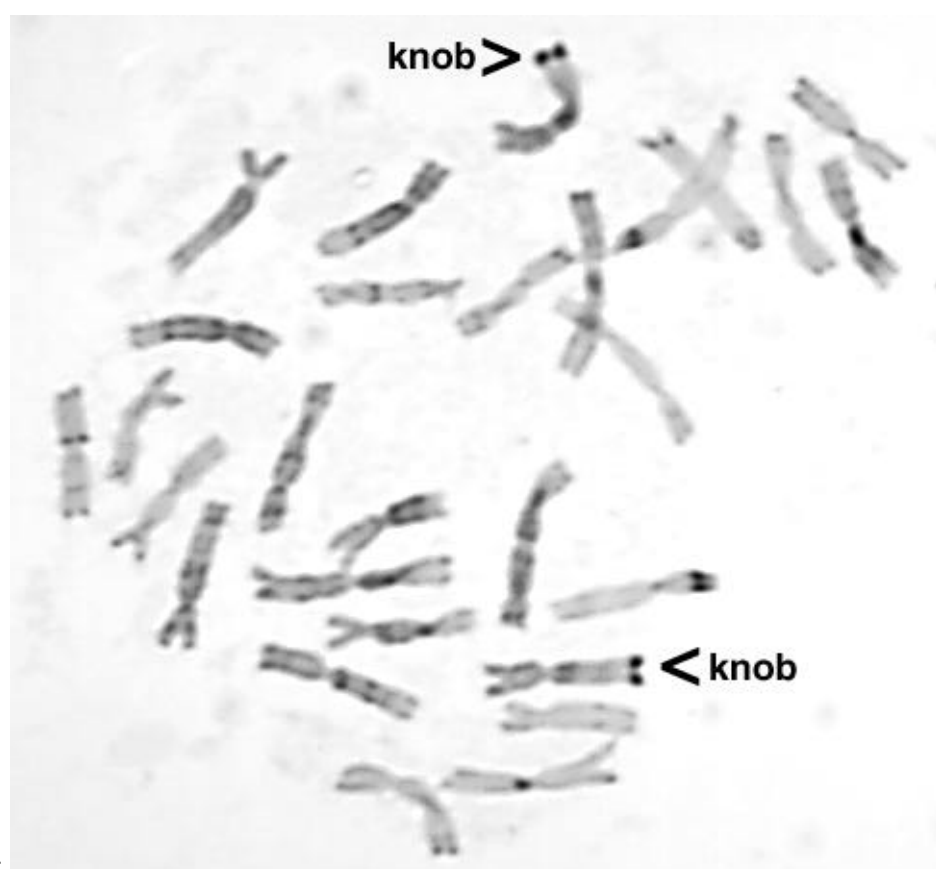
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Figure 1. C-banded chromosomes of F_3 plants segregating for zero, one, or two 5C chromosomes (arrows) with the long-arm terminal knob. A) Plant 12-D, homozygous, non-knob. B) Plant 70-C, heterozygous for the knob. C) Plant 71-B, homozygous, knob. Magnification is 630X.





C

GENOMIC TOOLS AND GERMPLASM FROM OAT X MAIZE CROSSES

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ABSTRACT

In hexaploid oat (*Avena sativa* L., $2n = 6x = 42$) both haploid oat plants and plants with one or more maize (*Zea mays* L., $2n = 2x = 20$) chromosomes added to an oat genome have been recovered from oat x maize crosses. This report describes the production and characterization of these materials including the generation of a complete set of individual maize chromosome addition oat plants for each of the ten maize chromosomes, the recovery of chromosome-segment additions following gamma radiation treatments, and illustrations of how these materials can serve as valuable oat and maize genetic tools and germplasm sources.

BACKGROUND

Maize pollination of emasculated florets of oat can lead to the recovery via embryo rescue of two types of viable offspring, plants with a complete haploid set of 21 oat chromosomes and plants with 21 oat chromosomes plus one or more maize chromosomes. These two types of plants result respectively from a complete or partial uniparental elimination of maize chromosomes during embryo development from an oat-maize hybrid zygote (Rines and Dahleen 1990; Rines et al. 1997). The majority of recovered plants are oat haploids with no retained maize chromosomes. These plants can serve to produce doubled haploids, either by colchicine treatment (Aung, 1998) or from unreduced gamete formation and self-pollination (Dahleen and Rines, 1990; Davis 1992). The low frequency of plant recovery (usually less than 1% based on total oat florets emasculated and pollinated in experiments to date) has limited the application of the technique for production of doubled haploids for breeding purposes (Rines et al. 1997). However, valuable oat genetic mapping tools in the form of aneuploids have been generated from these materials. Specifically, about one-third of offspring from self-fertilization of non-colchicine-treated haploid oat plants are aneuploid, apparently from fusions involving partially unreduced gametes (Davis 1992). Monosomic ($2n - 1$) plants produced in this manner have allowed the assemblage of a nearly complete set of monosomic lines (Jellen et al. 1998), which in turn has been used for the assignment of oat molecular marker linkage groups to physical chromosomes toward the production of an integrated physical-molecular marker map for hexaploid oat (Fox et al. 2000; Start 2000).

The second type of plants recovered from oat x maize crosses, haploid oat plants with added maize chromosomes, are unique in being the widest-cross partial hybrids of which we are aware. Much of our effort has focused on these plants because of their unique nature and the exciting prospects they afford for developing novel genetic tools and germplasm for both oat and maize and for studying interactions between their genomes.

Special efforts have been directed to forming fertile disomic ($2n = 42 + 2$) maize chromosome addition lines for each of the ten maize chromosomes, and using these to generate, through radiation treatments, translocation and other stocks with only a segment of a particular maize chromosome present in an oat plant.

MATERIALS AND TECHNIQUES

'Starter-1' oat, a single plant reselection of cv. Starter, was chosen for use in most of our studies because of the large seed, strong stems, and ease of emasculation of this cultivar. Other oat lines used include Sun II, Kanota, Preakness, MN97201, and two reselections of the experimental tissue culture line GAF-Park, GP-1 and GP-2. 'Seneca 60', a sweet corn hybrid chosen initially for its earliness and abundant pollen, was used almost exclusively as the maize pollen source to maintain a constancy for analysis of maize chromatin added to recovered oat plant genomes.

Techniques currently used for oat x maize crossing and plant recovery are essentially as described by Rines and Dahleen (1990) and Rines et al. (1997). One modification has been introduced in the last several months. To emasculate the oat florets, we now clip the pre-anthesis spikelet at the base of the secondary floret with scissors to remove most of the secondary floret and the distal ends of the anthers of the primary floret. A panicle with 20 or 30 clipped spikelets is then covered with a glassine pollination bag. Two days later the bag is removed. Any large anther remnants are carefully removed with forceps to expose the stigmas more fully. The florets are then sprinkled with freshly collected maize pollen, a few drops of water are put into the glassine bag, and the bag replaced on the panicle. After two more days, the panicle's florets are sprayed with a solution of 100 mg/L 2,4-D to promote embryo development. At the time of embryo rescue at 14-16 days after pollination, any oat caryopses produced by accidental selfing are readily distinguished by their plump size and are discarded. Caryopses with no embryo or with embryos from maize fertilization are smaller and partially shriveled from lack of normal endosperm development.

Detection of retained maize chromatin in initial F_1 plants from oat x maize crosses, in their progenies, or in plants obtained following radiation treatment of addition lines was made either by Southern hybridization using maize genomic DNA or by polymerase chain reaction (PCR) amplification of the long terminal repeat (LTR) sequence of the dispersed high copy maize retrotransposon sequence Grande-1 (Riera-Lizarazu et al. 2000). Genomic *in situ* hybridization (GISH) analysis of root-tip preparations using fluorescein-labeled maize genomic DNA as probe was used to verify presence of maize chromosomes and determine the number of maize chromosomes in addition lines and the size and location of segments in radiation products (Riera-Lizarazu 1996; 2000). Previously mapped maize chromosome restriction fragment length polymorphism (RFLP) and microsatellite (SSR) markers were used to identify which maize chromosomes were present in the addition lines and to characterize retained maize chromosome segments in radiation products as described in Riera-Lizarazu et al. (2000).

OAT-MAIZE ADDITION (OMA) LINES

During the past three years 70 F_1 plants containing maize chromosomes have been identified among about 200 plants recovered from 2,000 embryos rescued from more than 25,000 maize-pollinated oat florets. These oat-maize addition (OMA) plants are in addition to 36 OMA plants described previously (Riera-Lizarazu et al. 1996; Maquieira 1997). One small plant had six maize chromosomes but most surviving OMA plants had fewer. Plants having only a single added maize chromosome were the most common and were generally more vigorous than plants with multiple additions, probably due to detrimental effects of extra chromosomes. Some of the single chromosome addition plants were self-fertile, presumably due to meiotic restitution, producing disomic OMAs with a chromosome constitution of $2n = 42 + 2$. In not all F_1 plants in which maize chromosomes were detected, however, were the maize chromosomes transmitted; presumably either because the plant was initially chimeric for the maize chromosome or because the chromosome was lost somatically or during gamete production.

Single maize chromosome OMA F_1 plants have now been recovered for each of the ten maize chromosomes. Self-fertile disomic addition lines with nearly 100% transmission of the disomic maize chromosome have been obtained for maize chromosomes 1, 2, 3, 4, 6, 7, and 9. For maize chromosome 8 there is a self-fertile monosomic ($2n = 42 + 1$) line that transmits the added chromosome to about 8% of progeny. Colchicine applications are being used to try to recover fertile disomic versions of OMA F_1 plants with chromosome 5 and 10 additions. Although our sample is still somewhat limited, there does appear to be an influence of oat genotype on the frequency with which an OMA F_1 and its disomic version is obtained for a particular maize chromosome. For example, although two-thirds of our 90 OMAs have Starter-1 as an oat parent, we have never found a Starter-1 OMA with maize chromosome 10. Yet maize chromosome 10 was present in three OMAs of one genotype and two of another genotype for which in both cases we had many fewer total OMAs than for Starter-1. Also, although Starter-1 OMAs have been obtained for maize chromosomes 3, 7, and 8, self-fertile versions of these OMAs have been obtained to date only in other oat backgrounds.

Little is yet known about specific maize gene expression in these OMAs although the various maize chromosome additions often give distinct phenotypic effects and usually reduce plant vigor. The one instance where a phenotypic effect in an OMA is traceable to a specific maize gene on the added chromosome is for Sun II OMA 3 disomic addition line. In this line, the demonstrated ectopic expression of the *Lg3* gene on maize chromosome 3 appears to account for the liguleless phenotype of the OMA 3 lines (Muehlbauer et al. 2000).

RADIATION HYBRIDS

To further reduce the amount of maize chromatin present in an OMA, we irradiate the lines to induce chromosome breakage and obtain lines with only segments retained of individual maize chromosomes. For radiation treatments, disomic OMA plants were crossed to the oat parent to produce monosomic OMA seed. This seed was then treated with 30 to 50 krad gamma radiation and planted. DNA samples of surviving plants were tested by PCR for the high copy maize repeat sequence Grande-1 as an indicator of the presence of maize chromatin. Tests with a series of previously mapped maize markers and GISH analysis of root-tip chromosomes were used to characterize the lines containing maize chromatin. Maize chromosome modifications observed in these plants, termed "radiation

hybrids", included diminutive maize chromosomes with both terminal and interstitial deletions, oat-maize translocations, and combinations of the two (Riera-Lizarazu et al. 2000).

APPLICATIONS TO MAIZE AND OAT GERMPLASM DEVELOPMENT

The individual OMAs and the radiation hybrids generated from them represent a powerful tool for rapid, efficient mapping of maize DNA sequences. Maize sequences, including ones with no identified polymorphic form, can be readily assigned to chromosome by either Southern hybridization or PCR assay using DNA from an OMA series representing the ten maize chromosomes individually added to oat. Okagaki et al. (unpublished) used this system to map to maize chromosome 273 EST sequences from the Stanford Maize Mapping Project. Once assigned to chromosome, the maize sequence can then be mapped to position on the chromosome by tests with DNA from a selected series of radiation hybrids for that maize chromosome. For each chromosome a radiation hybrid set will be generated and arrayed to represent a series of overlapping segments of the maize chromosome. Mapping of the maize sequences is thus based on physical association of sequences rather than recombination. Riera-Lizarazu et al. (2000) report such a radiation hybrid panel for maize chromosome 9. We estimate that a panel of 100 informative maize chromosome 9 radiation hybrids with an average of 3 breaks per chromosome would allow mapping at the 0.5-1.0 Mb level of resolution.

From an oat genetics and germplasm development viewpoint, the most interesting oat-maize radiation hybrids would be those with a small segment of maize chromatin translocated into the oat genome. In those cases maize genes influencing such traits as disease resistance, heat stress tolerance, water use efficiency, novel proteins, or photosynthetic efficiency might be introduced free of linked deleterious genes. In addition to novel oat germplasm, a contribution arising out of this project is the identification of numerous sequences including SSRs and ESTs being mapped in maize but which also hybridize or amplify in oat. Thus, several potential oat site-specific PCR markers may be identified as well as additional oat genomics information produced. Other valuable genetic information to be generated relates to the nature of intergenomic interactions for gene regulation, suppression, and phenotype expression in such novel wide hybrid materials.

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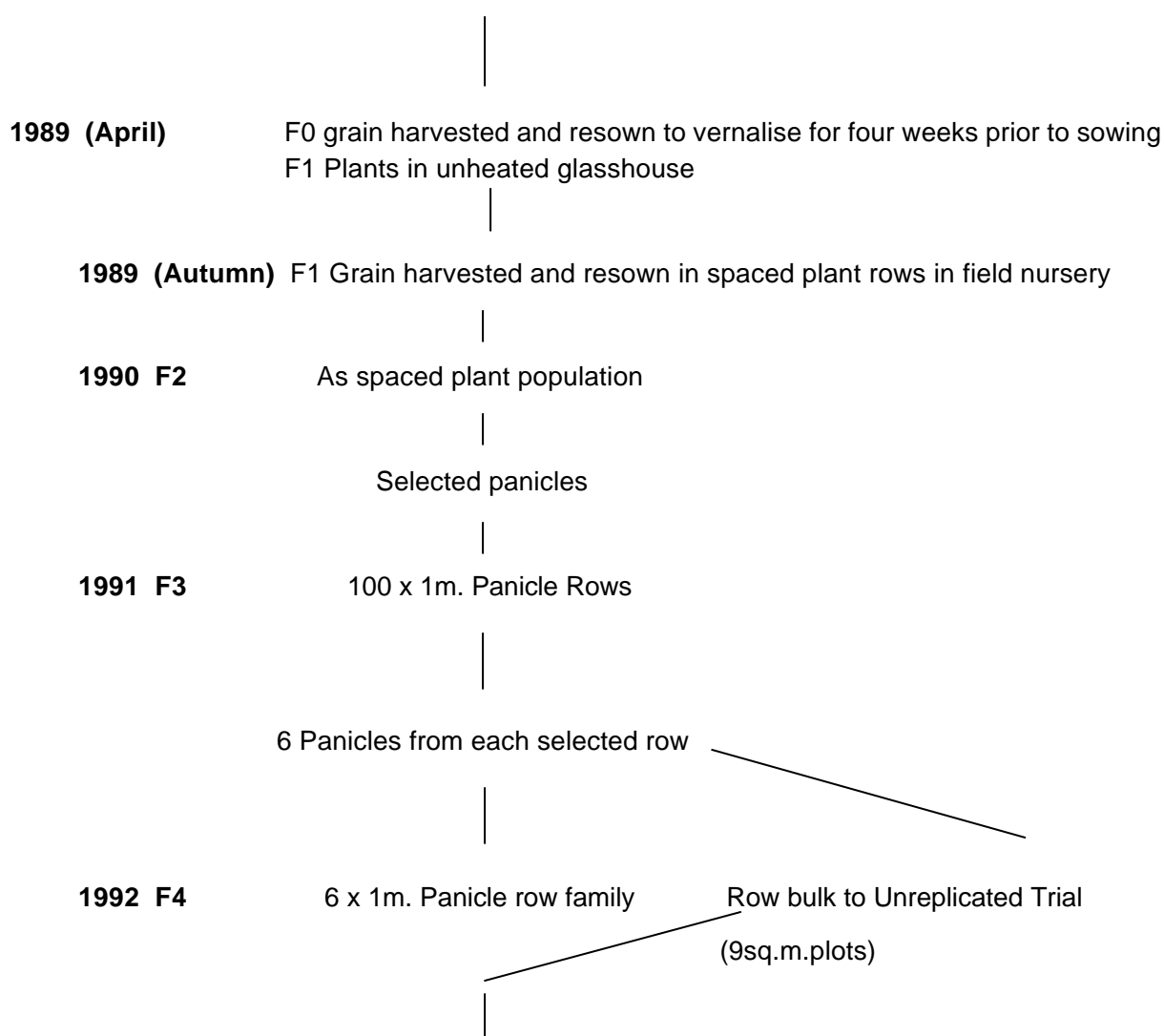
FROM CROSS TO VARIETY IN 10 YEARS - THE SELECTION OF 'JALNA' WINTER OAT

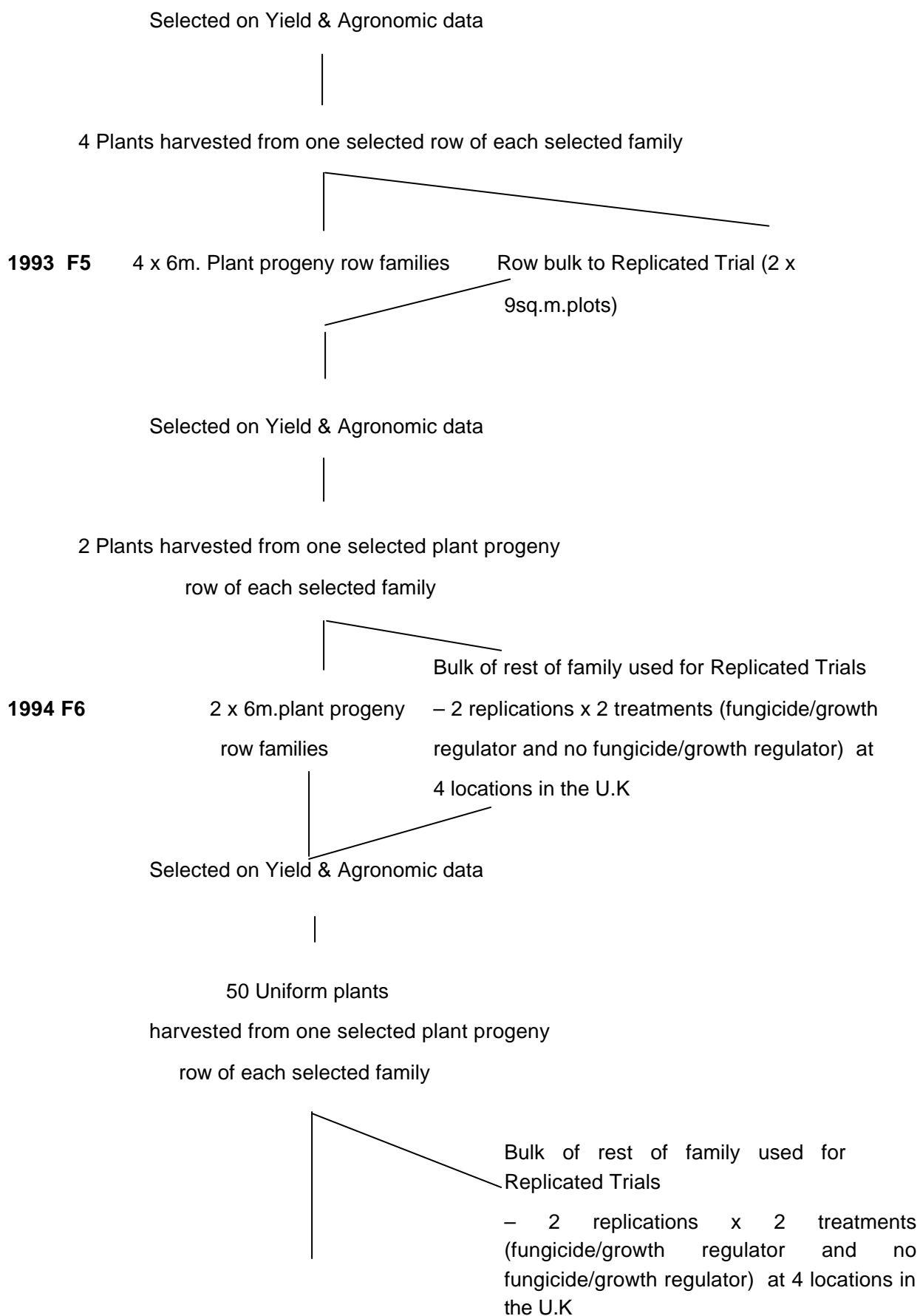
Alan Roffey

Semundo Cambridge U.K.

Breeding and selections techniques vary from breeder to breeder. The following flow chart indicates the methodology employed within one UK Oat breeding programme resulting in the breeding of the successful U.K. variety 'Jalna' which may be seen in the demonstration plots.

(January) Cross made, in lit, heated glasshouse between Varieties Craig & Solva





1995 F7

Detailed character description
undertaken on each of these plants
& each checked uniform plant sown
as up to 4 x 21m. spaced plant rows
(stocks) at 9 cm. spacing

Each stock is checked throughout growing
season for uniformity

One stock is selected and harvested for use in distinctness,
uniformity and stability (DUS) testing and further
multiplication during first year in national list testing.

300 panicles + 3kg seed
for DUS + 200 panicles
and 1Kg reserve

20Kg. seed for Value in Use
and Cultivation trials (VCU)

Progeny of 35 uniform plants
for further multiplication.

**1996 National List
Year One**

Independent Trials carried
out by the National Institute
of Agricultural Botany (NIAB)
at several representative sites
within the U.K.

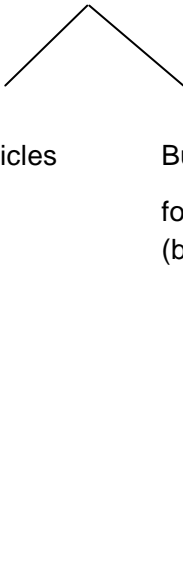
Plants checked against character
descriptions & progeny sown
at up to 4 x 21m. spaced plant
rows (stocks) each.

250kg. of seed for
multiplication (breeder's
seed)

20Kg. seed for Value in Use
and Cultivation trials (VCU)

One stock is selected for
National list year two breeders stock

Progeny of 30 uniform plants
for further multiplication.



1997 National List Year Two	Independent Trials carried out by the National Institute of Agricultural Botany (NIAB) at several representative sites within the U.K. After successful completion of which, variety is added to the U.K. National List of cereals.	1000 panicles	Bulk of seed for multiplication (breeder's seed)
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1998 Recommended List Trial	Independent trials carried out by NIAB after successful completion of which, variety is added to NIAB's list of varieties recommended for use in the U.K.	Further stock maintenance and production of pre-basic & basic seed
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1999 Jalna was recommended for use in the U.K.

SOME QUALITY GROAT CHARACTERS IN OAT WILD SPECIES

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ABSTRACT

This research presents the results of studying (1989-1997) 16 wild species with different ploidy level. The range of variability by quality parameters have been demonstrated and valuable forms have been identified by such characters as weight of 1000 grains, percent of huskness, groat protein and oil content, groat aminoacid and fatty acid composition. Relationship between geographical origin of the accessions studied and their quality characters was found.

INTRODUCTION

The data on yields and other characters indicated that the wild and weedy relatives possess genes that can increase the productive potential of the crops (3). Cultivated and wild oat, in addition to its agricultural traits, manifests high levels of grain and green matter quality (9, 11, 18). Protein content in oat grain averages 9-12%, though maximum content in some commercial characters may reach 20% and oil percentage in groats may be as high as 11% (14, 15) with well-balanced aminoacid and fatty acid composition (10, 13). However, in a number of cases grain yield shows adverse correlation with grain protein content. Interspecific hybridisation was more efficient in the breeding process targeted at this feature (1, 8). Some wild diploids and tetraploids had high groat oil content (12-13%) (17). Hexaploid weedy oat species appeared to have 27-28% (2) of protein in naked seed, being however reported sometimes to reach 35%. According to numerous reference sources, quite many forms of hexaploid species *Avena sterilis* and *A.fatua* have been analysed for this trait, and the samples identified by such analysis are presently used in oat breeding to obtain high-yielding lines and varieties with higher protein content in grain (12, 16). The forms of *A.sterilis* with high protein and oil content were reported to have cytoplasmic genes which are capable to provide a 20-30% increase in the yield of a hybrid population (2). The effect of such genes takes place without depressing the increase of grain protein content. In addition to qualitative parameters, such wild forms must possess a number of agricultural features which could provide for enhancement of other properties in cultivated oat (5, 6).

MATERIALS AND METHODS

Having at our disposal a rich collection of wild and weedy oat species, we started studying biochemical characters of oat grain, continuing, at the same time, the analysis of commercial traits (5, 7). This study involved about 180 forms of oat species with different ploidy levels: diploids (*A.pilosa*, *A.clauda*, *A.ventricosa*, *A.longiglumis*, *A.canariensis*, *A.hirtula*, *A.wiestii*, *A.atlantica*), tetraploids (*A.barbata*, *A.vaviloviana*, *A.magna*, *A.murphyi*) and hexaploids (*A.fatua*, *A.occidentalis*, *A.ludoviciana*, *A.sterilis*).

Sowing was performed at Pavlovsk Experiment Station of VIR in 1989-1997. *Borrus*, a released cultivar oat from Germany, was taken as the standard reference. Evaluation of original materials was based on the methods and descriptors of VIR (4). Protein content and aminoacid composition were analysed at the Laboratory of Protein and Nucleic Acids of VIR.

The purpose of this research was to identify interspecific differences in groat protein and groat oil content and aminoacid and fatty acid composition, disclose intraspecific variation of these parameters in correlation with the geographic origin of these forms, and to trace the dependence between grain quality parameters and cultivation conditions characteristic of these species.

RESULTS AND DISCUSSION

In this study, it was measured not only biochemical parameters, but weight of 1000 grains and percent of huskness. The results showed that among diploid species grain weight and percent of huskness was ranges 3.2 – 13.6 g and 42.8% - 74.5% respectively (Table). The highest groats protein content in *A.longiglumis*, *A.atlantica*, *A.wiestii* ranged from 19.9% - 22.1% and oil content more than 10% had forms of *A.canariensis* and *A.pilosa*. Groat oil fatty acid composition demonstrated that concentration of saturated (palmitic and stearic) fatty acids were higher in *A.hirtula* and *A.longiglumis*; monounsaturated (oleic) – in *A.hirtula*, *A.longiglumis* and *A.wiestii*; polyunsaturated – (linoleic) in *A.clauda* and *A.pilosa*, (linolenic) in *A.atlantica* and *A.longiglumis*.

The weight of 1000 grains in tetraploid species *A.barbata* was not high (6.4 g), but the degree of huskness was 51.6%. The average percentage of grain protein was 21.1%. The highest average values of this parameter for the study was demonstrated by the samples from Azerbaijan Iran and Portugal. Lysine content in the protein of this species averaged 5.6%, being less than in cultivated oat, but reliably higher than in hexaploid species. All accessions of *A.magna* had groat protein content more than 20.0%. Aminoacid composition in the present species was advantageously and reliably different from that in cultivated oat and other hexaploid species. In the forms of *A. barbata* the content of essential aminoacids (valine, methionine, isoleucine, tyrosine and phenylalanine) in the protein was reliably higher than in the reference cv. *Borrus*, lysine and threonine content was similar to cultivated oat, while leucine content was lower. These data indicate an increased nutritive value of the protein contained in this tetraploid species. The highest average values in tetraploids of groats oil content (more 8%) was demonstrated by the accessions from Azerbaijan, Spain (Canary Is.), Italy and Morocco (*A.magna*). Concentration of oil fatty acid showed that saturated (palmitic) fatty acid was higher in *A.barbata* and *A.vaviloviana*; monounsaturated (oleic) – in *A.barbata*, *A.vaviloviana* and *A.magna*; polyunsaturated – (linoleic) in *A.vaviloviana*, (linolenic) in *A.barbata* and *A.murphyi*. Correlation analysis showed that such qualitative parameters as the weight of 1000 grains and protein and oil

content in grain were directly proportional to each other, whereas grain size had inverse correlation with grain huskness.

Grain weight of hexaploid species *A.ludoviciana* was 15.6 g. Percentage of huskness was 44.9%. The highest mean values of grain protein content (21.2-22.6%) were reported in the samples from Azerbaijan, Iraq and Israel. Lysine content in the protein of this species appeared to be the lowest among all analysed species (0.65 g per 100 g) and was closely connected with grain protein content. At the same time, the content of a number of essential aminoacids (phenylalanine) was reliably higher than in *Borrus*, the content of threonine, valine, isoleucine, leucine and tyrosine was at cultivated oats level, while lysine and methionine content was lower; thus this species had practically the same nutritive value as cultivated oat. The highest mean values of groat oil content (more than 8%) were reported in the accessions from Azerbaijan, Georgia and Armenia. Grain weight in this species was inversely proportional to huskness and had a reliably direct correlation with the percentage of protein in grain, the latter being in its turn inversely linked with huskness.

Another hexaploid species *A.sterilis*, which is regarded in numerous publications as a donor of increased groat protein and oil content, in our research also manifested higher parameters of this trait than the other species of this group. Forms from Morocco, Turkey and Tunisia were identified for the grain weight which sometimes reached the level of cultivated oat (24.3-32.7 g). The level of huskness in these accessions was the highest among this group of species and amounted at the average to 53.6%. As for the percentage of grain protein, this species had the best parameters among hexaploid species. The highest mean values (more than 21%) for all years were manifested by the forms from Israel, Morocco, Lebanon, Algeria and Tunisia. It was identified a large group of forms accumulating an increased groat protein content which was stable during the years of study and amounted to 21.3-24.4%. These accessions were: WIR-142 (Morocco), WIR-473 (Lebanon), WIR-653 (Algeria), WIR-644 (Tunisia), WIR-502, WIR-529, WIR-550 and WIR-551 (Israel). Aminoacid content of protein in *A.sterilis* was in many aspects similar to the parameters of the previous species with nutritive value reaching the level of cultivated oat. Isoleucine and phenylalanine content reliably exceeded the reference; threonine, valine, leucine and tyrosine equalled the reference, while lysine and methionine content was lower. The highest mean values of groat oil content (more than 8%) for all years were manifested by the forms from Iraq, Israel and Algeria. It was demonstrated a large group of accessions accumulating an increased groat oil content: WIR-431 (Iraq), WIR-502 (Israel), WIR-653, WIR-1699, WIR-1887 (Algeria). Correlation analysis showed that the weight of 1000 grains was directly and reliably linked with huskness and adversely with grain protein content. The latter, in its turn, was adversely proportional to huskness of the samples.

The most early hexaploid species *A. fatua* was similar in many parameters to cultivated oat. The grain weight in this species ranged 13.9 g, and grain huskness was about 30% (at the cultivated level). Grain protein percentage in *A.fatua* was the lowest (18-19%) among all the species studied, but exceeded the level of cultivated oat. As for the composition of essential aminoacids, this species demonstrated the level higher than in cultivated oat in the content of leucine and phenylalanine; isoleucine and tyrosine equalled with the reference; whereas lysine, threonine, valine and methionine were below the reference level, which is an evidence of insufficient nutritive value of protein in this species. Groat oil percentage in *A.fatua* was the highest from Greece, Ukraine, Georgia, Kazakhstan and Tadjikistan. The results of correlation analysis witnessed that huskness was directly linked with grain protein content and adversely with the grain weight.

Fatty acid composition of oil in groat in hexaploids was demonstrated that in saturated (palmitic and stearic) fatty acid was higher in *A.fatua*, *A.ludoviciana* and *A.sterilis*; monounsaturated (oleic) – in *A.fatua* and *A.ludoviciana*; polyunsaturated – (linoleic) in *A.ludoviciana*.

CONCLUSION

Thus, on the basis of the studying wild and weedy oat forms, it was determined that diploid and tetraploid species, due to less ploidy, don't directly mating with hexaploid cultivated oat. On the other hand, a series of accessions were marked for higher protein and oil content in grain (*A.magna* ect.), and their aminoacid and fatty acid composition was balanced in essential aminoacids better than in other hexaploid species and better ratio of fatty acid of this species increased nutritive value. It is also worth mentioning that with a thrice lower weight of 1000 grains than in hexaploid species, the samples of this group, especially those from Azerbaijan, Portugal, Spain (Canary is.) and Morocco had the highest values of protein and oil content in grain. Direct correlation between grain size and grain protein and oil content witnessed to a possibility of using forms of this species in oat breeding practice. At the same time, many biochemical parameters of grain quality in this species were more strongly affected by changes in environments. And finally, the problems arising when inter-specific mating these species with cultivated oat would restrict the possibility to recommend it directly as a donor of high groat protein and oil content.

Hexaploid species *A.ludoviciana* and *A.sterilis* were similar to each other in many features with only one difference: the latter exceeded the former in the parameters of agricultural traits and in grain quality, especially the forms from Israel, Algeria and Tunisia. However, the parameters of grain size and percentage of huskness produced different effect upon grain protein and oil content in these species. In *A.ludoviciana*, forms with larger grain size had higher protein content in grain and less percentage of huskness. *A.sterilis* showed the opposite tendency in these parameters. At the same time, good combining ability with cultivated oat, high groat protein and oil content and nutritive value of protein and oil make it possible to recommend these species as donors in the breeding process for quality.

A.fatua did not possess a wide range of valuable agricultural traits compared with the previous species. In the percentage of protein and oil in grain they were at an intermediate level, especially the samples from Kazakhstan, Georgia and Ukraine, and exceeded the value demonstrated by cultivated oat, but they showed less nutritive value of protein. This species had the lowest percentage of grain huskness and thus it may be recommended as a donor for enhancement of quality in cultivated oat.

In the result of this evaluation it was disclosed intraspecific diversity of all parameters in correlation with the geographic origin of these species and forms. The accessions with high groat protein content mostly were origin from Israel, Morocco and Azerbaijan and the highest groat oil content forms usually were from Azerbaijan, Morocco, Ukraine and Georgia.

These studies confirmed that species *A. sterilis* and *A. ludoviciana* are the most promising and important both in terms of grain quality and in terms of transferring this trait onto cultivated oat. The research resulted in finding intraspecific variation in biochemical parameters under study, which opens a possibility to search for forms with a complex of commercially valuable properties and high grain quality.

Table. Average values of groat characters in oat wild species

Species	Weight of 1000 grains, g	Percent of huskness, %	Groat-protein content, %	Groat-oil content, %
<i>A. ventricosa</i> Bal.	3.9	68.9	15.4	8.7
<i>A. clauda</i> Dur.	4.7	55.0	10.2	8.9
<i>A. pilosa</i> M.B.	3.2	74.5	9.7	10.4
<i>A. longiglumis</i> Dur.	13.6	57.8	22.1	7.8
<i>A. canariensis</i> Baum	7.5	71.4	14.7	11.2
<i>A. wiestii</i> Steud.	5.1	59.3	19.9	8.8
<i>A. hirtula</i> Lag.	8.4	42.8	13.7	7.4
<i>A. atlantica</i> Baum	4.3	53.6	20.1	7.6
<i>A. barbata</i> Pott.	6.4	51.6	21.1	7.1
<i>A. vaviloviana</i> Mord.	8.3	41.9	17.8	6.8
<i>A. magna</i> Mur.et Terr.	19.6	65.5	21.9	7.6
<i>A. murphyi</i> Ladiz.	18.2	64.8	19.1	8.9
<i>A. fatua</i> L.	13.9	36.7	18.5	9.1
<i>A. occidentalis</i> Dur.	11.5	53.8	19.8	7.8
<i>A. ludoviciana</i> Dur.	15.6	44.9	18.7	9.6
<i>A. sterilis</i> L.	14.4	53.6	21.8	8.0

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MILLENNIUM - AN OAT FOR THE FUTURE

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The winter oat Millennium bred at IGER is a new variety with a range of exceptional characteristics. It has a distinctive large yellow thin-husked grain. The variety has a number of attributes making it well suited to milling for human consumption but it also has much potential for animal feed.

BRIEF HISTORY

Millennium is the culmination of a complex series of crosses aimed at combining high grains per ear with large grain size, stiff straw and resistance to diseases including oat mosaic virus.

Its pedigree is 78-1Cn 3/2/1/2 x ((Bardsey x Rosette) x 07198 CnI/3)

The first cross was made in 1980 between Bardsey, an IGER variety and Rosette a stiff-strawed but mildew susceptible line from Lochow-Petkus in Germany. The F₁ of this cross was then crossed with 07198Cn I/3 in 1981. A selection of 07198Cn I/3 was subsequently developed as Lustre, a large grained variety with resistance to oat mosaic virus and the PAV isolate of barley yellow dwarf virus and resistance to some forms of crown rust. These unusual characteristics derive from Cimarron (25% contribution to both Lustre and 07198Cn I/3), an American variety of unknown parentage derived from winter hardy survivors of a USDA winter hardiness nursery.

The selection with the highest numbers of grains and largest grain size was crossed with 78-1Cn 3/2/1/2 in 1987. 78-1Cn 3/2/1/2 was a sister line of Craig resulting from the cross between Pennal and Bulwark made in 1978. From this final cross, two lines entered breeders' trials in 1994 and National List trials in 1997.

87-42Cn I/2/2/1 was found to be the better selection. Although still at an early stage of development, it was named Millennium in 1998 as an expression of our confidence in the variety.

Millennium became the first variety to be added to the UK Recommended List in this millennium. C1 seed will be available autumn 2000.

AGRONOMIC CHARACTERISTICS

Millennium is a high yielding variety of oats with stiff straw, resistance to crown rust and excellent grain quality.

Yield

In terms of yield, it has yields 6% more than Gerald and 4.5% more than Jalna in fungicide-untreated official trials. It has yielded 1% less than Gerald and Jalna in treated trials. We believe that these figures understate the genetic potential of Millennium and the inclusion of more trials in the data matrix will result in the high yield potential of Millennium being demonstrated. Millennium has yielded 7% more than Gerald in 21 breeders' trials since 1995.

Disease resistance

Millennium is moderately resistant to mildew. It is resistant to common isolates of crown rust such as race 251 (virulent on the susceptible differential cultivars Appler, Bond and Saia) and race 205 (virulent on Appler, Anthony, Bond and Saia) but is susceptible to race 221 (virulent on Appler, Anthony, Bond, Trispermia and Saia) which was identified in one out of 18 isolates analysed by the Pathogen Virulence Survey in 1999 (Jones, 2000). It is resistant to Oat Mosaic Virus.

END-USE CHARACTERISTICS

Human consumption

Millennium scores better than all other recommended varieties on a number of ways.

First, it has large grains, hence there are less screening losses i.e. fewer grains which are too small to use (Table 1).

Table 1. Varieties in rank order of grain size.

	1000 grain weight (g)	Screenings (%<2.0mm sieve)
Millennium	42.0	4.4
Kingfisher	36.9	5.5
Jalna	34.8	8.5
Gerald	33.3	5.8
Image	32.9	6.2
Aintree	28.4	10.7

(Source: UK Recommended List 2000)

Secondly, its husks are readily removed so less energy is needed and there is higher throughput. Using a dehulling machine, Millennium was virtually completely dehulled in 40 seconds, Viscount in 70 seconds and 90-98Cn4/1 in 120 seconds. In other words, it took three times as long to remove husks from 90-98Cn4/1 as from Millennium, which would have considerable energy and throughput implications (Valentine *et al.*, 2000).

Thirdly, the husks are thin so that the proportion of kernel to total grain is higher (Table 2).

Table 2. Varieties in rank order of kernel content %.

	Kernel content %
Millennium	77.6
Jalna	76.7
Image	76.6
Kingfisher	75.9
Aintree	74.0
Gerald	73.7

(Source: UK Recommended List 2000)

Fourthly, the flakes themselves are larger, ideal for premium 'jumbo' flakes. The following table shows the higher proportion of large grains in Millennium compared to other varieties (Table 3).

Table 3. Varieties ranked according to the percentage of grain of passing over a 2.8mm sieve.

	>2.8 mm	>2.5 mm	>2.3 mm	>2.1 mm	<2.1 mm
Millennium	32.9	43.6	20.2	0.4	2.9
Image	15.7	47.7	31.5	0.6	4.4
Jalna	4.8	43.3	46.6	0.8	4.5
Gerald	4.7	51.0	38.8	0.6	4.9

Source: Breeder's mean data from three sites in 1999.

The husks of Millennium, being so well-filled, are also readily removed during combining. When harvesting this variety, it is important to check that the incidence of dehulled grains is not above 5% and to adjust combine settings if necessary in order to capitalise on its value to the milling industry.

A Belgian miller has described Millennium as being exceptionally well-fitted for the oat milling industry, with an unprecedented 1000 grain weight for European oats, and concluded that Millennium produced superb oats for milling.

Animal Feed

The thin husk of Millennium and high level of energy-rich oil make the grain particularly suitable for feeding to ruminants. IGER has found a predicted metabolisable energy ME value (Thomas et al 1988) of Millennium of 13.0 MJ/kg DM compared to 12.5 for Gerald in seven replicated tests between 1996 and 1999. (Table 4).

Table 4. Predicted metabolisable energy (MJ/kg DM) of Millennium compared to standard varieties and breeding lines.

	1996			1998			1999		
Name	Oil % DM	NCGD % DM	ME	Oil % DM	NCGD %DM	ME	Oil % DM	NCGD % DM	ME
Gerald	7.5	82.3	13.4	5.8	72.5	11.6	5.7	74.3	11.8
Image	7.5	83.8	13.6	6.7	75.2	12.3	6.5	77.3	12.5
Kingfisher	7.1	85.3	14.0				6.0	77.0	12.3
Millennium	6.7	86.6	13.9	5.7	76.3	12.1	5.8	77.9	12.4
91-33Cn 4/1				6.2	77.3	12.4	5.7	79.7	12.6
94-16Cn 2/1				6.7	78.8	12.7	6.2	77.9	12.5
95-56ACn 3							5.8	79.1	12.5

DM = dry matter

NCGD= neutral detergent cellulase gamanase digestibility

Wider implications of greater usage of oats in animal feeds

We consider that that the inclusion of thin-husked oats such as Millennium in ruminant diets, particularly as a home-grown feed, would bring many benefits.

- With falling meat and milk prices in the EU, the economics of buying in compound feeds is increasingly coming under question. Provided cost-effectiveness can be demonstrated, then there is now greater incentive for farmers to grow their own feed.
- Consumers are increasingly concerned with securing good quality animal products that have been produced, by Good Farming Practices, from animals that are healthy and that have been treated humanely. The use of oats would provide greater product traceability. It would provide the assurance that animals are fed with primary products which are natural and wholesome, safe and environmentally sustainable.
- There is evidence that feeding oats may produce animal health benefits such as positive effects on immune function or on gut bacterial infections, reducing the need for routine addition of antibiotics to feeds (reviewed by Lindberg, 1999).
- Returning to the situation where livestock farms grew cereals for feeding their stock would benefit the environment through increased crop diversity, and providing food for wildlife, such as previously common birds in lowland grassland areas.
- It may be possible to realise product quality benefits such as less saturated fat in milk and improved storage and processing properties.

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MAXIMISING ENERGY AND PROTEIN IN NEW DWARF NAKED OATS

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A new generation of dwarf naked oats offers great potential for use as a high protein, high energy feed for poultry and pigs. Success in this sector is dependent on achieving satisfactory yield and protein content.

A study to maximise energy and protein (MEP) in the dwarf, naked variety Icon, set out to produce a target yield in excess of 5 tonnes/hectare, 16% protein and 14% oil. Dwarf types are resistant to lodging and allow greater quantities of nitrogen to be applied, which will increase the protein yield.



Trial plots at Rosemaund, Herefordshire, during the 1998/ 1999 season

HOW GOOD COULD NAKED OATS BE AS A FARM FEED?

Icon represents the first of a new generation of dwarf winter naked types. Being naturally high in both protein and oil, an agronomic programme was designed to target a yield of 5 tonnes /hectare, 16% protein and 14% oil. The trial set out to explore how management and input could influence both protein and oil yields. With short stiff straw it was anticipated that high levels of nitrogen could be applied without inducing lodging.



The study was conducted during the 1997/98 season (Year 1) at two sites, Rosemaund and Abbots Ripton, and in the 1998/99 season (Year 2) at Rosemaund, using three varieties - Icon (naked), Krypton (naked) and Gerald, blocked in main plots to avoid shading and lodging effects. Each variety was assessed throughout the season and yields were measured with samples analysed for specific weight, TGW, oil and protein.

The nitrogen treatments used are substantially higher than the normal levels of nitrogen applied for conventional height varieties. The foliar urea was applied to assess the potential to further increase in grain protein and improve protein quality. Knowledge gained from the first year of the study was used to adjust the ammonium nitrate treatments and timing.

Table 1. Treatments – Year 1

Treatment	Ammonium nitrate (Kg/ha)	Foliar urea (Kg/ha)	Total nitrogen (Kg/ha)
1	100	0	100
2	100	60	160
3	130	0	130
4	130	60	190
5	160	0	160
6	160	60	220

Table 2. Treatments – Year 2

Treatment	Ammonium nitrate (kg/ha)	Foliar urea (kg/ha)	Total nitrogen (kg/ha)
1	0	0	NIL
2	60	0	NIL
3	120	0	NIL
4	180	0	NIL
5	0	60	NIL
6	60	60	NIL
7	120	60	NIL
8	180	60	NIL
9	0	0	CCC
10	60	0	CCC
11	120	0	CCC
12	180	0	CCC

AGRONOMIC ASSESSMENTS CONDUCTED:

- Plant populations
- Crop growth stages - recorded on a weekly basis for each variety
- Final tiller number
- Lodging assessment
- Grain analysis - grain yield and nitrogen content

RESULTS

Table 3. Mean yields and protein content for all treatments (Year 1 and Year 2)

VARIETY	MEAN YIELD T/HA			MEAN PROTEIN %			STANDING ABILITY
	Year 1		Year 2	Year 1		Year 2	Years1 and 2
	AR	Rosemaund	Rosemaund	AR	Rosemaund	Rosemaund	
ICON	4.0	4.6	6.07	15.00	12.86	14.00	++
KRYPTON	4.2	4.4	5.06	13.72	13.29	12.97	--
GERALD	7.5	6.5	8.00	10.29	9.86	11.03	-

NOTE: AR = Abbots Ripton

*Yield and protein content***Year 1**

Mean yields for all treatments were as in table 3. On a groat for groat basis the yield of Icon was similar to Gerald, at the Rosemaund site only. At Abbots Ripton Gerald gave a higher yield than both Icon and Krypton. Crown rust at Rosemaund was a contributing factor to the generally low yields, affecting Icon and Gerald. Results indicated that in the absence of disease Icon has the potential to out yield Krypton.

No yield response to ammonium nitrate or effect on final tiller number was noted at either site. At the nitrogen levels applied this was unexpected, and was possibly due to the late timing of the nitrogen application and the subsequent dry weather, which may have limited nitrogen uptake.

The addition of foliar urea produced no increase in yield due to late application, but did result in an increased grain protein content in all treatments at both sites, particularly at the lower ammonium nitrate levels. Results indicated a greater potential for an increase in protein content in Icon than in other varieties, but there was some interaction with other site factors. At 100 kg/ha ammonium nitrate, the application of 60 kg/ha foliar urea raised protein levels by approximately 1% in Icon and Krypton but only 0.2% in Gerald.

Negligible effects on specific weights due to ammonium nitrate and foliar urea were observed at both sites.

Year 2

The mean yield of Icon was 6.07 t/ha compared to 4.6 t/ha in Year 1. Very high levels of crown rust contributed to the lower yields in Year 1. Krypton yielded 5.06 t/ha, 1 t/ha less than the Icon due to its high early lodging. On a groat for groat basis the yield of Icon was once again equal to Gerald.

Grain protein contents were also higher in year 2; maximum values for Icon were achieved at 120 kg /ha and the varieties were ranked I>K>G. The addition of foliar urea and PGR treatments also produced a small increase in yield across the varieties and in the grain protein in Gerald and Icon.

Specific Weight

Specific weights for all varieties were higher in 1998/99 as the disease pressure was much lower than in the previous year. Thousand grain weights were also notably higher in the second year. No treatment effects on any of the varieties were noted.

Oil Content

In 1998/99 samples for two treatments on Icon were analysed for oil content to assess the effect of foliar urea application. There was evidence of a detrimental effect on oil content, but more studies would be needed to confirm this.

Oil is important as it is a major contributor to energy. Oats are naturally high in oil and if, through selection and management this can be advanced, then the value of the grain will be improved. In terms of energy, oil has more than twice the energy of starch.

Lodging

Year 1

Lodging severity at both sites was ranked Krypton>Gerald>Icon with the higher ammonium nitrate (AN) levels producing more lodging. Icon lodged only immediately prior to harvest and even then it was only partially lodged. This was a clear display of the superiority of Icon in respect to straw stiffness. The late season lodging of all varieties was not thought to have affected yield or grain quality.

Year 2

Lodging began earlier than in the previous season, so provided a good comparison of straw stiffness between the varieties. Krypton was again shown to be the weakest variety, with all treatments except nil ammonium nitrate resulting in lodging. As the season progressed into grain fill, lodging in both Krypton and Gerald continued, whereas no lodging was observed in Icon. The effects of PGR application in delaying lodging of Krypton and Gerald became apparent as the season progressed. At harvest all treated Krypton plots were flat and only the nil ammonium nitrate treatment of Gerald was standing. No lodging in Icon was apparent, even at very high ammonium nitrate levels.

Late rain in August affected yield and quality. Foliar urea treatments gave no significant effects on lodging.

Crop growth

Year 1

Final crop heights varied between varieties with

Krypton>Gerald>Icon. Height measurements from plots to which no PGR was applied showed little or no effect with Icon but significant effects for Krypton and Gerald.

Possible effects of PGR were, however, noted with Icon, resulting in lower yield. Due to limited data more studies are needed.

Year 2

Increasing rates of ammonium nitrate increased the final tiller numbers in Icon, in Krypton no increase was seen above 60 kg N/ha and in Gerald maximum numbers were seen at 120kg N/ha. Final crop heights agreed with those of the first year with Krypton>Gerald>Icon.

Absence of ammonium nitrate had a significant effect on crop heights, when nitrogen was applied there was no consistent effect. PGR affected the height of Krypton and Gerald but again produced no height effect in Icon.

CONCLUSIONS

Over the first two years of trials sufficient confidence was gained to indicate that the management of inputs could have a considerable influence on protein yield. The results confirmed the potential of Icon to yield grain with protein contents between 13.5% and 15% under high nitrogen regimes with little or no lodging risk.

The advent of dwarf winter material brings very exciting prospects to substantially uplift the value of oats when used in on-farm feeding systems. New lines with higher yields and better quality specifications, together with new chemistry strobilurins like Landmark will contribute to making this an especially interesting programme.

In the third year of trials the focus will again investigate how management and input can influence yield and quality. The new short variety Grafton is introduced for the first time and the strobilurin Landmark will be employed following encouraging results during screening trials in the season of 1999.

This project has thrown up some interesting propositions and provided a useful programme from which new protocols can be developed. Based on new concepts this MEP project will lead to new areas of research.

DISEASE ON OATS! WHAT DISEASE ON OATS?

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If we do concede that the cultivated *Avena species* do attract their fair share of diseases we should see if the basket of oat diseases in this part of the world is unique!

Australia is a Federation of States and the delivery of agricultural services has been by government based largely on the various states with their various abilities and perceptions. Therefore the disease priorities have often varied between states on more than scientific biological reasoning. The state boundaries have been almost miraculous in their ability to stop diseases, whether the boundary is a line on a map or a meandering river, it did not seem to matter. In recent years the main source of research funds in Australia has been the Grains Research and Development Corporation (GRDC), fortunately it has shown some common sense and has reduced the research areas from the state based six to a more pragmatic, agro-economic, three regions corresponding with the major grain growing areas of Australia: north, south and west. There is now a level of national coordination made possible by the interaction across the GRDC's three Regional Panels.

However the major research providers are still the state based Departments of Agriculture, as well as the Universities and the CSIRO, and I will address my remarks on the basis of this picture. Firstly the diseases as highlighted by the pathologists in each state and then the breeders response to these threats.

Cereals in Australia are grown in low input agricultural systems with disease control usually achieved with varieties having genetic resistance.

Several years ago, at their annual meeting, the Australia oat breeders listed all the factors important in our breeding programs. For the diseases, we came up with the following prioritised list. How do these breeding priorities compare to the priorities as seen by plant pathologists and other stakeholders?

Breeding priorities for oats in Australia – diseases.

	QLD Grazing	NSW Grain	NSW Dual Purpose	VIC	SA High Rain	SA Low Rain	WA High Rain	WA Low-Med Rain	TAS
Stem rust	4	3	3	4	4	2	3	- -	3
Leaf rust	5	5	5	4	3	1	-	-	3
BYDV	1	3	5	4	4	1	3	-	5
Bacterial blights	2	1	1	1	1	2	-	-	2
Septoria	1	1	1	3	3	1	4	-	-
Spermospora	-	1	1	2	1	1	-	-	-
CCN	-	1	1	4	2	4	-	-	-
Stem nematode	-	1	1	-	2	3	-		-
5 very high priority									
1 low priority									

QUEENSLAND¹

An average of 250,000 hectares of oats is grown in Queensland annually extending from the Central Highlands to the New South Wales border. Oats in this region is used primarily for grazing in the beef, dairy and sheep industries with less than 10% being harvested for grain, primarily to provide seed for sowing. The crop is grown during winter to provide quality fodder when native pastures are unproductive.

Leaf Rust *Puccinia coronata* f. sp. *avenae*

Stem Rust *Puccinia graminis* Pers. f. sp. *avenae* Erikss. and Henn

A major limiting factor to growing oats for forage or grain is the frequent occurrence of diseases such as leaf and stem rusts. Although the impact of stem rust is generally considered minor for oats grown and managed for forage.

The rapid build-up of rust spores can produce serious consequences. For example, in the rust outbreak of 1988, the economic loss was estimated at \$70 million. 'Fortunately, new oat varieties with leaf rust resistance can be continually produced through a plant breeding program.'??

Breeding response

Rusts are a major constraint and the main thrust of oat improvement is rust resistance. Historically, Queensland has relied heavily on North American germplasm for its oat improvement and continues to do so. It has been extremely difficult to attract the level of funding necessary to address the rust problem domestically in what is essentially a grazing crop. All recent releases have come from breeding programs in either Texas, the northern prairie states or Canada. While most of these were released as rust resistant, from fourteen varieties commercialised since 1990 only three are currently leaf rust resistant and none are resistant to stem rust.

Varieties currently resistant to leaf rust are :

Barcoo was released by Pacific Seeds in 1996 under PBR. It was selected from an introduction from Texas A & M University, USA. Barcoo has good leaf rust resistance. The leaf rust resistance of Barcoo has not been determined.

Gwydir was released by Pacific Seeds in 1999 under PBR. It was developed jointly by the University of Queensland/DPI/Pacific Seeds and was tested as PO519. Gwydir is a Queensland developed forage oat variety, compared to most varieties which were introduced from overseas. It has an leaf rust resistance which has not been determined.

Nugene is a joint release between DPI and Heritage Seeds for the year 2000. Nugene was developed by North Dakota State University, USA and was tested as ND1. The leaf rust resistance is conditioned by a new gene (Pc91) plus an unknown resistance gene acting in complement.

Oats from Canada and northern USA are particularly well suited to grazing in this region. They generally produce vigorous early growth which maximises dry matter production from limited soil moisture. In addition, their requirement for a lengthy cumulative photoperiod for head initiation, ensures they remain suitable for grazing into late spring after which time summer growing pastures or forage crops are usually ready to graze. The majority of current commercial varieties and pending releases are from these sources.

The Forage Oat Breeding Program of the Queensland Department of Primary Industry (QDPI) places greater emphasis on the development of leaf rust resistant varieties suitable for grazing. Pyramiding leaf rust resistance genes into adapted forage oat varieties is the current approach.

Dr R G Rees, previously a pathologist with QDPI, initiated a breeding program to pyramid resistance genes, and progeny from these crosses are currently being evaluated for forage production. Materials have already been developed that combined 3-4 resistance genes to current races of leaf rusts. Resistance genes were selected through rust screening and aided by molecular markers techniques to facilitate their identification. These materials are currently in the advance stages of yield trials with varietal release projected in year 2001. These varieties would combine durable leaf rust resistance and improved forage yield.

In recognition of the challenges posed by the rusts, Queensland Department of Primary Industries appointed its first oat breeder in 1996 to develop improved forage oat varieties with durable rust resistance. Mr Greg Platz was appointed to the position and has since been replaced by Dr Leonard Song.

The following comment whilst written for Queensland relates substantially to all the Australian cereal zone. Breeding for rust resistance in oats is hampered by the dearth of effective resistance genes; the continual release of varieties carrying these genes as the sole source of resistance and the ubiquitous nature of the alternative host - wild oats (*Avena fatua*, *A. ludoviciana*, *A. barbata*). Wild oats can be found growing at any time of the year. Rust surveys have identified pathotypes with virulence on genes to which the population has not been exposed in *A. sativa*. The alternate host (*Ramnus* spp) does not occur in Australia.

Crown Rot Fusarium graminearum Group 1

Crown rot is an important disease of wheat, barley and triticale in the northern grain belt of Australia. Crown rot survives in the soil as fungal threads of the fungus, *Fusarium graminearum* Group 1 in the residues of diseased winter cereals or infected grasses.

Oats can be infected by the fungus and may or may not show symptoms of crown rot. In 1999, a number of wheat crops succeeding oats had high levels of crown rot.

Breeding Response

The importance of this disease in oats is such that no breeding response is required.

NEW SOUTH WALES²

NSW Department of Agriculture

Predicted oat sowings for 2000 are reduced to 354,850 ha. Producers are planting higher value grazing wheats in place of oats due to better returns. Pasture availability has also been good in most districts, reducing the need for grazing cereals. An estimated 380,000 ha were sown in 1999. Interest in growing oaten hay for export has increased.

The major diseases of oats in New South Wales are stem rust, leaf rust, and BYDV.

Breeding Response

The breeder relies on selection under heavy disease pressure of parents and amongst breeding lines for resistance/tolerance. The main disease selection sites are at Temora in southern NSW, with heavy BYDV presence, and at the University of Sydney, Plant Breeding Institute field and greenhouse sites at Cobbitty, where extreme BYDV, leaf rust and stem rust pressure is applied.

An extract from the 1999 NSW Breeding Trials report, exemplifies the problem:

'Very widespread BYDV infections occurred at tablelands and slopes sites. This effected grain yield and quality. The mild wet spring resulted in very high levels of leaf and stem rust infection especially in grain only experiments. This resulted in grain yield and quality loss at most sites.'

The University of Sydney

The work of the University of Sydney, Plant Breeding Institute at Cobbitty on the cereal rusts is the only national Australian program researching diseases of oats. The PBI program services each of the state based breeding program reported in this paper. This service is achieved by screening the breeding material of each program for the two rusts and with BYDV and by conducting an annual rust survey across Australia.

Leaf Rust Puccinia coronata var. avenae

Pathotype Distribution

Leaf rust of cultivated and wild oats was widespread in 1999-2000. Virulence for *Pc68* was detected in samples collected in Qld in May, and later in NSW. The pathotype responsible, 0307-6,10, is regarded as a single-step mutant from the Cleanleaf pathotype, 0207-6,10. A second *Pc68* virulent pathotype, 0107-3,6,10, was also isolated. As in 1998-1999, pathotypes with virulence for genes *Pc38*, *Pc39* or *PcCleanleaf* were common in NSW and Qld but rare or not detected in SA and WA. Three pathotypes with virulence for Warrego were also isolated. Pt 4473-6,10 appeared to increase in frequency in Qld and Nth NSW. Triplet code pathotypes 0000 and 0001 tended to be the most common and were

recovered from all regions. The crown rust resistances of several oat cultivars released in north eastern Australia in recent years have been overcome by new pathotypes of *Puccinia coronata*.

The current differential set (Table 1) has been in use since 1995, and was developed by Dr. David Bonnett, a former Ph.D. student. The current pathotype nomenclature comprises a coded triplet value followed by a list of numbers which correspond to virulence on 12 supplementary differentials

The detection of virulence for cv. Warrego during 1998, and for the gene Pc68 in 1999 (Graza 68 and Moola) is yet a further example of the ability of *P. coronata* to rapidly overcome newly deployed resistance genes. Few of the current suites of oat cultivars possess effective seedling resistance to leaf rust. The resistance of Bettong, Barcoo, Nugene, and Gwydir continue to be effective.

Survey results indicate that the population of Oat Leaf Rust in Australia is clearly structured and there is good evidence of groups of pathotypes within which individuals were most likely derived via single step mutation.

Table 1 A. Coded triplet differentials:

Differential	Resistance gene	Octal Value
H458	PcH458	4000
WIX 4361-9	PcXIX1,WIX2	2000
Amagalon	Pc91	1000
Culgoa	PcCul	400
Cleanleaf	Pc39, 39, Cl	200
PC68	Pc68	100
TAM 0301	Pc58	40
TAM 0.312	Pc59	20
Pc61	Pc61	10
Pc38	Pc38	4
Pc39	Pc39	2
Swan	-	1

B. Supplementary differentials:

<i>Differential</i>	<i>Resistance gene</i>
1. Pc36	Pc36
2. Pc46	Pc46
3. Pc50	Pc50
4. Pc51	Pc51
5. Pc52	Pc52
6. Pc55	Pc55
7. Pc56	Pc56
8. Pc63	Pc63
9. Pc64	Pc64
10. Pc71	Pc71
11. X534	?
12. X716	?
Bettong	?
Barcoo	?
Warrego	?

Breeding Implications

The crown rust resistances of several oat cultivars released in north eastern Australia in recent years have been overcome by new pathotypes of *Puccinia coronata*.

By way of example the gene Pc68, transferred from *Avena sterilis* to *A. sativa* by Wong et al. (1983; Can. J. Genet. Cytol. 25, 329-335), was incorporated into two cultivars released by Agriculture Canada, A.C. Assiniboia and AC Medallion. These cultivars were released in Australia in 1997 under the names Graza 68 and Moola, respectively. A differential possessing Pc68 was included in the differential set used to assess pathogenicity of *P. coronata* in Australasia in 1995, and all isolates examined during years 1995 to 1998 were avirulent for this gene. In June 1999, leaf rust was noticed on Graza 68 and Moola in experimental plots in Queensland at two sites, Warwick and Kingsthorpe. Additional observations at Gympie also indicated heavy rusting of Moolah. Greenhouse tests with rust samples from both locations confirmed virulence for Pc68, and further indicated that the new pathotype had most likely arisen by a single step mutation to virulence for Pc68 in pathotype 0207-4,6,10 (the "Cleanleaf" pathotype). The designation for the Pc68 virulent pathotype is 0307-4,6,10 (the "Graza 68" pathotype).

The apparent ease with which *P. coronata* has overcome recently deployed resistance genes is a clear indication of the need to avoid releasing cultivars with single effective resistance genes. To date, virulence has not been detected for gene Pc91. It will be important to assess the value of newly characterised genes such as Pc94 and to try to deploy the genes identified as useful in combination to reduce the likelihood of new pathotypes with matching virulences.

The outcome is that sources of leaf rust resistance in the world's oat collections are becoming difficult to find, and sources of stem rust resistance are virtually exhausted.

Control of rust in oats has for various reasons been more difficult to achieve than control in wheat. The parasites appear to be more variable than those on wheat; more frequent susceptible varieties and wild oats permit much more inoculum to be present; the global industry is relatively small, and therefore there are fewer resources for research.

Although resistance is present in wild relatives of cultivated oat, traditional hybridisation and selection procedures for successful transfer take more than 20 years. Hopefully, developments in plant biotechnology and transformation will shorten this process.

Stem Rust *Puccinia graminis* Pers. f. *sp. avenae* Erikss. and Henn

Pathotype Distribution

The 1999-2000 survey recovered 316 cultures from 223 samples. The pathotype distribution was similar to previous seasons with pathotype groups 30, 41 and 94 prevailing. Groups 30 and 41 tended to be more frequent in the eastern states while 94 pathotypes were well distributed across all oat growing regions.

This virulence for Pga has become progressively more widespread, both in terms of geographical range and the number of pathotypes now incorporating this virulence. Approximately 22 % of isolates comprising 12 pathotypes showed virulence for Pga. Virulence for Pga continues to predominate in Queensland and northern NSW, although isolates have now been recovered from southern states including Victoria and South Australia. There are currently no effective resistance genes deployed for the oat stem rust pathogen.

The lack of effective genetic variability for stem rust resistance among important sources of germplasm used by Australian oat breeders is a major cause for concern.

Breeding Implications

The oat crop is the third most important cereal in Australia after wheat and barley. Stem rust caused by *Puccinia graminis* Pers. f. *sp. avenae* Erikss. and Henn. is a major constraint to oat production throughout the country. Despite the absence of barberry (*Berberis vulgaris* L.), the alternate host, the pathogen survives and multiplies on volunteer oat plants, wild oats and certain native and introduced grass species. The prevalence of widely virulent pathotypes throughout the country has enforced the need to seek new sources of resistance. Until the late 1980s, genes such as *Pg-8* and *Pg-13* and the resistance gene complex known as *Pg-a*, conferred resistance in Australia. However, with the appearance and spread of widely virulent pathotypes, such as 94+*Pg-13* and 41+*Pg-9+Pg-13*, genes *Pg-8* and *Pg-13* are no longer effective (Adhikari, 1996). The resistance known as *Pg-a* was shown to be based on two complementary recessive genes.

For oat breeders in Australia, the main sources of resistance to stem rust have been materials from the International Oat Rust Nursery and, more recently, the Quaker Oat Nursery. Many recent Australian breeding lines were selected from these materials or from crosses involving such lines. However, the genetic bases of resistance in the germplasm were largely unknown. Although the "*Pg-a* complex" was used extensively as a source of stem rust resistance, information on its distribution and inheritance is scant.

Experience has shown that genetic uniformity in germplasm leads to disease vulnerability. This could be a major threat to the Australian oat industry and comparable to the outbreak of southern leaf blight caused by *Helminthosporium maydis* Nisikado and Miyake on maize associated with *cms-T* cytoplasm in the USA in 1970 (Hooker & Saxena, 1971), and the triticale stem rust epidemic in Australia following the loss of resistance conferred by *Sr27* and *SrSatu* in the early 1980s (McIntosh & Singh, 1986).

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SOUTH AUSTRALIA³

South Australian Research and Development Institute (SARDI)

The major yield limiting diseases of oats in South Australia and Victoria are

- leaf rust (caused by *Puccinia coronata* f. sp. *avenae*)
- barley yellow dwarf virus
- stem rust (caused by *Puccinia graminis* Pers. f. sp. *avenae*),
- Cereal cyst nematode (*Heterodera avenae*),
- stem nematode (*Ditylenchus dipsaci*),

Red leather leaf (*Spermospora avenae* (Sprague et Johnson) Sprague)

Cereal pathology research is conducted by three closely-linked groups within SARDI:

- the Fungal Pathology group headed by Hugh Wallwork and
- the Nematology group headed by Sharyn Taylor provide pathology research and extension services, while also interacting with
- the Cereal Molecular Genetics laboratory of Kevin Williams on resistance-linked molecular marker development and pathogen genetics conducts research and provides a resource for the identification and management of fungal and nematode diseases of cereals in South Australia.

Breeding Response

The SARDI based Oat Breeding Program in cooperation with VIDA develops improved oat varieties for both Victoria and South Australia. The breeding program is focused on improving yield potential, disease resistance, and milling, feed, and hay end-use quality in both naked and husked oat varieties.

The disease screening programs are a cooperative effort with SARDI Field Crops Pathology and the Plant Breeding Institute, The University of Sydney. In addition, field evaluation sites are sown and assessed by members of the breeding program for these important diseases.

Linkages to other research programs in SARDI, the University of Adelaide, and the Cooperative Research Centre for Molecular Plant Breeding have resulted in projects to develop doubled haploid technology and molecular markers for quality and disease resistance in the Oat Breeding Program.

Molecular Markers

A genetic map is being produced to identify molecular markers linked to quality and disease resistance traits in a cultivated oat cross. This project is being funded by the Cooperative Research Centre for Molecular Plant Breeding, which is based at the University of Adelaide on the Waite Campus.

A single-seed descent population was produced from the cross Potoroo × Mortlock. This population is segregating for cereal cyst nematode and stem nematode resistance and tolerance derived from Potoroo

As a prelude to constructing a genetic map of this cross, restriction fragment length polymorphism (RFLP) screens are being conducted on the population parents, using mainly CDO and BCD probes chosen to give good coverage of linkage groups on the published hexaploid oat maps. To date, 165 RFLP probes have been tested, with 78 (47%) revealing polymorphism between the parents. The polymorphic RFLP markers will be used as anchor loci for map construction, with amplified fragment length polymorphism (AFLP) markers used to increase marker density.

WESTERN AUSTRALIA⁴

Oats in Western Australia are grown for grain, hay, grazing or silage. In 1995, about 350,000 hectares were sown to oats, of which 250,000 was for grain production, 70,000 was for hay and 30,000 for green feed and silage.

The important diseases of oats in Western Australia are:

- **Septoria avenae blotch**, is the most common oat disease in Western Australia. The disease is caused by the fungus *Phaeosphaeria avenaria* f.sp. *avenaria* (asexual stage: *Stagonospora* (formerly *Septoria*) *avenae* f.sp. *avenaria*). *Septoria avenae* blotch may cause up to 50 per cent yield loss and crop lodging in extreme cases but losses of around 10 per cent are more common in high rainfall areas.

Breeding Response: select for resistant or moderately resistant for disease-prone areas.

- **Stem Rust** *Puccinia graminis* var. *avenae* Under favourable conditions, stem rust is very damaging and can destroy a crop
- **Leaf Rust** *Puccinia coronata* var. *avenae* is potentially a very damaging disease, reducing both grain and forage yields. In 1992 the first serious epidemic of leaf rust occurred in Western Australian oat crops. In many areas this caused major yield losses in some varieties. Leaf rust now occurs regularly in the southern high rainfall regions, especially on early sown crops
- **Barley Yellow Dwarf Virus** (BYDV) is widespread in high rainfall areas of Western Australia. It infects cereals and grasses, but grasses (pasture and wild) are the

main reservoirs. The virus survives between growing seasons in grasses which persist through the summer. Infection is spread from the grass reservoirs to oats and other cereals through the migration of cereal and grass aphids.

Breeding Response

Select under field conditions and at the Plant Breeding Institute, Cobbitty for Stem and Leaf Rust and for BYDV.

Aphid arrival date is closely linked to pre-growing season rainfall, and that the amount of BYDV spread is affected by both aphid vector arrival date and the proportion of them carrying virus into the crop from external sources. A decision support system (DSS) is being developed to forecast the need for insecticides to control aphid vectors of BYDV in different districts each year.

Minor diseases

- **Ring Spot** is a common disease caused by the fungus *Drechslera campanulata* which is widespread throughout agricultural areas. The disease often occurs with *Septoria avenae* blotch and symptoms may easily be confused. No direct control measures are available nor does control appear to be warranted.
- **Cereal Cyst Nematode** (CCN) has been identified as a problem in small areas in Western Australia. The CCN-resistant South Australian varieties Marloo, Potoroo, and Wallaroo are suitable for production in these areas.
- **Bacterial blights**
 - Stripe blight (*Pseudomonas syringae* pv. *striaefaciens*) and Halo blight (*Pseudomonas syringae* pv. *coronafaciens*)

These bacteria need moist conditions to spread. Normally, crops outgrow the infection in spring. Losses are not known to be significant in Western Australia.

These diseases are not breeding targets.

GrainGuard™

All sectors of Western Australia's grains industry are working together under the banner of GrainGuard™ to maximise freedom from major grain pests, diseases and weeds and to minimise risk of chemical residues in grain. GrainGuard™ has been initiated as part of the State government's \$3.5 million commitment to improved industry protection through strengthened risk assessment, quarantine and emergency response. GrainGuard™ is supported by the industry based Agriculture Protection Board, the Pulses and Oilseeds Partnership Group and the Cereals Partnership Group.

Industry representatives (from growers to exporters) are working with Agriculture Western Australia to develop the GrainGuard™ framework.

NEW ZEALAND⁵

The major diseases of oats in New Zealand are Leaf Rust, BYDV, Stem Rust, and Bacterial Blight.

Aphids are important pests of New Zealand cereal crops. Five different kinds of aphid are found in cereal crops in New Zealand, all of which can transmit BYDV. Four of the five can cause yield losses of up to 30%.

There is a well developed Aphid Warning system which assists farmers in their planning for the use of insecticides.

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MAJOR DISEASES ON OATS IN SOUTH AMERICA

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ABSTRACT

The successful expansion of oat production in South America may be threatened by some diseases. Environmental conditions and genetic diversity found in our sub tropical region put pathogens like *Puccinia coronata* f.sp. *avenae* much ahead of the strength of the major resistance genes. Also, agricultural practices adopted by farmers in most areas, such as the direct seed drilling, favoured the outcome of diseases such as the kernel spot, caused by *Pyrenophora avenae*, and the head blight and root rot, caused by *Gibberella zeae*. The aim of this paper is to show the impact of these diseases in our agricultural system as well as the challenges we face to control them.

INTRODUCTION

Recently, oat (*Avena sativa* L.) crop grown in importance in South America, specially in Brazil, becoming one of the best crop alternatives to be used in the winter months. In the past, all the oat necessary for the human and animal consumption in Brazil was imported from Argentina, with great costs (FEDERIZZI *et al.*, 1997). The necessity for high quality oat grains in the Brazilian market called the attention of breeders for new, local varieties that would integrate a new agricultural system for grain production.

One of the consequences of this rapid expansion of the cultivated area with oats in south Brazil and other South American countries was the increase of inoculum and severity of fungi diseases that attack the culture. Among these, the most frequent and destructive is the crown rust, found in all parts of the world where oat is cultivated. More recently, however, two other diseases arose as new challenges to the direct seed drilling system, the kernel spot and the giberela.

The crown rust disease

Crown rust disease is caused by the fungus *Puccinia coronata* f.sp. *avenae*, which has the ability infect other grasses too. In South America its sexual stage was not found as yet and may not occur since there is no any of its known alternate hosts. Crown rust epidemics has been the chief effect in reducing oat yields in Brazil. Besides, it may reduce the cultivated area by generating unstable harvests and inadequate economic condition to the farmers. To maintain this disease at desirable levels, isolated methods, like the use of resistant varieties with major, race-specific genes, and fungicides, have been employed. Nevertheless, losses in effectiveness and the need for varieties reposition are frequent due to rapid changes in the population of the pathogen. Even with the progresses obtained the resistance levels present in the available cultivars are not enough to face the pressure present in the growth areas.

The ideal conditions for the occurrence and spread of the disease are temperature between 16 and 18 °C and high air humidity, which are common in the growing areas in South Brazil (MARTINELLI *et al.*, 1994). Under these conditions the rate of the disease growth is very high (**Fig. 1**) which can cause yield losses over 90% (**Table 1**). Besides, there is a fast replacement and specialisation of races of the fungus so many resistant varieties are quickly defeated. The methods employed to control the disease have been the use of chemicals and new resistant varieties. The use of fungicides may not be economic in many cases and cause side effects to the environment.

Under the Brazilian conditions, the short durability of the resistance is attributed (i) to the high mutation frequency of *P. avenae*, (ii) to the maintenance of the crop throughout all months of the year among the South American countries, (iii) to the presence of other susceptible grasses and, (iv) to the favourable environment, allowing a continuous infection period and sporulation (FEDERIZZI & STUTHMAN, 1998). All this form a single and an unique pathosystem which may help to fix the large number of mutants observed.

Crown rust samples revealed to be very diverse and complex in virulence (**Table 2**) with some of them carrying up to 26 virulence genes. The average of the number of virulence genes per race analysed were 20.5 in 1997, 14.8 in 1998 and 15.8 in 1999 (Leonard & Martinelli, not published).

This data indicated that structure of the *P. coronata avenae* population is at least comparable in complexity with any other countries in the world where the sexual stage occur. This scenario call attention for a deep reflection about the dynamics of the pathogen population, the interaction with its host and consequently, about the strategies to control it. For example, the strategy of pyramiding major genes, advocated by some researches in other countries, should be carefully analysed for our environment. Therefore, it is vital to search and utilise other, more stable types of resistance. The *slow-rusting* type of resistance has been suggested as one promising strategy to enlarge the durability of the resistance to the crown rust.

In South America, we are working with partial resistance since 1995, measuring its components such as pustule size, latent period, sporulation period and disease severity (AUDPC). So far, the results seems to be promising showing the existence of genetic variability among the genotypes (THOMÉ *et al.*, 1997; MELLO *et al.*, 1998; CHAVES & MARTINELLI, 1997).

Table 1. Yield and quality losses due to crown rust epidemic on two susceptible oat varieties.

Varieties	AUDPC	Yield (kg/ha)	% reduction	Yield	Industrial weight
1. UFRGS-14	2634	701	80		31
2. UFRGS-14 + fungicide	123	3628			47
3. UPF-16	3146	99	96		*
4. UPF-16 + fungicide	165	2720			57

* = not determined due small amount of seeds harvested.

Source: Roesch, F. E. & J. A. Martinelli, 1999.

Figure 1. Crown rust progress on the susceptible cultivar UPF-16.

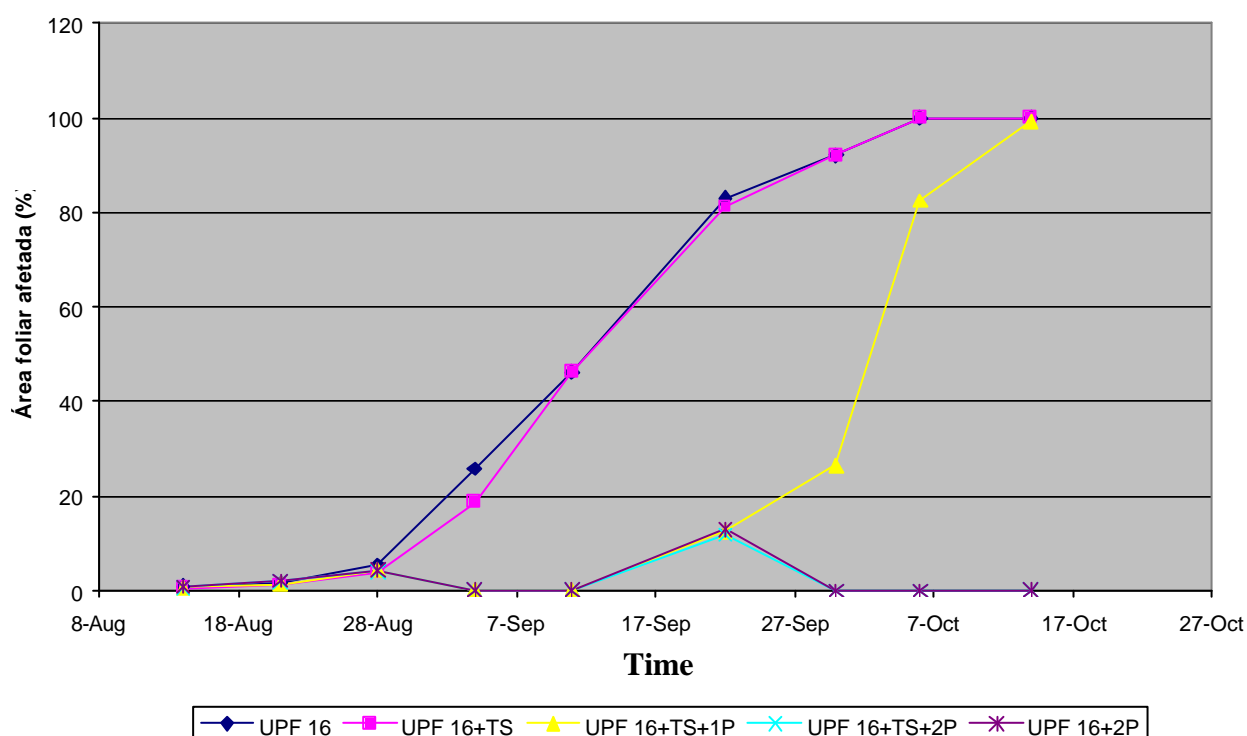


Table 2. Frequency of virulence of isolates of *Puccinia coronata* f.sp. *avenae* in South Brazil on the resistance genes during 1997, 1998 e 1999.

Gene de Resistência	% virulence 1997	% virulence 1998	% virulence 1999
Pc 14	89	86	88
Pc 35	43	45	46
Pc 36	55	66	72
Pc 38	8	36	33
Pc 39	79	38	66
Pc 40	85	88	79
Pc 45	92	17	39
Pc 46	92	45	70
Pc 48	62	21	21
Pc 50	4	10	10
Pc 51	49	45	52
Pc 52	30	17	10
Pc 53	42	2	5
Pc 54	89	22	43
Pc 55	77	41	66
Pc 56	47	66	74
Pc 57	100	62	70
Pc 58	38	2	5
Pc 59	25	40	45
Pc 60	96	78	84
Pc 61	94	66	67
Pc 62	25	3	10
Pc 63	8	28	20
Pc 64	90	19	36
Pc 67	94	34	31
Pc 68	0	3	0
Pc 70	40	42	59
Pc 71	81	32	62
Marvelous	100	100	100
H548	74	7	31
Dane	27	38	49
X4361-9	15	38	51
TAM-O-386-R	52	10	20
TAM-O-393	89	9	34
B604Xsel	91	14	36
Saia		27	
Vista			5
*	20,5	11,8	14,8

* = average of number of virulence genes per race.

Source: Leonard & Martinelli (not published).

PYRENOPHORA AVENAE

One of the consequences from the fast expansion of the cultivated area with oat in South America under the direct seed drilling system was the increase of inocula of some phytopathogenic fungi. Among these, the leaf blight and kernel spot, caused by *P. avenae* became more pronounced.

The presence of spotted kernels appears as a new and particular problem from the agricultural system adopted by farmers in south Brazil mainly, not being seen with such impact in any other country. The magnitude of this problem can be exemplified by losses imposed to farmers, reaching up to 20% at the harvest.

The presence of dark spots on oat kernels has been a limiting factor for their commercialisation in Brazil because they are less acceptable by the industries. The localisation of the mycelium of *Pyrenophora avenae* on the kernels and its enzymatic activity may be involved with the cause of the spots.

The mycelium of *P. avenae* is the main cause of kernel spots of oats and its growth is restricted within the cells of pericarp. *P. avenae* has good lipase and protease enzymatic activity but poor amylase activity (**Fig. 2**). Spotted oat kernels did not differ in the protein and lipid contents when compared with the healthy ones (**Table 3**). In particular, these contents are higher on those external tissues of the pericarp than the whole grain, independently of the presence or absence of spots. These data may explain the superficial growth of *P. avenae* mycelium on oats cariopsis and its association with the kernel spot.

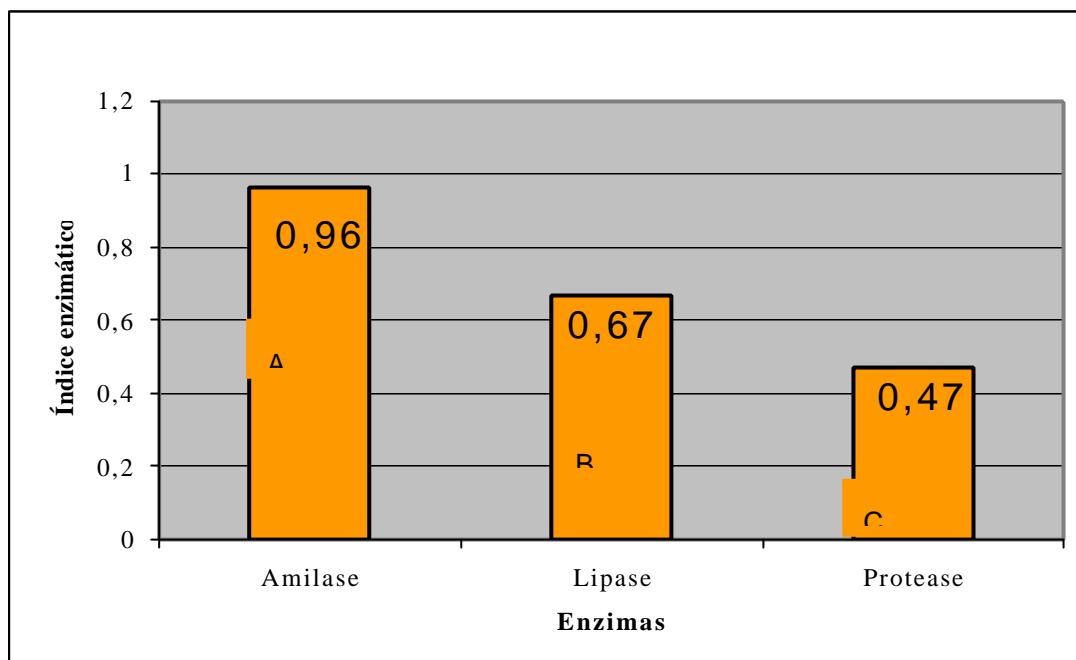
One analysis of existing variability on the Brazilian pathogen population, made by esterase isoenzymas on 108 *P. avenae* isolates, allowed us to establish different groups of similarities among them. Also, there was a significant interaction on the host-pathogen test.

Table 3. Percentage of proteins and lipids in oat kernels or in their superficial layers, with or without *Pyrenophora avenae*.

Tratamentos	% Gross Protein *	% Lipids *
1. Oat kernel	13,38 a	5,28 A
2. Spotted oat kernel	13,64 a	5,24 A
3. Pericarp and aleuroma	16,95 b	6,50 B
4. Spotted pericarpo and aleuroma	17,03 b	6,84 B

* Means followed by the same letters do not differ by Tukey's test at 5%.

Figure 2. Index ^(*) of the enzymatic activity of *Pyrenophora avenae* for amilase, protease and lipase. The values of the bars represent the relation of colony diameter the the halo diameter. Means followed by the same letters do not differ by Duncan's test at 5%. a 5%. C.V.: 9,55%



GIBBERELLA ZEAE

Fusarium graminearum, anamorph of *Gibberella zeae*, has gradually increased its frequency over oat plants, panicles and roots, as well as on corn. From 1998, the fusariosis appeared as a root rot disease on oats causing their rot and lodging when they were at the dough growth stage. Many plant crowns become pink and covered by perithecia. Inside the stems a profuse and pink micelium can be seen. The occurrence of this new form of attack on oats may be of great magnitude for the maintenance of the direct seed drilling system using oat as one of the key crops for the crop rotation model adopted in South America.

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Figure 3. Symptoms of *Gibberella zeae* on oat showing the crown rot and the pink mycelium inside the stem.

VIRAL DISEASES OF OAT

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ABSTRACT

By far the most important viral disease of oat is caused by the barley yellow dwarf viruses (BYDVs). BYDVs cause significant economic losses in many oat production regions worldwide. Host plant resistance or tolerance is the best method of control of BYDVs. A few of the viruses infecting oat other than BYDVs will be mentioned briefly, but because barley yellow dwarf (BYD) is by far the most important virus disease of oat the major emphasis will be on BYD and development of tolerant genotypes. Our objective in this paper is to summarize some of the research that we have done on the development of BYDV tolerant germplasm and the use of molecular markers associated with genes for tolerance to BYDV.

INTRODUCTION

Barley yellow dwarf (BYD) is the most economically important viral disease of oat (*Avena sativa*) and causes significant yield losses worldwide (D'Arcy, 1995, Lister and Ranieri, 1995). Other viruses that infect oats cause relatively minor losses, although some have been known to cause economic losses in specific locations and specific environments. Although 30 or more viruses have been reported to infect oat, less than 10 infect oat frequently in the field. Because BYD is the most important we will devote most of this paper to barley yellow dwarf. We will summarize some of the research we have done on the development of BYDV tolerant germplasm and the use of molecular markers associated with genes for tolerance to BYDV.

Viruses that infect oat

In addition to the BYD-causing viruses (BYDVs), Brome mosaic virus (BMV), Oat sterile dwarf virus (OSDV), Oat blue dwarf virus (OBDV), Oat golden stripe virus (OGSV), Oat chlorotic stunt virus (OCSV), and Oat mosaic virus (OMV) infect oat. Harder and Haber (1992) and the VIDE (Brunt et al., 1997) provide information on these and other viruses that have been reported to infect oat.

OGSV and OMV are vectored by the soilborne fungus *Polymyxa graminis* and are related to wheat soilborne mosaic virus (Chen et al., 1996). The viruses cause mottling and stunting in winter oats. The symptoms tend to be most evident in early spring and become less pronounced as the plants grow and temperatures become warmer. OMV has a narrow host range, generally only infects *Avena* species, and has been reported in the United States, United Kingdom, and possibly New Zealand. Recently, Coker 716 has been identified as a source of resistance to both viruses (Walker et al., 1998). OCSV also may be vectored by *Polymyxa* and has been reported in the United Kingdom (Boonham et al., 1997)

BMV infects a wide range of species in the Gramineae and probably occurs worldwide. BMV, a member of the *Bromovirus*, has also been reported in complexes with BYDV, and may be more important economically than is currently recognized (Harder and Haber, 1992). BMV is mechanically transmissible, but has been transmitted experimentally by

nematodes, beetles, aphids, and rust urediospores (Harder and Haber, 1992). The host range of BMV is very wide and includes several dicotyledenous species. BMV produces mosaic symptoms that may become progressively milder over time. The symptoms of BMV may mimic those of BYDV infection.

OSDV occurs in northern Europe where its vectors (planthoppers in the genus *Javesella*) occur. It has a relatively narrow host range in the *Gramineae*. OSDV has caused serious losses in some European countries, and cultural practices designed to reduce the number of planthoppers carrying the virus have been used for control of OSDV.

OBDV has been reported in North America and is obligately vectored by the aster leafhopper, *Macrostes fascifrons*. OBDV is persistently transmitted by leafhoppers and multiplies within the vector. Symptoms on oat include stunting, blue-green discoloration of the leaves, enations (abnormal outgrowths on the surfaces of leaves and stems), sterility, excessive tillering, blasting (often from the panicle tip downward), and some leaf necrosis.

BYDVs, phloem-restricted luteoviruses obligately vectored by aphids, infect a wide range of host species and cause economic losses in small grain cereal crops around the world (D'Arcy, 1995, Lister and Ranieri, 1995). BYD symptoms include leaf chlorosis, reddening of the leaves, leaf necrosis, stunting, reduced root growth, delay or prevention of heading, blasting of florets, and failure to fill kernels (Jensen and D'Arcy, 1995, Kolb et al., 1991). BYD symptoms vary depending on the host, virus strain, and environment.

Five or more species of BYDVs have been described.. The five best characterized species, which were based initially on the efficiency with which they are transmitted by different vectors (Power and Gray, 1995), have been divided into two genera. The genus *Luteovirus* includes: *Barley yellow dwarf virus* (BYDV)-MAV (transmitted by *Macrosiphum* (*Sitobion*) *avenae*); BYDV-PAV (transmitted by *Rhopalosiphum padi* and by *Macrosiphum avenae*). The genus *Polerovirus* includes: *Cereal yellow dwarf virus*-RPV (transmitted by *Rhopalosiphum padi*). Neither BYDV-RMV (transmitted by *Rhopalosiphum maidis*) nor BYDV-SGV (transmitted by *Schizaphis graminum*) have been assigned to a genus yet. At least 25 species of aphids have been reported to vector BYDVs (Halbest and Voegtlin, 1995). The most frequently reported vectors of BYDVs world-wide are probably *Rhopalosiphum* species.

Significant yield losses result from BYD in all small grains, including oat (Lister and Ranieri, 1995). Host plant resistance or tolerance is an important control strategy for reduction of losses due to the BYDVs; however, insecticides have been used to control the aphids that spread BYDVs in some production areas, especially where management is intensive and grain prices are high (Plumb and Johnstone, 1995). Use of insecticides to control aphids is most common in Europe. Generally, insecticide sprays have been more effective in autumn sown grains than in spring sown. Nevertheless, yield increases of up to 38 % have been reported in spring oats (Plumb and Johnstone, 1995). Control of infection at early plant growth stages is crucial since plants are damaged more severely when infected at an early stage. The seed treatment insecticide imidacloprid (Gaucho™) has also been effective in dramatically reducing yield losses in spring oats (Gourmet et al., 1996). In most oat producing regions the use of tolerant (Cooper and Jones, 1983) cultivars has been the only economic means of controlling damage due to BYD (Burnett et al., 1995). Many researchers have contributed to the development of oats with tolerance or resistance to BYDVs, and good levels of tolerance have been identified in oats (Burnett, et al., 1995, Kolb, et al., 1991).

METHODS USED FOR EVALUATION OF BYDV TOLERANCE

In our program we use a BYDV field nursery to evaluate genotypes for BYDV tolerance (Hewings et al., 1992). The techniques and facilities have been developed over a period of years. Oat genotypes to be evaluated for BYDV tolerance are planted in hills in the field with 15 seeds per hill. Aphids (*Rhopalosiphum padi*) carrying an Illinois isolate of BYDV-PAV are used to inoculate the hills. The aphids are reared on barley plants grown in 15 cm diameter pots. These plants (grown either in growth chambers or in greenhouses) grow for about one month before 20 to 40 viruliferous aphids are placed on the plants. To confine the aphids, the plants are covered with a tube made of netting (100 micron mesh size) and plexiglass. The aphids on the plants multiply to high levels in about two weeks. Aphids for inoculations are collected by removing the plexiglass tube and shaking the plants over large pieces of paper (about 75 x 100 cm). A small amount of talc sprinkled on the paper prior to aphid collection prevents the aphids from sticking together. Hills are inoculated using an aphid / corn meal mixture (1 : 1 volume / volume) dispensed through a custom-built apparatus. The corn meal serves as a carrier, and the light yellow color of the corn meal makes it easy to see if a hill has been inoculated, thus helping to prevent escapes. About 60 to 70 aphids are placed on each hill, and essentially all of the plants in a hill are infested and become infected. Hills are inoculated when the plants are in Feekes growth stage 1 or 2. An insecticide is applied about five days after inoculation to kill the aphids. Paired control and inoculated hills (separated by a buffer row) are grown in some experiments, but for routine evaluation of breeding lines control hills are not necessary. Hills are evaluated at Feekes growth stage 10.6 by rating each hill on a 0 to 9 scale. Hills are rated on the amount of leaf chlorosis, stunting, and blasting of florets in the panicles. On this scale, hills rated 0 exhibit essentially no chlorosis, no stunted tillers, and no blasting; hills rated 9 do not head and are very severely stunted.

Development of bydv tolerant germplasm

We have used these procedures to develop BYDV tolerant genotypes and have released varieties and germplasm lines with good BYDV tolerance. In 1991 we released seven germplasm lines with good levels of BYDV tolerance (Kolb, et al., 1991). Recently, we developed genotypes that exhibit essentially no BYD symptoms. A population from a four-way cross was used to develop these oat germplasm lines with a high level of tolerance to BYDVs. Our objective was to combine genes for tolerance to BYDVs from different sources and develop germplasm lines with an even higher level of tolerance to BYDVs. The four-way cross involved four BYD tolerant parents: IL86-1156, IL86-5698, IL86-6404, and Ogle. The F₃ population was space-planted in the field and inoculated with BYDV-PAV-IL when the plants were at Feekes GS 1. Plants that exhibited BYD symptoms were destroyed. About 780 of the most tolerant plants (based on lack of symptoms) were harvested individually. A single hill of each line was evaluated for BYDV tolerance in a BYDV-PAV-IL inoculated nursery, and 139 lines were selected. The 139 lines (plus the parents and checks) were evaluated for two seasons using three replications of paired control and BYDV-PAV inoculated hills. Because these lines exhibit little or no BYD symptoms, we evaluated BYDV tolerance based on virus titer using ELISA, percent stunting (height difference between control and inoculated hills), and percent yield loss (grain yield difference between control and inoculated hills). In addition to BYDV tolerance, lines were selected based on grain yield per se, kernel morphology, and absence of awns. Two cycles of selection in the F₃ and F₄ were effective in eliminating BYDV susceptible plants from this population. The lines vary in the amount of stunting and yield loss but, under our environmental conditions, none of the lines exhibit chlorosis or other symptoms

due to BYDV infection. Considering only plants that exhibited little or no visible symptoms, ELISA values indicated that virus replication was reduced in some plants without symptoms, but not in others. Based on all of the criteria used for selection, seven lines will be released as BYDV tolerant germplasm lines. These lines differ somewhat in height, maturity, and ELISA virus titer. All of the lines have excellent tolerance to BYDV-PAV. Several of the lines are approximately equal to Ogle for grain yield. They will be registered in *Crop Science*.

We have also used the evaluation procedure in combination with backcrossing to develop near-isogenic lines that differ only in BYDV tolerance. We crossed several different BYDV tolerant parents to Clintland 64 (BYDV susceptible) and backcrossed five times to Clintland 64 while selecting for BYDV tolerance. Several groups of near-isogenic lines that included both susceptible and tolerant lines were then derived from the same BC₅F₂ plant. We are in the process of releasing some of these near-isogenic lines which may be useful in research on BYDV and for use in conjunction with molecular markers. Some of these lines and a recombinant inbred line (RIL) population have been used in research on the identification of molecular markers associated with genes for BYDV tolerance (Jin et al., 1998, Jin et al., 2000). Other research programs in the U.S. and other countries are also involved in breeding for tolerance or resistance to BYDV (Burnett et al., 1995). Incorporation of BYDV tolerance into elite genotypes and combining a high level of BYDV tolerance with all of the other traits desired in varieties is an ongoing endeavor in our program as well as many other oat breeding programs.

Molecular markers associated with genes for bydv tolerance

Using amplified fragment length polymorphisms (AFLPs), three loci were identified that explained 35, 21, and 17 percent of the phenotypic variability for BYDV tolerance in a RIL population derived from a Clintland 64 (susceptible) x IL86-5698 (very tolerant) cross (Jin et al., 1998). The evaluation procedures described above were used to collect phenotypic data on BYDV tolerance. The alleles for tolerance at these three loci come from the tolerant parent, IL86-5698. The three loci were mapped to linkage groups 2, 8, and 36 of the Kanota x Ogle restriction fragment length polymorphism map (O'Donoghue et al., 1995, Jin et al., 1998, Jin et al. 2000). Taken together, these three loci explained about 50% of the genetic variability in BYDV tolerance in this data set. None of the three loci was associated with plant height or maturity. Using the same RIL population, we recently identified microsatellites (SSRs) that map to all three of the chromosomal regions identified with AFLPs. Some of these polymerase chain reaction markers were developed from a RFLP and others are randomly selected microsatellites. A poster describing this research is presented at this meeting.

Transgenic oat plants with resistance to BYDVs have been produced by Dave Somers, University of Minnesota, Allen Miller, Iowa State University, and investigators working with them (Koev et al., 1998). In the growth chamber there was a dramatic reduction in symptoms in the transgenic oat plants, and the transgenic oat plants flowered and produced seed, while the nontransgenic near-isogenic controls died. Symptom reduction was not as great in the field (personal comm. W.A. Miller). Additional research is in progress involving these lines and more recently produced transgenic lines.

CONCLUSIONS

- BYDV is the most important viral disease of oat.
- BYDV causes economic losses in many oat production regions.
- Host plant resistance is the best method for control of BYDV.
- Genotypes with excellent levels of tolerance to BYDV have been developed, but interactions among virus strain, environment, genotype, and vectors occur.
- Molecular markers associated with BYDV tolerance have been identified, but additional research is required.

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JUST HOW MISERABLE CAN THE RUST DISEASES MAKE OATS (AND OAT BREEDERS) IN HIGH-RUST AREAS?

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ABSTRACT

Average grain yields of 29 crown rust and stem rust-susceptible oat entries were 97% lower than for TAMO 397, a crown and stem-rust resistant cultivar, in the 1999-2000 season at Beeville (South Texas). Rust -susceptible oat entries at Thrall (Central Texas) had a 63% lower mean yield than did TAMO 397. Two other locations (one in each of these same areas) had much less rust damage. The results at Beeville and Thrall indicate that the rust diseases certainly can make oats very miserable in high-rust areas.

RESULTS AND DISCUSSION

Dramatic demonstration of the effect of crown rust on oat yields was seen in the "Elite" oat trials at four locations in South and Central Texas (two locations in each region) in the 1999-2000 season. Crown rust caused significant yield reductions for the eleven most susceptible entries at all locations (the lowest damage being 17% at McGregor and 14% at Uvalde, the low-rust locations) when their average yield was compared to that of TAMO 397, a crown-rust and stem-rust resistant cultivar grown in the same test. Yield reductions for susceptible entries at Thrall and Beeville were much more dramatic, with yield reduction (using the yield of TAMO 397 = 100%) of 63% at Thrall and with 97% yield damage at Beeville. The U.S.D.A. Uniform Oat Yield Nursery at Beeville also had a 97% lower yield average for 18 other susceptible entries than the yield produced by TAMO 397; this Texas cultivar is the rust-resistant check in this nursery.

When compared to TAMO 397, nine moderately susceptible to moderately resistant entries in the "Elite" test yielded 37.0 % as much at Beeville, 59.8% at Thrall, 88.6% at McGregor, and 101.4% at Uvalde. This is good evidence that crown rust was least damaging at Uvalde, which usually is a "high-rust" location. The highest yields among all 40 cultivars and experimental lines in the "Elite" tests at both Uvalde ($5.0 \text{ Mg ha}^{-1} = 133\%$ of TAMO 397) and at McGregor ($4.1 \text{ Mg ha}^{-1} = 122\%$ of TAMO 397) were for LA90113AFL, an experimental line exhibiting moderate crown rust resistance. This resistance was inadequate at both Thrall (57% of TAMO 397) and Beeville (28% of TAMO 397). The average yield of 20 crown rust and stem rust-resistant experimental lines was from 0.1 - 4.8% below that of TAMO 397 at the 4 locations, with the highest average yield produced by a Texas experimental line having a 4-location yield advantage of 11.6% ($.36 \text{ Mg ha}^{-1}$) over TAMO 397.

However, the average yield reduction of 97% for a total of 29 susceptible entries in the "Elite" trial and the Uniform Oat Yield Nursery (U.S.D.A.) at Beeville in the 1999-2000 season indicates that the rust diseases (primarily crown rust in this instance) can make oats very miserable. Even oat lines with moderate resistance were significantly affected (56% average yield reduction for 22 entries in the two trials at Beeville). TAMO 397 was the only commercial variety having adequate levels of resistance to crown rust and stem

rust; its yield was slightly superior to the average for 20 rust-resistant experimental lines at each location, although individual entries produced as much as 12% more than TAMO 397 (4-location average). Oat breeders are made very miserable by the rust diseases when new races (biotypes) overcome the resistance of previously-resistant varieties and/or promising experimental lines. Most oat breeders who work in the “high rust” areas have experienced the sense of loss associated with these dramatic shifts in rust virulence.

EFFECTIVENESS OF RECURRENT SELECTION FOR IMPROVING PARTIAL RESISTANCE TO OAT CROWN RUST

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ABSTRACT

Crown rust disease of oat is caused by the pathogen *Puccinia coronata* and produces frequent and severe yield losses in many regions of the world. In the past, this disease has been controlled with genetic resistance and fungicides. Most breeders have used major genes that confer complete race-specific resistance. This strategy provides protection for very limited periods of time because varieties become susceptible once the frequency of virulent races in the pathogen population increases. More durable alternatives are necessary and partial resistance is being explored as one. The objective of this research was to determine the effectiveness of rapid cycle recurrent selection as a method for improving partial resistance to oat crown rust. The source population was created using named varieties and high-yielding experimental lines. Recurrent selection for grain yield was practiced during seven cycles. The progeny of the C7 parents was selected for crown rust resistance and after four rapid cycles (1 cycle/year) of recurrent selection for partial resistance, the different sets of parents were compared in three environments to determine the progress from selection. Results indicate that rapid cycle recurrent selection produced a significant increase in the level of resistance to oat crown rust and could be used as an effective breeding strategy to provide protection from this disease. Keywords: oat, crown rust, partial resistance, recurrent selection

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INHERITANCE OF RESISTANCE TO STEM RUST (*Puccinia graminis* f. sp. *avanea*) RACE NA67 IN 'PAUL' OAT

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ABSTRACT

Stem rust (caused by *Puccinia graminis* f. sp. *avanea* Eriks & E. Henn.) is one of the most destructive diseases of oat (*Avena sativa* L.) in western Canada. In 1998, a new race of stem rust, NA67, with virulence on seedlings and adult plants of western Canadian oat cultivars was found in approximately 27% of the spore samples collected from western Canada. 'Paul' is resistant to NA67. Information on the inheritance of resistance to NA67 in Paul is not available. This study was conducted to determine the number of genes and types of action of genes conditioning the resistance of Paul to NA67. The results showed that two or three independently segregating genes with dominance epistasis for the susceptible phenotype controlled the expression of resistance to NA67 in Paul. The results also suggested that selection for resistance in the F₂ would most likely be ineffective in some crosses involving Paul due to the low frequencies of resistant plants. Consequently, selection for resistant genotypes should be deferred to later generations in which the frequency of resistant plants would be increased as a result of inbreeding (self-pollination), segregation and recombination of genes.

INTRODUCTION

Stem rust (*Puccinia graminis* f. sp. *avanea* Eriks & E. Henn.) is one of the most destructive diseases of oat (*Avena sativa* L.) in western Canada. It can cause significant grain yield and grain quality losses, and under severe epiphytotic conditions it can destroy an entire crop. Approximately 35% of the oat acreage in Manitoba was lost due to the stem rust epidemics of 1977 (McCallum et al., 1999).

Fungicides can be used to alleviate the yield losses associated with stem rust in oats; however, they are often ineffective and represent an additional economic input for the farmer. An alternative to fungicides is the use of resistant cultivars. Nearly all of the cultivars that were released for the rust-prone areas of western Canada in the last 25 years generally have been resistant to the prevalent races of stem rust. Nonetheless, new races of stem rust that are virulent on previously resistant cultivars evolve from time to time forcing plant breeders to search continuously for new genes and utilize them in breeding programs.

In 1998, a new race of stem rust with virulence on seedlings and adult plants of western Canadian oat cultivars was found in 27.1% of the spore samples collected from oat fields in Manitoba and eastern Saskatchewan (McCallum et al. 2000). The new pathotype, NA67, is virulent on genes *Pg1*, *Pg2*, *Pg3*, *Pg4*, *Pg8*, *Pg9*, *Pg13*, and *Pg15*, and is avirulent to *Pga*, *Pg10*, and *Pg16* (McCallum et al., 2000). More recently, resistance to NA67 were

discovered in "Paul" oat (McCallum, unpublished data). This discovery has led to greater interest in the use of Paul as a parent in oat breeding programs. However, information on the inheritance of stem rust resistance in Paul is not available. To effectively use this resistance in breeding programs, information on the mode of inheritance is essential. This study was conducted to determine the number of genes and types of action of genes conditioning the resistance of Paul to NA67.

MATERIALS AND METHODS

Four genotypes, 'AC Pinnacle', 'AC Kaufmann', OT799 and 'Paul' were used as parents in this study. AC Pinnacle was developed at the AAFC Cereal Research Centre, Winnipeg, MB from the cross 91RAT20/Dumont68. AC Kaufmann and OT799 were developed at AAFC Lacombe Research Centre, Lacombe, AB from crosses OT257/AC Medallion and AC Belmont/OT257, respectively. Paul (PI591809) was developed at North Dakota State University from a complex set of crosses (McMullen et al., 1997). All four genotypes possess genes *Pg2*, *Pg9* and *Pg13* (genes defeated by NA67), but only Paul carries unspecified genes conditioning resistance to NA67. For simplicity, Paul is hereinafter referred to as the 'resistant' parent, and AC Pinnacle, AC Kaufmann and OT799 are referred to as 'susceptible' parent(s).

The inheritance of resistance to NA67 was examined using the parental, F_1 , F_2 , F_3 and BC_1 populations of the Paul/AC Pinnacle, Paul/AC Kaufmann and Paul/OT799 crosses. These crosses are hereinafter referred to as 'Cross 1', 'Cross 2' and 'Cross 3', respectively. In each cross, Paul was used as the female parent. Seeds of the parents, F_1 , F_2 , F_3 and BC_1 generations of the three crosses were planted in 50 x 35 x 10 cm flats filled with soil-less potting mix (3 parts peat moss:2 parts vermiculite:1 part perlite supplemented with micronutrients). In each flat, seeds were planted ~2.5cm apart within rows; the rows were spaced ~5.0 cm apart.

Seedlings were inoculated with spores of NA67 when they were in the 2-leaf stage. The method used to inoculate the seedlings was similar to that described by Harder and Haber (1992). Disease reactions were recorded ~14 d after inoculation when typical lesions developed on leaves of susceptible plants. Seedlings were classified as either 'resistant' or 'susceptible'. Seedlings were classified as resistant when they showed no evidence of infection except for very small, yellowish-green flecks similar to those observed in Paul. Seedlings were considered susceptible if they showed large, sporulating lesions. The ratings were made on the first and/or second leaf of each seedling.

The observed numbers of resistant and susceptible seedlings were fit to expected genetic ratios. Chi-square values were calculated to determine the goodness of fit to the expected genetic ratios. Heterogeneity Chi-square values were also computed to determine whether the three crosses displayed similar genetic ratios. Chi-square values were considered significant at the $P < 0.05$ level.

RESULTS AND DISCUSSION

As expected, all seedlings of the resistant parent showed no visible symptoms of infection, except for a few yellowish-green flecks. All seedlings of the susceptible parents showed large sporulating lesions, with the lesions frequently coalescing. The F_1 and BC_1 populations of all three crosses expressed uniformly susceptible reactions indicating that recessive genes conditioned the resistance to NA67.

Seedlings of the F_2 and F_3 populations of the three crosses segregated into two phenotypic classes. One class contained resistant seedlings with only minute yellowish green lesions - similar to the reactions of Paul. The second class consisting of seedlings with varying percentages of sporulating lesions similar to those observed in the susceptible parents. The latter class showed a range in degree of infection, but the majority of the seedlings showed reactions similar to those observed in the susceptible parents. The numbers of resistant and susceptible seedlings in the parents, F_1 , F_2 , F_3 and BC_1 populations of the three crosses are shown in Table 1.

Segregation data for the F_2 populations of Cross 1 and Cross 2 were a good fit to the 15:1 (susceptible:resistant) ratio indicating that duplicate dominant epistatic genes were conditioning susceptibility in the two crosses. Segregation data in the F_3 populations of Cross 1 and Cross 2 showed a good fit to the 55 susceptible:9 resistant ratio expected for dominance epistasis in the F_3 generation.

The number of resistant and susceptible seedlings in the F_2 and F_3 generations of Cross 3 fit, respectively, the 63:1 and 967:57 ratio expected for trigenic inheritance (Table 1). It would appear that three dominant epistatic genes were controlling the expression of susceptibility to NA67 in this cross. Heterogeneity chi-square test revealed that the segregation ratios in the F_2 and F_3 populations of Cross 3 were significantly different from the segregation ratios observed in the F_2 and F_3 generations of the other two crosses. These results suggested that relative to AC Pinnacle and AC Kaufmann, OT799 carried at least one more gene for susceptibility.

If the gene symbols ' r_1 ', ' r_2 ' and ' r_3 ' are used to designate the trigenic segregation observed in Cross 3, then the genotypes of Paul, AC Pinnacle, AC Kaufmann and OT799 can be represented as $r_1r_1r_2r_2r_3r_3$, $R_1R_1R_2R_2r_3r_3$, $R_1R_1R_2R_2r_3r_3$ and $R_1R_1R_2R_2R_3R_3$, respectively. Similarly, the genotypes of the resistant seedlings in the F_2 and F_3 generations would be $r_1r_1r_2r_2r_3r_3$, whereas those of the susceptible seedlings would be:

$R_1_R_2_R_3_$
 $R_1_R_2_r_3r_3$
 $R_1_r_2r_2R_3_$
 $r_1r_1R_2_R_3_$
 $R_1_r_2r_2r_3r_3$
 $r_1r_1R_2_r_3r_3$ or
 $r_1r_1r_2r_2R_3_$.

Genes for resistance to NA67 are available from several sources including *A. sterilis* L. (CI9139 - source of *Pga*), *A. sativa* L. (CI2824 - source of *Pg10*) and *A. barbata* (line no. D-203 - source of *Pg16*). Although these genes can be used individually or concurrently to develop new cultivars, additional sources of resistance would be needed to diversify the genetic base and to increase the durability of the resistance genes. Wilson and Shanner (1989) have indicated that the resistance of a cultivar would be more durable if it is conferred by more than one gene. It is not clear from the present study if the genes

conferring resistance to NA67 in Paul are different from the *Pga* genes found in CI9139. If the genes in Paul are confirmed to be new, they could be stacked with *Pga*, *Pg10* and *Pg16* to augment the durability of the resistance by increasing the complexity of the genetic changes that would be necessary in the pathogen to overcome the resistance of the host. Even if the resistance genes in Paul are identical to those of CI9131, Paul would still be a preferred parent to use in breeding programs because of its resistance to the common races of stem rust, crown rust (*Puccinia coronata* Cda. f. sp. *avenae* Eriks.), loose smuts (*Ustilago avenae* (Pers.) Rostr.) and covered smut (*U. kolleri* Wille.) found in western Canada and its superior agronomic performance relative to the other known sources of resistance genes.

CONCLUSIONS

Results from this study suggest that the inheritance of resistance to NA67 in Paul is based on two or three independently segregating genes with dominance epistasis for the susceptible phenotype. Selection for resistance based on F_2 would most likely be ineffective in some crosses involving Paul due to the low frequencies of resistant plants in the F_2 and F_3 generations. In such cases, selection for resistant genotypes should be deferred to later generations in which the frequency of resistant plants would be increased as a result of inbreeding (self-pollination), segregation and recombination of genes.

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Table 1. Segregation for resistance and susceptibility to pathotype NA67 of Puccinia graminis f. sp. avenae in parental, F₁, BC₁, F₂ and F₃ generations of three oat crosses.

Generation	Expected Ratio	Observed no. of seedlings		i^2	Probability range
		Susceptible	Resistant		
S : R					
Paul/AC Pinnacle					
Paul	0 : 1	0	22		
AC Pinnacle	1 : 0	16	0		
F ₁	1 : 0	17	0		
BC ₁	1 : 0	23	0		
F ₂	15 : 1	122	9	0.013	0.90 – 0.95
F ₃	55 : 9	160	32	0.873	0.30 – 0.50
Paul/AC Kaufmann					
Paul	0 : 1	0	24		
AC Kaufmann	1 : 0	23	0		
F ₁	1 : 0	21	0		
BC ₁	1 : 0	22	0		
F ₂	15 : 1	205	12	0.089	0.70 – 0.90
F ₃	55 : 9	156	32	1.128	0.20 – 0.30
Paul/OT799					
Paul	0 : 1	0	23		
OT799	1 : 0	21	0		
F ₁	1 : 0	14	0		
BC ₁	1 : 0	19	0		
F ₂	63 : 1	168	3	0.011	0.90 – 0.95
F ₃	967 : 57	159	6	0.831	0.30 – 0.50

INHERITANCE OF RESISTANCE TO THREE PATHOTYPES OF LOOSE AND COVERED SMUT OF OATS

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ABSTRACT

Loose smut (caused by *Ustilago avenae* (Pers.) Rostr) and covered smut (caused by *U. kolleri* Wille.) are important diseases of oat in Canada. Many distinct physiological races of smut have been described, but A13, A60 and A617 represent the most common physiological races found in the prairie regions of western Canada. Breeding for resistance to these three pathotypes is hampered by a lack of information on the inheritance of these diseases. A study was conducted in 1999 to determine the mode of inheritance, number of genes and linkage relationships of the genes conditioning resistance to pathotypes A16, A60 and A617. The results showed that the inheritance of resistance to the three pathotypes was conditioned by either a single recessive gene or by two genes with dominant-recessive epistasis. The results also showed that resistance to the three pathotypes were conditioned by three different sets of genes. The simple inheritance and relatively few number of genes conditioning resistance to A13, A60 and A617 underscore the relative ease with which oat breeders would be able to develop smut resistant cultivars for western Canada using currently available germplasm.

INTRODUCTION

Loose smut (caused by *Ustilago avenae* (Pers.) Rostr) and covered smut (caused by *U. kolleri* Wille.) are major diseases of oat in almost all oat producing regions of the world. Although yield losses from these diseases are low (Thomas and Menzies, 1997), losses as high as 25% or more can occur if fungicides or resistant cultivars are not used (Green, 1968). Most of the cultivars grown in Canada are susceptible, in varying degrees, to both pathogens.

Fungicides can be used to control smuts in susceptible oat cultivars. However, the extensive use of fungicides is costly to farmers and may affect the environment. Use of resistant cultivars provides an effective, economical and environmentally friendly means of mitigating the adverse effects of the two diseases.

Attempts to develop resistant cultivars have caused oat breeders to seek a better understanding of the genetics of the resistance mechanisms, and the relationships among isolates and between isolates and host cultivars. Murphy and Coffman (1961) and Marshall and Shaner (1992) have reviewed most of the early literature on the inheritance of smut resistance in oats. Conclusions drawn from these reviews indicate that there is very little consensus among researchers on the inheritance of smut resistance in oats. Conflicting numbers of genes and types of action of gene ranging from a single dominant or a single

recessive gene to two, three or four dominant independent or dominant epistatic genes have been reported, and in a few cases the researchers have postulated quantitative inheritance for both diseases. In a recent study, Wilcoxson et al (1993) reported that the inheritance of resistance to the Minnesota population of *U. avenae* was multimodal and was conditioned by at least two genes. In almost all of the early studies, mixtures of races or unspecified pathotypes of smuts have been used further contributing to the ambiguity of the published reports.

Many distinct physiological races of smut have been described (Nielsen, 1977), but A13, A60 and A617 represent the most common physiological races found in the prairie regions of western Canada (Menzies and Thomas, 1997). Oat cultivars differ in their reactions to these pathotypes, and greater resistance is usually related to higher grain yield, vigorous growth and heavier test weight. Very little has been published on the inheritance of resistance to specific races of loose and covered smuts of oats, and in particular to the three pathotypes that are commonly found in western Canada. Our objective in this study was therefore to determine the mode of inheritance, number of genes, types of gene action and linkage relationships of the genes conditioning resistance to pathotypes A16, A60 and A617.

MATERIALS AND METHODS

The inheritance of resistance to smuts is very difficult to determine based on individual F_2 plants because of the amount of environmental variance. Even in a homozygous susceptible cultivar, not all inoculated plants will show infection (Marshall and Shaner, 1992). Therefore, to avoid the situation in which disease escapes confound the results of the study, F_2 derived F_3 families ($F_{2:3}$) were used. The $F_{2:3}$ families were derived from two crosses: AC Juniper/OT271 and OT548/AC Juniper. OT271 is an experimental cultivar developed at Agriculture and Agri-Food Canada, Cereal Research Centre, Winnipeg, Manitoba from a cross of W84499/OT237. OT548 was developed by the Svalof-Weibull Seed Company of Sweden from a cross of Sv88293/Dumont. AC Juniper was developed at Agriculture and Agri-Food Canada, Lacombe Research Centre, Lacombe, Alberta from a Dula/Cavel cross. OT271 and OT548 are resistant to pathotypes A13, A60 and A617; AC Juniper is susceptible to the three pathotypes.

The F_1 generation of each cross was grown in a greenhouse at the Lacombe Research Centre. The F_2 generations were grown in a winter nursery at Lincoln, New Zealand during the 1998/99 season. Seeds harvested from randomly selected F_2 plants were used to produce the $F_{2:3}$ families. One hundred eighteen families from the AC Juniper/OT271 cross and 77 families from the OT548/AC Juniper cross were used in the study. Seed from each family was divided into three sets, each set containing 30 seeds/family. Each set was inoculated with aqueous suspension of spores of one of the three pathotypes using the vacuum infiltration method (Nielsen, 1977). The concentration of the inoculum was 1 g L^{-1} . The three sets of seeds were then used to plant three separate but identical hill-plot nurseries; each nursery consisted of all of the $F_{2:3}$ families from the two crosses and was inoculated with spores of one of the three pathotype. The three nurseries were grown adjacent to each other on a Ponoka clay-loam soil (Orthic Thick Black Chernozem, Udic Boroll) at the Lacombe Research Centre in 1999. The land used for the nurseries was kept fallow in the previous summer. Fertilizer was applied in the spring at the time of seedbed preparation. The nurseries were hand-planted (30 seeds/hill) in hills centered ~ 30 cm apart in 6 m long rows. Rows were spaced 50 cm apart. A hill of each parent (30 seeds/hill) was planted at the beginning and end of each row; hence each row contained 2 hills of each

parent and 16 hills of $F_{2:3}$ families.

Disease reaction was recorded when typical symptoms developed on panicles of susceptible plants (~ 4 weeks after panicle emergence or Zadok's growth stages 60-65). For each hill, the number of infected and uninfected panicles were counted and the percent infection was calculated. Thereafter, families were classified as either 'resistant' or 'susceptible'. Families were considered resistant when they showed no visible symptoms of (0%) infection, and susceptible if they had one or more smuted panicles. Since it was difficult to differentiate segregating families from homozygous susceptible families, the two types of families were combined together and regarded as susceptible. The segregation data were fit to expected genetic ratios. Chi-square values were used for testing the goodness of fit to the expected genetic ratios. Chi-square values were considered significant at the $P < 0.05$ level.

RESULTS AND DISCUSSION

Although a high level of infection was obtained in all three nurseries, not all inoculated panicles of even the susceptible parent showed infection. The frequency of infection in the hills planted to AC Juniper averaged 81, 77 and 85% in the A16, A60 and A617 nurseries, respectively.

The results of testing 118 families from the AC Juniper/OT271 cross and 77 families from the OT548/AC Juniper cross are summarized in Table 1. In both crosses, the number of $F_{2:3}$ families in the resistant and susceptible classes fit the 7:9 ratio expected for dihybrid inheritance in the F_3 generation. It would appear that two genes, one dominant and the other recessive, and both with similar disease reaction were conditioning the resistance to pathotype A13 in OT271 and OT548 (Table 1). The number of $F_{2:3}$ families that were resistant and susceptible to A60 in the AC Juniper/OT271 and OT548/AC Juniper crosses gave a good fit to 3:1 ratio expected for monohybrid inheritance in the F_3 generation. It would appear that a single recessive gene was conditioning the resistance of OT271 and OT548 to A60. The $F_{2:3}$ segregation data for pathotype A617 also fitted the 9:7 ratio in the AC Juniper/OT271 cross and the 3:1 ratio in the OT548/AC Juniper cross (Table 1). These results suggested that the resistance of OT271 was based on duplicate genes with dominance and recessive epistasis, and that of OT548 was conditioned by a single recessive gene.

Paired comparisons of disease reaction were made for the $F_{2:3}$ families to determine if a gene that conditioned resistance to one pathotype also conditioned resistance to any of the other two pathotypes. The reactions of the $F_{2:3}$ families to the three pathotypes were not similar indicating that resistance to pathotypes A13, A60 and A617 were controlled by three different sets of genes.

The joint regression of the genes conditioning resistance to A13, A60 and A617 were also examined to determine whether the genes governing the resistance to one pathotype were linked to the genes conditioning resistance to any of the other two pathotypes. To simplify the analysis, families showing resistance to one of the pathotypes were selected, and within this group of resistant families the segregation ratios for the other two pathotypes were determined. If the genes controlling resistance to the three pathotypes were independent, then the frequency of resistant and susceptible families in the selected fraction would be expected to be similar to those observed in the whole cross. On the other hand, segregation ratios that deviate significantly from the ratios that were observed in the unselected population would indicate that the two sets of genes were linked. The

segregation data so examined suggested that the genes conditioning resistance to the three pathotypes were either located on different chromosomes, or if located on the same chromosome, they were at least 50 crossover units apart.

CONCLUSIONS

Information on number of genes, type of gene action and linkage relationship of genes is essential for the development of an efficient breeding strategy for cultivar development. The present study has shown that the inheritance of resistance to smut pathotypes A13, A60 and A617 was conditioned by either a single dominant gene or by two genes with dominant-recessive epistasis. The study also showed that the genes conditioning resistance to the three pathotypes were independent.

The simple inheritance and relatively few number of genes conditioning resistance to A13, A60 and A617 underscore the relative ease with which oat breeders would be able to develop new smut resistant cultivars for western Canada using currently available germplasm.

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Table 1. Segregation for resistance and susceptibility to smut pathotypes A13, A60 and A617 in $F_{2:3}$ families of two oat crosses.

Pathotype	Expected Ratio	Observed no. of seedlings		χ^2	Probability range
		Susceptible	Resistant		
S : R					
AC Juniper/OT271					
A13	9 : 7	64	54	0.121	0.90 – 0.95
A60	3 : 1	90	28	0.045	0.70 – 0.90
A617	9 : 7	67	51	0.001	< 0.95
OT548/AC Juniper					
A13	9 : 7	44	33	0.002	< 0.95
A60	3 : 1	58	19	0.004	< 0.95
A617	9 : 7	56	21	0.108	0.70 – 0.90

EFFECT OF MPTS LITTER EXTRACT ON GERMINATION, GROWTH AND BIOMASS PRODUCTION OF OATS VARIETIES

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ABSTRACT

MPTS are generally grown on field boundaries as well as in social forestry system in temperate to tropical parts of the world. The litter biomass of these WITS dramatically influenced the germination, growth and biomass accumulation of oats seedlings at room temperature (25°C) temperature. The aqueous extract of Mango (*Mangifera indica*) and Subabool (*Leucaena leucocephala*) on higher concentrations were very inhibitory. Light microscopy and measurement of root-shoot revealed that lower concentration (25 g litter biomass/liter water) of MPTS in water stimulate the germination, growth as well as dry biomass production of oats varieties. However, higher concentrations i.e. 50 and 75 g litter biomass/liter water drastically reduce the germination, growth and biomass production of oats varieties.

Out of 8.3 million ha cultivated area in fodder crops; oats being cultivated on about one lakh ha area in India. Although 15 species of Oats are popular in different parts of the world Oats which have their own identity due to moisture and nutrient stress tolerant ability. Therefore, the farmers which have limited/restricted supply of moisture/irrigation prefer to take cultivated as well as wild Oat with different MPTS combinations. Since most MPTS drops 1.5 to 8.0 t/ha litter biomass which otherwise improve the soil physico-chemical properties and serve as nutrient supplement (Lal and Singh 1998). Therefore, some of oats sp. Are traditionally popular in temperate-cum-hilly regions of J&K, H.P. and Utranchal (Photograph). The litter biomass of MPTS as well as Oats itself release innumerable chemical, bio-chemical and microbial reactions and derived number of intermediate compounds. Such natural products/ chemical released in the soil system and finally make available to the crops and MPTS after degradation (Prasad and Subbiah, 1982). The present study was conducted to study the effect of aqueous extract of WTS on the germination, seedling growth and final biomass production of Oats seedlings.

MATERIALS AND METHODS

A laboratory experiment was carried out to study the allelopathic effect of MPTS litter biomass on germination percentage, growth characteristics of roots and shoots and biomass production of Oats seedlings at Indian Grassland and Fodder Research Institute, Jhansi-284 003 India in 1997 and 1998. The aqueous extracts of litter biomass of Mango (*Magifera indica*) and subabool (*Leucaena leucocephala*) were prepared by soaking different quantity i.e. pure water, 25, 50, 75g/L. 75g/L + urea, 75 g/L + soil and field soil to compare in distilled water for 48 hrs. Aqueous extract thus obtained were filtered through whatman No I filter paper. Three varieties of Oats viz. kent, JHO-851 and JHO-822 were used in the text. Twenty seeds of each variety were placed in petri dishes of 10 cm diameter, 1.5 cm height lined with double layer of filter papers. The seeds were moistened with 10 ml of the extract on first day and 5 ml on. subsequent days. Distilled water was

used as control. Normal field soil where Oats generally grow was also used to compare with the treatments, Observations on germination, length of roots, height of shoots and fresh as well as dry biomass accumulation in seedling were recorded on eighth days after sowing.

RESULTS AND DISCUSSION

The litter biomass of Mango (*Mangifera indica*) contain phyto - chemicals such as gossypol, cenebic acid, Benzoic acid, Hepuric acid, caphic acid, benilic acid, chlorogenic acid, parahydroxy benzoic acid and subabool (*Leucaena leucocephala*) litter biomass contain; mimosine, guercetin, galic protocatechuic, ferulic, caffeic, P-coumaric acid etc., These secondary metabolites enhance the germination, elongation of root and shoot and biomass production of seedlings on lower concentration i.e. 25 g. Litter biomass/ litre water by 3 and 2% more germination due to mango and subabool litter extract respectively over control. Similarly shoot height increased by 0.3 and 0.5 cm, root length by 0.6 and 0.9 cm-4 fresh biomass by 88 mg and 105 mg and dry biomass by 9 and 14 mg due to mango and subabool litter biomass on lower concentrate i.e. 25g/ litre. Similar trend in germination 0/6, shoot height, root length, fresh as well as dry biomass production was also observed in JHO-851 and JHO-872 varieties of oats.

However, the higher concentration of extracts i.e. 50 and 75 g lower biomass/ litre water significantly inhibits the germination in all the varieties of oats (Table -1). The inhibition of germination retardate in shoot height, root length, fresh and dry biomass production was observed due to restriction of migration of food ;materials and get deposited on the joints of shoot- root in all the varieties. This inhibition effect was over come when litter biomass mixed with urea and soil. Similar adverse effect of phyto-chemicals of mango (*Mangifera indica*)- i.e. gossypol, cenebic acid, Benzoic acid, Hepuric acid, caphic acid, benilic acid, chlorogenic acid, parahydroxy benzoic acid and subabool (*Leucaena leucocephala*) litter biomass contain; mimosine, guercetin, galic protocatechuic, ferulic, caffeic, P-coumaric. acid etc was also reported by. Lai. (1999) and Lai and Singh. 1999.

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Table I: Effect of aqueous extract of NEPTS fitter biomass on germination, shoot length, root length and production of oats (8 DAS)

Oats Varieties treatments	Germination (%)		Shoot length (cm)		Root length (cm)		Biomass Production (mg)			
	Mango	Subabool	Mango	Subabool	Mango	Subabool	Fresh	Subabool	Dry	Subabool
Kent										
Distt. Water	so	80	7.2	7.2	10.4	10.4	270	270	48	48
25 g/L	83	82	7.5	7.7	11.0	11.3	358	375	57	62
50 g/L	77	75	7.0	6.9	7.2	7.6	219	231	34	36
75 g/L	60	60	5.1	5.2	5.4	6.5	156	168	20	22
75 g + Urea	84	89	7.6	7.8	10.3	10.2	270	285	46	48
75 g + Soil	89	91	7.8	8.0	10.2	10.1	312	308	48	49
Field Soil	82	88	7.4	7.6	10.0	10.0	293	288	48	49
JHO-851										
Distt. Water	78	78	7.0	7.0	11.0	11.0	278	289	48	48
25 g/L	83	87	7.9	7.5	11.7	11.7	342	363	53	57
50 g/L	74	72	6.6	7.0	7.8	7.1	220	238	32	36
75 g/L	62	61	5.1	5.0	5.6	5.3	156	163	19	20
75 g + Urea	85	90	8.1	8.3	10.5	10.7	257	271	48	49
75 g + Soil	91	94	8.1	8.3	10.5	10.6	311	325	51	53
Field Soil	84	83	7.6	5	10.1	10.8	298	305	49	50
JHO-822										
Distt. Water	82	82	7.2	7.2	10.4	10.4	280	280	49	49
25 g/L	83	86	8.2	8.0	11.0	10.6	368	360	55	53
50 g/L	74	71	6.5	6.7	7.0	7.1	235	238	35	34
75 g/L	62	60	5.1	5.2	5.0	5.1	165	162	20	21
75 g + Urea.	91	92	8.1	8.0	8.0	8.1	263	268	47	48
75 g + Soil	92	90	8.2	8.1	10.1	10.4	315	312	50	50
Field Soil	84	85	7.8	7.7	10.2	10.3	300	312	49	50

RESIDUAL EFFECT OF TREE LITTER BIOMASS AND N SOURCES ON YIELD AND QUALITY OF OATS AFTER SORGHUM, SWEETSUDAN AND MAIZE

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ABSTRACT

Application of 75% N through urea + 25% through MPTS litter biomass could influence the production to 10.96% over yield of dry biomass in 1994-95 and 13.08% in 1995-96 in comparison to without N. The increment in oats forage yield due to sole litter biomass of MPTS was 12.93% in 1994-95 and 14.6% in 1995-96 over without N application. Application of pure MPTS litter biomass increased the 29.7% in 1994-95 and 30.69% nitrogen content at harvest over without N application. Maximum N uptake was observed in sole litter biomass, application of MPTS in oats i.e. 31.25 kg in 1994-95 and 33.68kg in 1995-96 over without N application.

Out of 15 existing oats species over one dozen are found and cultivated/utilized in wide range of soil and climatic conditions in India. Although some of the oat species are traditionally popular in temperate-cum hilly tracts of H.P., J. & K., parts of U.P. and other northern states of India for livestock's like horse, cattle, donkey mithun, sheep, goat, poultry etc. Being rainfed tolerant and suitable for arid situations oats become popular in most sub-tropical areas. Being ancient practice for MPTS-oats get attention on the farmer's field due to socio-economic situation and agro-ecological conditions. Due to mixed population of various MPTS innumerable chemical, bio-chemical and microbial reactions naturally taken place and derived number of intermediate compounds. These secondary compounds released from plants may be volatilized from leaves, as leachate, decay of plant litter, decay from sloughed tissue from roots and their exudates (Rizvi and Rizvi 1992). The addition of organic matter through tree litter biomass as one of the major source of nitrogen to the Indian soils which otherwise are generally deficient in nitrogen (Prasad and Subbiah, 1982 and Lal and Singh, 2000).

MATERIALS AND NETHODS

A field experiment was conducted at Research farm of Division of Agronomy, Indian Agricultural Research Institute, New Delhi, during 1994-95 and 1995-96. (I) to study the allelopathic effect of MPTS litter biomass residues on yield of oats and (II) to quantify the application of optimum amount of tree biomass as nutrient supplement and (III) to study the effect of phyto-chemicals of MPTS as well as forage crops viz. Sorghum, sweetsudan and maize on bomass production as well as quality of oats. The experiment was laid out in split-plot design with three replications. The forage crops viz. Sorghum (PC-23), sweetsudan (SSG 59-3) and maize (African tall) were tried in main plot. litter biomass of three MPTS (*Mangifera indica*, L), *Syzygiuni cumini* L skeel and *Leucaena leucocephala*) in sub plot and four source of N (90 kg/ha) for all three crops in sub-sub plots (without N, 75% N through urea + 25% N through litter biomass (7.5q/ha) in case of *Leucaena leucocephala* and 12.5 q/ha in case of *Mangifera indica* and *Sy2ygjum cumini*), 100% N through urea and 100% N through litter biomass (30 q/ha in case of *Leucaena*

leucocephala and 50 q/ha each in case of *Mangifera indica* and *Syzygium cumini*). 'Me oat (Kent) was uniformly sown in the residual fields in both the years of experimentation without any additional N application neither by urea fertilizer nor by litter biomass of MPTS.

The experimental soil was sandy loam, which was poor in organic carbon and N, medium in P and rich in K with slightly alkaline in reaction. The oat crop was sown on Nov. 11, 1994 and Oct. 28, 1995 by tractor operated seed drill to get uniform plant population at 22.5 cm apart. The oat crop was harvested on March 3, 1995 and Feb. 25, 1996 on 75 % particle initiation to meet out higher protein demand.

RESULTS AND DISCUSSION

Fresh biomass production

The residues of urea fertilizer as well as litter biomass application in general increased the fresh forage yield over without N application (Table 1). N 75% through urea + 25% through litter biomass could influence the production to 12.06% over yield of fresh biomass in 1994-95 and 13.95% over fresh biomass yield in 1995-96 in comparison to without N. The increment in yield due to sole litter biomass was 12.7 % in 1994-95 and 16.02% in 1995-96 over without N application i.e. 6.37% in 1994-95 and 10.67% in 1995-96. Litter biomass application of *Mangifera* and *Syzygium* increased the fresh forage yield of oats in both the years of experimentation over *Leucaena* litter biomass Table 1).

The residues of urea fertilizer as well as litter biomass of NPTS application in general increased the dry forage yield over without N (Table 1). 75% N through urea + 25% through litter biomass could influence the production to 10.96% over yield of dry biomass in 1994-95 and 13.09% in 1995-96 in comparison to without N. The increment in yield due to sole litter biomass of MPTS was 12.93% in 1994-95 and 14.6% in 1995-96 over without N application. The least increases in yield was obtained due to sole fertilizer application i.e. 5.62% in 1994-95 and 9.24% in 1995-96 (Table 1). Similar trend was also observed in protein production. The increase in terms of fresh as well as dry forage yield and protein of oats was mainly due to carryover residual effect of treatments under favorable climatic conditions. Such residual effect of fertilizer on oats, which grown after kharif (Summer) crops were also reported by Thakuria. and Rafique (1993), Vashishatha (1993) and Shukla and Lal(1994). Previous crops as well as litter biomass did not influence the fresh as well as dry biomass production of oat at 120 days after sowing.

Nitrogen percent and in uptake (above ground parts)

The residues of urea fertilizer as well as litter biomass application in general increased the nitrogen content of oats on all stages of crop harvest over without N in both the years of experimentation. Application of pure litter biomass increased the 29.7% in 1994-95 and 30.69% nitrogen content at harvest over without N application (Table 2). Similarly application of pure urea increased the N uptake 10.1 kg in 1994-95 and 12.84 kg in 1995-96 over without N application in oat crop. N 75% through urea + 25% through litter biomass could increase N uptake by 24.66 kg in 1994-95 and 27.03 kg in 1995-96 over without N application. Maximum N uptake was observed in sole litter biomass i.e. 31.25 kg in 1994-95 and 33.69 kg in 1995-96 over without N application (Table 2). The results are in conformity with the results of Pradhan and Misra (1994) and Purushotarn et. al. (1995). However, the results revealed that neither kharif crops nor MPTS litter biomass could influence nitrogen uptake in Oats on final harvest at 120 days after sowing (Table 2).

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HIGH SEED RATES INCREASE OAT YIELD WITHOUT REDUCING GRAIN QUALITY

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SUMMARY

The recommended seed rate for oats in Western Australia, as previously determined using older varieties, is lower than the optimum seed rate observed for more recent varieties. The optimum seed rates for these more recent varieties are between 75 and 100 kg ha⁻¹ depending on variety. The quality of the grain was not affected by higher seed rates and was observed to be more responsive to changes in site location and growing condition.

BACKGROUND

In Western Australia oats are regarded as the poor cousin of the other cereals. As a result of this attitude, oats are not grown in a very professional manner. This fact, coupled with poor agronomic knowledge and research, has resulted in oat production remaining low in Western Australia. Much of this production traditionally came from the sheep production areas and was often of reduced quality. In recent years export markets have required grain of higher quality. In order to achieve grain quality of the standard required, growers now have a greater requirement for agronomic information. This research is improving the level of knowledge available to oat growers. Previous oat agronomic research conducted in Western Australia (Anderson and McLean, 1989) showed that the optimum seed rate was between 61 and 77 kg ha⁻¹ depending on variety. However, the varieties tested are no longer the dominant oat varieties and there is a need for the more recent, more widely grown varieties to be similarly tested. In addition the seed rates used by growers in Western Australia are commonly below 60 kg ha⁻¹.

AIM

To understand the effect of seeding rate on yield and quality of currently grown oat varieties in Western Australia.

METHODOLOGY

Varieties were sown at seven sites in a range of environments in Western Australia over three years. Three non-dwarf varieties (Mortlock, Coomallo and Hotham) and three dwarf varieties (Dalyup, Needilup and Wandering) were tested over this period with at least two of each plant type in each trial. These varieties were sown rates of 30, 60, 90, 120, 150 kg ha⁻¹. Trial plots were sown at 18cm spacing by eight rows using experimental cone seeders. The trials were fertilised so that there were no nutrient deficiencies to limit crop growth. All trials were monitored through the season and grain quality assessments (test weight, seed weight) were taken following harvest. Preliminary analysis of the data was conducted using the ASREML (NSW Agriculture) statistical program.

RESULTS AND DISCUSSION

For each site the yields of all varieties tested were standardised by relating the yield of all treatments to the yield of Mortlock at the lowest seed rate of 30 kg ha⁻¹. The results for each variety were then averaged and the yield response to seed rate for each variety was determined. Quadratic curves were then fitted to the data (Figure 1). All varieties showed positive responses to increased seed rates. At all seed rates the dwarf varieties were higher yielding than the non-dwarf varieties. The nature of the response was independent of the plant type, with the dwarf variety Dalyup having similar shaped curves as the non-dwarf varieties Hotham and Mortlock. Whilst the dwarf variety Needilup had a similar shaped curve to the non-dwarf variety Coomallo. These similarities are not related to the maturity of the variety with Hotham being a shorter season variety than both Mortlock and Dalyup.

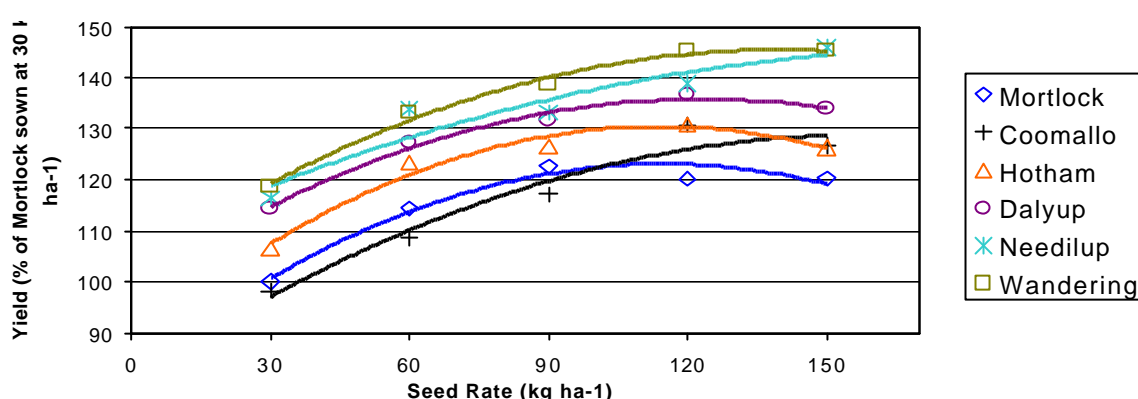


Figure 1. Relationship between relative average yield (percentage of Mortlock sown at 30 kg ha⁻¹) and seed rate (average LSD = 10%).

The optimum seed rate was taken to be the point on each curve at which the grain yield increase for each extra kg of seed was a 5 kg (or 0.23%) increase on the yield of Mortlock when sown at 30 kg ha⁻¹. The optimum seed rates (kg ha⁻¹) for the varieties Mortlock, Coomallo, Hotham, Dalyup, Needilup, and Wandering were 78, 98, 77, 76, 86 and 79 kg ha⁻¹ respectively. These seed rates are higher than those established for the same environment by Anderson and McLean (1989) of 61 to 75 kg ha⁻¹.

There was no relationship observed between grain quality and seed rate (Figures 2 and 3). However, there was no relationship between test weight and seed weight with Coomallo having the highest test weight and lowest seed weight. On the other hand, Dalyup had a low test weight and a low seed weight. Both test weight and grain weight varied considerably with trial site. There was evidence in some trials that a wet winter-spring period, usually associated with higher yields, resulted in lower grain quality (data not shown).

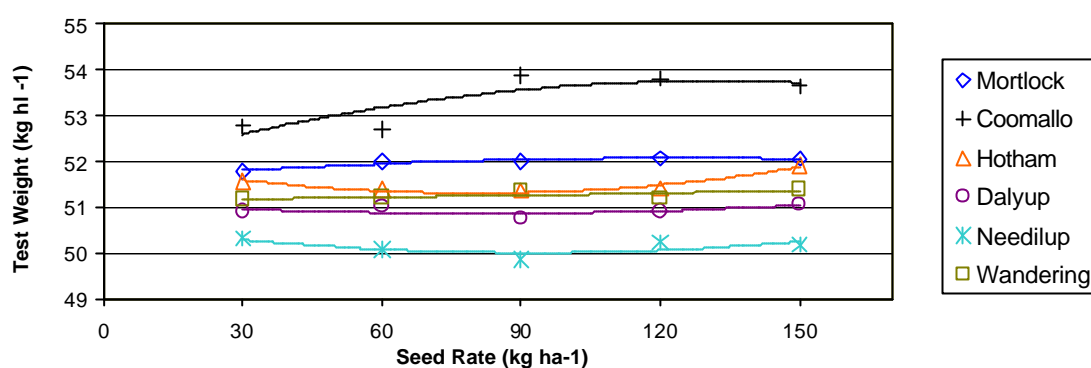


Figure 2. Relationship between test weight and seed rate (average LSD = 2.6 kg hl⁻¹).

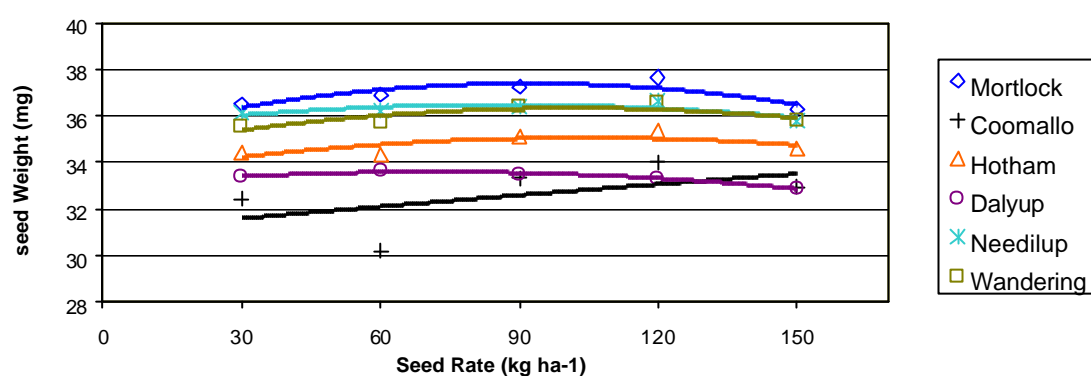


Figure 3. Relationship between grain weight and seed rate (average LSD = 4.2 mg).

CONCLUSIONS

- Currently recommended seed rates, and those often used by growers, are inadequate to reach the optimum yields for the varieties tested in these field trials.
- Seed rates between 75 and 100 kg ha⁻¹, depending on variety, should be used for oats grown in Western Australia.
- Increasing seed rates has very little effect on grain quality.

ACKNOWLEDGMENTS

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EFFECTS OF THE *Dw6* DWARFING GENE ON AGRONOMIC AND GRAIN QUALITY FEATURES OF OATS

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ABSTRACT

The *Dw6* gene has been used successfully to develop lodging resistant oat cultivars in Australia, but to our knowledge no agronomically successful oat cultivars possessing the *Dw6* gene have been developed in Canada or the United States. The contribution of the *Dw6* to yield or other characteristics has not been quantified. The effects of *Dw6* on agronomic and grain quality features of oat were examined at three locations in central Alberta, Canada, in 1997, 1998 and 1999 using seven pairs of dwarf (*Dw6/Dw6*) vs. tall (*dw6/dw6*) near-isogenic lines. The results showed that *Dw6* reduced plant height by an average of 40 cm and significantly increased lodging resistance. *Dw6* also reduced grain yield by ~26.0%, delayed flowering by ~8 days, slowed ripening by ~5 days, and reduced test weight and kernel weight by 7.1 kg hL⁻¹ and 6.4 mg/kernel, respectively. In addition, genotypes possessing the *Dw6* genes had lower oil content compared to their tall counterparts. The effects of *Dw6* on protein content were not consistent across the seven pairs of near-isogenic lines. The reasons for the differences other than height within pairs of near-isogenic lines were not readily discernible from the results of this study. Both linkage and pleiotropy have been proposed as possible causes for the undesirable association of *Dw6* with the agronomic and grain quality features of oat.

INTRODUCTION

Wheat (*Triticum aestivum* L.), barley (*Hordeum vulgare* L.), rice (*Oryza sativa* L.) and sorghum (*Sorghum bicolor* (L.) Moench) breeders have used dwarfing genes to develop lodging resistant cultivars. Lodging resistance allows farmers to increase N-fertilizer rates, apply irrigation if necessary and establish higher yield goals than what is possible with standard height cultivars. Lodging resistance also ensures proper grain filling, minimize harvest loss and help maintain grain quality. Additionally semidwarf cultivars may have higher harvest indices and reduced straw handling and associated field operation requirements, and therefore are ideal for use in intensive crop production systems. The rapid adoption of semidwarf wheat and rice varieties by farmers around the world represents one of the most sweeping agricultural changes in recent times.

With the advent of the *Dw6* dwarfing gene, there has been renewed interest in reducing the height of the oats. However, the use of dwarfing genes has not been as popular or successful in oat as in wheat or rice. Conflicting reports have been obtained by various breeders. Lodging resistant, semi-dwarf oat cultivars have been successfully developed and released for commercial production in Australia (Barr, 1986; Sims, 1963). Similar

attempts to develop semidwarf oat cultivars in Canada using the *Dw6* gene have not been successful. The main objective of the present study was to quantify and characterize the effects of the *Dw6* gene on agronomic and grain quality features of oats.

MATERIALS AND METHODS

Seven pairs of near-isogenic lines carrying the *Dw6/Dw6* and *dw6/dw6* alleles were used in the present study. All seven pairs of near-isogenic lines were developed by the Agriculture and Agri-Food Canada Research Centre, Lacombe, Alberta and released in 2000 (Kibite, in-press). The experiments were conducted at two sites (Lacombe and Breton) in 1997 and at three sites (Lacombe, Breton and Rotation O) in each of 1998 and 1999. A randomized complete block design in split-plot arrangement with four replications was used at each site and in each of the three years. Main-plot treatments consisted of seven genetic backgrounds, and sub-plot treatments consisted of stature (dwarf vs. tall). Sub-plots were four rows, 3 m long with a spacing of 22 cm between rows. Seeding rate was adjusted to 250 viable seeds/m². A self-propelled seeder equipped with six double-disc openers was used to drill the seeds at ~ a 4 cm depth. The outer two openers were dedicated to seeding winter wheat, which was used to separate adjacent sub-plots. Sub-plots were harvested using a Wintersteiger Nursery Master Elite combine. All four rows of each sub-plot were harvested for grain yield and grain quality determination.

Agronomic and grain quality traits measured on a sub-plot basis included number of days to flowering and to maturity, plant height, lodging resistance, grain yield, test weight, kernel weight, protein content and oil content. Data analysis was by analysis of variance (ANOVA) using a model for split-plot design. Initially each experiment was analyzed separately. Thereafter, the data from all experiments were combined and analyzed after confirming that the sub-plot error variances were homogeneous following Bartlett's test for homogeneity of variances (Steele and Torrie, 1980). All ANOVA were calculated using the Proc GLM procedure of the SAS System for Windows™ Release 6.12. For analysis of the combined data, a mixed model was used in which genetic backgrounds, environments (site-years) and replications were considered random effects and stature was considered as a fixed effect. Least significant difference (LSD) was used for mean separation when the F-test from ANOVA was significant ($\alpha \leq 0.05$).

RESULTS AND DISCUSSION

ANOVA for individual experiment showed that there were highly significant ($P \leq 0.01$) differences among the seven genetic backgrounds for all traits measured in each environment. The pooled ANOVA revealed that there were also highly significant differences ($P \leq 0.01$) among environments, genetic backgrounds and stature for all traits. In addition, highly significant ($P \leq 0.01$) stature-by-environment, stature-by-genetic background and stature-by-genetic background-by-environment interaction effects were observed for all traits that were examined in this study. These first- and second-order interaction effects were predominantly due to changes in relative performances rather than changes in the ranking of the dwarf and tall stature genotypes within pairs of isogenic lines since there were only a few cross-over type of interactions within pairs of near-isogenic lines. In other words, in all genetic backgrounds and environments the trends in response to the *Dw6* gene were similar and consistent differing only in degree from environment to environment and among genetic backgrounds.

The seven pairs of near-isogenic lines were developed using a program of single-seed descent that involved eight generations of self-pollination. In each generation of self-pollination heterozygosity was maintained at the *Dw6/dw6* locus while homozygosity was achieved at all other loci. Thus each pair of near-isogenic line traces to a single F_8 plant which in turn traces to a single F_2 plant (Kibite, In-press). In the absence of selection and/or linkage and after 8 generations of self-pollination, two members of a pair of near-isogenic lines will be expected to be very similar to each other, having about 99.6% of their germplasm in common, and differing at only about 0.4% of their loci. Thus they were ideal germplasm for comparing the effects of the *Dw6/Dw6* and *dw6/dw6* alleles.

The average effect of the *Dw6* gene across the seven genetic backgrounds was to delay panicle emergence by about 8 days, to delay maturity by about 5 days, and to reduce plant height and grain yield by 33.8 and 26.0%, respectively. The *Dw6* gene also increased lodging resistance, but reduced test weight by 7.1 kg hL⁻¹, and kernel weight by an average of 6.4 mg/kernel (Table 1).

The reasons for the undesirable effects of the *Dw6* gene are not readily discernible from the information on hand. The reductions in grain yield, test weight and kernel weight, and the delay in flowering and maturity may have been due to the *Dw6* having pleiotropic effects on genes governing these traits. An alternative explanation for the differences other than height within pairs of nearly-isogenic lines may be that the genes governing and/or modifying the above traits were tightly linked to the *Dw6/dw6* locus and were transferred intact (i.e. without recombination) from the *Dw6* and *dw6* donor parents to the respective dwarf and normal height progeny. After 8 generations of self-pollination, and concurrent selection for heterozygosity, a segment of the parental chromosome, about 7.1 centimorgans in length would be expected to remain intact around the *Dw6/dw6* locus. If there is interference from the centromere and/or if the chromosome carrying the *Dw6/dw6* locus is short, the size of the parental-type chromosome segment that would have remained intact after 8 generations of self-pollination will be longer than 7.1 centimorgans. Thus, the observed differences within pairs of near-isogenic lines may also be related to the size of the parental-type chromosome segments that despite 8 generations of self-pollination may have remained intact and were inherited by the dwarf and tall near-isogenic lines.

If pleiotropy is the cause of the undesirable association of *Dw6* with the agronomic and grain quality features of oat, there is very little that plant breeders can do other than using alternate dwarfing genes or height reducing genetic system that do not have deleterious effects. On the other hand, if the undesirable associations are due to linkage, then techniques such as intermating and/or irradiation could be used to break the undesirable linkage blocks and facilitate recombination of genes.

CONCLUSIONS

The *Dw6* gene reduced the height and significantly increased the lodging resistance of the oat genotypes used in this study. However, dwarf plants carrying the *Dw6* allele were significantly inferior to their tall counterparts in grain yield and grain quality features including test weight, kernel weight, protein content and oil content. The *Dw6* gene also delayed flowering by an average of 8 days and maturity by almost 5 days. The undesirable effects of the *Dw6* gene may have been due to pleiotropy and/or linkage.

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Table 1. Genotype x stature and environment x stature interaction effects on grain yield, grain quality and agronomic characteristics on 7 pairs of near-isogenic oat lines.

Genotype	Grain yield			Days to flowering			Days to maturity			Plant height			Lodging score		
	<u>Drf.</u>	<u>Tall</u>	<u>Dif.</u>	<u>Drf.</u>	<u>Tall</u>	<u>Dif.</u>	<u>Drf.</u>	<u>Tall</u>	<u>Dif.</u>	<u>Drf.</u>	<u>Tall</u>	<u>Dif.</u>	<u>Drf.</u>	<u>Tall</u>	<u>Dif.</u>
	(kg-1ha)			(d)			(d)			(cm)			(%)		
LAO517-01	3689	5689	64.8	72.5	63.1	9.4	116.9	113.9	3.0	74	114	-40	0	20	-20
LAO521-02	5885	7611	77.3	72.9	61.8	11.1	135.5	116.4	19.1	73	115	-42	0	10	-10
LAO521-03	5544	7967	69.6	69.9	62.3	7.6	121.6	117.6	4.0	77	115	-38	0	10	-10
LAO524-02	6016	7625	78.9	72.3	63.8	8.5	118.6	115.3	3.3	84	124	-40	0	11	-11
LAO525-01	5418	7460	72.6	75.4	69.3	6.1	122.9	118.0	4.9	86	124	-38	0	18	-18
LAO525-02	4437	6893	64.4	76.3	67.7	8.6	120.5	116.1	4.4	77	119	-42	3	21	-18
LAO525-03	6529	7464	87.5	71.3	66.8	4.5	121.3	118.8	2.5	93	135	-42	2	20	-19
LSD	270			0.8			2.0			2.8			1.2		

	Test weight			Kernel weight			Protein content			Oil content		
	<u>Drf.</u>	<u>Tall</u>	<u>Dif.</u>	<u>Drf.</u>	<u>Tall</u>	<u>Dif.</u>	<u>Drf.</u>	<u>Tall</u>	<u>Dif.</u>	<u>Drf.</u>	<u>Tall</u>	<u>Dif.</u>
	(kg-1hL)			(mg)			(%)			(%)		
LAO517-01	38.8	45.9	-7.1	24.7	30.4	-5.7	12.0	12.3	-0.3	7.5	8.5	-1.0
LAO521-02	44.1	51.6	-7.5	30.4	39.7	-9.3	11.2	12.0	-0.8	6.3	6.5	-0.2
LAO521-03	43.9	52.0	-8.1	34.2	38.5	-4.3	12.1	11.2	0.9	5.7	7.0	-1.3
LAO524-02	45.6	51.9	-6.3	30.9	37.7	-6.8	11.6	12.3	-0.7	5.9	6.3	-0.4
LAO525-01	45.7	51.9	-6.2	31.0	37.2	-6.2	12.6	12.3	0.3	5.5	6.1	-0.6
LAO525-02	40.7	49.1	-8.4	25.4	32.4	-7.0	12.6	12.3	0.3	6.7	7.7	-1.0
LAO525-03	44.7	50.8	-6.1	30.6	36.0	-5.4	11.5	12.1	-0.6	5.9	6.8	-0.9
LSD	0.6			1.1			0.4			0.3		

PLANT EMERGENCE AND GROAT YIELD OF DIRECT SEEDED HULLED OAT, HULLESS OAT AND BARLEY

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ABSTRACT

Hulless oat has gained increased popularity in western Canada because of its excellent nutritional quality in animal feeds, higher test weight compared to hulled oats, and lower production costs compared to hulless barley. Management that aims at increasing seedling emergence may increase groat yields of hulless oats to the same level as hulled oats.

Field experiments were conducted at each of two locations in Alberta, Canada, during the 1997, 1998 and 1999 growing seasons. The results showed that increased seeding rate increased seedling emergence of both hulled and hulless oats. However, the increased seedling emergence did not translate into higher groat yields. Hulless oats showed lower seedling emergence compared to hulled oats at each seeding rate and each seeding depth indicating that a higher seeding rate should be utilized for hulless oat cultivars. Seeding rate and seeding depth affected a number of other variables, such as maturity, that would provide benefits to the producer growing oat. Higher seeding rate and shallow seeding depth should also increase the competitiveness of oat for weed management in direct seeded cropping system.

INTRODUCTION

Oat is grown widely across Western Canada both as a food and a feed grain. The advantage of hulless oat is excellent nutritional quality, less mass and volume for the producer to handle, it is an alternative use to sell into specialty markets, and production costs are lower compared to hulless barley. The disadvantages are poor emergence compared to hulled types, often attributed to an exposed caryopsis (Peltonen-Sainio, 1994), low grain yield (Peltonen-Sainio, 1997) and no general marketing pool. Hulless oat grain yields are measured without the hull, so that realistic comparisons with hulled varieties should be compared after the hulled varieties have been de-hulled. The average groat yield differences between hulled and hulless oat was 10% in Finland, mostly associated with improved seedling emergence (Peltonen-Sainio, 1994). Management that aims at increasing seedling emergence may increase groat yields of hulless oat to the same level of hulled oat.

Briggs and Aytenfisu (1979) have reported interactions with seeding rate, cultivar and seeding date with wheat and recommended that new cultivars should be examined under various production practices to exploit the favorable interactions to maximize grain yield. Similarly, management practices that combine conservation tillage, varieties, seeding rate and seeding depth may improve oat yield in central Alberta.

The objective of this study was to increase plant emergence and groat yield of oat through adjustment of seeding rate and seeding depth in direct seeded systems.

MATERIALS AND METHODS

Trials were conducted at the Fort Vermilion Experimental Farm (58° N) and the Lacombe Research Centre (51° N) in the 1997-1999 growing seasons. A randomized complete block design in a 4 X 3 X 2 factorial arrangement and four replicates was used. Cultivars were two hulled oats (AC Juniper and CDC Pacer), a hullless oat (AC Belmont) and a hullless barley (Falcon). Seeding rates were 150, 250 and 350 seeds m⁻² and were seeded at two depths of 2.5 cm and 6.3 cm. Plot size was 4m X 15m with 30 cm row spacing. Seeds were not treated with a fungicide prior to seeding because of possible phytotoxic effects in the hullless varieties. Weeds were controlled as required each year with herbicides at recommended rates. Plant emergence, yield components, silage yield, groat yield, maturity, and quality characteristics were measured. Data analysis was determined by ANOVA. Separation of means was determined by the least significant difference at P=0.05.

RESULTS AND DISCUSSION

Plant Emergence

Significant effects were detected for Location X Seeding Depth, which indicated that for both the hulled and hullless varieties seedling emergence was 18-42% higher when seeded at 2.5 cm compared to 6.3 cm depth (Table 1). The exception was at Fort Vermilion in 1999 where emergence was similar at both seeding depths. The seedling emergence of AC Juniper and CDC Pacer, hulled oats, decreased 19% and 9%, respectively when seeds were planted at the 6.3 cm depth compared to the 2.5 cm depth (Table 2).

<i>Table 1. Emergence (plants m⁻²) of plants seeded at 2.5 cm and 6.3 cm at Fort Vermilion and Lacombe, Alberta from 1997-1999.</i>							
	Fort Vermilion			Lacombe			Mean
	1997	1998	1999	1997	1998	1999	
Seeding Depth							
2.5 cm	156	140	127	186	135	159	151
6.3 cm	124	121	125	157	95	120	124
L.S.D =	9						4

Table 2. Emergence (plants m^{-2}) of oat and barley varieties at two seeding depths averaged over six site years between 1997-1999 at Fort Vermilion and Lacombe.

	Seeding Depth		Mean
	2.5 cm	6.3 cm	
Hulled Oat			
AC Juniper	177	143	160
CDC Pacer	180	164	172
Hulless Oat			
AC Belmont	116	96	106
Hulless Barley			
Falcon	129	94	111
Mean	151	124	
L.S.D. = 0.8			

Seedling emergence of hulless oat was reduced 17% when seeded at 6.3 cm compared to 2.5 cm. In comparison, hulless barley seedling emergence at 6.3 cm was reduced by 27% from the seedling emergence at 2.5 cm.

Table 3. Emergence of hulled and hulless oat and hulless barley at three seeding rates averaged over six site years between 1997-1999 at Fort Vermilion and Lacombe.

	Seeding Rate (Seeds m^{-2})			Mean
	150	250	350	
Hulled Oat				
AC Juniper	104	159	217	160
CDC Pacer	109	172	234	172
Hulless Oat				
AC Belmont	66	112	140	106
Hulless Barley				
Falcon	67	117	150	111
Mean	87	140	185	
L.S.D. =	9			6

Increasing seeding rate improved the number of seedlings emerged for the hulled oats, hulless oat and hulless barley (Table 3). Emergence of CDC Pacer was 73, 69 and 67% when seeded at 150, 250 and 350 seeds m^{-2} , respectively. The hulless oat, AC Belmont, only had seedling emergence of 44, 45 and 40% when seeded at 150, 250 and 350 seeds m^{-2} , respectively. However, increasing the seeding rate from 150 to 250 seeds m^{-2} resulted in a 55% increase in seedling emergence for hulled oat types and a 72% increase in seedling emergence for the hulless types. The relatively small cost of increased seeding rates would justify higher seeding rates for both the hulled and hulless types.

Groat Yield

Significant cultivar X seeding rate X seeding depth effects were detected for groat yield of oat. Groat yield is a method of factoring the hull content into the yield measurement so that comparisons can be made of hulled and hulless oat. Groat yields were generally similar from both hulled and hulless oat. However, groat yield of hulless oat decreased when seeded at 150 seeds m^{-2} and 6.3 cm soil depth compared to the low seeding rate and the shallower seeding (Table 4). Increasing seeding rate at the 6.3 cm seed depth increased the hulless groat yield significantly, whereas at the shallower seeding depth the groat yield was similar at all seeding rates.

CONCLUSIONS

Increased seeding rate increased seedling establishment in both hulled and hulless oat. The low per cent emergence of the hulless (40%) indicates that higher seeding rates should be utilized, particularly if the seed is placed more than 2.5 cm into moisture. Higher seeding rates increased seedling establishment of hulled oat as well, however, the increased seedling establishment did not translate into higher groat yield. Higher seeding rates would increase the competitiveness of oat for weed management in cropping systems. Seedling emergence of hulless oat was similar to that of hulless barley. Seeding rate and seeding depth affected a number of other variables, such as maturity, that would provide benefits to the producer growing oat.

Table 4. Groat yield of hulless and hulled oat averaged over six locations during 1997-1999.

		Groat Yield ($kg\ ha^{-1}$)			
		150	250	350	Mean
Hulled Oat	Seeding Depth				
AC Juniper	2.5 cm	4810	4970	4930	4910
	6.3 cm	4840	4820	4860	4840
CDC Pacer	2.5 cm	5020	4830	4720	4860
	6.3 cm	4750	4820	4860	4750
Hulless Oat					
AC Belmont	2.5 cm	4600	4720	4600	4640
	6.3 cm	4300	4590	4650	4510
L.S.D. =		190			110

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STUDIES ON THE WINTER HARDINESS AND FROST RESISTANCE OF WINTER OAT VARIETIES

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ABSTRACT

Efforts to cultivate winter oats in Hungary have made little headway due to problems in overwintering. Breeding is aimed at the development of winter oat genotypes with reliable winter hardiness and frost resistance, good yielding ability and agronomic traits. For this purpose the winter hardiness, frost resistance and chemical quality of oat varieties used as crossing partners were determined, in five consecutive winters in the phytotron and field nursery. The results suggest that it should be possible to develop winter oat genotypes with frost resistance approaching that of moderately resistant winter barleys, enabling them to overwinter more reliably under Hungarian conditions.

INTRODUCTION

Spring oats were grown in Hungary on an average of 220 thousand hectares in the 1930s, while the sowing area has now dropped to 50–70 thousand ha. Despite this decline in the sowing area, oats are regarded in Hungary, as elsewhere, as one of the most valuable feeds for brood and young animals and for racehorses. Many baby foods are made from oatflakes or oatmeal and products containing oats are also becoming popular with adults.

Due to their higher yields, efforts to grow winter oats in Hungary and to select frost-resistant types are by no means new. In 1901 Cserhádi sowed seed from Erfurt in Germany, but the crop was destroyed by frost. In 1912 Gyárfás wrote that the frost resistance of winter oats had improved considerably, but was far from perfect. Winter oats developed by Legány yielded 800 kg more per hectare in 1918 and 400 kg more in 1919 than spring oats, but in 1920 frost killed all his lines. The conclusion was that winter oats produced a far higher yield in Hungary than spring oats, but until a completely frost-resistant winter oat variety was available the crop could not be recommended to farmers (Kükedi, 1958; Lelley, 1971).

Winter oats, unlike spring oats, do not continue to grow in chilling temperatures. They have a rather decumbent growth habit, and they are resistant to freezing or 'winter hardy' (Marshall, 1976), an essential requirement for the growing of oats during winter (Marshall and Kolb, 1982). Selection methods using controlled freezing tests in the laboratory have been developed and should be useful in breeding for improved winter hardiness (Marshall and Kolb, 1982; Podyma and Krzeczowska, 1993).

Oat breeding has been underway in the Martonvásár institute since 1993 and is aimed at developing winter oat genotypes with reliable winter hardiness and frost resistance, good yields and disease resistance, and high β -glucane contents, suitable for growing under normal production conditions in Hungary. This paper presents a comparison of the winter hardiness, frost resistance, yield and chemical quality parameters of winter oat varieties obtained from various parts of the world.

MATERIALS AND METHODS

The experiments were carried out in the phytotron and field nursery of the Agricultural Research Institute of the Hungarian Academy of Sciences. Winter oat varieties originating from various oat growing regions of the world, and winter wheat, barley, triticale and durum wheat were used in the experiments.

For the phytotronic frost test, germinated seeds were sown in wooden boxes measuring 42 × 30 × 13 cm. The growth medium was a 3:1:1 mixture of garden soil, humaszka (humus-containing additive) and sand. The plants were grown in nine rows per box, with 20 plants per row. Each box represented one replication and there were four replications in each experiment. The preliminary growth stage lasted for six weeks, with a weekly reduction in temperature, to simulate natural conditions. Preliminary growth was followed by two-phase hardening. The first phase took place in the autumn-winter chamber used for preliminary growth and the temperature fluctuated daily between +3 and –3°C for a week. The second, 4-day hardening phase was carried out in the frost testing chamber at –4°C immediately prior to freezing.

The temperature was gradually reduced and freezing took place at –10 and –12°C for 24 hours. The temperature was then raised by 1°C an hour and after the two-day thawing period the boxes were transferred to growth benches. At the end of the third week of further growth plants which had survived freezing and started developing could be readily distinguished from those which had died. A detailed description of the M29 programme used in the frost testing method was reported by Tischner et al. (1997).

For the field experiments germinated seeds were planted in wooden boxes in mid-October. The boxes were placed on the soil surface in the nursery. In late March plants which had overwintered and begun to develop were clearly distinguishable from those which had died. Winter hardiness was expressed as the percentage of overwintered plants compared to the original plant number.

The evaluation of the experimental data was carried out using one-factor analysis of variance. Differences between means were tested by least significant differences (LSD) ($P=0.05$, 0.01 and 0.001).

RESULTS AND DISCUSSION

The winters were mild in the 5 years tested, so the winter oat varieties suffered no losses in the small-plot field experiments, but the temperature 3–5 cm below the surface, where the tillering node is located, was lower in the boxes on the soil surface than in the ground, so substantial frost damage was inflicted in this treatment (Table 1).

Table 1. Winter hardiness of winter oat varieties in boxes placed on the soil surface or sunk into the soil (overwintering %).

Varieties	1993/94	1994/95		1995/96	1996/97	1997/98	Mean
	F	F	S	F	F	F	
Kenoat	-	85.0	100.0	59.8	42.5	40.8	57.0
Walken	-	76.0	100.0	67.0	49.5	50.8	60.8
Szegedi oszi	68.7	36.3	100.0	28.4	6.2	38.7	35.7
H 84 1121	-	-	-	37.6	7.5	33.1	26.1
Joker	-	-	-	18.8	0.0	22.1	13.6
Gerald	50.0	0	91.2	6.7	0.0	3.7	12.1
Emperon	41.2	2.5	100.0	0.0	0.0	4.6	9.7
Chamois	23.7	1.2	100.0	0.0	0.0	2.3	5.4
Mean	45.9	33.5	98.5	27.3	13.2	24.5	
Bánkúti 1201	87.7	91.3	96.7	82.0	85.0	100.0	89.2

F = boxes placed on the soil surface

S = boxes sunk into the soil

LSD_{5%} = 17.1, LSD_{1%} = 23.9, LSD_{0.1%} = 31.4 between any two values,

LSD_{5%} = 4.9 between means

Compared with the overwintering values of the winter wheat variety Bánkúti 1201 the mean overwintering of the winter oat varieties was significantly lower at the 0.1 % level. Significant differences were also observed between the overwintering values of different varieties. The American oat varieties Kenoat and Walken had better winter hardiness than those bred in the UK, Germany and France. In 1994/1995 winter oat varieties grown in boxes sunk into the soil suffered hardly any losses, like those grown in the small-plot field experiment. In boxes placed on the soil surface the greatest frost damage was suffered by the winter oat populations, the mean overwintering rate of which was less than 30 %.

In order to determine differences in the frost resistance of cereal species testing was carried out at four freezing temperatures in the phytotron (Table 2). Of the winter wheat varieties the results achieved for one variety with excellent (Martonvásári 4), one with moderate (Bánkúti 1201) and one with poor (NS Rana 2) frost resistance are presented. The three winter triticale varieties included are those successfully introduced into cultivation in Hungary in the early 1990s. The three winter durum wheats were bred or introduced by the Martonvásár institute and have the best winter hardiness at present. Two of the winter barleys have acceptable frost resistance, while the third is poor. Two of the winter oat varieties have the best frost resistance known for the species, while the Hungarian-bred variety has moderate resistance.

The difference in frost resistance between the species is clear from the data. In general the frost resistance of winter cereals decreases in the following order: wheat and rye, triticale, durum wheat, barley and oats. This order, based on mean values, may change for certain varieties due to the considerable differences observed within the species, but even the most frost-resistant winter barley and oat varieties had lower survival rates than the poorest winter wheat variety. Using the best oat genotypes for this trait it may prove possible to develop lines with frost resistance equivalent to that of moderately resistant winter barleys.

Table 2. Frost resistance of cereal species (survival %).

Species/Varieties	Freezing temperatures			
	-11°C	-12°C	-13°C	-15°C
Winter wheat Martonvásári 4	-	100.0	100.0	95.4
Bánkúti 1201	-	82.2	60.4	48.1
NS Rana 2	-	69.3	52.0	5.1
Winter triticale Presto	-	94.1	91.6	68.9
Tewo	-	91.6	89.2	61.4
Moniko	-	95.8	86.5	63.9
Winter durum wheat Odmadur 1	-	89.3	83.4	57.7
Odmadur 2	-	70.1	74.8	58.9
Martondur 1	-	88.9	69.2	61.6
Winter barley Kompolti korai	74.6	68.6	40.1	1.3
Kompolti 4	72.7	67.1	50.5	0.0
Rex	-	37.8	18.8	0.0
Winter oats Kenoat	55.5	44.4	17.0	0.0
Walken	41.5	20.9	16.8	0.0
Szegedi oszi	1.8	3.8	1.4	0.0

LSD_{5%} = 17.5

Oats are the richest protein source among the cereals. In addition, increasing attention has been paid in recent years, especially by experts in nutrition and medicine, to the high β -glucane content, which reduces the blood cholesterol level and has a favourable effect on the blood sugar level. It is thus important to investigate whether the ratio of these compounds in winter oat varieties is similar to that in spring varieties.

Under Hungarian conditions the most frost-resistant varieties gave the lowest yields, though their protein and β -glucane contents were above-average (Table 3). In the three years examined the winter oats gave higher yields than the spring varieties in two years and a lower yield in one. The protein and β -glucane contents were slightly higher in the spring oat varieties than in the winter oats, though the chemical quality of certain winter varieties was practically equal to that of the spring oats, indicating that winter oat varieties could also be suitable for human consumption. No correlation was found between chemical quality and winter hardiness for the varieties examined, suggesting that it should be possible to develop winter-hardy genotypes with good chemical quality.

Table 3. Phytotronic frost resistance, yield and chemical quality of winter oat varieties.

Varieties	Phytotronic frost resistance (survival %)		Yield (kg/plot)			Protein %	β-glucane %
	-10°C	-12°C	1998	1999	2000		
Winter oats							
Kenoat	96.0	85.8	2.99	3.31	3.81	14.5	3.72
Szegedi oszi	50.0	27.1	3.60	3.49	4.69	13.6	4.43
Gerald	16.0	6.0	3.76	4.06	4.01	12.8	3.44
H 84 1121	2.0	2.0	3.69	4.47	4.28	12.7	3.95
Spring oats							
Bakonyalja	-	-	3.68	4.39	3.10	13.8	4.24
GK Pillangó	-	-	3.13	4.32	3.02	14.2	5.03
LSD _{5%}	18.4	17.1	0.31	0.32	0.36	1.17	0.34

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OAT YIELD AND QUALITY: EFFECTS OF NITROGEN FERTILIZATION AND SEEDING RATE

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ABSTRACT

Increased demand for high-quality oats (*Avena sativa* L.) from western Canada has increased the prominence of oats in today's cropping systems, and thus the need for management strategies to optimize oat yield and quality. A three-year study was initiated to determine the impact of nitrogen rate and seeding rate on oat yield and quality. Over three years, from 1998 to 2000, 18 site years of data has been collect in two Canadian provinces, Saskatchewan and Manitoba, containing 27 to 47 kg NO₃⁻-N ha⁻¹ to 60 cm. At each site, a randomized complete block design consisting of four replicates of a factorial combination of five nitrogen rates (15, 30, 60, 90, 120 kg N ha⁻¹) and five seeding rates (150, 225, 300, 375, 450 plants m⁻²) was established using AC Assiniboia or CDC Pacer. Increasing seeding rate consistently increased both plant and panicle density. Increasing the seeding rate increased yield when competition from wild oats (*Avena Fatua* L.) occurred or poor crop emergence existed. When good crop emergence occurred and wild oats were not present in the field seeding rate had no affect on yield. The responses to N varied among sites. In the first two years of the study, maximum grain yields were achieved at N rates of 30 to 60 kg N ha⁻¹ at four sites and at 120 kg N ha⁻¹ at one site; additional N did not further increase yield. In contrast, at three of eleven sites, low to moderate rates of applied N produced greater yields than higher rates of N. At the remaining three sites, significant interactions between nitrogen rate and seeding date were evident. Increasing the nitrogen rate tended to reduce test weight. The impacts of seeding rate and N rate on the % thin kernels and thousand kernel weight appear less consistent.

COMPARATIVE PERFORMANCE OF OATS VARIETIES ON ROW SHAPE AND DIRECTION ON SALT-AFFECTED SOILS IN SUB-TROPICAL INDIA

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ABSTRACT

An investigation was carried out during 1997-98 and 1998-99 to know the comparative performance of Kent, JHO-851 and JHO-822 varieties of oats on different row shape as well as directions on sodic soils in Indo-Gangatic plains. The germination, green forage, dry biomass and protein production of oats varieties was estimated. The germination of oats varieties was significantly increased when sown as double rows on raised beds in north west direction over other treatments. The similar trend in production of green as well as dry biomass and protein was observed in both the years of experimentation. The existing check var. Oats kent was still found superior over JHO-851 and JHO-822 under sodic soil conditions of Uttar Pradesh.

Key words: Oats, row shape, row direction, sodic soils, sub-tropics, growth, yield, quality

About 8.3 million ha cultivated area of India is under fodder crops and there is hardly any scope of expansion due to high pressure on arable land for food and commercial crops. Under such circumstances the option left for the farmers to cultivate the problem soils that are pre-dominantly found in Indo-Gangatic plains. Since these soils differ from normal soils and show wide variation in morphological features, physical properties and chemical characteristics from one region to another (Abrol and Dhurvanarayan, 1990). Although in India about 8.5 million ha area is affected due to salinity problem in crop root zone and this problem has become more acute with expanding irrigation sources (Agrawal, et.al, 1979). About 8 lakh ha of salt-affected soils are spread in to 23 districts in central U.P. due to acute sodicity impediment of drainage and shortage of water, vast area is rendered uncultivated as wasteland. These lands are highly fertile but less productive because of the serious limitation imposed by high concentration of sodic salt, poor drainage and presence of impervious hard layers beneath one meter depth from the surface (Lal, 1997).

MATERIALS AND METHODS

A field experiment was conducted on aquack and aric netrualtalf which consist of ustalf, ochrepts and orthants as per seventh genesis classification (Boul, et. al. 1980) of inceptisols of central U.P. at NARP center, Daleepnagar of C.S.A. University of Agricultural and Technology, Kanpur for two years during 1998 and 1999. The soil of the experimental site was low in organic carbon and nitrogen, medium in phosphorus and high in potassium. The physico-chemical properties of upper soil layer (0- 15 cm) was 53% sand, 28% silt and 19% clay with < 0. 1 % organic carbon, >40 ESP, > 10 pH in 1:2 suspension and 2.23 dsm-1, electrical conductivity on 25 °C temperature. Therefore, these soils rated as saline -sodic soils of Indo-Gangatic plains of alluvium. Since these soils are not suitable for commercial as well as food crops due to presence of hard pan of Ca Co₃ and excess amount of salts in the root zone. The experiment was laid out in split-plot design with four replications. The treatments consisted of three row shapes viz. flat sowing, raised bund

20 cm single row sowing and raised bund 20 cm double row sowing, three row directions viz. North-East, North-South and North-West. Three cultivated varieties viz. Kent, JHO-851 and JHO-822 were sown on these row shape and directions. The sowing of experiment was done in the last week of Oct. 1997 and 1998. After proper establishment in the saline root zone conditions, the periodic plant samples were collected for protein estimation (Noroziamesky, et. al, 1974). A basal dose of 40 Kg N, 60 Kg P₂O₅ and 60 Kg K₂O/ha were applied at the sowing time. Remaining 40 Kg N was top-dressed after crown root initiation (30 DAS). The irrigations were applied at 30 days interval to saturate the root zone for crop demand. The chemical analysis of water indicated pH values 7.8 to 8.6, E.C. 0.56 to 1.45 dsm-1 and SAR 1.89 to 6.03. On the basis of these characteristics the irrigation water grouped in to S1C2 to S2C3 class (Ramamurthy, 1964).

RESULTS AND DISCUSSION

Germination of oats varieties was significantly increased (85 and 86%) when sowing was done on Northwest direction in both the years (1997-98 and 1998-99) of investigations respectively over North-east (82%) and North-South (81 and 81.5%) in the study years (Table-1). Similarly germination of oats increased by 3.5 and 4.7% in the study years when the crop was sown as single row raised bund over flat sowing (Table-1). Similar trend in enhancement of germination was observed in double row sowing over flat sowing. However, non-significant difference in germination % of oats varieties was observed.

Kent variety of oats could produce maximum green (235 and 239 q/ha) as well as dry (44 and 45 q/ha) forage yield in both the years of experimentation respectively. Like wise the germination of oats varieties, North-West direction of row could produce higher green (247 and 249 q/ha) and dry (46 and 49 q/ha) in 1997-98 and 1998-99 respectively. The yield level was significantly superior over North-East direction of sowing. However, non-significant difference among North-South and North-West was observed in terms of green as well as dry forage yield production (Table-1).

Double row sowing on raised bund could produce 30.6 and 34.6% higher green fodder and 68.9 and 67.7% higher dry fodder over flat sowing in 1997-98 and 1998-99 respectively. While single row sowing on raised bund could produce only 22 and 25% higher green fodder and 49 and 50% higher dry fodder over flat sowing in the respective years of experimentation (Table-1). Oats variety i.e. JHO-851 and JHO-822 could maintain 0.02 unit more nitrogen % on 30, 60 days after sowing in both the years of experimentation (1997-98 and 1998-99). However, on later stages of crop growth reverse trend in N% was observed i.e. Kent variety maintain 1.08% N in both the years of experimentation on harvest, which was 0.01 unit more in comparison to JHO-851 as well as JHO-822 (Table-2). Therefore, the protein production was significantly higher in Kent i.e. 4.75 and 4.81 q/ha in 1997-98 and 1998-99 in comparison to JHO-851 (4.17 and 4.28) and JHO-822 (3.95 and 3.85 q/ha) respectively.

North-West direction of sowing could maintain enrichment in N % on all stages of crop growth as well as protein production on harvest (4.9 and 5.29 q/ha) which was higher than North-East (4.44 and 4.54 q/ha) and North-South (4.49 and 4.69 q/ha) in the respective years of investigations. Similarly double row sowing on raised bunds could maintain more enrichment of N% as well as protein production on harvest (5.34 and 5.07 q/ha) in 1997-98 and 1998-99 respectively which is much superior over flat sowing (3.10 and 2.99 q/ha) in the respective years of investigations. Similarly single row sowing on raised bund could

maintain more N % on all stages of crop growth as well as protein production on harvest in comparison to flat sowing (Table-2). These suggest that Kent variety of oats should be sown on sodic soils on North-West direction on raised bund with double row sowing.

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Table-1 Effect of row shape and direction on germination, fresh and dry forage yield of oats varieties

Treatments	Germination %		Forage yield (q/ha)			
			Fresh		Dry	
	1997-98	1998-99	1997-98	1997-99	1997-98	1998-99
<i>Varieties</i>						
Kent	82.0	84.0	235	239	44.0	45.0
JHO-851	83.0	83.7	228	225	39.0	40.0
JHO-822	83.0	83.5	201	202	37.0	36.0
C.D. 5%	NS	NS	20.0	21.0	3.2	3.2
<i>Row direction</i>						
North-East	82.0	82.0	202	205	41.5	42.5
North-South	81.0	81.6	230	235	42.0	43.5
North-West	85.0	86.0	247	249	46.0	49.0
C.D. 5%	0.45	0.45	20.2	18.5	3.4	3.3
<i>Row shape</i>						
Flat	78.0	77.0	188	182	29.0	28.0
Raised bund 20cm single row	81.5	81.7	230	228	43.0	42.0
Raised bund 20cm double row	82.0	82.6	248	245	49.0	47.0
C.D. 5%	0.56	0.57	20.0	18.0	3.5	3.1

Table 2 Effect of row direction and row shape on nitrogen % and protein production (q/ha) of oat varieties

Treatments	1997-98				1998-99				Protein (q/ha)	
Prod.	N% (DAS)				N% (DAS)					
	30	60	90	120	30	60	90	120	1 st Yr	2 nd Yr
<i>Varieties</i>										
Kent	1.23	1.19	1.10	1.08	1.24	1.20	1.10	1.08	4.75	4.81
JHO-851	1.25	1.21	1.11	1.07	1.26	1.22	1.11	1.07	4.17	4.28
JHO-822	1.25	1.21	1.11	1.07	1.26	1.22	1.10	1.07	3.95	3.85
C.D. 5%	0.001	0.005	0.006	0.005	0.005	0.005	0.005	0.005	0.46	0.23
<i>Row direction</i>										
North-East	1.22	1.18	1.10	1.07	1.21	1.20	1.10	1.07	4.44	4.54
North-South	1.23	1.19	1.10	1.07	1.21	1.19	1.09	1.08	4.49	4.69
North-West	1.22	1.18	1.11	1.08	1.23	1.19	1.09	1.08	4.90	5.29
C.D. 5%	NS	NS	NS	NS	NS	NS	NS	NS	0.45	0.42
<i>Row shape</i>										
Flat	1.23	1.19	1.10	1.07	1.23	1.19	1.10	1.07	3.10	2.99
Raised bund 20 cm single row	1.24	1.21	1.12	1.08	1.24	1.20	1.11	1.08	4.60	4.53
Raised bund 20 cm single row	1.25	1.22	1.12	1.09	1.24	1.21	1.12	1.08	5.34	5.07
C.D. 5%	0.006	0.005	0.005	0.005	0.004	0.004	0.004	0.004	0.54	0.52

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ABSTRACT

In the UK the oat crop is attractive to growers, as it is a good break crop, which competes well agronomically with the alternative crops such as barley, pulses or oilseeds. However the limiting factor to increasing the area under production is the lack of sustainable markets. Since 1995 both Government and commercial companies, have supported projects aimed at identifying new markets, within a coordinated approach.

The OATEC project which reports in 2001, will report in 2001 on the feasibility of an advanced oat fractionation plant to be sited in the Marches area of the UK, including an assessment of fractionation techniques and their associated markets.

INNOVATION investigated genotypic, husbandry and environmental effects on grain composition, and an assessment of the functionality of components for food use

AFENO will investigate the role of naked oats in avian diets.

THE OATEC PROJECT

Oatec will produce a feasibility study on the construction of a high-technology oat processing plant within the Marches area of the UK. The project was awarded funding under the European Union's Objective 5b scheme, which is directed at sustaining rural populations in areas designated to be suffering from social deprivation. All funding must be matched by commercial sponsors on an equal basis and the project was therefore supported by the Countryside Agency who had funded a precursor study, Semundo Ltd, a UK breeding and crop development company with interests in oats, The Superioat Co. Ltd, who research, develop and market naked oats, and Shropshire County Council in whose region the project is taking place.

The project was split into two phases

Phase 1

Phase 1 objectives were defined in order to give an overview on the feasibility of a European plant and its main conclusions were reported in June 1997:

High technology oat processing facilities existed, but there were also opportunities for innovative new technologies, as well as some existing 'low' technology processes. Therefore process technology was not a barrier to the construction of a plant. However, the most appropriate technology for processing UK winter oats would not be known until products most suitable for the European market had been identified.

Whilst advances had been made in identifying the various existing commercial enterprises concentrating on industrial oat processing there was evidence that other plants might exist in Europe and elsewhere which could affect the viability of a UK plant.

Some high technology oat products produced in North America were being sold into the European market, and other products were undergoing full US registration for their pharmaceutical properties. This proved that there were real markets for new products, but did not quantify whether the European market could sustain its own production facility.

Companies already involved in the new processes wished to collaborate with *Oatec* as they did not rule out the possibility of a UK located plant being built in the future.

The UK winter sown oat has a significantly different nutrient profile to the spring sown North American oat which may offer unique opportunities to extract distinct actives at competitive costs. Significant variations had also been noted between varieties, and considerable environmental effects on certain nutrients were apparent.

Oatec was becoming internationally known as a research group that had extensive knowledge on industrial oat processing, and companies were approaching it for further information thus increasing the interest in a new plant.

A large UK pharmaceutical company, Boots plc had indicated a strong interest in becoming involved in Phase 2 to assess the role of oats in their cosmetic lines.

Phase 2

Phase 2 started in 1997 and is scheduled to produce a detailed feasibility study on the siting of a high technology oat processing plant in the UK in 2001.

The nine areas to be studied are as follows:

Raw Material: Initial results from Phase 1 have indicated significant varietal differences in β -glucan, oil, and protein in winter-sown oats and it is clear there are also environmental and yearly effects. Phase 2 is assessing the 1997, 1998, 1999 and 2000 oat crops to determine the most suitable quality oats to be used in a UK industrial process, and to determine the degree of variation within commercial crops and their affect of processing efficiency and product quality.

Product Assessment: Phase 1 had identified a number of high technology products currently being manufactured and some of these had been offered to *Oatec* for product assessment. This gave a reasonable range of products, but it was felt necessary to undertake the manufacture of additional oat based products that were thought to have commercial potential.

Process Design: To consider potential processes and recommend an appropriate design taking into account quality aspects of UK grown oats and the potential product market. Oatec had visited a number of process plants in Phase 1, mainly in Canada and America, but it was recognised that other facilities existed in Scandinavia, and these were visited during Phase 2.

Markets: The commercial feasibility of the proposed new plant would largely depend upon the size and value of the European market. Initial assessments had indicated that there was an inherent interest in the cosmetic, pharmaceutical and functional foods in the form of 'natural' products from oats, but few of the companies contacted had any degree of knowledge about oat products. It was also clear that current suppliers were concentrating on the high value, low volume markets, whereas it was felt important to be able to test the price-volume ratios across the range from lower priced products it is hoped that this information will lead to a clearer understanding of the potential market for oats within Europe.

Supply Chain: A prime factor in determining the efficiency of plant operation centres on the homogeneous nature of the raw material presented to the process. Phase 2 will assess the suitability of both conventional husked oats and naked oats for the process, and recommend a range of agronomic practices to maximise the raw materials' quality profile. It is envisaged that the proposed plant will wish to operate under full traceability for its raw material, and may wish to adopt a HACCP (Hazard Analysis Critical Control Point) system. Phase 2 will recommend a suitable closed loop supply infrastructure.

Location of Plant: A number of factors will be considered in recommending site location, including local infrastructure, environmental considerations, grants available, proximity of a skilled labour force, and supply logistics to the plant

Social Impact: Since Oatec is funded under an EU Objective 5b scheme, which requires the maintenance of a rural infrastructure, the project will determine the number and type of jobs likely to be created both directly and indirectly by the proposed plant.

Finance: To determine potential sources of finance for a plant.

Cosmetic Assessment: The project partner Boots plc will undertake to screen products for their suitability for use in cosmetics and skin care products.

A number of other activities are included in the project, such as an ongoing patent monitor, which will assist in assessing the rate of change within the industry. Much of the project's success lies in its interaction with commercial companies and it has continued to attend further conferences in order to gain increased publicity.

Whilst the formal termination of the project will result in the publication of a feasibility study in 2001, a major European company has now joined with OATEC, to assess specific market sectors with the view to construct a bespoke processing plant.

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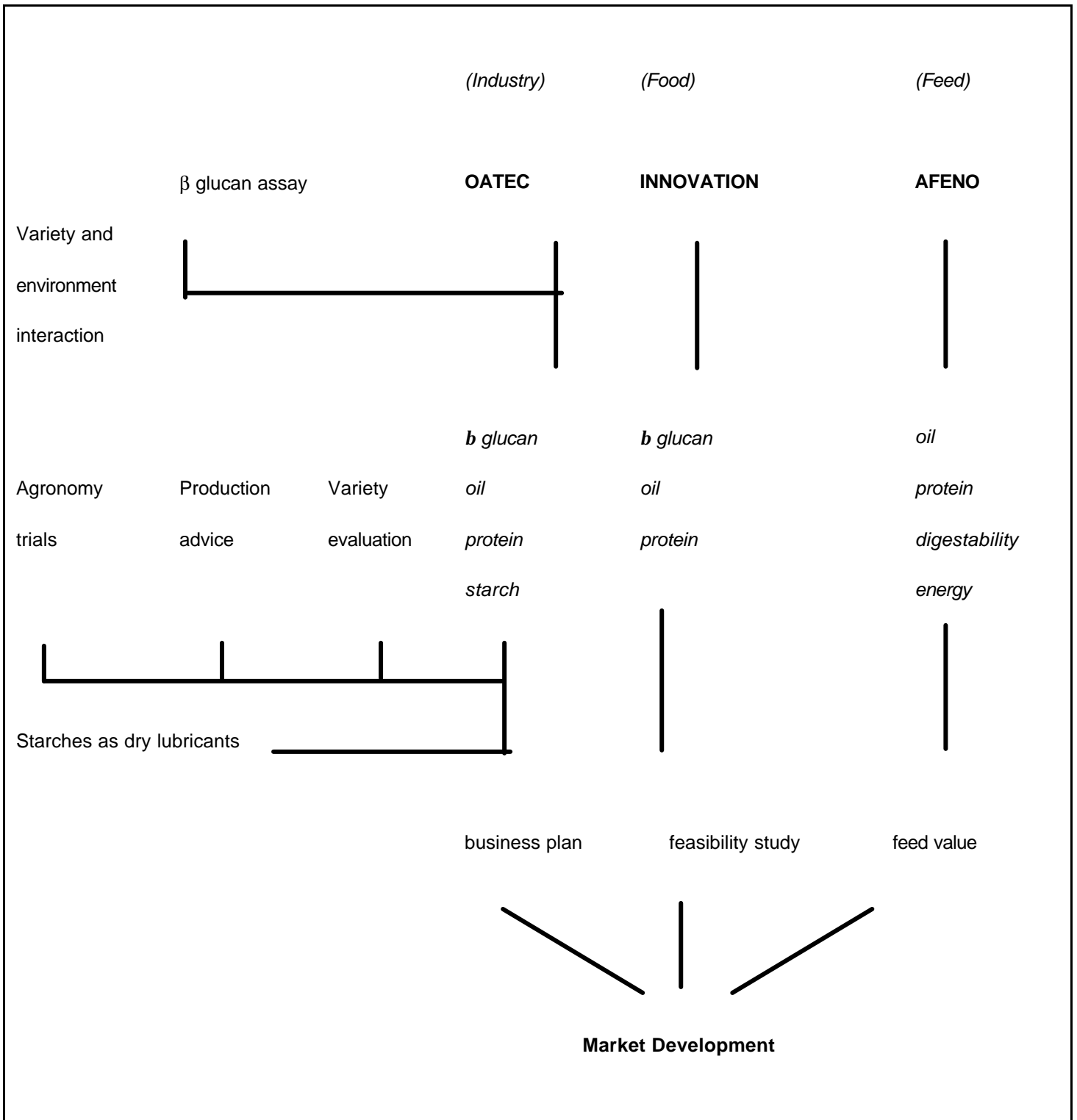
ABSTRACT

The OATEC project which reports in 2001, will report in 2001 on the feasibility of an advanced oat fractionation plant to be sited in the Marches area of the UK, including an assessment of fractionation techniques and their associated markets

Phase I concluded that advanced oat fractionation was feasible, and oat products derived from advanced processes were now being successfully marketed. Phase II will focus on the potential market opportunities available to a UK plant, and the design of a suitable fractionation plant to produce sufficient product.

As part of the project OATEC is researching industry attitudes to advanced fractionation, and a questionnaire will be distributed to all conference delegates as part of this exercise.

Oat Research Strategy In UK



Objectives for Oatec:

Feasibility study of an extraction plant and its design, including impact on employment;
Development of oats as an industrial crop in the 'Marches' region of England and Wales.

Objectives for Innovation:

Evaluation of milling and fractionation processes for extraction of components;
Investigation of genotypic, husbandry and environmental effects on grain composition;
Examination of the effects of grain composition on milling and fractionation efficiency;
Characterisation of structure and properties of components;
Assessment of the functionality of components for food use.

Objectives for Afeno:

Assessment of agronomic effects on grain quality and yield for naked oats;
Evaluation of nutritional properties of naked oat for broilers and turkeys;
Characterise meat quality derived from high-oat diets;
Assess feasibility of an industry-led short chain production contract.

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