Vernon Burras

PROCEEDINGS OF THE FOURTH INTERNATIONAL OAT CONFERENCE

VOLUME III

GENERAL SESSIONS

Edited by: Andrew R. Barr, Robyn J. McLean, John D. Oates,
Glenn Roberts, John Rose, Ken Saint and Suzanne Tasker.

October 20th and 23rd, 1992

Hilton International Hotel

Adelaide, South Australia

Hosted and organised by the Fourth International Oat Conference Inc.
on behalf of the International Oat Conference Committee.

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PREFACE

The Fourth International Oat Conference, of which these are the Proceedings, was held in Adelaide from 19th – 23rd October, 1992.

In the business meeting at the close of the Third International Oat Conference held at Lund, Sweden in 1988, the International Organising Committee under the chairmanship of Dr Robert Forsberg was elected to organise the next conference. Adelaide was chosen as the venue. The final date of the Fourth Conference and the outline of the program, including selection of the main speakers, were suggested by the International Committee but local arrangements and finalisation of the program were delegated to a local sub-committee comprising staff from the South Australian Department of Agriculture, the Australian Barley Board, the Uncle Tobys Company and the Australian Oat Breeders Group. I wish to record my appreciation of the work done by this local committee in assuming various organisational responsibilities over the three years prior to the conference.

The Conference was organised into two special symposia ("The Changing Role of Oats in Human and Animal Nutrition", "Wild Oats in World Agriculture"), two days of general sessions (Crop Protection, Molecular Biology, Breeding Methodology, Economics and Marketing, Cytogenetics/Genetics, Physiology, Forage) and a field tour of the Lower North district of South Australia.

The Fourth International Oat Conference acknowledges the generous assistance from the following sponsors:

South Australian Department of Agriculture

Crawford Agricultural Trust

Australian Tourist Commission Convention Assistance Scheme

Qantas

Australian International Development Aid Board

Ansett Australia

Australian Barley Board (Oat Growers Pool)

The Uncle Tobys Company

Grains Research and Development Corporation

In addition, **The Quaker Oats Company** is a sustaining member of the IOC

PREFACE continued

Special thanks to:

Sue Tasker, Tom Hoppo, and Dean Wardle: for managing the oat breeding program during conference organising.

Geof Palmer: for efficiently managing finances as Treasurer

Dick Medd: for help, advice and encouragement in all aspects of the Wild Oats in World Agriculture Symposium.

Elisabeth Eaton: Principal of the Conference Secretariat (Festival City Conventions) for outstanding service and attention to detail.

Alan Dube: arranging sponsorship for delegates from Bulgaria, India, Czechoslovakia and Poland.

David Sparrow: liaison with the Crawford Agricultural Trust and Southern Foods to assist delegates from Bulgaria and Poland

From the outset there was a firm commitment to make the Conference as international as possible and every effort was made to provide a program that would attract participants from all parts of the world, from a wide range of scientific disciplines and the oat industry.

At the time of printing 100 full time delegates, 35 part-time, 2 students and 30 accompanying persons from 22 countries were registered.

I wish the next International Oat Conference every success in advancing the knowledge, production and quality of the oat crop.

Andrew R Barr
Chairman
Fourth International Oat Conference, Inc.

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Oat Breeding, Biotechnology and Value-Added Traits

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Introduction

Oat breeding has a proven record of developing high yielding, agronomically suitable varieties for a wide range of geographic and climatic areas. Consequently, producers, processors and end-users have been able to utilize and profit from the use of these varieties. However, recognized scientists and business persons see the future more in terms of value-added grain as opposed to the traditional commodity[1]. This paper reviews the opportunities that value-added traits, biotechnology and breeding may have for oats and some of the hazards that will have to be negotiated to reach a given objective.

Oats production in the US in 1991 was 3,500,000 metric tons with a farm-gate value of US$310,000,000. It is estimated that 1,300,000 metric tons were milled with an end-user value of US$358,000,000. The remaining production was used as feed, seed and industrial ingredients with an end-user value of an additional US$600,000,000. The end-user market should be the target of value-added traits in oats.

In the early 1960s, The Quaker Oats Company had an objective to develop oat varieties with a protein level of 18-20%. The business goal was to be able to label finished product as high protein and to advertise such in the market place. The objective was reached in the mid-1970s with the release of high protein varieties such as Dal, Hinoat, Otee, Goodland and others.

Two things occurred that prevented taking advantage of this trait in the market place. First, the United States Food and Drug Administration (USFDA) changed the label standards such that nutritional components had to be expressed in terms of percent Recommended Daily Allowance (RDA) and in grams per serving instead of as a simple percentage of the product. The regulations made it virtually impossible to differentiate between 15% and 17% protein. Initially, the consuming public found it very confusing and the marketing advantage was totally removed. Secondly, the high protein varieties did not command a premium in the grain markets to justify the identity-preserved handling that was required. Today, the USFDA regulations are undergoing changes which may give the oat industry the opportunity to make a nutritional content claim that oats are a good source of protein.

The preceding history clearly illustrates that value-added traits can be incorporated into oats by conventional plant breeding. However, it also shows that a rather simple rule change coupled with the market's inability to pay for the trait can foil the very best of plans. The expectations for the use of biotechnology in developing value-added traits have been widely publicised in the media. Unfortunately, the perceived risks of biotechnology have received more headlines than the real benefits. In May, 1992, the USFDA announced that genetically engineered food products will not receive separate or special regulatory attention[5]. This issue will ultimately be resolved in the courts.

Recognizing that government regulations, environmental groups, the media and consumer groups will influence the use of biotechnologically assisted development of value-added traits, a clear definition of the benefits of value-added traits must lead the challenge. Goss[3] indicates that the benefits of a value-added trait will be recognized if it results in a cost savings to the end user, if improved products are derived from it or if a unique product can be created from it.

Value Adding

Value-added traits are not new and in fact, have been used since recorded history. Fermentation of specialty grains by early man resulted in beer and tasty bread products.

Today, endosperm mutants of corn (i.e. Wx and Ae) are used to produce distinctive starches, sweeteners and alcohol for use in food and industrial products. The current interest in low-fat diets has stimulated the development of fat substitutes derived from grains such as corn and oats. Hard white winter wheat varieties have been developed at Kansas State University for use in bread which results in a whole grain product that is bright, mild flavored and requires up to 50% less sugar, thus reducing ingredient costs[4].

According to Burrows[1], in cool climates where corn and soybeans are not grown, naked seeded oats offer pig and poultry farmers a high quality feed that can be grown locally to avoid high transportation costs of feed ingredients. Frey (pers. comm.,1992), in cooperation with breeders in Norway, is developing oats that are so high in oil that they can be grown as an oil crop in northern climates where soybeans cannot be grown. Winter durums are being developed at Oregon State University that will yield as well as the soft white winter wheats that Oregon and Washington are famous for producing. Herbicide resistant corn hybrids, high-solids tomatoes, food-grade yellow corn hybrids, and soybeans with specialty proteins and oils are fast approaching the market place. Obviously, many more examples can be mentioned to illustrate that the use of value-added traits is not new and that the future will be interesting and exciting.

There are at least two risks that these products face. One is the chance that a value-added trait in a given species could become very popular and quantities could become so large that it could become a commodity itself and the required premium price would disappear. Secondly, some form of protection must be in place to justify the research and development costs. Cutler[2] has surveyed producers who are willing to grow specialty grains and handle them separately in order to receive a premium price which compensates them for their efforts. It seems that their opportunities are best, if they can deal directly with a processor or their own cooperative or be a part of a totally vertically integrated system. In order to justify premium prices, processors or end-users need to have a unique methodology which differentiates their product from others in the market place.

This methodology or trade secret may, in fact, be the end-users' best protection. However, the opportunity to patent genetically engineered plants and plant products offers protection much more extensive than Plant Variety Protection (PVP). Patent protection offers companies and individuals the justification to invest in value-added trait research and development. The possibility of restricted germplasm exchange due to patent rights is a major issue. However, Goss[3] states that "it is Du Pont's opinion that patents will be granted for plants expressing novel or enhanced quality traits, but in most instances the claims will be drawn to the specific germplasm or nucleotide sequences rather than broad claims for the quality trait itself. This will provide companies with a means of protecting their products from conversion by others, but will also allow for the commercialization of products derived by using several different methods to achieve a similar benefit." Again, the future effects of patent protection will be determined in the courts.

Future of Plant Breeding

Plant breeding will continue to be the delivery mechanism for value-added traits, but biotechnology used in conjunction with breeding will greatly enhance the process. Restriction fragment length polymorphisms (RFLPs), random amplified polymorphic DNA (RAPDs), isoenzymes, etc. are powerful analytical tools that will make the breeders much more efficient in their quest for value-added traits. Consumer demand for a value-added trait must exist or very strong assurances that it can be created must exist before substantial time, money and effort can be invested. If the end-users have adequate protection and the producers have an opportunity to share in the profits generated by these traits, then the probabilities of successfully developing a value-added trait greatly increases.

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Status of Oat Quality (1988–91) — German Cultivars, Industrial Oats

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Peter Kölln, Köllnflockenwerke, Elmshorn, FRG

Summary

Extensive quality investigations with different German oat cultivars confirmed again that certain varieties with constant high milling quality characteristics and crop yield are available and could be recommended to the farmers, f.i. over several years var. Alfred.

Though German milling oats are usually of good grain physical quality, there is a shortage in oats during the last years because of reduced oat cultivation area. Futhermore its use for human consumption products is often limited because of grey-black looking and damaged grains affected by bad harvest and storage conditions. The required imported oats are of different external grain quality and nutrient content. By quality checkups — as referred in this presentation — suitable oat lots had to be selected for effective oat milling and processing high quality oat products.

Introduction

The economic efficiency in oat milling depends to a high degree on the obtainable extraction rate, which for its part is directly influenced by oat quality. The negative relation between hullcontent of oats and extraction rate resp. groat yield in practical milling was recently studied by Vorwerck[4]. Figure 1 demonstrates the results established in different oat mills European and worldwide; the studies presumed oats with 13% water content and quality demands as referred in Table 4.

For more information about milling oat quality we regularly investigate both oat samples from variety trials performed by the Agricultural Board of Schleswig-Holstein and Hannover at different locations in the crop years 1988–91 and samples from usually handled industrial oats from different origin.

Variety Trials

External oat quality

Table 1 shows the main parameters thousand grain weight and hullcontent (hand dehulling) for 17 German oat varieties. The mean values for the single years confirm the well known fact that oat quality is dependent on the different year's growing conditions. So in the years 1988 and 1991 oat quality was good with low hull content, whilst 1989 severe dryness caused smaller groat development and high hullcontents.

The German law for grain market structure demands for oats a minimum TGW of 27 g dm and maximum 26% hullcontent. In 1989 from 10 test varieties the demand for TGW was fulfilled by 5 and for hullcontent only by 2 varieties (Nero, Lupus).

Table 1 demonstrates that independent of the different growing conditions in the years and the trial locations the individual varieties showed a variety typical quality development for TGW and hullcontent.

In Table 2 relative figures for TGW and hullcontent from means of the 4 crop years were represented and derived from it so called "quality value numbers". In addition yield datas are given in Table 2.

The best quality varieties over several test years are Alfred, Pilot, Lupus, Tomba and to a less degree Nero. Remarkable high hullcontents were established with Adamo, Lorenz and extremly Klaus. Comparable results were referred in earlier studies[1,2,3].

Several new cultivars — first tested 1991 — gave sufficient TGW with low hullcontent (Alf, Jumbo, Gramena). Unfortunately Sanova's very low hullcontent is connected with relative low grain yields.

Nutrient content

Protein and oil contents of the groat — dehulled with a laboratory air pressure huller — are shown in Table 3.

The higher protein values (Lorenz, Klaus, Nero) respective the low contents (Alfred, Flämingsvita, Flämingsregent, Pilot) were established in every single test year and on the different growing locations. Protein content in the dry year 1989 was about 4% higher compared to the other crop years.

Our studies confirm the known fact, that oil content of oats is highly variety typical. And there are wide variations in potential for oil production from rel. 127 (9,2% — Bruno) down to 75 (5,2% — Sanova).

The special favourable dietetic effect of oat gum gave rise to extend the nutrient analysis to ß-Glucan determination (McCleary — enzymic method). In Table 4 preliminary results for different cultivars are represented. ß-Glucan content obviously is genetically influenced (f.i. Alfred, Lorenz, Gramena with high values) and dependent on growing conditions (higher values 1989).

Industrial Milling Oats

External quality

For oat milling industry the quality status of oat lots usually handled in the market as industrial oats is of importance.

Table 5 represents the results for German oats grown 1988-91 in North-German areas and in addition the demanded quality requirements for industrial oats are specified. Though there are only small variations in hl-weight the grain quality was evidently worse in 1989 — a year with a special dry vegetation period. So the grains were light in TGG and TGTW, had more hulls and a smaller grain size value (GSV), and relative many samples did not achieve the requirements for the different quality features; f.i. the maximal limit for hullcontent was exceeded by 49 from 64 samples (= 77 %).

So German oats normally develop a sufficient kernel content to give a good milling quality, its use for human consumption products of high quality is often limited because of grey-black appearance and damaged grains affected by bad conditions during harvest (weather) and storage.

In Germany each year 10–20,000t West Australian oats were processed because of its excellent grain quality and appearance (Table 6). Though the content in hulls, foreign matter and double oats is high, the TGTW is superior — not to mention the favourable water content of about 9–10 %.

Table 7 demonstrates oat quality values from other possible European oat growing countries. The contradiction between high TGW and low grading resp. GSV for Australian oats compared with the inverse proportion f.i. to German oats is conditioned by the longer and more compact kernel shape of Australian oats.

Oats imported from England and Scotland 1991 were distinguished by special light grain weights. High quality oats can also be produced in Sweden and Finland. The Turkish samples are more of theoretical interest.

Nutrient content

The groat protein and oil content of German milling oats show only small variations in the different crop years (Table 8). However the dryness in 1989 resulted in remarkable higher protein and mineral contents. Between the presented oat provenances remarkable differences could be established as demonstrated in Table 9: West Australian and to a lesser extent South Australian oats are relative poor in protein and especially in minerals (K, C, & P) in contrary to North-European origin oats — caused by higher fertilization and environmental conditions. Nevertheless Australian and in 1991 English oats contain much more oil in the groats.

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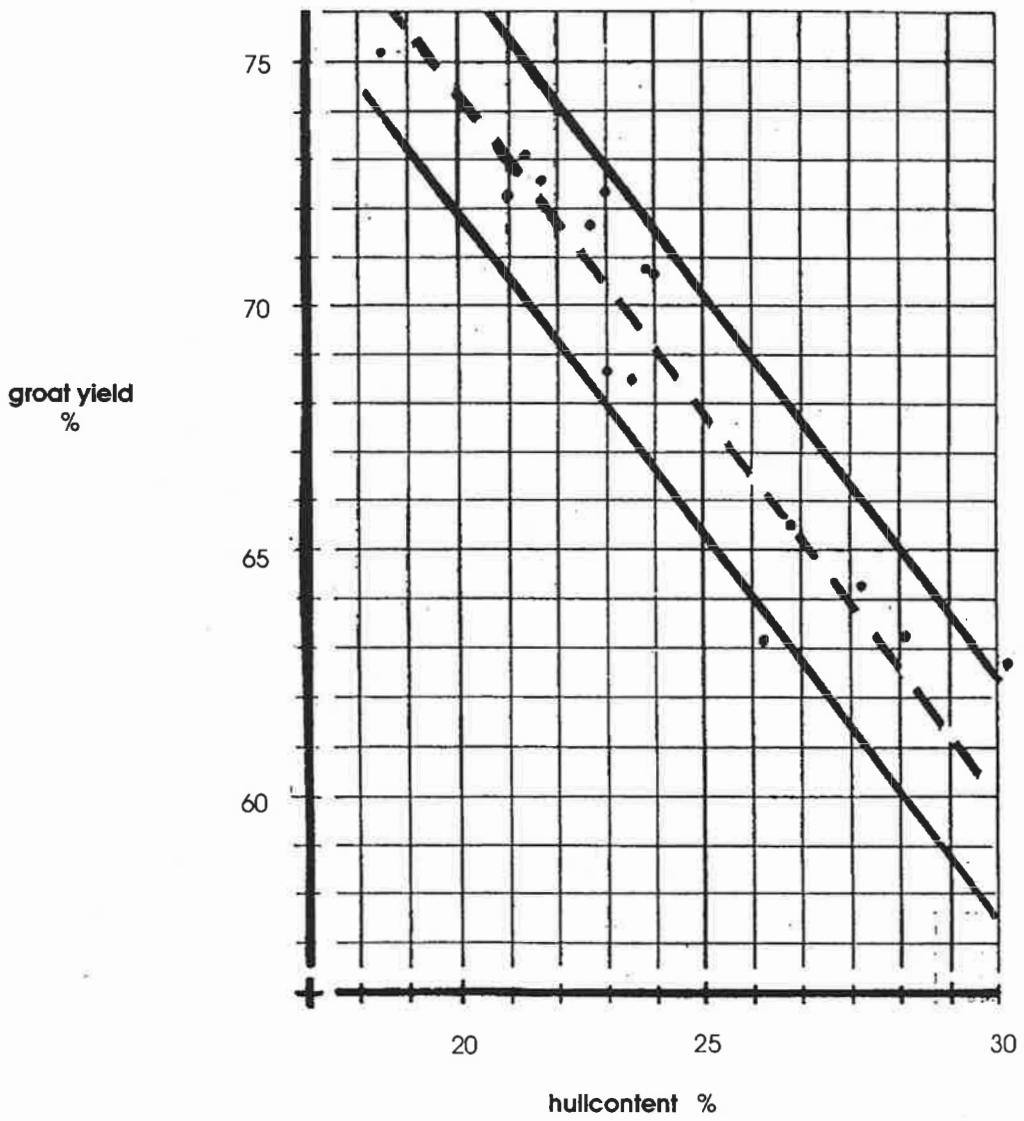

Figure 1: Groat yield (dm) dependent on hullcontent (hand dehulling)

Table 1. Thousand grain weight and hull content
Variety trials Agric. Board Schleswig-Holstein/Hannover 1988–91

		Thousand grain weight (g in dm)				*Hull content (% in dm)*			
		1988	*1989*	*1990*	*1991*	*1988*	*1989*	*1990*	*1991*
Variety	*n*	*13*	*13*	*13*	*15*	*13*	*13*	*13*	*15*
Alfred	54	32,9	27,6	31,2	30,5	24,3	27,9	26,1	23,5
Flämingsvita	54	30,2	26,6	29,4	28,2	25,1	28,3	26,7	24,8
Adamo	52	33,3 *	27,7	30,5	29,1	26,–	29,6	28,4	27,3
Flämingsregent	17	28,8	25,7 *	–	–	25,5	28,6	–	–
Lorenz	26	31,6	26,9	–	–	25,4	30,2	–	–
Pilot	26	31,5	28,4	–	–	23,1	26,9	–	–
Nero	21	29,6	26,8 *	–	–	21,7	25,5	–	–
Lupus	16	31,8	28,– *	–	–	23,4	25,1	–	–
Fuchs	26	–	25,5	28,8	–	–	27,7	25,5	–
Tomba	26	–	28,2	31,5	–	–	27,8	24,7	–
Wiesel	28	–	–	28,8	27,1	–	–	26,3	25,1
Bruno	28	–	–	29,5	28,2	–	–	27,5	26,3
Klaus	28	–	–	31,–	27,8	–	–	31,–	29,8
Gramena	15	–	–	–	28,8	–	–	–	25,6
Alf	15	–	–	–	28,9	–	–	–	23,8
Sanova	15	–	–	–	28,2	–	–	–	21,3
Jumbo	15	–	–	–	29,2	–		–	24,–
mean	462	31,–	27,2	30,1	28,6	24,3	28,–	27,–	25,1

n number of locations * not on all locations

Table 2. Comparative quality and yield of oat varieties (1988 - 91)

Variety	*TGW Rel. values*	*Hulls* *	*Quality value number TGW + = high*	*Hulls += low*	*Relative grain yield*	*crop year*	*rel. 100 (dt/ha)*
Alfred	104	97	+1	+1	102		
Flämingsvita	98	102	-1	0	101	1988 - 91	65
Adamo	103	107	+1	-2	106		
Flämingsregent	94	104	-2	-1	101		
Lorenz	100	106	0	-2	98		
Pilot	103	96	+1	+1	98	1988 - 89	58
Nero	97	90	-1	+3	97	1989 - 90	
Lupus	103	93	+1	+2	96		
Fuchs	95	97	-2	+1	100		
Tomba	104	95	+1	+2	97		
Wiesel	95	99	-2	0	101	1990 - 91	74
Bruno	98	103	-1	-1	103		
Klaus	100	117	0	-4	100		
Gramena	101	102	0	0	98		
Alf	101	95	0	+2	100		
Sanova	99	85	0	+4	95	1991	78
Jumbo	102	96	0	+1	102		

* Rel. 100 = mean TGW resp. hull content in each year (see Table 1)

Table 3. Comparison of protein and oil content (1988–91) of German oat cultivars

Variety	*n*	*Protein* *Relative values* *	*Oil*
Alfred	52	97	106
Flämingsvita	52	97	87
Adamo	50	101	114
Lorenz	24	105	119
Pilot	24	97	101
Nero	21	103	85
Flämingsregent	17	96	90
Lupus	16	102	82
Fuchs	24	101	78
Tomba	24	102	103
Wiesel	28	100	95
Bruno	15	99	127
Klaus	15	106	115
Gramena	15	102	106
Alf	15	100	78
Sanova	15	99	75
Jumbo	15	99	91

* Rel. 100 = mean protein resp. oil content in each year

	1988	*1989*	*1990*	*1991*	*1988 - 91*
	(% in dm)				
mean protein	14,3	18,1	14,3	13,4	15,0
mean oil	6,7	6,7	7,5	6,9	7,0

Table 4. ß-Glucan in German oat cultivars (1988–91)

	1988	*1989*	*1990*	*1991*
	(% in dm)			
Alfred	4,9	4,9	4,4	4,4
Flämingsvita	4,1	4,6	3,9	4,2
Adamo	4,7	4,9	4,0	4,2
Lorenz	4,8	5,1	–	–
Pilot	4,3	5,5	–	–
Fuchs	–	4,5	4,2	–
Tomba	–	4,6	4,0	–
Wiesel	–	–	4,2	4,2
Bruno	–	–	3,8	4,0
Klaus	–	–	4,3	4,4
Gramma	–	–	–	4,8
Alf	–	–	–	4,4
Sanova	–	–	–	3,6
Jumbo	–	–	–	4,2

Table 5a. Oat quality — German milling oats

Crop Year	*n*	*M %*	*HL-W kg*	*TGW g dm*	*TGTW g dm*	*Hulls % in dm*
1988	78	13,7	57,3 (13)	30,6	23,2	24,3 (2)
1989	64	13,3	57,1 (11)	27,1 (29)	19,8	27,1 (49)
1990	62	12,8	57,2 (3)	29,3 (9)	21,8	25,6 (16)
1991	50	13,7	56,8 (9)	29,2 (7)	21,9	24,9 (6)
mean 1988-91	254	13,4	57,1	29,1		25,4
demands		max. 15,5	min. 55	min. 27		max. 26

appearance: no grain discolouration, no damage, dark groats
smell: sound, not musty and sour

M Moisture
TGW Thousand Grain Weight
TGTW Thousand Groat Weight
HL-W Hectolitre Weight
n test numbers
(n) Demands not obtained

Table 5b. Oat quality — German milling oats

Crop Year	*Grading a%*	*b%*	*c%*		*GSV*	*FG %*	*FM %*	*DO %*	*HO %*	*TGC %*
1988	46	32	15	(8)	96	1,9 (12)	1,– (32,0)	0,2 (1)	11,–	77
1989	17	35	31	(56)	64	1,8 (11)	0,8 (14)	0,7 (21)	6,4	73
1990	30	35	23	(28)	79	1,3 (7)	0,8 (11)	0,2	10,2	76
1991	30	40	22	(12)	83	1,9 (8)	0,7 (10)	0,2	8,3	76
mean 1988-91	32	35	22		82	1,7	0,8	0,3	9,1	75
demands: a + b + c = min. 90						max. 3	max. 1	max. 0,8		

FG Foreign Grain
DO Double Oats
FM Foreign Material
HO Hulled Oats

Grading with slit sieve: a => 2,5 mm, b => 2,2 mm, c => 2,0 mm
GSV (Grain Size Value): a x 1,4 + b x 0,8 + c x 0,4
TGC (Total Grain Content): CO – (CO x Hulls) + HO
CO (Cleaned Oats): 100,0 – (FG + FM + HO)

Table 6a. Oat quality — Australian milling oats

Crop Year	*n*	*M %*	*HL-W kg*	*TGW g dm*	*TGTW g dm*	*Hulls % in dm*
1988	4	9,4	61,1	33,7	24,1	28,5
1989	9	9,8	61,3	33,1	24,3	26,7
1990	7	9,–	60,8	33,1	23,6	28,7
1991	10	9,1	61,–	32,1	22,9	28,8
mean 1988-91	32	9,4	61,–	32,8	23,6	28,1
demands		max. 15,5	min. 55	min. 27		max. 26
appearance:	no grain discolouration, no damage, dark groats					
smell:	sound, not musty and sour					

Table 6b. Oat quality — Australian milling oats

Crop Year	*Grading a%*	*b%*	*c%*	*GSV*	*FG %*	*FM %*	*DO %*	*HO %*	*TGC %*
1988	14	41	32	65	1,2	2,6	0,7	14,5	73
1989	18	48	25	74	1,–	1,6	0,4	14,1	76
1990	12	39	35	62	1,4	1,8	0,6	12,2	73
1991	10	39	35	59	1,7	2,–	1,5	6,1	71
mean 1988-91	13	42	31	64	1,3	1,8	0,8	10,8	73
demands: a + b + c = min. 90					max. 3	max. 1	max. 0,8		

Table 7. Oat quality - European / Australian oats, harvest 1991

	n	*M %*	*HL-W kg*	*TGW g dm*	*TGTW g dm*	*Hulls % in dm*	*Grading a%*	*b%*	*c%*	*GSV*	*DO %*
West Australia	10	9,1	61,0	32,1	22,9	28,8	10	39	35	59	1,5
South Australia	1	9,0	53,6	32,1	22,7	29,3	6	30	43	50	0,6
Germany	50	13,7	56,8	29,2	21,9	24,9	30	40	22	83	0,2
England	7	12,6	56,–	25,5	19,–	25,3	20	37	27	68	0,4
Scotland	2	12,5	57,–	26,4	19,9	24,8	28	41	22	81	0,5
Ireland	1	–	61,1	28,4	21,9	22,9	35	43	16	90	0,1
Sweden	1	–	60,6	30,2	23,–	23,9	17	46	29	72	–
Finland	1	–	59,6	27,5	21,4	22,3	14	43	32	67	0,2
Poland	2	–	55,8	30,–	21,5	28,2	8	48	33	63	1,6
Turkey	2	–	51,–	24,3	17,4	28,2	0	3	30	14	0,8

Table 8. Nutrient content of German milling oats (dehulled groats)

Germany	*n*	*Protein (N x 6,25)*	*Oil*	*Ash*	*K*	*Ca*	*P*
			% in dm			*mg % in dm*	
1988	55	15,2	6,9	2,14	480	65	478
1989	47	17,3	7,1	2,15	489	66	481
1990	51	15,3	7,1	2,04	443	66	466
1991	53	14,5	6,9	2,05	450	63	462
1988-91	186	15,6	7,0	2,10	467	65	473

Table 9. Nutrient content of European (1991) / Australian (1988–91) milling oats (dehulled groats)

Origin	*n*	*Protein*	*Oil*	*ß-Glucan*	*K*	*Ca*	*P*
			(% in dm)			*(mg % in dm)*	
Western Australia	13	12,7	9,6	3,80	343	53	348
South Australia	2	13,8	8,8	3,60	354	65	345
Germany	33	14,5	6,9	(4,20)	450	63	473
England	6	13,8	8,2	3,72	413	64	395
Ireland	1	12,3	5,8	3,36	399	69	402
Sweden	1	13,9	6,0	3,45	421	67	441
Finland	1	16,1	6,5	4,58	474	51	489
Poland	1	14,5	6,9	4,44	457	63	513
Turkey	2	15,6	7,9	3,89	331	73	339

Global Oats 2000

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Summary

The principal oat growing countries are Canada, China, Commonwealth of Independent States, Czechoslovakia, France, Finland, Germany, Norway, Poland, Sweden and the United States of America in the northern hemisphere, and Argentina and Australia in the southern hemisphere. From a peak of 50.2 Mt in 1972/74, oat output is projected to fall to 35.2 Mt in 1991/92, representing a fall of around 30 per cent. Most oats are consumed in countries of origin, with about four per cent of production entering international trade each year. World trade in 1991/92 is forecast to be 1.4 Mt, compared with 1.3 Mt in 1990/91 and 1.8 Mt in 1989/90. The most significant development in world trade in the 1980s was the emergence of the United States of America as the foremost oat importer, followed by the European Community, Commonwealth of Independent States, Switzerland and Japan. Major oats exporters are Canada, Finland, Sweden, Australia and Argentina.

Major Oats Importers

United States of America

The United States is a major contributor to world oats area and production, and is estimated to account for almost 11 per cent of global oats area and 11.8 per cent of world output for the period 1989/90 to 1991/92, with yields above world averages[21]. Oat production has been declining for four decades, due in part to increasing farm mechanisation and lower incentives provided for oats under the various farm programmes, as compared with other commodities such as barley, corn and wheat.

In the 1980s, consumers were quick to respond to the perceived medical and nutritional benefits of the water soluble properties of oats, resulting in a rise in food usage[9]. The gap between domestic demand and falling production was met by increasing levels of imports from a number of overseas suppliers, including Finland, Sweden, Argentina and Canada. As the decade progressed, oat imports rose, reaching a plateau of 67.7 per cent of world trade in 1990/91, with a forecast of 64.4 per cent in 1991/92[12]. Within the United States, oat processors adjusted their respective production capacities accordingly[8,17].

The 1991/92 oats harvest projection of 3.5 Mt is around 30 per cent below the 5.2 Mt estimate for 1990/91 and follows an earlier fall from 5.4 Mt in 1989/90. The 1991/92 outturn is reckoned to be the second smallest on record, with the area harvested a record low. The tightening oats supply is reflected in a fall of 17 per cent in the December 1, 1991 stocks, in contrast to the situation one year previously[22]. Food, seed and industrial (FSI) usage continues to increase, despite reductions in seed use as planted area falls. In 1991/92, FSI utilisation is forecast at 1.8 Mt, up from 1.7 Mt the previous year. This rising trend is primarily due to greater food application.

European Community

The Treaty of Rome in 1957 ushered in the European Community, and there were six member countries initially. Now the Community comprises 12 member countries; Belgium, France, Denmark, Ireland, Italy, Germany, Greece, Luxembourg, Netherlands, Portugal, Spain and the United Kingdom. While oats are grown in each member country, production has declined some 50 per cent over three decades, despite a 25 per cent lift in yields. The most significant falls have occurred in Belgium, Luxembourg, Greece and the Netherlands,while France and Germany are the main oat producers[18]. Marketing and policy are closely interwoven, and the Common Agricultural Policy covers high support prices,export subsidies, stocks and import protection.

Such arrangements are decided annually by agriculture ministers of member countries, and include support prices for soft wheat (quality wheat, bread wheat and feed wheat), durum, corn, barley, sorghum and rye for the period 1990/91 through to 1995/96[19]. Oats are not included in the CAP price regime, and as a free grain do not have guaranteed prices. In practice, oat prices are usually geared to feed barley and research has focussed on barley, corn and wheat, for example, to the disadvantage of oats[4].

What the CAP does provide is a threshold price on the entry of oats from third countries and the import levy is intended to protect other EC cereals, as well as oats. Oat shortfalls in some member countries have been met in part by France and Germany, in addition to imports from Scandinavia and Australia. EC oat imports peaked in 1984/85, with 14.1 per cent of international trade, but this share has declined considerably to a forecast 2.3 per cent, which includes the former east German Republic, which had been an important buyer of foreign oats in the 1980s.

Commonwealth of Independent States

The group of 15 republics which formerly comprised the Soviet Union, is estimated to account for half the world's oats area, and approximately 42 per cent of global production for the period 1989/90 to 1991/92, with yields below world averages. From 1985 to 1987 oats made up 10 per cent of the total Soviet grain area, and 97 per cent was in the Soviet heartland, with the remainder in the Baltic States[20,21]. The former Soviet Union has taken about 19 per cent of coarse grain imports globally, with about the same percentage of the world wheat trade, between 1986/87 and 1991/92[12].

Oat imports have been highly variable, but have averaged around nine per cent for the same period. While in the 1970s and early to mid 1980s, the Soviet-Union was mainly a cash buyer, with some barter trade activity, the various republics now purchase on credit, rather than on commercial terms. The emphasis is principally on barley, corn and wheat, mainly from the EC and USA. However, Finland provided credit terms for oats, along with barley, in 1991[12]. Finland, Sweden and Australia have been the chief oat suppliers, and in 1991/92 oat imports are forecast at 6.8 per cent of international trade.

Switzerland

The major agricultural activity in Switzerland is dairying and requires substantial feed inputs, particularly in winter. In this regard Switzerland is a traditional oats importer, accounting for about six per cent of global trade but this is declining. France and Scandinavia have been the principal external oats exporters in the recent past[12]. Swiss agricultural policy is under review, with a strong focus on developments in Europe and the current GATT discussions. Switzerland would like to be in a position to successfully apply for EC membership at a mutually convenient time[24].

Japan

Approximately two thirds of Japan's food requirements emanate from foreign sources, having regard to the westernisation of the Japanese diet. Cereals feature prominently in these imports (except for whole grain rice) and Japan is a regular oats importer, obtaining supplies from Australia and Canada. Japan's share of the international oat trade is around the six per cent level. Health conscious Japanese consumers are increasingly looking towards fibre fortified foods and beverages which could lift the consumption of oats and imports to this country.

Major Oats Exporters

Canada

Oats are the third most important cereal crop in Canada, estimated to account for about seven per cent of global oats area and production, with yields marginally above world averages, for the period 1989/90 to 1991/92[21]. In common with most other oat producing countries, most of the oats are used domestically[6]. A major structural marketing change

occurred in August, 1989, when the Canadian Wheat Board, which had the oversight for oats for four decades, was relieved of this responsibility by the federal government. In effect, the 1988/89 oat pool was the last operated by the Board, and subsequently growers became free to contract directly with merchants or processors for the disposition of their oats. The Board still retains the responsibility for barley and wheat[5].

Severe logistical and transportation constraints hindered the export of Canadian oats, as well as low prices, until the early to mid 1980s. As recently as 1984/85, Canada was still only a minor exporter, accounting for only 1.3 per cent of the international oats trade, however,the expanding US market provided an opportune outlet for Canadian oats. For 1991/92, Canada is forecast to lead the global oats trade, accounting for 30.5 per cent, with most of the exports directed towards the United States[12]. Foreign oat customers also include Cuba, Belgium, Luxembourg, the Netherlands and Japan[6]. For the 1992/93 season, Canadian oat growers are planting more. This is in response to stronger prices and sound prospects for sales to the United States as a consequence of anticipated declines in the availability of oats from Scandinavia[23].

Finland

Oats are the second most important crop after barley, and oat area and output are estimated to account for less than two per cent of world oat area and 3.5 per cent of production, with yields almost double world averages, for the period 1989/90 to 1991/92[21]. Finland is a major oats exporter, ranking third in 1989/90, first in 1990/91, and is forecast to occupy second place in 1991/92[12]. The marketing of grain is carried out by the Finnish Grain Board, which has the responsibility for importing wheat, when appropriate, and exporting barley and oats. Oats have been exported to the former Soviet Union, several European countries and the United States. Policy changes being implemented will result in a gradual deregulation of agriculture, increasing the area to be set aside, thus reducing grain production and export availability.

Sweden

Oats rank third in cropping importance, after barley and wheat. Oats is reckoned to account for 1.7 per cent of world area and 3.8 per cent of global output, with yields more than double world averages, for the period 1989/90 to 1991/92[21]. Most grain is either imported or exported by the Swedish Grain Trade Association, in conjunction with the Swedish Farmers Supply Association. The Swedish co-operative movement exercises an extremely important role in the rural economy, and its significance surpasses those in other comparable western countries[16]. Sweden is an important contributor to the international oats market, however, its performance has fluctuated, ranging from a 34.7 per cent share in 1986/87 to a forecast 20 per cent in 1991/92. If the latter is realised, Sweden would be the world's third largest exporter. Sweden's external oat markets have been the former Soviet Union and the United States of America. In the period 1983 to 1989, Sweden supplied 36.1 per cent of US oat imports, but this declined to 17.1 per cent in 1989/90. Sweden lost market share to Canada, whose proportion of the US market rose from 42 to 63 per cent[10,11].

In 1990, the Swedish government decided to introduce a new food policy, entitled "Agricultural Reform" for introduction July 1, 1991. Under the new programme, open ended price support systems and export subsidies would be abolished, and border protection lowered, in line with trade liberalisations discussions under GATT[24]. The impact on Swedish oats is likely to mirror developments in Finland, reducing the quantity of oats available for export.

Australia

Oats are Australia's third most important winter cereal, estimated to account for 5.5 per cent of world oats area and 3.9 per cent of global production, with yields below world averages, for the period 1989/90 to 1991/92[3]. Oats are grown in each of the grain states, and the five year averages to 1990/91 were: New South Wales (38.2%), Western Australia (30.7%), Victoria (19.2%), South Australia (9.8%), Queensland (1.2%), and Tasmania (0.9%)[21]. Around 75 per cent of oats are utilised as feed, mainly for cattle, goats, horses and sheep[15]. Feed usage depends on seasonal conditions, with droughts occurring in 1982/83

and 1989/90, with the latter continuing into the following season. These adverse seasons were attributable to the climatic variable, "El Nino"[1,14], with the greatest impact in eastern Australia, and produce, including oats, being shipped from west to east to augment seriously depleted grain harvests and stocks. Food usage of oats rose through the 1980's, peaking at an estimated 4.3 per cent of output in 1990/91, and is forecast to decline to 3.6 per cent of production, in 1991/92[3]. Oats have had a major impact on food consumption patterns, providing for oat based products in breakfast cereals, bread, biscuits, cakes, muffins and muesli snackfoods[4]. In relation to marketing, there are no constraints nor price support programmes for Australian oat growers, and marketing activity is spread across a plethora of merchants, processors, cooperatives and boards[7]. The percentage of oat output directed to exports varies in a band from 10 to 16 per cent[3]. As the world's fourth largest exporter, estimated to account for 14 per cent of international trade from 1989/90 to 1991/92, Australia's oats customers include Japan, Ecuador, Spain, the Netherlands and Germany, with occasional shipments to the former Soviet Union[3].

Argentina

Oats are overshadowed by other grains and oilseeds and, accordingly, are consigned to a lesser role in the rural economy, being mainly used for feed. However, interest in oats was stimulated in the second half of the 1980's, following developments in the US oats market. While ranking fifth in international oat trade, export performance has been falling in recent years, ranging from 0.8 per cent in 1986/87 to 23.9 per cent in 1987/88, and its forecast share is 3.4 per cent in 1991/92[11,12]. While marketing is carried out by the private sector, export taxes were still in place at the end of 1990 for coarse grains, rice and soybeans. These taxes may be replaced by value added taxes, imposed by the Argentine Government[13].

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Swedish Oats on the International Market regarding Quantity, Quality and Economics

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Introduction

Last year Sweden was the largest exporter of oats on the international market. Oats has however been one of the major grains in Sweden for over 200 years. Oats became more commonly grown at the end of the 18th century. In the middle of the 19th century the acreage of oats increased because of good exporting possibilities. Swedish oats was exported as horsefeed to London, for example, where at this time lots of horses were used[4].

At the end of the 19th century oats were grown over more than 800,000 hectares and were the major grain crop in Sweden. The export of oats was very important for the Swedish economy at this time, financing modernization of both farms and industries[4].

Today, when horses are no longer used to the same extent, barley is the most common feed grain in Sweden and oats is mainly used as feed for dairy cows and racehorses. For that reason the acreage of oats has decreased to about 400,000 hectares, which is approximately 30 per cent of the Swedish grain area of 1.5 million hectares[5].

Production of Oats in Sweden

Oats is well suited for growing in the Swedish climate. Low temperatures and good soil moisture after planting in spring are favourable for the growing of oats. Long days with many daylight hours and cool weather in the early summer gives good conditions for formation of panicles and kernels[4].

Yield and production may vary quite considerably between the years (Table 1). On average, for the last ten years, the yield has been 3,680 kilograms per hectare. The total production is, on average, 1.5 million tons with an export of 25%. Last year, however, more than 30 % of the Swedish oat crop was exported. Most of the domestic use is as feed but during the last four years the use of oats for feed has decreased. For human consumption only 30,000 tons is used[5].

This season Sweden has had a very bad drought. The production of oats and barley will only be enough to supply the domestic market. Therefore the forecast for 1992/93 is that Sweden will not have any export of oats.

World Trade in Oats

World trade in oats has increased during the last few years due mainly to the demand in the United States (Table 2) . The trade reached in 1991/92 was 1.8 million tons. Imports by the former USSR and the United States are expected to rise this following season[3].

Last year Sweden was the largest exporter on the international oat market with about 30 per cent of the world trade[3]. Most of the Swedish oats is exported to the United States[5]. Feed for horses, especially racehorses, is still the most common use. The demand for milling oats is however rising.

Table 1. Production and use of oats in Sweden 1982/83-1991/92, Aug/July[5].

Year	*Production (1,000 tons)*	*Domestic use (1,000 tons)*	*Export (1,000 tons)*	*Yield (kg/ha)*
1991/92	1426	965	461	4130
1990/91	1584	1054	530	4310
1989/90	1455	1108	347	3538
1988/89	1330	1054	276	3134
1987/88	1440	1220	220	3624
1986/87	1486	1164	322	3261
1985/86	1668	1191	477	3751
1984/85	1904	1125	543	4444
1983/84	1268	1125	143	3139
1982/83	1663	1336	327	3486

Table 2. World trade in oats 1987/88-1991/92, July/June. 1,000 tons[3].

	1987/88	*1988/89*	*1989/90*	*1990/91 estimated*	*1991/92 forecast*
Importers:					
EEC	8	84	14	15	20
JAPAN	79	78	66	110	90
SWITZERLAND	114	99	65	62	70
USSR (former)	57	144	452	35	150
USA	599	904	1160	1166	1300
Others	176	234	251	207	210
TOTAL	1033	1543	2008	1595	1840
Exporters:					
ARGENTINA	290	143	138	20	25
AUSTRALIA	216	260	232	213	200
CANADA	282	658	727	414	400
EEC	8	9	1	2	5
FINLAND	—	43	497	487	490
SWEDEN	189	230	319	355	605
USA	7	8	12	6	—
Others	41	192	82	98	115

Quality of Swedish Oat Exports

All shipments of Swedish oats to the international market are controlled so that they are sound oats with high quality, free from live insects, heat damage and moulds. Swedish oats are well known for being clean and having large heavy kernels. Pesticides are seldom needed either in the field or in store due to the Swedish climate.

Test weight

The test weight was on average 61.3 kg/hl (47.6 lbs/bu) for exported oats in 1982/83 to 1991/92. The variation between different years is small with a minimum average value of 59.9 kg/hl (46.5 lbs/bu) in 1987/88 and a maximum of 62.2 kg/hl (48.3 lbs/bu) in 1986/87. The variation between different growing areas is very small[5].

Other grains and foreign matter

During the last 10 years the exported oats has on average been mixed with 1.6% other grains and 0.4% foreign matter. Purity in other words, is on average 98.0%. Barley is the most common other grain mixed with the oats with less than 1.0% on average. The variation in purity between years and regions is very small (Svensk Spannmalshandel, unpublished data).

Protein content

Analysis for protein content has only been made since 1988/89 on Swedish export oats. Average value for the last four years is 12.1% protein on dry matter basis (N*6.25). Variation between the years depends on growing season and the yield. Since 1988/89 the variation in protein content has been between 11.1% and 13.2% DM. Comparisons between growing regions shows that protein content is about 0.5% higher in the eastern growing areas than in the south and the west. The protein content in dehulled oats is approximately 15.0% DM[5].

Results of a Study of Quality Criteria important for the Industrial Utilization of Oats

To give a short description of quality criteria important for the industrial utilization of oats, a study has been made of exported oats from the last two harvests. One hundred samples each year have been analysed representing about 10% of the export in 1990/91 and 1991/92. The samples have been divided into growing areas depending on where the shipments were made; in the east, west or south of Sweden.

Kernel size, thousand kernel weight, hull content and fat content

On average, 76.4% of the oat kernels are bigger than 2.2 mm and the mean value for thousand kernel weight is 31.3 grams (Table 3). Between the two growing seasons there was a small variation in kernel size and thousand kernel weight with higher values in 1990/91 due to better growing conditions. In comparison, between the regions the oat kernels are slightly bigger and heavier in the western growing areas of Sweden than in the east and the south. Variation in hull content and fat content are small between the years and the regions.

Dietary fibre

Since fibre content in oats is of interest from a nutritional point of view, a small study of 20 samples each year in 1990/91 and 1991/92 were made. Soluble and insoluble dietary fibre were analysed on dehulled oats in accordance with AACC method 32-05.

The mean value for soluble dietary fibre was 4.7% and for insoluble dietary fibre 6.6% (see Table 4). 42% of the total content of dietary fibre is soluble which is about the same as in earlier studies of Swedish oats[1].

Table 3. Average value for kernel size, 1000 kernel weight, hull content, and fat content 1990/91 to 1991/92 (n=200).

	Kernel size (% > 2.2 mm)	*1000 kernel weight (g)*	*Hull content (% DM)*	*Fat content (%DM)*
Sweden	76.4	31.3	26.3	5.4
East	71.8	30.8	26.2	5.5
West	83.8	32.2	26.0	5.3
South	74.4	30.8	26.9	5.0

Table 4. Average value of soluble, insoluble and total dietary fibre in dehulled oats in 1990/91 and 1991/92, per cent of dry matter (n=40).

	Soluble dietary fibre	*Insoluble dietary fibre*	*Total dietary fibre*
1990/91	4.6	7.0	11.6
1991/92	4.9	6.1	11.0
Mean value	4.7	6.6	11.3

Discussion

Swedish oats is well suited to the needs of the international market. The quality meets the specifications for milling oats both in Europe and in the United States[2]. The demand for heavy oats from Sweden as feed for racehorses is rising and we will probably find new markets in the future.

However, the Swedish oat production is very much dependent on guarantee prices and export subsidies. Swedish farmers have a guarantee price for oats on the international market of 180 USD per ton in comparison with the price on the international market of about 100 USD per ton.

The Swedish parliament has decided to reduce the subsidies for grain and other agricultural products. But since last year, when Sweden asked for membership in the European Community, the future in our grain production will very much depend on the agricultural policy in the EC.

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An Economic Analysis of the Breeding of a Special Purpose Oat

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Summary

The project analysed here is the breeding of Potoroo, a dwarf feed grain oat (*Avena sativa*) with resistance and tolerance to cereal cyst nematode, (*Heterodera avenae*). Potoroo is intended to replace all varieties of oats intolerant of cereal cyst nematode and tolerant varieties used for feed grain production where cereal cyst nematode is a problem. An economic analysis of the breeding program and subsequent industry benefits indicates an extremely favourable benefit cost ratio of 69 to 1, using a real discount rate of 5%.

Introduction

In late 1991 the Australian Grains Research and Development Corporation commissioned a series of benefit-cost studies, focusing exclusively on grains research and development. This particular study was just one of 21 projects analysed. The benefit-cost studies aimed to "obtain a measure of the benefits of research in the grains industries, and to strengthen accountability to the fund providers, the farmers and the Federal Government"[4]. Another aim was to develop an efficient and easy to use method to help allocate research resources[4]. Given that the new variety Potoroo is unlikely to be grown abroad, the cost reduction methodology[5] was chosen, which yields a conservative estimate of research and development benefits.

The Potoroo breeding program began in July 1984 with the aim of breeding oat varieties that were resistant and tolerant to cereal cyst nematode (CCN), which is the most economically important disease of wheat (*Triticum aestivum*), barley (*Hordeum vulgare*), and oats in South Australia and Western Victoria. With the advent of the dwarf varieties Echidna and Dolphin, the yield potential of oats in areas not infested with CCN rose by between 30 to 40%. This project sought the combination of CCN resistance and tolerance in a semi-dwarf genotype with the high yield potential and plant type of Echidna. The development of such a semi-dwarf resistant and tolerant variety ensures the highest possible profit is gained from the "root disease break crop" part of the rotation.

For the purpose of the current analysis the project was deemed to have commenced in 1985, with the research phase completed in 1990 and the extension phase in 1992. The project has been funded by both the South Australian Government and the Australian Grains Research and Development Corporation (and its predecessors).

Potoroo has excellent yield potential, averaging one per cent higher than Echidna over all rainfall districts of SA where CCN is not a yield limiting factor and often double where CCN is a severe yield limiting factor[2]. Potoroo produces grain that is larger than Echidna's, but higher in screenings and lower in hectolitre weight[2]. The grain is longer and thinner than Echidna's and is therefore not regarded as suitable for milling, but is more suitable for ruminant feeding[2].

Assumptions Used in the Analysis

Potoroo substitutes directly for the currently used Wallaroo, Marloo and Echidna varieties in those geographic areas of South Australia and Victoria which are infested with CCN. These oat regions cover an area of 151 300 ha[1]. Based on yield relativities, the yields assumed for Echidna and Potoroo in CCN infested areas are 0.9 t/ha and 1.8 t/ha, respectively, with Wallaroo and Marloo yielding 1.3 t/ha. Yield relativities, rather than assumed yields, are a

key parameter in the following analysis. Following the adoption of a CCN resistant and tolerant oat in the rotation in CCN areas, increased subsequent wheat yields are estimated by the SA Department of Agriculture at 10%, which equates to a cost reduction of $12/t ($1991). The choice of a discount rate, or the rate at which future expenditures and revenues are discounted to present (1991) value, significantly alters the estimated financial ratios. Two plausible after inflation or real rates of 5% and 10% are used[5].

Analysis

The analysis considers only the grain yield benefits of Potoroo and does not evaluate the additional benefits of grazing or hay making that will result from the oat breeding project, especially of the concurrent development of an oaten hay variety yet to be named. Hence, the results reported are a conservative estimate of the benefits.

It is estimated that in 1992, 1000 tonnes of seed was available commercially, sufficient for planting around 20 000 ha. The estimated adoption profile for Potoroo will see one third of South Australian (and other Southern Australian) oat areas planted to it by 1994. That profile is expected to be maintained thereafter. The benefits to producers in terms of oat yield increases over existing varieties have been discussed earlier.

The five-year average farm gate oat prices (in $1991) are; number 1 grade $116/t, number 2 grade $111/t and number 3 grade $108/t (6). In evaluating this project it is assumed that Wallaroo, Marloo and Potoroo fetch the number 3 grade price while Echidna fetches the number 1 grade price.

Calculations of unit cost reductions

A) **Before new technology**	Wallaroo/Marloo	Echidna
Ave. variable cost $/ha	78	78
Yield t/ha	1.3	0.9
Ave. variable cost $/t	60	87
Ave. fixed cost $/t	48	29
Ave. total cost $/t	108	116

B) **With new technology** (Potoroo)	Substitute Potoroo for Wallaroo or Marloo	Substitute Potoroo for Echidna
Ave. variable cost $/ha	78	78
Yield t/ha	1.8	1.8
Ave. variable cost $/t	43	43
Ave. fixed cost/ha	62	26
Yield t/ha	1.8	1.8
Ave. fixed cost/t	34	14
Ave. total cost $/t	77	57
Unit cost saving $/t	31	59

Summary of Results

Table 1 presents the costs and benefits in 1991 dollars of the oat breeding project over the forty year period 1985 to 2024. These results were compiled with the aid of a purpose built spreadsheet titled "REVS"[3].

From Figure 1, the pattern of cash flows is illustrated with money spent initially on research and extension, with no offsetting benefits. However from 1992 onwards the benefits outweighed any costs, reaching a maximum net present value ($1991) of nearly $7 million in 1994.

Table 1. Results of a benefit-cost analysis of the Potoroo breeding program: 1985-2024.

Financial Parameters	5% Discount Rate	10% Discount Rate
Present Value of Costs $	1.8 m	2.2 m
Expected Present Value of Benefits $	126.6 m	72.1 m
Expected Net Present Value $	124.8 m	70.0 m
Expected Internal Rate of Return %	57	57
Expected Benefit Cost Ratio	69	34

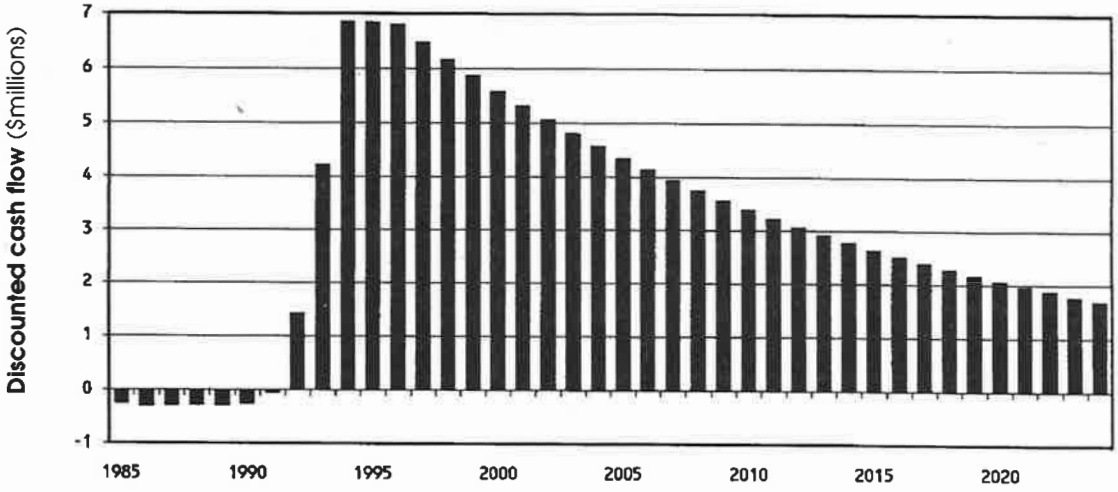

Figure 1. Annual discounted cash flows (@ 5% discount rate) for the Potoroo breeding project, 1985 to 2024.

The process of estimating the benefits of the Potoroo breeding program required various assumptions such as the geographic area to which Potoroo would be applicable and the adoption profile. This process is extremely useful in forcing researchers to focus on outputs, and the process of adoption. Also, the benefit-cost approach is a useful tool in guiding the allocation of resources within a research and development portfolio not only for research scientists, but their managers.

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Oat Marketing

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The Australian Barley Board operates in both South Australia and Victoria, and is currently responsible for marketing oats, barley and grain legumes. It is a well established professional organisation with over 50 years experience in grain quality, handling, marketing and shipping. The Board became involved in oat marketing back in 1978 and since that time has become a reliable supplier of quality oats.

A considerable amount of time is spent in quality assessment, with staff undergoing extensive training to ensure they are capable of conducting the various tests necessary to determine the quality grade of each truck-load delivered by growers. Oats received by the Board are sampled and tested a number of times as they move from the farm to the customer. This not only guarantees quality during storage and handling but also means stocks can be selected to meet the specific requirement of each buyer.

The parameters which are examined to determine oat quality include

- ❒ moisture
- ❒ cultivar
- ❒ density
- ❒ screenings
- ❒ other cereals
- ❒ weed seeds
- ❒ weather stained grains.

In South Australia, the major oat growing regions are Eyre Peninsula, the Mid North and Upper South East, while in Victoria they are the Wimmera, Northern Mallee and Loddon Campaspe districts.

With higher yielding cultivars being bred and released by the oat breeding team of the South Australian Department of Agriculture, a swing to these varieties has taken place.

Statistics of areas sown to oats now show that approximately 65% and 70% respectively of the total Victorian and South Australian oat crops are now planted to these varieties.

The marketing of oats in South Australia and Victoria shows two distinct directions, with the bulk of the South Australian crop being exported while in Victoria the usage is primarily domestic.

Playing to Win Against Oat Rusts

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Summary

The development of oat, *Avena sativa* L., cultivars with more durable resistance to crown rust, *Puccinia coronata* Cda. var. *avenae* Fraser & Led., and stem rust, *Puccinia graminis* Pers. f. sp. *avenae* Erikss. & E. Henn., is essential for stable production of oats in "subtropical" areas, where both diseases frequently cause serious damage. Strategies for accomplishing this important breeding goal are presented in this paper.

Durable Resistance

One of my primary breeding goals is to develop oat cultivars with more durable resistance to crown rust and stem rust. Although it probably is not realistic to expect resistance to be "permanent", increasing the relative durability of resistance would pay great dividends in commercial agriculture, and would allow the breeder some needed "breathing room" to devote additional effort to improving other important agronomic traits. My ideas on developing oat germplasm lines and cultivars with relatively durable resistance are based on my own experience in South Texas and South American rust "hotbeds". I believe that there are some factors which make these subtropical production areas rather unique in terms of the level of resistance that is required. These include the much longer growing season for fall-planted ("winter") oats, and the optimal environmental conditions for rapid and sustained disease development throughout most of the growing season in the areas in which the rust diseases are most devastating.

In discussing durable resistance, it is important to define just what "durable" means. My office dictionary[8] defines durable as: "able to exist for a long time without significant deterioration". In his excellent review of durable resistance to plant diseases, R. Johnson[3] of the Cambridge Plant Breeding Institute gave the following definition: "Durable resistance to a disease is resistance that remains effective during its prolonged and widespread use in an environment favorable to the disease."

Therefore, the test for durable resistance must include the two elements of time (long) and production area (large), each of which is subject to interpretation. Johnson[3] states that durable resistance cannot be identified on the basis of testing genotypes only in small-scale experiments, even if they are grown repeatedly at many locations and over many years, since the total area occupied by such tests is small compared with the area occupied by a cultivar in commercial use. He cited the example of the triticale, *X Triticosecale* Wittmack, cultivar 'Coorong', selected from the CIMMYT program and grown in Australia after it had been tested at many locations. Shortly after commercial production began, a new race of *P. graminis* f. sp. *tritici* Eriks. & E. Henn. pathogenic for the gene *Sr27* was detected and the resistance of Coorong was shown to depend solely on this gene. Subsequent tests showed that resistance in a high proportion of CIMMYT triticales was due to *Sr27* and all were vulnerable to this race, despite the earlier tests at many locations in which this resistance remained effective. I had a similar experience in oats. Experimental oat lines I subsequently released as the cultivars 'TAM 0-301' and 'TAM 0-312'[4] had among the lowest crown rust infection ratings in the International Oat Rust Nurseries grown in many locations before their release; however, neither proved to have durable resistance when grown commercially in South Texas.

Johnson[3] stated that testing with many races of a pathogen from existing collections is a weak test for durability, particularly of a newly introduced source of resistance. For example, it is very probable Coorong triticale could have been tested to all races of *P. graminis* in culture collections in the world (possibly except Australia) without detecting pathogenicity for *Sr27*. Yet the experience in Australia showed that its resistance was not durable[3].

Johnson[3] also made the point that resistance cannot be described as durable if it has only been used briefly on a large scale. This would be an unusual scenario, but possible. In oat breeding, we may have had such an example with the 'Victoria' source of crown rust resistance. A large number of both spring and winter oat cultivars having crown rust resistance derived from Victoria were released in the period 1941-1945. Although there was no perceptible increase in the Victoria-attacking crown rust races between 1941 and 1945, when the acreage of Victoria derivatives increased from zero to about 80% of the USA total[1], widespread devastation of these cultivars by Victoria Blight, *Helminthosporium victoriae* Meehan & Murphy, caused them to be replaced as rapidly as possible[7]. By 1957, crown rust races virulent on Victoria comprised about 70% of all collections made in the USA, with the increase attributed to expansion in acreage of Victoria derivatives in the South[1]. It seems quite probable that the Victoria crown rust resistance would have proved even less "durable" had Victoria Blight not prematurely curtailed the production of varieties having this resistance in the spring-oat area.

Another important point made by Johnson[3] is that durable resistance may have several underlying causes. There are numerous examples of durable resistance conditioned by single genes (although not many in small grain rust diseases), and many examples of single-gene resistance which has not proved durable. Johnson[3] states that cases in which single-gene resistance has proved durable, though unusual, provide an important contrast to the notion that resistance will remain effective only if it is under polygenic or complex control. He also points out that there are many examples of durable resistance conditioned by more than one or two "major" genes, and that this does not necessarily indicate that a large number of genes are involved, as might be inferred from the term polygenic. Johnson[3] stated that it is often assumed that incomplete resistance will be under polygenic control and that such resistance will be race non-specific. However, there are many examples in which incomplete resistance (including slow-rusting of wheat, *Triticum aestivum* L., to stem rust, *P. graminis* f. sp. *tritici*, and to stripe rust, *P. striformis* West.) has been found to be highly race-specific. Thus, incomplete or "partial" forms of resistance may not prove durable. Therefore, Johnson[3] states: "Consequently, durable resistance cannot be recognized or defined by the degree of its effect on the epidemiology of disease."

Another important point which Johnson[3] mentioned is that resistance that has remained effective for a long period of time despite widespread use (which he defines as the "most powerful test for durability of resistance", assuming that production of the resistant cultivar(s) exhibiting the durable resistance took place in an environment favoring disease) may not continue to do so in the future. Certainly, we have had a good example of this phenomenon recently in small grains. The *T* gene for resistance to stem rust, *P. graminis* f. sp. *tritici* in barley, *Hordeum vulgare* L., had been used throughout North America for over 70 years[2]. In small grains, this undoubtedly was the best example of durable, single-gene resistance. However, in 1989 a new stem rust race which could overcome this resistance appeared in Kansas (B. Steffenson, pers. comm., 1992). Johnson[3] makes the point that "durable" is a relative term; if resistance in cultivars usually remains effective for no more than three or four years, and another cultivar grown under similar conditions remains resistant for 14 years, this resistance may merit the "durable" designation. It is clear that each additional year of resistance durability in a popular cultivar is far more valuable than resistance in a newly released one. Since several years are needed for a cultivar to come into widespread use on the farm, each additional year of profitable production of a popular cultivar has a much larger economic impact than do the years immediately following its release.

Two other ideas expressed in Johnson's review of durable resistance[3] are important considerations in undertaking the very difficult task of breeding for durable resistance. He states that if epidemics of disease are rather rare due to the combined influences of environmental conditions and resistant cultivars, there may be great difficulty in deducing that any particular cultivar or group of cultivars possess(es) genetic components giving greater durability than usual. In the rust "hotbed" areas in which I work, this would not pose much constraint to success, but in areas having light and/or sporatic disease pressure, it is a factor which must be considered. He also states: "If resistance in a cultivar is to be the only method used to control disease, it must be at an adequate level to inhibit the development of epidemics" (emphasis mine). The level of resistance required to provide adequate protection against crown rust and/or stem rust in various oat-producing areas (environments) may be very different!

My own philosophy about resistance to oat rust diseases is based on my own experience, and is admittedly biased. I recognize that some systems "work" (provide adequate protection to plant diseases) in some areas, but that these same systems may not be suitable for others. Therefore, my overall philosophy is that whatever system of breeding produces resistance adequate to provide effective disease protection in a given situation is a good system. I firmly believe that "if it ain't broke, don't fix it" is a good motto. Dr. Kenneth B. Porter produced some of the most popular wheat cultivars in the U. S. Great Plains without much effort in breeding for resistance to wheat leaf rust, *P. recondita* Rob. ex. Desm., as this disease generally does not cause much yield loss in the areas in which his wheats are best adapted (High Plains of Texas, Kansas, and Colorado). I was always envious of him, as he made great strides in improving yield of Hard Red Winter wheat in a relatively short period of time (probably much more progress than would have been possible had he been working in an area having high disease incidence). However, I am absolutely sure that the most important "yield" gene(s) that can be incorporated into improved oat cultivars in areas having high incidence of crown rust and/or stem rust are genes condititioning resistance to these diseases. Any other "yield" genes simply cannot be expressed in a plant killed by rust in the juvenile stage of growth.

I also am convinced that under the severe-disease situations we have in South Texas and in many of the oat production areas of South America, only high-level resistance provides adequate protection against rust diseases; slow-rusting, rate-reducing forms of resistance or plant "tolerance" do not give sufficient protection in subtropical rust "hotbeds". I also do not think that variety mixtures or multiline varieties containing a significant proportion of susceptible genotypes will produce acceptable yield and grain quality under the heavy epidemics characteristic of such areas. Reasons that the partial forms of resistance are not adequate in subtropical areas are: 1. Early infection is likely, particularly if oats are planted early for grazing. I have seen volunteer oats at Dallas "livid" with crown rust in late September. Early-planted oats (and wheat) for grazing in Texas frequently become infected with rust in the two-leaf stage. In seasons having mild winters, disease cycling is "nonstop" until plants approach maturity in the spring, or at least until plants are killed. Not only is grain yield devastated, but forage yield is severely reduced, and the grazing season can be shortened dramatically; 2. Length of the active disease season for fall-seeded vs spring-sown oats is very different, with many more cycles of rust possible for fall-seeded oats. If fall-sown oats become infected in October, disease cycling may be active for seven months before plants approach maturity in May in South Texas.

It is my understanding that delaying the "peak" of the crown rust epidemic in Iowa by three weeks will prevent severe damage. Delaying the peak of the epidemic by three weeks in South Texas only delays the death of the plant by three weeks; this would not have much positive effect on either grain yield or quality in years in which crown rust infection occurs in the fall and conditions are favorable for continuous disease activity throughout the entire growing season. Even in years in which we have some "winter" weather in the Coastal Bend area of South Texas (the exception rather than the rule, as winter wheats with normal vernalization requirements frequently do not head due to inadequate exposure to temperature below 4°C), crown rust is not really "stopped" for any significant time-span. Pustules survive and provide adequate inoculum to generate heavy infection as soon as temperatures moderate following the infrequent periods of cold weather. If oats survive, it appears that crown rust also survives. Although the disease can be held in check by cold weather, it is like a "crouching tiger", waiting to spring forth as soon as temperatures begin to warm in the late winter (by mid-February in South Texas); 3. Environmental factors (temperature, humidity, and dew deposition) favor development of very heavy epidemics much earlier in the plant's life-cycle in fall-sown oat crops grown in these subtropical areas. One could not hope to design a better inoculation chamber than the one nature provides in the field at Beeville, Texas, in my opinion. With heavy inoculum present on virtually every susceptible plant in the field, and the optimum environment for reinfection, it is no wonder that rust epidemics are devastating in this area. In Texas, crown rust becomes much less severe to the north and west. Winter temperatures are somewhat cooler (though generally quite mild) in the Central Texas Blacklands; this, or some other rather subtle environmental difference usually prevents the development of devastating crown rust epidemics from Waco northward. It is interesting to note that this environmental "barrier" does not prevent the routine development of very heavy epidemics of wheat leaf rust in this "light" crown rust area.

Chemical Control

Fungicides can help control disease losses in high-disease areas, but are a relatively poor substitute for effective plant resistance. Systemic seed treatment fungicides such as Baytan and Dividend could be used to prevent or greatly reduce fall infection of crown rust if they become approved for use on oats. These chemicals probably could be used on oats planted for grazing, as the length of time grazing currently is prohibited following emergence of Baytan-treated wheat is not excessive. The seed-treatment systemic fungicides do offer some promise, and probably would significantly alter disease epidemiology if they were used on all oats seeded in the high-disease areas, thus eliminating or greatly reducing the "crouching-tiger" inoculum largely responsible for rapid disease increase in the late winter or early spring, later culminating in very heavy rust epidemics.

However, it appears unlikely that systemic foliar fungicides will ever be approved for oats utilized for grazing. In Texas, only 20-25% of the planted oat acreage is harvested for grain, with the rest being "harvested" exclusively by grazing livestock (both cattle and sheep). Residue problems in green forage treated with foliar-applied systemic fungicides almost certainly would preclude grazing. In addition, it is obvious that high-level plant resistance is much more economical as well as effective in preventing loss from rust diseases. Our experience with many fungicide trials over the past seven crop seasons is that yield increases as large as 60 bushels per acre (2.2 metric tons per hectare) have been obtained from timely application(s) of effective experimental sterol-inhibitor chemicals to susceptible oat genotypes. The commercial sterol-inhibitor Tilt is being used successfully to protect the commercial oat crop in the Entre Rios area (Parana state) of Brazil. Two applications of the high recommended rate of Tilt are used; this approach to oat disease control has certainly improved and stabilized oat production in this area, which is subject to heavy losses from both crown rust and stem rust. However, this chemical is not yet registered for use on oats in the USA. As previously stated, it seems very unlikely that any systemic chemical will ever be approved for use on oats utilized for grazing, so fungicidal control of rusts is not likely to be the answer in Texas. In addition, we have found that although yields and test weights of susceptible oat genotypes can be improved dramatically by fungicide treatment, they still fall far short of those produced by untreated resistant genotypes. Genotypes with a high level of resistance to rusts have not shown any significant improvement in either grain yield or volume weight in response to fungicide treatment in any of our South Texas trials. Since genetic resistance provides more effective protection against oat rusts than any chemical we have tested, it appears obvious that breeding for resistance should remain a high priority in areas having heavy disease epidemics. Both seed treatment and foliar fungicides (if approved for use on oats) could be used to provide a "second line of defense" when needed. Development of oat cultivars with more durable resistance would reduce the frequency of "emergency" situations in which fungicide use would be required.

Breeding Strategy

Another of my own strong personal "Gospel-Truth" beliefs about resistance to oat rust diseases is that resistance is useless, unless it can be put into an acceptable agronomic "package". My plant pathology associates are prone to tell me that I should be using the polygenic resistance of some old cultivars, such as the Red-Rustproof type. However, the suggested parent almost always is very tall, weak-strawed, and late-maturing. Crossing with this kind of parent gives the plant breeding equivalent of the "Humpty-Dumpty" story — all the king's horses and all the king's men have little chance of putting either good agronomic type or the polygenic rust resistance back together again in segregates from such crosses, and virtually no chance of combining good agronomic type with the desired polygenic resistance. Backcrossing to genotypes having desirable agronomic characteristics improves the chance that desirable types can be selected, but further reduces the chance that all components of the polygenic resistance will be recovered, especially since identification of such genotypes is very difficult, as this type of resistance is quite subject to strong environmental influence. Therefore, my opinion is that this approach is unlikely to produce the desired type unless the breeder is unusually lucky.

Regional deployment of resistance genes probably would help stabilize production and increase durability of resistance in many cases. However, recent changes in virulence of crown rust biotypes in both spring and winter oat areas of the USA despite deployment of different resistance genes in cultivars in the two areas demonstrated that this strategy will not prevent development of virulent races and damaging epidemics in each area. Oats still should benefit to some degree, as new races in the two areas generally are not virulent on cultivars in the other area, so "imported" inoculum should be a weaker factor in disease epidemics.

As previously noted, we have had only a few examples of relatively long-term durable resistance to rust diseases in small grains. The *T* gene for stem rust resistance in barley certainly is the best example of durable single-gene resistance to small grain rusts in the USA. Stem rust resistance of US spring wheats and Australian wheats, both based on different "pyramids" of a relatively small number of genes, also has proved quite durable. Durability of resistance of US spring wheats may have been increased by interregional diversity of resistance in the Hard Red Winter and Hard Red Spring wheat areas of the U.S., with the *Tmp* gene derived from 'Triumph' providing resistance to all North American stem rust races except 15 and 56 in the winter wheats, and different genes providing resistance to these races in the spring wheats[6].

I believe that the best hope we have of developing oat cultivars with durable resistance to rust diseases lies in the old adage "there is safety in numbers". We have numerous examples in which combining several genes for resistance has provided protection against races for which none of the individual genes were effective. The durable resistance of Australian wheat varieties to stem rust is based on four "obsolete" resistance genes. The history of development of this gene "stack" is interesting. In 1960, 'Mengavi' with stem rust resistance conditioned by *Sr36* (derived from *T. timopheevi* Zhuk.) was released. New races with pathogenicity for *Sr36* were soon identified, and Mengavi was withdrawn. In 1964, the cultivar 'Mendos', which possessed *Sr7a, Sr11, Sr17, and Sr36*, was released but soon met the same fate. In 1967, 'Timgalen', possessing *Sr5, Sr6, Sr8, and Sr36*, and later 'Timson', 'Cook', and 'Shortim', with the same combination of resistance genes, were released. According to Johnson[3] all these cultivars remained resistant in the field in Australia despite widespread use (durability of 17 years to the time when Johnson's review was published). Therefore, this resistance has been very durable, although races with pathogenicity for *Sr5, Sr6, and Sr8* were common in surveys and it appears that the continuing resistance is mainly or solely due to *Sr36*, despite the earlier failure of resistance depending on this gene. Johnson[3] stated "Thus, present evidence indicates that this durable resistance is due to a combination of genes, each of which is know to be race-specific, and none of which provided durable resistance when used separately or in other combinations."

Since it is impossible to determine which genetic combination will prove to be durable during the developmental process, we should keep in mind that there is safety not only in "stacking" as many genes as possible, but also in developing a number of different gene stacks. It appears that this is the "strategy" which the crown rust fungus is using against us. According to Kurt Leonard of the USDA Cereal Rust Laboratory, field isolates of the oat crown rust fungus in the USA have a large number of virulence genes (average 30), including many that correspond to resistance genes that have never been used commercially in American oat cultivars (K. Leonard, pers. comm., 1991). This argues strongly against the notion that unnecessary virulence genes reduce the reproductive fitness of the fungus, and that biotypes containing such genes would have a strong selective disadvantage in nature.

I had an interesting gene-stacking experience with the Texas oat cultivar 'TAMO 386'. Its pedigree is Coker 75-12/4/'Coker 227'/'Coker 234'/3/TAM 0-301/TAM 0-312/2/CI9221 /5/TAM 0-312/Coker 227. It had excellent resistance to crown rust races to which the TAM and Coker parent cultivars were susceptible. When the cultivar became susceptible to a new South Texas biotype in 1991, about 1% of the plants remained resistant. We presume that these plants had a gene or genes for resistance not carried by the bulk of the population. This is quite possible, as both the Coker 75-12 and CI 9221 parents had some resistance to crown rust, though they were used primarily to improve lodging resistance (Coker 75-12) and stem rust resistance (CI 9221). It is interesting that resistant selections from our breeder's seedlot of TAMO 386 have exhibited a range of maturity, height, and seed type. In addition, a high percentage of lines derived from resistant panicle selections have been found to

segregate to crown rust, with segregation patterns which were also found to vary considerably. We do not yet have a good explanation for the "hidden heterogeneity" in this cultivar, or for the strong residual heterozygosity in resistant selections from it. A good number of resistant selections appear to have the same phenotype as TAMO 386, and we expect to release a reselected version of this cultivar within the next two years.

In developing a strategy for breeding for stable rust resistance based on gene stacking, one obvious question is "How many genes should we try to "stack", and what kinds of genes should we be using?". The relatively short life of varieties with the *Pc38 + Pc39* combination of crown rust resistance genes released by Canadian and North Central US breeders provides evidence that more than two "strong" genes should be used. In some cases, "weak" resistance genes may prove to be important. Dr. Marr Simons (Simons, unpublished data) once was shocked to learn that a gene from *A. sterilis* L., which conferred resistance to the most virulent crown rust biotypes then know in the U.S.A., was completely susceptible to an old biotype thought to be among the most avirulent in his collection. It is obvious that this "strong" gene from *A. sterilis* could still be useful, but that it would need to be combined with any of a number of "weak" genes that confer resistance to the avirulent culture.
A similar case has recently occurred in wheat stem rust. When the *T*-gene resistance of barley was overcome, there was some concern that wheats would be susceptible to this new biotype. Much to the amazement of everyone, the "universally susceptible" soft red winter wheat cultivar 'McNair 701', which has been used by USDA Cereal Rust Laboratory personnel as a stem rust "trap" genotype in wheat nurseries throughout the U.S.A., exhibited a resistant reaction to this biotype; obviously, it has a gene for resistance, though it was previously thought to have absolutely no resistance to the stem rust pathogen. Use of the *T*-gene biotype should allow the extraction and use of the McNair 701 resistance gene, even if other gene(s) in wheat confer resistance to his culture.

Some oat cultivars such as 'Portage' (released by H.L. Shands of the Univ. of Wisconsin in 1960) have exhibited rather stable intermediate-type reaction to crown rust for many years (D. Stuthman, pers. comm., 1991 and 1992). The resistance of Portage appears to be due to a "stack" of genes conditioning partial resistance. Dr. Stuthman noted that not all intermediate resistance has a polygenic "base"; individual genes conditioning partial resistance to many biotypes have been identified. The Oat Research Group at the Univ. of Minnesota and cooperators at Purdue Univ., Univ. of Queensland, and Univ. of Tel Aviv propose to combine a number of such genes to produce cultivars with durable resistance. They are attempting to "tag" a number of these genes with RFLP markers (preferably having each of the genes flanked at 5 map units or less) to allow identification of genotypes having all the desired genes. Use of genes conditioning partial resistance (rather than "stronger" genes conditioning higher-level resistant reactions) may or may not result in an adequate level of resistance for subtropical production areas. If such genes act in an additive manner, it might be possible to "build" an adequate level of resistance for severe-disease environments if a sufficient number of genes are combined. If all or most of the genes conditioning partial resistance are race-non-specific (a rather big "if"), the high-level resistance derived from their combined effect also would be expected to be race-non-specific, and durable. However, if genes conditioning the incomplete resistance are race-specific, the derived resistance would likely be less race-non-specific. As Johnson[3] pointed out, it really is not possible to prove conclusively that any resistance is not race-specific, as non-specificity is only recognized by the absence of specificity. At most, resistance that has not shown any specificity after prolonged testing could be classified as apparently race-non-specific. Nelson[5] stated that all resistance genes are race-specific when acting alone or combined in small numbers, and that they provide race-non-specific resistance when combined in larger numbers. If this is true, there probably would be no long-term advantage of using genes conditioning intermediate levels of resistance over genes conditioning complete resistance.

Conclusions

In my view, there is adequate evidence that combining an adequate number of resistance genes conditioning either incomplete or higher-level resistance (or combining genes conditioning both types of resistance) offers the best possibility of producing the desired stable resistance we need. To me, the question is not whether "to stack, or not to stack?",

but "how to stack?". Previous gene-stacking efforts have been based on using pathogen biotypes to identify the resistance genes being combined; the only alternative was to use test-cross data to determine the number of genes if differential biotypes could not be identified. In either case, stacking more than 3 or 4 genes becomes very difficult, if not impossible. However, some of the emerging biotechnological methodology may make it much easier to track genes in plants. As previously mentioned, Univ. of Minnesota workers currently are developing RFLP markers which should allow identification of plants having specific resistance-gene combinations. In addition, the development of a suitable method for producing doubled haploid plants in oats would allow determining the number of homozygous resistance genes on the basis of segregation of a single F_2 testcross progeny. Therefore, we may be on the threshold of a new "era" of capability in terms of producing and identifying genotypes having a number of genes conditioning resistance to crown and/or stem rust. Hopefully, this will result in our being able to develop and utilize oat cultivars with much more durable resistance to the rust diseases.

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Partial Resistance of Oats to *P. coronata* f. sp. *avenae*

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Summary

Several oat cultivars (*Avena* sp.) were inoculated on the 1st (primary), 2nd and 4th leaves with race 264 of *Puccinia coronata* f. sp. *avenae* (*Pca*) to characterise and determine components of partial resistance (slow-rusting). Panfive was the only cultivar to exhibit partial resistance giving a moderately susceptible reaction but expressing a lower infection efficiency, fewer and smaller uredia and a lower spore production compared to the susceptible cultivars Algerian and Sual for all three leaf ages tested. Of the components measured, uredium density gave the best indication of partial resistance across the three leaf ages tested for Panfive.

Introduction

Oat cultivars with complete or near complete resistance to leaf rust (*Pca*) have a relatively short field life due to the great genetic variability in the *Pca* populations[1]. Partially resistant (PR) or slow-rusting lines which place less selection pressure on the pathogen and act to slow the rate of epidemics are now being sought in an attempt to prolong the field life of cultivars. Plants expressing partial resistance exhibit longer latent periods, lower infection efficiences, fewer and smaller uredia and/or reduced sporulation when compared to susceptible cultivars[3,7,12,15,23,24]. In an endeavour to develop a glasshouse screening procedure to select for PR plants, an experiment was conducted to indentify which components gave the best indication of PR. In addition, the effect of leaf age on the expression of each of the components was investigated.

Methods

The oat cultivars Ascencao, Panfive and Sual were included in the experiment due to their moderately susceptible to moderately resistant reactions in the 1989 field trials at Toowoomba, Qld. Garry, cited in the literature as a slow-rusting cultivar[9], was also included in the experiment. Algerian and Saia were used to represent susceptible and resistant controls respectively. The 1st or primary leaf and the 2nd and 4th leaves of the plants were inoculated with race 264 of *Pca*. The leaves were laid flat on cardboard, abaxial side up and held in place by two rubber bands. Plants were placed in a spore settling tower[2] and inoculated with 10 mg of uredospores. A deposition of 540 uredospores/cm^2 (coefficient of variation 27%) was obtained using this method. Plants were incubated overnight in a dew chamber at 20 ± 1°C. They were then transferred to a temperature controlled growth cabinet maintained at 24 ± 2°C and subject to natural light fluctuations.

Plants were assessed for disease reaction 12 days after inoculation using the ratings system described by Murphy[13]. The disease components measured included latent period (in days), infection efficiency (no. uredia/no. spores deposited), uredium density (no./cm^2 leaf area) and size (mm^2) and spore production (no./cm^2 leaf area). Analysis of the data was by single or multiple analysis of variance and comparisons between means were made at the $P < 0.05$ level of significance[19].

Results and Discussion

Panfive which was moderately susceptible to *Pca* in the field at Toowoomba, Qld, expressed a lower infection efficiency (Table 1) and fewer uredia (Table 2) when compared to the susceptible cvs Algerian and Sual for all three leaf ages tested. Panfive also expressed a lower infection efficiency and a reduction in spore production compared to

the susceptible cultivars. All of these factors would contribute to a reduction in the rate of an epidemic and therefore Panfive appears to express partial resistance. Panfive was selected from a cross between Lodi and PI267989 (*A. sterilis*)[5] and contains at least one dominant gene *Pc* 36 which confers resistance to race 264 and others[22]. The PR of Panfive appears to be controlled by a single recessive gene (Martin, Brake, Irwin: unpublished data). While the durability of this incomplete resistance cannot be predicted, the level of resistance expressed by Panfive may be sufficient to effectively reduce losses caused by leaf rust epidemics.

Table 1. Cultivar and leaf age differences in infection efficiency.

Cultivar	*Infection efficiency*		
	1st leaf	*2nd leaf*	*4th leaf*
Algerian	0.90a	1.11ab	0.67a
Ascencao	0.04b	0.16d	0.05b
Garry	0.33c	0.80bc	0.73a
Panfive	0.35c	0.65c	0.09b
Saia	0.01b	0.10d	0.004b
Sual	1.15d	1.18a	0.36ab

Within columns, numbers followed by the same letter are not significantly different ($P < 0.05$). l.s.d across rows ($P < 0.05$) Algerian - ns; Ascencao - 0.06; Garry - 0.34; Panfive - 0.31; Saia - ns; Sual - 0.38

Table 2. Cultivar and leaf age differences in uredium density.

Cultivar	*Uredium density (/cm^2)*		
	1st leaf	*2nd leaf*	*4th leaf*
Algerian	64.60a	47.20a	20.69a
Ascencao	5.45b	5.78b	0.75b
Garry	29.29c	50.47a	13.83c
Panfive	30.85c	22.40c	7.61d
Saia	2.94b	0.39b	0.03b
Sual	54.04d	52.79a	23.46a

Within columns, means followed by the same letter are not significantly different ($P < 0.05$). l.s.d across rows ($P < 0.05$) Algerian - 7.41; Ascencao - 0.34; Garry - 9.38; Panfive - 8.07; Saia - 1.08; Sual - 6.93

Although Garry was considered slow-rusting when compared to Algerian in the mid 1970s[9], evidence obtained from this work has indicated that this cultivar was more like the susceptible cvs Algerian and Sual both in the field and the glasshouse, producing large numbers of medium to large uredia.

Uredium density which has frequently been found to be an indicator of slow-rusting[6,7,10,11,12,15,21], gave the best differentiation between cultivars for the three leaf ages tested. Infection efficiency also appeared to give a good indication of slow-rusting reflecting closely the results for uredium density.

Latent period, uredium size and spore production did not give good differentiation between cultivars, although all of these components have been reported as being indicators of slow-rusting[3,4,7,8,10,12,14,15,16,17,18,20,21]. The susceptible cultivars Algerian, Garry, Panfive and Sual all expressed a latent period of 6 days regardless of leaf age. In contrast, the highly resistant cvs, Ascencao and Saia expressed slightly longer latent periods of 7 to 10 days. Uredium size similarly failed to give clear differentiation between cultivars as all cultivars including the resistant Ascencao and Saia, produced uredia comparable in size. Spore production, as expressed as the number of spores/cm^2 of leaf tissue, gave clear differentiation between cultivars although statistically the differences were not significant due to the amount of variability present in this component. These components which did not clearly differentiate between the cultivars in the seedling stage, may be expressed in the adult stage in the field.

In general, disease resistance increased with an increase in leaf age for all of the components measured although there was a slight increase in susceptibility in the second leaf of some cultivars for various components including infection efficiency and uredium density (Tables 1 and 2). While only seedlings were inoculated in the glasshouse, the reactions of the cultivars reflected their field response with respect to the relative rankings. It is therefore envisaged that by inoculating the 1st or 4th leaves and by measuring uredium density, it would be possible to select for partially resistant cultivars in the glasshouse.

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Stem Rust Resistance Genes in Mexican Oat Germplasm

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Summary

Oat stem rust is the principal oat disease in the oat growing area in Mexico. This study was undertaken to determine the resistance in Mexican oat germplasm. One hundred and three oat lines and varieties, were tested. This material was evaluated in adult plant stage at the Glenlea field station at Winnipeg, Canada in the summer of 1991. All the lines were artificially inoculated with a composite of races NA8, NA16, NA25, NA26, NA27, and NA55. All lines were also evaluated in the seedling stage individually to the above races in the greenhouse tests. Of the 103 lines, 29 were resistant to all the six races, indicating the presence of gene combinations or perhaps gene *Pga*. The remaining lines showed variable reactions, with some lines indicating the presence of gene *Pg2*. The field data indicated more variability, with reactions ranging from resistant to susceptible. The results indicate a promising level of resistance in the Mexican oat germplasm, warranting further genetic and environmental evaluation.

Introduction

Oat breeding began in Mexico in 1959. The emphasis in this project has been to develop suitably adapted cultivars with earliness, stem rust resistance, high yield, and high quality. However, less attention has been paid to source of stem rust resistance and the development of appropriate resistance breeding strategies.

The main disease affecting oat in the high plateau region of Mexico (200, 000 hectares) is stem rust caused by *Puccinia graminis* Pers. f. sp. *avenae* Eriks. & Henn, and oat workers at Cd. Cuauhthemoc, Chih. have become more concerned with this disease. The virulence of the natural rust population in Mexico[(4)] is similar to that in Canada[(1)], with race NA27 predominating. In our plant breeding program we are interested in identifying effective genes for stem rust resistance. The objective in this study was to determine the level of resistance to a range of virulence phenotypes of *P. graminis avenae* in the Mexican oat breeding germplasm.

Methods

One hundred and three lines and varieties from the Mexican oat breeding program were evaluated in greenhouse and field tests at the Agriculture Canada Research Station, Winnipeg. In the field tests the lines were planted in single 1 meter rows, with a row of mixture susceptible line planted every fifth row as rust spreaders. The spreader rows were inoculated with a composite of six races NA8, Na16, NA25, NA26, NA27, and NA55 of stem rust *P. graminis* f. sp. *avenae* in the first week of July. Rust severities were evaluated August 12, 1991 using the modified Cobb's scale. In the greenhouse all lines were evaluated in the seedling stage individually to the above races. Infection types 0, ;, 1, 2, and 3 - were considered resistant and infection types 3 and 4 as susceptible.

Results and Discussion

The seedling reactions to the individual races are shown in Table 1. Few identifiable resistant genotypes emerged from this test. From these results 28% of the lines had resistance to all races (Table 1 row a), and could contain either gene *Pga* or a combination of genes.

another possible genotype is gene *Pg2* (Table 1 row e). There were a significant number of lines that could not be fitted to known resistance genotypes.

Table 1. Numbers of lines and reaction patterns (resistant (R) or susceptible (S)) to six races of *Puccinia graminis* f. sp. *avenae*.

	No. of lines	*Percent of lines*	*Race*					
			NA8	NA16	NA25	NA26	NA27	NA55
a.	29	28.2	R	R	R	R	R	R
b.	7	6.8	R	R	R	S	R	R
c.	8	7.8	R	R	S	R	R	R
d.	30	29.1	R	R	S	S	R	R
e.	12	11.7	R	R	S	S	S	S
f.	1	1.0	S	S	R	R	R	R
g.	1	1.0	S	R	S	S	S	S
h.	3	2.9	R	R	S	S	S	R
i.	9	8.7	R	R	S	S	R	S
j.	1	1.0	R	R	R	S	S	S
k.	1	1.0	R	R	S	R	R	R
l.	1	1.0	R	R	S	R	S	R

The classification of the field reactions are shown in Table 2. The natural level of oat stem rust occurrence in Manitoba in 1991 was light[1], therefore the field reactions in this test are representative of races used.

Table 2. Classification of field reactions of Mexican oat lines to a artificially inoculate races of *Puccinia graminis* f. sp. *avenae* at Winnipeg, Manitoba in 1991.

No. of lines	*Percent of lines*	*Reaction class*
15	14.6	Resistant/moderate resistant
28	27.2	Moderate resistant/moderate susceptible
28	27.2	Moderate susceptible
21	20.4	Moderate susceptible/susceptible
11	10.6	Fully susceptible

Due to the use of race composites and possible environmental and growth stage effects, the field reactions are not as definitive as are the seedling tests. A factor to consider is the possible presence of gene *Pga*. This gene (or gene complex) is less effective in the adult plant stage than in seedling stage[2].

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Slow Crown Rusting in Oat

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Summary

The pathogenic plasticity of *Puccinia coronata* has made it difficult to develop durable resistance to crown rust of oat using major genes for hypersensitivity. As an alternative genetic control, we are investigating slow rusting, a form of partial resistance. In experiments in the greenhouse. *P. coronata* did not develop as prolifically in three accessions of *Avena sterilis* as in a susceptible cuitivar of *A. sativa.* The *A. sterilis* accessions had smaller pustules compared to the susceptible cultivar. Two of them had fewer pustules per unit of leaf area, and one had a longer latent period compared to the susceptible cuitivar. Reduction in pustule size, with attendant reduced spore production may be a major component of slow crown rusting in *A. sterilis.*

Introduction

Crown rust continues to be one of the most destructive diseases of oat in North America despite attempts for more than 60 years to control this disease by use of genetic resistance. The pathogen is highly polymorphic for specific pathogenicity — the ability to overcome the effects of specific resistance genes in the host. An alternative approach to the use of race-specific, hypersensitive resistance is to use partial resistance, e.g. slow rusting. Slow crown rusting was described and characterized more than 20 years ago[1,3]. However, slow rusting has not been employed by oat breeders in North America for control of crown rust. Lack of proven procedures for phenotypic selection and the abundance of genes for hypersensitive resistance from *Avena sterilis* may be why. However, the hypersensitivity from *A. sterilis,* like that from *A. sativa,* has provided only ephemeral control of crown rust. Our work was undertaken to identify slow rusting lines and to develop protocols for detecting slow rusting in monocyclic infection studies in the greenhouse. We found evidence for lower receptivity, smaller pustules, and slightly longer latent periods in three accessions of *A. sterilis,* compared to Clintford.

Methods

Avena sterilis line PI 412163 was selected for study because it had a low severity but susceptible reaction type to crown rust in the field in Iowa. *A. sterilis* lines Ts 1469 and Ts 7204 were obtained from U. Brodny in Israel, who described them as slow rusting. *Avena sativa* line MN 841824 was one of several lines bred and selected for consistent moderate resistance in the buckthorn nursery by M.B. Moore at the University of Minnesota. Seed of these accessions and of Clintford, the fast rusting check, were sown in flats of soil and placed for one month in a cold room a 3°C with a 12 hour photoperiod. After this cold treatment, seedlings (1- to 3-leaf stage) were transplanted individually into 15 cm diameter pots that contained a standard soil-peat mix.

Experiments commenced once plants had jointed. Five replicate plants of each cultivar were inoculated in a randomized complete block design. The uppermost fully expanded leaf, usually flag -1, -2, or -3, was inoculated by spraying it with urediniospores of race Pc 54 of *Puccinia coronata* var. *avenae* that had been suspended in Soltrol 750. After the oil evaporated from the leaves, plants were placed in a moist chamber overnight (5pm–9am the following morning). Prior to closing the chamber, plants were misted with water.

Isolate Pc 54 of *P. coronata* was obtained from A. Epstein of Iowa State University. It was originally collected in 1982 because of its virulence on TAM-0-301 (gene Pc 58). It is also virulent to Ukraine, Trispernia, IA Y344, TAM-0-312, and IA Y349.

Beginning 8 days after inoculation, erupted pustules on the adaxial surface of each leaf were counted, either on a measured segment of leaf or in 10 equidistant circular areas of 6 mm diameter. Pustules were counted daily in the same area on each leaf until no new uredinia appeared. Lengths of five arbitrarily chosen pustules were measured with a measuring magnifier calibrated to 0.1 mm. Latent period was calculated as the time required for 50% of the final number of pustules to erupt by probit analysis[5].

Results and Discussion

Pustules began erupting on most plants by 8 days after inoculation. Typically, pustules continued to erupt until 15–17 days after inoculation. The rate at which new pustules erupted diminished with time. Although cultivars differed significantly in latent period, the range in mean time required for 50% of the pustules to erupt was only 2 days (Table 1). The variation among experiments was highly significant, as was the experiment x cultivar interaction. This interaction could not be ascribed to any one cuitivar. All cultivars except Ts 1469 had long latent periods in some experiments and short latent periods in others. Ts 1469 had a consistently long latent period (10 days or longer).

The cultivars also differed in the final number of pustules that developed (Table 1). On average, Ts 1469 had less than one-fourth as many pustules per square centimeter as did Clintford. This parameter of rust development also varied among experiments, and the cultivar x experiment effect was significant. In two experiments all of the cultivars had only a few pustules per square centimeter, whereas in two other experiments there was a greater difference between Clintford, MN 841823, and Ts 7204 on the one hand, and PI 412163 and Ts 1469 cn the other.

Pustule length varied greatly among cultivars (Table 1) pustules on Clintford and MN 841823 were large. Those on Ts 7204 were intermediate. and those on PI 412163 and Ts 1469 were small. In three experiments the infection type was recorded for each plant at the time pustules were measured (Table 1). Within each cultivar there was variation among plants, due partly to genetic differences among plants of a cultivar. The accessions with the smaller pustules had a higher frequency of pustules with chlorotic or necrotic borders, but pustules that lacked a distinct chlorotic or necrotic border on these accessicns were not noticeably larger than those that did.

Pustules were measured twice, at 12 and 15 days after inoculation in two experiments and at 13 and 16 days after inoculation in a third. Pustule length increased on Clintford between the two times. Length increased slightly on MN 841824, but remained constant or decreased slightly on the *A. sterilis* lines.

For each experiment and cultivar we calculated the coefficient of variability. Latent period, calculated as T50, was least variable, with most CVs in the range of 9 - 18%. The number of pustules per square centimeter was most variable, with most CVs in the range of 40 - 120%. Most CVs for pustule length were in the range of 20 - 37%. The *A. sterilis* accessions were more variable for infection type, which suggested that this material was more genetically heterogeneous than the inbred *A. sativa* cultivars. However. such heterogeneity was not indicated by greater CVs for latent period, pustule density, or pustule size compared to the *A. sativa* cultivars.

Our work with three accessions of *A. sterilis* revealed components of slow rusting similar to those identified in earlier studies with *A. sativa* and A. *byzantina*[1,3,9]. All three *A. sterilis* accessions had smaller pustules than Clintford's: two accessions had fewer pustules per square centimeter, but only one had a longer latent period.

The greater variation in infection type and the lower number of pustules per square centimeter on the *A. sterilis* accessions compared to Clintford and MN 841824 leads us to speculate that there is variation among infection sites on same leaf of the kind described for slow rusting *A. byzantina* line CI 4876[2].

This variation results in arrest of fungal growth in some infection sites and to restricted pustule growth in others. Evidence for restricted hyphal growth in the accessions we studied is the fact that pustules ceased growing sooner in *A. sterilis* compared to Clintford and final size

was smaller. This is similar to what has been observed in slow leaf rusting wheats[6]. Presumably these smaller pustules would produce fewer spores which would impair the reproductive ability of the fungus in the field[1,7].

If slow rusting is to be included as a selection criterion in breeding programs, methods of reliable phenotypic selection must be developed. Field screening is subject to the vagaries of weather and occurrence of other diseases which may interfere with crown rust development. An alternative is to use controlled inoculations in the greenhouse. The characteristic of slow rusting used for selection must be amenable to easy and rapid measurement, and have a high heritability. The present study provides no information about heritability, but it provides some guidance about choice of a character for selection. In our studies with wheat slow leaf rusting, we have found that latent period is a major component[4,7,8]. This character is not highly sensitive to inoculum dose and therefore strictly quantitative inoculation is not required. In this study we found that latent period did not vary greatly among oat lines, and that even on the susceptible cultivar Clintford the latent period was much longer than what is typical for a wheat cultivar susceptible to leaf rust. Within limits, pustule size is not greatly influenced by pustule density[6], so this may be a feasible character for measurement and selection of slow crown rusting genotypes of oat. Pustule density would be much more difficult to use as a selection character because inoculum application and control of moisture on leaf surfaces would need to be carefully controlled in order to ensure that the number of germinated spores per unit area of leaf was uniform on a large population of plants. In two of the four experiments reported here pustule number evidently did not reach its potential on all accessions. It is likely that attempts to select on the basis of pustule density would lead to many more misclassifications of individual plants than would selection for pustule size.

Slow rusting in oat may be a durable form of resistance[1,3]. If this is so, and if reliable and rapid selection techniques for this character are developed, it can be used routinely in breeding programs where crown rust is a persistent problem.

Table 1. Slow rusting components of five oat accessions compared to Clintford.

Accession or cultivar	*Latent period (days)*	*Pustules/ cm^2 (no.)*	*Pustule length (0.1 mm)*	*Infection type frequency*[a]				
				P	PC	C	CN	N
Ts 1469	11.5 c	2.6 a	3.8 a	8	1	6	2	2
PI 412163	10.6 bc	5.7 ab	3.9 a	15		4	3	1
Ts 7204	10.0 ab	11.8 c	6.8 b	7	2	9	3	3
841824	9.5 a	6.9 b	10.7 c	5	4	5		
Clintford	10.2 ab	12.1 c	15.5 c	18		6		

a P=pale green around pustule. C=chlorosis around pustule. N=necrosis around pustule. PC is intermediate to P and C. CN is intermediate to C and N.

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Dew Period Length — A factor in selection for aggressiveness in Crown Rust of Oats caused by *Puccinia coronata avenae*

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Summary

Length of dew period was tested as a means of detecting differences in aggressiveness between known pathogenic races Pc-59 and 264-B of the oat rust pathogen. *Puccinia coronata avenae* race 264-B appears to be able to penetrate and establish itself in a shorter period of dew (6 hours) and consistently produced larger quantities of urediospores throughout the period of this study (4 months) than Pc-59. These findings raise the possibility that dew period length may be a factor for selection of aggressiveness within pathogenic races.

Introduction

Variation in pathogen populations has been and continues to be of great concern to Plant Pathologists. This concern is based on experience with pathogens which has shown that there are advantages of gene recombination at the population level as proposed by Fisher[2] and Felsenstein[1] which apparently enhance the effectiveness of genes for pathogenicity. In the cereal rusts pathogenicity is conditioned by genes that exhibit simple mendelian inheritance in small or finite populations[5,8]. Recombination of individual loci has been reported in certain pathogen populations and is thought to be advantageous (fitness) to the pathogen[3]. There is now convincing evidence that sexually reproducing populations of *P. coronata* are more aggressive[4,6,7]. A number of traits have already been described and characterized as contributing to the aggressiveness of various pathogenic configurations of *P. coronata* on oat[6]. However it occurs to the authors that the so-called latent period encompasses a rather lengthy period of time[6,7]. We decided to check on the length of time required for germination and establishment by two races (264-B and Pc-59) of *P. coronata* by inoculating them on a susceptible oat cultivar and exposing them to varying lengths of leaf wetness periods.

Materials and Methods

All inoculations were conducted using the variety Markton (universal suscept). Plants (15 per pot) were grown in 10.2 cm diameter clay pots in a standard greenhouse mix soil (2;2;1 — soil, peat, perlite) pasteurized in an aerated steam soil treater. Inoculations were carried out when plants were in the first leaf stage just prior to emergence of the second leaf.

Inoculum consisted of urediospores produced on the variety Markton. Freshly harvested spores (80% germination or higher on 2% water agar) were applied in "Isopar" oil (Exxon) prepared to contain 1 mg of spores per cc of oil. The inoculum (3cc) was applied in 4,4,– second bursts via an atomizer at an elevation of ½ meter over the plants which were on rotating platforms at the bottom of a spore settling tower. The atomized inoculum was allowed to settle for 6 minutes after which the plants were placed in a dew chamber (Percival) held at 16°C air temperature with water at 23°C and walls at 14°C. Plants were removed from the dew chamber at intervals of 6,12,24 and 48 hours and placed on a greenhouse bench with 16 hours of light and temperature at 17°C for further incubation. After 8 days the plants were examined for number of pustules per leaf and weight of spores which were collected at 3 day intervals following eruption of approximately ¼ of the pustules. Spores were collected by gently tapping the infected leaves with a glass rod while

the plants were held in a horizontal position over a sheet of high gloss paper (Canson Special Airbrush) 30 cm x 38 cm within a three-sided polyethylene tent. The spores were then gently scraped toward the center of the collection paper with a single edge razor blade and shaken on to a preweighed sheet of glassine paper (7.5 cm x 12.6 cm) for weighing.

Results and Discussion

Pustule numbers and spore production in milligrams by race and dew period length are presented in Tables 1 and 2. The moist period required for establishment of infection by race 264-B was shorter than that of Pc-59. Production of urediospores by 264-B exceeded that of Pc-59 throughout the spore collection period of this test. Surprisingly the longest dew period (48 hours) appeared to depress the production of spores. The size of pustules produced by race 264-B following the minimal dew period (6 hours) appeared more variable than those resulting from longer dew period.

Dew periods have long been recognized as requisite for the development of rust outbreaks and some parameters have been established as necessary for the development of severe outbreaks. It is tempting therefore to speculate on the possible impact of the length of those dew periods upon the overall populations of the pathogen. Would 24 hours of continual dew result in a more diverse population of rust races or would it favor those races requiring a longer dew period? i.e. are there members that are less fit or are there so many infections that competition is causing a depression in spore yield? Conversely would more extreme conditions favor more aggressive genotypes (better fit)? Race 264-B is certainly better able to establish itself under short dew periods than Pc-59 however it also appears to be more aggressive in terms of inoculum production than Pc-59 at all dew regimens. It will be interesting to test these procedures on field collections of *P. coronata*.

Table 1. Numbers of pustules

		Dew Period (in hours)	*Replicates* I	II	III	IV	*Mean*
1.	Pc-59						
		6	0.0	0.0	0.0	0.0	0.0
		12	1.27	1.33	1.31	1.17	1.27
		24	3.31	4.13	3.59	3.43	3.61
		48	17.14	9.29	16.64	18.98	15.51
2.	264-B						
		6	1.35	4.7	3.5	4.4	6.53
		12	46.10	45.76	61.89	53.10	51.71
		24	63.02	48.46	52.28	59.68	55.86
		48	43.91	39.61	47.65	43.49	43.66

* Significantly different from Pc-59 at the 99% level of confidence (95% Tukey HSD).

Table 2. Weight of Urediospores Produced (in Mg)

	Dew Period (in hours)	*I*	*II*	*III*	*IV*	*Mean*
1.	Race Pc-59					
	6	0	0	0	0	0
	12	12.0	15.7	9.1	13.5	12.57
	24	22.3	27.1	35.7	39.5	31.15
	48	16.0	8.1	10.2	16.8	12.77
2.	Race 264-B					
	6	0	0	0	0	0
	12	30.8	37.5	49.7	55.6	43.40
	24	53.9	46.9	53.1	42.4	49.07
	48	34.2	36.7	40.9	23.8	33.90

* Significantly different from race Pc-59 at the 99% level of confidence (95% Tukey HSD).

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Field Research and Germplasm Evaluation Methodology for Barley Yellow Dwarf Virus in Cereals

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Introduction

Barley yellow dwarf is the most economically important virus disease of cereals. It has a worldwide distribution affecting over 100 species in the family Poaceae, including barley, wheat, oats, sorghum, rye, triticale, maize, rice and a wide variety of wild grasses[4]. BYD is caused by a continuous, often overlapping range of luteoviruses that are more or less related serologically[9]. Symptoms of BYD are sometimes difficult to identify; the characteristic stunting of the plant and reddening or yellowing of leaves are often misinterpreted as nutritional deficiencies or environmental insults. BYDVs are grouped into strains on the basis of their transmissibility by over 30 species of aphids[1,5]. Once the virus is acquired, the vector is potentially infective for life. No means, other than the aphid, is known for naturally or experimentally infecting graminaceous hosts. Rochow[8] characterized five BYDV strains found in New York State, USA and gave each an acroynym based on the genus and specific epithet of the principal vectors. Thus, MAV is transmitted specifically by *Sitobion avenae* (previously *Macrosiphum avenae*), RPV by *Rhopalosiphum padi*, RMV by *Rhopalosiphum maidis*, and SGV by *Schizaphis graminum*. PAV is transmitted non-specifically by *R. padi* and *S. avenae*.

In North America, the only practical means of reducing cereal yield losses from BYDV is through development of tolerant or resistant (*sensu* Cooper and Jones, 1983[2]) cultivars. Evaluation of germplasm is efficient only if a reliable means of inoculating materials of interest is found. To accomplish this end, some programs have amplified already high levels of natural infection through management practices such that reliance on artificial inoculation is unnecessary[6,10]. In one or more states of the American Midwest, BYDV epidemics occur nearly every year, but in any given area disease incidence varies. Thus, to ensure year to year continuity in the cooperative Department of Agronomy - USDA ARS Cereal Virology BYDV breeding program, artificial inoculation techniques were developed by H. Jedlinski and C.M. Brown and modified by us to infect thousands of entries each spring and fall with BYDV-PAV-IL, a moderately severe, well-characterized isolate (1986). Artificial inoculation has a number of advantages: germplasm response to a single BYDV or a known combination of BYDVs can be evaluated in trials replicated in both time and space, uniformity of infection is assured and levels and timing of infection can be controlled.

Methods

Virus isolate and aphid vector maintenance

Our laboratory maintains 7-10 different cereal aphid species and an equal number of characterized BYDV isolates. Each BYDV isolate is kept in infected plant cultures: at least one infected plant culture is kept without aphids and one or more with aphids (viruliferous colonies). Many more virus isolates are kept as plant cultures and are infested with vectors only when needed. Each aphid species is maintained as a non-viruliferous colony. Vector colonies are transferred regularly, the schedule determined by the biology of the aphid species. Avoiding inadvertent mixing of aphids or BYDVs is a simple task if careful attention is paid to scheduling transfers and isolating different vectors. The purity of vectors is monitored at every transfer and the identity of the BYDV isolates is tested at regular intervals by serology and by luteovirus PCR[7]. To establish colonies, seeds of a cereal preferred by each aphid species are sown in clay pots. When the plants are at growth stage 5 or 6 (Feekes scale), 10-30 aphids are transferred to the plants and confined in cages.

The cages are made of tubular Plexiglas® with two large windows cut in the sides for ventilation. The windows and the top of the cage are fitted with plankton netting of a mesh size (100 micron) that will confine even the smallest nymph. To guard against aphid escapes, the top of the pot and the cage are sometimes wrapped in Parafilm or the cage/soil interface is sealed with finely sieved soil.

Distribution of aphids in field inoculation

To inoculate approximately 10,000 hills and have vectors available over a period of 2–3 weeks each spring and fall, 50 viruliferous vector colonies are established each week for 3 weeks. About 7 weeks before field inoculations begin, 3 or 4 Hudson barley seeds (a cultivar that withstands both infection with the virus and heavy aphid pressure) are planted in 15 cm clay pots; 3-4 weeks later the plants are infested with viruliferous *R. padi.* Up to 150 colonies at one time are reared on greenhouse potting benches, fitted with Plexiglas® enclosures and window air-conditioners. The potting bench enclosures serve as an extra precaution against aphid escapes and help to maintain temperatures at 20–25°C. After establishment, colonies are held in the enclosures while the aphid populations increase. The day before field inoculations, the colonies are moved to a cool transfer room. Early the next morning the cage is removed from each colony and the vectors are shaken onto a piece of butcher paper that has been dusted with talc to prevent the aphids from sticking together. After several colonies have been shaken, the paper is rolled into a cone to transfer the aphids to a waxed cardboard container for transport to the field. In the field, the aphids are mixed with corn meal (usually 1:2/v:v) and placed into a dispensing device dubbed a "bug blaster" by our group. The bug blasters are modifications of devices developed at CIMMYT and by Wiseman[11]. The amount of cornmeal can be increased or decreased to regulate the number of vectors that will be dispensed in one aliquot. Thousands of hills can be inoculated quickly and efficiently with a small crew. In the past, before the vector dispenser was used, 50-100 aphids were swept from the waxed containers onto each hill with a sable brush. This method was very effective, but the number of aphids placed on each hill varied, and every member of the crew had to crawl on the ground to carefully place the vectors into the center of each hill. The use of the bug blaster has more than halved the amount of time needed to inoculate, it allows for more uniform inoculation of hills compared to the sable brush method, and fewer aphids are used per hill. Five to ten days after infestation, the aphids are killed with Cygon. Response to BYDV infection is evaluated one or two times after panicles emerge using a 0-9 scale[6,10].

Design of germplasm evaluation and enhancement fields

After the soil is worked, preferably into a moderately fine seedbed, the field is marked into a grid; furrows, 90 cm on center, run the length of the field and shallow furrows cross the field at 30 cm intervals. Thus, the rows of hills are planted 90 cm apart and the hills within the rows are planted 30 cm apart. Paired hills of each entry are planted side-by-side snaking in parallel up and down the field. Traditional corn punch planters have been modified to create a 3 cm diameter hill. A dense barrier row of winter oats or winter wheat is pushed in between the rows of inoculated and control hills to minimize infestation of the control hills. Spring oat barrier rows are preferred in the Midwest for fall planting because they do not survive the harsh winter, leaving only the test and control hills in the field in the spring. Winter wheat barriers are used in spring because they do not head. Sometimes the barrier rows are removed after the field has been treated with insecticides to kill the aphids used for inoculation. Maintenance of uninfected controls in years of high BYDV incidence can be a problem. BYDV is most damaging when infection occurs at an early growth stage. By planting at the earliest possible date (late March or early April in central Illinois), control hills can be in the early boot stage before the first large aphid flights arrive in mid-May. Thus, a good comparison between a hill artificially inoculated in late April and a control hill inoculated naturally in mid-May can be made. Symptoms in oats are sufficiently dramatic to obviate the need for control hills. The response of breeding material is usually compared with known standards instead of control hills. In contrast, BYDV symptoms in spring and fall wheat are generally more subtle and control hills are planted for comparison.

Yield plots for replicated experiments

The methods first developed for germplasm evaluation and enhancement have been adapted to a variety of research projects including crop loss modeling, yield loss studies, and investigations of the dynamics of BYDV spread. There are a number of advantages to using yield plots: they are quickly planted with readily available equipment, treatments can be adequately randomized and replicated within a single field, the plots are narrow enough to allow collections of plant tissue or vectors without entering the plot and perturbing the vectors, and yield data is very easy to collect.

Foci of infection can be established to evaluate BYDV spread by dispensing one or more aliquots of viruliferous vectors with the bug blaster into the plot. If a random infection pattern is desired, the aphid/cornmeal mixture is dispensed with the bug blaster into a small plastic container with 0.5 cm holes in the top. The aphids are then randomly shaken over the plot. Levels of infection (foci or randomly generated) for crop loss models are established in the same way. Random application of a large number of aphids can be used for uniform infection of plots for yield loss studies.

Epidemiology in areas of high natural BYDV incidence

In areas of high BYDV incidence data generated from the spread of virus that has been artificially introduced into an experimental field is often confounded by naturally occurring infections that originate from outside the plot. Many BYDV isolates collected as part of a state-wide incidence survey have been characterized and a few are unique. These isolates are serologically indistinguishable from the BYDV-PAVs that occur every year in our area yet their banding patterns differ when analyzed by the luteovirus PCR technique. Using these isolates for our epidemiology studies in the field allows differentiation between artificially introduced and naturally occurring BYDV-PAVs.

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Characterisation of Resistance to Crown Rust in Oat

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Abstract

Crown rust, caused by *Puccinia coronata* Cda. var. *avenae* Fraser and Led., has historically been the most destructive fungal disease throughout the world on oat (*Avena sativa* L.). Control of this pathogen through breeding depends on identification of diverse and stable resistance from *A. sativa* as well as its related species. The objectives of this research are to 1) identify oat lines that express resistance to crown rust, and 2) characterise the expression of this resistance.

Two spring oat lines, MN84-1804 and MN84-1811 were identified as having moderate resistance, a host phenotype of infection type 2. Both lines expressed incomplete hypersensitivity and very limited pustule development when infected with race Pc-54 of *P. coronata*. In field testing, two F_2 populations, derived from crosses between a susceptible line, MN84-1824, and each moderately resistant line, were found to be continuously distributed for latent period, but lacked transgressive segregation. The mean latent periods of the two F_2 populations were intermediate and significantly different from either parent, but were significantly shorter than midparent value. Quantitative determination of three rusting components measured in the greenhouse showed that the two F_2 populations were intermediate and significantly different than either parent for latent period, pustule density and pustule size. In contrast to the field study, the latent period distributions for both F_2 populations tested in the greenhouse were shifted toward the resistant parents. MN84-1804 and MN84-1811 were both found to possess adult-plant resistance, as shown by their susceptible seedling reaction and moderate resistant adult reaction to three cultures of crown rust.

Annual Ryegrass Control in Oats with Pre-Emergence Diuron

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Summary

The results of two experiments in which diuron and mixtures of diuron with other grass herbicides were used for pre-emergent control in oats (*Avena* sp.) are presented. In the first experiment diuron + metolachlor gave excellent ryegrass control with large yield increases. In the second experiment diuron alone at high rates was the best treatment on a diuron tolerant variety, while diuron + pendimethalin was the best treatment on the diuron sensitive variety. The role of diuron as a pre-emergent herbicide for oats is discussed.

Introduction

A smaller range of herbicides has been available in Australia for weed control in oats when compared to the other main cereal crops. This has been most evident with grass selective herbicides where only the herbicide chlorsulfuron has been registered for post-emergent control of annual ryegrass, *Lolium rigidum*, while no herbicides are currently registered for the pre-emergent control of any grass weeds in oats. While chlorsulfuron was initially considered to be safe when used as a pre-emergent application on oats[3] it was not subsequently registered for this use. Diuron has been previously reported as providing ryegrass control in barley either alone or when used in mixtures[2]. Oats were considered to be sufficiently tolerant to diuron (J. Pierce, pers. comm., 1988) that experiments on the use of diuron as a pre-emergent herbicide for ryegrass control in oats would be worthwhile conducting.

This paper reports results of two experiments in which diuron either alone or in combination with other grass selective herbicides was used for annual ryegrass control in oats.

Methods

Experiment 1

Two sites (duplex soil, sandy loam over clay) with expected populations of annual ryegrass were seeded with Mortlock oats at 50 kg/ha. Herbicide treatments (Table 1) were applied immediately after seeding, and weed counts were made 50 days after seeding. The trial design was a strip plot using three replications of plots 3m x 10m. The area harvested in each plot was 1.4 x 10m. Yield results were analysed using a nearest neighbour technique[4].

Experiment 2

A duplex soil (loam over gravelly clay) was seeded with two oat varieties at 50 kg/ha. Annual ryegrass seed was spread on the trial area prior to seeding in order to give a population density greater than 400 plants/m^2. Herbicides (Table 2) were applied immediately after seeding and at the two leaf stage in the case of chlorsulfuron. Weed biomass ratings were made 47 days after seeding. The trial design was a strip plot with four replications of plots 3m x 10m. The area harvested in each plot was 1.4 x 10m. Yield results were analysed using a nearest neighbour technique[4].

Results and Discussion

Experiment 1

The best treatments for annual ryegrass control were diuron + metolachlor and metolachlor, and this was reflected in yield with the diuron + metolachlor treatments giving the highest yields at both sites (Table 1). While the higher rate of diuron alone was able to provide ryegrass control equivalent to metolachlor at site 1, at site 2 diuron was generally inadequate. However diuron did give acceptable yield increases at both sites. The mixtures of diuron with the dinitroaniline herbicides, pendimethalin and oryzalin, generally gave poor ryegrass control but did result in significant yield increases. This result may be due to the inhibition of root growth by the dinitroanilines[1] which causes less competition for nutrients in early crop growth.

Table 1. The effect of five herbicides applied pre-emergent on annual ryegrass density and yield of Mortlock oats in 1989.

Treatment	*Rate (kg a.i./ha)*	*ARG density (plants/m²)*		*Yield (t/ha)*	
		Site 1	*Site 2*	*Site 1*	*Site 2*
Diuron	1.0	80	300	1.91	2.38
Metolachlor	1.44	73	108	1.90	3.24
Diuron + Metolachlor	0.5 + 0.72	20	33	2.02	3.90
Diuron + Pendimethalin	0.5 + 0.33	73	250	1.81	2.19
Diuron + Oryzalin	0.5 + 0.125	183	200	1.88	2.37
Untreated		216	383	1.35	1.23
LSD (P=0.05)		70	202	0.12	0.43

Experiment 2

Both diuron treatments gave excellent ryegrass control and in the case of the line 81Q/346 a yield increase of 35% was achieved (Table 2) The decline in yields at the higher diuron rate would indicate that diuron was damaging the crop and this was observed with oat death in some rows (particularly in Dalyup). The diuron + pendimethalin mixture gave the highest yield response in Dalyup even though ryegrass control was inferior to the diuron treatments. The standard post-emergent treatment of chlorsulfuron was better than the ratings suggest as nearly all ryegrass plants were strongly suppressed and had very poorly developed root systems. However both varieties were also strongly affected by the herbicide and at harvest were up to 20% shorter than the untreated plots. The yields in the chlorsulfuron treatments were reduced below those of the untreated plots and this would indicate that for both the level of weed control achieved and the yields obtained significant crop damage has occurred.

Table 2. The effect of five herbicides on annual ryegrass control and yield of two oat varieties in 1991.

Treatment	*Rate (kg a.i./ha)*	*ARG control (rating)*[a]	*Yield (t/ha)*	
			81Q/346	*Dalyup*
Diuron	1.0	8.5	5.35	4.74
Diuron	2.0	9.0	5.19	4.47
Pendimethalin	0.5	2.75	4.95	4.74
Diuron + Pendimethalin	0.5 + 0.33	5.75	5.11	5.18
Chlorsulfuron (Z12)[b]	0.01875	6.25	3.64	4.30
Untreated		0	3.96	4.43
LSD (P=0.05)		1.25	0.96	1.24

a biomass rating: 0=no effect ; 5= 50% reduction ; 10=complete control
b applied post emergence at Zadoks *et al* [5] Decimal Growth Stage 12.

The results presented here indicate that diuron either alone or in combination with other grass selectives has the potential to control annual ryegrass in oats when the herbicides are applied after seeding. The crop damage suffered by the oats from chlorsulfuron in experiment 2 is one reason why an alternative herbicide strategy is needed for oats in Western Australia. Oats which are grown on sites in the higher rainfall areas are prone to chlorsulfuron damage whereas diuron in the same situation has generally proven safe (Bowran, unpublished). Diuron also controls a range of weed (such as toadrush, *Juncus bufonius*; silvergrass, *Vulpia* species; stonecrop, *Crassula* species) which are commonly found in higher rainfall situations. Diuron and its combinations with other grass selective herbicides may also be useful in controlling chlorsulfuron resistant annual ryegrass where the resistance is due to site of action mechanisms, and as an alternative herbicide to use in rotating different chemical groups between crops.

The yield results from Experiment 2 also indicate that oat varieties may differ in their tolerance to diuron. Previous work (Bowran, unpublished) had shown that the line 81Q/346 was more tolerant to diuron than a range of other advanced lines and that Mortlock was only slightly less tolerant of diuron than 81Q/346. An exploration of genetic diversity amongst oat lines in response to diuron would be desirable as it could lead to higher use rates of diuron for improved weed control.

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Recent changes in Pathogenicity of Oat Crown Rust on New Zealand Spring Oats

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Since the mid 1970s Agriculture Canada (Winnipeg) and DSIR Crop Research (Palmerston North) have cooperated in an oat breeding project principally to improve Barley Yellow Dwarf Virus (BYDV) tolerance in oats, a cereal disease that is prevalent in the Southern North Island (SNI) of New Zealand (McEwan, 1986). Cultivars bred in New Zealand, particularly Omihi have demonstrated good tolerance of this disease in the field. Early generation breeding material, principally sourced from Agriculture Canada, but regularly containing a component of New Zealand adapted material is screened in the SNI each year. An additional advantage to the New Zealand cooperators is the resistance to Oat Crown Rust (OCR) which is normally contained in the material, as this disease is also a significant problem in the SNI.

Lines containing the OCR resistance genes PC 38 and PC 39, particularly when in combination have given good field resistance in the SNI and resistant cultivars have been selected from this material. Samples of OCR infected material have been collected for several seasons in the SNI for later rust race typing in Winnipeg.

In the 1989/90 season, of six such collections, three were found to be virulent on the PC 38 carrying differential, each showing a different combination of reactions to the other differentials (Table 1). Also during this season late sowings of previously OCR resistant material were found to have susceptible reaction type pustules, though these were not tested for pathogenicity at the time.

Table 1. Race surveys of oat crown rust from 1989/90 season

OCR Genotype	*No. Samples*	*No. Races*
PC 38	3	3
PC 39	0	0
PC 38, 39	0	0
Others	3	3
Total	6	6

The following season (1990/91) many oat lines previously resistant to OCR suffered early and severe infection. Samples race-typed at Winnipeg Indicated that the previously effective genetic combination for resistance of PC 38, 39 had now been overcome by a number of new pathogenic races. (Table 2).

The most prevalent pathogenic race, virulent on differentials carrying PC 38, PC 39, PC 55 and PC 63 was represented by 16 samples (50%) though a number of other combinations also virulent on PC 38, 39 were also recovered.

In the 1991/92 season OCR was again prevalent on material carrying PC 38, 39 and a collection of samples of OCR infected material again showed the prevalence of the PC 38, 39 attacking races (Table 3). As sampling of OCR has been principally from PC 38, 39 carrying lines, the large proportion of races carrying virulence for the PC 38, 39 is to be expected. Sampling from older OCR susceptible material lacking PC 38, 39, revealed some races capable of attacking PC 38, 39, and others lacking this capacity.

Table 2. Race surveys of oat crown rust from 1990/91 season

OCR Genotype	*No. Samples*	*No. Races*
PC 38	1	1
PC 39	3	3
PC 38, 39	28	7
Total	32	11

Table 3. Race surveys of oat crown rust from 1991/92 season

OCR Genotype	*No. Samples*	*No. Races*
PC 38	0	0
PC 39	1	1
PC 38, 39	23	8
Other	1	1
Total	25	10

Again the principal pathogenic race was virulent on PC 38, PC 39, PC 55 and PC 63 and represented by 11 samples (44%).

Several virulence combinations typed out on the differential set were known North American OCR races, but a number of the combinations were unique.

The exposure of the PC 38, 39 genetic combination for OCR resistance has apparently resulted in a parallel but independent shift of pathogenicity in both countries.

It has been observed that some of the early generation breeding material may carry only PC 38 or 39. This may have led to a step-wise overcoming of the PC 38, 39 combination by the pathogen.

The rapid erosion of the effectiveness of the combination of the OCR resistance genes PC 38, 39 has had a major effect on the selection strategy for oats in the SNI.

However, a number of breeding lines with good OCR resistance in the field remained in the programme and will form the basis for further breeding work. Sources of effective resistance derive from USA germplasm and also Agriculture Canada and New Zealand breeding stocks.

The genetic bases of these resistances will need to be identified with a view to broadening the genetic base for OCR resistance. It has been observed that a number of identified PC genes retain effective resistance to present OCR races in New Zealand.

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Evaluation of Random vs. Focus Inoculation on Visual Incidence and Yield of Barley Yellow Dwarf Virus in Noble Spring Oat

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Summary

Compensation among yield components occurs in oats and other cereals. Because cereals tiller, compensation may affect yield loss due to barley yellow dwarf and the method of artificial inoculation may affect the amount of compensation. An experiment was designed to determine the effect on yield loss of initiating infections with random or focused inoculation patterns. Covariate analysis was used to determine that there were no inoculation technique by disease incidence interactions. Thus, compensation effects on Noble oat may not have an effect on yield loss and the convenient method of establishing disease foci to evaluate yield loss can be used with confidence.

Introduction

Barley yellow dwarf virus (BYDV), spread by aphids, has increased in prevalence and severity during the past 30 years and is now considered the most destructive disease affecting oats in the United States. Oats, like other cereals and grasses are known to compensate among the three yield components. Reestman[(5)] reviewed the effect of virus infection on the production of ware potatoes and discussed the effects of compensation by healthy plants surrounding diseased plants. He noted that the intensity of compensation by healthy plants is probably the main factor affecting yield loss in the field. Compensation may occur when healthy plants overgrow infected plants early in the growing season or uninfected and diseased plants may grow at similar rates early in the season, but over time the healthy plants fill all or some of the space occupied by the diseased plants. Compensation is more likely to occur if the infected plant is stunted or dies while the rest of the crop is actively growing. There may not be compensation under conditions of low fertility, drought, or low plant density and it is more likely to occur under the opposite conditions of high fertility, sufficient water supply, and dense planting. It is theoretically possible that at certain percentages of incidence there is no effect on yield because of optimal compensation. Because of the tillering capacity of oats, compensation may be a factor in assessment of yield loss due to barley yellow dwarf virus on spring oats and the method of artificial inoculation may affect the ability of the oats to compensate. Artificial inoculation to create foci of infection (see Hewings *et al.* in this volume) has been used previously in yield loss studies[(1)]. In this method, a disease epidemic is initiated by placing viruliferous aphids on one to three adjacent plants in a yield plot. The aphids spread the virus by moving from the focus of infection to feed other plants in the plot. Only the uninfected plants on the edge of this expanding focus can compensate for the infected plants. Another approach to generating an epidemic within a yield plot is to shake the same number of aphids that were used for a focus inoculation over the plot to create a random pattern of infected plants. Since the diseased plants would be interspersed with uninfected plants, compensation could contribute to a reduced yield loss. The random inoculation technique probably approximates more closely natural infection in cereal fields. A field experiment was designed to determine the effect, if any, of inoculation technique on yield loss assessment in spring oat.

Methods

A well-characterized, non-specifically transmitted isolate of barley yellow dwarf virus (BYDV-PAV-IL) was used for all experiments[(2)]. Noble oat, moderately sensitive to BYDV, was

planted in 6 row yield plots (0.9m x 2.5m) in two locations, Urbana Illinois in 1991 and DeKalb, Illinois (about 150 miles north of Urbana) in 1992. In a randomized complete block design, disease was established by infesting the plots with 0-3 levels of viruliferous *Rhopalosiphum padi* using random or focus inoculation methods. Each treatment was replicated 5 times. Incidence was assessed by determining visually the percentage of diseased plants in each plot. Disease incidence was determined at approximately weekly intervals when the oat plants were at Feeke's growth stages 10, 10.5, and 11[3]. The data were analyzed using SAS (Statistical Analysis Systems, North Carolina). Covariate analysis was used to determine if the response of yield to BYDV infection varied with the method of inoculation. The model tested was: yield = disease incidence, inoculation method, disease incidence by inoculation method, and block. Block and inoculation method were class variables and disease incidence was the covariate. With this model, the regression of disease incidence on yield is determined within each inoculation method. The test of the interaction of inoculation method and disease incidence is a test of homogeneity of slopes of these regressions and determines if the response of yield to BYDV incidence is the same for both inoculation techniques[4].

Results and Discussion

Previous research has indicated that visual disease assessment at growth stage 10.5 had a significant relationship to yield loss[1]. This work confirms their study. In addition, in this study there were no inoculation technique by disease incidence interactions at either location. Therefore, for these locations the estimate of yield, based on disease incidence will not vary with the method of artificial inoculation used to infect the oats in the plot. This suggests that compensation effects on this cultivar of spring oat may not have important effects on yield loss. From a practical standpoint, both methods of inoculation can be used with confidence for yield loss studies.

Table 1. Result of analysis of covariance of two experiments. Block and inoculation technique (random vs. focus inoculation) are class variables and disease incidence is a covariate. A significant inoculation technique by disease incidence interaction would indicate that the response of yield to disease pressure varied with inoculation technique.

	Location	
Source of Variation	*Urbana, 1991*	*DeKalb, 1992*
Block	**	NS
Inoculation Technique	NS	NS
Disease Incidence	**	**
Inoculation Technique by Disease Incidence Interaction	NS	NS
Coefficient of Variation	8.1	13.4
R^2	0.71	0.75

** = Significant F calculated, $P < 0.01$

Table 2. Estimated regression lines describing the relationship between BYD severity and yield loss for two different inoculation techniques in two locations.

	Estimates of the Regression Lines	R^2	*CV*
Urbana 1991			
Focus Inoculation	3699.615 - 23.098X		
Random Inoculation	3487.06586 - 23.125X	0.71	7.9
DeKalb 1992			
Focus Inoculation	3496.056 - 21.666X		
Random Inoculation	3288.548 - 21.666X	0.76	13.1

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Selection for Barley Yellow Dwarf Virus (BYDV) Tolerance in Segregating Populations using Modified Single-Seed Descent

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Summary

Barley yellow dwarf (BYD) is an important aphid-transmitted viral disease of small grains. Elimination of BYDV sensitive genotypes from early generation segregating populations would increase the efficiency of breeding for BYDV tolerance. Our objective was to compare the BYDV tolerance of populations resulting from: no selection in the F_2 or F_3, populations inoculated with BYDV in the F_2 only, and populations inoculated with BYDV in both the F_2 and F_3. Populations of F_2 and F_3 plants from four intraspecific spring oat, *Avena sativa* L., crosses were grown in the greenhouse using a modified single-seed-descent method with 100 plants per 13 cm pot. Plants in infected subpopulations were infected with the BYDV-PAV-IL strain by inoculation with viruliferous *Rhopalosiphum padi* L. We hypothesized that inoculated sensitive genotypes would produce fewer seeds than tolerant genotypes at the high plant density used. Response to selection was evaluated in the F_5 and F_6 in the field using hills inoculated with the same BYDV-PAV-IL strain. The BYDV inoculation procedure did not increase the frequency of tolerant genotypes in the four crosses studied.

Introduction

Barley yellow dwarf is an important disease of small grains throughout the world, and is the most economically important viral disease of oats in the U.S. The disease is induced by one or more virus strains belonging to the luteovirus group[3,5,7] that share a common host range and induce symptoms of chlorosis and stunting in graminaceous hosts. Developing tolerant cultivars is the most efficient and practical method of controlling the disease[1,4].

A major consideration in the development of improved cultivars is the speed at which such improved cultivars can be made available to farmers. The single-seed descent (SSD) breeding procedure is well-suited for oat breeding when generations are advanced in the greenhouse. We use a modification of the SSD technique in the Univ. of Illinois spring oat breeding program[2]. Plants are grown at high density under limited soil fertility and moisture. About 100 seedlings are grown in each 13 cm clay pot. Most of each pot is filled with sand and only 2 to 3 cm of soil is placed on top of the sand. Plants subjected to these cultural stresses produce only one or a few seeds and reach maturity in approximately 60 to 75 days. Two to three generations can be grown during the winter. We asked the question: Could the modified SSD procedure be used in combination with BYDV inoculation to eliminate BYDV sensitive genotypes from segregating populations grown at high density in the greenhouse? Our hypothesis was that the additional stress of BYDV inoculation would prevent sensitive genotypes from forming any seed, thus reducing the frequency of BYDV sensitive genotypes in later generations. The higher frequency of tolerant genotypes in later generations would increase the efficiency of breeding BYDV tolerant cultivars.

Methods

We compared the BYDV tolerance of populations resulting from : no selection in the F_2 or F_3 (control population), F_2 generations inoculated with BYDV, and F_2 and F_3 generations both inoculated with BYDV.

Four populations developed by intraspecific hybridization (IL 8983-54, IL 8983-57, IL 8983-17 and IL 8983-49) were evaluated. These four populations were studied because one parent in each cross was very tolerant but the BYDV tolerance of the second parent varied from sensitive to very tolerant (Table 1.).

Seeds from F_1 plants were planted at a rate of 100 seeds per pot on 18 Sept. 1989, in the greenhouse in 13 cm clay pots. Two pots were planted for each population. Seeds were covered with 2 to 3 cm of a soil mixture consisting of 1 sand: 1 peat moss: 1 topsoil. Plants were grown in a greenhouse equipped with metal halide lamps operating on a 14 hour photoperiod with day and night temperature of approximately 21 and 16°C, respectively. Approximately 2.5 grams of water-soluble fertilizer (20 N - 19 P - 18 K) were dissolved in one liter of water, and 50 ml of this dilute fertilizer solution was applied to each pot three times during the growth of the plants.

The oat seedlings were inoculated at the 2-3 leaf stage with *Rhopalosiphum padi* L. carrying BYDV-PAV-IL. Seedlings were caged for 3 days for inoculation access before a dilute malathion (0,0 dimethyl phosphorodithioate of diethyl mercaptosuccinate) spray (2.6 ml of malathion per liter of water) was applied to kill the aphids.

One seed was harvested from each F_2 plant. The F_3 populations were divided into two subpopulations. One half of the F_3 plants underwent another cycle of inoculation, and the other half were grown without inoculation. At maturity, one random seed was harvested from each plant. F_4 plants were grown without inoculation. For the control populations, the same procedure was repeated, but the F_4 generation was grown in the field in rows. At maturity, 100 random panicles were harvested from each row. For evaluation of BYDV tolerance, 30 seeds were harvested from the main panicle of each plant and F_5 plants were grown at the Agronomy-Plant Pathology South Farm of the University of Illinois at Urbana-Champaign. Seeds were planted on 24 April 1991 in hills (15 seeds per hill) arranged in a randomized complete block design (RCBD) with two replications. At the 2-3 leaf stage, the plants were inoculated with BYDV-PAV-IL. Three days were allowed for inoculation access before the application of a dilute Cygon® 400 (Dimethoate (0,0-dimethyl S-(-N-(methylcarbamoyl) methyl) phosphorodithioate) spray to kill the aphids. After panicle emergence, each hill was rated for BYDV tolerance using symptom expression as described by Schaller and Qualset[6] on a scale ranging from 0-9, with 0 indicating no visual symptoms and 9 severe symptoms. Seeds harvested from each hill were planted on 14 April 1992 for reevaluation in the F_6.

Results and Discussion

The mean BYD scores of control subpopulations (no inoculation with BYDV) were either significantly better than or did not differ from the mean BYD scores of subpopulations inoculated in the F_2, and F_2 and F_3 (Table 1). Our expectation was that we would eliminate most sensitive genotypes in the subpopulations inoculated with the virus, and that the greatest change would occur in the sensitive x tolerant population, IL 8983-54; however, the mean BYDV tolerance of the control plants was equal to the mean BYDV scores of the other subpopulations. The percentage of plants rated 5.5 was similar in all subpopulations. The distribution of BYDV tolerance for genotypes in the subpopulations varied depending upon the cross, but the distributions for the control subpopulations were similar to the subpopulations that had been inoculated (data not shown).

As with other procedures, the modified SSD method causes some genotypes in each generation to be lost. Using a density of 60 seedlings per pot, Cisar *et al.* [2] reported that after two generations of modified SSD up to 34.5% of the original population was lost due to barrenness and that an increasing number of plants were lost as population density was increased. In our experiment, the percentage of plants that produced one seed differed depending upon the treatment. We hypothesized that the largest percentage of plants not producing any seed would be the inoculated subpopulations. Since one parent in each of the populations IL 8983-54 and IL 8983-17 was not very tolerant to BYDV, we also hypothesized that, compared to IL 8983-49 and IL 8983-57, these populations would have a higher percentage of plants that failed to produce any seed when inoculated. The number of plants producing at least one seed in the F_2 subpopulations varied from 23% to 87% and from 38% to 96% in the F_3 subpopulations. The percentage of plants producing at least one

seed varied depending upon the cross but was not altered by inoculation with BYDV. Surprisingly, the highest percentage of plants not producing seeds (77%) occurred in the tolerant x very tolerant control population, IL 8983-49.

In conclusion, inoculation with BYDV under modified single-seed descent was not effective in eliminating BYDV sensitive genotypes. The use of the technique favors those genotypes which have the ability to set seeds under the stress of low nutrient levels and high competition. In this study, elimination of genotypes seemed to be independent of the level of BYDV tolerance.

Table 1. Barley yellow dwarf virus (BYDV) tolerance for F_5 and F_6 oat populations evaluated under field conditions.

Cross	*Population*	*Sub-population*	*Score (0-9)*[a]	*SE*
Sensitive x Very Tolerant				
Don x IL 85-6467	IL 8983-54	F_2 Inoc.[b]	6.14 a[c]	0.12
		F_2 & F_3 Inoc.	5.09 b	0.12
		Control	5.09 b	0.09
Moderately Tolerant x Very Tolerant				
Larry x IL 86-5698	IL 8983-17	F2 Inoc.	4.69 c	0.13
		F_2 & F_3 Inoc.	4.75 c	0.10
		Control	4.33 d	0.09
Tolerant x Very Tolerant				
Newdak x IL 85-2075	IL 8983-49	F_2 Inoc.	4.97 e	0.13
		F_2 & F_3 Inoc.	4.82 e	0.11
		Control	4.31 f	0.09
Very Tolerant X Very Tolerant				
IL 85-6467 x IL 86-1158	IL 8983-57	F_2 Inoc.	4.61 g	0.10
		F_2 & F_3 Inoc.	4.65 g	0.10
		Control	4.47 g	0.09

a Score: 0 = no symptoms, 9 = severe symptoms
b Inoc. = inoculated with BYDV-PAV-IL.
c For comparisons made within each cross, means with the same letter are not significantly different.

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Barley Yellow Dwarf Virus in Cereals in the High Rainfall Zone of South Australia

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Summary

Five experiments were conducted in the south east of South Australia during the period 1987–91 to determine the effect of natural infection of Barley Yellow Dwarf Virus (BYDV) on a range of oat and wheat cultivars. BYDV was controlled in split plot experiments by spraying control plots with Ambush® (permethrin 500g/l). BYDV occurred in four of five years. In oats, New Zealand Cape was rated as susceptible, Echidna as moderately tolerant and Dolphin as tolerant. In wheat, reaction to BYDV varied from susceptible (cultivars Spear, Halberd and Talent) to moderately tolerant (cultivars Osprey and Warrigal). Moderately tolerant cultivars had a common parent in WW15, synonymous with Anza. Percentage yield reduction of Spear wheat was related to the summer-autumn rainfall before sowing which it is postulated affected the number of aphids that survived the summer. The relationship was calculated to be:

Yield Reduction (%) = 0.17027 rain (Dec–May mm) - 5.9185, $R^2 = 0.72$.

Introduction

Cereals and pasture grasses in southern Australia are susceptible to infection by Barley Yellow Dwarf Virus (BYDV); principally the PAV isolate[6]. Artificial inoculation by infective aphids prior to tillering can reduce wheat grain yields by up to 79%, while later inoculation can reduce yields by up to 9%[3]. A field survey of wheat crops throughout Victoria in 1984, showed that infection with BYDV ranged from 0–20% with estimated yield losses from the most affected crops being 20%[5]. As little was known about the likely yield loss caused by BYDV in the high rainfall zones of South Australia or about the disease reaction of commonly grown cereal cultivars, a series of experiments was initiated in 1987 to investigate the effects of natural infection of cereals with BYDV.

Materials and Methods

In 1987 and 1988 oat and wheat cultivars were sown near Naracoorte in the south east of South Australia. From 1989 onwards only wheat cultivars were tested. Experimental design was a split plot with aphid sprays as main plots and cereal cultivars as sub-plots. Plot size was 4.5 m long by 8 rows at 15 cm row spacing and 8 replicates were used. All experiments were sown in late May or early June except in 1991 when sowing occurred on 2 July. At sowing nitrogen was applied at 20 kg/ha while herbicides and trace elements were applied as needed. Fungicide (either Bayleton® or Tilt®) was applied prior to heading to control any other foliar diseases.

After crop emergence, at approximately 14–21 day intervals until flowering, Ambush® (permethrin 500g/l) was applied at 200 ml/ha to the control plots. From 1989, 10 leaves were taken at random from each plot of 5 selected wheat cultivars, after flowering, to be tested for the presence of BYDV by ELISA. At maturity, grain yields, protein content and 1000 grain weights were measured.

Results and Discussion

Variation existed between the oat cultivars for tolerance to BYDV (Table 1). New Zealand Cape was susceptible, Echidna moderately tolerant and Dolphin tolerant with an average yield reduction of 31, 12 and 5% respectively. Grain weight of all three cultivars was only slightly affected by BYDV. In oats, only early infection reduces grain weight to any degree[1].

Table 1. Effect of BYDV on oat grain yield and grain weight.

Cultivar	*1987*				*1988*			
	Yield kg/ha		*% Yield Redn*[1]	*% Redn 1000 Grain Weight*	*Yield kg/ha*		*% Yield Redn*	*% Redn 1000 Grain Weight*
	Control	*Nil*			*Control*	*Nil*		
New Zealand Cape	2074	1459	30	8	3401	2305	32	1
Echidna	3694	3180	14	3	6236	5555	11	1
Dolphin	3380	3140	7	2	7048	6773	4	3

[1] redn = reduction

Variation existed between wheat cultivars for tolerance to BYDV with Spear being susceptible and Osprey moderately tolerant (Table 2). Other susceptible cultivars were Halberd and Talent. Osprey and several other moderately tolerant Australian cultivars tested such as Warigal and Kiata, have WW15 as a parent. WW15 is a synonym of Anza which is regarded as one of the most tolerant wheat cultivars to BYDV[(2)]. Grain weight of wheat was reduced by BYDV but the percentage reduction did not account for the total reduction in yield (Table 2).

Table 2. Percent reduction in grain yield and 1000 grain weights in Spear and Osprey wheat caused by BYDV over five years.

Year	*% Grain Yield Reduction*		*% 1000 Grain Weight Reduction*	
	Spear	*Osprey*	*Spear*	*Osprey*
1987	32	16	9	4
1988	40	28	15	12
1989	24	12	7	6
1990	5	2	1	3
1991	20	not tested	4	not tested

The percentage yield reduction caused by BYDV varied from year to year (Table 2) with significant yield reductions for the susceptible cultivar Spear in four of the five years in which experiments were conducted. In 1990, however, BYDV did not occur. This was confirmed by ELISA tests for the susceptible cultivar, Halberd which for the untreated plots showed 23, 0 and 16% of leaves affected in the years 1989, 1990 and 1991 respectively. The greatest yield reduction occurred in 1988 following 2 days of hot winds during grain fill. This was probably caused by reduced root system and leaf area due to BYDV[(4)] which resulted in the earlier senescence of plants affected by BYDV. Although oats were not tested after 1988 the likely yield reduction of susceptible oat cultivars may be inferred. In 1987 and 1988 the yield reductions of Spear wheat and New Zealand Cape oats caused by BYDV were similar and it is likely that susceptible oats would have suffered approximately a 20% yield reduction in 1989 and 1991 but been unaffected in 1990.

Over the five years of experiments the percentage yield reduction of the susceptible wheat cultivar Spear, was closely related to the rainfall accumulated during the period December to May (Figure 1). This rainfall ranged from 67mm in 1990 to 254mm in 1987. It is postulated that increased rainfall over summer and autumn enabled greater numbers of aphids to survive. Perennial grasses in the high rainfall zone of southern Australia act as a reservoir for BYDV allowing surviving aphids to infect cereals soon after emergence. Early infection causes greater yield reduction[(3)].

Under high rainfall conditions in southern Australia BYDV is an important disease. In these experiments BYDV occurred in 4 out of 5 years and caused yield reductions of susceptible cultivars of up to 40%, therefore a major breeding aim should be for BYDV tolerance. Current oat cultivars that yield well in the south east of South Australia are rated at least moderately tolerant of BYDV.

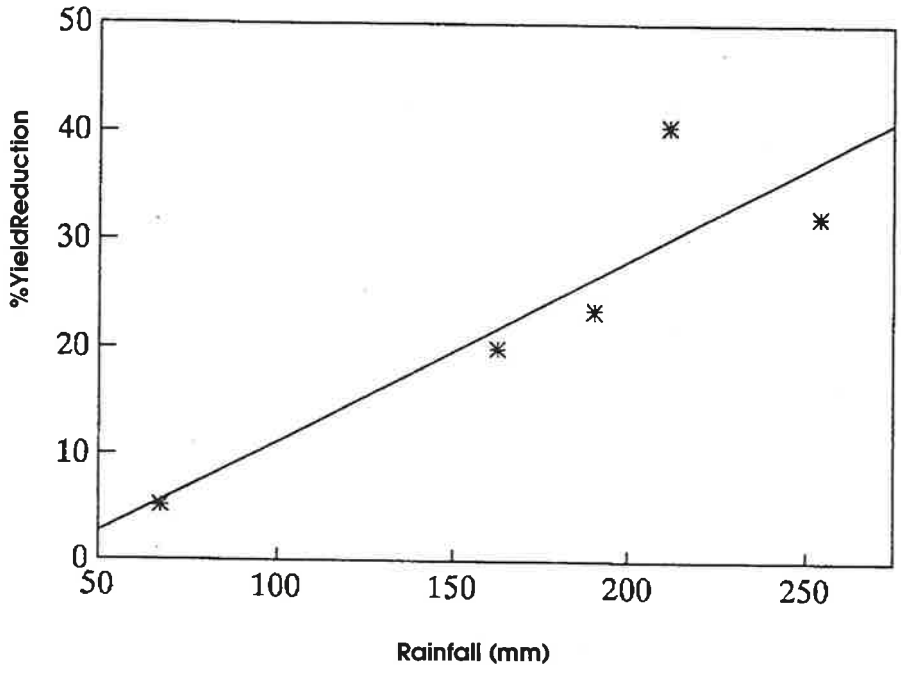

Figure 1. Relationship between summer-autumn rainfall before sowing (Dec-May) and percentage yield reduction in Spear wheat caused by BYDV.
Yield Reduction (%) = 0.17027 Rain (mm) - 5.9185, $P<0.05$, $R^2 = 0.72$

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Breeding for Resistance and Tolerance to Oat Stem Nematode (*Ditylenchus dipsaci*) in South Australia

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Summary

A range of oat cultivars and advanced lines from the South Australian oat improvement program were assessed for resistance and tolerance to oat stem nematode (*Ditylenchus dipsaci*). A wide range in hosting ability and tolerance to the nematode was found. Excellent levels of both resistance and tolerance were detected. Results from these and other experimental sites have led to the submission for registration of a stem nematode resistant variety suited for hay in South Australia.

Introduction

Stem nematode is one of the most devastating nematode diseases. The first report of stem nematode damage on oats in South Australia occurred in 1973[(1)]. Since then it has spread to many districts including the Mid-North, Lower-North, Yorke Peninsula and Fleurieu Peninsula[(4)]. These are the areas where most of South Australia's export and domestic oaten hay and over 20% of the grain is grown. In some cases, whole paddocks of oats have been destroyed with no hay cut or grain set.

Options for management of the disease include crop rotation and resistant/tolerant cultivars[(3,4,6,7)]. Crop rotations traditionally used to control other cereal root pathogens may however be disastrous for control of stem nematode as faba beans and to a lesser extent peas, which are important "break" crops for other cereal root pathogens, have been identified as host crops to this nematode[(6)]. Resistant and tolerant cultivars would therefore seem the most effective management tool against the oat stem nematode particularly since the nematode is able to survive for long periods between host crops and the host status of S.A.'s weed flora is largely unknown. Furthermore, fields with low populations increase very rapidly to damaging levels when a susceptible crop is grown. Oat stem nematode may be efficiently transferred both within South Australia and interstate in hay. Growing resistant and tolerant cultivars in infected areas would slow down the spread of the nematode to new areas.

Initial studies on oats showed assessment of tolerance by visual symptoms was correlated with resistance/susceptibility and substantial progress was achieved in selecting resistant lines in field experiments conducted on stem nematode infested sites. From these initial studies, five sources of resistance were identified and have been used in the South Australian oat breeding program viz:

1. Lines carrying the Grey Winter gene, shown to be effective in S.A.[(6)], including Panema and the New Zealand breeders line, 279.01.
2. A wild oat accession (*Avena fatua*) collected from a heavily infested paddock at Northfield, S.A.
3. Many entries from the Quaker nurseries for South America including Quaker-84-187, Quaker-85-183, Quaker-84-150, Quaker-83-200 and Quaker-83-265.
4. Echidna, which presumably obtains its resistance from its Canadian parent OT207.
5. New Zealand Cape, a source of moderate resistance.

This study reports the evaluation, in two experiments, of the resistance and tolerance of breeders lines derived from four of these sources of resistance as well as a range of oat cultivars currently grown in South Australia.

Methods

In the first experiment, thirty two lines in advanced variety testing in South Australia were sown in a stem nematode infested paddock at Freeling, in the Lower-North of South Australia, in 1991. Four weeks after sowing, nematode invasion was determined by counting the number of nematodes extracted from five plants per plot by the mister technique[5]. Six weeks before harvest nematodes were extracted from the lower 20 cm of the stems of five plants in each of three replicates, using the whitehead tray technique (modified baerman funnel method)[2].

In the second experiment, four cultivars were sown in demonstration plots (100 m. by four rows) adjacent to experiment one. Three of these lines were resistant to oat stem nematode, each one from a different source and were compared to Swan, a susceptible cultivar. Nematode recovery was assessed for each plot using the technique described above and grain yield was measured.

Results and Discussion

Experiment One

Initial nematode invasion was low and ranged between zero and twelve nematodes per plant with an average of 6.5 nematodes per plant a month after sowing. This low initial nematode density did not damage even susceptibile plants and permitted an excellent assessment of hosting ability (= "resistance") of the different oat lines. Higher initial densities would have adversely affected some susceptible lines early in the season not allowing their full potential as hosts to be assessed.

Nematode numbers recovered from the oat plants six weeks before grain harvest are shown in Figure 1 and ranged from 28,000 per plant in Dalyup to 16 per plant in the breeders lines OX86;061R-8 (IORN-84-70/Mortlock//Mortlock/Echidna) and OX82;059-58-10 (Mortlock/Echidna). As an indication of the potential of each genotype as a host for the nematode, the highest number of nematodes recovered per plant are shown.

At low initial nematode numbers resistant lines are an effective barrier to nematode multiplication, therefore in this experiment a number of lines were assessed to have excellent resistance. Further experiments will determine if these lines are resistant when initial nematode invasion numbers are high.

Experiment Two

Initial nematode invasion was also low in this experiment, allowing assessment of the hosting ability of the four cultivars. The three resistant cultivars were poor hosts to the nematode and show very low nematode numbers (Table 1) compared with Swan. In comparison, the susceptible cultivar Swan suffered substantial yield loss and was an excellent host for the nematode, increasing nematode numbers by 3000 fold. The three resistant genotypes yielded as well (OX82;104-12) or better (Quaker-84-187) than they would have compared to Echidna in a non-infested site (Table 1).

Assessment of the stem nematode resistance and tolerance, yield data from thirty experiments for grain and six experiments for hay-grazing have led to the submission of Quaker-84-187 for registration as a multi-purpose cultivar with particular suitability for hay.

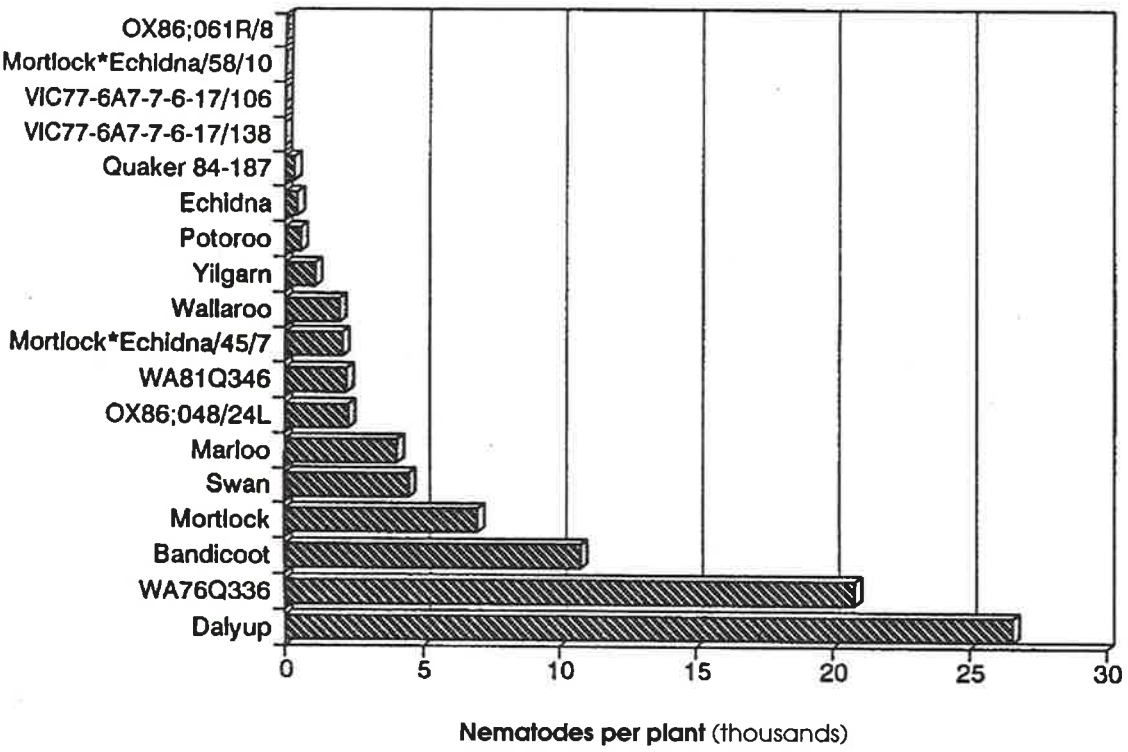

Figure 1. Hosting Ability of 18 Different Oat Lines at Freeling, 1991

Table 1. Nematode Number and Yield of Demonstration Experiment, Freeling 1991

Oat Cultivar or Breeders Line	*Mean Nematode Nos Recovered in 20 Plants*	*Yield (kg ha^{-1})*	*Yield (% of Echidna) in Infested Experiment at Freeling, 1991*	*Yield (% of Echidna) in Non-Infested Experiments[2] (no. of expts.)*
Echidna	14	4411	100%	100%
Swan	29 354	2434	55%	70% (172)
OX82;104-12[1]	6	3194	72%	75% (3)
Quaker-84-187	441	4037	92%	81% (36)

1 South Australian breeders line from the cross 279.01/SWAN//MORTLOCK. 279.01 has the "Grey Winter" gene for stem nematode resistance.

2 Data from Oat Breeding Database of experiments conducted since 1977.

Future Directions

Further studies are required to determine if the resistant genes outlined in this paper are effective against all stem nematode populations in Australia and if the genes from the five sources are actually different. These resistant lines will be monitored to check for the appearance of resistance breaking races.

The gene in OX82;104-12 is being transferred to higher yielding lines with semi-dwarf growth habit and Cereal Cyst Nematode (*Heterodera avenae*) resistance/tolerance.

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A Virus Attacking Winter Oats in the UK

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A conspicuous and possibly serious viral disease has occurred sporadically in the winter oat breeding nursery at Aberystwyth since 1986. The worst affected tillers are severely dwarfed and have spirally twisted leaves with golden yellow and elongated streaks. Panicles are poorly developed, are twisted and hardly emerge from their leaf sheaths(1).

Virus particles associated with these symptoms are isometric and c. 35 nm in size(2), in contrast to oat mosaic and oat golden stripe viruses which have rod-shaped particles. The exact method of transmission is unknown but observations on known infected sites suggest that it might be soil-borne. An embryo wounding technique(3), successfully used for maize white line mosaic to which this disease has some similarity, has been used to artificially transmit the virus.

Susceptibility appears to be mainly associated with non-UK unadapted lines and segregating breeding material containing parents of diverse origin.

In 1991, the virus was identified in commercial crops cv. Aintree on a farm near Brecon, some 70 km away from Aberystwyth. In one field, it was estimated that about 10% of plants were stunted.

In a replicated variety trial in this field in 1992, infection ranged from 0.1 to 11.9 tillers/m^2. Good levels of resistance probably exist for this disease within existing UK varieties but constant monitoring of resistance levels, particularly when introducing new germplasm, may be necessary.

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* ADAS is an executive agency of the Ministry of Agriculture, Fisheries and Food and the Welsh Office.

Association between Vesicular-Arbuscular Mycorrhizal Fungi and Oats

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Summary

A survey was conducted to determine the occurrence of mycorrhizal fungi in soils with various cropping histories. Mycorrhizae were found associated with plant roots in all soils, however the percentage of roots infected was highly variable ranging from 26.5 – 71.3% on corn, 35.3 – 67.3% on "prairie" and 34.4 – 48.4% on land previously cropped with soybeans. Subsequent investigations in the laboratory have indicated that spores of the mycorrhizal fungi are stimulated to germinate in the presence of certain soil flora — in particular, species of streptomyces.

Introduction

Certain fungi existing in symbiotic association with plant roots referred to as "Mycorrhizae" were first described over 100 years ago[4]. The endomycorrhizae, especially those with aseptate hyphae in the family Endogonaceae, are ubiquitous on the roots of most cultivated herbaceous plants. These fungi form large vessicles and arbuscules (tree-shaped bodies) in the cortical cells of the host plant roots and are commonly referred to as vessicular-arbuscular (VA) mycorrhizae[12].

During the past 20 years the VA mycorrhizal fungi (VAM) have been shown to function in the uptake of minerals and water by plants from soil[3,5,11].

There is virtually no literature on the relationships between VAM fungi and oats. This is largely assumed from work on other small-grains. For maximum colonization and plant growth effect to occur, VA mycorrhizal inoculum must be present and root infection must occur in high enough incidence early in the plants development[7,8,9]. Additions of *Glomus mosseae* or *Glomus Caledonius* increased the dry weight of barley in soils with low levels (8-13 ppm) of phosphorus[11]. Soil microflora appear to have a variety of strong affects on the ability of VAM fungi to germinate and colonize their host plants[1,2,8,10,13,14]. This research was undertaken to determine the extent of mycorrhizal association with oat in Iowa and to attempt to define parameters under which mycorrhizal associations might be of benefit to oat production.

Methods

The VAM fungal content of soils from 11 sites in Central and North Central Iowa was determined. Seven of these sampling sites were in cultivated fields, three in recently established prairie sites and one in a native prairie. The cropping histories of the cultivated fields were varied but all were in oats at the time of sampling.

Soil samples consisting of 3 cores 10 cm in diameter x 20 cm deep from each of 3 sites were collected from 3 sites in each sampling location. The cores from each collection location were transported to the laboratory, blended and then utilized in a variety of procedures.

Seeds of Avena sativa var. Ogle and Don were planted in pasteurized vermiculite and watered with steriiized water to produce VAM-free seedlings. Week-old VAM-free seedlings were transferred to 12 cm clay pots previously autoclaved then half-filled with pasteurized greenhouse mix 2.2.1 (soil-peat-pearlite). Filling of the pots was then completed using 50 grams of soil from each of the collection locations upon which the seedlings (one per pot) were placed and then covered with enough greenhouse mix to bring the whole to proper

level for watering. Each pot was double potted to minimize any cross contamination. Each location (11) by variety 2 by treatlnent (3) (field soil, sieved field soil, and pasteurized soil) was replicated four times in a randomized block design. Plants were allowed to grow until heading at which time they were harvested Roots of each plant were removed and washed free of soil placed in 10% KOH for clearing then stained with acid fuchsin and assayed for the presence of VAM fungi using the gridline-intersect method[6].

Spore germination studies using a variety of techniques were carried out using methods modified from those of Schenck[13]. Spores of *Glomus intraradices* and *Glomus etunicatum* were surface sterilized in 2% chloramine-T amended with 200 ppm streptornycin sulfate. These were then placed on agar or on rootlets of oat seedlings in close proximity to but not in direct contact with field soil, sieved soil and cultures of several species of streptomyces.

Results and Discussion

The mean percentage of oat roots infected by native populations of VAM fungi varied greatly depending upon source and irrespective of oat variety (Table 1). The inoculum from a commercial field and an old prairie had significantly higher infection percentages (71.3% and 67.3%) than any of the other sources. In commercial fields the preceding crop appeared to have no influence. There was no consistent difference in wet or dry weights between mycorrhizal and non-mycorrhizal plants. Spores of VAM fungi (*Glomus intraradices, Glomus etunicatum* and *Gigaspora gigantea* commonly found in lowa oat fields failed to germinate in a sterile environment, even in the presence of live oat roots, but did germinate in the presence of volatile agents produced by unsterilized soil and cultures of *streptomyces orientalis.*

This information could lead to methods of stimulating earlier and more consistent colonization of oat roots by VAM fungi.

Table 1. VAM — Percent root Infection by inoculum source

Location	Previous Crop	Mean % Infection	Significance
Hampton	Corn	71.3	a
Ames (Curtiss 1)	Prairie	67.3	a
Ames (Hinds Farm)	Wheat	51.1	b
Fayette	Soybeans	48.4	b
Jordan	Prairie	43.3	bc
Ft. Dodge	Soybeans	42.3	bcd
Stratford	Soybeans	37.0	cd
Ames (Norton Farm)	Prairie	36.7	cde
Ames (Curtiss 2)	Prairie	35.3	de
Hudson	Soybeans	34.4	de
Boone	Corn	26.5	e

Comparison of the mean percentage infection of Native V-A mycorrhizal fungi on two oat varieties: *Avena sativa* var's Don and Ogle. Numbers followed by the same letter are not significantly different. LSD = 5.0, T = 2.03452 and Pr>F = 0.007 with 33 df.

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Twenty-Five Years of Recurrent Selection in Oat

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Summary

Nearly a quarter century of recurrent selection for grain yield in oat has produced annual gains exceeding 2.5%. In addition to this direct response to single trait selection, there has been a number of correlated responses, some desirable and others unwanted. Some of these changes most likely have contributed to the yield increases while others, if left unchecked, would diminish the breeding value of the material. The current emphasis in the program is to mainstream the advanced cycle material back into the breeding program and to conduct experiments with the derived material to elucidate the underlying reasons for the substantial gain in grain yield. The latter will ultimately include efforts to map QTLs for grain yield.

Introduction

During the last two decades, recurrent selection for a number of traits in self-pollinating crops has become increasingly popular. The oat breeding program at the University of Minnesota initiated its version of recurrent selection in 1968. It includes several features not common in other efforts: 1) evaluation of near-homozygous rather than early generation progeny; 2) relatively limited testing prior to parental selection for the succeeding cycle, i.e., five replicates of microplots at only one location-year; 3) selection both among and within families; and 4) a systematic crossing scheme to achieve the intermating between cycles of selection.

Next season we will evaluate cycle six (C_6) progeny to enable selection of parents to initiate the next cycle. To date, our efforts have focussed on the following objectives: 1) assess the cumulative genetic gain from continued selection; 2) evaluate modifications of the selection protocol to determine whether greater efficiency can be achieved; 3) measure correlated responses to enable a post-facto analysis of phenotypic changes; and 4) because of anticipated undesirable correlated responses, compare several methods of mainstreaming advanced-cycle parents back into our breeding program. Procedural details and results obtained prior to 1988 were discussed at the Third International Oat Conference in Lund, Sweden[12].

In this report, we briefly review our earliest results, summarize the results of our more recent efforts and describe our future plans.

Materials and Methods

Cumulative genetic gain

Parents from each of the first five cycles of selection, along with the initial parents, were evaluated extensively at two locations in 1988 and 1989 in both micro- and standard-row plots[11]. Grain yield, seed weight, plant height, and heading date were measured and seed number was calculated for all parents and seven check cultivars.

Selection procedure modifications

Early generation (F_3) bulks of every C_5 family were evaluated at one location in 1989 for grain yield, heading date, plant height, test weight, and lodging[1]. In the following year, F_4 bulks, bulks of F_6 lines and 10 F_6 lines from each family, as well as the 21 C_5 parents, were grown at two locations. The bulks were grown in standard row plots and the lines and their parents in microplots. The same traits were again measured. The parents and lines were also

evaluated for Barley Yellow Dwarf (BYD) reaction at the University of Illinois with the cooperation of Anna Hewings and Fred Kolb.

Correlated response

A number of traits have been evaluated for possible correlated responses and the initial results reported earlier[4,8]. In addition, in an extensive series of yield trials C_4 parents were compared to the initial parents to ascertain changes in stability of grain yield, test weight, lodging resistance, groat percentage, as well as percentage of oil and protein in the groat. Four different locations were utilized to grow either standard row plots or microplots or both during the years of 1986-89. In addition, special disease nurseries utilizing artificial inoculations were established at St. Paul and Rosemount, Minn., and Urbana, Ill., to measure changes in reaction to crown rust, smut (a combination of loose and covered) and BYD, respectively.

More recently, seed samples of parents from cycles 0, 1, 3, and 5 were evaluated for kernel length, width, perimeter, area and shape using digital imaging analysis[5]. Grain yield, kernel weight and number had been previously measured. Changes in kernel size and shape as well as changes in the relationships with grain yield, kernel weight and number as the result of selection for grain yield were determined.

Methods of mainstreaming

Following initial indications that there were several undesirable correlated responses accompanying our successful recurrent selection for yield only, we modified the selection criteria to control increases in plant height and maturity. While continuing the original selection protocol, we initiated a second protocol substituting sibs of selected parental lines. The substituted lines were nearly equivalent in grain yield but had more desirable height and/or maturity. Progeny from the two protocols were then compared directly to assess the effect of secondary trait selection pressure[9].

In a further attempt to correct undesirable correlated responses, the crossing scheme was "opened" by crossing all C_4 parents biparentally to three exogenous genotypes. These genotypes were earlier and/or shorter than the C_4 parents (Figure 1). The "closed" intermating using the partial diallel crossing scheme was also continued. Progeny from the opened crossing scheme were then directly compared with those produced with the original closed scheme.

The progeny from the opened crossing scheme were subsequently subjected to selection first among crosses within a half-sib family and then selection of the best line within each selected cross. Seven 'Ogle' and seven 'Starter' derivatives were chosen for further selection efforts (Figure 1). These individuals were used to produce three different kinds of populations which might typically be used to introgress germplasm into an adapted gene pool. First, the Ogle group was biparentally mated to the Starter group to produce 49 "double cross" combinations. Second, each of the 14 derivatives was crossed to two additional outsider genotypes chosen principally for good agronomic type and superior BYD reaction to produce 28 three-way crosses. Third, the Starter derivatives were backcrossed to Starter. Advanced generation progeny from the three types of crosses were then compared to determine which type of cross is most likely to produce genotypes which have the best composite-trait value.

We have also initiated three new recurrent selection populations (Figure 1). In one, a single advanced-generation line was selected from each of the 17 best "double cross" families. These lines have been intercrossed in a partial diallel to produce 51 new cross combinations. Additionally, a single advanced generation line was selected from the best 11 three-way cross families. These lines have been intercrossed in a complete diallel to produce 55 more combinations. Recurrent selection will be applied to each of these new gene pools to identify genotypes with the best combination of important traits including grain yield, BYD rating, height, maturity, and lodging resistance.

Finally, C_5 progeny were evaluated for BYD tolerance in the University of Illinois-USDA/ARS aphid-inoculated nurseries and the best five lines (each from a different cross), regardless of their yield potential, were selected and intercrossed in a complete diallel (10 crosses).

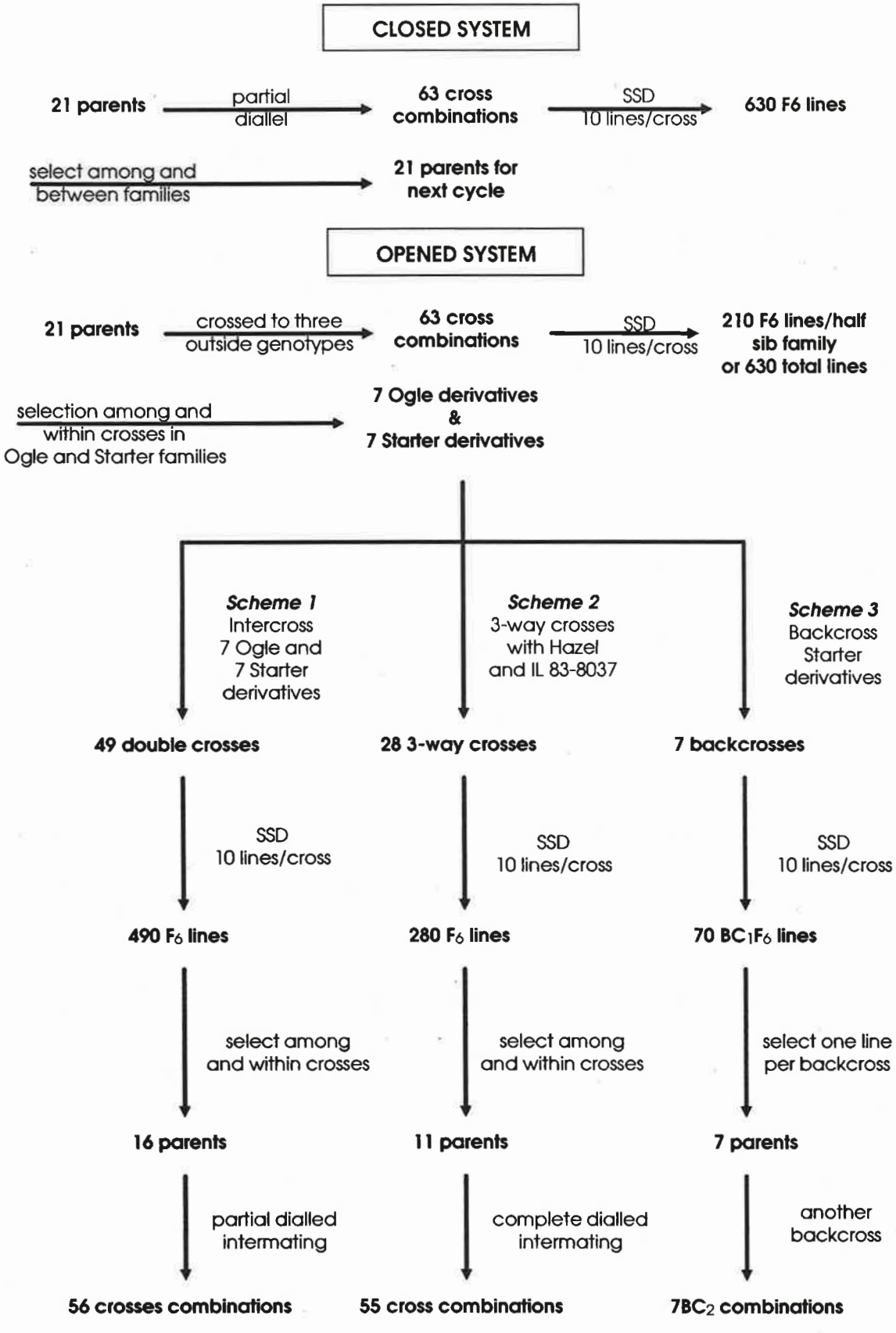

Figure 1. Schematic of closed and opened recurrent selection systems.

Advanced generation progeny will be evaluated at the University of Illinois for BYD reaction. In a separate effort, these five selections were also biparentally mated to four of the BYD tolerant germplasm lines recently released by the University of Illinois[7]. Progeny will be evaluated for transgressive segregants. Such genotypes presumably would have received genes from our recurrent selection gene pool which are different from those in the Illinois germplasm lines.

Results and Discussion

Cumulative genetic gain

Over the first five cycles of recurrent selection, grain yield has been increased 7.9% (measured in microplots) and 7.5% (measured in row plots) per cycle (Table 1) as measured by weighted linear regression[10]. These results provide conclusive evidence that: 1) recurrent selection for grain yield is effective in oat; and 2) the particular selection protocol we used was relatively efficient producing an annual rate of gain exceeding 2.5%. Because the response was primarily linear over the five cycles, we can also conclude that genotype x environment interaction had little negative impact on our results even though only five replicates of microplots were grown in one environment to provide the progeny evaluation used to select parents for the next cycle.

Table 1. Yield gain from recurrent selection based on performance of parental groups across four environments.

Cycle	*Plot type*	
	Microplots g/m^2	*Standard row plots* g/m^2
0	198.8	172.4
1	206.7	189.2
2	215.4	192.9
3	227.0	194.8
4	247.9	215.1
5	281.4	246.6
Current cultivars	218.5	229.4

The comparison given in Table 1 of the performance of current cultivars is also noteworthy since the parents of the most advanced cycles yielded more than these cultivars, especially when evaluated in microplots. The relatively better performance of the checks in row plots may be due to superior lodging resistance of the checks. All other traits measured in these tests, plant height, heading date, and seed weight and number, were also increased as the result of the repeated selection for grain yield.

Selection procedure modification

Even though our genetic gain (2.5% per annum) exceeds that for most systems of recurrent selection for grain yield in any species, we continually strive for greater cost effectiveness for our system. If early generation (F_3) bulk performance would predict those families in our partial diallel crossing scheme which are more likely to produce a parent for the next cycle, we could concentrate our progeny testing on those families. We then could effectively double our progeny testing (use either two locations or row plots rather than microplots), thus increasing its precision and probably increase our annual genetic gain. Briefly summarizing our results testing this approach, there were no differences among F_3 bulks for grain yield and F_4 bulk performance was not correlated with the average of the 10 F_6 lines per family for grain yield. Our next approach will be to assess evaluating F_4 lines rather than F_6 lines and thereby reduce the cycle time to two years. That reduction is possible when we use a winter nursery to produce the F_3 generation.

Correlated responses

In addition to the 2.5% annual genetic gain for grain yield, there have been a number of other changes, some desired and others unwanted. All plant parts which we have measured, as well as grain growth rate and seed number, have increased; most of these trait changes have probably contributed to yield increases. Smut resistance and lodging

susceptibility were also increased. Further, based on an extensive series of yield trials, we concluded that the advanced-cycle parents were more responsive to favorable production environments than were the original parents. In contrast, decreases have been observed for harvest index, BYD tolerance, bushel weight and groat percentage[11].

Our most recent efforts on correlated responses have utilized digital imaging analysis to measure changes in grain size and shape[5]. Kernel size including length, width and area increased with cycles of selection for yield (Table 2), but kernel shape was not changed. Kernel number was also increased, thus there was a large increase in the sink capacity of the plants of the advanced-cycle parents. Caution should be exercised, however, when comparing specific increases for kernel weight versus kernel number because these values are somewhat dependent on the individual environments from which the data are collected. Regardless, it does appear that both source and sink capacity (the former based on results of Bregitzer *et al.* [4] and Payne *et al.* [8]) have been increased while grain yield was being increased. The exact nature of the cause and effect relationships among these traits, however, requires more study before definite conclusions can be made.

Table 2. Percentage increase per cycle for grain yield and kernel size parameters, kernel weight, and kernel number over five cycles of recurrent selection for grain yield, two locations in 1989.

Trait	*Microplot*	*Row plot*
Grain yield	10.71	5.70
Kernel area	1.84	1.82
Perimeter	.92	.77
Length	1.00	.76
Width	.74	.92
Weight	2.60	3.87
Number	7.68	1.22

Other reports on recurrent selection in oat including Baltenberger *et al.* [2] and Branson and Frey[3] have observed fewer correlated responses than we. Both did several cycles of random mating before initiating selection, but whether such crossing produced greater genetic equilibrium among important loci thereby making their gene pools less vulnerable to correlated responses is unclear.

Methods of mainstreaming

The first attempt[6] at secondary trait selection to control increases in height and maturity was at best modestly successful (Table 3). The corrections expressed by the substituted parents themselves were of the magnitude which we desired for the progeny. However, the reduction in plant height and maturity for the progeny were not enough to justify continuation of the approach per se. It may be that with only 9 of 21 parents substituted, there was too much dilution by the other 12 original parents.

Our second attempt[9], crossing each of the 21 C_4 parents to three exogenous genotypes, produced more desired results (Table 4). The average height of all open-crossing-system progeny was shorter than the original closed system progeny, yet the two were equivalent in grain yield and maturity. Ogle progeny were higher yielding than the original C_4 progeny, equal in heading date but somewhat shorter. Starter progeny were equal in yield but earlier and shorter. Progeny of Mn 82214, an OT207 dwarf derivative, were lower yielding and shorter but also later than the C_4 progeny. These comparative results are to be expected when the phenotypes of the 21 C_4 parents are compared to those of the three outside parents.

Further, when multiple trait selection criteria (yield, height and heading) were applied to Ogle, Starter and closed system progeny, 45% of the Ogle and Starter progeny were saved while only 13% of the original C_4 progeny were retained.

Table 3. Means of RS-1 and RS-2 parents and progeny grown at one location in 1984 and two locations in 1985.

Character	*1984*		*1985*	
	RS-1†	*RS-2*	*RS-1*	*RS-2*
Parents				
Grain yield (g plot^{-1})	38.9	37.1	38.2	39.4
Maturity (days to heading)	59.9	57.9**	61.0	59.8**
Plant height (cm)	118.4	112.4**	121.4	117.4**
Progeny				
Grain yield (g plot^{-1})	38.3	38.2	43.6	42.1**
Maturity (days to heading)	59.8	59.2	60.5	60.1
Plant height (cm)	115.1	113.9	119.6	117.3*

*,** Differences significant at 0.05 and 0.01 probability levels, respectively.
† RS-1 = original system, RS-2 includes substituted sibs for parents.

Table 4. Mean values for measured traits from the closed and open systems of recurrent selection and from parents used to initiate the open system, one location, 1987.

System or parent	*Heading (days after planting)*	*Height (cm)*	*Yield (g m^{-2})*
Closed system progeny	45.7 b†	93.6 a	277.6 b
Open system progeny	45.9 b	86.6 c	269.0 b
C4 x Starter progeny	45.2 c	86.7 c	266.8 b
Starter	42.1 *	74.6 *	180.6 *
C4 x Ogle progeny	45.8 b	88.9 b	303.4 a
Ogle	44.7	82.4 *	300.2
C4 x Mn82214 progeny	46.8 a	84.2 d	237.8 c

* Indicates a significant difference between a progeny group and its respective parent, no data for Mn82214 *per se*.
† Values sharing the same letter are not significantly different at the 5% level, based on contrasts.

Based on the results given in Table 4, the Ogle and Starter families were chosen for further crossing and multiple trait selection efforts. The double crosses between these two groups were higher yielding than the three-way crosses; however, the three-way crosses with Hazel or an Illinois breeding line produced a higher proportion of chosen progeny when several multiple trait selection indices were used. The Starter backcross progeny were the shortest and earliest of the three groups but were also the lowest for grain yield.

During the 1992 field season, additional data were obtained on the double cross, three-way cross and backcross progenies to compare the three approaches for successful multiple trait index selection. In addition, the crosses for the new recurrent selection populations within the double crosses and within the three-way crosses have been made. Second backcrosses to Starter are also underway.

Acknowledgements

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Evaluation of Grain Yield Potential of Oat Germplasm in São Carlos-SP, Brasil

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Summary

Oat germplasm has been selected for forage production since 1985 in São Carlos, SP. Since the black oats (*Avena strigosa*), commonly used in this region do not produce seed satisfactorily, the forage selection study was followed by seed yield evaluation for final recommendation of oat cultivars. Promising grain production ability was demonstrated in some of the lines. This may be very important as the state of São Paulo is the main oat growing area in the country, although significant grain production has not been carried out here in the past.

Introduction

In the region of São Carlos, state of São Paulo, oats are cultivated mainly for forage production during the winter months. Black oats, *Avena strigosa*, are commonly used, but since they do not produce seeds satisfactorily in this region seed is brought from the southernmost states of Brasil. The same occurs with oat grain. In 1985, EMBPAPA/UEPAE de São Carlos initiated a program to evaluate oat germplasm for forage production[7]. This study program was followed by evaluation of the germplasm grain yields, with the objective of selecting material that would allow local seed production.

Methods

The present study was conducted in the same experimental plots as previously described forage production trials (Godoy *et al.* 1992. Oat evaluation for forage production in São Carlos, SP-Brasil. Fourth Int. Oat Conf.), using half of the plots to evaluate seed production. In 1985, 21 accessions were evaluated; from these, eight were selected and evaluated in 1986, together with four new accessions. In 1987, nine accessions selected from the 1986 trial were evaluated and finally, in 1988, six selected accessions were evaluated. It is important to point out that in all cases selection was performed upon forage production. In 1985, two accessions were discarded for low seed production. Seed was hand harvested from the central rows of half of each plot and yield calculated in kg/ha.

Results and Discussion

From the forage yield results, cultivars UPF 3, UPF 7 and São Carlos (UPF 79S115) were recommended for the state of São Paulo. The average seed yields in 1986, 1987 and 1988 are shown in Table 1. Seed yields were not evaluated in 1985.

Among the recommended forage cultivars UPF 3 presented the best average seed yield (2523 kg/ha). This was similar to the best results obtained in Rio Grande do Sul with UPF 3, as reported previously[4,5,3,1,2]. UPF 7 presented lower yields than those reported by these same authors whose results ranged from 1990 to 3582 kg/ha. UPF 2 had yields in São Carlos closer to those obtained by the authors in Rio Grande do Sul (1218 to 2392 kg/ha). The São Carlos cultivar, although presenting a lower average seed yield than that described by Forcelini *et al.* [6] in Passo Fundo, RS, offers the possibility of local seed production (Table 1), which is not possible with the common black oats cultivated in the São Carlos region.

Other tested accessions such as UPF 791174-3 and UFRGS 79A65 showed promising grain yields suggesting that oat seed and grain production is feasible in this region of Brasil.

Table 1. Average seed yield of oat accessions at São Carlos, SP. Brasil, 1986-88

Seed yield (kg/ha) *Accession*	*1986*	*1987*	*1988*	*mean*
UPF 3	4423b*	1136a	2009ab	2523
UFRGs 79A65	3246de	1148a	2423a	2272
UPF 79I17A	2690e	1179a	1703b	1857
UPF 7	3367cde	384de	1515bc	1755
UPF 2	2443e	583cd	1154cd	1393
São Carlos (UPF 79S115)	800gh	427de	877d	701
UPF 8	2945e	995ab	—	1970
UPF 79331-3	1627fg	814bc	—	1221
UFRGS 7806	1375e	423de	—	899
UPF 5	7386a	—	—	—
UPF 78211-2	4034bcd	—	—	—
Black oats (control)	284h	133e	236e	218
Mean	2991	722	1417	
C.V (%)	18.45	22.84	29.90	

* means followed by the same letter, within each column, do not differ statistically (Duncan, 5%).

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Oat in Portugal — Breeding an Old Cereal for Sustainable Agricultural Systems

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Summary

Oat is one of the components of crop rotations that sustain animal production in the Mediterranean areas of Portugal. Since the agricultural systems are based on cereal and animals, oat takes a crucial place in the farming systems. However, its value as cereal crop is very low as compared with other cereals, due to the EC economic policy. Farmers use oat for grazing, hay and for grain. This situation influences breeding strategies at National Plant Breeding Station (NPBS) at Elvas. Our philosophy is based in broaden genetic diversity for specific uses of oat to obtain a cheap crop.

Introduction

Portugal is located in the southwestern part of Europe between parallels 37^0 and 42^0 N, occupying a total area of 8,893,000 ha.

In spite of the small area, big differences can be found in environmental conditions affecting agriculture. The Northern part is hilly, cooler and with a high percentage of small farms (less than 5 ha.). The South, more affected by a Mediterranean climatic pattern, with lower and more erratic rain distribution, is the main cereal production area.

Wheat, maize, potatoes, wine and olive oil represent about 42% of total crop production.

Small grain cereals (wheat, barley, triticale and oat), are cultivated in approximately 600,000 ha from which oat represents around 180,000 ha.

Oats in Portugal have been traditionally faced as a low input crop, growing after long runs of other cereal crops acting, in this place of the rotation, as an extremely useful take-all break.

On the other hand, in the marginal areas of Portugal, this cereal is a component of a farming system of which livestock is the most important component. Oat is used for grazing, production of hay (mixed with vetches) and grain. The yield has remained unchanged over the last years except for the fluctuation associated with rainfall patterns. Almost 100% of total grain production is consumed by livestock, direct animal consumption and industry.

This crop is not directly supported by EC, (there is not an intervention "market") but, as a low input cereal, farmers really want to continue growing oats.

Once breeding must be concerned with all aspects involving the crop, the breeding program of Cereal Department at NPBS is targeting to improve the yield (grain and biomass), quality and acceptance of oats both on the farm and in the market.

Type of Germplasm

The introduction of germplasm developed for high input agricultural systems has been unsuccessful in marginal areas. There is a high risk of crop failures due to climatic and soil conditions, what makes farmers reluctant to the use of large amounts of inputs such as fertilisers, pesticides and herbicides.

In Portugal the genetic base of cultivated oats has been extremely narrow, based on local land races, Argentinean mixtures (Barradas and Bagulho, 1967) and more recently on some Australian material. In the early sixties the National Program located at Elvas (NPBS)

introduced through J.T. Reeves from South Perth Department of Agriculture, a set of lines where Avon, Fullmark and some other had shown excellent performance. During more than two decades Avon and Swan were the most spread varieties into cultivation due to the work in this station.

Avon and Swan are early cultivars for grain production. Another introduction coming from Morocco in that decade still has today the first place as forage variety. This cultivar called Boa F) produces high biomass and the growth cycle is suitable to use mixed with vetch.

Nevertheless, Avon was the most important introduction, not only in terms of cultivated area, but also as a parent in the National Oat Breeding Program (Table 1).

Table 1. Pedigrees of cultivars from Cereal Department at NPBS

Varieties	*Pedigree*	*National Catalogue*
S. MATEUS	S. Mamede x (S. Francisco x GI Innes)	included
S. ALEIXO	Avon x Avena Cartuja	"
S. ROMAO	S. Mateus x Avon	Under Registration
S. VINCENTE	(S. Jose) x Ballidu) x Avon	"
AE 9001	Avon x Tam - 0 - 301	"

In the last decade new introductions from Australia have shown interesting characteristics to be used in several crosses.

Breeding Efforts at NPBS

In order to take this crop suitable to our farming system, for example maintaining straw palatability and potential to grow in mixtures with vetches, the breeding efforts at ENMP are dealing with:

a) broadening the genetic base of germplasm using different sources from Australia, USA, Canada and Europe.

b) Evaluation of germplasm in different conditions considering traditional and new end uses (cereal breakfast).

c) Breeding for resistance mainly to *Puccinia coronata* and BYDV.

Breeding methodology includes artificial crossing, pedigree modified method with panicle selection on F3 bulked to produce F4. Long crosses were used but it was realised that was difficult to handle the tremendous variation obtained. Now single, top crosses and sometimes top crosses with one back cross are used, and excellent materials are coming out from the program by a better exploitation of the transgressive segregation.

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Oat Breeding at the University of Rio Grande do Sul, Brazil

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Summary

The oat breeding program at the University of Rio Grande do Sul, began in 1960 with the objective of developing new oat varieties with high and stable grain yield. Other traits sought were short plant stature, earliness and good grain quality. Before 1987, the segregating populations were obtained through the Quaker Oat International Nursery from the University of Wisconsin and Texas A & M. Twelve improved varieties with high grain yield and better adaptation to the cropping systems utilized in South Brazil were developed from the "QOIN".

Introduction

The oat breeding program at UFRGS began in the 1960s, with the introduction of pure lines from Wisconsin (Program USAID — Wisconsin — UFRGS). The objective was to introduce genotypes with good forage and grain yield and resistance to crown and stem rust. In the late 1970s the area sown to oats for grain in the states of South Brazil was very low and most of the oats utilized was imported from Argentina. In 1975, the objectives of the program were changed and emphasis was placed on the development of oat varieties with high and stable grain yield[1]. A massive program of introduction of F_3 populations was commenced through Dr H. Shands of Wisconsin, and later through the Quaker Oat International Nursery (Universities of Wisconsin and Texas A & M). The objective of the present work is to record the progress obtained in the oat breeding program at University Federal of Rio Grande do Sul, Brazil.

Methods

The environment

The University Experimental farm is located in the county of Eldorado do Sul at 51°39' W and 30°05' S, 46 m above sea level . The average temperature, rainfall and solar radiation during the growing season for oats is presented in Table 1.

The germplasm

Before 1987, all segregating populations were introduced from the Quaker Oat Nursery, and a pedigree method based on single panicle selection was mainly used. Strong selection pressure was placed on short stature, early maturity, good agronomic type and high grain yield potential. Since 1987, crosses have been made on site and most of the current selections have been developed from this material. In 1992, the first yield tests of more than 100 lines selected in previous years were conducted.

Results and Discussion

Currently, 12 new varieties have been released to the farmers. These are designated UFRGS 1 to UFRGS 12. The variety, year of release, pedigree, plant height and days to maturity are listed in Table 2. These are the earliest varieties to be released in Brazil and they allow farmers to plant double-crop soybeans at the ideal sowing time after an oat crop. UFRGS 7 is also the shortest variety of oat ever grown in Brazil. The grain yield of these twelve varieties grown in different regions of Brazil are shown in Table 3. Since 1985, UFRGS 7 and UFRGS 10 have shown the highest grain yield, exceeding the average of all varieties grown by 18% and 20% respectively.

Over the last three years the area sown to UFRGS 7 by farmers has increased steadily. The oat varieties developed in this program are much better adapted then previous varieties and in consequence the area sown to oats is increasing and oat production is now meeting Brazilian needs.

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Table 1. Average temperature, solar radiation, rainfall, and relative midity from June to November, Eldorado do Sul, Brazil

	Temperature (°C)	*Solar Radiation Cal/cm²/d*	*Rainfall (mm)*	*R.H. (%)*
June	13.9	206	168	85
July	14.2	213	145	84
August	15.0	248	145	78
September	17.0	322	128	79
October	18.9	414	103	74
November	21.0	509	107	72

Table 2. Variety, year of release, pedigree, plant height and days to maturity of twelve oat varieties developed at University of Rio Grande do Sul, Porto Alegre, Brazil

Variety	*Year release*	*Pedigree*	*Plant Height (cm)*	*Maturity (d)*
UFRGS 1	82	DAL x CDA 292	130	145
UFRGS 2	82	DAL x CDA 292	125	145
UFRGS 3	82	CDA 28 x Goodland	95	155
UFRGS 4	85	DAL x CDA 292	135	142
UFRGS 5	85	Coker 234 x X2626-2	140	145
UFRGS 6	85	Swan x X2616-2	140	150
UFRGS 7	86	X 1205 x FLA 1093	105	140
UFRGS 8	86	OA 338 x X2682-1	125	135
UFRGS 9	86	Daible x S8 Parents	125	137
UFRGS 10	87	C1217 x (Coronado-BCRA)	130	150
UFRGS 11	87	Quadcross 2 (16 parents)	100	143
UFRGS 12	87	734470-2 x (Coker 234-74xC17)	125	150

Table 3. Variety, year of test, grain yield average and percentage over the best check of twelve oat varieties grown in different environment of South Brazil

Variety	*1979 1981*	*1982 1984*	*1983 1987*	*1985 1988*	*% Best Check*
UFRGS 1	2936				169
UFRGS 2	2782				160
UFRGS 3	2496				143
UFRGS 4		2254			108
UFRGS 5		2899			138
UFRGS 6		2922			140
UFRGS 7			2616		118
UFRGS 8			2671		120
UFRGS 9				2617	114
UFRGS 10				2928	128
UFRGS 11				2356	103
UFRGS 12				2732	120

Oats Situation in South America

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Argentina

Approximately 2,000,000 hectares are sown in Argentina, of which only 450,000 ha. are harvested. Oats are generally destined to a double purpose. Production normally ranges around 550/600,000 tons.

Oats can be sown during two seasons, early autumn or in winter. Those sown in autumn have a double purpose while those sown in winter are exclusively for harvest. Crops are not fertilized and weed control is infrequent. The grower that sows to harvest pays greater attention to crops. It's a crop sown in a wide area but of little importance.

Brazil [2][3]

Oat production has significantly increased during the last fifteen years. In 1991, 246,000 hectares were harvested giving an average yield of around 1,200 kg/ha, with a national production of 250,000 tons. This figure shows the explosive evolution of oat production in Brazil.

The most important breeding programs are those of the University of Passo Fundo, University of Rio Grande do Sul, and of the Mixed Agrarian Cooperative of Entre Rios Ltd. Quaker, since some years ago, keeps a close relation with these experimental stations and each year sends them genetic material from the Universities of Wisconsin and Texas. In general, stabilized lines and segregating materials are sent, which are later selected in Brazil according to their behaviour in the different regions. Oat production regions are situated in the states of Rio Grande do Sul, Santa Catarina and Parana.

Diseases in Brazil are particularly virulent and in order of importance they are: leaf rust (*Puccnia coronata avenae*), stem rust (*Puccnia graminis avenae*), BYDV, Halo Blight, helministosporiosis (*Pyrenophora avenae*) and septoriosis (*Septoria* sp), limiting oat production. At present, genetic resistance or tolerance is being investigated while most big farmers use fungicides.

In the south of Brazil, oats is used as forage during winter and is either sown alone or in association with rye grass or with some legumes. In the last years, oats has also been used as a soil cover to control erosion.

The most popular varieties are: UPF 2, UPF 5, UPF 13, UFRGS 12, UFRGS 7 and UFRGS 10. Work is being done on tissue culture and the first steps in the search for stem rust resistance are being taken. Another objective to achieve is the improvement of grain quality.

Chile [1]

Average yield 2,400 kg/ha. Production: 120,000 tons.

Chile is also part of Quaker's South American Research Program since 1979, just as Argentina. Oat crop evolution can be divided into different stages:

1. First, where yields are very low.
2. Second, where yields significantly improve.
3. Third and fourth, where the greater oat production is due to the increase of yields and not to the increase of the sown area.

The area where oat is grown is a cold one, the soil has a high percentage of organic matter and also powdery mildew (*Erysiphe graminis avenae*) has been observed during the last years.

In Chile, breeding works are carried out at three experimental stations: Carrillanca, Quilamapu and La Platina. At La Platina test on diseases are being performed. In order of importance the diseases are: Halo Blight, BYDV (barley yellow dwarf virus), rust; but they do not constitute a limitation to production.

The following works are carried out at Carrillanca and Quilamapu:

- ❒ Breeding : crossing. Probably the experimental station to have made the greatest amounts of crossings.
- ❒ Grain quality : groat %, protein %, weight test, lodging resistance.

The genetic breeding program incorporates a different agronomic type and a marked yield increase. Genes resistant to rust and lodging were also incorporated.

Chilean oats are of the Canadian type, having a long growth period. There are two possible sowing times: winter and spring although better yields are obtained during the winter sowing.

A great difference exists between the national average and what was obtained by the best farmers. In a more or less easy way yields of about 5,000 kgs can be obtained but the problem in Chile is that there are too many small growers and they do not have storage capacity.

Commercialization is being currently organized through representatives. The most spread varieties are: Llaofen, Ancafen, Yecufen and America.

Chile exports very good quality oats.

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Oat Breeding in Argentina

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Oat breeding began in the year 1923, when Eng. E. Klein released the first variety. In 1969 the Suregrain variety is registered, being one of the most important in Argentina. In the late 1970s and early 1980s Quaker Oats Co. assumed funding responsibilities for South American oat research. Dr. Shands, Dr. Brinkman, Dr. Schrikel and Dr. Brunette were some of the people that formed part of the program, currently integrated by Dr. Sam Weaver and I from Quaker Oats Co. and by Dr. Forsberg and Dr. McDaniel from the University of Wisconsin and from the Texas A&M University respectively. The main breeding activities of the Quaker South American Program are either handled individually by Dr. McDaniel or by Dr. Forsberg. Both perform the crosses to produce new segregating populations and develop the list of the test lines and segregating populations for each South American country.

Breeding work is carried out at the experimental stations of Inta Castelar, Bordenave and at Barrow.

Castelar experimental station

Work on resistance to diseases are made at this station. Investigations on stem and leaf rust are carried out in a greenhouse as well as in the farm. Eng. Antonelli determined various sources of resistance. All the materials such as lines and segregating populations are also tested at this station. In Argentina plant diseases, in order of importance, are the following: leaf rust, BYDV, stem rust, Halo Blight.

Barrow experimental station

Situated in the city of Tres Arroyos in the heart of the wheat region. Programs on breeding, herbicides, fertilization, grain quality and grain yield are carried out here:

- ❒ Breeding: regrowth after grazing since oats in Argentina are generally used with a double purpose.
- ❒ Lodging resistance: old oats were of an agronomic kind which rendered them very susceptible, while new oats have a very good behaviour.
- ❒ Crossing: at present, and with the technical advice of Drs. McDaniel and Forsberg, many crosses are made at this station.
- ❒ Disease resistance: studies on resistance to leaf rust are very important for this area.
- ❒ Herbicide program: the main objectives are: a) application time, b) weed control. Investigations on alternative herbicides to the use of MCPA Tordón are being carried out.
- ❒ Grain quality: great emphasis has being place on this trait, on the search for oats with a better hull/grain relation, better protein percentage, better weight of 1,000 gr, etc. A minimum protein parameter is to be established for the future, as a condition for the selection of milling oats. For said purpose, all samples will be tested to determine: hull/grain relation, protein percentage and weight of 1,000 gr.

Two new varieties were developed at this station: *Bonaerense Paye* and *Bonaerense Gringa*. Yields per hectare are superior to other commercial varieties.

Bordenave experimental station

Placed to the southwest of the Barrow station, it has a colder and drier climate. In Argentina many oats are sown in this kind of region, which is why this work is very important to the country. Works are being done on regrowth after grazing, frost resistance, drought resistance, disease resistance, grain quality and lodging resistance. Recently work was initiated on resistance to green bug (*Schizaphis Gramminum*). Two new varieties have been developed: *Cristal Inta* and *Millauquen Inta.*

Another small breeding program is being done at the University of La Plata, where resistance to green bug is being studied. As a result of this investigation *Tambera* oats was released, with a certain tolerance to said disease.

Oat programs had not released many cultivars until three years ago. Cultivars retain popularity for longer periods of time in areas where races of pathogens do not change frequently. The newest cultivars released in Argentina have been significantly better than the older cultivars in one or more traits.

Another important aspect of the breeding program is the team work between Quaker Argentina and the experimental stations. For the production and multiplication of new oats, production agreements are being signed with the farmers through big grain companies. Certified seeds are used exclusively (this was a success and a very important technical advance both for Quaker Oats, due to oats quality, and for the experimental stations on account of the income of funds) and the payment of royalties to the pertinent party is established as a condition. At the same time, pursuant to agreements entered into with the experimental stations, these new funds will be directed to research.

Also milling tests on an industrial scale are performed as part of the oats program in order to accurately determine the new varieties' behavior at the mill.

The Achievements of Oat Breeding in Finland since 1920

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Summary

The present study evaluated the genetic changes in the structure of stands of oats, *Avena sativa L.*, in Finnish growing conditions during this century. The most important traits, alterations in which contributed to increased grain yields of up to 20-30%, were decreased plant height, increased vegetative phytomass, increased panicle weight, improved panicle filling rate, and increased size of flag leaf. Furthermore, modern cultivars are likely to be source-limited whereas the older ones are sink-limited.

Introduction

During the past ten years numerous studies reporting genetic gains of 30-40% in the grain yield production of oats have been published[4,5,10,12,14]. In addition to improved productivity, the modern cultivars are known to have shorter straw length, associated with lodging resistance and improved HI. The objective of the present study was to evaluate, by comparing 17 morpho-physiological traits, how the structure of the oat plant and the oat stand have changed due to breeding.

Methods

The oat material consisted of 13 Finnish oat cultivars released between 1921 and 1988, 3 foreign cultivars, and 13 breeding lines developed at the Hankkija Plant Breeding Institute. The cultivars were evaluated at the Viikki Experimental Farm of the University of Helsinki (60°13' N) in 1988 and 1989. Completely randomized block design was employed. The plots were fertilized at the recommended rate (80 kg N ha^{-1}).

Grain yield (g m^{-2}) and the following morpho-physiological traits were measured on each plot: days to flag leaf emergence, heading, and yellow ripeness; grain-filling period (d); plant height (cm); lodging (%); panicles per m; phytomass (g $plant^{-1}$); panicle weight (g); number of grains per panicle; single grain weight (mg); harvest index (HI, %); panicle-filling rate (mg $plant^{-1}$ day^{-1}); grain-filling rate (mg $grain^{-1}$ day^{-1}); area of flag leaf (cm); flag leaf area index (FLAI); and rate of plants infected by barley yellow dwarf virus (BYDV, %). The historical trends in the various traits due to oat breeding were tested by Spearman's rank correlation analysis.

Results and Discussion

Finnish oat breeding has resulted in yield improvements of up to 35% during this century[10,12]. In the present study yield increases of 20-30% were detected by comparing cultivars released between 1921 and 1988.

Straw length

Since the onset of the intensive breeding programs, cereal breeders have emphasized selection for short- and stiff-strawed lines (Table 1). This has resulted in reductions of up to 15-20% in plant height in modern oat cultivars as compared to those released in the 1920s.

However, Lawes[4] showed that the newer cultivars are better adapted to high-yielding environments, even though breeders had aimed indirectly at improving phenotypic stability through selection for short and stiff straw. This is in agreement with the findings in Finnish growing conditions[11], and may result from increasingly homogeneous plant populations, which are less able to compensate in adverse environments, and from reduction in the extent of the root system[5]. Thus, further shortening of straw in no longer as essential as it once was.

Table 1. Significant Spearman's rank correlations between morpho-physiological traits and year of cultivar release.

Trait	*1988*	*1989*
Grain yield	0.73^{**}	0.51^{ns}
Grain-filling period	-0.43^{ns}	-0.67^{*}
Plant height	-0.72^{**}	-0.79^{***}
Phytomass	0.60^{*}	0.54^{ns}
Panicle weight	0.76^{**}	0.53^{ns}
Harvest index (HI)	0.69^{**}	0.21^{ns}
Number of grains per panicle	0.71^{**}	0.52^{ns}
Panicle-filling rate	0.81^{***}	0.68^{**}
Area of flag leaf	0.60^{*}	0.74^{**}
Flag leaf area index	0.25^{ns}	0.77^{**}

*** $P \leq 0.001$ ** $P \leq 0.01$, * $P \leq 0.05$ ns non-significant

Source-sink interaction

Selection for short straw length has resulted in improved HI[2]. This was also found to be the case in the present study (Table 1), although correlation between HI and year of cultivar release was significant only under the exceptionally dry conditions of 1988. The unfavorable environment highlighted the superior capacity of the modern cultivars to allocate assimilates into the sinks of economic importance. In fact, Finnish oat breeders have not increased panicle weight at the expense of above-ground vegetative biomass[7]. Rather both of these components have improved: panicle weight by 21 kg ha^{-1} yr^{-1} and vegetative phytomass by 13 kg ha^{-1} yr^{-1}.

Sims[13] found that a decreased number of secondary tillers associated with a higher proportion of head-bearing tillers was the most important factor contributing to the increased HI of oats. However, tillering capacity has only limited importance in northern latitudes because the long days inhibit tillering[3]. The present study confirms this, as no changes in the number of panicles per m were identified.

CO_2-exchange rate of one Finnish cultivar of the 1920s decreased very steeply at the early part of the grain-filling period[8] due to the low number of grains. This was an indication of limited sink capacity. However, improvements in HI have turned yield formation into a source-, rather than sink-limited process in the modern cultivars.

Prolonging of leaf area duration (LAD) has been one of the methods used to overcome the source limitation of modern cultivars. Recently, Ehlers[1] concluded that increased LAD is the critical factor responsible for the improved yielding ability of the modern oat cultivars. However, in regions where the growing period is brief, later maturity class could not have been used as a selection criterion[6], which is one reason for the absence of significant correlation between year of cultivar release and maturity class.

However, improved productivity has also been obtained in such marginal areas — not through prolonged LAD, but rather through development of cultivars with a shorter grain-filling period (Table 1) and a panicle-filling rate increased by some 30%.

In fact, prolonging of the pre-anthesis phase at the expense of the post-anthesis phase is one of the possible reasons for the increased generative sink capacity. Another factor positively contributing to the panicle-filling rate is that breeding has been able to increase the size of flag leaf (Table 1) by 20-30%; this has overcome somewhat the source limitation, assuming that the increase has not been associated with decreased CER per unit leaf area.

An additional factor contributing to durable green area is resistance to pathogens. Barley yellow dwarf virus (BYDV) is the only important pathogen destroying oat canopies in Finland. It can cause remarkable yield reductions of up to 40%[9]. However, due to the lack of intensive BYDV-resistance breeding, no improvements in BYDV-tolerance were detected in the present study.

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Recent Advances In Oat Molecular Biology

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Summary

Oat is rapidly becoming a more feasible and attractive subject for plant molecular biology research. Advances in oat gene isolation and characterization, continued development of systems for production of transgenic plants and the completion of molecular maps for hexaploid oat and some diploid relatives will complete the spectrum of technologies required for molecular biology research and its application to oat improvement.

Introduction

Remarkable progress has been accomplished in the field of plant molecular biology over the past decade. It has been less than ten years since the first reports of transgenic plants[18], plant restriction fragment length polymorphism (RFLP) maps[15], and sequencing of the entire tobacco chloroplast genome[13]. In the few years since the establishment of these and other important benchmarks, there has been an impressive revolution in the field of plant biology which has led to transformation systems and molecular maps for most crop plants. One measure of this recent progress is indicated by the scale of near-term goals established for research in and applications of plant molecular biology. Examples include commercialization of transgenic plants, map-based cloning of genes and sequencing of the entire nuclear genomes of plants such as *Arabidopsis*. Some of these goals will be achieved in the very near future.

Relatively few workers have chosen oat as a system for plant molecular biology investigations. In contrast, quite a number of significant physiological and metabolic studies have been conducted using oat; including much of the early work on auxins and phytochrome. One obvious scientific explanation for the apparent low interest in applying molecular biology approaches to elucidating the molecular mechanisms underlying these physiological studies stems from the fact that oat has been perceived as a less than ideal genetic system for basic research. The enormous and comparatively uncharacterized hexaploid genome of oat and the absence of a genetic transformation system likely were deterrents to conducting molecular biology research in oat.

The objective of this paper is to discuss the recent advances in oat molecular biology. In oat, major recent advances have been achieved in the areas of RFLP mapping, gene isolation and genetic transformation. Aspects of all of these breakthroughs are presented in talks and posters at this meeting. To avoid excessive duplication with these presentations and because progress on the *Avena* RFLP maps will be covered at this meeting, this paper will be limited to a discussion of recent progress and future challenges in the areas of gene discovery and genetic transformation of oat.

Results and Discussion

Gene Discovery for Oat Improvement

Progress in oat gene isolation and characterization has important implications for understanding the molecular relationship(s) between genes, gene products and plant traits. Plant morphology, development, metabolism, response to environment and to pests, and the composition of the grain are traits controlled by gene networks about which more information is required concerning their underlying "gene-enzyme-trait relationships" before molecular manipulation strategies can be devised for crop improvement. Unfortunately the list of isolated and characterized oat genes is short compared to those in most crop species.

Three oat gene systems that have been characterized at the molecular level are briefly reviewed below.

Significant progress has been achieved in the isolation and characterization of cDNAs encoding oat tubulin subunits[9]. Dimers of alpha- and beta-tubulins self-assemble to form microtubules which play key roles in cell division, cell enlargement and cell wall deposition. At least 6 to 10 genes each of alpha- and beta-tubulin were detected per hexaploid genome using genomic DNA blot analysis[9]. The levels of tubulin transcripts increased during gibberellic acid induced cell elongation and tubulin transcript levels were correlated with cell wall deposition during cell elongation[9]. These results provide an insight into the role of tubulins in oat plant growth and development.

Genes encoding the oat kernel storage proteins, avenins and globulins, have been isolated and characterized[2,5,6,14]. Oat globulins, which make up 50% to 80% of the kernel protein, resemble legume globulins in amino acid composition thus explaining the nutritionally balanced amino acid content of oat protein[1,7]. The avenins have structural homology to wheat gliadins and comprise 10% to 20% of the kernel protein[2]. Recent work is focused on investigations of the regulatory mechanisms that control avenin and globulin gene expression and protein deposition in the endosperm. During kernel development, avenin mRNA levels are greater than globulin mRNAs[2,5]. However, more globulin accumulates in the mature kernel. These results suggest that storage protein accumulation is regulated both transcriptionally and post-transcriptionally in oat[2,5] demonstrating a unique mode of storage protein gene regulation among the cereals. Further progress in understanding the molecular basis of transcriptional and post-transcriptional regulation, and protein deposition in determining the unique amino acid composition of oat kernel protein will elucidate genetic manipulation strategies for further grain quality improvement. However, investigations to acquire this information are dependent on development of oat gene transfer systems.

Genes encoding oat (1-3,1-4)-ß-glucanase, an enzyme that hydrolyses mixed linkage ß-glucan, have been isolated and characterized[19] (S.J. Yun *et al.* — these Proceedings). A 1.5 kb full length glucanase cDNA clone has been characterized in detail[19]. Glucanase genes comprise a small multigene family which have been assigned to a homoeologous group of chromosomes (W. Rooney and E. Jellen, University of Minnesota unpublished data). Glucanase transcripts have been detected at high levels in elongating leaves and in the endosperm of 10-d-old immature kernels as well as in the aleurone layer of germinating kernels. The transcript levels generally parallel glucanase activity in these tissues. Future research is focused on investigating the role of ß-glucanase activity in endosperm development and in vegetative cell expansion and will involve genetic transformation.

Genetic transformation strategies both require and may be used to discover genes that are useful for crop improvement. Two general categories of transformation strategies can be delineated based on manipulations that involve changes in expression of oat genes and those that involve introduction of genes from any organism. Changes in expression of existing oat genes involve either overexpression or down-regulation of the gene of interest. Overexpression can be mediated by reintroduction of a gene under the control of a promoter sequence that confers elevated expression or a unique pattern of tissue- or developmental-specific expression[18]. Down-regulation of a specific gene may be mediated by antisense[16], cosuppression[11,17] or ribozyme technology[8]. All of these approaches require having at least some DNA sequence of the target gene as well as promoter sequences that would regulate the appropriate expression of the transgene. Overexpression and down-regulation are elegant strategies for elucidating gene-enzyme-trait relationships. Furthermore these approaches have been used in plant improvement programs to manipulate a number of traits.

Genetic transformation also has been used to express exogenous genes that may be isolated from any organism in the target species. This removal of sexual compatibility barriers is the hallmark of transformation. Indeed transgenes isolated from diverse plants, bacteria and viruses and, in a few cases, from animal and insect systems have been expressed in plants[18]. Therefore the sources of genes useful for plant improvement would appear to be unlimited. Manipulations involving exogenous genes can be subdivided into two subcategories.

Exogenous genes can be used to over-ride endogenous pathways to increase levels of a specific endogenous product. Exogenous genes also are used to introduce completely new traits into the target species. Recent reports of transgenic plants with increased herbicide, disease and insect resistance, plants that produce novel compounds such as the industrial feedstocks, pharmaceutical peptide hormones or industrial enzymes and plants with altered product compositions demonstrate the potential applications of this strategy in oats.

A matter for debate will concern the origin of genes that will be useful for oat improvement. Central to this debate is whether the most useful genetic transformation strategies involve manipulation of expression of oat genes or will the genes come from either related species or other organisms. Because so few oat genes have been characterized, near-term oat genetic transformation goals will by necessity involve non-oat genes. For example, current efforts to transfer the barley yellow dwarf virus coat protein genes into oat to investigate virus resistance may represent the first application of this transformation strategy in oat improvement (R. Lister, these Proceedings). Promoters for tissue- and development-specific expression of transgenes also are lacking. Exogenous promoter sequences from other plants may be expected to regulate transgenes in oat properly. Furthermore, promoters from other organisms may be discovered that confer a desired expression pattern and level in oats. However, to fully utilize the potential of transformation in oat it seems inevitable that at least some effort must be undertaken in oat to isolate and characterize a battery of promoter sequences that specify a broad array of gene expression patterns.

A major challenge will be isolating and characterizing oat genes that have either qualitative or quantitative control over traits that have so far only been characterized on the phenotypic level. For example, it would be extremely worthwhile understanding the molecular genetic basis of yield component traits such as tiller number per plant, number of seeds produced per panicle and seed size. However, almost nothing is known about the genes and gene products underlying these types of traits. Therefore, the genes must be isolated based solely on the phenotype they confer. Advances in gene mapping, gene isolation and transformation techniques have resulted in development of strategies that may be applied in oat to determine the molecular basis of phenotypic traits. These strategies include RFLP map-based gene cloning, chromosome segment-specific libraries and transposon tagging.

Map-based gene cloning relies on a high resolution RFLP map to pinpoint the locus of interest[10,15]. A very large (ca 100 kb) cloned oat genomic insert is then isolated that is syntenic to the linked RFLP markers. The genomic insert containing the gene of interest is further subcloned and analysed by various methods that can be used to identify the open reading frames of genes encoded on the insert[10]. Identity of the gene of interest can be confirmed by transforming the putative gene back into oat to determine its effect on plant phenotype. This map-based cloning procedure would be facilitated in oat through the production of chromosome segment-specific libraries. Chromosome-specific libraries may be constructed from isolated chromosomes or chromosome fragments. Subtractive hybridization using deletions or possibly even ditelosomics and aneuploids also may be used to construct region-specific libraries. The end result of either of these procedures is to produce a genomic library from a specific genomic region, thereby increasing the probability of isolating a mapped gene encoding a phenotypic trait.

The maize transposable elements Ac and Ds have been transferred into a number of species and have been shown to transpose properly[3]. If an Ac, Ds system were transferred into oat, progeny could be screened for mutants created by Ac, Ds element transpositions into genes that effect the phenotype of interest. The inserted transposable element sequence then could be used as a tag to isolate the gene into which the element had inserted[12]. Oat genomic sequences flanking the transposable element would then be used to isolate either cDNA or genomic clones of the target gene. Again, transformation could be used to verify the effect of the isolated gene on plant phenotype. Strategies for isolation of agronomically important oat genes require substantial effort and improvements in the RFLP map, genomic libraries and transformation system. However, it is important to consider these potential strategies as we plan for the future of oat molecular biology.

Current Status of Oat Transformation

Fertile, transgenic oat plants have been produced that transmit transgene sequences and phenotypes to their progeny. The procedural details of this transformation system are described in a poster presentation (Somers et al., these Proceedings). Briefly, DNA delivery was accomplished using acceleration of particles encoated with transgene DNA into cells of friable, embryogenic callus. Bombarded tissue cultures were selected for expression of an introduced selectable marker gene *bar* which confers resistance to the herbicide phosphinothricin (PPT). Tissue cultures resistant to PPT were shown to be transgenic using Southern blot analysis as were plants regenerated from the transgenic tissue cultures.

In the initial transformation experiments about 50% of the regenerable transgenic tissue cultures produced male sterile plants whereas the remainder appeared to be completely sterile. Some cross-fertilized, transgenic progeny were produced on these plants by hand pollination. To date numerous self-fertile plants have been regenerated from two transgenic tissue cultures. Segregation for the presence and absence of transgene sequences and phenotypes in progeny of some plants regenerated from both transgenic tissue cultures approximates a 3:1 ratio suggesting disomic inheritance of the transgenes. We are in the process of examining the inheritance in the R_2 progeny of the transgenic plants to confirm stable transformation.

The current transformation process that we have developed takes about six months from the time of microprojectile bombardment to production of seed on regenerated plants. Although our results with this prototypical transformation system indicate that oat has been transformed, several alterations are required before this system can be efficiently applied to oat molecular biology research and crop improvement. The cost and time required to produce a transgenic tissue culture must be reduced. The frequency of fertile plants must be increased. In our most recent experiments, the frequency of fertile plants appears to be much higher because of our use of younger tissue cultures for microprojectile bombardment. The selectable marker *bar* gene (herbicide tolerance) cannot be used in selection of transgenic plants that are intended for field testing because of the high probability that this gene may be transferred to wild oats, an eventuality that is amply documented at this meeting. Most of these adjustments in the procedure represent technical details which can be overcome with existing and developing technologies.

Future Prospects

As progress in gene isolation, gene transfer and gene mapping in oat gather momentum, I believe that oat will gain respectability as an experimental organism. The demonstration that oat is a "good" system for molecular biology research, because all requisite tools are in place, will increase research efforts on oat. Possibly the oat research community will expand because of research progress reviewed in this paper and presented by other investigators at this conference. The outcome of this increased effort will eventually result in improved oat cultivars.

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Novel Oat Grain Protein Genes

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Abstract

To study gene expression during development of oat cells we first isolated a 3B3-like cDNA (p3B3) from oat seeds (Fabijanski *et al.* 1988). The bipartite/chimeric features of this sequence encouraged us to screen another oat seed cDNA library which revealed one other type of 3B3-like sequence (c3B3). Since the amino acid sequence predicts a 16kDa oat storage protein, we believe these cloned DNA sequences code for the 16kDa protein, the N-terminal amino acid sequence of which has been determined by Pernollet *et al.* (1989). These 16kDa proteins may act as chaperonins in the upper deposition of the major protein fractions, globulins and prolamins. These new 3B3 sequences contain features distinct from the globulin family of genes (that are deposited in one fashion) and those of prolamin genes (that are deposited differently) (Lending *et al.* 1989). It would be of great interest to know if this 16 kDa protein is part of some, as yet unidentified, matrix within the bodies. This will allow for an understanding of the mechanisms of protein deposition in plant cells. This information is needed if the application of generic engineering techniques to crops is to be successful.

Toward an Integrated Chromosomal/Molecular Genetic Map in Oat

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Summary

DNA restriction fragment length polymorphism (RFLP) bands on Southern blots are being used to identify syntenic groups of markers and to associate these groups to chromosomes using aneuploid stocks of cvs. Sun II and Kanota in cultivated oat (*Avena sativa* L.). Nine distinct nullisomics were identified in Sun II and twelve distinct monosomics identified in Kanota. RFLP analysis demonstrated that in each cultivar set several monosomics were deficient for the same chromosomes. Four tentative homoeologous groupings have been identified among the Kanota monosomic series. Improved C-banding procedures combined with chromosomal morphological features have enabled cytological identification of all 21 oat chromosomes.

Introduction

Although common cultivated oat *Avena sativa* L. and common bread wheat *Triticum aestivum* L. have similar allohexaploid genomic structures (2n=6x=42), detailed knowledge of the genomic organization of oat has lagged behind that of wheat due to a paucity of genetic markers, aneuploid cytogenetic stocks, and means of physically identifying individual chromosomes in oat. In this report we summarize our progress using RFLP markers, various aneuploid stocks, and computer-enhanced chromosomal C-banding pattern analysis toward the development of an integrated physical/molecular marker map in oat.

Methods

Plant materials

Seed was obtained for oat cv. Sun II monosomics, nullisomics, and ditelosomics from Dr. H. Thomas, Welsh Plant Breeding Station, Aberystwyth, Wales, and cv. Kanota monosomics from Dr. T. Morikawa, University of Osaka Prefecture, Sakai, Japan. Monosomics were rapidly identified based on the presence of a high proportion (>30%) of microspores with micronuclei. Putative nullisomics often were identified based on distinctive plant morphologies and confirmed by cytological and RFLP analyses.

RFLP Analysis

DNA extractions, restriction digests, Southern blotting and hybridization procedures all followed protocols described by Sambrook *et al.* [12], with minor modifications. Probes used were known genes (i.e. ß-tubulin, globulins, avenins); oat genomic (OG probes) and cDNA clones from etiolated leaves (CDO probes) obtained from Drs. L. O'Donoghue, M. Sorrells, and S. Tanksley, Cornell University; and cDNA clones isolated from a cv. Ogle oat endosperm cDNA library (UMN probes). In analyses involving nullisomics or ditelosomics, absence of a band in lanes containing DNA from the nullisomic or ditelosomic line places the sequence normally detected by the probe to the missing chromosome or chromosome arm. Analysis of monosomics is similar except that one is dependent on detection of a reduced band intensity or dosage effect rather than a band absence from a lane. Because only one of the bands present in a three-band lane might be expected to be associated with the chromosome deficiency, the other two bands, which presumably associate to the homoeologous chromosomes, should be present at normal intensity and thus serve as internal checks for DNA loading variations.

To detect dosage-related intensity differences, short-term exposure autoradiograms were scanned into a Macintosh IIx computer using an Applescanner and Applescan software and analyzed using Image 1.43 (National Institute of Health) software. To check consistency of results, two different plants from the same monosomic line were analyzed. The whole test was repeated to confirm initial assignments. In some cases it was possible to confirm the dosage-based band assignment by analyzing DNA from monosomic F_1 plants obtained from crosses of the monosomics by a cultivar with a polymorphism for that band. A complete absence of one polymorph in the band pattern from the monosomic F_1 served to confirm the association of the band sequence to the deficient chromosome.

C-banding protocol

Root tips after 24-hour ice-water bath treatment were fixed in 3:1 ethanol:glacial acetic acid, squashed after 2 hours in a drop of 45% acetic acid, and examined under phase-contrast. Images of selected cells with well-separated chromosomes were captured using the NIH programs Image 1.22 or 1.43 on a Macintosh IIx computer with a Cohu 4815-2000 CCD video camera mounted atop a Zeiss Axioskop microscope. Chromosomes were subsequently C-banded by a variation of the protocol of Giraldez *et al.* [3] using Wright's stain[6]. Captured images of C-banded chromosomes together with chromosome arm measurements obtained from phase-contrast images were used to construct graphical ideograms of cv. Kanota chromosomes.

Results and Discussion

Analysis of RFLP patterns on Southern blots using DNA extracts from nullisomics or ditelosomics in oat provides an efficient means for identifying syntenic groups of markers (ones present on the same chromosome or chromosome segment). These procedures have allowed the localization of 55 RFLP sequences to 9 putatively different chromosomes in cv. Sun II. Nullisomics were obtained and DNA from leaf tissue analyzed for 12 of the 18 available Sun II monosomics. However, certain groups of the 12 were missing the same RFLP sequences and hence appear to involve deficiencies of all or at least a portion of the same chromosome. Nullisomics I, IV, VI, XI, XII, and XVIII each appear to be distinct while II/XIII, VII/XIV, and VIII/IX/X are groups whose members are missing the same sequences. Since nullisomics were placed within a grouping exhibit differences in phenotype (4; H. Thomas, pers. comm.), these nullisomics probably contain genetic background differences. In addition to the nullisomics in Sun II, four different Sun II ditelosomics have been analyzed using 28 markers. Two of these lines, D VII and D XIV, represent ditelosomics missing different arms of the same chromosome.

In cv. Kanota, where 21 monosomics have been reported[9], nullisomics were obtained only from monosomics 8, 19, and 21. The technique of monosomic dosage analysis was applied to the remaining Kanota monosomics to identify chromosome locations for RFLP markers that give a simple three-band pattern. In certain cases where polymorphism for the marker existed in another cultivar, the chromosome assignment could be verified by generating and analyzing the appropriate F_1 monosomic. As in the Sun II aneuploid series, RFLP analysis of the Kanota monosomics revealed that some lines which were thought to be missing different chromosomes were each deficient for the same markers. Other types included various monosomics missing some RFLP sequences in common and some not in common. Such differences possibly reflect translocation differences among these monosomics. Overall, 12 unique monosomics were tentatively identified among the 21 Kanota monosomic lines available with possible translocation variations present in three of them (Fig. 1).

Three complete homoeologous groups and a partial group of two homoeologous chromosomes were tentatively delineated using the criteria that homoeologous chromosomes would be deficient in different sequences (bands) hybridized by a given probe sequence (Fig. 1). Each homoeologous grouping was determined from patterns involving 3 to 5 probes. However, in each grouping, there were 1 or 2 probes which identified an alternative chromosome as a member of that set. Again, these variations were taken to reflect translocations. Translocations appear to be quite prevalent in oat based on cytological evidence[8,10,13] and early RFLP linkage map data (L. O'Donoghue and M. Sorrells, per. comm.). Homoeology for some chromosomes will probably be best determined by molecular markers close to the centromere.

Each of the three tentative complete groupings of homoeologs in Kanota (Fig. 1) contains one dark-staining chromosome, which presumably represents the C-genome homoeolog of the group since several studies[1,2,5,7] have indicated C-genome chromosomes are more heterochromatic than those of the A and D genomes. Conclusions from RFLP analysis that certain Kanota monosomics (e.g. 5, 10, 15, 20) were each deficient for the same chromosome, or at least a major portion of it, were supported by C-banding karyotype analysis of monosomics[6]. In addition to translocation differences among stocks, some of the apparent duplications of deficiencies we detected among the Kanota monosomics may have been due to monosomic shifts or seed handling errors; however, based on RFLP and C-banding analysis neither the Sun II nor the Kanota monosomic series are complete. Still, much progress has been made toward the development of an integrated physical/molecular genetic marker map in oat. Analysis of additional monosomics now being obtained from haploids recovered from oat x maize crosses[11] may enable the delineation of all seven homoeologous sets of chromosomes in hexaploid oat.

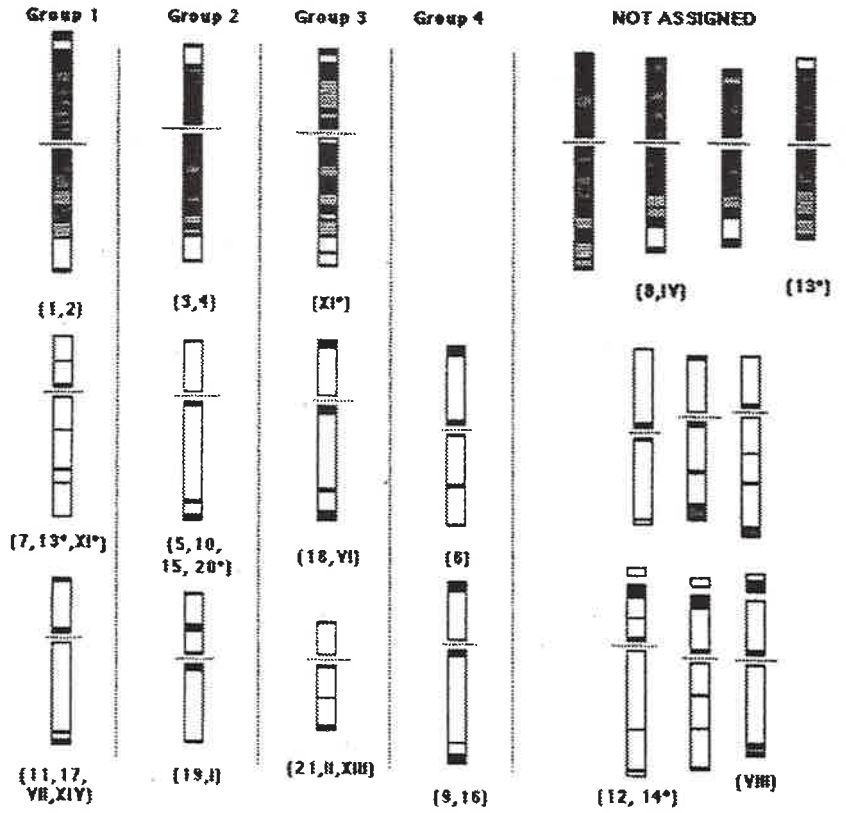

Figure 1. Idiogram of Kanota C-banded karyotype with chromosome designations and homoeologous groupings based on RFLP and C-banding analysis of monosomics. Arabic numerals designate Kanota monosomic lines that are deficient for a particular chromosome. Roman numerals designate Sun II monosomic lines that are deficient for the chromosome. Asterisks denote lines missing translocated portions of the chromosomes. Adapted from Jellen[6].

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Developments in Oat Biotechnology

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Summary

Significant progress has been made on the development of an hexaploid oat RFLP map. Diploid maps have been completed for *Avena atlantica x Avena hirtula* and *Avena strigosa x Avena wiestii* crosses. Several crown and stem rust genes have been mapped in both diploid and hexaploid oats. Studies are in progress to map a number of quantitative traits.

A transformation system has been developed for cultivated oats. Stable and reproducible gene insertion has been achieved by microprojectile bombardment of friable, embryogenic callus and suspension cultures of a GAF/Park line. Research is in progress to refine the transformation system and to evaluate transgenic disease resistance mechanisms.

Introduction

Biotechnology is expected to provide the basis for many major advances in crop improvement in the twenty-first century. Although it will not replace the traditional methods of crop improvement, many of the classical approaches will be modified in order to realize the benefits of the new knowledge and technology.

The purpose of this presentation is to provide an assessment of progress by oat researchers in RFLP and transformation technologies and a brief overview on food safety issues associated with genetically modified organisms.

Results and Discussion

RFLP Map Development

In November, 1989, a cooperative effort was initiated by researchers at Agriculture Canada (Ottawa), Cornell, Iowa State, Minnesota, USDA (Minnesota, Iowa State & Aberdeen) and The Quaker Oats Company to develop an oat RFLP map.

Cornell and Iowa State initiated their mapping programs by focusing on the development of diploid maps. The purpose of the diploid maps would be to assist in the assignment of probes to specific linkage groups for the hexaploid map and to aid in evaluating ancestral relationships. Concurrently, Cornell screened potential parents for the hexaploid mapping population. Candidates for the hexaploid mapping population were selected on the basis of their coefficient of parentage[11].

Diploid Maps

Cornell utilized 44 F_3 families from an interspecific A-genome cross *(Avena atlantica x Avena hirtula)* produced by M. Leggett to develop an RFLP map[6]. A total of 192 markers obtained primarily from oat and barley cDNA libraries were assigned to seven linkage groups. The linkage groups varied in size from 30 to 118 cM for a total map length of 614 cM.

Iowa State developed a separate diploid map utilizing 88 F_2 lines derived by crossing *Avena strigosa* with *Avena wiestii*[8]. This population has the advantage that it provides the opportunity for evaluation of resistance loci to *Puccinia coronata* (crown rust). The *strigosa* parent is resistant to infection by at least 40 races of crown rust while the *wiestii* parent is susceptible to all these races. Note, a more detailed summary of the Iowa State work is presented in the poster session of this conference[8]. One Hundred Seventy markers obtained from an oat root cDNA library were assigned to 15 linkage groups covering a distance of 2139 cM. Seven rust genes have been mapped on this population.

Interestingly, they are all located on the same linkage group within an area representing a genetic distance of about 80 cM.

In comparison, Huen, *et al* [3] obtained a map size of 1096 cM for barley and the map for *Triticum tauschii* (the D-genome of wheat) is 1554 cM[2]. It is likely that the recombination frequency for the *A. hirtula x A. Atlantica* cross was reduced due to its interspecific nature resulting in a smaller map size. Work is currently in progress to integrate the two maps.

Hexaploid Oat RFLP Mapping

The level of polymorphism in hexaploid oats appears to be more than sufficient to allow mapping in cultivated varieties. Sorrells (personal communication) surveyed the parents of several crosses which had a very low coefficient of parentage[11]. This data indicates a high level of polymorphism for low copy cDNA probes. On the basis of this data, the RFLP mapping group selected a primary (Kanota x Ogle) and a backup (Kanota x Marion) cross for developing the hexaploid oat map. Both populations have been advanced via single seed descent to the F_7 generation. Mapping is underway and currently more than 350 markers have been scored on the primary population. The results to date are very encouraging! A preliminary map will be completed in early 1993 for review by the mapping team. The next steps will be determined on the basis of the results of this evaluation.

In addition to the development of the molecular map, efforts are underway to map a number of quantitative and qualitative traits. Both mapping populations were grown in replicated yield trials in Aberdeen, Idaho and in hill plots at the other cooperating locations this summer (1992). Yield, seed morphological characteristics, disease resistance, seed composition and selected agronomic traits will be measured on each line within the two populations. The results of these analyses will be used to develop an initial evaluation of key loci within the oat genome.

Concurrent with the development of the hexaploid map numerous other related research projects are in progress. Cornell and South Dakota State Universities are conducting projects to develop RFLP fingerprints for a large number of hexaploid lines. Several locations are developing populations to map specific traits. Already several rust genes have been linked to molecular markers using backcross derived lines. Penner, *et al* [7] identified a RAPD marker which maps to within 6.0 ± 2.8 cM of a loci for the stem rust Pg3 resistance. Rooney, *et al* (personal communication) have identified markers which are closely linked to new sources of crown rust resistance derived from the genotypes Amagalon and Obee/Midsouth.

Several complementary technologies are being investigated/developed as part of the RFLP program. The University of Minnesota group is utilizing existing cytogenetic stocks to assign markers to specific chromosomes. Initial studies are being conducted with the Sun 11 (developed by H. Thomas, Welsh Plant Breeding Station) and Kanota (provided by T. Morikawa, University of Osaka). (The results of this study are presented in detail at this meeting by H. Rines, *et al* [9]). These studies show that the existing stocks do not provide a complete set of chromosome deletion stocks. The Minnesota data to date has identified nine distinct nullisomics in the Sun 11 series and 12 monosomics in the Kanota series. These have proven to be very useful in assigning molecular markers to specific chromosomes. Four tentative homologous groups have been identified using this approach. The Minnesota group has also initiated efforts to develop a more complete set of cytogenetic stocks using oat haploids developed from wide crosses[1].

The Agriculture Canada Oat Genome group is evaluating microdissection as a potential means of producing chromosome specific genomic libraries. The results to date are very encouraging. Successful development of this technique could provide assistance in producing molecular probes which map to specific chromosomal regions. Additionally, this technique should be very useful in screening libraries for markers which map to specific chromosomes.

Oat Transformation

Stable oat transformation has been reported by Somers, *et al* [10]. Friable, embryogenic oat callus and suspension cultures of GAF-30/Park were bombarded with microprojectiles

coated with DNA constructs coding for phosphinothricin (PPT) resistance and B-glucuronidase (GUS). Regenerated plants exhibited stably integrated transgene sequences which cosegregated with PPT resistance and GUS activity in progeny of these plants. Currently, transformation is limited to the GAF/Park line. This experiment has been repeated several times with different GAF/Park culture lines. Additional research is in progress to improve the efficiency of transformation and to evaluate alternative selection systems. The selection system is an issue since PPT is a herbicide and because oats are known to outcross with wild relatives at an appreciable rate. Although PPT is not currently utilized on small grains there is some interest in getting it approved for use on wheat. Thus, there will be some environmental considerations which must be addressed when seeking approval for general release of transformed oats if they contain a herbicide resistance gene.

Concurrently with the refinement of the transformation system, efforts are underway to evaluate potential viral and fungal disease resistance mechanisms. The most advanced program is a cooperative effort between Somers' group at the University of Minnesota and Lister (Purdue Univresity)/Larkins (University of Arizona), whose objective is to develop barley yellow dwarf virus (BYDV) resistant oats. The Lister and Larkins group have developed gene constructs based upon virus coat protein sequences[12,13]. This mechanism has proven to be successful in providing resistance to a number of viral diseases in other crops[4,5]. The BYDV coat protein construct has been bombarded into the GAF/Park line and is under selection and regeneration.

Regulatory/Safety Issues

Food safety/regulatory issues must be carefully considered when one contemplates gene transfer as a solution to a research problem. Regulatory policy has been slow to develop for genetically modified organisms because of sociological issues and the lack of a technology/experience base which the regulatory agencies can utilize. Due to the long term nature of this research, it is critical to consider all issues well in advance so that one can maximize success from both a research and a regulatory point of view. The following represents a brief overview of food safety issues for genetically modified organisms currently under discussion in the United States.

On May 29, 1992, the US Food and Drug Administration published a policy statement entitled "Foods Derived from New Plant Varieties" in the US Federal Register 57:22984-23005. The agency identified several key scientifically based questions which the developers of genetically modified foods should answer to assure the safety of the new products. These are:

> *Have New Substances been introduced into the Food that raise Safety Questions?* Transferred genetic material (nucleic acids) would not be expected to be the subject of regulation because they are present in all living organisms. However, the focus will be on the expression products of the transferred genes. It is anticipated that many substances being introduced into new plant varieties will not require pre-market approval by the FDA. In general, when the introduced substance is one that is already present at comparable or greater levels in currently consumed foods, there is unlikely to be a safety issue sufficient to call into question the presumed GRAS (Generally Recognized As Safe) status of such naturally occurring substance. However, substances that are added to foods as a result of genetic modification which raise safety questions (because they are not substantially similar to substances commonly found in foods such as proteins, fats and carbohydrates, or that has no history of safe usage in food) may be regulated as "food additives". For example, casein added to a food via genetic engineering would be considered to be GRAS while a novel protein sweetener would require a food additive petition.
>
> *Has an Allergen not commonly found in the Plant been introduced?* The allergenicity of a food is a major consideration for genetically modified foods and is addressed in detail by the policy statement. Examples of foods which are commonly implicated in allergies include milk, eggs, wheat, soybeans, shellfish and nuts. The sensitive population is

ordinarily able to identify and avoid the offending food. However, if the allergen were moved into a new plant variety that never before produced the allergen, the susceptible population would not know to avoid the food unless properly warned. Thus, if one were to use the previous example of adding casein to a new food you would be required to label the food as containing "milk" or some other informative descriptor unless scientific evidence is available to demonstrate that the added casein protein is not the cause of milk allergies in the susceptible population.

Have the Levels of Important Nutrients Changed? The FDA recognizes that an unintended consequence of genetic modification of the plant may be a significant alteration in the levels of important nutrients. In addition, changes in bioavailability of a nutrient or the presence of increased levels of other constituents that effect absorption or metabolism of nutrients must be considered for potential impact.

Have the Levels of Naturally Occurring Toxicants in the Plant been increased? Plants are known to produce naturally a number of toxicants and antinutritional factors, such as protease inhibitors, hemolytic agents, and neurotoxins, which serve the plant as natural defense compounds against pests or pathogens. Many of these toxicants are present in today's food at levels that do not cause acute toxicity. Others, such as cassava and some legumes have sufficient levels to cause severe illness or death if the foods are not properly prepared. The developer must demonstrate that in plants with known toxicants that the new varieties do not have significantly higher levels of these components than other edible varieties of the species.

In all cases, the developer of the recombinant plant must be able to demonstrate that *'Accepted, Established Scientific Procedures were followed in the Development of the New Plant'* and that *'the Genetic Material and its Expression Products have been well characterized'*. In this case, the source of the transferred gene is very important. For example, an oat lipase wouldn't raise any issues while a lipase from *Clostridiurn botulinurn* would, even though both have a common function.

As previously mentioned, the current oat transformation protocol utilizes a herbicide resistant gene as selectable marker which may raise a regulatory question from an environmental point of view. However, this is probably much more acceptable than an antibiotic resistance gene from a food safety point of view. These and other questions must be answered as we move toward the development of commercially viable transgenic oats. Resolution of these questions will certainly become easier as the regulatory community develops experience with the issues associated with management of genetically altered organisms.

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Characterization and Expression of Oat (1-3, 1-4)-ß-Glucanase Genes

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Summary

(1-3,1-4)-ß-glucanase activity is expressed in oat leaves, roots and developing and germinating kernels. To investigate the role of (1-3,1-4)-ß-glucanases in oat leaf and kernel development, a 1.5-kb full-length (1-3,1-4)-ß-glucanase clone was isolated from an etiolated leaf cDNA library. The polypeptide sequence encoded by the oat cDNA exhibited 90% identity to amino acid sequences of barley (1-3,1-4)-ß-glucanases. The cDNA was cloned into an *E. coli* expression vector and the purified gene product specifically hydrolysed (1-3,1-4)-ß-glucan. (1-3,1-4)-ß-glucanase mRNA was detected in oat leaves 2- to 14-d after emergence from the coleoptile and in endosperm of 10-d-old immature kernels.

Introduction

Cell wall (1-3,1-4)-ß-glucan metabolism is proposed to be important in cereal grain germination[1] and cell elongation[3,8]. Previous reports indicated that ß-glucanase activity was present in mature oat kernels[6]. In a preliminary study to investigate the potential role of (1-3,1-4)-ß-glucanases in mixed linkage ß-glucan accumulation and kernel development, expression of (1-3,1-4)-ß-glucanase activity was surveyed in various developing oat tissues. (1-3,1-4)-ß-glucanase activity was highest in 5-day-old developing kernels and decreased rapidly as the kernels matured. Most of the activity seemed to be associated with endosperm tissue[10]. High levels of activity also were detected in tissue cultures, aleurone layers of germinated kernels and in developing primary leaves[10]. Buffer-soluble endo-(1-4)-ß-glucanase activity also was determined because the substrate (Azobarleyglucan) used to assay (1-3,1-4)-ß-glucanase activity was known to be hydrolyzed by (1-4)-ß-glucanases[5]. In developing kernels and leaves, the expression pattern of endo-(1-4)-ß-glucanase activity was similar to that of (1-3,1-4)-ß-glucanase. These results indicated that glucan hydrolase activity detected in developing kernels and leaves was due to either a mixture of (1-3,1-4)- and endo-(1-4)-ß-glucanase activities or the action of endo-(1-4)-ß-glucanase alone. The presence of high levels of endoglucanase activity in rapidly developing kernels suggests that ß-glucan hydrolases are involved in ß-glucan metabolism in the cell walls of developing oat kernel tissues. The objectives of this study were to 1) isolate and characterize an oat (1-3,1-4)-ß-glucanase cDNA clone and 2) use the cDNA to further investigate expression of (1-3,1-4)-ß-glucanase activity in developing kernels.

Methods

A 1448-bp cDNA clone, pOGL1, was isolated from an oat leaf cDNA library[10]. This library was screened with a 30-mer oligonucleotide probe whose sequence was based on a highly conserved amino acid sequence present near the mature polypeptide amino-terminus of barley (1-3)- and (1-3,1-4)-ß-glucanases[2,4,7]. Glucanase assays were conducted using azobarley glucan as described by the manufacturer[5]. Thin layer chromatography was conducted to identify the major reaction products of the pOGL1-encoded gene product on various glucan substrates[9].

Results and Discussion

The pOGL1 cDNA clone had a short 5' untranslated region, an open reading frame (ORF) for 334 amino acids, and a 3' untranslated region. Sequence comparisons with barley

(1-3,1-4)-ß-glucanase (2,4,7) suggested that the ORF encoded a putative 28 amino acid signal peptide plus a 306 amino acid mature polypeptide. The pOGL1 DNA sequence encoding the mature polypeptide shared about 92% and 89% identity with barley (1-3,1-4)-ß-glucanase EI[4,7] and EII[2] coding sequences, respectively. Deduced amino acid sequence of the mature polypeptide coding region exhibited 95% and 90% identity to barley (1-3,1-4)-ß-glucanase isozyme EI and EII polypeptides, respectively. A Val-Glu-Ser sequence that precedes the signal peptide cleavage sites of barley and wheat (1-3,1-4)glucanases[7] was also found in the deduced amino acid sequence of pOGL1. However, the 3' untranslated nucleotide sequence of pOGL1 showed little homology with those of barley (1-3,1-4)-ß-glucanase genes.

To confirm that pOGL1 encoded a (1-3,1-4)-ß-glucanase, the mature polypeptide coding sequence of pOGL1 was subcloned into the pGEX-2T fusion gene expression vector (Pharmacia), and the fusion protein was purified from transformed *Escherichia coli* cultures. The purified fusion protein encoded by pOGL1 had (1-3,1-4)-ß-glucanase activity and substrate specificity to barley (1-3,1-4)-ß-glucan, but it did not hydrolyze (1-3)-ß-glucan, carboxymethylcellulose, or starch (Table 1). Major reaction products of the enzyme encoded by pOGL1 on barley ß-glucan appeared to be oligo-(tri- and tetra-) saccharides linked by (1-3)- and (1-4)-linkages (data not shown) confirming that pOGL1 encoded a (1-3,1-4)-ß-glucanase.

Table 1

Substrate	*Glucan Linkage*	*(1-3,1-4)-ß-glucanase Activity (µg of glucose equivalent/µg enzyme)*
ß-glucan	ß (1-3,1-4)	51.6
laminarin	ß (1-3)	< 0.5
CM-cellulose	ß (1-4)	< 0.5
starch	α (1-4,1-6)	< 0.5

Genomic Southern blots with copy number reconstructions probed with pOGL1 indicated that oat (1-3,1-4)-ß-glucanase genes are present at low copy numbers and are members of a small multi-gene family.

Northern analyses using pOGL1 as a probe showed that oat (1-3,1-4)-ß-glucanase mRNAs are expressed in expanding leaves and endosperms of developing kernels. High levels of (1-3,1-4)-ß-glucanase mRNA were detected in the aleurone of germinated kernels. Low levels of mRNAs hybridizing to pOGL1 were detected in shoots, roots, and young panicles. Elevated expression of (1-3,1-4)-ß-glucanase mRNAs in developing endosperms and leaves suggests that (1-3,1-4)-ß-glucanase may play a role in mixed linkage ß-glucan metabolism involved with cell expansion in rapidly growing monocot tissues.

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Characterization of Wide-Cross Derived Oat Haploids and their progeny

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Summary

Haploid plants of oat (*Avena sativa* L.) may be produced by applications of maize (*Zea maize* L.) pollen to emasculated oat florets in a process involving alien chromosome elimination and embryo rescue of developing embryos. Recovered oat plants usually have 21 chromosomes but analysis of root tips revealed retention of 1 to 4 maize chromosomes in about 20% of the plantlets. Haploid oat plants with 21 chromosomes are partially self-fertile producing both euploid and aneuploid progeny. Aneuploid progeny are being characterized as stocks for mapping RFLP genetic markers. Euploid progeny show potential as instant homozygous lines for breeding.

Introduction

The production of haploid plants of oat (*Avena sativa* L., 2n=6x=42) from oat x maize crosses was initially described by Rines and Dahleen in 1990 (7). Prior to that time, only six haploid or aneuhaploid plants had been reported in oat, five of spontaneous origin[3] and one from anther culture[6]. The process of haploid plant formation in oat appeared similar to that reported earlier in wheat (*Triticum aestivum* L.) x maize crosses[2] with rapid elimination of maize chromosomes during early cell divisions of the hybrid embryos. However, we recently discovered that about 20% of the plantlets recovered from embryo rescue following the wide-cross hybridizations retained 1 to 4 maize chromosomes in addition to the haploid oat chromosome complement. Furthermore, the haploid plants which did have only the expected 21 oat chromosomes were often self-fertile producing both euploid and aneuploid progeny. In this report, we describe characterizations of wide-cross derived oat plants and their progeny and evaluations of them for gene transfer, genetic mapping, and breeding purposes.

Materials and Methods

Haploid and progeny plant production

The scheme for production of oat haploids with and without retained maize chromosomes and of progeny from self-fertilization of 21-chromosome oat haploids is outlined in Figure 1. Oat and maize plants were grown, crosses made, and embryos rescued as described by Rines and Dahleen[7]. Root-tip chromosome counts were made on plants regenerated from embryos produced in crosses of reselections of the oat cultivars 'Starter', 'Sun II', and 'Kanota' with the maize F_1 hybrids 'Seneca 60' and 'A188 x W64A'. Only progeny from self-fertilized Starter haploids have been analyzed to date although seed has been recovered from self-fertilized Kanota and Sun II haploids as well. Haploids were designated as S_0, and their progeny derived by self-pollination were designated S_1.

Cytological analysis

Chromosome counts on root-tip cells of embryo-rescued plants from oat x maize crosses and of 2-day post-germination seedlings from seed produced on self-fertilized oat haploids were performed using a modified procedure described by Mujeeb-Kazi and Miranda[4]. Genomic *in situ* hybridization of root-tip chromosomal preparations was conducted using digoxigenin-labeled maize genomic DNA mixed with 10 x unlabeled oat genomic DNA.

The unlabeled oat DNA served to block oat-specific and in-common sequences allowing specific hybridization to maize chromatin. Procedures similar to those described by Mukai and Gill[5] were followed.

RFLP analysis

Oat DNA sequence probes, Southern blot preparation techniques, and detection of monosomic dosage effects was conducted as described by Rines *et al.* (these Proceedings).

Agronomic analysis

Oat lines derived from euploid progeny of Starter haploids were grown in hill plots sown 30 seeds per hill on 30 cm centers with 5 replications at each of two locations, St. Paul and Rosemount, Minnesota. Dunnett's test was used to compare the derived lines to the original parent line for maturity, plant height, seed weight, vegetative biomass, and grain yield.

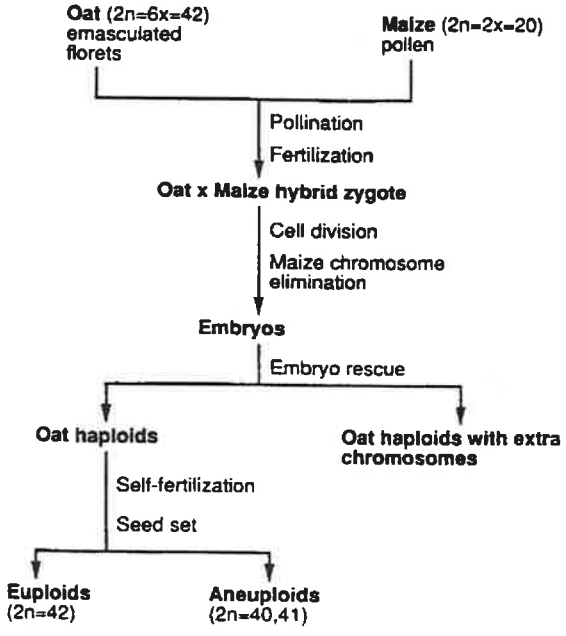

Figure 1. Oat x maize hybridization. Origin of haploid oat plants and derived progeny.

Figure 2. Oat root tip cell with expected 21 oat chromosomes plus two smaller maize chromosomes (arrows).

Results and Discussion

Plants with retained maize chromosomes

In an experiment involving 2017 maize-pollinated oat florets, 244 developing embryos were isolated onto embryo-rescue medium and 26 plantlets recovered. Chromosome counts in root-tip cells from 16 of the plants obtained revealed that three contained more than the expected 21 chromosomes. The three plants were slower growing and had thicker, darker leaves than other oat plants recovered from the same experiment. Root-tip cells of two of these plants had three extra chromosomes and root tip cells of one had one extra chromosome. The other 13 plants checked mitotically had the expected 21 chromosomes. In another experiment ten plants were recovered and two of them had extra smaller chromosomes; one had four and the other had two (Fig. 2). The size of the smaller chromosomes in all cases conformed to that expected for maize chromosomes. Chromosome *in situ* hybridizations using total genomic DNA clearly demonstrated that the smaller extra chromosomes were of maize origin. RFLP probes are being used to identify the maize chromosomes retained. Attempts will be made to exploit oat materials with retained maize chromosomes in gene transfer and in the isolation of maize chromosomes or maize chromosome-specific DNA.

Self-fertility in haploid plants

Haploid oat plants derived from oat x maize crosses are surprisingly fertile with up to 23% seed set from self-pollination[7]. Fertility can not be attributed simply to somatic doubling because numerous (about 13%) of the progeny are aneuploid with monosomics (2n = 41) being common (about 11%). Also, cytological analysis of meiotic cells from the haploid plants revealed a frequent occurrence of meiotic restitution due to failure of meiosis I, thus giving rise to microspore dyads which are presumed to be the source of functional gametes[1]. Uneven distribution of univalent chromosomes at meiosis I would account for the production of deficient gametes and hence aneuploid progeny. Mean rod bivalent formation at meiosis I ranged from 1.50 ± 0.84 to 3.14 ± 1.31 in four haploid plants analyzed with ring bivalents and multivalents each being rare (<0.1)[1]. A possible relationship between bivalent formation frequency and frequency of meiotic restitution is being examined.

Aneuploid progeny

Mitotic and meiotic screening of 344 S_1 progeny from six haploids of Starter identified 39 monosomics, 7 double monosomics, 12 interchanges, and 2 paracentric inversion heterozygotes. RFLP analysis using monosomic dosage analysis identified five putatively different monosomics among six characterized by this technique. Monosomics recovered as progeny from self-fertilized progeny may enable the identification of a complete monosomic series in oat.

Euploid progeny

Twenty-two lines representing either three or four euploid (2n=42) progeny from each of six Starter haploids were studied[1]. Each line was derived by two generations of seed increase from an individual S_1 plant and should correspond to a "doubled haploid" line in being fully homozygous. These six sets of haploid derived lines were then compared to the Starter parent line in agronomic evaluations based on small-plot field tests. From one haploid, all four derived lines were inferior to the Starter parent line, indicating that the haploid may have contained some detrimental gametoclonal variation. Sets of derived lines from two other haploids contained two types of individual lines, ones that were inferior and ones not significantly different from the control parent line. The presence of two types of derived lines in each set indicated that the variation may have been produced during gamete formation in the haploid parent plants since only a portion of the progeny lines appeared to be affected. The ten members of the remaining three sets of haploid progeny derived lines performed not significantly different from the control parent line. Thus, lines comparable to the starting parent line could be recovered by this technique. These results indicate that oat x maize crosses may have value for producing instant pure-breeding lines for genetics or breeding purposes if the frequency of haploid oat plant recovery could be markedly increased above the 1% of oat florets pollinated, as is now commonly obtained.

Acknowledgements

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Pedigree Assessment in Cereal Crops using RAPD-DGGE

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Summary

We have optimized a denaturing gradient gel electrophoresis (DGGE) system that, when used in combination with random amplified polymorphic DNA (RAPD) analysis, greatly facilitates the detection of reproducible DNA polymorphism among closely related plant lines. We have successfully used this approach to estimate pedigree relationships among a spectrum of plant lines in wheat *(Triticum aestivum)*, barley *(Hordeum vulgare)* and oat *(Avena sativa)*. Based on analysis with 1 or 2 primers, we were able to distinguish soft from hard winter wheats and 2-rowed from 6-rowed barley lines. Further analysis using additional primers allowed resolution of polymorphisms among very closely related lines in highly selected populations. We placed 17 cultivars of oat into two distinct clusters that differed significantly from previous oat pedigrees.

Introduction

Assessment of the degree of relatedness among lines or populations is useful for the selection of parents in crosses for hybrid or cultivar development. Methods for estimating relatedness are generally based on plant breeding records and plant phenotype[4,5,7] or biochemical markers[1,8]. However, DNA fingerprinting strategies are limited by the amount of DNA fragment polymorphism detectable across related lines. Lack of DNA polymorphism is the greatest hindrance to DNA-based pedigree assessment in many self-pollinating crops. Here we present a DNA fingerprinting method based on the combination of random amplified polymorphic DNA (RAPD)[9] analysis and a denaturing gradient gel electrophoresis (DGGE) system[6].

Methods

The spring oat, spring barley, and red winter wheat lines used in this study were selected from previous pedigree assessment studies[4,5,6]. Spring barley lines were kindly provided by Dr. Tom Blake (Montana State University) and Dr. J.F ranckowiak (North Dakota State University). Genomic DNA isolation was performed on 2-week old seedling tissues using a modified procedure of Gawel and Jarret[2].

Oligonucleotide primers (10-mers) were purchased from Operon Technologies (Alameda, CA). The polymerase chain reactions (PCR) were performed according to He *et al.*[3]. The PCR products were run on 1.2% agarose in 0.5X TBE, 12% acrylamide in 1X TAE or 12% acrylamide with a gradient of denaturant[3]. RAPD profiles were scored from DGGE visually. Relationships among samples were evaluated with a phenetic cluster analysis, using the unweighted pair group method for arithmetic average (UPGMA), and plotted as a phenogram. All computations and statistical analyses were performed using SAS (version 6.0) programs.

Results and Discussion

Comparisons of agarose (1.2%), polyacrylamide (12%) and DGGE of identical RAPD products revealed little or no visible polymorphism among wheat and barley lines in agarose. Polyacrylamide improved resolution, but both gel systems were inferior to DGGE for the enhanced detection of DNA polymorphism. DGGE is designed to allow the resolution of sequence differences among fragments of similar or identical size[6].

The procedure takes advantage of the fact that even single base pair differences will alter fragment melting properties (Tm), resulting in altered gel migration rate.

Analysis of 1056 reproducible amplified DNA sequences was possible from a total of 8 gels and 8 primers (Table 1) applied to 14 cultivars of soft red winter wheat (SRWW) and 2 cultivars of hard red winter wheat (HRWW). Our study indicated that SRWW lines comprise a heterogenous group with an average similarity of 85%, differing ($P < 0.08$) from the HRWW cultivars. Among the SRWW, two significantly different subgroups were observed. Cultivars Oasis, Abe, Beau, Arthur and Monon form one cohesive subgroup and cultivars Fillmore, Benhur and Caldwell form the other. This classification indicated good agreement with that of Murphy *et al.*[5].

Of the 16 lines of spring barley used in this study, 6 are 6-rowed and 10 are 2-rowed per spike cultivars. Cluster analysis of 986 DNA amplified sequences obtained from 5 gels and 5 primers (Table 1) indicated that all the barley cultivars tested comprise a single heterogenous group with substantial subgrouping. Most of the 2-rowed cultivars differed from the 6-rowed. Among the 6-rowed cultivars, Larker, Morex and Bonanza form a cohesive subgroup. Among the 2-rowed cultivars, Lewis, Clark, Hector, Bearpaw and Bonus form a cohesive subgroup that differs from cultivar Gallatin. The moderate variability among barley cultivars selected for this study may be the consequence of intensive selection focused on malting quality, resulting in a significant reduction in germplasm diversity[4].

Analysis of 1170 reproducible amplified DNA sequences obtained from 17 cultivars of hexaploid oat *(Avena sativa)* and one line of diploid oat *(Aveva strigosa)* using 6 gels and 8 primers showed that *A. sativa* cultivars cluster to two significantly different ($P < 0.05$) groups A and B with one subcluster within group B. Both *A. sativa* groups were more similar to each other than either to the accession of *A. strigosa*. The 17 cultivars used in this study belong to 5 different clusters in a previous pedigree assessment study[7]. The differences in classification between our study and that of Souza and Sorrells[7] may reflect differences in resolution of methods used for determining relationships among the oat lines. The previous studies of oat[7] relied primarily on estimates of coefficient of parentage, dependent on the accuracy of plant breeding records and on the estimation of relative genetic contributions from the various ancestors to a cultivar. The RAPD-DGGE method provides a means for verification of genetic relationships without the dependence on additional sources of information that may be subject to human error or aberrant genetic segregation. The observation of adequate polymorphism to allow the distinction of even the most closely related materials used in this study will be significant for future studies of this type and promises to be of great value in gene mapping and marker-assisted selection programs.

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Table 1. Oligonucleotide (10-mer) primers used in the study and the fragment polymorphism resolution achieved using RAPD-DGGE.

	Primer	*sequence*	*resolution**
Wheat	A05	AGGGGTCTTG	3
	A09	GGGTAACGCC	3
	A11	CAATCGCCGT	3
	A15	TTCCGAACCC	3
	A17	GACCGCTTGT	2
	A07/A16	GAAACGGGTG/AGCCAGCGAA	1
	A16/A17		1,3
	A07/A18	/AGGTGACCGT	3
Barley	A05		3
	A11		1,3
	A15		1
	A17		1,2
	A16/A17		1
Oat	A05**		3
	A09		3
	A11		2,3
	A05/A18		1,3
	A12/A18	TCGGCGATAG/	3
	A16/A17		3

* 1: distinguishes primary clusters

2: distinguishes subclusters within primary groupings.

3: distinguishes between individual lines within a cluster.

** All primers tested with oats distinguish *A. sativa* from *A. strigosa*.

Initial Genetic Studies of Putative Isozyme Loci in Cultivated Hexaploid Oat

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Summary

Oat is a major crop with limited mapping information. Isozyme genes have helped to build maps in other crops and thus a project was initiated to examine the potential of isozyme genes to supplement gene mapping efforts in oat. Initial findings are reported for phosphoglucomutase and isocitrate dehydrogenase. These findings indicate that previously uncharacterized isozyme genes will also be useful in chromosome mapping and gene tagging in oat. Additional isozyme systems will be investigated.

Introduction

Although oat, *Avena sativa* L., has international importance as a food and feed crop, little has been reported about the genome organization of this crop species. Maps for several crops were initially based on morphological and physiological traits and were later supplemented with isozyme and other protein loci. More recently, DNA markers have allowed a high degree of map saturation in several crop species such as maize, *Zea mays* L.[4], barley, *Hordeum vulgare* L.[3,5], and soybean, *Glycine max* L. Merr.[7]. The hexaploid nature of the common cultivated oat has likely contributed to a lack of simple markers as triplicate forms of genes might often be active, one per genome. However, a few isozyme bands in polyploid *Avena* species have been demonstrated to be under monogenic control and therefore may be useful for chromosome mapping and gene tagging[2,8,9,12,14]. The objective of this research was to observe the inheritance patterns of additional isozyme loci in cultivated oat and to use the information to supplement mapping efforts currently in progress.

Methods

Extracts of leaves of greenhouse-grown plants were used for electrophoresis and were prepared in the same manner as described previously[6] except that wicks were flash frozen in liquid nitrogen and stored at -70°C for subsequent gel runs. A TRIS-citrate/lithium borate pH 8.3 starch gel system[10] was used to resolve phosphoglucomutase, and a histidine pH 6.5[1] gel system was used to resolve isocitrate dehydrogenase. The TRIS-citrate gel was run at 220 constant volts while the histidine gel was run at 6 watts constant power. After four or five hours of electrophoresis, the fronts had migrated eight to ten centimeters as indicated by a red food color dye. The gels were sliced and then stained for the above enzymes following the protocols of Soltis *et al.* [11]. Gels were scored and data generated from segregating populations were analyzed by the Linkage-1 program[13].

Results and Discussion

Phosphoglucomutase (PGM, EC 2.7.5.1) is a glycolytic enzyme commonly examined in plant isozyme surveys. Studies have shown that PGM isozymes are monomers and are encoded by two nuclear genes in most diploids. The product of one locus is usually active in the plastids and the product of the other in the cytosol. However, in maize, no PGM activity has been detected in organelles, suggesting that two PGM isozymes are active in the cytosol. In observing the PGM zymogram for 'Ogle', 'Kanota' and resulting progeny (Fig. 1), the more anodal bands appear to be segregating forms, and the lower band could be the product of one or more non-segregating loci.

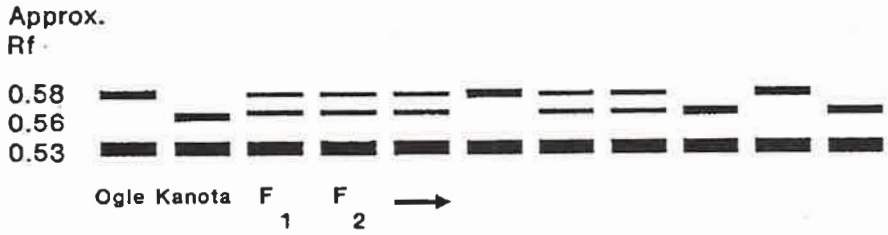

Figure 1. Zymogram of parential, F_1, and F_2 arrays observed phenotypes of PGM.

The intracellular location of PGM products has not been determined in oat. In testing the hypothesis that the upper bands were controlled by codominant alleles of a single locus, a close fit to a 1:2:1 ratio was observed (Table 1). An alternative hypothesis would be that each of the more anodal bands represents a distinct locus segregating for presence of detectable active product, and each would also likely fit a monosomic 3:1 ratio. However, a double "null" condition was not observed in this population. Additional genetic tests need to be conducted to further verify the genetic basis of PGM bands in oat.

Table 1. Single-locus goodness of fit to either a 1:2:1 of 3:1 ratio for putative isozyme loci scored for segregation among 88 Ogle/Kanota F_2 individuals.

Proposed locus	*Ogle Type*	*Hetero zygous*	*Kanota Type*	χ^2	*P*
Pgm-1	22	42	24	0.273	0.80 - 0.95
(expected)	(22)	(44)	(22)		
Idh-1	61	–	27		
(expected)	(66)	–	(22)	1.515	0.20 - 0.50

Isocitrate dehydrogenase (IDH, EC 1.1.1.42) is one of the enzymes involved in the oxidation of citric acid in the tricarboxylic acid cycle. In most plant species studied, it is controlled by one locus. Exceptions include maize, barley, and soybean where two loci have been reported to code for IDH. The variation observed between Ogle and Kanota appears to be in the number of loci expressing (Fig. 2). The three-banded pattern of Kanota can be explained by two functional gene products forming an interlocus heterodimer if the enzyme is dimeric as commonly reported. The five-banded pattern observed for Ogle could result from the expression of a third locus that is apparently "null" in Kanota. In the F_1 and F_2 arrays, only the parental bands were observed and the scores fit a 3:1 expected for dominant monogenic inheritance (Table 1). No significant deviation from independent assortment was detected between the segregating PGM and IDH isozymes indicating that the loci controlling these proteins are not linked.

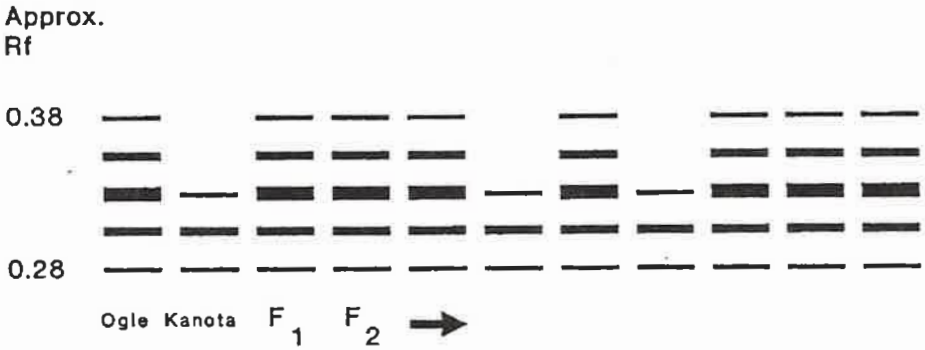

Figure 2. Zymogram of parential, F_1, and F_2 arrays observed phenotypes of IDH.

These results indicate that some isozyme markers may be a useful supplement for the genome map of oat, but one must be cautious in interpreting the isozyme phenotypes. Genetic tests involving crosses among several phenotypes are recommended. Other enzyme systems that may have useful polymorphism between Ogle and Kanota, but not presented here, include peroxidase, diaphorase, esterase, 6-phoshogluconate dehydrogenase, malate dehydrogenase, and shikimate dehydrogenase.

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Development and Application of an RFLP Linkage Map in Diploid Oat

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Abstract

Two diploid oat populations have been produced by crossing *Avena strigosa* with *A. wiestii* and *A. nudibrevis*. These materials are being used to pursue several objectives: 1) to construct an RFLP linkage map for diploid oat species representing the *A.* genome; 2) to identify genetic linkage between RFLP loci and genes for resistance to *Puccinia coronata* (crown rust); and 3) to investigate the genetic basis of morphological and physiological traits important to oat improvement programs. The *strigosa* parents are immune to infection by at least 40 races of crown rust while the other parents are extremely susceptible to the same races. An oat root cDNA library is being screened to identify RFLPs for each population. Six hundred cDNA clones have been screened against the parents. One hundred and forty clones detect RFLPs in the *strigosa/wiestii* population. One hundred clones detect RFLPs in the *strigosa/nudibrevis* population. Linkage analysis of the RFLPs and rust reaction will be conducted in the F_3 and F_7 generations consisting of 130 families in each population. The populations will also be useful for studying the genetics of resistance to stem rust, BYDV, test weight, hull percentage and several other morphological traits.

Transgenic Oat Tissue Cultures and Regenerated Plants

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Summary

Transgenic friable, embryogenic oat tissue cultures were selected for phosphinothricin (PPT) resistance following microprojectile bombardment with a plasmid containing the *bar* gene and the gene encoding ß-glucuronidase (GUS). To date 111 PPT-resistant tissue cultures have been shown to be transgenic based on Southern blot analysis. Plants were regenerated from 38 of the 111 transgenic tissue cultures. Regenerated plants generally exhibited male sterility. However, more than 30 plants regenerated from a transgenic tissue culture were fully fertile. GUS activity in seed on fertile regenerated plants and PPT resistance in progeny of these plants cosegregated with *bar* and GUS transgene sequences demonstrating stable inheritance of the transgenes.

Introduction

Allohexaploid cultivated oat (*Avena sativa* L.) has been recalcitrant to transformation, as have many other gramineous monocotyledonous (cereals) crops, primarily because of problems encountered in DNA delivery into totipotent cells and the availability of marker genes useful for selection of transformed tissue cultures. Microprojectile bombardment[7] currently exhibits the greatest potential for cereal transformation. DNA delivery by microprojectile bombardment into cells in tissue cultures[3,4,6,13,15,16], or into the scutellum of immature embryos of some cereals such as rice[for review see 2] is followed by selection for transformed tissue cultures. Regenerated transgenic plants have been isolated from maize[3,4,16], rice[2], wheat[15] and many other crops[2] demonstrating the broad applicability of the microprojectile bombardment procedure. The objective of this study was to develop a microprojectile bombardment DNA delivery procedure and a tissue culture selection system for isolation of transgenic oat tissue cultures.

Methods

Friable, embryogenic oat callus and suspension cultures of the highly culturable genotype GAF-30/Park[1,10] were bombarded with DNA-encoated tungsten microprojectiles using the Biolistic PDS-1000 particle acceleration device. The pBARGUS plasmid[3] contains the *E. coli uid A* gene, which encodes ß-glucuronidase (GUS)[5], under control of the maize alcohol dehydrogenase I (Adh1) promoter/intron 1 enhancer[3,9]. The plasmid also contains the *Streptomyces hygroscopicus bar* gene[14], which confers plant cell resistance to phosphinothricin (PPT), under the control of the cauliflower mosaic virus (CaMV) 35S promoter and Adh1 enhancer. Following microprojectile bombardment, tissue cultures were plated on filter paper disks overlying PPT-selection medium callus maintenance medium[1] lacking L-asparagine and containing 3 mg/l PPT. After 8 to 16 weeks on PPT selection medium, surviving sectors of the tissue cultures were isolated from the filter papers and plated directly onto selection medium to further select and increase the PPT-resistant tissue cultures. Uniformly PPT-resistant tissue cultures (16 to 20 weeks on selection medium) were stained for GUS activity[5,8] to determine coexpression frequency and sampled for Southern blot analysis[11,12].

Results and Discussion

Transgenic tissue cultures

Three microprojectile bombardment experiments were conducted in which all PPT-resistant tissue cultures were stained for GUS activity and were analyzed for the presence of *bar* gene sequences using Southern blot analysis. These experiments were conducted over a period of about 1 year on 21 different oat tissue culture lines initiated from 16 immature oat embryos isolated from the GAF-30/Park genotype. The objective of conducting these experiments was to determine the reproducibility of the transformation system. Tissue cultures resistant to PPT were recovered in all three experiments from 10 of 21 bombarded tissue culture lines. A total of 331 PPT-resistant tissue cultures were recovered after approximately 20 weeks selection on PPT-containing medium.

Southern blot analyses using the *bar* gene as a probe were performed on DNA extracted from the 331 PPT-resistant tissue cultures isolated in the three experiments to determine the number of transgenic tissue cultures. The *bar* gene sequence was detected in 111 of the 331 PPT-resistant tissue cultures (Table 1). Furthermore, the *bar* probe hybridized only to the high molecular weight fraction of undigested DNA isolated from the PPT-resistant tissue cultures indicating integration into genomic DNA (data not shown). Substantial variation in copy number and fragment sizes of the *bar* transgene was observed among the transgenic tissue cultures. Copy number reconstructions indicated that the copy number of the *bar* gene ranged from one to more than twenty copies per genome equivalent among the various transgenic tissue cultures.

Significant variability in the yield of transgenic tissue cultures per bombardment was observed among tissue cultures. Over all three experiments, a range of 27 to 37% of the PPT-resistant tissue cultures were determined to be transgenic. These frequencies convert to an overall recovery of 1.9 transgenic tissue cultures per microprojectile bombardment treatment (Table 1). Coexpression of GUS activity was observed in about 75% of the transgenic tissue cultures (Table 1).

Table 1. Relative efficiency of three oat transformation experiments.

Experiment number	*Number of transgenic tissue cultures per plate bombarded*	*Frequency of transgenic tissue cultures with GUS coexpression*	*Frequency of transgenic tissue cultures with plant regeneration*
1	45/24 = 1.9	33/45 = 73%	16/45 = 36%
2	57/17 = 3.4	41/57 = 72%	17/57 = 30%
3	9/17 = 0.5	9/9 = 100%	5/9 = 56%
Overall	111/58 = 1.9	83/111 = 75%	38/111 = 34%

Transgenic Plants

Plants were regenerated from 38 of the 111 transgenic tissue cultures (Table 1). Each of ten plants regenerated from one transgenic tissue culture selected in Experiment #1 exhibited PPT resistance confirming *bar* gene expression in regenerated plants. Furthermore, regenerated plants exhibited the presence of the *bar* transgene sequences and integration of the transgene into high molecular weight oat DNA. In the first two experiments (Table 1), plants regenerated from transgenic tissue cultures were either fully sterile or male sterile. Male sterile plants were regenerated from about 50% of the transgenic tissue cultures. A portion of the male sterile plants were crossed with pollen from the cultivar Starter. Four testcrossed seed were produced from crosses with male sterile transgenic plants regenerated from one cell line. One of the outcrossed progeny was transgenic based on Southern blot analysis using the *bar* probe and expression of GUS activity in the seed (data not shown).

The tissue cultures that were bombarded in Experiment #3 had been initiated approximately 26 weeks prior to microprojectile bombardment treatment. Of the 9 transgenic tissue cultures isolated in this experiment, 5 maintained plant regeneration capacity. Plants regenerated from 4 transgenic tissue cultures selected in this experiment appeared to be male sterile. However, one of the transgenic tissue cultures produced completely fertile plants. More than 30 plants were regenerated from the fertile transgenic tissue culture and all were fully fertile and produced normal appearing seed upon self-pollination. Seed produced on these plants segregated for GUS activity demonstrating expression of the transgene in the progeny of transgenic oat plants. Furthermore the progeny plants exhibited segregation of PPT resistance. Southern blot analysis conducted on the progeny plants indicated cosegregation of *bar* and GUS genes. Of 15 plants tested, 11 plants exhibited both the *bar* and GUS gene sequences indicating a close fit to a 3:1 segregation ratio expected for disomic inheritance of dominant genes and thus indicated stable transmission of the transgenes to the progeny of the transgenic plants. Of the plants tested for GUS activity and herbicide tolerance, there was strict cosegregation of the phenotype and the presence of the transgene sequences.

Our evidence for stable transformation of hexaploid oat tissue cultures and regenerated plants includes 1) detection of transgene (pBARGUS) sequences integrated into high molecular weight oat DNA, 2) expression of PPT-resistance and, in some cases, GUS activity in tissue cultures and regenerated plants, and 3) inheritance of transgene sequences and phenotypes in progeny of regenerated plants. Transgene integration patterns, variation in copy number, and coexpression frequencies were similar to those reported in maize transformed via microprojectile bombardment[3,4,16]. Detailed characterization of the inheritance of the transgene sequences and phenotypes is underway. This oat transformation system is being used to investigate resistance mechanisms to barley yellow dwarf virus conferred by coat protein constructs in collaboration with J. Vincent and R. Lister, Department of Botany and Plant Pathology, Purdue University.

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Cytogenetic Studies in *Avena*

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Summary

Cytogenetic techniques utilizing aneuploid stocks of the cultivated oat *A. sativa* have been employed in attempts to identify chromosomes carrying specific genes and to map the position of these genes on the relevant chromosome.

Introduction

Cytogenetic techniques involving the use of conventional light microscopy for the identification of whole chromosomes and chromosome segments and the study of mitotic and meiotic divisions in relation to chromosome homology between and within species, has remained basically unaltered for many years. With the advent of aneuploid series in some of our crop species, much has been learnt about the structure and function of individual chromosomes. More recently, the application of numerous and varied techniques has meant that such conventional microscopy, in conjunction with these techniques, has dramatically increased our knowledge of chromosomes in terms of their macro- and micro-structure, and their function. For example, chromosome banding (C-banding) and silver staining techniques have greatly enhanced our knowledge of the structure and function of chromosomes and their respective genomes[4,5,16,17].

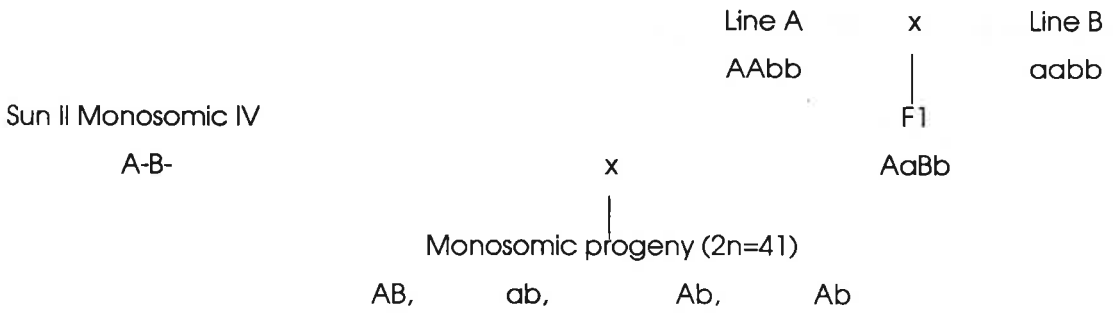
Similarly, the visualization of particular DNA sequences using specific DNA probes[1,3], and latterly the use of total genomic DNA probes for in-situ hybridization[2,8] has provided a great deal of information with regard to the identity of particular chromosomes or chromosome segments. Whilst such technologies are routinely used in other crop species, they are only now emerging in the oat crop.

At present, the only full sets of monosomics in *Avena* isolated in a Japanese variety by Morikawa[10] is not compatible with European germplasm. However, the monosomics which are available in the cultivar SunII, have been put to good use in assigning and mapping genes to a particular chromosome(s), and demonstrating conclusively that the cytogenetic architecture of the genus is based on polyploidy with its inherent genetic duplication[13]. This paper describes some recent research at IGER utilizing monosomic analyses.

Mapping Chromosome IV

Chromosome IV of *A. sativa* is known to carry at least five major genes[11]. One of these genes inhibits the expression of the fatuoid phenotype in the cultivated oat, such that none of the florets are awned or shed their seed. Thus, deletion of this pair of chromosomes (i.e. the nullisomic) produces the fatuoid phenotype, whilst in the monosomic condition, there is a distinct single awn on the primary floret only, and the seed does not shed.

The ability to identify monosomic IV lines by phenotype alone, has been used to advantage in a modified scheme of monosomic analysis to map these five genes. The scheme involves crossing appropriate lines of the cultivated oat and using the F1 hybrid as the male parent in crosses onto the standard monosomic IV of Sun II. The crossing scheme used was as follows:



Since over 80% of the female gametes formed by the monosomic will have 20 chromosomes, the proportion of monosomic progeny from the cross monosomic IV x F1 hybrid will be high and can be readily recognized by their phenotype. Because the monosome must derive from the F1 hybrid, the segregation of the alleles at the two loci can be scored, providing they are expressed in the hemizygous state. Using this modified scheme of monosomic analyses, the linkage between the loci controlling chromosome synapsis (Syn), inhibition of the fatuoid character (Fi), the dwarfing gene (DW), large grain size (Lg) and fluorescence of the glumes (Fl) has been determined. The tentative genetic map incorporating the information derived from this analyses is shown diagrammatically in Fig 1.

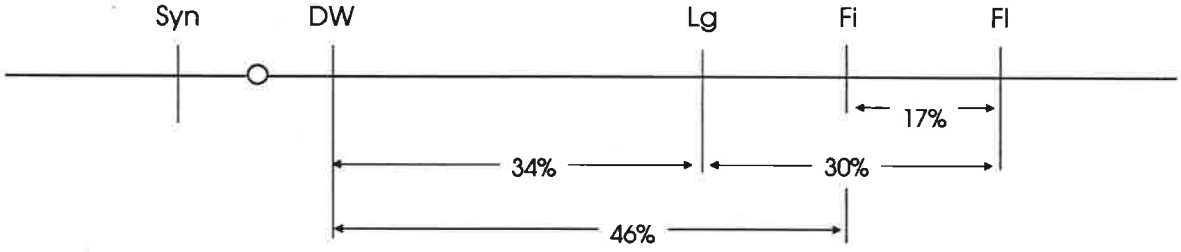


Figure 1. Diagrammatic map of five major genes on chromosome IV of the cultivated oat *A. sativa.*

No linkage was detected between the locus for chromosome synapsis and any of the other loci, and it is known from a previous report[15] that Syn and Fl are located on different chromosome arms.

Distribution of Quantitative Trait Loci

The distribution of some loci with quantitative effects on certain morphological characters was determined by a study of intervarietal chromosome substitution lines. In this study, individual chromosomes of the cultivar SunII were substituted by the corresponding chromosome of a high protein line (Cc6501) derived from *A. sterilis* crosses. The intervarietal substitution lines were established by standard backcrossing procedures using monosomic lines. The substitution lines were compared to the recipient and donor lines in a completely randomized block design. The effect of the substituted chromosome on a number of agronomic characters was assayed by comparing the substitution lines with the recipient line. The results are summarised in Table 1.

Table 1. Summary of the effect of specific chromosomes on the expression of different phenotypic characters.

Character	*Chromosome having an effect.*
Heading date	IV VIII IX XV
Culm length	IX XIII
Panicle length	III XIII
Total height	IX XIII
Panicle number	V XI
Total weight	II III IX XI XII XIII
Grain yield	XI XII XIII
100 Grain weight	IV V VIII IX XV
% Nitrogen in grain	IV V VIII XIV XV

It is of interest to look at the relationship between total height and the two components of height, culm and panicle length. Chromosome III had an effect only on panicle length, and chromosome IX on culm length, but only chromosome IX had an effect on total height, while chromosome XIII had an effect on all three characters. Chromosome XI had a significant effect on total weight and grain weight, whilst the effect of chromosomes IX, XII and XIII on total growth were mainly due to vegetative growth. These results give some indication of the distribution of quantitative trait loci on specific chromosomes.

Control of Chromosome Pairing

One of the biggest problems in assessing the relationship between oat species, or the transfer of useful genes from the wild to the cultivated oat, is the restriction of pairing to homologous chromosome pairs. Such a restriction not only prevents recombination between homoeologous chromosomes, but might also mask the actual relationship between species.

Evidence for such a mechanism has been described by a number of oat workers[7,12,14] and is evident from the lack of chromosome pairing in haploid plants derived from hexaploid oats, where there is very limited inter-genomic pairing[6,9].

In an attempt to identify the chromosome(s) carrying the gene(s) responsible for suppressing the pairing of homoeologues, the wild tetraploid *A. agadiriana* which has very limited (less than 12 %) chromosome pairing in hybrid combination with the hexaploid cultivated oat, was crossed to the eighteen available monosomics in Sun II background. The results are presented in Table 2.

Table 2. Mean chromosome pairing in hybrids between *A.agadiriana* and the monosomic series of Sun II.

Monosomic	*IV*	*III*	*II (ring)*	*II (rod)*	*I*	*xta*	*% chromosomes paired*
I	-	0.06	-	2.44	28.94	2.56	17.31
II	-	0.02	-	1.92	30.10	1.96	14.00
III	-	0.04	-	1.78	30.32	1.86	13.37
IV	-	-	-	1.48	31.04	1.48	11.31
V	-	0.17	-	2.82	27.86	3.16	20.40
VI	-	0.02	-	1.82	30.30	1.82	13.43
VII	-	-	-	2.10	29.80	2.10	14.86
VIII	-	0.06	-	2.88	28.06	3.00	19.83
IX	-	0.07	0.01	2.30	29.17	2.46	16.66
X	0.01	0.10	-	2.37	28.92	2.59	17.37
XI	-	0.06	-	2.65	28.52	2.77	18.51
XII	-	-	-	1.68	30.64	1.68	12.46
XIII	-	0.06	-	1.52	30.78	1.64	12.06
XIV	-	0.02	-	2.32	29.30	2.36	16.29
XV	0.01	0.18	-	2.46	28.50	2.88	18.57
XVI	-	-	0.04	2.72	28.48	2.80	18.63
XVII	-	0.04	-	2.54	28.80	2.60	17.71
XVIII	-	0.05	-	2.08	29.68	2.16	15.20
Euploid 1	-	0.06	-	1.92	30.98	2.04	11.49
Euploid 2	-	0.08	-	1.96	30.98	2.12	11.89

If the chromosome carrying the pairing control gene were absent, then it would be expected that the chromosome pairing in that particular monosomic hybrid line, would be greater than that of the euploid hybrid, in which the pairing control mechanism would be operative. Bearing in mind the percentage of chromosome pairing (11.32 – 21.95%) observed in haploids and aneupolyhaploids of the hexaploid cultivated oat[6,9], it is evident from the data presented in Table 2 that none of the monosomic lines has a level of chromosome pairing that might be expected if the pairing control genes had been eliminated.

Two deductions can be made from the results obtained: 1) the critical chromosome is one of the three monosomics not yet available; 2) the pairing control mechanism is spread throughout the three genomes. If the latter is the case, then it is improbable that the pairing control mechanism can be knocked out by deleting whole chromosomes, as this would almost certainly result in inviable plants.

Conclusion

Emerging molecular technologies will undoubtedly furnish oat workers with much needed tools to identify and mark chromosomes and genes, thus providing vital information with regard to the structure and function of individual genes, chromosomes and genomes.

The construction of genetic maps in *Avena*, would be greatly accelerated by the availability of complete aneuploid stocks, and a better understanding of homologous/homoeologous relationships within the genus. However, the present interest in molecular approaches for the construction of genetic maps and accelerated genetic selection, is imposing pressure on the allocation of funds for conventional cytogenetic studies.

Since some genes are pleiotropic, the introduction of a single alien gene to the cultivated oat is likely to influence the expression of other genes not associated directly with the character transferred, hence altering the phenotype. Thus, when molecular technology can be used routinely in oat breeding programmes to transfer specific genes, cytogenetic studies will still be an essential supplement to the breeding effort.

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Pollen Size in *Avena*, and Cytogenetics of Octoploid-Tetraploid Crosses

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Summary

Pollen grain size among species of different ploidy levels of the genus *Avena* was examined. Results indicate that pollen size in oats increases in proportion to chromosome number. The average size of oat pollen grains was 39.3 µm for the diploid, 41.7 µm for the tetraploid, 46.9 µm for the hexaploid, and 47.8 µm for the octoploid accessions tested. The same octoploid and tetraploid accessions were crossed, and F_1 hybrid plants contained 40 or 41 chromosomes. Depending on the accessions used in crosses, averages of 5.4 to 10.0 bivalents were observed during metaphase I. Higher chromosome associations were also observed. F_1 plants were highly sterile.

Introduction

Pollen size in many genera has been positively correlated with chromosome number[1]. Furthermore, differences in pollen size within the same anther in *Solanum* and *Medicago*, and pollen shape of *Trifolium pratense* have been indicators of pollen grains bearing unreduced gametes[5]. Gornall[2] used size and exine ornamentation of *Avena* pollen grains as a taxonomic factor to study the evolution of oats. This study was initiated to determine pollen grain size in relation to ploidy level of *Avena* species, and to observe any differences for pollen grain size within the same anther as an indicator of unreduced gametes.

The tetraploid oat accessions used for the pollen study were also crossed with octoploid lines to determine the cytogenetic behavior of chromosomes in the obtained hybrids. The octoploid lines used were artificially synthesized by doubling the chromosome number of sterile hybrids between hexaploids and either tetraploid[3] or diploid lines[4].

Methods

Pollen size of six *Avena* species of different ploidy levels and 10 oat octoploids was determined. The group of diploid oat species was represented by *A. strigosa* (four accessions); the tetraploid group by *A. abyssinica* (three accessions), *A. barbata* (eight accessions), *A. maroccana* (two accessions), and *A. vaviloviana* (seven accessions); the hexaploid group by *A. sativa* (eight cultivars); and the octoploid group by 10 lines. The plants were grown at the University of Wisconsin West Madison Farm in the summer of 1991. Pollen grains were sampled from one to six plants per line. One to two ripe but unopened anthers, obtained from the basal floret of each sampled spikelet, were placed on a slide and pollen grains were squeezed out of the anther with tweezers. A 1% acetocarmine solution was used as staining agent. Photographs were taken at a 125-fold magnification. The largest and smallest diameters were measured, and the flat-field area was calculated. The accessions used in the pollen study were also used to obtain hybrids between octoploid and tetraploid lines. Crosses were performed during winter in the greenhouse in a 3-year period (1990-1992), and hybrid seeds were planted in field nurseries. Panicles were collected on sunny mornings between 9-10 a.m., when the base of the flag leaf was 3-7 cm above the second leaf, and were fixed in carnoy fixative. After 24-48 hrs in fixative, the panicles were stored in 70% alcohol until their evaluation.

Results and Discussion

The mean size and the range of the largest diameter of pollen grains for each species are given in Table 1. For the accessions studied, pollen grain size increased with ploidy level. While the average size of diploid oat pollen grains was 39.3 µm with a range of 37.9 to 41.4 µm, it increased to a mean diameter of 41.7 µm for the tetraploid group with a range of 39.0 to 43.9 µm, and to 46.9 µm for the hexaploid oat group with a range of 43.8 to 49.1 µm. Finally, the octoploid pollen grain had an average diameter of 47.8 µm with a range of 44.8 to 50.8 µm. Calculation of pollen grain flat-field area gave a mean of 1014.9 μm^2 for the diploid, 1166.5 μm^2 for the tetraploid, 1484.2 μm^2 for the hexaploid, and 1627.5 μm^2 for the octoploid groups. The correlation between length and width was positive and high (r=0.94), thus pollen grain length, width, or area can be used for statistical differentiation.

Table 1. Pollen grain size of different species of the genus *Avena*.

Ploidy	*Species*	*No. of pollen grains*	*Pollen diameter*	
			Mean (µm)	*Range (µm)*
2n=2x=14	*strigosa*	300	39.3	37.9 - 41.4
2n=4x=28	*abyssinica*	150	42.0	40.2 - 43.8
	barbata	330	41.8	40.1 - 43.9
	vaviloviana	480	42.3	40.5 - 43.9
	maroccana	45	39.5	39.0 - 40.0
	abyssinica x *strigosa*	90	40.8	40.8
2n=6x=42	*sativa*	551	46.9	43.8 - 49.1
2n=8x=56	*abyssinica* x *sativa*	225	47.7	46.9 - 48.5
	barbata x *sativa*	310	46.9	44.8 - 50.0
	canariensis x *sativa*	66	49.8	49.8
	pilosa x *sativa*	52	50.8	50.8

For the purpose of this study the largest diameter of the pollen grain was used. Analyses of variance of the above material gave highly significant differences between ploidy levels ($F=37.27$; d.f.=3,7; $p<0.0001$). Pollen grain sizes of species within the same ploidy level were not significantly different, while lines within the same species show highly significant variation ($F=7.19$; d.f.=31, 137; $p<0.0001$). Analysis of the measurement data reveals that there is a high positive correlation ($r=0.86$) between oat pollen grain length and ploidy level, and that a linear regression line ($Y=35.91+1.56X$) can fit the data. No difference in pollen grain size among the five tetraploid was found. The tetraploid group contained three species (*A. abyssinica, A. barbata, and A. vaviloviana*) plus derived tetraploid CI 7232 with the AB genome, and one species (*A. maroccana*) with the AC genome. Differences, however, were observed in pollen grain size between lines within the same tetraploid species, indicating that even with the same genome configuration, genetic factors could control size pollen grain. One of the tetraploid lines showed variability in pollen grain size within the same plant. The size of the large pollen grains produced by this line are comparable to pollen produced by the octoploid lines. Further study of meiosis in tetraploid line PI 412767 in relation to the larger pollen grains is underway. The amphiploid lines at the octoploid level also did not show any difference in pollen grain size, although they have been developed by crossing the ACD genome with the AB genome, or with the C or the A genomes.

Thirty-two hybrids from octoploid x tetraploid crosses were obtained out of 1,248 crossing attempts (2.6%), while 50 hybrids were obtained out of 124 attempts (40.3%) when the octoploid lines were used as pollinators.

However the germination ability of tetraploid x octoploid hybrid seeds was low (18%) compared to the octoploid x tetraploid seeds (96%). Most hybrids were completely self-sterile but on rare occasions one or two seeds were set.

Three of the hybrids studied cytologically had either 40 or 41 chromosomes, indicating that tetraploid gametes contributed n=14 chromosomes. Chromosome pairing of the hybrids is summarized in Table 2. The genomic constitution of tetraploid PI 412767 (*A. vaviloviana*) is AABB and of octoploid EG88-746 is AAAcAcCCDD. Accession CI 7232 is a tetraploid derived from an advanced generation of a highly sterile triploid hybrid (*A. abyssinica* x *A. strigosa*) and its genomic configuration is AABB. Octoploid line CI 7898 is the progeny of a decaploid oats artificially synthesized from *A. abyssinica* (AABB) x *A. sativa* (AACCDD). It is not possible to determine which genomes or chromosomes were lost from the original decaploid during the process of reduction to the octoploid level.

Table 2. Chromosome pairing of the F1 hybrids between octoploid-tetraploid accessions.

Cross	*Chromosome No.*	*No. of cells*	*Mean number of I*	*II*	*III*	*IV*	*V*	*VI*
CI 7898 x CI 7232	40	11	14.55	10.00	1.55	0.09	0.09	0.00
CI 7898 x CI 7232	40	19	13.63	8.68	1.63	0.95	0.00	0.05
PI 412767 x EG88-746	41	12	20.58	5.42	2.42	0.25	0.17	0.08

Chromosome pairing in the two CI 7898 x CI 7232 hybrids indicates that the octoploid line retains some of its BB genome chromosomes contributed by the tetraploid parent, since high frequency of bivalent pairing occurred. A weighted mean of 13.97 univalents in the same hybrids indicates that chromosomes from the C and D genomes are also present. Observed trivalents, quadrivalents, or higher order chromosome associations are due to partial homology. At anaphase I of meiosis, one or two bridges were observed in a number of cells along with an average of 12.3 laggards, which tended to divide longitudinally with chromatids migrating to opposite poles. Most chromatids were incorporated in the nuclei but one or two micronuclei per cell were present in some cells at telophase I. Ninety-six per cent of the microspores contained micronuclei, ranging from one to seven. Both hybrid plants were sterile.

The PI 412767 x EG88-746 hybrid plant had a genomic configuration of AAAcBCD and 41 chromosomes. Bivalent pairing can be attributed to A-genome chromosomes, while partial homology between the Ac and A genome can explain the trivalent associations. Quadrivalents or higher order associations were also observed and were all chains of four or more chromosomes. On average, 17 laggards were present in anaphase I and divided longitudinally into chromatids that moved to opposite poles. Most cells at the end of meiosis I contained one or more micronuclei. Pollen stainability was low (17.1%).

Based on F1 chromosome number, unreduced gametes (2n=28) were not found in this small sample of functional male or female gametes in these tetraploid lines.

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Cytogenetic and Inheritance Studies of Crown Rust Resistant Hexaploid Oat Translocation Lines

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Summary

Genetic and cytogenetic studies (a) of inheritance for reaction to crown rust and (b) of chromosome pairing in three Wisconsin oat translocation lines and in F_1, F_2, and F_3 progenies of translocation-line x *Avena sativa* crosses were conducted. The translocation lines possess crown rust resistance from diploid *A. strigosa* transferred from 6x-amphiploids or derived-tetraploid C.I. 7232 via monosomic alien substitution lines. Despite chromosome loss during meiosis, the translocation lines always had 42 chromosomes and showed continuous resistance to crown rust. A common meiotic abnormality at metaphase I was "mispositioned bivalents" where one or more bivalents moved away from the main group at the time of centromere orientation. All F_1 plants of all crosses and reciprocals (14 in all) were resistant to crown rust indicating that genes for resistance are dominant and are transferred through both pollen and eggs. Segregation in F_2 included normal 3R:1S single-gene ratios and others where fewer-than-expected resistant plants occurred. Chromosome loss in F_2 plants led to fewer-than-expected resistant plants in F_3 lines.

Introduction

During the past three decades, workers at Wisconsin have developed crown rust resistant oat translocation lines. Two different bridging types were used to transfer resistance from diploid *Avena strigosa* L. The first type was a 6x amphiploid (3,4,5) developed by doubling the chromosomes of triploids from *Avena abyssinica* L. (tetraploid) x *Avena strigosa* (diploid) crosses[1]. The second bridging type was derived-tetraploid C.I. 7232[6], which was selected from progeny of an *Avena strigosa* x *Avena abyssinica* cross by Zillinsky *et al.* [7]. Crosses between the two bridging types and *Avena sativa* led to monosomic alien substitution lines (MAS) from which the translocation lines were derived following an irradiation program to translocate a *strigosa* chromosome segment carrying a gene for resistance to a *sativa* chromosome[2]. Genetic and cytogenetic studies were undertaken to determine meiotic chromosome behavior in translocation lines N569-42-52 and N770-105-1, from the 6x-amphiploid program, DCS 1789, from the derived-tetraploid program, and in their F_1 hybrids with *Avena sativa*.

Methods

Seven crosses and their reciprocals between the three translocation lines (N569-42-52, N770-105-1, and DCS 1789) and three *Avena sativa* cultivars (Holden, Froker, and Marathon) were studied. Pollen mother cells from the three translocation lines, two *Avena sativa* cultivars (Holden and Froker), and 11 F_1 hybrids were examined cytologically. Segregation ratios for resistance to crown rust in F_2 populations of the fourteen crosses were determined in field and greenhouse tests using race 264B. Pollen mother cells from F_2 plants of four crosses (N569-42-52 x Holden and its reciprocal, N770-105-1 x Holden, and DCS 1789 x Holden) were examined cytologically. Crown rust reaction in F_3 lines and families was studied in the same four crosses. Pollen stainability was determined for the three translocation lines, the *Avena sativa* cultivar Holden, and F_1 and F_2 plants of these four crosses as an indication of pollen development.

Results and Discussion

Translocation line N770-105-1 demonstrated a higher level of resistance than both N569-42-52 and DCS 1789 suggesting that the gene(s) for resistance in line N770-105-1 is not the same as that in N569-42-52 or in DCS 1789. The continued expression of resistance to crown rust generation after generation indicates that the translocation lines are homozygous and homogeneous for crown rust resistance. Cytological observations revealed that the translocation lines always contain 42 chromosomes, but chromosome loss was observed during meiosis. Uniformity of translocation lines in their reaction to crown rust year after year, despite chromosome loss during meiosis, suggests that male and female gametes do not function unless they contain the haploid chromosome number (n=21) including the gene for resistance to crown rust. Meiotic abnormalities observed were mispositioned bivalents in metaphase I, chromosome lagging and bridges in anaphase I, mispositioned chromosomes in metaphase II, and chromosome lagging in anaphase II, all of which may trace back to the irradiation treatment used in the development of the translocation lines. It was observed that all bivalents moved to the cell plate at metaphase I, and then rearranged such that centromeres were oriented toward opposite poles. However, some bivalents moved away at the time of rearrangement, and these bivalents were called "mispositioned" bivalents. Mispositioned bivalents are thought to be the result of either nonhomoeologous translocations or spindle abnormalities. Examination of pollen grains revealed that a high percentage was normal (stainable). Chromosome deficiency in polyploids such as oats does not necessarily result in pollen abortion.

All F_1 plants of the seven crosses and their reciprocals were resistant to crown rust indicating that genes for resistance are dominant and that they transfer through the pollen as well as the egg. Cytological examination of F_1 plants revealed the presence of rod bivalents, univalents, and quadrivalents at metaphase which demonstrate lack of complete homology between translocation-line chromosomes and *Avena sativa* chromosomes. Chromosome and genome differentiation which occurred during the development of the translocation lines are responsible for the lack of complete homology between translocation-line and *Avena sativa* chromosomes. The genomic constitution of the 6x amphiploids was $A^d{}_sA^d{}_sA^t{}_sA^t{}_sBB$. However, there has likely been some differentiation between $A^d{}_s$ chromosomes of diploid *Avena strigosa* and $A^t{}_s$ chromosomes of *Avena abyssinica*. In addition, chromosomes of genome B are partially homologous to A_s chromosomes. Chromosome rearrangements occurred among these genomes, differentiating 6x-amphiploid genomes from genomes in other species. More chromosome differentiation probably occurred after crossing 6x amphiploids with *Avena sativa*, and irradiation also induced other effects such as mutations and translocations. The series of crosses among parents with differentiated genomes, followed by selfing and irradiation, likely induced chromosome arrangements which made translocation-line chromosomes not completely homologous with *sativa* chromosomes. Other meiotic abnormalities observed in meiosis in F_1 plants, i.e., mispositioned bivalents, chromosome lagging, and bridges, are thought to be results of irradiation.

Segregation ratios for resistance to crown rust in F_2 populations indicated that resistance is conditioned by a single but not identical gene in the three Wisconsin translocation lines. However, segregation ratios were inconsistent from test to test because of fewer-than-expected resistant plants in F_2 populations. Reduced frequencies of transmission of resistance through the pollen vs. through the egg were observed. The inconsistent segregation ratios in F_2 populations are circumstantially connected with meiotic abnormalities in F_1 plants. Although all F_1 plants of all crosses showed meiotic abnormalities, strong 3R:1S ratios were obtained for at least one F_2 test even for those crosses showing abnormal segregation ratios in other tests. These results may be due to pollen certation when translocation lines were used as males, and/or to selective elimination of eggs or zygotes containing chromosome deficiencies. Fewer meiotic abnormalities were observed in F_2 plants than in F_1 plants. This indicates that meiotic abnormalities might be decreased by additional crosses to *Avena sativa* followed by selfing, leading to improved chromosomal balance. Meiotic abnormalities were observed in both resistant and susceptible plants, indicating that chromosome loss was not limited to the chromosome carrying the gene for resistance.

Fewer-than-expected homogeneous resistant F_3 lines suggests that chromosome loss occurred in some F_2 plants during meiosis. Another observation was that some heterozygous F_2 plants, expected to produce progenies which segregated 3R:1S within F_3 lines, produced fewer resistant progenies than expected. The proportion of resistant plants in some abnormal F_3 lines was less than 50%. These abnormalities in F_3 segregation ratios must have resulted from meiotic abnormalities in F_2 plants. Meiotic abnormalities in plants in abnormal segregating F_3 lines were higher than abnormalities in other classes (homo R, normal segregating, or homo S). The F_2 parent plants of abnormal segregating F_3 lines had higher percentages of meiotic abnormalities than did F_2 parent plants of F_3 lines with a normal 3R:1S segregation ratio.

Cytological studies of pollen mother cells from F_1, F_2, and F_3 plants showed a sharp decrease in abnormal chromosome pairing and other meiotic abnormalities from F_1 to F_3. These results demonstrate that crossing translocation lines with *Avena sativa* followed by selfing decreased meiotic abnormalities and increased the dosage of *sativa* chromatin which leads to more chromosomal balance in successive generations. More backcrosses to *Avena sativa* might hasten chromosomal balance and cytological stability.

Through pedigree breeding, these genes were transferred into enhanced breeding stocks worthy as parents in an applied oat breeding program. Cultivars Centennial, Horicon, and Dane, products of this program, were resistant to prevalent races at the time of release.

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Use of *Avena sterilis* and A. *maroccana* derived *A. sativa* Germplasm to increase Groat Protein Concentration in Oat for Western Canada

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Summary

A. *sativa* genotypes derived from an A. *sterilis* background and selected for high groat protein concentration at Iowa State consistently demonstrated high groat protein in trials at Saskatoon during 1989-1991 and are being used as donors of increased protein in the U. of Sask. breeding program.

Genotypes derived from an A. *maroccana* background at the Welsh Plant Breeding Institute did not demonstrate as high a protein concentration as expected, although line Av2027/1/3/27 appears to have some potential as high protein donor parent. Advanced lines with acceptable performance and a 1.0-2.0% protein increase are being evaluated.

Several foreign cultivars consistently demonstrated increased groat protein compared with local checks, including: Elen and Maldwyn from Wales; Otee, Trucker and SN404 from the USA; Karhu from Finland and Leila from Norway.

Introduction

A major objective of our oat breeding project is to develop genotypes with improved market end-use quality, especially for the U.S. market. Historically, Canadian varieties have had excellent milling quality, but relatively lower protein concentration than American varieties. A moderate (1.0 to 2.0%) increase in groat protein concentration without a loss of physical grain quality or yield potential is our goal.

Sources of Increased Protein

Based on reports at the 3rd International Oat Conference[1,2] and one subsequent report[3], we decided to utilize materials derived from *Avena sterilis* and A. *maroccana* as potential donors. Four A. *maroccana* derived A. *sativa* lines were obtained from the Welsh Plant Breeding Institute and twenty A. *sterilis* derived A. *sativa* lines were obtained from Iowa State University. Other foreign introductions have been evaluated for protein concentration and subsequently for other important physical quality and agronomic traits over three years (1989-1991) at Saskatoon.

Materials and Methods

Materials were grown at Saskatoon and evaluated for groat protein concentration as follows:

1989. Unreplicated groups of four hill plots each of 20 A. *sterilis* derivatives and 4 A. *maroccana* derivates and unreplicated yield trial plots of 50 introductions from the USSR, Czechoslovakia, Sweden, Wales, U.S.A., Norway and Germany.

1990. Two replicate hill plot test, two locations, 32 genotypes: 10 local checks, 4 A. *marocanna* derivatives, 11 selected A. *sterilis* derivatives and 7 foreign cultivars. Unreplicated yield trial plots of 27 introductions.

1991. (a) Two replicate yield trial, two locations, 25 genotypes: 7 local chks, 2 A. *maroccana* derviatives, 11 A. *sterilis* derivatives, 3 U.S. and 2 Welsh varieties. (b) 39 F_5 lines from A. *maroccana* derivative/local line hybrid in unreplicated yield trial plots. (c) 94 F_5 lines from A. *maroccana* derivative/local line hybrid and 66 F_5 lines from local line/Otee hybrid in hill plot trials.

Results and Discussion

1989. Initial evaluation of the A. *sterilis* derivatives were encouraging (Table 1) and, based on protein concentration and agronomic features, 11 genotypes were selected for further evaluation. While A. *maroccana* derivatives were not as high in protein, the interesting features of these materials encouraged continued evaluation. Eight of fifty introductions demonstrated higher protein (Table 2) combined with acceptable agronomic features and were selected for 1990 trials.

Table 1. Groat Protein Concentration of A. *maroccana* (Av) and A. *sterilis* (J + L) Derivatives, Saskatoon, 1989

Name	*% Prot.*	*Name*	*% Prot.*	*Name*	*% Prot.*
Av2401/2	18.2*	J706-4	21.5	J758.3	21.5*
Av2402/4	17.9*	J806-4	18.8	J778-3	20.4
Av2027/3/1/32	20.3*	J762-1	21.2*	J756-3	21.7*
Av2027/3/1/27	n.a.	J894-4	19.1	J775-1	21.2*
J772-3	20.3	J828-4	19.2	J706-1	21.6*
J756-1	22.4*	X2-1	20.7	J606-1	18.4
J674-2	18.4	J773-3	21.7*	J773-1	21.6
J740-3	21.1*	J829-3	20.2*	Local check	17.5
J794.4	22.1*	L966-3	22.3*		

* Selected for evaluation in 1990.

Table 2. Groat Protein Concentration of Six Foreign Oat Genotypes, Saskatoon, 1989

Name	*Origin*	*n*	*% Protein*	*Name*	*Origin*	*n*	*% Protein*
Calibre	CAN	3	19.1±0.5	Elen	WAL	1	23.9
Cascade	CAN	4	19.9±0.7	David	CZE	1	22.1
Otee	USA	1	24.1	Sv38529	SWE	1	23.0
SN404	USA	1	22.8	Karhu	FIN	1	20.2
Maldwyn	WAL	1	22.7	Leila	NOR	1	21.5

1990. Detailed evaluation confirmed the higher protein concentration of all A. *sterilis* derivatives, one of four A. *maroccana* derivatives and several introduced genotypes as compared to the dominant Canadian varieties Calibre and Cascade (Table 3). In addition, ten of the eleven A. *sterilis* lines and the U.S. varieties Otee and SN404 demonstrated significantly higher protein concentration than the local "high" protein check, Riel. The higher protein of five foreign introductions was confirmed (Table 4).

Table 3. Groat Protein Concentration of Selected Oat Genotypes as grown at Two Locations, 1990

Name	*% Prot.*	*Name*	*% Prot.*	*Name*	*% Prot.*
Calibre	16.3	Av2402/2	16.7	J762.1	20.6**
Cascade	16.2	Av2402/4	16.9	J773.3	20.6**
Riel	17.9*	Av2027/3/1/27	18.4*	J758-3	21.8**
Otee	20.6**	Av2027/3/1/32	17.4	J756-3	21.1**
Maldwyn	18.8*	J740-3	20.4**	J775-1	20.2**
Elen	19.0*	J756-1	21.4**	J706-1	20.6**
David	16.9	J794-4	20.9**	J829-3	19.1*
		L966-3	20.1**	Std error	0.42

* Significantly greater than $\bar{X}$ of Calibre and Cascade by LSD at P = 0.05. LSD = 0.82.
** Significantly greater than Riel by LSD at P = 0.05.

Table 4. Groat Protein Concentration of Selected Foreign Oat Genotypes, Saskatoon, 1990

Name	*Origin*	*% Protein*	*Name*	*Origin*	*% Protein*
Calibre	CAN	18.2	Maldwyn	WAL	21.6
Cascade	CAN	18.7	Sv38529	SWE	20.1
Karhu	FIN	20.2	David	CZE	19.5
Leila	NOR	20.4	Av2027/3/1/32	WAL	19.7

1991. All A. *sterilis* derivatives and the A. *maroccana* derivative Av2027/3/1/27 continued to demonstrate significantly higher protein concentration compared with the cultivars Calibre and Cascade, as did all selected introductions (Table 5). As in 1990, the same genotypes, plus Av2027/3/1/27, were higher in % protein than the "high" protein check Riel.

Clearly these lines are not agronomically equal to the checks, being generally lower yielding, earlier maturing and less desirable in terms of physical grain quality. However, in the group with significantly higher protein than Calibre and Cascade; Maldwyn, Elen and J829-3 offer good potential, demonstrating acceptable yield levels and, especially for J829-3, reasonble kernel quality. The A. *maroccana* derivative Av2027/3/1/27 while low in yield potential combines high protein with good grain quality.

Of the remaining A. *sterilis* derivatives, J775-1 offers the best potential demonstrating comparable yield and maturity with Riel with fair kernel quality. Lines J756-1 and J758-3 combine consistently high % protein with good kernel quality. The U.S. variety Otee is of interest based on very high protein with good test weight and reasonable grain size.

Preliminary results indicate that the increased protein concentration of Otee and Av2027/1/3/27 can be transferred to locally adapted materials. The best lines appear to have a 1.0-2.0% protein improvement combined with acceptable agronomic performance and grain quality. Further testing of these materials and advanced lines from crosses with A. *sterilis* derivatives is underway in 1992.

Table 5. Combined Analysis, Oat Yield Trial, RCBD, 2 Reps at 2 Locations, 1991

Name	*Gr. Yld. (kg/ha)*	*% Prot.*	*T.wt. (kg/hl)*	*Kernel wt. (mg)*	*% Plump*	*Mat. Score §*	*Prot. Yld. (kg/ha)*
Calibre	4815	16.0	56.5	37.5	70	4	770
Derby	5289	15.0	57.3	39.5	76	4	793
Cascade	5434	15.9	54.9	35.1	63	3	864
Riel	4728	17.7*	55.3	37.1	63	4	837
Otee	3161	21.5**	54.8	29.1	46	1	680
Maldwyn	4239	18.4*	54.3	25.7	29	2	780
Elen	5028	17.9*	51.9	27.4	30	4	900
Trucker	3862	18.1*	58.2	35.2	71	2	699
SN404	3802	20.5**	55.6	29.1	37	4	779
Av2027/3/1/27	3608	19.4**	52.6	31.2	60	4	700
Av2027/3/1/32	5229	16.8	52.0	30.9	47	4	878
J706-1	3751	21.0**	52.9	31.3	37	2	788
J740-3	3921	20.1**	52.9	34.8	49	3	788
J756-1	3886	21.6**	55.9	33.5	53	1	839
J756-3	3383	20.0**	54.9	30.2	49	1	677
J758-3	3568	22.1**	55.1	33.8	59	2	789
J762-1	3706	21.4**	54.3	34.8	56	2	793
J773-3	3728	22.1**	55.3	33.2	49	1	824
J775-1	4926	20.4**	53.6	31.0	35	3	1005
J794-4	3559	20.8**	55.7	31.3	53	2	740
J829-3	4540	18.4*	54.2	35.2	60	4	835
L966-3	3327	21.1**	47.5	29.2	18	3	702
Std. error	285	0.7	1.0	1.5	9.2	—	—

* Significantly greater $\bar{X}$ of Calibre and Cascade, P = 0.05
** Significantly greater than Riel, P = 0.05
§ 1 = earliest

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Isozyme and Chromosome Variations of the *Avena* Species in the Canary Islands and Morocco

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Summary

Isozyme and chromosome variations within four species, *Avena Canariensis, A. agadiriana, A. moroccana* and *A. longiglumis,* from the most probable area of origin of the polypoids were examined. Variable loci and heteozygosity of *A. canariensis* from Fuerteventura were the highest of all the species examined. However, the plants from Lanzarote tend to possess lower level of variation than those from Fuerteventura. Ecotypic differentiations were observed in three species with the exception of *A. maroccana.* These growth habits were positively correlated with isozyme and chromosome types. The earlier flowering ecotype had much more numbers of satellite chromosomes than the late types in *A. agadiriana* and *A. longiglumis* but vice versa in *A. canariensis.* These ecotypes were further emphasized by a reciprocal translocation.

Introduction

All the biological species of *Avena* coexist in the area roughly between Southern Spain, Morocco and the Canary Islands. The most probable area of origin of the polyploids is where the putative lower ploidy ancestors and their higher ploidy descendants overlap. Clearly Southern Spain, Morocco and the Canary Islands represent the only area which meets such a demand. In order to clarify intra- and inter-specific diversities of *Avena,* isozyme and chromosome variations were examined in the wild populations of the Canary Islands and Morocco.

Methods

Forty one natural populations consisting of four species, *A. canariensis* (2x), *A. agadiriana* (4x), *A. maroccana* (4x) and *A. longiglumis* (2x), collected from the Canary Island and Morocco were used in this study. Electrophoresis was carried out according to Morikawa and Leggett[1]. Meiotic and mitotic chromosomes were observed according to Morikawa and Leggett[2].

Results and Discussion

Mean genetic variability in four *Avena* species of 41 natural populations is shown in Table 1. *Avena canariensis* is restricted to the Canary Islands. We recorded an average of 53.8% variable loci, 1.76 alleles per locus and an expected heterozygosity of 0.226 in Fueteventura. But all the values in Lanzarote were less than those of Fuerteventura. No heterozygous individuals were found in any of the arrays at the first generation. The populations from northern Lanzarote which is a xeric rocky mountain area, were monomorphic but had a peculiar allozyme. The intraspecific variation of *A. canariensis,* as indicated by morphological plasticity, variation of chromosome shape and isozyme polymorphism, has further been emphasized by the loss of a pair of satellites , a very irregular cytomixis and a reciprocal translocation. These often cause meiotic irregularities and distort the structures or disrupt the process to bring about varying degrees of sterility or aberrant gameres. *A. canariensis* has distinctive ecotypes, which are divided into early and late flowering types. The late flowering ecotype has a late heading date, prostrate growth habit and pubescence, whilst the early flowering ecotype is early, erect and glabrous. These growth habits are positively correlated with isozyme and chromosome genotypes.

The early type always had Est-3S, Est-2N, Got-3M and Pgi-2F alleles, whilst the late type had Est-3F, Est-2F, Got-3S and Pgi-2S. The same trend was observed in the satellite chromosome numbers. The early flowering ecotype always had a pair of satellite chromosomes whilst the late flowering ecotype always had two pairs (Table 2). The early flowering types were adapted mainly to disturbed habitats along ditches and roadsides. The later flowering types were collected in the southern part oF Fuerteventura and the northern part of Lanzarote, mainly at high elevations in habitats that were basically undisturbed by cultivation.

Table 1. Mean genetic variability in the natural populations of *Avena* species in the Canary Islands and Morocco

Species	*No. of plants exam.*	*No. of popu-lations*	*alleles /locus*	*Variable loci (%)*	*Hetero zygosity expected*
A. canariensis (Fuerteventura)	189	9	1.76	53.8	0.226
A. canariensis (Lanzarote)	215	10	1.54	43.1	0.127
A. agadiriana	107	5	1.50	46.3	0.154
A. maroccana	355	11	1.82	44.3	0.182
A. longiglumis	168	6	1.78	38.3	0.160

Avena agadiriana is the newly described tetraploid species, which is very similar to *A. canariensis*. This species was distributed from Casablanca to Tiznit along the Atlantic coast of Morocco. Moreover, its distribution area is divided into two parts by the Haut-Atlas mountains (alt. 4164m). The northern part of the mountains has very heavy clay soils, whilst the southern part is very dry and has sandy soil. The genetic variability of the 6 populations was as follows; an average of 46.3% variable loci, 1.50 alleles per locus and an expected heterozygosity of 0.154 were recorded (Table 1). A dendrogram, resulting from a UPGMA cluster analysis, showed a major dichotomy between the southern and northern populations. Chromosome variations, the loss of satellites and a translocation, were observed by hybridisation between the groups. The northern group (3 populations involving CAV6743) of late maturing types always had two pairs of satellite chromosomes. The southern earlier flowering group always had three pairs of satellite chromosomes (Table 2). A reciprocal translocation was involved between the groups. Intraspecific variations of isozyme and chromosomes in *A. agadiriana* were very similar to those of *A. canariensis*. The genetic differentiations of *A. canariensis* were mainly associated with the elevation of habitats, but those of *A. agadiriana* were associated with specific soil characters, edafic factors and precipitation.

Avena maroccana is a typical weedy species forming massive stands mixed with *A. sterilis* in cereal fields on heavy alluvial soil, an environment to which its large spikelet is well adapted. It has been discovered and repeatedly found only in the triangle between Tflet-Rommani-Tedders in Morocco. It has been stated that *A. maroccana*, which is closely related to the hexaploids on the basis of morphology and meiotic affinities, appears to have a combination of A and C genomes. This species is restricted to a small area and there is no sign of ecotypic differentiation within the species. However, the genetic variability of 11 populations was relatively larger than the former two species. An average of 44.3% variable loci, 1.82 alleles per locus and an expected heterozygosity of 0.182 were recorded (Table 1). A dendrogram showed two distinct clusters, which are roughly correlated with the geographic distance, and two independent populations (M7 and M9). Each population of *A. maroccana* appears to be adapted to a microhabitat. Chromosome analysis on this species is now in progress.

Table 2. Intraspecific differentiation of two distinct ecotypes and relationship to satellite chromosome numbers in *Avena*

Species	*Ploidy*	*No. of populations with*			*No. of pairs of satellites*		
		Total	*Early*	*Late*	*Early*	*Late*	*Previous report*[3,4]
A. canariensis (Fuerteventura)	2X	9	2	7	1	2	2
A. canariensis (Lanzarote)	2X	10	5*	5	1	2	–
A. agadiriana	4X	6	3	3	3	2	2
A. maroccana	4X	11	–	–	–	–	3
A. longiglumis	2X	6	1	5	2	1	2

* Two types are mixed.

Avena longiglumis is sporadically distributed in the Iberian peninsula, North Africa and Israel. It has very long slightly subequal glumes and very large anthers; the floret is the dispersal unit. It consists of two ecotypes. The first is a coastal type of robust, tall plants with large drooping panicles. The other is a desert type of shorter, slender plants with small panicles. Both ecotypes are adapted to sandy soils. The genetic variability of 6 populations was recorded as follows; an average of 58.3% variable loci, 1.78 alleles per locus and an expected heterozygosity of 0.160 (Table 1). Out of 6 populations, one was the desert type and five were the coastal types. Isozyme differentiation between the ecotypes was not detected, but Clinal variations for several allozymes were observed from north to south. The desert type (early flowering) had two pairs of satellite chromosomes whilst the coastal type (late flowering) always had one pair.

From the evidence we have accumulated from studies of three species of *Avena*, with the exception of *A. maroccana*, it would seem that the species of *Avena* probably evolved through chromosomal rearrangements, and did not involve hybridization.

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Fungicide Application and Genotype X Environment Interaction of Oat Grain Yield

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Summary

Eleven oat genotypes were evaluated for grain yield stability and the effect of fungicide application on the genotype x environment (GXE) interaction in seven locations in Southern Brazil during 1985–1990. Eberhard and Russel's[3] parameters (x, b and Sdi) were adopted and analyses were performed acording to two models: with fungicide application and without fungicide. Results indicated a strong GXE interaction, although no genotype showed stable grain yield, as shown by the high regression deviations observed. The genotype stability was similar with and without application of fungicide.

Introduction

Genotype x environment interactions (GXE) analysis has been suggested as a means to help breeders evaluate elite, stable genotypes in breeding programs[2,3,4]. This interaction assumes special importance in areas of high environmental variation, where the genotypes may perform distinctly over different conditions. Large environmental variation occurs in Southern Brazil during the cold season, especially from one year to another, and therefore desirable genotypes for this region are those with wide adaptability[3]. Unpredictable situations during the growing season could cause stress affecting plant development, altering cultivar stability. All the models for GXE interaction analysis are based upon environmental variation which occurred in the past, and they are not useful for predicting future genotype performance. However, the technique presents some problems due to the limited duration of genotypes in variable environments, caused mainly by disease[1]. Thus, chemical control, utilizing fungicides, has been proposed as a way to increase genotypic stability in conditions of high pathogen incidence, as occurs in Southern Brazil. The objectives of the present study were to evaluate the effect of fungicide on the genotype x environment interaction and grain yield stability of different oat genotypes grown in Southern Brazil.

Methods

Eleven oat genotypes (Table 1) developed at the University of Passo Fundo (UPF) and Federal University of Rio Grande do Sul (UFRGS) were evaluated for grain yield stability in seven locations (Eldorado do Sul, Ijui, Passo Fundo and Vacaria in the State of Rio Grande do Sul; Campos Novos in the State of Santa Catarina; Ponta Grossa and Entre Rios in the State of Paran), during six years (1985–1990). Two trials, with and without fungicide application, were conducted in each location, except during 1985, for all locations, at Vacaria for all years and Ijui in 1988, when fungicide was not applied. Randomized blocks with three replications were used. Each plot was comprised of four rows 5.0 m long and 0.20 m apart. For yield measurement, three rows only were harvested. In the experiment sprayed with fungicide, two applications of propiconazole (0.5 L/ha) were used. The first appliction was made when varieties were in the boot stage, and the second fifteen days later. Analysis of variance was performed, assuming genotypic effects as fixed and other factors as random. Stability parameters were estimated by Eberhart and Russell's model, separately with and without fungicide applications.

Results and Discussion

Analysis of variance (not shown) revealed that all the main effects (genotype, year, location and fungicide) were significant, as were the interactions between genotypes and the other factors. Mean grain yield, linear regression coefficients and deviations from regression are presented in Table 1. Two genotypes UFRGS 7 and UFRGS 10 gave high grain yield in the two analysis and the genotype UPF 4 was the lowest yielding. In the analysis of trials without fungicide, the linear regression coefficient was b < 1 for genotypes UPF 4 and UFRGS 7, and b > 1 for UPF 5 and UFRGS 10. For the other genotypes, b =1. With the application of fungicide only UPF 4 had b < 1, and UPF 6 and UFRGS 10 had b > 1. The deviations from the regression for most genotypes were significant, with the exception of UPF 3 and UPF 4 without fungicide, and UFRGS 10 with fungicide. The three parameter analysis did not give evidence of a superior genotype for grain yield stability, since no genotype fulfilled the assumptions of the model used. Utilization of fungicide as a means of increasing grain yield stabiity, does not appear important. The relative performance of genotypes did not vary with fungicide appliction, the mean grain yield being the only variable affected, by this treatment. Therefore, although fungicide application contributes strongly to increased grain production, it does not assure grain yield stability.

Table 1. Mean grain yield, regression coefficient and regression deviation (Sdi) for genotypes tested with and without fungicide during 1985 to 1990 in different locations of South Brazil

Genotype	Without fung. mean (kg/ha)	bi	Sdi	With fung. mean (kg/ha)	bi	Sdi
UPF 3	2077	1.09	267	2487	1.05	349[3]
UPF 4	1670[2]	0.81[3]	329	2029[2]	0.75[3]	373[3]
UPF 5	2065	1.29[3]	480[3]	2385	1.00	463[3]
UPF 6	2317	0.99	365[3]	2767	1.26[3]	431[3]
UPF 7	2407	0.99	350[3]	2702	0.90	410[3]
UPF 8	1930	1.10	530[3]	2254	1.01	524[3]
UPF 9	1880[2]	1.07	513[3]	2414	0.98	475[3]
UFRGS 7	2886[1]	0.87	605[3]	3188[1]	1.03	587[3]
UFRGS 8	2394	0.82	625[3]	2477	0.80	556[3]
UFRGS 9	2364	0.78[3]	455[3]	2476	0.92	418[3]
UFRGS 10	2692[1]	1.20[3]	434[3]	2930[1]	1.29[3]	269
Mean (std)	2244 (361)			2555 (323)		

[1] = Mean + 1 St. D.
[2] = Mean - 1 St. D.
[3] Significantly different to b = 1.
[4] Significant at 5%.

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Variability in *Avena sativa, Avena sterilis* and their Hybrids: Morphologic, Cytogenetic and Electrophoretic Evaluations

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Summary

Crosses were performed between *Avena sativa* L. and wild accessions of *Avena sterilis* L. with the objective of identifying the best wild introductions to broaden the germplasm pool of oats in Brazil. Hybrids were identified by spikelet morphology and chromosome pairing. The high homology of the two species made the identification of the hybrids by the esterase enzymatic system difficult. The meiotic pairing observed in the hybrid plants makes feasible the use of accessions of *Avena sterilis* in the improvement of oats in southern Brazil.

Introduction

The reduction of genetic variability in cultivated species of plants is a contemporary phenomenon, especially in areas of high environmental stress as observed in southern Brazil. In oat, the wild species have been used in interspecific crosses to broaden the genetic variability and to transfer specific characters of agronomic importance[1,2,3,5]. This study was made with the objective to make crosses between cultivated genotypes of *Avena sativa* and wild accessions of *Avena sterilis* of different origins; and to investigate the hybrid conditions by spikelet morphology, meiotic behaviour and electrophoretic pattern.

Material and Methods

Artificial hybridisations were made between cultivated genotypes UFRGS 7, UFRGS 8 and UPF 7 with different accessions of *Avena sterilis*, including reciprocals. Analysis was made of hybrids (F_1) and parents grown in the field in 1989. Spikelet morphology was analysed by the presence and absence of awns, degree of pilosity and shattering. Electrophoresis was performed using the α and ß esterases and zymograms have been compared by Jaccard's Similarity Index[4]. For meiotic pairing analysis, inflorescences were fixed in Newcomer's (1953) solutions and pollen mother cells were stained with propionic acid. Crosses were made in 154 panicles with 1220 flowers pollinated. 140 grains were obtained with a seed set of 11%.

Results

Despite the pollination being carefully made by hand, the seed set obtained was very low. However, all the hybrids obtained were fertile. The difference between the hybrids and the parents was easily observed through the spikelet morphology. The hybrid shows one awn, pilosity at antecious I and is non shattering. The *sativa* type is awnless, glabrous and non shattering. Finally, the *sterilis* group has awns at antecious I and II, pilosity and natural shattering. The results obtained with the analysis of electrophoresis pattern through the Jaccard's Similarity Index showed more similarities between the *sativa* and *sterilis* types than inside each species itself. These results show more variability for the esterase system among the genotypes of the same species than between the two species. The electrophoresis analysis was not efficient for identification of hybrids. High chromosome regularity was observed in the parental genotypes (*sativa* and *sterilis*), and most cells analysed showed 21 bivalents (Table 1).

However, hybrids (F_1's) showed an increase in the number of univalents and multivalents. The observation of multivalents may represent structural differences, but the preferential pairing by bivalent indicates a high homology between the two species and the feasibility of introgression of *Avena sterilis* genes into *Avena sativa*.

Table 1. Meiotic pairing in cultivated genotypes of oats (*Avena sativa*), wild introductions (*Avena sterilis*) and their hybrids. Agronomy Department/UFRGS, 1989.

Genotypes	*Number*		*Means/cell*		
	plants	*cells*	*bivalents*	*univalents*	*multivalents*
UFRGS 7*	9	288	20.98	0.03	0.003
UFRGS 8*	8	281	20.91	0.13	0.000
TOTAL	17	569	20.94	0.10	0.002
I 325	9	198	20.86	0.14	0.000
I 378	7	213	20.97	0.06	0.000
TOTAL	16	411	20.95	0.10	0.000
HYBRIDS	24	1810	20.69	0.31	0.070

* cultivated genotypes

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Gene Effects for Fodder Yield in Oats

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Abstract

Three *A. sativa* lines viz; Kent, Nodaway and WA 1470 each were crossed with an *A. sterilis* accession PI 295932. The populations developed for each of the three crosses were parental, F_2, F_3, B_{11}, B_{22}, B_{1s} and B_{2s} generations. The joint scaling test suggested by Cavalli (1952) was applied to test the adequacy of genetic models as well as for estimating the genetic parameters for green and dry fodder yields.

The main effects, additive (d) and dominance (h), were significant in all three crosses for both green and dry fodder yields except in Kent x PI 295932 for green fodder where the additive effect was insignificant. Among the epistatic effects, additive x additive (i) was significant for green and dry fodder yields in Kent x PI 295932 and for dry fodder yield in Nodaway x PI 295932. Whereas additive x dominance (j) was significant for dry fodder yield in Kent x PI 295932 and dominance x dominance (l) was significant for green and dry fodder yields in Kent x PI 295932. Epistasis observed in all the crosses were of duplicate type.

Methods like modified recurrent selection and/or adoption of biparental matings will be useful under such a situation.

Use of a Chromosome Translocation for Genetic Studies in Oat

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Summary

Chromosome translocations are useful for gene mapping in diploid species, but such use of translocations in allopolyploids has been of limited value. We describe methods for determining linkage distance between a locus in an interchanged chromosome segment and the interchange breakpoint in hexaploid oat, *Avena sativa* L. We suggest uses for oat chromosome translocations to 1) facilitate oat genetic mapping studies; 2) develop stable genetic stocks with specific gene dosage; and 3) produce stable, unique combinations of alleles conferring crown rust resistance for use in oat breeding.

Introduction

Translocation differences occur frequently among oat cultivars[6,8,11]. An understanding of segregation from translocation heterozygotes may allow their exploitation to interpret gene mapping data, develop genetic stocks for deletion mapping, and evaluate gene dosage effects. Chromosome translocations are useful for gene mapping in diploid species[1,2,4,10], but such use of translocations in allopolyploids has been of limited value. Genetic buffering, due to the presence of homeoalleles in hexaploid oat, compensates for chromosome loss in duplication-deficiency (Dp-Df) gametes produced by translocation heterozygotes. In contrast to diploid species, translocation differences in hexaploid oat may not result in semi-sterility[3] and therefore genetic ratios may be expected to differ from those produced by diploid translocation heterozygotes.

The oat cultivars, Steele and Dumont, differ by a chromosome interchange with *Pc-38* in an interchanged segment, resulting in F_2 segregation ratios of 15 resistant (R):1 susceptible (S) when inoculated with a crown rust isolate avirulent on *Pc-38* [6]. Inheritance studies indicate *Pc-38* is allelic or tightly linked with crown rust resistance genes *Pc-62* and *Pc-63* [5]. Evaluation of progeny resulting from Dumont/Dif-63 (Dif-63 is a germplasm line homozygous for *Pc-63*) hybrids indicate Dumont possesses *Pc-38* in an interchanged position relative to its allele in Dif-63, Steele, and other germplasm lines[6].

We used the backcross method to provide a direct estimate of recombination in an interchanged segment in hexaploid oat interchange heterozygotes. Detection of crossovers between the crown rust resistance locus (*Pc* locus) and the interchange breakpoint would allow the production of lines with combinations of *Pc-38*, *Pc-62*, and *Pc-63* previously not possible. The objectives of this study were to 1) obtain recombinant genotypes with *Pc-63* in the interchanged position; and 2) determine the linkage distance of the *Pc* locus to the interchange breakpoint.

Methods

A backcross derived line, with 'Fraser' as the recurrent parent, developed with a single dominant crown rust resistance gene, *Pc-63*, [5] was obtained from Agriculture Canada Research Station, Winnipeg, Manitoba. This line was designated Dif-63 for this study. D8, a $F_{4:5}$ line derived from Dumont, lacks *Pc-39* and has *Pc-38* in the Dumont interchanged position[6]. Dumont and D8 (both denoted D) possess *Pc-38* in an interchanged position relative to Dif-63. D lines and Dif-63 were crossed to produce F_1 seed heterozygous for *Pc-38*, *Pc-63*, and the translocation. D/Dif-63 F_1 hybrids were backcrossed to Dif-63 using the F_1 as the female, and subsequent selfing of BC_1F_1 plants produced BC_1F_2 seed for rust evaluation.

Crown rust isolate 181 (CR 181), which is virulent on *Pc38* and avirulent on *Pc63*, was obtained from J. Chong (Agriculture Canada Research Station, Winnipeg, Manitoba). Standard inoculation procedures were used with spores suspended in 'Soltrol 170' oil (Phillips Petroleum Co.) applied to the leaves of 6-7 day old seedlings. After development of infection, an infection type (IT) was assigned to individual seedlings according to the 0-4 scale developed by Murphy[9]. Plants with an IT greater than 2 were considered susceptible.

The avirulence/virulence relationship of CR 181 to *Pc-63* and *Pc-38* allowed identification of seedlings that contain at least one dose of *Pc63* in Dif-63//D/Dif-63 BC_1F_2 seedlings. Recombinant genotypes were identified by examining BC_1F_2 segregation ratios. Three ratios are possible in the BC_1F_2; 15R:1S, 3R:1S, and all resistant. An expected 15R:1S ratio results from duplicate dominant gene action in recombinant BC F_1 plants. All segregating populations were tested for goodness of fit using a chi-square test. A minimum family size of 50 was used to distinguish between a 15:1 and 3:1 ratio at the .05 confidence level[7].

To estimate the frequency of recombination, the number of backcross F_1's producing segregation ratios of 15R:1S in the BC_1F_2 was multiplied by 2 to account for recombinant genotypes segregating 3R:1S. The frequency of recombination was calculated as follows:

$$\text{Frequency of Recombination} = \frac{\#\text{ of recombinant BC } F_1 \times 2}{\text{Total Backcross } F_1\text{'s}}$$

The frequency of recombination is an estimate of the distance between the locus and the breakpoint in map units. Double crossovers are not detectable using this method.

Results and Discussion

Inoculation of 151 BC_1F_2 families with CR 181 identified 11 families segregating 15R:1S. Of the remaining 140 families, 64 were all R and 70 segregated 3R:1S. A recombination frequency of .152 was calculated after correction for unidentifiable recombinants segregating 3R:1S. *Pc-63* was determined to be linked in repulsion 15.2 ± .0296 cM distal to the translocation breakpoint.

If the *Pc* locus and the breakpoint were tightly linked or pairing and recombination were reduced in the region of the translocation, few or no recombinants would be expected. The ratios produced suggest pairing of the interchanged with noninterchanged homologous segments was nearly normal and Dp-Df gametes were transmitted with frequencies similar to balanced gametes. The recombinants detected provide an estimate of recombination that occurs in an identifiable oat chromosome segment smaller than a whole chromosome arm. Analysis of translocation heterozygotes should allow use of the breakpoint as a genetic marker for assessment of order and direction from the centromere of linked genes.

Recombinant genotypes segregating 15R:1S possess *Pc-63* in the interchange and noninterchange positions, which can be confirmed by testcrosses to a universal susceptible cultivar, and would allow recovery of plants with four doses of *Pc-63*. This will allow evaluation of the effect of increasing doses of *Pc-63* on rust reaction. In addition, construction of a genotype simultaneously homozygous for *Pc-62* and *Pc-63* may be possible. However, the recombination frequency calculated in this study would lead to genotype instability with regard to combining *Pc-62* and and *Pc-63* in a true breeding line. Other combinations of the three resistance alleles will allow evaluation of possible interactions and dosage effects.

Near isogenic Dp-Df lines that differ by presence or absence of chromosome segments are being produced by repeated backcrossing of a deficiency *Pc-38* genotype to a homozygous duplication *Pc-38* line used as the recurrent parent. Subsequent selfing and rust evaluation allows recovery of the homozygous crown rust susceptible Dp-Df genotypes. Near isogenic reciprocal Dp-Df lines have been produced. The resulting near isogenic lines differ by the presence or absence of the segments involved in the translocation and linked genes in the interstitial segments. These lines should be useful to examine dosage effects of genes located in interchanged segments. Translocation heterozygosity allows evaluation of dosages from 0 in deficiency lines to 4 doses in duplication lines.

Dp-Df lines combine certain aspects of other aneuploid stocks with some advantages relative to other aneuploids for mapping genetic markers. Discrete partial chromosome segments involved in the translocation are available for analysis. Dosage can conveniently be maintained at 0 (nullisomic condition), 2 (disomic in either position) or 4 (tetrasomic) doses and transiently created for 1 (monosomic) or 3 (trisomic) using the same material. This manipulation requires less effort than other aneuploids. Deficiency mapping, exploiting Dp-Df differences of near isogenic lines, should allow identification of molecular markers in the interchanged segments. Expected segregation of molecular markers associated with chromosome interchange segments will change in a manner that parallels the genetic ratios of the crown rust resistance genes in the interchange segments.

The frequent occurrence of translocation differences among oat cultivars suggests the development of Dp-Df lines can be a planned process, and planned crosses could identify various useful translocation stocks. The translocation difference in this study was phenotypically identifiable due to 1) transmission of viable Dp-Df gametes and; 2) the presence of a dominant resistance gene, *Pc-38*, in an interchanged segment. These two conditions resulted in the expression of a recessive phenotype (S) in the F_2 progeny of a cross between cultivars exhibiting resistance conferred by the same allele[6].

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Gene Effects for Harvest Index in *Avena sativa* L. x *Avena sterilis* L. Oat Crosses

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Abstract

Three *Avena sativa* L. cultivars (Kent, Nodaway and WA 1470) and one *Avena sterilis* L. accession (PI 295932) were used for developing the experimental materials. The gene effects were estimated using parental, F_1, F_2 and backcross (B_1 and B_2) generation means for each of the three crosses, i.e. Kent x PI 295932, Nodaway x PI 295932 and WA 1470 x PI 295932. The χ^2 test and estimates of different parameters (Cavalli, 1952) indicated the adequacy of the five parameter model in the cross Kent x PI 295932, detecting highly significant estimates of additive, dominance, additive x additive and dominance x dominance effects. In crosses Nodaway x PI 295932 and WA 1470 x PI 295932 only the additive-dominance (three parameter) model was found adequate. In both these crosses the additive effect was more predominant than the dominance effect, however both the estimates were highly significant.

Early generation selection and intermating among F_2/F_3 generation selected plants is proposed for further improvement in the harvest index.

Inheritance of Plant Height and Heading Date of Different Oat Crosses

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Summary

Plant height and heading date are two of the most important traits for oat adaptation in the environments of southern Brazil. Most oat varieties grown in the region are very tall (more than 140 cm), and yield losses due to lodging are frequent. In addition, early varieties with good grain yield are desirable because most farmers grow soybean after the oat crop. An experiment was performed with the parental, F_2 and F_3 generations of twelve oat crosses involving short, intermediate and tall plant types, and early and late maturing types. Brazilian genotypes had either one or two major genes determining plant height and heading date.

Introduction

For most crop plants, modifications in a few loci with large phenotypic effects may represent drastic changes in adaptation and final fitness to the environment. Plant height and heading date are two of the most important traits for oat adaptation in the environment of southern Brazil. Use of the oat crop for grain production is increasing steadily in the region. Most oat varieties grown are very tall (greater than 140 cm) and yield loses due to lodging are frequent. In addition, early varieties with good grain yield are desirable because soybean is grown after the oat crop. In oat (*Avena sativa* L.) the impact of genes for short stature has been limited due to multiple end uses for the crop (grain or forage) and because oats are often grown in low-yield environments. All reports of genetics of dwarfness in oat have described single-gene inheritance, and five of seven genes are dominant for short stature[1,3,4,5]. No previous attempts have been made to introduce dwarf genes (specially DW 6 and DW 7) into the Brazilian germplasm, and few varieties are short (less than 100 cm). High yield potential has been obtained by selection of early oat varieties[2]. The objectives of the present study were to determine the inheritance of plant height and heading date in the current germplasm avaliable in southern Brazil.

Methods

Twelve crosses were made involving genotypes in the same or different phenotypic classes for plant height and heading date (Table 1). An experiment in field conditions with parents, F_2 and F_3 generations of all twelve crosses was grown in a randomized block design with two replicates. A replicate usually consisted of four rows of each parent, 20 rows of each F_2 populations and 40 F_2-derived F_3 lines. A row was 5 m long, with seeds spaced 0.30 m apart, in row spaced 0.30 m. Heading date was obtained for each plant individually in number of days from seedling emergence to the emergence of the panicle from the leaf sheath. At maturity, plant height was measured from the soil surface to the top of the panicle on the main tiller of each plant. A genetic hypothesis of one or two major genes was tested for goodness of fit by chi-square analysis on F_2 and F_3 populations for each cross.

Results and Discussion

Standard deviations for plant height and heading date for all genotypes were very similar, indicating that the environment had a similar effect on the phenotypic expression of each genotype utilized.

Table 1. Parental characteristics observed in a field planting at Eldorado do Sul, Brazil, in 1991

Cultivar	*Heading (days)*	*Plant height (cm)*	*Phenotypic Class*
UFRGS 86A1194-2	128 + 4.0	130 ~~110~~ + 4	Late - Tall
UFRGS 881920	105 + 3.5	127 + 5	Intermediate-Tall
UFRGS 871547	104 + 3.4	93 + 4	Intermediate-Short
UFRGS 10	103 + 2.3	130 ~~120~~ + 5	Intermediate-Tall
UFRGS 7	98 + 3.2	97 + 4	Early-Short
UFRGS 884095	95 + 3.3	68 + 4	Early-Dwarf
UFRGS 8	91 + 2.3	135 ~~105~~ + 5	Early-Tall

The segregation pattern observed for plant height in the crosses studied indicate that one or two genes were responsible for the variation obtained. A gene dominant for short stature was present in UFRGS 884095 (a derivative of OT207), a single recessive gene was present in UFRGS 871547 and two recessive genes were present in UFRGS 7 (the shortest variety grown in Brazil). One or two genes determining heading date were observed in all crosses. The genotype UFRGS 8 has a single major gene for earliness, which is dominant over all others. UFRGS 7 and UFRGS 884095 carry two dominant genes for earliness, but they have a small effect relative to the gene present in UFRGS 8. The intermediate group of UFRGS 881920, UFRGS 871547 and UFRGS 10 each carry one gene with a small effect on earliness. These genes are different and can be recombined. The late genotype UFRGS 88A1194-2 is recessive for both genes. The observations can be summarized with the following genotypes proposed for the parents at the two loci for heading date and plant height respectively:

UFRGS 86A1194-2	aabb	-
UFRGS 881920	AAbb	AAbb
UFRGS 871547	AAbb	aabb
UFRGS 10	aaBB	AABB
UFRGS 7	AABB	aab1b1
UFRGS 884095	AABB	*
UFRGS 8	A*A*	AAbb

* The genotype UFRGS 884095 is a derivative of OT207 and it carries the gene DW6 which showed a single gene dominance over all others in this study. Analysis of the genotypes shows that the same phenotype can be obtained by different combinations of genes for both traits, and the variation observed can be recombined in different forms to increase the final adaptation and grain yield potential of the crop.

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A Further *Avena Macrostachya* Hybrid

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Summary

Chromosome pairing in the hybrid *Avena macrostachya* x *A.canariensis* is similar to that of the other *A.macrostachya* x diploid *Avena* hybrids, indicating that the two species are only distantly related.

Introduction

Avena macrostachya Bal. ex Coss. et Dur. is unique within the *Avena* as it is an outbreeding, perennial, autotetraploid, whilst all the other species in the genus are inbreeding annuals. In recent years, oat breeders have become interested in this species because it possess a number of attributes which would be beneficial to the cultivated oat crop if a genetic transfer could be effected. Apart from its perenniality (which could be of considerable value to the forage oat crop), it is tolerant of cold conditions[4], resistant to some isolates of barley yellow dwarf virus (A. Comeau, pers. comm. 1990) and resistant to the aphid *Rhodopalosiphum padi* (L.)[8].

The perennial habit and outbreeding nature of this oat, together with the high degree of isobrachiallity of chromosomes, and lack of variation in chromosome size, are considered to be indicative of primitive types[6]. This would suggest that *A.macrostachya* is the oldest member of the genus, and is therefore also of interest in terms of the evolution of this important crop species.

Methods

The *Avena macrostachya* accession used in this study was CAV5264 obtained from Gene Resources Canada, Ottawa, Canada, and the *A. canariensis* accession from an unidentified site in the Canary islands. In all crosses, *A. canariensis* was used as the female parent. Developing embryos were excised about twenty days after fertilization, and cultured on Gamborg's B5 medium without 2,4-D or kinetin in a dark incubator at 20°C until the shoot was about two centimetres long. The developing seedlings were then placed in natural daylight at room temperature until the second leaf emerged when the plantlet was transferred to a soil filled pot in the glasshouse. For meiotic analyses, immature panicles were taken and fixed in Carnoy's solution. Anthers at the correct stage were stained according to Snow[7] and squashed in 45% acetic acid.

Results and Discussion

Chromosome pairing in the hybrids (Table 1) was characterized by the formation of seven bivalents (mainly ring configurations) and seven univalents in 89% of pollen mother cells (PMC's). Four V shaped trivalents and two non-chiasmate pseudo trivalent associations orientated as a V and a straight chain were recorded. The maximum pairing observed was eight bivalents and five univalents, and the minimum pairing was one trivalent, four bivalents and ten univalents.

Due to the autotetraploid nature of the *A. macrostachya* parent, any hybrid between *A. macrostachya* and any of the annual species of *Avena* would be expected to have seven bivalents (mainly ring configurations) at meiotic metaphase because of the duplication of homologous chromosomes in the *A. macrostachya* gametes. Consequently, any chromosome pairing in excess of seven bivalents in triploid hybrids must be attributable

either to the pairing of homologous/homoeologous chromosomes, or to translocation differences between the species.

Table 1. Mean chromosome pairing per PMC at metaphase I in the *A. canariensis* x *A. macrostachya* hybrid.

	No. of Cells	*I*	*II (rings)*	*II (rods)*	*III*	*Mean chiasmata*
A. canariensis x *A. macrostachya*	100	7.06 (5-10)	5.90 (2-8)	1.01 (0-4)	0.04 (0-1)	12.86

* Range in parenthesis

Chromosome pairing in the *A. canariensis* x *A. macrostachya* hybrid reported here, would be expected to be similar, if not identical to that of the hybrid *A. damascena* x *A.macrostachya* [5], since despite their different morphology, and geographic isolation, *A. canariensis* and *A. damascena* in hybrid combination, have complete and regular chromosome pairing[3]. This assumption is borne out by the chromosome pairing observed in the *A. canariensis* x *A. macrostachya* hybrid reported here, which does not differ significantly from the chromosome pairing observed in the triploid hybrids between *A. macrostachya* and the A genome diploid species *A. atlantica* [1,2] or *A.prostrata* [1,2].

In the *A. canariensis* x *A. macrostachya* hybrid reported here, apart from the expected seven bivalents formed by the homologous *A. macrostachya* chromosomes, few chromosomes formed chiasmate associations. In only four PMC's were more than fourteen chromosomes paired. Three of these involved the formation of a trivalent whilst the fourth contained an extra bivalent, making eight in all. These trivalents and the extra bivalent could be formed either by the pairing of homoeologous chromosomes, or by the pairing of a translocated chromosome segment, but must involve chromosomes from the *A. canariensis* parent. As with other triploid hybrids involving *A. macrostachya*, the trivalent frequency is very low, which indicates that the translocation or homoeologous segment must be very small.

It is clear from the lack of chromosome pairing in this, and other hybrids between *A. macrostachya* and the annual species of *Avena*, that unless true chromosome homology is masked by the preferential pairing of the *A. macrostachya* chromosomes, then *A. macrostachya* must be very distantly related to the annual species of the genus.

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Differentiation among Sandy Oat (*Avena strigosa* Schreb.) Populations

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Summary

The structure of variation in 56 sandy oat populations from Europe and South America was investigated by using various morphological characters measured on plants grown in Radzików. Factor analysis was used to identify trait complexes that accounted for major proportions of the total variation among populations. Subsequently, the populations were clustered into seven distinct groups based on their similarity for factors. Each group showed a close association to specific geographic or environmental factors. These results confirm the existence of a 'geographic axis' of variation for indigenous plant material. Apart from groups previously described, South American populations clustered in an easily distinguishable group.

Introduction

Sandy oat (*Avena strigosa* Schreb.) is a crop plant which originated from Europe, and was frequently cultivated in mountainous regions in the past. The Polish Gene Bank pays special attention to collecting ecotypes and land races which still exist in Poland in small, private farms[4]. During collecting missions of indigenous germplasm we collected samples of *A. strigosa* [3]. However, we found that the present situation has changed markedly and *A. strigosa* plays no role as a cultivated plant or as a weed. The statement that *A. strigosa* is a disappearing synanthropic species in Europe influenced us to study the availability of genetic resources and variability of the species.

The objectives of this study were (a) to classify accessions of *A. strigosa* into groups on the basis of morphological traits, (b) to assess which traits were important in establishing groups, and (c) to determine the contribution of each trait to total variability among accessions.

Methods

For this study 57 accessions of *A. strigosa* were used. The *A. strigosa* accessions were evaluated in an experiment grown at the Plant Breeding and Acclimatization Institute, Radzików, Poland. During the season 38 traits were recorded. Analyses were computed by using population means for all quantitaive traits. For qualitative traits, the percentages of lines within a population that expressed certain character states were used. Factor analyses were applied using SPSS/PC procedures[7]. The axes cumulating variance higher than 85% were rotated. Cluster analyses were computed by using values of factors for populations. As a similarity measure Euclidian distance was used. Populations were clustered by Ward and UPGMA methods[1].

Results and Discussion

The factor analysis showed that the first three factors accounted for 22, 12 and 10%, respectively, of the total variation among traits in oat landraces. The Varimax rotation of 13 axes (85% of variation) showed that the first factor was highly correlated with characters describing the shape of floret: length of kernel, length of glume, length of second glume, length of lemma, length of lemma tip, and length of awn. A score for the second factor was highly correlated with the angle of flag leaf to culm, and the place of insertion of awn on the lemma. The trait significantly correlated with the third factor is the hairiness of lemma.

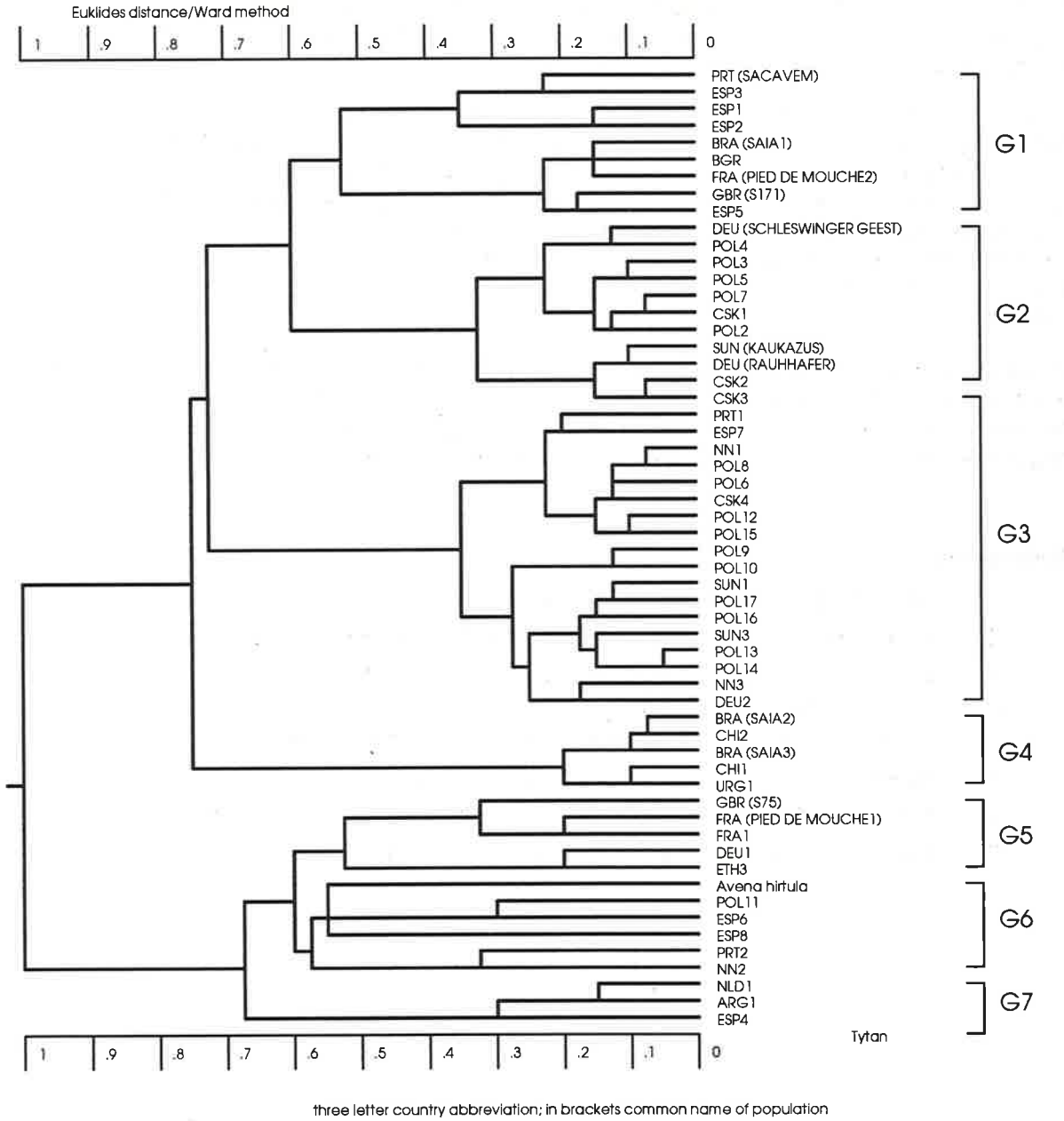

Figure 1. Dendrogram of the similarities of 56 sandy oat populations and population of *Avena hirtula*.

The dendrogram that resulted from the cluster analysis of *A. strigosa* is presented in Figure 1. The accessions were grouped in seven major clusters, at a similarity level (r-value) of 0.6.

Cluster 1 contained populations from Western Europe, exept SAIA 1. The populations in this cluster had a high thousand seed weight and the longest upper internode.

Cluster 2 had populations originated from Central and Eastern Europe. The populations were early and had wide and long leaves. These oat populations had long glumes, lemma, tips of lemma, and longest awns.

Cluster 3 also contained mainly populations from Central and Eastern Europe. These populations had a long vegetation period, and a short culm. The populations in cluster 3 differ from those in cluster 2 in the height of the plant, the number of florets per panicle, and in earliness.

Cluster 4 contained populations from South America. The cluster was easily distinguishable from others. These oat populations had a high thousand grain weight, small leaves, high insertation of awn on lemma, short awn, low number of levels and florets per panicle.

Clusters 5, 6 and 7 contained populations, originated mainly from Western Europe, which did not cluster very strongly to each other. Similar results occurred with the UPGMA method where these populations were farthest from the other groups.

These associations of clusters of similar oat populations with certain geographic regions that have dominating environmental factors support the view that 'geographic axis' of variation exist for indigenous plant materials[2]. Characters describing the shape of floret are most correlated with this axis. Cluster analysis revealed that relatedness of germplasm was stronger between Eastern European populations than those originating from Western Europe where the centre of origin of *A. strigosa* is located[5]. Our analysis indicated though they historically originated from Europe, we observe the formation of a new 'centre of variability' of the species.

In our study, representation of some regions of distributions was limited because of lack of representation of germplasm in collections. Scandinavian populations are well described in botanical literature even though they do not have any representation in gene banks. Other regions with high variability such as the British Isles[6] are represented by few accessions.

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An Ideal Combination of Morpho-Physiological Traits in Oats: Development of an Ideotype

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Summary

The present study focused on developing an ideotype for oats, *Avena sativa L.*, for optimal growing conditions in the northern agro-climatological zone. Traits characterized in the ideotype were associated with grain yield or otherwise required for yield production. Traits of hypothetical oat model that are expected to enhance yield potential include: high VGR and PGR; high phytomass; short straw length; high panicle weight resulting from high number of grains and high PFR; HI of about 55%; LAI with maximum peak value of five; and delayed aging processes of the uppermost leaves followed by rapid collapse in photosynthetic apparatus to permit the necessary early maturation.

Introduction

The main selection criteria used in Finnish breeding programs to date have been very easily measured, plant height and lodging resistance being two examples. Selection for short straw length has resulted in an improved HI[1]. However, further increases in HI are likely to be of no benefit and might be even disadvantageous or unattainable. Thus, new morpho-physiological traits, i.e., increasingly laborious selection criteria, must be characterized and utilized in the future if further improvements in yield are to be achieved.

Methods

The plant material — consisting of 19 oat cultivars and breeding lines adapted to northern growing conditions — was evaluated in field experiments at the Anttila Experimental Farm of the Hankkija Plant Breeding Institute (60°25′ N) in 1986–87 and at the Viikki Experimental Farm of the University of Helsinki (60°13′ N) in 1988–89. A total of 21 morpho-physiological characteristics of oats were measured. The monitored traits were as follows:

1) grain yield (g m^{-2}),
2) the architecture of an individual plant and the plant stand {namely, plant height (cm); lodging (%); number of panicles per m; phytomass (g $plant^{-1}$); vegetative phytomass (g $plant^{-1}$); panicle weight (g); number of grains; single grain weight (mg); and harvest index (HI, %)},
3) the canopy structure {namely, size (cm^2), dry weight (mg), and angle (°) of flag leaf; leaf area index (LAI)}, and
4) the growth cycle {days to heading and to yellow ripeness; length of grain-filling period (days); vegetative growth rate (VGR, mg $plant^{-1}$ day^{-1}), phytomass growth rate (PGR, mg day^{-1}), panicle-filling rate (PFR, mg day^{-1}), and grain-filling rate (GFR, mg day^{-1}).

More precise presentation of the methodology is in the references[8,10,11].

The significance of differences among lines in morpho-physiological traits was tested using ANOVA. Correlation between grain yield and different traits was tested by linear regression analysis.

Results and Discussion

The correlations between grain yield and morpho-physiological traits were mostly insignificant in 1987 when the growing season was cool and rainy, and in 1988 when crops were exposed to exceptionally low precipitation. In the favorable growing conditions of 1986 and 1989 several associations were significant (Table 1). The present study thus describes an oat model for favorable growing conditions in northern latitudes.

Table 1. Significant correlations between grain yield and morpho-physiological traits in 1986 and 1989. Insignificant associations are not presented.

Trait	*Correlation with grain yield*	
	1986	*1989*
Days to heading	0.27^{ns}	0.65^{**}
Days to yellow ripeness	0.62^{**}	0.88^{***}
Grain-filling period	0.58^{**}	0.73^{***}
Plant height	0.48^{*}	0.40^{ns}
Vegetative phytomass	0.30^{ns}	0.68^{***}
Vegetative growth rate	0.27^{ns}	0.66^{**}
Phytomass	0.52^{*}	0.66^{**}
Phytomass growth rate	0.39^{ns}	0.59^{**}
Panicle weight	0.69^{***}	0.58^{**}
Single grain weight	0.48^{*}	0.73^{***}

*** $P \leq 0.001$ ** $P \leq 0.01$ * $P \leq 0.05$ ns non-significant

Maturity class

In regions where the length of growth period is restricted, as in Finland, early maturation is one of the most important characteristics of an ideotype. Therefore, future improvements in yielding ability cannot be obtained by introducing cultivars with a longer growth period, although days to yellow ripeness correlated positively with grain yield (Table 1). However, one possibility for improving productivity without prolonging the growth cycle from sowing to ripeness is to alter the relative length of the pre- and post-anthesis phases. Lengthening of the post-anthesis phase at the expense of pre-anthesis phase is particular interest. However, shortening of pre-anthesis phase may result in cultivars with decreased number of florets per panicle. A recent study of this question (Peltonen-Sainio and Peltonen, unpublished data) showed that an oat cultivar with shorter pre-anthesis phase produced a lower number of florets but a higher number of grains per panicle than did cultivar with a longer pre-anthesis phase. Therefore, modification of pre- and post-anthesis phases does not necessarily reduce grain yield.

Architecture and function of the canopy

Efficient interception of solar radiation results from compatible leaf characteristics, which change in synchrony according to the requirements of the economic sinks. In spring cereals the optimum peak value of LAI — an indicator of absorption of photosynthetically active radiation (PAR) — varies between four and six. In the present study the LAI of one oat cultivar examined was close to eight due to the abundant production of sterile secondary tillers. The average LAI of the lines was about five and the cultivar characterized by extremely high LAI had the lowest grain yield. Therefore, a LAI of about five is likely to be optimal in northern latitudes, too.

The present study showed that the LAI of oats decreased steeply from its peak value near the beginning of the grain-filling period[7]. Cultivars with even moderately larger green area produced higher grain yields. These findings suggest that delayed aging processes associated with rapid collapse in photosynthetic apparatus would be especially promising in Finnish growing conditions[10].

Characteristics of the flag leaf are also of special interest. In this study the size of flag leaf did not correlate with grain yield, although this trait has been increased by 20% by domestic plant breeding[8]. Possibly, the larger area is associated with reduced CER per unit area[10]. Moreover, the angle of the flag leaf[7] would seem to have only limited importance in northern latitudes.

Other characteristics of an ideotype

In the future, more attention should be placed on the production of cultivars with both high vegetative potential and high panicle weight (Table 1), so as to maintain HI close to the present level of about 55%. High phytomass should result not from lodging-sensitive long straw but from short straw with a high stem diameter associated with an increased area of vascular tissue[3]. Further shortening of straw is no longer as essential as it once was, and may result in cultivars with a shallow root system[5] and consequent sensitivity to drought. Furthermore, in northern growing conditions, production of high phytomass should not result from a high number of sterile secondary tiller; rather, the oat stand should consist solely of abundant uniculms[7,9].

Increased panicle weight should result from a higher number of grains rather than increased single grain weight. Grain number correlates more strongly with panicle weight and is less laborious to manipulate[9]. Moreover, Lawes[4] has shown that 1 000-grain weight is one of the most stable yield components.

Due to the restricted length of the growth period in Finland, production of high vegetative phytomass requires improved VGR and PFR. The author[10] and Frey with his co-workers[2,12] showed that enhanced VGR contributed to improved grain yield (Table 1).

Phenotypic stability

Ideotype breeding carried out in favorable environments, as recommended here, may result in cultivars with poor stability over adverse environments. However, the evaluation of present oat material[11] with several stability analyses showed that by screening for the stability parameters high yielding lines with relatively stable yield performance can be identified.

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Correlation Regression Analysis of Winter Oats Yield and Some Components

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Summary

An agrobiological investigation on the productivity (Y), winter hardiness (X_1), days to heading (X_2), days to maturity (X_3) stem height (X_4), lodging (X_5), resistance to *Puccinia graminis* f.sp. *avenae* (X_6), panicle weight (X_7), panicle length (X_8), 1000 grains mass (X_9), husk percentage (X_{10}) and raw protein content in the grain (X_{11}) has been conducted on 128 varieties selected from the winter oats collection. The correlation between characters was used to construct appropriate selection indices which were then used to choose the best parents for a yield improvement program. The correlation/regression analyses show that the determining factors for the yield in winter oats are: winter hardiness, length of the vegetative period, stem height, lodging resistance, panicle length, 1000 grains mass and protein content in the grain.

Introduction

Winter oats generally have great advantages over spring oats in Bulgaria. Unfortunately they are not widely grown despite the weight of experimental evidence. The purpose of this investigation was to perform a complete agrobiological study of the winter oats collection, to measure the correlation/regression coefficients between pairs of traits and to determine their usefulness in a breeding program.

Methods

The investigation commenced in 1987. Twelve characters were measured for each variety using the descriptors published by IBPGR[2,4]. Student's "t" test was used to test correlation coefficients for significance. The calculations were made using a standard statistical package on an IBM AT computer[1,3]. The following abbreviations are used in the paper: Y = grain yield (kg/dka), X_1 = winter hardiness (%), X_2 = days from January 1 until heading, X_3 = days from January 1 until ripening, X_4 = stem height (cm), X_5 = lodging (%), X_6 = *Puccinia graminis* f.sp. *avenae* resistance (%), X_7 = panicle weight (g), X_8 = panicle length (cm), X_9 = 1000 grains mass (g), X_{10} = husks (%), X_{11} = crude protein content by Kjeldal (%). Winter or spring habit was determined by serial sowing dates: 1st - autumn sowing (30 October), 2nd - early spring sowing (1 February), 3rd - spring sowing (1 March) and 4th - late spring sowing (1 April). Varieties were also grouped according to their origin. American varieties formed the biggest group of 47 varieties, followed by 21 Italian, 10 English, 5 French and 12 Bulgarian which included 10 breeding lines. Single varieties originated from Sweden, The Netherlands, Germany, Czechoslovakia, Romania, Yugoslavia etc.

Results and Discussion

With a view to determining the contribution of individual characters to the total grain yield, we compared the correlation coefficients between pairs of characters. Response to selection in these characters can be predicted from Table 1. Yield depended mainly on 6 characters - X_1, X_2, X_3, X_4, X_5 and X_{11}. Winter hardiness (X_1) is strongly correlated with days to heading (X_2) and days to maturity (X_3) and 1000 grain mass (X_9) and is strongly dependent on X_4, X_5 and X_{11}. Panicle weight and 1000 grain mass (important selection characters) are strongly correlated with the length of the vegetative period and stem height.

Table 1. Correlation coefficients between grain yield and ten other traits for 128 oat varieties

	Y	X_1	X_2	X_3	X_4	X_5
X_1	.64053**					
X_2	−.21873**	−.22681*				
X_3	−.23567**	−.19407*	.64163**			
X_4	−.44601**	−.36114**	.28366**	.30057**		
X_5	−.61572**	−.38409**	−.03648	.15572*	.38986**	
X_6	−.12432	−.12864	.15826*	.14172*	.10751	.13026
	X_6	X_7	X_8	X_9	X_{10}	X_{11}
Y	−.12432	−.10817	−.00902	−.02087	−.06604	−.33768**
X_1	−.12864	−.08196	−.04294	−.14176*	−.10573	−.28532**
X_2	.15826	.52365**	−.06318	−.50320**	−.03163	−.03554
X_3	.14172	.42475**	.05807	−.29540**	.06823	−.09927
X_4	.10751	.28804**	.16665*	−.07579	−.01679	.06288
X_5		.13822	.05181	.20649*	.07025	.27102**
X_6		.12913	.02277	−.05688	.05719	−.14184*
X_7			−.01185	−.24482**	.04854	−.08444
X_8				.07876	−.00921	.05079
X_9					−.04326	.17126*
X_{10}						.11302

* P (=0.05) = 0.1393; ** P (=0.01) = 0.2271

Future objectives of a breeding program will be to overcome the deleterious correlations. The data obtained for grain yield gives us reason to be optimistic. The highest relative yield of 131% was obtained from the American varieties, lines 83106026 and 83106028 which also had an average height of about 100 cm. Almost all varieties with a height over 120 cm had a yield equal to or below the mean. The data also suggest that breeders have made a change in the architecture of the oat plant. The decrease in plant height has also led to a decrease in lodging. We believe the correlation of lodging with 1000 grain mass and protein content will be a serious problem to breeders. The strong correlation between traits is probably related to the large differences in plant type found in oats.

The selected varieties were divided into three groups on the basis of growth habit: 1. spring type (55 varieties) 2. semi-spring type (54 varieties) 3. winter and semi-winter types. Group 3 consisted of S-172, Kyu-78-448. Lustre, Elan, Maris Quest, Prieure, Joker, Peniarth and 11 lines from Italy. The yield of Groups 1 and 2 was strongly effected by the factors:X_1, X_3, X_5, X_8 and X_{11}. In Group 3 the relationship between yield and the time factors X_1, X_2, and X_3 is statistically nonsignificant. This may be due to the natural winter hardiness in the latter part of the vegetative period found in the varieties from this group. The most frequently occurring correlations between characters for the first, second and third groups are: X_4, X_5, X_8 and X_{11} have a strong effect on X_1, X_3, X_4, X_7 and X_9 have a strong effect on X_2, X_4, X_5 and X_9 have a strong effect on X_3, X_5, X_7 and X_{11} have a strong effect on X_4, X_8, X_9 and X_{11} have a strong effect on X_5. X_{10} and X_{11} have a strong effect on X_6. X_9 strongly effects X_7, and X_{11} effects X_9. The optimal regression equations were found after consecutive elimination of the insignificant correlation coefficients. Linear regressions of the type $y = a_o + a_i x_i$ were formed. Grain yield for the whole group of 128 varieties tested is determined by X_1, X_5 and X_9. However in group 1 alone grain yield is determined by X_1 and X_3.

In group two grain yield is determined by X_1, X_5, X_8 and X_{11}. In group three only X_8 occurs in the equation. However the contribution of other factors in this equation is not ignored because the determining factor (X_8) is strongly negative in relation to X_1 ($r = 0.59^{**}$) and positive in relation to X_4 ($r= 0.47^{*}$) and X_5 ($r = 0.57^{*}$) within this group.

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Dormoat — A Possible Role in Sustainable Agriculture

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Summary

Dormancy genes from wild oat, *Avena fatua* L., have been successfully incorporated into high performance, non shattering cultivars of covered and naked seeded dormoats. They were bred to raise oat yield levels in Canada by virtue of their early spring germination which encourages extensive root growth, extensive tillering, differentiation of large panicles with many florets, disease and insect escape characteristics and lodging resistance. Because of an inability to control and synchronize germination behaviour to grow dormoat as an annual crop, a different management system based on growing it continually on the same site for up to five years was devised. The system is successful and meets the specifications required of a sustainable agriculture system.

Introduction

Dormoat[(1)] is an experimental crop bred at the Plant Research Centre (PRC), Agriculture Canada, from hybrids between *Avena fatua* L., and commercially grown cultivars of the spring oat, *Avena sativa* L. Dormoat strains combine all or a portion of the seed dormancy traits of wild oat with the desirable agronomic qualities of commercial oat cultivars and the seeds do not shatter like wild oats. Tall, semi-dwarf, dwarf, high protein, high fat, naked and covered seeded, daylength sensitive and insensitive, disease resistant or susceptible, dormoat strains have been bred and are stored in PRC collections. Originally it was intended to breed a crop whose dormant seeds could be sown in autumn. They would remain dormant during autumn and winter but would germinate in springtime and take advantage of cool temperatures and abundant moisture to develop a high yield potential. Unfortunately, in spite of devoting much effort to the project in which literally hundreds of quite different hybrids were made, the project stalled because we were unable to isolate selections whose germination behaviour matched the idealized dormoat. When selections were made for high dormancy in autumn, emergence in springtime was too low (5-10%) and the crop showed a weedy characteristic in subsequent years. When strains were selected for good emergence in springtime, too many seeds (40-50%) germinated in autumn. No strains were found that failed to germinate in autumn but germinated highly in springtime. It was clear that a breeding and selection approach was not going to produce the desired result.

From laboratory studies it was found that for a dormoat seed to emerge in springtime, the freshly harvested seed had to first after-ripen to remove primary dormancy. However, during that process the seed had to be induced into a state of secondary dormancy to prevent it from germinating in autumn and to make it eligible to germinate in springtime. These processes normally take place in soil in the field over a period of weeks or years but attempts to "manage" or "synchronize" the seed immediately after harvest by employing different treatments before autumn planting, often improved spring emergence values but no practical efficient protocol has yet been discovered to give the desired result.

Discussion

Recent initiatives to develop production systems that conform to the principles of sustainable agriculture have opened up new possibilities for the dormoat. These principles have forced a re-examination of management strategies to satisfy the criteria of sustainable agriculture (i.e. practices that will reduce petroleum and chemical use; prevent soil erosion and compaction; improve soil tilth, structure and organic matter; combat weeds; escape diseases; lower costs of production; maintain or improve grain quality while

maintaining the traditional uses of oat for pasture, forage and grain). Instead of viewing the dormoat as an improved oat, I now view it as an improved wild oat. My inability to synchronize germination may now become an advantage.

Instead of following the cropping pattern of the common oat which involves utilizing a piece of land for one year and then changing the following year to another crop in the rotation, the objective now is to grow the dormoat continually on one site for five or more years. The oat is an annual but the site is being managed as if it was a perennial. Each year a grain crop is harvested and a portion of the harvested seed is returned to the soil during harvesting to maintain the reservoir of dormoat seed in the soil. When the producer wants to change the rotation, the crop is cut for green feed to reduce the soil seed reservoir. The site is either sown to a forage legume or perennial grass where volunteer oats are cut for forage and fed to livestock or a different crop is grown and sprayed with a herbicide to destroy the oat along with weeds.

Culture of dormoat

The land chosen for dormoat culture should be land that the producer would prefer to "leave in oat" for five or more years. This land would most often be marginal, poorly drained, arid, rocky or sloping land where erosion is a problem.

To begin converting the land site to dormoat culture, it is easier to purchase and sow non-dormant seed in springtime. Non-dormant seed is easily obtained by storing harvested seed in a dry state in a granary for approximately one year. The crop is grown using the same techniques used to grow commercial spring-type oat. At harvest time, a portion of the harvested grain is returned to the surface of the soil. This can be normal combine losses and/or harvested seed. A means must be found to distribute the seed evenly from the combine. If the crop is cut for silage, regularly spaced strips of oats can be left in the field until the seed matures when they can be harvested and the straw and grain spread evenly over all the land. If manure is added, it should be spread at this time and the manure, seed, straw residue plus weeds incorporated into the soil with one tillage operation. Spreading the seed on the surface is analogous to the seed dispersal mechanism of the wild oat. Dormoat seed does not need to be treated with fungicides because they, like the wild oat, have been selected to withstand fungal attack in soil for many years.

Autumn seeding rates must be higher than normal rates of sowing spring oats because the number of seedlings emerging in springtime in only a fraction of the seeds sown. Enough seed must be sown in autumn to both suppress the establishment of winter annual and perennial weeds in autumn as well as give good oat stands in springtime to provide competition with annual weeds. It is probably more economical and more beneficial to the environment to invest in the cost of seed then to invest in herbicides.

The fate of autumn sown dormant seed can be divided into four categories. Some seeds lose their dormancy quickly and emerge in autumn. The plants provide fall pasture, prevent soil erosion, and trap snow to raise soil moisture reserves. A second fraction germinates in springtime and produces a crop. Any smut spores, *Ustilago avenae* Pers. Rostr., on the seeds in soil will be destroyed by winter. Seedlings emerging in springtime are usually late enough to escape spring frosts but early enough to give the plants a head start to escape severe infection from crown rust, *Puccinia coronata* Cda. f. sp. *avenae* Erikss. and Henn., and stem rust *Puccinia graminis* Pers. f. sp. *avenae* Erikss., although in some years the plants become infected late in the growth cycle. The early start also reduces barley yellow dwarf virus infections because aphids are usually not present. Lodging is reduced because the lower internodes are short and thickened due to the cool growing temperatures. Root systems are favoured and yield potentials rise because the cool moist conditions favour the differentiation of large panicles with many florets.

Yield increases of between 10–24% have been realized by sowing dormant seed in autumn compared to sowing non-dormant seed of the same strains in springtime. Yield increases could even be greater in years where spring seeding of standard commercial oats is delayed by persistent and frequent spring rains. The yield potential will naturally drop as fertility levels in soil drop with each succeeding year of cropping. Fertilizer, especially nitrogen, must be added each year as a top dressing. Dormoat should also prove beneficial in more arid regions because the land does not have to be worked in springtime

to produce a seed bed thus reducing soil moisture losses. Working the land in springtime for existing commercial spring oats is not only costly in terms of fossil fuels and operator time but it reduces yield potential because of the time delay and tillage encourages weed growth. Every time land is worked, soil structure is damaged and weed growth is encouraged.

The third portion of seed remains dormant throughout the next year because it has not been conditioned to germinate. It will either come up the next autumn or the following spring or it will remain dormant and respond the third year. This is the weediness factor associated with dormoat. However, it is a harvestable plant quite unlike the wild oat.

The fourth portion of seed dies. The seeds may begin to germinate but are destroyed by frost or eaten by soil organisms.

The seeding protocol is again repeated in years two, three, four and five unless it is decided to terminate the rotation. In year five or six the fields can be sown to legumes or grasses or used to grow other crops providing the herbicides that are used will control dormoats. No herbicide is required if the land is being used to produce hay or clover because volunteer oat will just add to the forage dry matter production.

The dormoat thus represents an interesting experimental crop to try to meet the criteria required for sustainable agriculture in Canada and parts of the northern USA. In fact, if it is successful, it is possible to project that some Canadian and USA producers could produce all the oat required in a very economic manner from marginal soils with a minimum of chemical inputs and tillage costs.

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Fructan and its Possible Effect on the Freezing Tolerance of Oat

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Summary

On a fresh weight basis more than half of 273 oat accessions had total fructan levels not significantly (P<0.05) different from Dicktoo barley, however, all but one accession had significantly (P<0.05) less high degree of polymerization (dp) fructan (dp>4) than Dicktoo. Using the percentages of 5 carbohydrates the accessions were grouped into 8 clusters. One of the 5 species analyzed was alone in a cluster; the remaining species were spread across several clusters. Of all the carbohydrates measured mg total sugar (Sucrose+glucose+ fructose) per g fresh wt. was most closely correlated to freezing tolerance.

Introduction

Most winter cereals such as wheat, barley and rye accumulate large amounts of a fructose polymer called fructan in vegetative tissues during cold hardening when photosynthetic input exceeds utilization. Winter oat, under the same conditions, accumulated one third as much high degree of polymerization (dp) fructan as wheat, barley and rye but almost twice as much dp3-6 fructan[4].

The purpose of this study was to investigate the genetic variability of fructan accumulation in oat and to see if any measured carbohydrate was related to freezing tolerance in controlled freezing tests.

Methods

Plant material/growing conditions

Two hundred and seventy three germplasm lines and cultivars from US spring and winter oat breeding programs and the National Small Grains Collection were tested. Plants were grown for 5 weeks at 15°C and hardened for 3 weeks at 2°C under controlled conditions in plastic tubes as described elsewhere[4].

Carbohydrate extraction

Approximately 1 cm of the stem was cut, weighed and then ground in a stainless steel grinder[3]. Water soluble material was extracted from the ground tissue 3 times with water and an aliquot of each sample was filtered through a 0.45 µm filter in preparation for HPLC analysis.

Chromatography

Carbohydrates were separated by HPLC, detected by a refractive index detector, identified by co-chromatography with external standards and quantified by comparison of unknown peak areas to peak area response curves of standards.

Statistical analysis

The experimental design was a randomized complete block with 2 replications over time. Because of the large number of accessions the experiment was separated into 4 sets which were grown and analyzed at different times.

Cluster analysis was used as a means of grouping the accessions based on their percentages of five types of carbohydrates: dp>4, dp4, dp3, sucrose, and monosaccharides (glucose+fructose). Clustering was done using the centroid method with squared Euclidean distance as the measure of closeness[6].

Freeze test

Twenty three accessions were selected from the original 273 to represent a range of carbohydrates. Six plants in each of 2 replications were used for freeze testing and 6 were used for carbohydrate analyses. After hardening, roots and shoots were trimmed and plantlets were placed in damp sponges and prefrozen for 48h at -3°C. After the -3°C prefreeze one set of 6 plants was removed for carbohydrate analysis as described above. The remaining 6 plants of each accession were taken to -11°C at a rate of 1°C/h. They were kept at -11°C for 2h and then thawed at 4°C/h. After thawing, roots were completely trimmed and plantlets were transplanted into a soil mix and allowed to regrow for at 15°C in a growth chamber. After 3 weeks, plants were visually rated on the basis of shoot and root regrowth on a scale of 0 (dead) to 5 (undamaged). The average survival of 6 plants was considered one replicate.

Results and Discussion

No significant difference was found among oat accessions in set 1 or 2 (data not shown) for mg total fructan nor in set 1 for mg dp>4 fructan presumably because the accessions included in sets 1 and 2 contain less genetic variability for fructan accumulation.

Sixty-seven percent of the accessions in set 3 and 54% in set 4 (data not shown)had total fructan levels not significantly different from Dicktoo barley. In fact, several accessions in set 3 had more total fructan than an average of 2 Dicktoo barley values (a nonsignificant difference). This suggests that the photosynthetic capacity necessary for initial fructan production is present in more than half of the accessions analyzed.

Using carbohydrate percentages, accessions were separated into eight clusters in each set (Figure 1. — numbers in parentheses along the X axis are the number of members in the corresponding clusters).

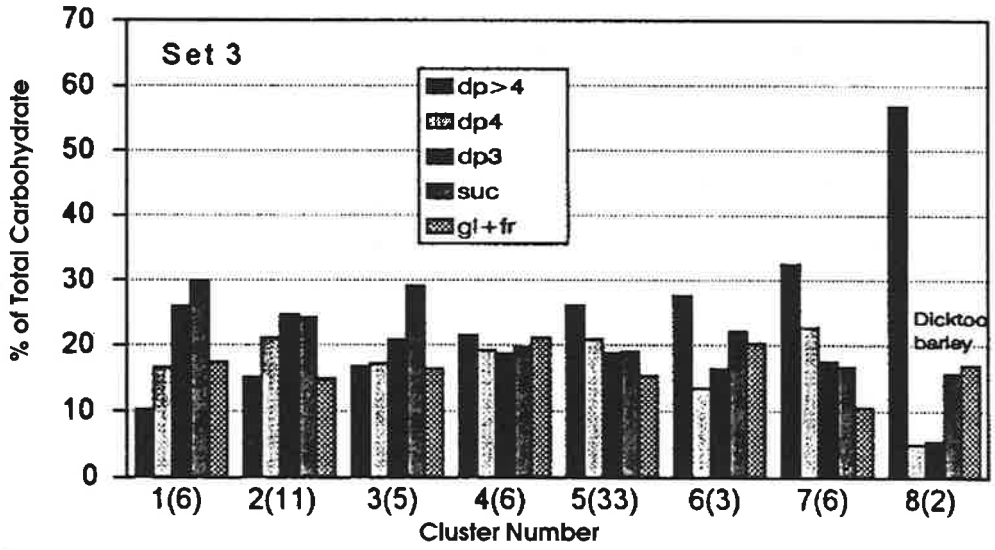

Figure 1. Cluster means for one set of 273 oat accessions.

Of the 5 variables used in the clustering procedure, % dp>4 fructan appeared to have the greatest effect on cluster formation, probably due to the greater range of % dp>4 fructan as compared to the other carbohydrates.

As expected, Dicktoo barley was the only accession in both sets in a cluster with the highest mean % dp>4 fructan and the lowest mean % dp3, dp4 and sucrose (Figure 1. (Results are presented from set 3 only)).

Set 3 contained oats from 5 *Avena* species. With the exception of *A. abyssinica* and *A. fatua*, considerable variation in carbohydrate composition was observed within species. The 7 *A. abyssinica* accessions tested were in clusters 1 and 3 which had relatively low % fructan and comparatively high % sucrose (Figure 1). The 5 *A. fatua* accessions were all in cluster 5 (Figure 1).

Under conditions used here fructan dp>6 had the lowest correlation with survival rating (r=0.287) of all the carbohydrates measured. In fact, spring habit cultivars in general had more fructan dp>6 than those of winter habit (our unpublished data) and yet they had very low survival ratings (Figure 2 — Don was the most freezing tolerant of the spring accessions tested). If sugar used in cryoprotection is a product of fructan hydrolysis[5,7] and accessions differ in their conversion of fructan to sugar during a –3°C prefreeze then the low correlation with survival rating ***after*** the prefreeze is not unexpected. Since spring cultivars had low levels of sugars after the prefreeze (Figure 2 — each point is the mean of 2 replicates) it is possible that enzymes hydrolyzing fructan during the prefreeze are not as active in spring cultivars as in winter cultivars. Under conditions used here the highest correlation (r=0.939) of any carbohydrate or combination thereof with freezing tolerance was total sugars (glucose + fructose + sucrose). This agrees with much of the research on carbohydrates and their relationship to freezing tolerance in plants[1]. The regression line of sugar verses freeze-test rating intercepted the X axis at approximately 15 mg/g fresh weight (Figure 2).

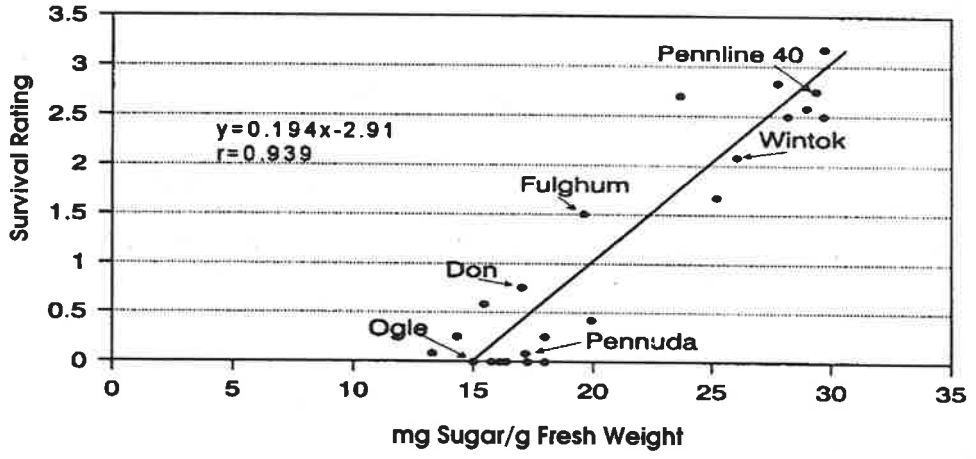

Figure 2. The relationship of sugars to survival rating in 23 oat accessions.

It is possible that this represents a minimum concentration of sugar necessary before cryoprotection by sugars can occur. This was very close to the amount of sugar at the convergence point of three barley cultivars which was also suggested as a minimum carbohydrate level necessary before cryoprotection begins[2].

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Sowing Rate and Competition Effects on Tall and Dwarf Oats

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Summary

In an experiment in the south east of South Australia the dwarf oat Echidna and its tall parent West were grown at a range of sowing rates with and without competition using wheat to simulate a grassy weed. Echidna outyielded West by 1.23t/ha without competition and 0.62t/ha with competition. Both cultivars had a similar effect on wheat heads/m^2 and grain yield. At the optimum sowing rate for oats the wheat yielded about 1.1 t/ha. Without competition both oat cultivars produced the same biological yield (11.47 t/ha) but harvest index for Echidna was 0.52 and for West was 0.39. Without competition the optimum sowing rate (where increase of 1 kg of grain increased yield by 10 kg/ha) was 272 grains/m^2 for Echidna and 198 grains/m^2 for West.

Introduction

Dwarf oats in North America, while more tolerant to lodging than conventional oats, have rarely outyielded conventional cultivars[3,4,5]. In Australia the cultivar Echidna was released in 1984[2] and is a cross between West and OT 207 which carries the Dw6 dwarf gene[3]. Echidna has outyielded conventional cultivars[1,2] and exhibits the maximum yield advantage when sown early[1]. While dwarf oats have sometimes responded to increased sowing rates[3], it was unknown how Echidna would be affected. Also it was unknown how Echidna would compete with grass weeds. Therefore an experiment was established to compare Echidna with its conventional parent West when grown at a range of sowing rates with and without competition from grassy weeds.

Materials and Methods

An experiment was sown on 13 June 1986 near Naracoorte in the south east of South Australia. Trial design was a split-split plot with the cultivars West and Echidna as main plots, sowing rates as sub plots and presence or absence of wheat as sub-sub plots. Plot size was 10 m long by 10 rows at 18 cm row spacing and four replicates were used. Wheat (cv. Aroona) was used to simulate a grass weed and was sown at 75 seeds/m^2. Oat sowing rates (Table 2) were adjusted for grain weight and germination. Fertilizer (ON:8.6P:OK) at 150 kg/ha was applied at sowing while all weeds were controlled by Glean® (chlorsulfuron 750 g/kg) at 25 g/ha. At heading Bayleton® (triadimefon 125 g/L) was applied at 1 L/ha to control stripe rust in the wheat. Prior to harvest, quadrats (1 m x 4 rows) were taken from each plot to determine yield components. Plots were machine harvested and grain yields were determined.

Results and Discussion

The effect of sowing rate and competition on grain yield of Echidna and West oats is shown in Figure 1. While the cultivar by rate interaction was not significant ($P>0.05$) there was a signfficant interaction between cultivar and competition ($P<0.001$) with Echidna outyielding West by 28% with no competition and 19% with wheat competition (Table 1). Most of the difference between Echidna and West was accounted for by grains/m^2 where Echidna produced 32% and 26% more grains/m^2 than West without and with competition respectively. The main effects of competition were to reduce oat panicles/m^2 by 20% and grains/panicle by 10%.

Increased oat sowing rate decreased the number of wheat heads/m2 from 227 to 78 (P<0.001 LSD(0.05)= 36.3) and wheat yield from 2.60 to 0.62 t/ha (P<0.001 LSD(0.05)= 0.048) (Figure 1). Neither oat cultivar nor cultivar x sowing rate interaction was significant (P>0.05) indicating that both oat cultivars competed with the wheat to the same extent. At the oat sowing rate that gave maximum oat yields, wheat yield was approximately 1.1 t/ha. Dwarf oats have also been grown in South Australia with vetch (*Vicia sativa* L.) as a hay crop. The straw strength and canopy structure of the dwarf oat has produced high yields of oat/legume hay.

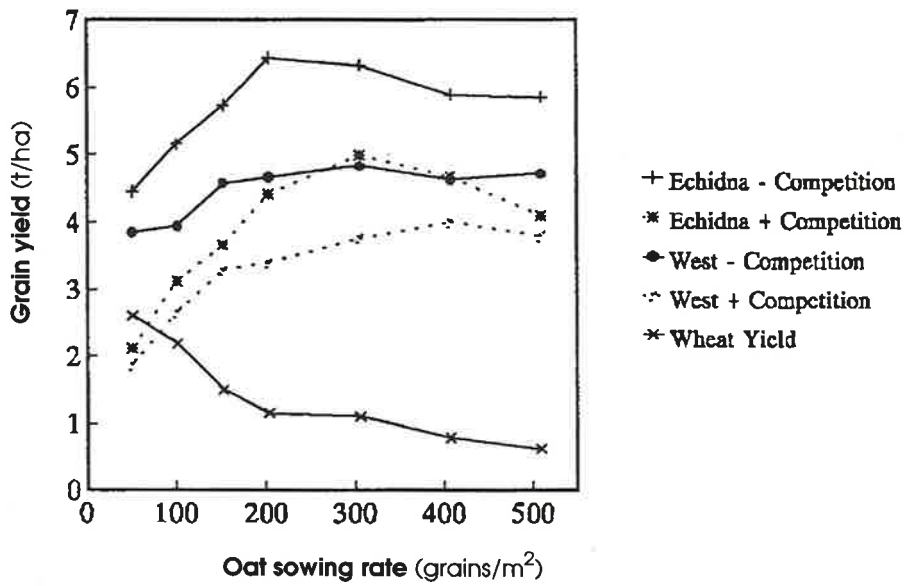

Figure 1. Effect of sowing rate and competition on grain yield of Echidna and West oats and the effect of oat sowing rate on grain yield of wheat

Table 1. Mean grain yield and grains/m^2 of Echidna and West oats with and without wheat competition (means of all sowing rates).

Cultivar	*Grain yield (t/ha)*		*Grain number (/m^2)*	
	Echidna	*West*	*Echidna*	*West*
Control	5.694	4.459	12210	9274
Competition	3.869	3.252	8321	6623
Significance	P<0.001		P<0.05	
LSD(0.05) within columns	.144		676	
between columns	1.754		3174	

As most oat crops in the south east of South Australia are grown with good weed control the effect of sowing rate on Echidna and West oats is shown for the non-competition treatments only. Increased sowing rate from 51 to 510 grains/m^2 increased the number of oat panicles/m^2 from 216 to 408 (P<0.001 LSD(0.05)= 43), decreased the number of grains/panicle from 45.2 to 25.4 (P<0.001 LSD(0.05)= 4.8) but had no effect on grain weight (P>0.05). At low sowing rates the biological yield of West was greater than Echidna (Table 2), however, the maximum biological yield achieved by both cultivars was the same (mean of 11.47 t/ha). Echidna oats produced more grains per panicle than West (37.9 compared to 32.8 (P<0.05 LSD(0.05)= 4.2)) and more grains/m^2 (Table 1) to produce a greater harvest index than West (0.52 compared to 0.39 (P<0.001 LSD(0.05)= 0.01)).

Table 2. Biological yield of Echidna and West oats as affected by sowing rate without competition with wheat.

Sowing rate (grains/m$^{2)}$	*Biological yield (t/ha)* 51	102	153	204	306	408	510
Echidna	7.693	8.418	11.140	11.320	11.560	11.370	10.650
West	10.690	9.675	10.840	11.020	10.550	11.380	10.920

Significance P<0.05, LSD(0.05) within rows = 0.163, between rows = 0.220

The optimum sowing rate was taken as the point on the quadratic regression fitted to yield/sowing rate data where grain yield increase for each extra kg of grain was 10 kg/ha[1]. These optimum sowing rates were 272 and 198 grains/m^2 for Echidna and West without competition and 304 and 292 grains/m^2 with competition. The optimum rates without competition are very similar to those determined in Western Australia which were calculated to be 296 and 210 grains/m^2 for Echidna and West[1].

The practical implication of this experiment is that dwarf genotypes such as Echidna can produce greater grain yields than conventional tall oats in southern Australia. However, to do this the dwarf oats have to be sown at higher sowing rates than conventional oats and weeds must be controlled to allow the full yield potential of the dwarf cultivar to be exploited. The biological yield of dwarf oats like Echidna is no lower than conventional oats with the grain yield increase being accomplished by increasing the harvest index. Whether harvest index can be increased further above the 0.52 reported here has been questioned[6]. Implications for further crop improvement are that yield increases are likely to be achieved by yield protection strategies such as disease resistance and by increasing the biological yield of dwarf genotypes rather than increases in harvest index.

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Response of Czech Oat Varieties to Heavy Metals and Dry Matter production

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Abstract

Productivity in oat varieties ranged from 6.0 to 6.5 t ha^{-1} in official trials in Czechoslovakia. The Zlatk, Ardo, Auron (CS) and Flämingsnova (D) varieties were tested in pot experiments with sludge municipal waste water. Varietal response to increased levels of nutrients, in particular N and heavy metals (Cd, Zn, and Cu), was evaluated at four growth stages (DC 31, 49, 81, 91). The average increase in plant biomass weight in contaminated variants was 50%, and plant biomass dry matter was 62%. Varietal response in biomass production was different at particular growth stages. The highest increase was found in the Zlatk and Ardo varieties. The course of heavy metal uptake by plants was different. The lowest Cd content at growth stage DC 91 in dry matter was determined in the Zlatk var., and in grain in Flämingsnova. The lowest Cu content in both plant and dry matter was determined in the Ardo variety. Zlatk showed the lowest values of Zn content in grain. The correlation analysis revealed close relationships between Cd-Zn and Cu-Zn uptakes into plant biomass and dependence of Cd and Zn translocations into grains on their uptake by plants.

Phenology of Rust-Resistant Forage Oats in Sub-Tropical Australia

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Summary

Rusts, especially crown (leaf) rust, are major constraints to oat production in the sub-tropical north-eastern cropping area of Australia. Rust resistant cultivars have recently been introduced and the phenology of these has been studied. When sown before April, cultivars differentiated clearly into groups on the time to appearance of the first node. This became increasingly less obvious with later sowings. Similarly substantial differences of more than 20 days for the period sowing to heading were recorded from only the pre-April sowings. Limited phenological data suggested that all varieties had a noticeable response to photoperiod and this response extended well beyond the appearance of the first node. The time to first node appearance was variable and correlated with the time from planting to heading. These factors have important implications for the optimal grazing use of the different cultivars.

Introduction

About 300 000 ha of oats are sown annually in Queensland, almost entirely for forage. The crop is planted during autumn-early winter to provide grazing in winter-early spring, a time when native grasses are dormant. Rusts, especially crown (leaf) rust (caused by *Puccinia coronata* Corda) frequently devastate oat crops with serious consequences to the grazing industry. Crown rust is a major limitation to reliable oats production and has had the effect of restricting the amount planted.

In recent years, a major effort has resulted in cultivars resistant to crown rust being selected from lines introduced from North America. These cultivars are or soon will be available to growers but little information is available on their phenology in the sub-tropical environment of Queensland. This paper reports two experiments undertaken to provide such information.

Methods

Experiment 1

Nine oat cultivars recently released or about to be released (Table 1), plus four current commercial cultivars were examined. The cultivars Minhafer and Algerian were included as reference examples of 'quick' (Minhafer) and 'slow' (Algerian) developing commercial oats. Two-metre rows of each cultivar were sown at Toowoomba at 3 weekly intervals from February to August, 1991. Records of the time to first node (decimal growth stage 31) and 'heading' (50% inflorescence emerged, g.s. 55) on the main stem were recorded for each cultivar. Time to first node was taken as a measure of the latest time to initial grazing.

Table 1. Rust-resistant oats for sub-tropical Australia.

Cultivar	*Origin*	*Released by*	*Available*
Amby	Texas	Queensland DPI	1991
Cleanleaf	N. Dakota	Pacific Seeds	1992
Cluan	Quebec	Tasmanian DA	1990
Culgoa	Texas	Queensland DPI	1991
Nobby	Texas	Queensland DPI	1994
Pan 5	Minnesota	Panorama Seeds	1988
Quamby	Quebec	Tasmanian DA	1990
Riel	Manitoba	Queensland DPI	1993
Talgai	Texas	Queensland DPI	1994

Experiment 2

The same varieties were grown in the field at 2 plantings (5 March and 2 June) with and without a photoperiod extension to 18 hours using incandescent lights strung 25 cm above the crop.

Results and Discussion

In Experiment 1, cultivars, planted during February to May, differed substantially in time to appearance of first node and were separable into two groups, the quicker Minhafer types and the slower Algerian types (Fig 1a, b). Both day length and temperature were declining during the February-May period.

Cultivars also differed substantially in time to heading from February-early March plantings, but the differences declined by the late March planting (Figs 1c, d). The Canadian-derived cultivars Cluan and Quamby tended to be slower to head irrespective of planting date. Similarly, the Texas line Talgai tended to be quicker to heading than other cultivars, especially from early plantings.

In Experiment 2, all cultivars tested had a significant response to photoperiod which extended well into the elongation phase. There was some evidence of a slight non-obligatory vernalisation response in cultivars, Algerian, Quamby, Cluan and Culgoa and possibly in cultivar Nobby. Further work is required to establish this response and particularly its effect, if any, on growth habit (prostrate versus erect).

The period from planting to first node provides a measure of the latest grazing event which will allow subsequent regrowth of the grazed tiller. The period from planting to heading is an indication of how late in a season a variety could be expected to produce useful forage. Both measures show extreme interactions between cultivar and planting time with the greatest differentiation exhibited from early plantings.

There is a role for both slow and quick developing oats in Queensland. Varieties of each group have different applications and management requirements. Detailed information on rate of growth and the influence of photoperiod and vernalisation on newly released cultivars will allow better grazing management and maximise forage production.

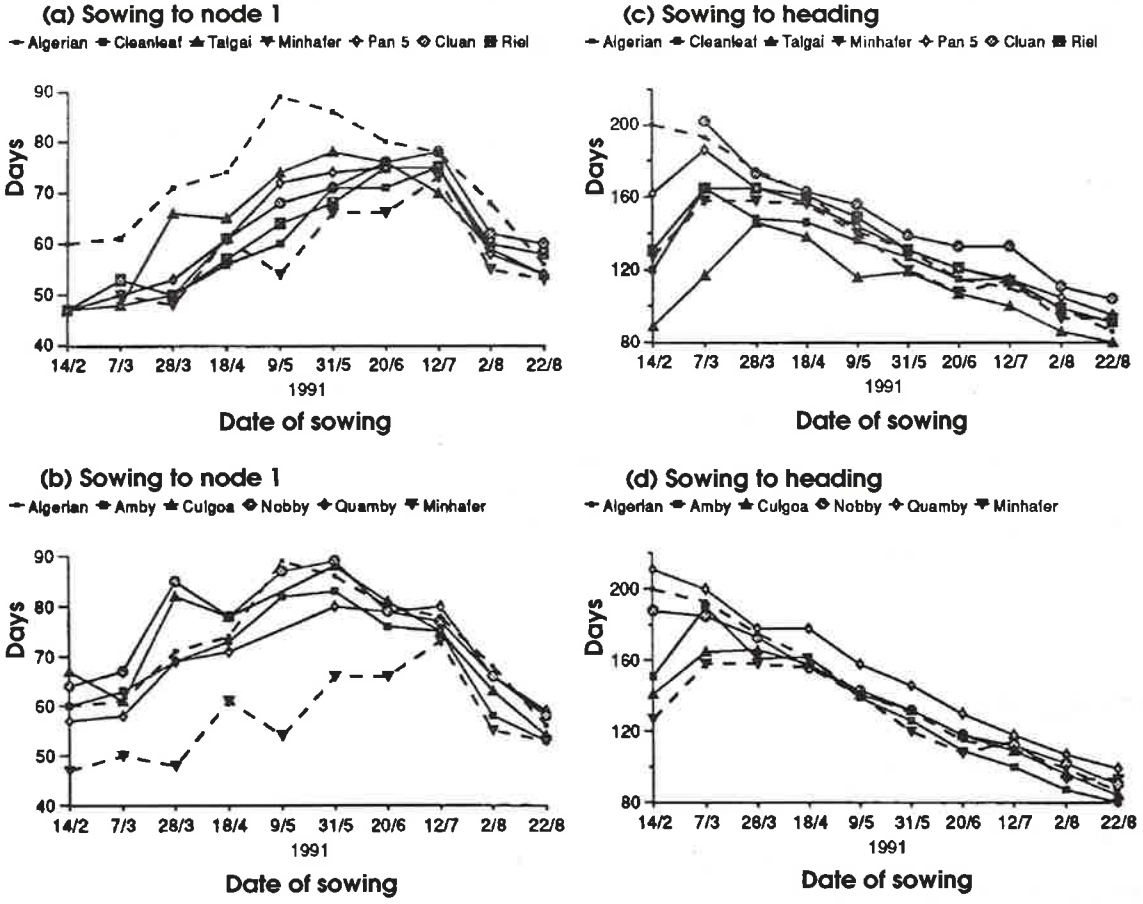

Figure 1. Development of 9 rust resistant oat cultivars from different sowing dates in sub-tropical Australia.

a,b: from sowing to node 1

c,d: from sowing to heading

Use and Management of Dwarf Oat, *Avena sativa*, in the North Central United States

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Summary

Since 1975, the oat breeding program at Minnesota has been developing and improving dwarf oat genotypes for evaluation of agronomic performance and potential cultivar release. Several research studies have been conducted in ensuing years to evaluate the use of dwarf oat in the North Central U.S. in companion crop forage production as well as in monoculture grain production systems. Dwarf oats were less competitive with weeds and underseeded alfalfa than conventional cultivars. Reducing row spacing from 18 to 10 cm did not enhance agronomic performance of the dwarfs. Prospective producer acceptance of dwarf cultivars appears to be good but release of dwarf cultivars could accentuate weed problems.

Introduction

Lodging is one of the major constraints to the production of oat in the North Central United States. It is particularly damaging when there is an underseeded forage legume such as alfalfa, *Medicago sativa*. Also, grain yields in monoculture are sometimes lowered due to suboptimal N fertility practices used to reduce the threat of lodging. Lodging has been greatly reduced in crops such as wheat, *Triticum aestivum*, and rice, *Oryza sativa*, by the introduction of dwarf stature through plant breeding. Until recently, dwarf genotypes with suitable agronomic qualities were not available in oat. However breeding efforts since 1975 have resulted in development of agronomically attractive genotypes for evaluation of performance in various agronomic systems.

In earlier studies at Minnesota[2], four experimental dwarf genotypes were compared to four conventional height lines over three years for grain and straw yields and other agronomic characteristics. Plant populations were also varied from 210 to 480 plants/m^2. There were no differences in grain yield among the genotypes in two of the years. In the third year, the highest yielding dwarf genotype gave significantly less grain than the best conventional cultivar. The highest grain yielding dwarf genotypes in each year produced straw yields that were 80 to 90% of the highest grain yielding conventional cultivars. Harvest indexes for the highest yielding dwarfs were similar to the conventional height genotypes, even though the dwarfs were about 30% shorter in stature. These earlier dwarf genotypes displayed the negative characteristic of incomplete exsertion of the panicles.

Marshall *et al.* [1] compared conventional height cultivar Ogle to the semidwarf Pennlo in two years at different row spacings, seeding rates and nitrogen levels. Ogle yielded from 13 to 18% more grain although it lodged severely in some treatments which hindered its harvestability. The dwarf produced 29 to 33% less straw. Neither cultivar responded differentially to the narrowing of row spacing from 18 to 13 cm.

Companion crop forage production systems involve growing one crop, usually oat, in association with a forage legume for the time needed to establish the forage seedlings. The practice dates back at least two centuries in the USA and provides added soil protection, weed suppression and forage biomass production in the seeding year compared with the practice of direct seeding of the forage legume. With the contemporary emphasis on agricultural sustainability, soil conservation and reduced pesticide use, the practice of companion cropping has assumed renewed interest. Recent studies at Minnesota found that a dwarf oat was less competitive with alfalfa that the conventional oat genotype evaluated when grown in a companion crop system[3]. In a recent survey of forage producers in Minnesota, oat was found to be the companion crop of choice for 87% of those who used companion cropping practices. Almost half of the survey respondents were favorably disposed to growing a dwarf companion crop were one available[4].

This paper summarizes results of studies conducted at Minnesota in recent years with advanced generation dwarf genotypes under both monoculture grain production and companion crop forage production systems.

Methods

The studies reported in this paper were conducted over the period 1987 through 1991. In one set of experiments, conducted in 1987, 1988, 1989 and 1991 at St. Paul, MN, four dwarf genotypes, one of which was common to the study of Meyers *et al.* [2], and four conventional height cultivars, Don, Hazel, Starter, and Steele were evaluated for grain production and agronomic properties in a monoculture production system. Row spacings (10 and 18 cm) were also a variable in the experiment on the hypothesis that the dwarf genotypes might be more competitive and give differentially higher yields in narrow row spacings than conventional cultivars.

In another study conducted in 1987, 1988 and 1989, the conventional height cultivars Preston and Starter were compared with an experimental dwarf genotype in a companion crop system at St. Paul, MN. Alfalfa was seeded with and without an oat companion crop in the experiments and subsequent forage yields were measured either at boot or soft dough stages of development in the oat. Weeds were controlled in the 1987 and 1988 experiments, but were allowed to grow in 1989 to evaluate the relative suppression of weeds by the companion crop genotypes.

Relative competitiveness of dwarf oat with green and giant foxmil weeds, *Setaria sp.*, was evaluated at Rosemount, MN in 1990 and 1991. Eight genotypes, including one dwarf, were grown in weedy and weed-free plots. Biomass production of the foxtails and of the oat was monitored as an indicator of competition between the crop and weeds.

Results and Discussion

The more advanced dwarf genotypes evaluated in monoculture proved to be more productive for grain than the earlier developed genotype, MN 805928. One of these genotypes always ranked in the top three in each year of the experiments. However in only one year was a dwarf, MN60228, the top ranking genotype. This was a particularly high yielding year with appreciable lodging of the conventional cultivars Don and Steele. In the other years, which were considerably lower yielding, the conventional cultivars Don and Hazel produced the most grain. The more advanced dwarf genotypes had higher harvest index than the earlier developed dwarf. The dwarf MN60228 had the highest harvest index (0.47), averaged over all years, compared to indexes 0.45 for Don and 0.42 for Hazel. Narrowing of row spacings did not have a differential effect on the yield of the genotypes evaluated. We conclude that considerable progress has been made in breeding agronomically desirable dwarf genotypes, such as MN60228. Under high yield conditions where lodging is likely, such genotypes appear to be favorably adapted. Harvest index has been slightly increased in the dwarfs compared to the conventional cultivars, but not to the same extent as for other cereals such as rice or wheat.

As expected in the oat companion crop experiments, yields of total dry matter for treatments where oat was included were consistently higher at either the boot or soft dough harvest than for the direct seeded (solo alfalfa) treatment. Averaged across all oat genotypes evaluated, the companion cropped treatments averaged 1749 kg/ha more dry matter production at boot harvest than the direct seeded treatment This advantage was reduced to 577 kg/ha by the soft dough harvest. Total dry matter production in the establishment year was 1014 kg/ha higher when an oat companion crop was included in the system compared to the direct seeded alfalfa treatment. The conventional height cultivar Preston usually gave slightly higher initial harvest or total season dry matter production. Alfalfa grown in association with dwarf oat genotype MN60246 tended to produce more dry matter at the soft dough harvest in 1989, which is consistent with earlier observations that shorter companion crops can reduce competitiveness with the underseeded alfalfa[3]. Greater initial growth of alfalfa, however, did not usually translate into higher alfalfa yields at the subsequent harvests in the seeding year.

Weed biomass was greatly suppressed in 1989 by the presence of an oat companion crop compared to the direct-seeded alfalfa treatment, especially at the soft dough harvest. All oat genotypes, regardless of stature, were similar in their abilities to suppress weed growth.

In evaluation of oat competitiveness with foxtail weeds, genotypes possessing conventional stature, "leafy" growth habit, and enhanced tillering usually suppressed foxtail biomass to the greatest extent. The dwarf genotype evaluated was associated with the highest level of foxtail production. Foxtail did not appear to differentially suppress the biomass production of the eight oat genotypes evaluated.

We conclude that future release of an agronomically-elite dwarf oat cultivar would be favorable for reducing lodging potential in monoculture grain production and companion crop systems. Dwarf cultivars should also enhance growth of underseeded forage legumes in companion crop systems. In monoculture grain production, the use of dwarfs could accentuate weed growth. Narrowing row spacing to favor dwarf oat production does not appear warranted.

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Oat Germplasm Evaluation for Forage Purposes in São Carlos-SP Brasil in 1991

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Summary

Forage production of selected oat germplasm provided by the University of Passo Fundo, was evaluated in 1991 by EMBRAPA/UEPAE de São Carlos. In a preliminary evaluation trial of 50 genotypes, fifteen appeared to have good characteristics and were selected for further testing. In a second trial where more detailed evaluations were performed, six genotypes were selected. All selected material showed potential for local seed production.

Introduction

The first cultivars of forage oats developed by EMBRAPA/UEPAE de São Carlos, were released in 1990[1]. A continuing program of germplasm selection is considered necessary mainly because of the threat of leaf rust. In 1991 material provided by the University of Passo Fundo was tested in two trials to evaluate its potential for forage production. Preliminary evaluation was carried out on fifty genotypes for disease resistance, forage yield and forage crude protein content. In another trial, 13 lines previously evaluated by the University of Passo Fundo for the same purpose, went through a more detailed evaluation.

Methods

In the preliminary evaluation experiment, each of the 50 genotypes was planted in two 3 m rows, 0.20 m apart, with a 1 m separation between genotypes. Planting was performed on May 27, using 80 seeds/m in an area irrigated by aspersion. Forage production was estimated through three harvests of a 0.40 m^2 area and dry matter yields in kg/ha were calculated. Harvests were performed on August 8, September 9 and November 11. At each harvest the crude protein and seed yields of each accession were determined.

In the second experiment, thirteen oat genotypes previously tested by the University of Passo Fundo, were tested in a randomised block design trial with three replications. UPF 3 and common black oats were used as controls. The experimental plots were 10 m x 5 rows with 0.20 m row spacing. Planting took place on the same date and in the same experimental area as the preliminary evaluation trial. Harvests were also performed on the same dates. In both cases no disease or pest control were performed. Forage yields were evaluated on half of the three central rows and seed yields on the other half.

Results and Discussion

In the preliminary trial, total dry matter yields varied from 3596 to 12428 kg/ha. Since no serious pest or disease problems occurred forage production at each harvest was the only selection standard used. Considering late forage production is of more interest in this region as this is when very little forage is available in the field, special attention was paid to yields in the second and third harvest.

On the basis of second harvest dry matter yields, nine genotypes were selected: UPF 85357, UPF 86155, UPF 85238-10, UPF 86066, UPF 78237-1b, UFRGS 7, UFRGS 6, UPF 85375 and UPF 81350. Their yields in the second harvest ranged from 5734 to 4251 kg/ha and crude protein content from 9.2% to 15.7%.

UPF 87097, UPF 87111, UPF 86081 and UPF 83340 were selected for their third harvest dry matter yields, which ranged from 6265 to 7133 kg/ha. Crude protein content of these lines

ranged from 7.2 to 11.4%. UPF 87111 presented a high degree of lodging and UPF 83340 had the longest cycle. UPF 84297 and UPF 82016 were selected for their dry matter yields in the first harvest, which were 6398 and 3129 kg/ha respectively. Their crude protein contents at this harvest were 24.0% and 20.5%. This group of 15 selected genotypes includes seven with highest total yield. All of them demonstrated good seed yielding ability and are being observed with more detail in 1992.

In the second trial traces of leaf rust were found on some genotypes but the disease did not progress. Some genotypes were susceptible to Barley Yellow Dwarf Virus. Lodging did not occur. The average forage yields and crude protein content of each genotype are shown in Table 1.

Table 1. Average dry matter (DM-kg/ha) yields obtained in three harvests and respective crude protein (CP - %) contents — Sao Carlos, 1991

Accession	*Total DM*	*1st harvest DM*	*CP*	*2nd harvest DM*	*CP*	*3rd harvest DM*	*CP*
UPF 84330	5319a*	2271a	19.8	1419abcde	12.9	1628 bcde	9.8
UPF 86301-6	5259a	1102 fg	23.1	1427abcde	12.7	2730a	8.6
UPF 86112	5205a	1301 efg	21.9	1854ab	10.3	2050 bc	10.2
UPF 83340-9	5112ab	1349 defg	21.3	1484abcde	10.8	2279ab	8.6
UPF Preta/87	5012ab	1354 defg	24.0	1993a	10.6	1664 bcd	8.4
Control (B.O)	4823abc	2025ab	18.9	1739abc	9.9	1059 def	10.4
UPF 84324	4767abc	1095 fg	22.0	1585abcd	12.9	2087 bc	10.1
UPF 86136	4664bcd	1601 bcde	20.1	1367 bcde	11.3	1696 bcd	8.2
UPF 81359	4445abcde	1856abc	17.8	1029 de	13.0	1560 cde	8.9
UPF 86155	4425abcde	1591 bcdef	18.2	966 e	12.6	1868 bc	7.5
UPF 86045	4379abcde	994 g	21.5	1448abcde	13.3	1937 bc	7.6
UPF 79302-1	3987 bcde	1810abcd	18.9	1476abcde	10.9	701 f	12.1
Control (UPF3)	3798 cde	1848abcd	18.2	895 e	14.4	1055 ef	10.1
UPF 86126	3587 de	1610 bcde	20.8	995 de	14.1	982 ef	10.2
UPF 80265	3359 e	1361 cdefg	18.7	1220 cde	13.0	779 f	11.2

* Means followed by the same letter do not differ statistically (Duncan, 5%).

Forage yields obtained for the controls in 1991 were markedly lower than their three year average, described by Godoy and Batista[1], when total yields were 7828 and 6828 kg/ha respectively for UPF 3 and common black oats.

Selection criterion in this case was yield 10% higher than common black oats, and within this criterion, UPF 84330 was selected for its first harvest yield, UPF Preta/87 for its second harvest yield, and UPF 84324, UPF 86045 and UPF 86155 for their yields in the third harvest. Seed yields were recorded and were reasonable for all selected genotypes, except for UPF 87/preta (630 kg/ha). Even so its seed yield was higher than the common black oats yield. Considering UPF 87/preta is a selection performed at the University of Passo Fundo within common black oats, it seems to be reasonable to initiate a selection program with *Avena strigosa* to make local seed production possible.

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Oat Evaluation for Forage Production in São Carlos, SP. Brasil

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Summary

With the objective of offering new options of forage oats to dairy producers in the São Carlos region (central region of the state of São Paulo Brasil) the dry matter yields of several genotypes of oats were compared over four years starting in 1985. As a result of the study EMBRAPA is recommending three cultivars; UPF 3, UPF 7 and São Carlos.

Introduction

Forage production is markedly reduced in São Paulo during the winter months due to low temperatures and lower rainfall, which causes a considerable water deficit. The use of winter forage crops, irrigated if necessary, is a viable alternative to overcome this problem. Forage oats are one of the best options due to their productivity and quality. Motta *et al* [6] verified that forage oats were similar to corn silage for milk production and quality. Coser *et al* [3] concluded that irrigated oats can be safely grazed from June through September by 2.5 to 4.5 AU/ha, and the daily average milk production was 11kg/animal. In Mato Grosso do Sul, Martinez and Costa[5] obtained oat yields of 5.38 t/ha of dry matter and 1.59 t/ha of crude protein.

In São Paulo there is little available data on utilisation of oat as a forage crop and only black oats, *Avena strigosa*, have been used. This work was conducted with the objective of offering new options of forage oats to the dairy producers of the São Carlos region which is located in the central region of the state of São Paulo, at 22°1' S lat. and 47°53' W long.

Methods

This work was conducted in an area irrigated by aspersion on soil with pH = 5; O.M. = 4.4 (%); P (resin) = 6 $\mu g/cm^3$; Ca = 3.74, Mg = 1.4, H+Al = 3.8, S = 4.96 and CEC = 8.76 meq/100 cm^3 of soil. In 1985 small amounts of seed of 21 accessions received from the University of Passo Fundo were preliminarily evaluated in unreplicated 6 m x 4 row plots. Six of the accessions were also evaluated in a three-replication experiment. At planting (80 seeds/m), soil was fertilised with 80 kg/ha of P_2O_5.

Two harvests were performed to evaluate dry matter yield at 70 and 100 days after planting in half of the two central rows. After the first harvest 30 kg/ha of N and 50 kg/ha of K_2O were applied. Common black oats was used as a control in the experiment. The same type of fertilisation and of control (common black oats) was used in both experiments. In 1986, twelve accessions were tested in a randomised block design with three replications. These twelve accessions consisted of four from each of the 1985 experiments, and four provided by the Secretary of Agriculture of Rio Grande do Sul State. Plots were 6 m x 10 rows with 15 cm row spacing. To evaluate dry matter yields, half of the six central rows were harvested 70 and 140 days after planting.

In May 1987, nine accessions selected from the 1986 experiment and a control were planted in 10 m x 20 row plots with 15 cm row spacing. Trial design was a randomised block with 3 replications. Forage production was measured at 70 and 130 days after planting, by harvesting a 4.80m^2 area from each plot. Six of the accessions went through a similar trial for final evaluation in 1988, where 30 m x 10 row plots were used. In the latter experiment, the crude protein content of each accession was determined at each harvest.

Results and Discussion

In the 1985 unreplicated oat trial, dry matter yields ranged from 1786 to 7102 kg/ha. The selected accessions, UPF 7, UPF 79S115, UPF 8 and UPF 80266 yielded respectively, 7102, 5622, 5233 and 4833 kg/ha, while the control (common black oats) yielded 4812 kg/ha. In the replicated trial, no statistical differences ($P > 0.10$) were detected, although dry matter yields ranged from 2542 to 4656 kg/ha. Only two accessions were deleted because of low seed production. In 1986, since none of the accessions showed any major pest or disease problems, the eight accessions with better total forage yields were selected. These ranged from 8457 to 10902 kg/ha. Five of the selected accessions had greater yields than the control, while the other three did not show statistical difference ($P > 0.10$). Moreover, UPF 3 was selected due to its high yield in the first harvest, a very desirable characteristic if oats are to be cultivated without irrigation in this region. Dry matter yields observed in 1987 were somewhat different from those obtained before with the control ranking last. The five better dry matter yielding accessions, which had total yields ranging from 6564 to 7988 kg/ha and UPF 79I174-3 which had very good seed production, were selected for final testing. In 1988 the forage yields obtained were overall higher than those of 1987, varying from 2520 kg/ha for the control to 2019 kg/ha for UPF 7. Again, all accessions had better total and second harvest yields than the control. In the first harvest, UPF 2, UPF 7 and UPF 79S115 showed better crude protein contents (26%, 23% and 25% respectively) than the control (20%), while in the second harvest, the crude protein contents were similar, around 11%. It is important to consider the average forage yields obtained when the accessions were tested with replications. Three year averages are presented in Table 1. In the first harvest, UPF 3 had an average yield greater ($P < 0.05$) than the control. UPF 2, UPF 7, UPF 79S115 and UFRGS 79A65 had greater ($P < 0.05$) forage yield than the control in the second and total of the two harvest. The average black oat yield obtained in this study was higher than those reported by Alvim *et al* [1] for Minas Gerais, and by Martinez and Costa[5] for Mato Grosso do Sul, suggesting very good conditions for growing forage oats in Sao Carlos.

Table 1. Average three year dry matter yields of selected oat accessions. São Carlos, SP. Brasil 1986-88

Accession	*Dry matter yields (kg/ha)* *1st harvest*	*2nd harvest*	*total*
UPF 2	2547 c*	6255a	8802a
UPF 7	2734 bc	5975a	8709a
UPF 79S115 ('São Carlos')	2871 bc	5553ab	8423a
UPF 3	3755a	4073 cd	7828ab
UFRGS 79A65	3009 bc	4804 bc	7813ab

* Means followed by same letter within each column, do not differ statistically (Duncan, P=.05).

Based on these results, EMBRAPA is recommending UPF 3 for the state of São Carlos without irrigation. According to Floss[4], UPF 3 originated from the cross Coronado x 1779-2. This came from Wisconsin, USA, and was introduced to Brazil as an F_3 in 1977. UPF 3 was described by Calvete and Santos[2] and was considered to be moderately resistant to leaf rust.

UPF 79S115, a line originating from selection within the Cherokee cultivar, was considered leaf rust resistant in Passo Fundo and Sao Carlos and was released by EMBRAPA as a new forage oat cultivar, named 'São Carlos'.

UPF 2 presented very good second harvest yields, but in the experiment without replication was considered by Calvete and Santos[2] as susceptible to leaf rust.

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The Potential Use of *Avena sativa*/Annual Legume Mixtures in the Pasture Phase of Cereal-Annual Legume Rotations

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Summary

Sowing oat cultivars resistant to cereal root diseases into legume pastures was evaluated as a means of replacing volunteer grasses in the cereal/livestock zone of southern Australia. Three pasture types (volunteer grass + medic, grassfree medic and sown oat + volunteer grass + medic) were compared at two stocking rates (8.4 and 12.6 DSE) under grazing. Four harvests were taken from July to September. The oat+grass+medic pasture type had a faster growth rate and maintained higher levels of pasture availability at each harvest. Sheep body weight gain showed no significant differences. Results suggest sowing oats into legume pastures has the ability to improve the carrying capacity of pastures by increasing both early winter and total dry matter production. Improvements in pasture botanical composition and grass and broad-leaved weed control are also achieved.

Introduction

The livestock carrying capacity of legume pastures in southern Australia is predominantly set in early winter and is directly related to the timing of rainfall and availability of early feed. Rapidly-growing volunteer annual grasses (usually rye-grass, *Lolium rigidum*, barley grass, *Hordeum leporium*, brome grass, *Bromus diandrus* and B. *rigidus*, silvergrass, *Vulpia* spp. and wild oats, *Avena fatua*), have traditionally provided useful early winter pasture growth compared to the slower growth of annual legumes (*Medicago* spp. and *Trifolium* spp.). Unfortunately these grasses pose problems in cereal-pasture rotations, acting as major hosts of the cereal root disease Take-All, *Gaeumannomyces graminis* and in the case of wild oats, Cereal Cyst Nematode, *Heterodera avenae* both of which are carried over to following cereal crops[2]. Livestock (particularly sheep) can also be injured and suffer wool contamination by the awned caryopses of barley grass, brome grass and silver grass[1] (D. Little, pers. comm., 1992).

Removal of the grasses with herbicides can lead to problems including lack of early grazing feed in winter, an increase in livestock diseases associated with legume-dominant pastures (e.g. redgut, bloat, scouring), invasion of broad-leaved weeds, resistance to grass herbicides and the potential to increase soil acidification in low pH soils.

A cutting experiment by Roberts (unpublished data) examined various mixtures of oats with *Medicago truncatula* (barrel medic, cv. Paraggio). Total winter early-spring production of the sown pasture components varied only slightly amongst treatments with the mixtures containing oats providing significantly dry matter (DM) in early winter. There was a linear correlation for grass and broadleaf weed DM to be reduced as oat density increased. A experiment was established in 1991 to assess the use of oat/annual *Medicago* mixtures in southern Australian pastures.

Methods

The field experiment was conducted at Roseworthy campus the University of Adelaide, 50 km North of Adelaide, South Australia. Three pasture types (volunteer grass+medic, grass-free medic and sown oat + volunteer grass + medic) established in winter (June) were grazed by one and a half year old merino wethers at two stocking rates (8.4 DSE and 12.6 DSE) with three replications.

The medic used was *M. truncatula* cv. Paraggio and the oats cv. Marloo (resistant to Cereal cyst nematode and Take-All). Volunteer grasses (barley grass, wild oats and annual ryegrass) were sprayed with the grass selective herbicide Targa™, (active constituent 94g/litre Quizalofop-P-ethyl) to provide the grass-free pasture type.

Pasture dry matter availability (DM), growth rates and botanical composition were measured by four harvests taken 59, 77, 92 and 112 days after plant emergence using regularly moved cage exclosures. Sheep body weight was measured at the same time.

Targa™ is a registered product of Du Pont.

Results and Discussion

Pasture production and botanical composition.(Figures 1 and 2)

Late opening rains delayed plant emergence until June 3 reducing the early winter sampling period. There was a significant Pasture Type Harvest interaction. Figure 1 shows the effect of Pasture Type on dry matter availability of the pasture components at the four harvests. Total available pasture was higher at all harvests in the oat+grass+medic pasture type, with the oats component as the main contributing difference. Oat DM provided 49%, 58%, 66% and 61% of the available pasture over the four harvests respectively. Medic yield was significantly suppressed in the oat+grass+medic pasture type from Harvest 2 onwards.

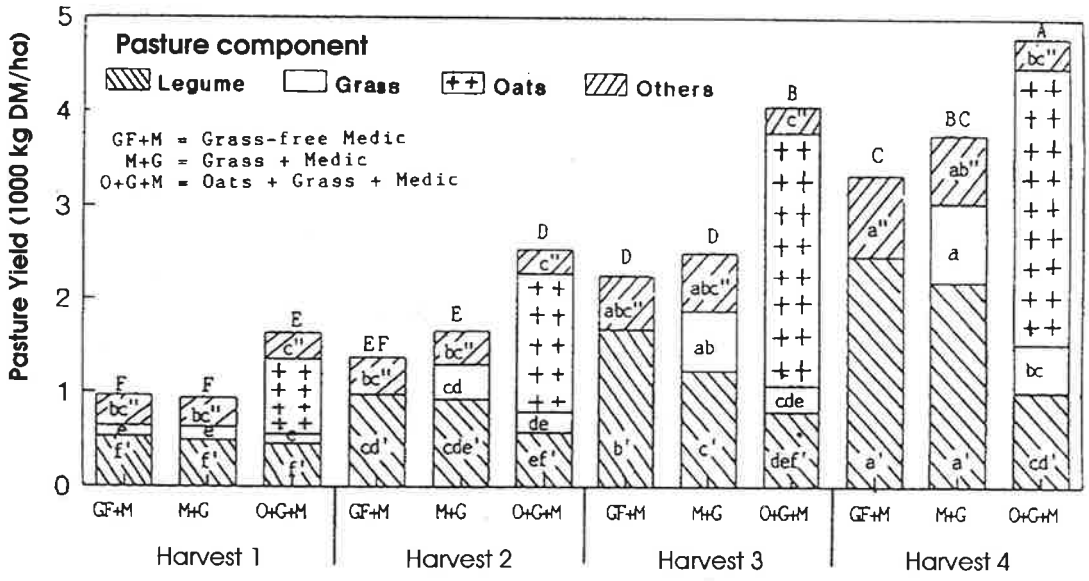

Figure 1. Botanical composition and dry matter production of three pasture types at four harvests.

Within pasture components yields associated with the same lower case letter are not significantly different ($P<0.05$). For total pasture, corresponding significant differences are denoted by upper case letters.

The results suggest that sown Marloo oats have an advantage over volunteer annual grasses with their ability to establish vigorous seedlings quickly and provide more DM throughout the growing season. The yield of the oats+grass+medic pasture type was largely dependent on the oat component which almost always made up over half the total available herbage on offer. Importantly the increase in total DM was not at the expense of legume growth until Harvest 2, when it appears the grazing pressure was inadequate at both stocking rates.

The yield of available grass increased over time but at a greater rate in the grass+medic pasture type compared to the oat+grass+medic mixture (Figure 2).

The regression equations are:

Grass + Medic Grass DM=145(± 26.67) + 13.6 (± 0.821)days
r^2= 0.99, P < 0.05

Oat + Grass + Medic Grass DM=80(± 36.59) + 7.73(± 1.126)days
r^2= 0.95, P < 0.05

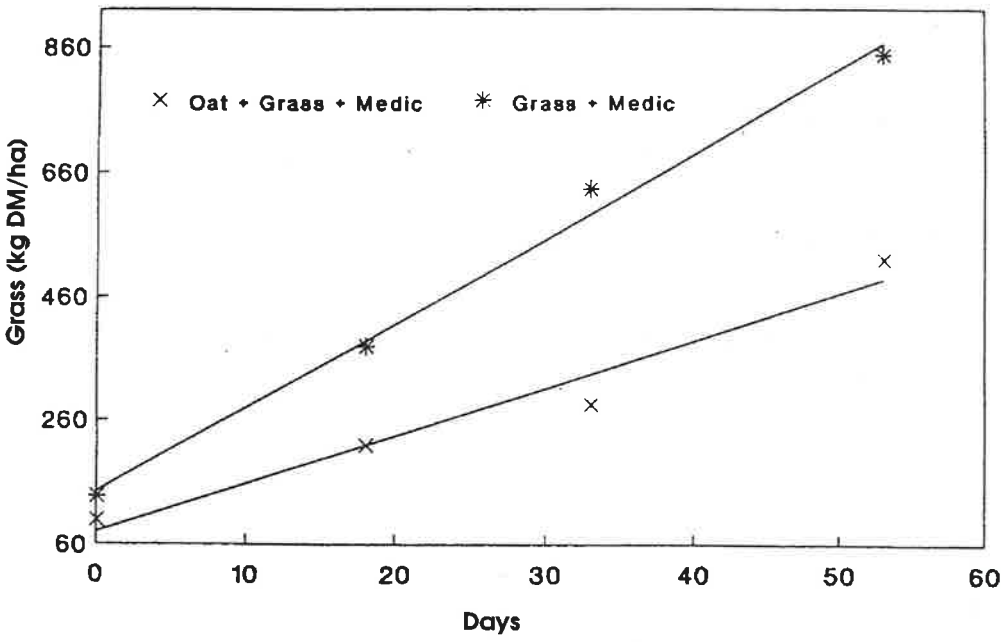

Figure 2. Regression of grass against time in grass+medic and oat+grass+medic pasture types

From plant emergence until Harvest 1 the oat+grass+medic pasture type had a growth rate 1.7 times greater than the other two pasture types. Thereafter there were no significant treatment differences in growth rates. The mean over the 54 day sampling period for the three pasture types and two stocking rates was 75 kg/ha/day.

Sheep Body weight

There were no significant differences in sheep body weight between pasture types or stocking rates. The regression equation for mean sheep body weight for the 54 day period is

Body weight = 53.5(± 0.793) + 0.226(± 0.022)days
r^2= 0.98, P < 0.001

Continuing research will focus on developing a pasture system that provides early winter grazing, suppression of weeds and reduces the carryover of cereal root diseases while optimising legume production.

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Breeding Oats for Irrigation in Australia

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Summary

Glen Innes, on the New England Tablelands, has proven to be the best centre for breeding oats for the heavy soils of the Riverina at Leeton, southwestern New South Wales. Plant selections made on the black self-mulching soils of the Glen Innes Research Station have resulted in the varieties Acacia, Bundy, and Mugga; all now replaced by Blackbutt. Both areas require resistance or tolerance to stem rust, water logging, red legged earthmites, Barley Yellow Dwarf Virus, lodging, shattering and second growth. Avon, a high yielding grain oat from West Australia, was found to be unsuitable because of its tendency to remain green for too long, holding back harvest operations. Although frost damage is less of a problem in the irrigation areas than on the Northern Tablelands, the frost resistant bulks from the cross F.Ga(1183G57)xVRAF, VRSF(1309G57) demonstrated good tolerance to water logging on heavy soils. One of these lines, Blackbutt, currently excells as a dual-purpose oat and as a grain oat variety and is recommended for both northern and southern irrigation areas. The concept of a 'triple-purpose' oat is introduced.

Introduction

Oats are regarded as needing more water to produce a unit of dry matter than any other small grain cereals except rice[(1)]. Rice is the most important irrigated crop in the Riverine Plain of New South Wales. Wheat, however, is also extensively grown under irrigation but is very prone to crop failure if it is susceptible to rust diseases[(6)]. Oats is less affected by rust diseases, and soil-borne pathogens than wheat and therefore often yields high under irrigation.

Methods

The Department of Agriculture has conducted dual-purpose and grain only oat trials for many years in the Riverine Plain of New South Wales. The early varieties, P4315, Avon, Cooba and Coolabah were compared with the late varieties, Blackbutt, Acacia, Algerian, Klein 69B and Mugga (Table 1). The varieties were kept in 2 separate groups, for ease of harvesting. The mid-season variety Bundy was common to both early and late trials. Due to the frequent tendency of Avon to make second growth and to delay harvest, early varieties sometimes were over-ripe and suffered some shattering losses as a result. Grazing yields are not given in these trials as they are usually too lenient in character to assess grazing potential under irrigation.

Discussion

Hull bulks topped the yields both in the grain only and in the grain recovery after grazing trials (Table 1). Similarly, Table 2 compares only grain recovery (grazing yields excluded) with grain yields on dryland in the Riverina. P4315 tops both sections without irrigation. This line therefore demonstrates a triple-purpose capacity, that is high dual-purpose and high grain only yields. Blackbutt, under irrigation (Table 3) showed the same capacity but the earlier compounded bulk, P4315, was more adaptable, being triple-purpose under both irrigation and dryland conditions.

Most virgin soils of the Riverine Plain have extremely low infiltration rates[(6)]. Gypsum has made possible successful pasture establishment[(2)]. On these soils, pasture establishment and rotation provide a sound basis for arable cropping.

The original nature of these soils, for which Australia has an unlimited water supply from the Snowy Mountains, still requires oat varieties resistant to occasional waterlogging. For this reason, selected varieties at Glen Innes like Acacia, Bundy, Mugga[4] and the Hull bulks have demonstrated their tolerance to these conditions, as have Klein 69B, Coolabah and Cassia[3] but should not be considered here because of poor quality grains *per se*. Resistance to summer storms at Glen Innes is also useful under irrigation. More recently, Sydney University's rust resistant Algerian cultivar Sual, has given high yields under irrigation although the straw is tall and weak, which requires this variety to be grazed. This is impossible if water-logging occurs.

Table 1. Comparisons of early and late maturing cultivars under irrigation in the Riverina for a 10 year period for grain recovery (pG) and grain only (G).

Cultivars (no.)	*G (7 trials) mean t/ha*	*pG (4 trials) mean t/ha*
P4315[a] (38)	3.76	2.88
Coolabah[a] (105)	3.61	2.40
Cooba[a] (22)	3.42	2.06
Bundy (15)[a]	3.36	2.54
Avon (101)[a]	3.30	–
Blackbutt (11)	4.36[b]	3.26[c]
Bundy (15)	4.00[b]	2.75[c]
Mugga (58)	3.79[b]	2.22[c]
Coolabah (105)	3.57[b]	–
Cooba (22)	3.23[b]	–
Klein 69B (53)	–	2.213[c]
Acacia (1)	–	2.06[c]
Algerian (70)	–	2.03[c]

Trials were conducted in the Murrumbidgee Irrigation Area, New South Wales, under irrigation from 1963-73. [a] early maturing cultivars; [b] late maturing cultivars, 2 trials; [c] late maturing cultivars, 4 trials.

Table 2. Comparisons of grain recovery (pG) and grain only (G) yields in the Dryland Riverina for a 10 year period.

Cultivars (no.)	*G (9 trials) mean t/ha*	*pG (4 trials) mean t/ha*
P4315 (38)	2.03	1.59
Cooba (22)	1.90	1.47
Avon (101)	1.88	1.55
Coolabah (105)	1.80	1.32
Bundy (15)[a]	1.71	1.38

[a] The low yields of Bundy, a drought tolerant cv, suggests an abundance of soil moisture in these trials, with P4315 exhibiting a triple-purpose capacity. Trials were conducted in the dryland irrigation regions of the Riverina, New South Wales from 1963-73.

Conclusions

Oat breeding for irrigation should consider the following characteristics; 1) Resistance to waterlogging especially in heavy soils. Acacia x Lampton lines by Carroll at Glen Innes were outstanding in this respect in the 1960s. 2) The strong straw of the HvII lines seems to derive from the tall strong-strawed variety, Garry. The shorter culms of P4315, for instance, had thicker stronger walls than those of Cooba, a variety without Garry parentage. It is for this reason that Cooba is not suitable for grain only, especially under irrigation. 3) A separate issue to No. 2) is that of the harvest index, or grain-hay ratios. Yield improvements to Ballidu, Orient and Avon have been attributed solely to an increase in harvest index[7]. Results reported concurrently[5] suggest that 1309 has a higher harvest index than Cooba with a hay yield equal to that of Cooba. Both Cooba and 1309 have high quality grain and good milling characteristics, therefore 1309, the parent of the Hull, is a better choice for crossing, or black-crossing, than Cooba, which is moreover lower in frost resistance. The grain/hay ratios concurrently reported[5] demonstrates that 856 G59 has the highest harvest index recorded and yet is significantly higher in hay yields to both Cooba and 1309. This high harvest index appears to be derived from Fulghum.

Table 3. Year 24 of testing Blackbutt oats: F_{29} generation trial, irrigation versus dryland.

Cultivar (no.)	Irrigation site[a] G[c] t/ha	Cool dryland site[b] pG[d] t/ha
Blackbutt (47)	5.29	2.40
Cassia (103)	4.89	–
Hakea (109)	4.78	–
Echidna 206)	4.76	1.58
Dolphin (205)	4.63	–
Bundalong (204)	4.36	–
Barmah (202)	4.25	–
Nile (209)	4.05	2.85
Carbeen (41)	3.75	2.31
Cooba (22)	3.61	2.01
Yarran (114)	3.02	2.12
Coolabah (105)	2.89	1.90
Mortlock (208)	2.89	2.00
Bulban (203)	2.71	–
West (214)	2.62	–
Rysun, rye	–	1.94
Malebo, barley	–	1.94
Quarrion, wheat	–	1.77
Rosella, wheat	–	1.66
Osprey, wheat	–	1.35
Forrest, barley	–	1.22
Diff. for sig.	n.a.	0.44
Date of sowing	11.4.85	26.3.85

[a] Coleambally trial, lodging prevalent; [b] Adelong; [c] Grain only trial; [d] Grain recovery after grazing, which was not measured by a pasture cut. n.a. = not analyzed.

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A Rapid, Low-Technology Method of Breeding High-yielding Oats with Dual Purpose Characteristics

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Summary

This paper reports the result of 34 years of oat breeding and testing of dual-purpose varieties (for grazing and grain recovery) by the New South Wales Department of Agriculture. A high vigour cross (Hvll 57-75) is identified which led to the release of Blackbutt (an F_4 directed bulk type) in 1975, and Carbeen (an F_6 plant progeny of the normal pedigree system) in 1981. This cross also produced a number of high yielding F_4 directed bulk types and F_2 plant progenies bulked in the F_3 as a result of their relatively high phenotypic uniformity. The highest yielding F_3 bulk was numbered P4315, which although classed as an early oat, out-yielded all other varieties, including Blackbutt, for total biomass, following early sowings, and over a wide range of soils and climates.

Introduction

The New South Wales Department of Agriculture has been a world leader in the breeding of dual-purpose oat cultivars since 1921[9]. This Department also has a strong tradition of releasing uniform oat varieties. These may take up to 15 years from making of the cross to release to farmers[4,5,6]. With the present restriction of funds to Australian agricultural research, benefit/cost ratios in oat breeding research could be greatly improved by adopting a rapid "directed bulk" oat breeding method. In this article, such a method is briefly outlined.

Methods

The early generation plan in Table 1 enables F_3 bulks and F_4 directed bulks to enter drill-testing respectively at 2 years and 4 years after the cross is made. For example, P4315 (F_3 bulk) entered trials in 1960 whereas Blackbutt (F_4 directed bulk) entered trials in 1962. Only certain crosses (phenotypically not too dissimilar) described concurrently[8] should be attempted. The morphology and pathology of the high vigour cross parents, described in this article, is given in Table 2.

Table 1. Rapid method of breeding oats for large biomass yields

Generation	Date sowing	Date harvest	Growing season	Stage
F1	31.3.58	9.10.58	6 months	Glasshouse[a] increase
F2	19.11.58	7.4.59	4.5 months	Spaced plant rust test
F3 earlier (normal)	7.5.59	31.12.59	8 months	Spaced plant grain class
F3 later (duplicate)	11.8.59	7.1.60	5 months	Smut and maturity test
F4	1.3.60	17.12.60	9.5 months	1st grazing and grain trial (2 years after cross)

[a] Field cross 26 x 21 made on 15.10.57

Table 2. Morphology and pathology of parents of High-vigour cross[a]

Cross A	*Female*	*Male*
Pedigree	F.Ga (1183 G57) G0-56-0-10(F5)	VRAF.VRSF (1309 G57) G0-102-H0-G0-0-0-2 (F8)
Homozygosity	Fixity proven	Fixity proven
Early growth	Prostrate	Prostrate
Mature height	Tall (122 cm)	Short (90 cm)
Harvest index	Medium	High 47.2%[b]
Grazing-frost	Very hardy (1/6)	Very hardy (1/6)
Foliage	Medium broad	Narrow leaves
wt. g/1000 seeds	32.30	44.00
groat %	70.50	74.00
kg/hectolitre	51.13	54.24
milling suitability	too small	excellent
grain articulation	50% *A. sativa*	100% *A. byzantina*
(specific trait)	50% *A. byzantina*	—
Ustilago (smut)	Resistant	Susceptible
Crown rust[c]	MR (2/6)	MR (3/6)
Stem rust	R (0/6)	S (6/6)

[a] Data obtained from row averages at Glen Innes 1959 [b] Harvest index determined subsequently at Tamworth 1961 [c] Crown rust is less important because grazing and cool winters discourage rank foliage growth.

Results and Discussion

With the much higher and more stable yields of the new bulk varieties (Tables 3, 4 and 5), 4 years of testing instead of the usual 7 years would therefore be sufficient for cultivar release. This would be the case especially if the number of testing sites could be increased. Instead of the usual 15 years under the pedigree system, which should be run concurrently, the time from cross to farmer can be halved to 6 years for F_3 bulks and 8 years for F_4 directed bulks. New possibilities are opened up by introducing a rapid breeding technique for producing dual-purpose oat cultivars. For New South Wales oat research programs to be attractive to funding, it will probably need to replace the popular variety Cooba with a variety that yields at least 20% higher. From Tables 3,4 and 5, the F_3 bulk, P4315, tested from 1960 to 1976, was at times up to 100% higher in yield but lacked milling suitability. It may soon be that this stipulation will be waived by the Agriculture Department, allowing such potential cultivars to be released. As well as P4315 there is a millable F_4 directed bulk, P4318, which is also tolerant to Barley Yellow Dwarf Virus, as is P4315. There could be little, if any, advantage in releasing a high yielding F_3 bulk to a farmer who is interested in growing oats for grain only. On the other hand, farmers who are in need of supplementing their winter pastures[4], and who practise optimum soil and crop management[5] stand to gain significantly. Supporting the latter farmers would increase Australia's relatively low average oat yields (approximately 1.4 tonnes/hectare), bringing them closer to the yields reported in this article. The model farmer will extend both seed and knowledge to make long-term profits. A further recommendation based on the results of the New South Wales Department of Agriculture is that F_3 bulks and F_4 directed bulks should be maintained indefinitely, not alone as gene banks similar to Suneson's composites[1,13], but also to monitor yield changes, if any, over time, relative to all the check varieties, including Algerian, Fulghum and Cooba.

Table 4 shows the overall superiority of Glen Innes bred oats over southern bred lines for frost resistance, cold weather growth to supplement pastures, long season intensive grazing with hay recovery on the richer type of soil in the summer rainfall regions. Table 5 shows the value of grazing, by return of nutrients through the grazing animal[15] in boosting grain yields, an option not usually open to specialized grain oats, wheat or barley varieties. Cassia, Coolabah, Hakea[12] and Yarran[11], although suitable for lenient grazing, are not true grazing-hardy, dual-purpose oats as is the high vigour line, P4315.

Carbeen is handicapped by its straw being taller than Blackbutt, while Hakea is taller and weaker than Carbeen. Yarran is susceptible to Barley Yellow Dwarf Virus. Tolerance to this disease is essential under high and summer rainfall conditions.

Lenient oat grazing dry matter yields in South Australia[3] were only 14% of those of continuously grazed pasture. By contrast, Algerian oats seeded at 90 kg/ha yielded 4 times that of ryegrass-clover pasture[4]. The same variety seeded at 180 kg/ha with 67 kg/ha of nitrogen carried 30 ewes per hectare or 8 times the carrying capacity of the pasture at Orange[4]. At Armidale, which is similar to Canberra and typical of much of eastern Australia, the ratio of oat to pasture growth in areas of dormant winter pastures (no sub-clover) was 10 to 1[14].

The results of this study indicate that heavy grazing, that is four or more pasture cuts, are essential to assess the true dual-purpose capacity of oat varieties.

Table 3. Second testing of Hv bulk oats in north-west New South Wales, contrasting cooler elevated site (Tamworth) with warmer plains site (Narrabri): F_5 generation trial.

			Tamworth (mild but frosty)					Narrabri
Cultivar (no.)	*CWG*[a] *t/ha*	*Frost*[b] *(0-6)*	*T4P*[c] *t/ha*	*pG*[d] *t/ha*	*TY*[e] *t/ha*	*pH*[f] *t/ha*	*G/H*[g] *%*	*G*[h] *t/ha*
P4315 (38)	1.71	0	6.97	1.63	8.60	3.61	45.2	1.09
F.Ga (30)	1.44	1	6.06	2.48	8.54	–	–	0.52[i]
Klein 69B (53)	1.40	0	6.45	1.78	8.23	4.15	42.8	2.69
871 G59 (42)	1.61	1	6.56	1.60	8.16	3.51	45.1	1.19
A x Lag (4)	1.24	0	5.37	2.31	7.68	–	–	0.24[i]
856 G59 (39)	1.40	0	6.15	1.46	7.61	2.88	48.6	0.71
Fulghum (27)	1.05	1	6.03	1.49	7.52	3.12	48.0	–
K69 B.G.R. (54)	1.19	1-	5.29	2.15	7.44	–	–	–
Acacia (1)	1.33	0	5.66	1.59	7.25	–	–	0.5[i]
886G59 (46)	1.11	1	5.35	1.79	7.14	–	–	0.28[i]
Algerian (70)	0.93	4	4.91	2.09	7.00	–	–	1.05
Cooba (22)	1.34	3	5.99	0.86	6.85	2.07	44.8	0.82
Mugga (59)	1.02	0	4.86	1.91	6.77	–	–	0.05[i]
1309 (23)	1.14	1	5.20	1.05	6.25	2.18	47.2	0.69
Bundy (15)	0.83	2+	4.58	1.59	6.17	–	–	1.38
843 G59 (37)	0.75	4	4.76	1.29	6.05	–	–	0.74
Burke (17)	0.58	4	4.11	1.24	5.35	–	–	1.71
Belar (9)	0.52	3	3.82	1.14	4.96	–	–	2.09
Orient (210)	0.22	6	4.18	0.43	4.61	–	–	4.38
Diff. for sig.	0.31	–	1.61	0.55	–	0.46	–	0.41
Date of sowing:	14.3.61		(high soil fertility)				3.5.61	(high soil fertility)

[a] Cold weather growth measured by 3rd cut; [b] Frost damage score of 3 and over lowers grain recovery yields; [c] Total of 4 pasture cuts, each immediately followed by sheep grazing trial area down close to ground level on 16.5.61, 10.7.61, 23.8.61 and 19.6.61; [d] Grain yields after grazing; [e] Total yield of c + d; [f] Hay recovered after grazing at grain ripeness stage; [g] Relative harvest index, grain as a percentage of hay; [h] Grain only trial; [i] Specialized winter oats, too late maturing for the north-west plains. All yields in tonnes/hectare, with pasture as dry matter.

Table 4. A comparison of southern and northern New South Wales bred cultivars under intensive grazing and hay recovery: F_{10} generation testing of HvII lines.

Cultivar (Ref. No.)	*5P (t/ha)*	*pH (t/ha)*	*5P+pH (t/ha)*	*tillers killed*[a]	*F score (0-10)*	*July P (t/ha)*
P4315 (38)	6.55	3.62	10.17	4	1	1.45
856 G59 (39)	6.21	3.70	9.91	0	1–	1.23
Blackbutt (11)	6.67	2.86	9.53	4	1	1.35
871-I G59 (43)	5.66	2.97	8.64	0	2	0.83
871 G59 (42)	5.60	2.99	8.59	36	2	0.74
Klein 698 (53)	5.01	3.37	8.38	0	2+	0.72
Cooba (22)	5.18	2.21	7.39	14	3+	0.95
Fulghum (27)	4.87	2.20	7.07	30	3	0.64
F x Vic (122)	4.21	2.47	6.68	19	4+	0.52
Coolabah (105)	4.09	2.08	6.17	76	6+	0.45
F x Avon (121)	3.89	2.23	6.12	43	4+	0.36
Avon x Fk (116)	3.96	1.93	5.90	40	7+	0.28
Avon x Os (117)	4.04	1.81	5.85	157	8	0.33
F x Avon (120)	3.45	2.11	5.57	106	7	0.23
Fulmark (107)	3.78	1.70	5.48	165	9	0.20
M1305 (118)	3.36	1.48	4.85	132	7	0.25
Algerian (70)	3.38	0.60	3.98	35	8	0.19
Sig. diff.	0.90	0.99	1.54	–	–	0.34

[a] No. per row; 5P = 5 pasture cuts as DM (dry matter); pH = air dried hay after pasture; F = frost (0 = no damage, 10 = extreme); Date of sowing 25.3.66 at Hawkesbury Agricultural College, rich alluvial soil, no irrigation; dry season (rainfall 50% of 86 year mean); seeding rate 72 kg/ha; rate of fertilizer, in seed drill only, 22.4 Kg N + 22.4 P_2O_5/ha. Cultivar reference nos. with 3 digits were bred in southern regions (winter rainfall) and those with 2 digits were bred in northern regions (summer rainfall).

Table 5. Lenient grazing and grain trial: F_{17} generation testing of HvII bulk oats.

Cultivar (Ref. No.)	*T2P*[a]	*pG*[b]	*TY*[c]
P4315 (38)	0.58	19.83	20.41
Sual (63)	0.49	19.66	20.15
Cassia (103)	0.47	16.14	16.61
Blackbutt (11)	0.48	14.50	14.98
Cooba (22)	0.62	10.36	10.98
Klein 69B (53)	0.57	7.26	7.83
Coolabah (105)	0.51	7.31	7.82
Bundy (15)	0.54	5.95	6.49
Algerian (70)	0.47	5.98	6.45
Mugga (58)	0.45	5.62	6.07
Avon (101)	0.43	3.92	4.35
Acacia (1)	0.53	3.80	4.33
Sig. Diff.	0.08	1.71	–
Coeff. var.	10.8%	12.4%	–

[a] Total of 2 pasture cuts to measure 2 grazings; [b] Grain recovery yields - a Department of Agriculture record for oat yields; [c] Total yield of grazing (as dry matter) and grain in tonnes/hectare. Excellent season; crown rust and stem rust severe but not affecting P4315 or Sual. Date of Sowing 4.5.73 at Tamworth Research Station.

Conclusions

A clear distinction must be made between blends or multilines versus varieties compounded in F_3, F_4 or F_5. Acceptable uniformity was achieved with an F_5 line of soyabeans[2] and with Blackbutt oats. A blend is artificially compounded of unrelated homozygous subpopulations subject to "natural selection", meaning yield change, and unable to maintain equilibrium. By contrast the early generation compounded variety has aggregate homeostasis, that is, stability and flexibility in yield, and this can be advanced by making the right cross, with a view to individual homeostasis, or buffering, by the parents selected.

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Wild Species of Oats from USSR as an Initial for Plant Breeding

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Summary

From preliminary testing, we found that some morphological characters and agronomic traits were correlated. Thus, these results may have application for choosing initial material for plant breeding till full maturity in the field. Attention also should be given to the fact that altitude where these forms were distributed, was correlated with important traits for crop improvement. The field data of evaluation presented in this paper show where we can find forms with needed agronomic characters belonging to different species with different ploidy levels.

Introduction

Wild and weedy species are considered to be of great potential value for oat breeding. They not only possess wild genetic variability in a number of important characters, but also most are closely related to the cultivated species, since they share the same chromosome number. Hexaploid weedy species are members of the primary gene pool. Diploid and tetraploid wild forms can be regarded as the secondary gene pool of the common oat. Many forms from both groups seem to have particularly useful genes for improving such traits as disease resistance, earliness, good tillering capacity, kernel size and quality[1,3,4,8].

The Vavilov Institute contains about 2000 accessions of wild and weedy species with different ploidy levels[5,6]. Collection of wild and weedy forms from former territories of the USSR (now CIS) currently number about 300 entries, as a result of collecting expeditions undertaken in the late of 60's and early 70's. More than 85% of them are hexaploid[6]. These expeditions suggest that the Caucasus area has a concentrated diversity of wild and weedy species of oats. The Caucasus mountains are a part of the Asia Minor centre of origin of the *Avena* genus after Vavilov's classification[9]. The investigation of this area has determined that in the Caucasus territory there are nine wild and weedy species of oats after Rodionova and Soldatov's classification (1982). These are wild species (*A. clauda, A. pilosa, A. ventricosa, A. bruhnsiana, A. wiestii and A. barbata*) and weedy species (*A. fatua, A. ludoviciana and A. sterilis*).

In the Caucasus, the diploid and the tetraploid wild species of oats are distributed in the territory of Azerbaijan. They are dispersed over the shore of the Caspian Sea, the Apsheron Peninsula, Lenkoran lowland and in the Shemakha plateau. A few entries of *A. barbata* are found in Turkmenistan only. Most of hexaploid weedy entries are dispersed over a vast area of the Caucasus too. Among weedy species, *A. sterilis* is found on the seashore of the Black Sea in Russia/Krasnodar region and in Georgia only. *A. ludoviciana* is also distributed throughout the territory of the Caucasus. These forms are found very often in mixed populations with *A. fatua*, but generally at lower altitude than *A. fatua*. *A. ludoviciana* is more diverse in Azerbaijan and it was collected in 25 districts in this area, in Georgia in nine districts, in four districts of Armenia and in Dahgestan and Krasnodar region of Russia. A few entries were found in the Crimea mountains of Ukraine and in the mountains of middle Asia. *A. fatua*, which is a common noxious weed, is distributed over the territory of the CIS from Arkhangelsk region (Russia) in the north to Tadjikistan in the south.

Methods

Samples of 253 wild and weedy oats which originated from the CIS were evaluated for variation in different morphological characters and agronomic traits. The countries and regions where these entries were collected and number of accessions from each are shown in Table 1.

All entries were grown in an experiment that was sown in 1990 and 1991 at Pushkin near St. Petersburg in Russia.

Table 1. Collection of wild and weedy species of *Avena* from territory of former USSR.

	pilosa	*clauda*	*ventri-cosa*	*bruhn-siana*	*weistii*	*barbata*	*fatua*	*sterilis*	*ludo-viciana*
Azerbaijan	19	7	1	6	13	6	6		97
Georgia							5	1	16
Armenia							6		6
Russia							14	4	5
Ukraine							8		5
Tadjikistan						1	7		1
Uzbekistan							1		
Kazakhstan							1		
Total	19	7	1	6	13	7	48	5	130

The data were analysed using plot means for all traits. Further, we calculated all possible correlation coefficients among traits. For preliminary testing, we also would like to find relationships between some morphologic characters and agronomic traits.

Results and Discussion

Significant positive correlations were found between juvenile growth type on the one hand and duration of different parts of vegetative period and duration of growth cycle on the other hand[(2)]. Decumbent juvenile growth and the rather long first part of vegetative period and growth cycle were positively correlated (0.61; 0.50; 0.46) for diploids, tetraploids and hexaploids, respectively. The most important traits for our conditions for using wild species is the duration of growth cycle, because many entries have a very long vegetative period with prolonged early stages. The shorter period till heading is very important in the case of mating with cultivated oats. In our experiment, the duration of the first stage of vegetative period was positive correlated with growth cycle. The significant correlations were those for duration of the period from germination to shooting and growth cycle, 0.93; 0.87; 0.64 for diploids, tetraploids and hexaploids, respectively. The duration of the period from germination to heading and growth cycle were also positively correlated, 0.82; 0.77; 0.69 for diploids, tetraploids and hexaploids, respectively. Another important trait is lodging resistance. In the field, it was positively correlated with thickness of straw and negatively with plant height, especially in diploid and tetraploid forms. Correlations were 0.50 and –0.45 for diploids and 0.61 and -0.44 for tetraploids, respectively. For hexaploids this relationship was not as strong. Low correlation existed between thickness of straw, -0.43, and plant height, 0.15, and lodging resistance. We consider the period from germination to shooting to have a more important influence on duration of the growth cycle of weedy and especially wild species of oats.

Diploids

Among diploid forms, *A. weistii* had the shortest mean of duration of period till heading from 41 to 58 days. The shortest duration of growth cycle ranged from 78 to 86 days for *A. pilosa*. The early accessions of *A.bruhnsiana*, *A.clauda* and *A.pilosa* were all from Azerbaijan. The shortest plant height in the collection of *A. bruhnsiana* ranged from 45 to 100 cm and about 50 per cent of all accessions were shorter than 100 cm. Diploid forms were tested for resistance to the diseases. They were moderately tolerant to crown rust only.

Tetraploids

A. barbata forms had the more prolonged first part of vegetative period (45-55 days) and also long growth cycle (79-103 days). Plant height of these collections ranged from 85 to 135 cm with a high mean (119 cm). Lodging resistance was not so high because they had a rather large plant height and middlesized thickness of the straw. *A. barbata* from Azerbaijan was moderately resistant to crown rust and tolerant to BYDV. These accessions were tolerant to frit fly as they had stems with moderate pubescence. They had the highest mean values for protein percentage (25.0%) and the lowest 1000 groat weight (5.5g).

Hexaploids

Among the hexaploid *A. ludoviciana*, a correlation was found between altitude of collecting the accessions and juvenile growth type and the duration of the first part of vegetative period. In *A. fatua* a negative correlation existed between altitude on the one hand and the duration of growth cycle and presence of pubescence on the other hand and positive correlation with resistance to crown rust. The more prolonged first part of vegetative period had *A. ludoviciana* entries from Ukraine (mean 49.5 days) and a shorter one for Armenia (mean 41.0 days). This period influenced the duration of the growth cycle. The mean was 101.0 days and 81.5 days from Ukraine and Armenia respectively. The earliest entry was from Azerbaijan. Among accessions there were forms which need vernalisation and they look like winter types especially from Crimean mountains, Ukraine and Azerbaijan. Entries mean plant height was 98.8 cm and this material had moderate lodging resistance. More resistant accessions to crown rust were from Georgia and Armenia and they had the largest yield per plot in *A. ludoviciana* group. BYDV tolerant accessions of this species were found in Azerbaijan. In *A. sterilis*, forms had duration of vegetative period ranging from 97 to 107 days. A few entries from Russia need vernalisation. Mean plant height was 111.0 cm which was similar to cultivated forms.. They had good resistance to all tested diseases, scoring 1-3, except BYDV. Among hexaploid species, accessions of *A. fatua* had the shortest parts of vegetative period and duration of growth cycle. The shortest country mean was found for Tadjikistan collection (47.0 and 86.6 days till shooting and growth cycle, respectively) but the shortest entry was from Russia. Among these forms the shortest accessions were from Azerbaijan (70 cm), from Armenia (72 cm) and from Russia (77 cm). Most of them had good lodging resistance. Field evaluation showed that these accessions had moderate resistant to crown rust. Russia, Azerbaijan and Armenia had the best mean scores (1-3) for crown rust. Tolerant entries to BYDV were from Georgia and Ukraine. Protein content ranged from 17.8% to 20.8%. The highest country mean was observed for collections from Tadjikistan and Ukraine. 1000-groat weight ranged from 13.8 to 31.8 g. The highest country mean was for Russia and Tadjikistan.

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