



# Conference Programme



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# Sponsors

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Oats2020 organised by

**The Institute of Biological, Environmental and Rural Sciences**

at



We are grateful to the following sponsors for their generous support



# Welcome to Oats2020

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## *Welcome to Oats2020*

On behalf of Aberystwyth University and Senova it is our great pleasure to welcome you to this conference.

Food sustainability and climate change are high on the political and agricultural agenda but so too is the production of quality and nutritious food. Oats are undergoing a resurgence, not only for human food, but are increasingly recognised as a high quality animal feed and a high value feedstock for industrial application. Environmentally benign, the oat grain is arguably the most nutritious cereal yet faces real challenges if its true potential is to be realised.

Adopting the title **Oats2020** this conference aims to bring a visionary approach to how those challenges can be overcome, providing a forum where researchers, producers and processors can share and exchange knowledge in formal and networking sessions. Our aim is to disseminate outcomes of projects and research from Europe and North America, provide an opportunity to put recent research on oats in the context of human health and nutrition, provide a forum for the identification of breeding and research targets that meet end-user requirements, identify future opportunities for oats along the supply chain and encourage alliances and new collaborations. The programme includes oral presentations and posters from researchers across the whole of the oat supply chain as well as contributions from a range of end-users of the oat crop.

A meeting such as this would not have been possible without the generous support of our sponsors. We gratefully acknowledge the Biotechnology and Biological Sciences Research Council (BBSRC), whose support has enabled a number of early career scientists to attend this conference. We also acknowledge the contributions from PepsiCo, Morning Foods, Weetabix and DuPont.

We hope you enjoy Oats2020 and thank you all for your valuable contributions to this conference.

# Oats2020 Conference timetable

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## Monday 23<sup>rd</sup> November

10:00 – 13:30	Registration
10:00 – 10:30	Coffee break
10:30 – 12:30	Oat Global Workshop
12:30 – 13:30	Buffet lunch
13:30 – 15:10	Oats2020 Conference welcome & presentations (Session 1.1)
15:10 – 15:40	Coffee break
15:40 – 17:15	Presentations (Session 1.2)
19:30	Poster session with drinks and buffet dinner (20:00)

## Tuesday 24<sup>th</sup> November

06:30 – 09:00	Breakfast sponsored by Morning Foods
09:00 – 10:40	Presentations (Session 2.1)
10:40 – 11:10	Coffee break
11:10 – 12:40	Presentations (Session 2.2)
12:40 – 13:45	Lunch
13:45 – 15:15	Presentations (Session 2.3)
15:15 – 15:45	Coffee break
15:45 – 17:30	Presentations (Session 2.4)
19:30	Drinks followed by conference dinner (20:00)

## Wednesday 25<sup>th</sup> November

06:30 – 09:00	Breakfast sponsored by PepsiCo
09:00 – 10:45	Presentations (Session 3.1)
10:45 – 11:15	Coffee break
11:15 – 13:00	Presentations (Session 3.2) and closing remarks
13:00	Lunch and depart



# Oats2020 Scientific programme

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## Monday 23<sup>rd</sup> November

10:00 – 13:30	Registration
10:00 – 10:30	Coffee break
10:30 – 12:30	Oat Global Workshop
12:30 – 13:30	Buffet lunch

## Oats: current status and future perspectives

### Session 1.1, Chair: Athole Marshall

13:30 – 13:40	Introduction and welcome <i>Mike Gooding, IBERS Aberystwyth University</i>
13:40 – 14:05	Oats...32,000 years in the value chain <i>Chris Green, Senova</i>
14:05 – 14:30	The current situation for oat breeding in Europe - opportunities and challenges <i>Steffen Beuch, NORDSAAT Saatzzucht GmbH</i>
14:30 – 14:50	The future for oats - a market analyst's view <i>Helen Plant, AHDB</i>
14:50 – 15:10	Public – private partnerships <i>Tom Jenkins, Innovate UK</i>
15:10 – 15:40	Coffee break

## Oats: current status and future perspectives

### Session 1.2, Chair: Chris Green

15:40 – 16:05	Oats - a growers perspective <i>Robert Law, Farmer</i>
16:05 – 16:30	Nutraceuticals, cosmeceuticals and beyond <i>Cark Maunsell, Oat Services</i>
16:30 – 16:55	American perspective <i>Bruce Roskens, Grain Millers Inc.</i>
16:55 – 17:15	Support for collaborative research <i>James Phillips, BBSRC</i>
19:30	Poster session with drinks and buffet dinner (at 20:00)

## **Tuesday 24th November**

06:30 – 09:00 Breakfast sponsored by Morning Foods

### **Opportunities for oats: health, milling, feed, industrial uses and new technologies**

#### **Session 2.1, Chair: Cark Maunsell**

09:00 – 09:30 Cardiovascular benefits of eating oats: evidence explained and mechanisms explored

*Frank Theis, University of Aberdeen*

09:30 – 09:55 Potential health benefits of oats consumption: dose - response relationships

*Richard Bracken, University of Swansea*

09:55 – 10:20 Oats: a minor grain with major potential

*Fred Gates, Campden BRI*

10:20 – 10:40 Enhancing milling quality through variety development

*Irene Griffiths, IBERS*

10:40 – 11:10 Coffee break

### **Opportunities for oats: health, milling, feed, industrial uses and new technologies**

#### **Session 2.2, Chair: Jon Moorby**

11:10 – 11:35 Oat metabolism - genetic and environmental drivers and future enhancement targets

*Derek Stewart, James Hutton Institute*

11:35 – 11:55 Full enhanced utilisation of oat: does it hold the potential to assist the transition to a bioeconomy?

*Steve Bowra, Phytatec*

12:05 – 12:20 Why oats fit into a healthy gluten-free diet

*Luud Gilissen, Bioscience - Wageningen University and Research Centre*

12:20 – 12:40 Oats in south-east Asia?

*Yung-Fen Huang, National Taiwan University*

12:40 – 13:45 Lunch

### **Opportunities for oats: health, milling, feed, industrial uses and new technologies**

#### **Session 2.3, Chair: Tim Langdon**

13:45 – 14:10 Oil in oats: some molecular insights

*Anders Carlsson, Swedish University of Agricultural Sciences*

14:10 – 14:30 Breeding oats for improved animal feed

*Sandy Cowan, IBERS Aberystwyth University*



- 14:30 - 14:55      The value of oats in ruminant diets  
*Jon Moorby, IBERS Aberystwyth University*
- 14:55 - 15:15      T3/Oat: relational database for oat genotypes and phenotypes  
*Clare Saied, Cornell University*

15:15 - 15:45      Coffee break

### **Opportunities for oats: health, milling, feed, industrial uses and new technologies**

#### **Session 2.4, Chair: Catherine Howarth**

- 15:45 - 16:15      The state of oat genomics: no more blind dates!  
*Nick Tinker, Agriculture & Agri-Food Canada*
- 16:15 - 16:40      Oat genomics at IBERS  
*Tim Langdon, IBERS Aberystwyth University*
- 16:40 - 17:05      *Avena strigose*: from metabolic gene clusters to genomics  
*Anne Osbourn, John Innes Centre*
- 17:05 - 17:30      Is genomic selection possible in oats?  
*Alf Ceplitis, Lantmannen Agriculture*
- 19:30                Drinks followed by conference dinner (at 20:00)

### **Wednesday 25th November**

06:30 - 09:00      Breakfast sponsored by PepsiCo

### **Challenges facing oats: disease, mycotoxins, and agronomy**

#### **Session 3.1, Chair: Athole Marshall**

- 09:00 - 09:25      Opportunities and challenges of oat agronomy  
*Sarah Clarke, ADAS*
- 09:25 - 09:50      Improving oat crop for stress resistance through multidisciplinary approaches  
*Elena Prats, Institute for Sustainable Agriculture - CSIC*
- 09:50 - 10:10      Development and evaluation of oat varieties with enhanced disease resistance  
*Catherine Howarth, IBERS Aberystwyth University*
- 10:10 - 10:25      Effect of grain development and nitrogen fertilizer on grain quality parameters  
*Pilar Martinez Martin, IBERS Aberystwyth University*
- 10:25 - 10:45      Population structure of European oat germplasm using the 6K oat SNP array and association analysis of frost tolerance  
*Giorgio Tumino, CRA-GPG Italy*



10:45 - 11:15      Coffee break

**Challenges facing oats: disease, mycotoxins, and agronomy**

**Session 3.2, Chair: Dhan Bhandari**

11:15 - 11:40      T-2/HT-2 in UK oat crop – 2014 and 2015 crops

*Derek Croucher, BOBMA*

11:40 – 12:05      Fusarium mycotoxins in UK oats

*Simon Edwards, Harper Adams University*

12:05 – 12:25      Cropping factors influencing the occurrence of dominant *Fusarium* species  
and mycotoxins from Swiss harvest samples

*Torsten Schirderwahn, Agroscope Switzerland*

12:25 - 12:45      Reducing DON content in oats through breeding

*Selamawit Tekle Gobena, Norwegian University of Life Sciences*

12:45 – 13:00      Closing remarks

13:00                Lunch and depart

# Oat Global

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## *The Oat Global workshop*

*Chair: Catherine Howarth*

Oat Global is a new strategy platform for the oat community which emerged as a grass-root initiative between private millers and public leaders in the North American, Latin American, European, and Australian community. It was acknowledged that the oat R&D community is too small in size to afford isolation or regionality. Many challenges in oat production and processing are of global nature and transferability of knowledge across geographies is key to success.

The goal of this platform is to help the public and private oat community to develop and fund cohesive R&D strategies for pre-competitive traits and germplasm. The platform operates at two levels: a strategy level where key resource owners, decision-makers, and influencers are connected in order to leverage available resources (intellectual and financial), and a project level where teams of scientists execute funded projects.

Oat Global started in 2014 and is “on the road” in 2015 to engage a broad base of oat workers both public and private. The aspiration is to move into 2016 with a well-developed international network and a worldwide approach to active and new initiative funded through this platform.

In order to engage the European oat community, Oat Global is being hosted by Oats2020 for a two-hour session where Oat Global will be further introduced. The Oat Global session will be chaired by Catherine Howarth, and Bruce Roskens will initiate and moderate an open discussion with the participants to set direction for a maximum benefit of Oat Global to the European oat community and for maximum engagement of the latter with the former.

# Oral presentation abstracts

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## *Session 1.1 - Oats: current status and future perspectives*

*Chair: Athole Marshall*

### *Oats 32,000 years in the Value Chain*

Christopher Green

*Senova Limited, 49 North Road, Great Abington, Cambridge, CB23 6AS*

Researchers in Italy have recently identified starch found on stones used in grinding grains to have come from oats believed to have been grown some 32,000 years ago. We have come a long way in product innovation and despite increased awareness on the health benefits associated with oats, in human or animal nutrition, and pharma, the global oat production is in decline. The reduced area devoted to oats impacts on the plant breeding industry. As a result of poor value capture on seed and its associated intellectual property consolidation is inevitable.

Whilst there are some examples of strong dedicated value streams, such as that for organic or for gluten free production, the oat value chain is somewhat dysfunctional. In part, this is due to a knowledge gap and disconnect between the various stakeholders that exist along the value chain.

This presentation reflects on the market status and highlights challenges that lie ahead from a plant breeding and seed marketing perspective. It will exemplify some specific communication challenges whilst portraying possible mitigating strategies to re-align the value and ensure sustainable inward investment for the continuance for a vibrant plant breeding activity on oats.

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## **Notes**

## *The current situation for oat breeding in Europe - opportunities and challenges*

Steffen Beuch

*NORDSAAT Saatzucht GmbH, Zuchtstation Granskevitze, Granskevitze 3, Germany*

There is strong economic advice for an upcoming higher competition between different food value chains. In the future, competition between companies or firms inside an individual food value chain (such as oat food) will be of minor importance. In Europe, there are many limits for private financed oat variety breeding as part of the oat value chain. On a national level, domestic oat breeding only can be economically sound if the oat seed market has a sufficient size. Additionally, in too many European countries the use of certified oat seed is limited. Consequently, the refinancing of breeding new oat varieties cannot be guaranteed and resulted in a reduced oat breeding input during the last 20 years.

Despite the decreased breeding activities an annual increase of the oat grain yield of 1.00 % has been detected in German official oat variety trials between 1983 and 2012. Varietal impact was the main significant factor for this increase of the grain yield potential in the trials, whereas agronomic issues have been of minor importance. During the same time the oat grain yield at farming increased by  $16 \text{ kg} \cdot \text{ha}^{-1} \cdot \text{year}^{-1}$  (resp. 0.37 %) only. The yield gap between official trial and farm yield is still significant increasing by 0.71 % per year.

Yield and grain quality remain key factors for successful oat production. Strong variation over environments (locations, years) affects breeding for a higher and more stable oat grain yield. Consequently, a safe assessment of the oat yield potential needs a quite high number of field trials. However, mainly due to financial reasons many European oat breeders as well as National Plant Variety Boards do not reach this number. Furthermore, specific weight still dominates the quality discussion in European oats but has no significant interaction with more relevant grain quality characters.

The introduction of innovative plant breeding techniques offers the possibility to bring oats "state of the art" compared to other arable crops. Oat breeders have to consider the potential of these biotech tools with care. With the view to the European cereal breeding (wheat, barley, triticale etc.) tissue culture techniques offer the possibility to create a faster breeding progress also in oats. In contrast, up to now marker assisted selection is only useful for breeding traits where single genes have greater impact.

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### **Notes**

## *The future for oats – a market analyst's perspective*

Helen Plant

*AHDB Cereals & Oilseeds, Stoneleigh Park, Kenilworth, Warwickshire, CV8 2TL*

UK consumption of oats has grown steadily over the past 20 years, driven primarily by an expansion of milling demand. The amount of oats used for human and industrial purposes has nearly doubled since 1995/96, with around half a million tonnes now milled annually. However, the area planted to oats and production did not follow the same pattern – tightening supplies. Exceptional weather conditions led to a spike in the oat area, and thus, production in 2013, but the area has been contracting again in the two years since. This presentation explores the implications for the UK oat market, should demand continue to grow.

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### **Notes**



## *Public – private partnerships*

Tom Jenkins

*Innovate UK, North Star House, North Star Avenue, Swindon, Wiltshire, SN2 1UE*

Innovate UK is the UK's innovation agency supporting business to help take forward new ideas, technologies and concepts towards commercialisation to generate wealth creation and jobs for the British economy. Since our inception in 2007 (as the Technology Strategy Board) we have invested more than £1.5bn of public funding in innovation, drawing in a further £1.5bn from businesses. This £3bn public-private investment has supported over five thousand UK companies, adding an estimated £7.5bn to the UK economy and creating, on average, 7 new jobs in each of the businesses that have worked with us.

The Sustainable Agriculture and Food Innovation Platform (SAF-IP) is a £90m initiative to support UK innovation across the agri-food sector. Since 2010 a series of thematic competitions has been run to help UK companies focus on specific challenges facing the sector such as crop protection, sustainable protein production and food processing & manufacturing efficiency. With the publication of the Government Agri-Tech Strategy (ATS) in July 2013, Innovate UK has been implementing the investment of £70m through the Agri-Tech Catalyst to support innovation in primary production. A further investment of £90m is being used to strengthen UK capability in agriculture through the creation of new Centres for Agricultural Innovation.

The paper will provide an overview of the work Innovate UK has taken forward to deliver the SAF-IP and ATS, with examples of collaborative projects that are helping UK companies with their 'concept to commercialisation' journey to take new technologies and products to market.

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### **Notes**

## *Session 1.2 - Oats: current status and future perspectives*

*Chair: Chris Green*

### *Oats – a growers perspective*

Robert Law

*Thrift Farm, Baldock Road, Royston, Herts, SG8 9NN*

Robert Law has been involved with the growing of oats for every harvest since 1972, when as a 12 year old school boy he remembers being fascinated by a crop that was taller than him at the time and was a real rarity! From helping on a farm that grew 8 hectares of oats 44 years ago he has progressed from school, agricultural college, farming scholarships abroad, working on and managing farms in England to building up his own farming business which extends to 2,100 hectares. The oat area that he is involved with has in that time multiplied by some 37 times to its present level of 300 hectares or 7% of his farmed area.

The farming business is centred on the Hertfordshire, Essex and Cambridgeshire county borders. Arable crops occupy 75% of the farmed area while grassland used to support a 2,500 ewe sheep flock makes up the balance.

The growing of oats on the farms has been, and continues to be, an essential part of the farming system. They act as a valuable break crop for other cereal crops and help to reduce the levels of soil borne diseases and pests. All oats grown on the farms are under contract with some 80% grown for milling while the remaining 20% are grown for seed.

The emphasis for the future growing of oats on our farms is very much on improving quality and increasing field yields as well as the percentage of the crop that makes an end oat product from the volume of material harvested off the field. This is being achieved by better plant breeding, on farm trials and the pooling of knowledge between like-minded growers.

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### **Notes**

## *Natural Actives: nutraceuticals, cosmeceuticals and beyond!*

Cark Maunsell

*Oat Services, The White House, 226 Bassett Avenue, Southampton, Hampshire, SO16 7FU*

Cark Maunsell of Oat Services Ltd will review the natural activity of oats in non-food applications and trace the commercial development of products within these markets.

Although principally known for their cholesterol lowering activity, oat actives also show excellent remedial properties over a wide range in cosmetic and pharmaceutical activity.

In assessing the future development of the food, cosmetic and pharmaceutical markets, oats have recently become well-placed as a nutraceutical ingredient but have the opportunity to be in the vanguard of the new hybrid sectors of cosmeceuticals and nutricosmetics:

A nutraceutical is a product isolated or purified from foods that is generally sold in medicinal forms not usually associated with food. A nutraceutical is demonstrated to have a physiological benefit or provide protection against chronic disease.

Cosmeceuticals are cosmetic products with biologically active ingredients purporting to have medical or drug-like benefits

When ingested, nutricosmetics support the function and the structure of the skin, nails, and hair, having a preventive or reactive effect.

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### **Notes**

## *Oats 2020 – North American Status in 2015*

Bruce Roskens

*Grain Millers Inc.*

Oat production in North America continues with its long-term downward trend in acreage, with only mild gains in yields. Acreage continues to push generally north as more productive crops – particularly corn, soybeans, and canola continue to make faster gains in yield, due considerably to GMO technologies. While there is some renewed interest in small grains, including oats, in areas of sustainable crop rotations and conservation and erosion control, oats continues its image with farmers of being the “the poor man’s crop”, or the “crop of no respect”.

After many years of decline, oats research efforts in the U.S. have seemingly stabilized in terms of funding at land grant universities and with the USDA funded programs. In fact, in the past 2 years we have witnessed breeding positions and efforts reinstated in South Dakota, Minnesota, and Wisconsin, and more support in research work by the USDA. Much of this has been promoted by oat industry companies, and includes some work in the organic farming scenerios.

Publicly funded oats research in Canada is primarily focused at two AAFC locations – Brandon, Manitoba, and Ottawa, Ontario, with testing locations managed by these two programs across several provinces. At least 3 private seed company oats programs are active in the country, and are releasing new varieties in both eastern and western Canada. Also of note is a seemingly increased effort by some seed companies in Canada to test multiple lines from several other countries, including the EU, the US, and South America.

Increases in yield, improvements in disease resistance and/or control, and improvements in nutritional traits continue to be of primary interest from the NA oats industry. Breeding strategies are ramping up to incorporate the new technologies and genome mapping capabilities that have been recently advanced through the efforts of Oats Global and its predecessor – CORE.

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### **Notes**

## *BBSRC: Supporting collaborative research to deliver innovations in agri-food*

James Phillips

*BBSRC, Polaris House, North Star Avenue, Swindon, Wiltshire, SN2 1UH*

The Biotechnology and Biological Sciences Research Council (BBSRC) is one of the seven Research Councils that form RCUK. We invest in world-class bioscience research and training which supports around 1600 scientists and 2000 research students in universities and institutes across the UK. BBSRC is the UK's main public-funder for agriculture and supports science that will contribute to overcoming challenges in Food Security, Bioenergy and Industrial Biotechnology, and Bioscience for Health. We fund collaborative research which generates innovation throughout the entire agri-food supply chain with a variety of mechanisms. Programmes such as the Research Technology Clubs bring together groups of companies and other research users, to support high-quality projects in the research base that respond to challenges identified with industry. We also support collaborations that are nearer to market, often by working with our partners at Innovate UK in programmes such as the Agri-Tech Catalyst. For further information please visit: [www.bbsrc.ac.uk/business](http://www.bbsrc.ac.uk/business).

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### **Notes**

## *Session 2.1 - Opportunities for oats: health, milling, feed, industrial uses and new technologies*

*Chair: Cark Maunsell*

### *Cardiovascular benefits of eating oats: evidence explained and mechanisms explored*

Frank Thies

*University of Aberdeen*

There is increasing evidence from both observational and intervention studies that high consumption of whole-grain food is associated with low risk of chronic disease such as cardiovascular disease and type 2 diabetes. The bulk of the evidence for the benefits of wholegrain comes mainly from observational studies, but evidence of benefit in intervention studies is increasing. However, the difference in composition between types of whole grain food could determine different physiological responses with regard to cardiovascular risk markers. Research has particularly focused on  $\beta$ -glucan-rich cereals such as oats for their potential effect on serum cholesterol concentration and postprandial glycaemia, with inconsistent results. Other mechanisms responsible for the beneficial effects of oats on cardiovascular risk have been suggested, and include lowering blood pressure and inflammatory markers, improving vascular function and increasing satiety. The presentation will critically review the evidence to date regarding the cardiovascular benefits of increased oat-based products intake particularly focusing on long-term intervention studies that investigated the effects of oats or oat bran on cardiovascular risk factors.

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#### **Notes**

## *Potential Health Benefits of Oats consumption: Dose - response relationships*

Richard Bracken

*Applied Sport, Technology, Exercise and Medicine Research Centre (A-STEM), Swansea University*

Oats are processed to convert them into a palatable and nutritious food. The outer layer of the groat is an important source of protein, neutral lipids,  $\beta$ -glucan, phenolics and niacin, and is sometimes separated from the groat to produce oat bran. The inner endosperm consists of proteins, starch carbohydrate and  $\beta$ -glucan while the germ contains mainly lipids (sterols, fatty acids) and proteins and bioactive peptides. Beyond cleaning and grading and dependent on the exact processing conditions (dehulling, heating, drying and cutting) the final grain can provide metabolisable nutrients of potential benefit to human health. This talk will focus on the effects of consumption of whole grain and/or individual components on relevant metabolic pathways pertinent to the development of non-communicable diseases (obesity, cardio-vascular disease and type 2 diabetes) and examine amounts necessary to exert a potential positive effect.

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### **Notes**

## *Oats: a minor grain with major potential*

Fred Gates, Simon Penson and Julian South

*Campden BRI, Station Road, Chipping Campden, GL55 6LD*

Oats were a major cereal crop until the internal combustion engine replaced horses in the early 20<sup>th</sup> century. They have advantages in being a low input crop compared to wheat, perform well on marginal land, are also a valuable break crop, and for reducing pests and weeds in cereal rotations.

Since the 1980s there has been considerable research interest in the link between the consumption of soluble fibre from sources such as oats and various health benefits. The US Food and Drug Administration (FDA) and the European Food Safety Authority (EFSA) have approved health claims to be made for foods containing oats, providing that they meet certain criteria.

Oats have a 'clean' image and are often chosen as ingredients for this purpose. Health claims focussing on 'natural' often assume that the product is free of contaminants. However, this is not always the case and there are numerous chemical hazards which can be found in oats, both in organic and traditional growing systems. These include agrochemical and environmental contaminants, mycotoxins and chemicals (such as acrylamide) that may be formed during processing. There are many types of contaminants (Hutton *et al.*, 2011) and they should be considered in relation to their source, whether they are residues from agricultural production and storage (e.g. pesticides), environmental (e.g. heavy metals) or formed during processing (e.g. acrylamide). Some of the key contaminants to consider in oat products are considered here. With careful selection of grain samples for processing, and monitoring of residues in the harvested grain, oats can provide an excellent cereal to include in healthy products.

The high lipid content and active enzyme systems make oats susceptible to rancidity. For this reason most commercially available oat products (e.g. flakes, flour and bran) are stabilised using a heat treatment to inactivate the lipid hydrolysing enzymes. This process also modifies the technological quality of the product and may contribute to food safety by reducing microbial loads. Native oat has a mild, sometimes grassy flavour, however the heat treatments that are traditionally used in oat processing generate a number of flavour compounds. Flavour is determined by the precursors present in the groat and thermal processing. Further processing such as cooking the oatmeal, extrusion or baking will modify the flavour as new compounds are formed and volatiles are evaporated. These can be characterised using advanced techniques such as quadrupole time of flight gas chromatography mass spectroscopy (Q-TOF GC/MS), which can rapidly determine an aroma profile for a sample.

Oat is a minor grain that has received renewed interest in the past few years. This has been mainly driven by consumer perception of oats as naturally healthy and the health benefits of oat beta-glucan. There is considerable scope to expand the range of products that include oats to help increase the level of fibre in the diet. Achieving the level of addition required to make a health claim



in a commercially viable product is challenging. Developing well-defined and widely accepted specifications for quality attributes would benefit this growing market.

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## Notes

## *Enhancing milling quality through variety development*

Irene Griffiths, Sandy Cowan, Catherine Howarth, Tim Langdon and Athole Marshall

*IBERS, Gogerddan, Aberystwyth University, SY23 3EE, Wales, UK*

There has been an oat breeding program based in Aberystwyth since 1919 producing varieties primarily for the U.K. Since 2001, over 30 winter and spring oat varieties have been included on the UK National and Recommended Lists. This includes a number of innovative oat varieties including the winter oat, Gerald which won the NIAB Cereals Cup voted as the variety most profitable by farmers and Mascani which is at present grown on the vast majority of the winter oat area. Currently 67% of the oats grown in the UK were bred in Aberystwyth. The general targets are to produce economically competitive varieties which are high yielding, disease resistant, easy to crop and meet end user requirements. In the UK, approximately 70% of oats grown are used for human consumption and the market for cereal products is expanding by 5% per annum. For the milling industry, the goals are high yielding varieties with high specific weight, high kernel content, that are easy to dehull combined with appropriate grain composition. The programme has strong links with the UK milling industry, which provides validation of breeding targets and undertakes analysis of the milling quality of selected varieties.

Producing new varieties is a long process. The first stage is to identify genetic variation for the traits of interest and to incorporate that into U.K. adapted material. Following the initial cross a rigorous selection process is undertaken integrating a range of high throughput phenotypic and genetic tools. In early generations plants are selected for traits such as height, disease resistance, flowering time and maturity. As selections progress through the breeding program, multi-locational field trials are used and grain quality traits (e.g thousand grain weight, specific weight, kernel content, hullability and  $\beta$ -glucan content) are assessed as well as grain yield. Together with the agronomy results these criteria form the basis for variety creation. Quicker and more efficient methods of DNA analysis are allowing the integration of marker technology into the breeding program. This enables a more directed selection approach in which only plants with the desired markers for traits of interest are taken forward into the next generation. The application of these techniques with regards to the development of high quality milling oats will be discussed.

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### **Notes**

## *Session 2.2 - Opportunities for oats: health, milling, feed, industrial uses and new technologies*

*Chair: Jon Moorby*

### *Oat Metabolism - Genetic and environmental drivers and future enhancement targets*

Derek Stewart, FRSC

*The James Hutton Institute, Invergowrie, Dundee, DD2 5DA, Scotland, UK*

The beneficial health and wellness stories centred on oats mean that it occupies an excellent position in the consumers view. Exploitation of this for existing and new products is still in its relative infancy compared with other cereals. Oats have a good nutritional and health beneficial component portfolio and these have been the target of an increasingly intense breeding effort. To ensure a resilient supply chain the environmental and agronomic aspects have been, and continue to be, studied to ensure that quality maintenance and enhancement is realised in different environment and conditions.

As part of several oat-based projects, including QUOATS ([www.quoats.org](http://www.quoats.org)), we have adopted a metabolomics approach to oat analysis alongside geneticists, breeders and agronomist to deliver a more complete story on the development of oat quality. Metabolomics, by definition, deals with metabolites many of which in isolation or through processing deliver the desirable end-user parameters. In broad terms well designed field trials were exploited and identified that there were expected outcomes from agronomic practices, e.g. increasing applied N impacted on amino acids content and composition, but also unexpected ones, e.g. impacts on phenolic content and composition. This will be dealt with in greater detail for key quality components.

Using real industry examples we will also show how metabolism (raw material quality) impacts on product quality, shelf life and health benefits, and where some potential targets for future enhancement may lie and the implications of this for new product development.

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#### **Notes**

*Full enhanced Utilisation of Oat; does it hold the potential to assist the transition to a bioeconomy?*

Steve Bowra

*Phytatec, Plas Gogerddan, Aberystwyth, Ceredigion, SY23 3EE, Wales, UK*

Biobased economic development is the stated vision for the 21<sup>st</sup> Century, which places particular emphasis on greater utilisation and exploitation of biomass and biotechnology. The driving principles underpinning the vision are sustainability, reduced dependence on fossil fuels and mitigation of climate change.

The goal of the presentation is illustrate the need to integrate the value chain and make a case that crops such as Oat as having the potential to support sustainable agriculture and therefore sustainable biomass production and thereby sustainable economic development.

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**Notes**

## *Why oats fit into a healthy gluten-free diet*

Luud JWJ Gilissen

*Bioscience – Wageningen University & Research centre, The Netherlands*

Oat is a healthy, nutritious and sustainable crop. It contains high amounts of unique soluble fibres (cholesterol-lowering beta-glucans), especially in the bran fraction. The unsaturated fatty acid content, also in the endosperm, is high (reducing risks of heart and vascular diseases). Oat starch is slowly but completely degradable (low glycaemic index favourable in glucose and weight control). Specific polyphenols and avenanthramides have antioxidant and anti-inflammatory properties. The oat protein contains all essential amino acids in amounts according to human need. Oat protein is safe to people with coeliac disease (CD), because the known CD immunogenic epitopes are absent. Increasing food research data also confirm the safety of oat in the gluten-free diet. Five EFSA health claims can be applied to oats, making this crop a healthy and welcome supplement to the gluten-free diet. Since 2009, according to European legislation, oat products may be sold as gluten-free, provided a gluten contamination level below 20 ppm. To achieve this level, a gluten-free production chain has been established in The Netherlands with very strict rules for agronomy and production throughout the entire chain. Presently, the gluten-free oat product diversity is still low, but several innovations have been started in breakfast cereals, bakery products (e.g. dough-based oat bread), and sweet and salty snacks.

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### **Notes**

## *Oats in South-East Asia?*

Yung-Fen Huang<sup>1</sup>, Chia-Shen Chen<sup>2</sup>

<sup>1</sup>Department of Agronomy, National Taiwan University, Taiwan; <sup>2</sup>Hengchun Branch, Taiwan Livestock Research Institute, Taiwan

Oat is a popular forage crop which may be grazed, cut-and-carried, made into hay, silage or balage. Dairy cattle farms in Taiwan depend heavily on the imported oat forage for animal feed. However, the international oat forage trade is becoming unstable and the price increasing. To provide alternative forage options to Taiwan's dairy cattle industry, an integrative forage research project is initiated and oat breeding is one of the components. Historically, oat research has been started in Taiwan at latest since 1930's. In the 1980's, a forage oat variety has been welcomed with enthusiasm by grower and dairy cattle farmers. Oat has therefore a proved potential to be grown under the climate condition in Taiwan. The renaissance of oat breeding in Taiwan is made possible through the participation to the Quaker International Oat Nursery and the generous germplasm sharing from Agriculture and Agri-Food Canada. We are collecting preliminary phenotypic data and aim to share our results to the community, particularly to regions sharing similar natural conditions.

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### **Notes**

## *Session 2.3 - Opportunities for oats: health, milling, feed, industrial uses and new technologies*

*Chair: Tim Langdon*

### *Oil in oats: some molecular insights*

Anders Carlsson,

*Department of Plant Breeding, Swedish University of Agricultural Sciences*

Starch, proteins and, to a minor extent, lipids are the main reserve nutrients in cereal grains. Compared to the other cereals, oat grains are unusual since they contain relatively high amounts of lipids. Oat species of different ploidy levels carry a great variation in not only the oil content but also in such as fatty acids and lipid composition, which are important traits that influence the oat oil quality. Previous work has shown the great potential in breeding for cultivars with different oil contents. A key in the understanding of the uniqueness of the oil in oat is its unevenness distribution in the oat grain. A major part of the lipids (86–90%) are found in the endosperm and “high-oil” cultivars have oil content in the endosperm compared to “low-oil” ones. There are also differences in the appearance of deposited oil in the compartments of the oat grain from discrete oil bodies in the aleurone layer, scutellum and embryo, to oil collections with diffuse boundaries in the endosperm. This suggests that not only the trait for high oil content but also the ability of accumulating the oil as mainly TAG and perhaps also to deposit the oil in the endosperm are highly influenced by the genotype.

The presentation will discuss the clear differences in the oil deposited across the compartments of the oat grain, the different proportion of the deposition of oil between “high-oil” and “low-oil” varieties, and the utilization of the different oil sources during germination. Finally, it will present some recent genetic data on regulation of oil synthesis by oat transcriptional factor.

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#### **Notes**

## *Breeding oats as high quality animal feed*

Sandy Cowan, Irene Griffiths Catherine Howarth, Tim Langdon and Athole Marshall

*IBERS, Aberystwyth University, Gogerddan, Aberystwyth, SY23 3EE, Wales, UK*

In contrast to many other parts of the world, oats in the UK are mainly used for human consumption with oats not of milling quality sold for animal feed. However some dedicated markets for feed oats exist including feed for racehorses. At IBERS we breed husked and naked varieties of winter and spring oats that are marketed by our commercial partners Senova Ltd.

There has been considerable effort in recent years aimed at the development of naked oats predominantly for poultry and monogastrics. Naked oats have some of the highest metabolizable energy (ME) values of the cereals and we have made good progress breeding high yielding naked oat varieties with high energy and protein. Recent studies in the Quoats project demonstrated the value of naked oats for animal feed. Their high oil content together with good protein content and the composition of essential amino acids make them an ideal ingredient. Naked oats also have some established niche markets such as inclusion into feed for companion animals, racehorses and as wild bird food. However they have not yet achieved mainstream adoption as animal feed probably due to the lower yield compared to husked oats.

Husked oats produce higher yields and are more widely available than naked oats. For the ruminant market we are now developing oat varieties that combine a high oil groat with low lignin husk (trade mark "HiDioat" Senova Ltd). The high oil provides the high ME value for the feed ration and the low lignin husk is more digestible than a standard husk, making an ideal ruminant feed and as a husked oat will immediately be 20-30 % higher yielding than naked oat.

The use of marker assisted selection (MAS) and high throughput phenotyping (using NIRS) to incorporate traits such as high oil content and low lignin husk into new lines is discussed.

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### **Notes**



## *The value of oats in ruminant diets*

Jon Moorby

*IBERS, Aberystwyth University, Gogerddan, Aberystwyth, SY23 3EE, Wales, UK*

Oats have long been known to be good as part of the diet of ruminant livestock. Ruminants, such as cattle and sheep, benefit from the use of microbes in their rumen to help ferment fibrous feeds, and they can make use of the energy in the whole grain of the husked oat. Energy values for husked oats (ranging between 12 and 14 MJ digestible energy per kg dry matter [DM]) tend to be lower than barley (about 15 MJ digestible energy/kg DM, another feed grain used extensively in livestock diets). Lignin is an indigestible component of the cell wall of plants, and is present in high concentrations in the husk of oats. Higher lignin concentrations make the oat grain less digestible for ruminants, which means less energy is provided by feeds (including oats) with high lignin contents, and recent IBERS oat-breeding objectives have aimed to reduce the lignin content of oat grains to make them more digestible.

The protein contents of oats and barley are roughly similar, at about 10-12% of DM, although the fat content of oats, tends to be much higher than that of barley. The fatty acid content of oats varies greatly, depending on the variety of the oat: naked or husked, spring or winter grown. The high oil concentration of some oat varieties limits the proportion of oats that can be fed to cattle and sheep, but the fatty acid profile of oats is such that ruminant products – meat and milk – from oat-based diets may have a fatty acid profile that is beneficial to human health when consumed. High oil concentrations in feed has a toxic effect on rumen microbes, which reduces the effective digestion of that feed, particularly the fibre components. Although the amount of oats used in livestock feeds is generally no more than about 30% of the complete diet due to their nutritional composition, the relatively high costs of production, particularly of naked oats, limits their use when used in least-cost formulations. The higher fibre content of oats, compared with other cereal grains, coupled with a generally lower starch content, means that the risk of rumen disorders (such as acidosis) is lower when oat grains are fed to ruminants.

Methane, a potent greenhouse gas, is produced in insignificant quantities during the fermentation of feeds in ruminant guts, and it is well known that an increase in the fat content of feeds can help reduce the amount of methane that cattle and sheep produce. Using in vitro and in vivo studies, recent work at IBERS has shown the methane production by rumen microbes was reduced as the fat content of oat grains increased. This suggests that oats, which have a lower nutrient requirement for their growth than some other grains, may also be useful in reducing the environmental impact of livestock production.

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### **Notes**

### *T3/Oat: Relational data for oat genotypes and phenotypes*

Clare Saied<sup>1</sup>, David Matthews<sup>2</sup>, Clay Birkett<sup>2</sup>, James Clohessy<sup>1</sup>, Yung-Fen Huang<sup>3</sup>, Nicholas Tinker<sup>3</sup>, Jean-Luc Jannink<sup>2</sup>

<sup>1</sup>Cornell University, Ithaca NY, 14850; <sup>2</sup>USDA-ARS, Ithaca NY, 14850; <sup>3</sup>Agriculture and Agri-Food Canada, Ottawa ON, K1A 0C6.

The oat breeding and genetics community has seen a tremendous growth in the quantity of data that it produces in recent years. Data management, analysis and accessibility are increasingly important to ensure that biological knowledge does not lag behind data generation and to realize the potential benefits of 'big data' for the wider oat community.

T3/Oat (<https://triticeaetoolbox.org/oat/>) is the repository of international oat phenotype and genotype data for the Oat Global project. Data stored in T3/Oat is open access and all users are able to submit data, establishing the database as a tool to support coordinated or individual trialing efforts. T3/Oat provides flexible queries for extracting desired datasets for analysis as well as integrated visualization tools for comparing trials, and analytical tools for genomic prediction and association. Applying modern computational techniques to large-scale, shared data in this manner will support scientific publications and variety releases, and will maximize the returns on the increasing volume of data produced by the oat community.

T3/Oat currently holds data from over 1,000 publicly funded phenotype trials, including Collaborative Oat Research Enterprise (CORE) trials and the Uniform Early and Midseason Oat Performance Nurseries, as well as genotype data generated by the CORE project. A publicly funded oat genotyping initiative was initiated this year to further oat improvement through collaboration and to enhance the genotype data available in T3/Oat. Public sector oat breeding programs in North America submitted over 1,300 breeding lines, and the resulting genotyping-by-sequencing (GBS) allele data will be made publicly available through T3/Oat.

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#### **Notes**

## *Session 2.4 - Opportunities for oats: health, milling, feed, industrial uses and new technologies*

*Chair: Catherine Howarth*

### *The state of oat genomics: no more blind dates!*

Nick Tinker

*Agriculture & Agri-Food Canada*

The oat genome is like a wonderful city full of diverse and interesting people. Unfortunately, the roads in "Oatopolis" are bewildering, and most of its inhabitants have no fixed address. Finding a partner in Oatopolis is based on spontaneous dates – often with the wrong person in the wrong place. Stable, long-term relationships are rare.

So it is with the genes of oat: we work with an enviable diversity of oat phenotypes, but the genes that control these phenotypes are often unmapped, elusive and unpredictable. It has not helped that oat varieties often contain variable chromosome rearrangements. The lack of a consistent oat map has led to difficulties in establishing robust genetic predictions that can be integrated into a reliable inventory of targets for selection. In my personal experience, this has a psychological cost: It is hard to make long-term commitments to genes that seem..."flakey".

Despair no more: the Collaborative Oat Research Enterprise (CORE) has embraced diversity! CORE teams have developed a new high-density oat consensus map that is based on the most common and consistent chromosome configurations within a sample of 20 oat parents. Importantly, we have also documented differences among the component maps from which the consensus was developed – suggesting locations where extra care may be needed when making predictions. The new map provides positions of approximately 17,000 SNPs from two public platforms: a 9K Illumina SNP array, and a genotyping-by-sequencing (GBS) technique. Diversity and association-mapping studies have demonstrated that these marker platforms, together with the latest consensus map, are poised to deliver a bountiful new harvest of robust genetic predictions.

This presentation will provide a users' guide to new tools for oat genomics. A case study in the dissection of a marker-trait association will be illustrated using a visually-intuitive interface that is part of a new GBS pipeline.

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#### **Notes**

## Oat genomics at IBERS

Tim Langdon<sup>1</sup>, Robert Vickerstaff<sup>1,2</sup>, Maciej Bisaga<sup>1</sup>, Debora Giorgi<sup>3</sup>, Sergio Lucretti<sup>3</sup>, Sandra Prusaka<sup>1</sup>, Chris Creevey<sup>1</sup>, Matt Hegarty<sup>1</sup>, Ziya Dumlupinar<sup>4</sup>, Adriana Ravagnani<sup>1</sup>, Catherine Howarth<sup>1</sup>, Athole Marshall<sup>1</sup>

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An *Avena* reference genome has been constructed, based on approximately 40-fold sequencing coverage of the wild diploid *Avena atlantica* with map information provided by survey sequencing of selected progeny of a population of *A. atlantica* x *A. strigosa*. Homology evidence and gene prediction were used to annotate the assembly with gene models. Transcriptome data from eleven *A. atlantica* tissues was used to further catalogue gene content and expression. This provides an overview of a typical wild *Avena* genome and gives some indication of the specific pathways and adaptations that distinguish oat from other cereals. We are currently using this information to guide assembly of genomic information from the hexaploid oat *A. sativa*, and to identify markers and candidate genes for agronomically important traits in the oat crop. A novel chromosome sorting method developed by our collaborators has greatly improved the efficiency of our hexaploid sequencing and is being applied to the common parent in our Nested Association Mapping (NAM) population. Genotyping-by-sequence and survey sequencing of NAM progeny will allow mapping of the hexaploid assemblies, and simplify association of traits and candidate genes in this population. Developing grain transcriptomes of the NAM parents are also being used to examine variation in expression in the hexaploid.

Longer term projects to understand oat domestication and to access useful genetic variation from historic or wild material will also be described.

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## Notes

## *Avena strigosa: From metabolic gene clusters to genomics*

Anne Osbourn

*John Innes Centre, Norwich Research Park, Norwich NR4 7UH, UK.*

Identifying novel natural product pathways in plants is extremely difficult because plant genomes are much larger and more complex than those of microbes. However, the recent discovery that genes for some types of plant natural product pathways are organised as physical clusters is now enabling systematic mining of plant genomes in the quest for new pathways and chemistries. The Osbourn lab has defined a large multi-gene cluster for the biosynthesis of antimicrobial triterpenes (avenacins) that protect oats against soil-borne pathogens such as take-all, and has now cloned and characterized all of the genes and enzymes of the pathway. Current projects include investigation of the origins of this gene cluster in oat, and metabolic engineering of triterpene biosynthesis into other plant species (e.g. *Arabidopsis thaliana*, rice, tobacco and wheat). In a collaborative project with Professor Bin Han (Shanghai Institute of Plant Physiology and Ecology) the genome sequence of our diploid oat reference species *Avena strigosa* (accession S75) has been determined *de novo* using whole genome shot-gun sequencing (>90% coverage; genome size 3.92 Gb) and will soon be frozen in preparation for assembly and annotation.

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### Notes

## *Is genomic selection possible in oats?*

Alf Ceplitis

*Lantmännen Lantbruk*

Genomic selection – i.e. the method of estimating breeding values from marker data only – has revolutionized cattle breeding, and is receiving increasing interest also from the plant breeding community. To date, research on and implementation of genomic selection in plant breeding has focused mainly on larger crops such as maize, rice, wheat and barley. In order to implement genomic selection it is necessary to have access to suitable genomic tools, i.e. reliable, efficient and high-throughput genetic marker systems (typically SNP markers). Due to the complex nature of the oat genome and generally low levels of research investments compared to many major crop species, relevant genomic tools have long been lacking in oats. Nevertheless, a recently developed 6k SNP chip now opens up the potential for genomic selection in oats.

Here, I will present some results on genomic selection in a Swedish spring oat breeding program. In particular I will show how prediction accuracy – i.e. how precisely markers can predict phenotypes – varies depending on the trait under study, the composition of the training populations used to develop the prediction model, and the choice of prediction model, using real data (not simulation or cross-validation). I will also discuss the relevance of these findings for oat breeding.

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### **Notes**

## *Session 3.1 - Challenges facing oats: disease, mycotoxins, and agronomy*

*Chair: Athole Marshall*

### *Opportunities and challenges of oat agronomy*

Sarah Clarke

*ADAS Gleadthorpe, Meden Vale, Mansfield, Notts., NG20 9PD*

Managed well, oats have the potential to be a high-yielding break-crop for growers. Current estimates of average oats yields for the 2015 harvest (ADAS Harvest Reports) are 6.2 t/ha, slightly above the final Defra estimate for 2014 (6.0 t/ha). However, the 9.3 t/ha average yield of the control varieties in the 2014/15 AHDB Recommended List Trials shows there is potential for growers to make more of the crop.

There are opportunities throughout the season for growers to optimise inputs to maximise yields. Fertilisation is one such area. Current guidelines for Nitrogen fertiliser recommend a maximum of 140 kg N/ha, but recent research has shown that this may be an underestimate and that optimum Nitrogen rates are often over 200 kg N/ha. Optimising other nutrients is also important to maximise yields. Potassium is a significant element for oats since it is important for straw.

A key challenge often cited for oats is grass-weed control. Although there are a number of chemicals authorised for use in oats to control weeds such as blackgrass, cultural control methods are also useful tools. Growers should consider rotations, siting the crop and how they prepare the seedbed.

Growing oats should certainly be considered for a wide range of situations. However, there are some agronomic and physiological questions which, if answered, could help growers understand the crop and maximise output.

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### **Notes**

## *Improving oat crop for stress resistance through multidisciplinary approaches*

Elena Prats<sup>1</sup>, Francisco Canales<sup>1</sup>, Gracia Montilla-Bascón<sup>1,2</sup>, Javier Sánchez-Martín <sup>1,3</sup>, Diego Rubiales<sup>1</sup>, Nicolas Rispail<sup>1</sup>

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Resistance to biotic and abiotic stresses is one of the most desirable traits for many crops as it is directly related to both yield and yield stability and in extreme cases it can be responsible of the 100% of the losses. Oats are susceptible to many pathogens and environmental stresses some of them world-wide distributed and others restricted to particular regions. Breeding for stress resistance is one of the most effective, economical, and environmentally friendly means to control plant diseases and also reduce yield losses due to abiotic stresses. However, breeding of complex traits such as stress resistance is a difficult task which should take into account the importance of the genetic variability in order to find appropriate sources of resistance, integrate different selection tools based both on phenotype and on molecular (not only genetic) markers, and last but not less important it should be based on a sound understanding of the underlying resistance mechanisms. In addition considerations such as the genotype x environment interaction, or biological knowledge of the more durable resistance mechanisms to pathogens are also crucial in order to get stable cultivars. Taking this into account we will explain different approaches carried out by our group for breeding oats adapted to the agro-climatic and stressful conditions of the Mediterranean area including biotic and abiotic factors.

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### **Notes**



## *Development and evaluation of oat varieties with enhanced disease resistance*

Catherine Howarth<sup>1</sup>, Irene Griffiths<sup>1</sup>, Sandy Cowan<sup>1</sup>, Maciej Bisaga<sup>1</sup>, Tim Langdon<sup>1</sup>, Ron Stobart<sup>2</sup>, Jane Thomas<sup>2</sup>, Athole Marshall<sup>1</sup>

<sup>1</sup>IBERS, Gogerddan, Aberystwyth University, SY23 3EE, UK; <sup>2</sup>NIAB, Huntingdon Road, Cambridge CB3 0LE UK

Crown rust (*Puccinia coronata* f.sp. *avenae*) and powdery mildew (*Blumeria graminis* f. sp. *Avenae*) are highly successful pathogens that can reduce oat yields by up to 50% and also impact on grain quality, reducing the value of the grain to the milling industry and other end-users of high quality grain. Powdery mildew is particularly important in the cooler, humid regions of cultivation and in Great Britain it is the most prevalent fungal disease of oats. Crown rust is of worldwide distribution and is important in the main oat growing regions in the US, Australia and Europe. The disease is favoured by warm and humid weather and mild winters and severe attacks have been more common in Great Britain in recent years. Genetic host resistance offers disease control that is potentially far more desirable than the application of fungicides. However, the rapid evolution of pathogen virulence has nullified many single genes for resistance. Aberystwyth University has exploited the genetic variation that exists within oats and capitalised on developments in genomic techniques to not only identify genetic markers associated with both mildew and crown rust resistance but also to use them to select improved oat varieties in both our spring and winter oat breeding programmes. This builds on the extensive underpinning research on oat genomics and genetics at IBERS. It is important also that new varieties developed maintain yield and grain quality. In this paper the development of new varieties using marker assisted selection is described along with results from two years of field testing.

Funding for this work comes from a number of sources including BBSRC and a project co-funded by InnovateUK and Senova.

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### **Notes**

## *Effect of grain development and nitrogen fertilizer on grain quality parameters*

Pilar Martinez Martin, Irene Griffiths, Sandy Cowan, Catherine Howarth

*Institute of Biological Environmental & Rural Sciences (IBERS), Gogerddan, Aberystwyth University, SY23 3EB, Wales, UK.*

Nitrogen fertilisation is an increasing economic and environmental concern, becoming a more important factor in developing sustainable production systems for cereal crops. Nitrogen is a vital nutrient for plant growth and yield formation. Understanding and enhancing the efficiency of nitrogen use is important in improving the economic competitiveness of oats but also has environmental benefits through reduced greenhouse gas emissions and reduced N leaching and run-off.

Additions of nitrogen have been shown to increase grain yield by increasing tiller survival and therefore the final shoot numbers and grain number per unit area. However it is important that the quality of that grain is maintained. Despite this, a clear understanding of the major effects regarding nitrogen influence on grain quality parameters is lacking. Results from a previous study on the genetic and environment effects on quality parameters showed that there was a differential effect of environment on grain chemical and physical parameters. On the basis of these results, in 2013-2014 and 2014-2015, four oat winter varieties, Mascani, Tardis, Balado and Gerald, were grown under six different levels of nitrogen fertilisation. After harvest, the grain was analysed by non-destructive methods (MARVIN), in addition to specific weight, kernel content, hullability, thousand grain weight, oil, and protein and  $\beta$ -glucan content determinations in order to identify the influence of nitrogen on grain quality parameters.

This PhD project is part-funded by AHBD-Cereals and Oilseeds (RD 2012-3774)

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### **Notes**

## *Population structure of European oat germplasm using the 6K oat SNP array and association analysis of frost tolerance*

Giorgio Tumino<sup>1</sup>, Roeland E. Voorrips<sup>2</sup>, Fulvia Rizza<sup>1</sup>, Franz W. Badeck<sup>1</sup>, Caterina Morcia<sup>1</sup>, Roberta Ghizzoni<sup>1</sup>, Christoph U. Germeier<sup>4</sup>, Maria-João Paulo<sup>3</sup>, Valeria Terzi<sup>1</sup>, Marinus J.M. Smulders<sup>2</sup>.

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Among winter cereals, oat is the most frost-sensitive and its winterhardiness is insufficient in areas with severe winters. Fall-sown winter oats have a longer growth cycle, earlier maturity and higher productivity than spring oats, hence improving frost tolerance is an important goal in oat breeding. The availability of new genotyping tools, such as SNP arrays, made Genome-Wide Association Study (GWAS) a suitable approach for QTL mapping in oat.

A diverse set of European oat germplasm, including landraces and modern varieties from different countries of origin, was genotyped using the Infinium 6K SNP Array (Tinker et al. 2014). The data were analysed based on hybridization intensities, which were used as continuous scores, rather than calculating discrete values by genotype calling. PCA and Ward's clustering revealed the presence of two main groups related to different European areas of origin. These groups roughly corresponded to Central+Eastern Europe and Western+Southern Europe, although a total of 8 subgroups can be distinguished.

The accessions were phenotyped for frost tolerance under controlled conditions by measuring fluorescence quantum yield of photosystem II after a frost stress (Rizza et al. 2001). Genome-wide association analyses were performed by a linear mixed model approach. Two models including principal components or genetic distances were used for population structure correction. The most robust associations detected six QTLs, three of which co-mapped with QTLs identified in previous studies based on bi-parental mapping populations. The approach used in the present work shows that QTL mapping of winterhardiness-related traits in oat is possible based on data obtained under controlled conditions. A higher marker density would increase the association between markers and QTLs, therefore increasing the probability to detect QTLs.

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### Notes

## *Session 3.2 - Challenges facing oats: disease, mycotoxins, and agronomy*

*Chair: Dhan Bhandari*

### *T-2/HT-2 in UK oat crop - 2014 and 2015 crops*

Derek Croucher

*British Oat and Barley Millers' Association (BOBMA)*

This presentation will summarise BOBMA data on mycotoxins collected from the 2014 and 2014 UK oat crops. Specifically regional data on T-2 and HT-2 mycotoxins will be reviewed in the context of Commission Recommendation 2013/165/EU, along with an overview of the co-occurrence with other Fusarium toxins.

The presentation will include data showing the reduction in mycotoxins through cleaning prior to "first stage processing"

The process adopted by the UK in terms of investigation of the relatively high T-2/HT-2 levels in the 2014 crop will be presented.

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#### **Notes**

## *Fusarium mycotoxins in UK oats*

Simon Edwards

*Harper Adams University, Newport, Shropshire, TF10 8NB, UK*

*Fusarium* mycotoxins are fungal toxins produced by species belonging to the *Fusarium* genus during infection of crops. Small grain cereals are susceptible to a disease called head blight which can result in harvested grains containing fusarium mycotoxins. Several different species of *Fusarium* can cause head blight and different species produce different mycotoxins. Worldwide, oats are generally considered less susceptible to head blight compared to wheat and barley.

In 2006 the European Commission set legislative limits for the fusarium mycotoxins deoxynivalenol (DON) and zearalenone (ZON) for cereals and cereal products intended for human consumption and guideline limits for feedstuffs. The legal limits for DON and ZON in oats intended for human consumption are 1750 and 100 ppb respectively. In 2013 the European Commission published a Recommendation that set indicative limits for the fusarium mycotoxins HT2 and T2, with a combined limit of 1000 ppb (HT2+T2) for oats intended for human consumption. The Recommendation requested Member States to continue monitoring HT2 and T2 in cereals and cereal products and to conduct investigations when indicative levels were exceeded, to determine why exceedances occurred, with an aim to consider legislative limits in 2015.

Surveys of commercial UK oat crops conducted from 2002-2008 identified that the legislative limits for DON and ZON were rarely exceeded in oats but that 16% of samples exceeded the indicative limit of 1000 ppb HT2+T2. Modelling of the associated agronomy data identified that variety and cereal intensity were key determining factors of HT2+T2 concentration in harvested oats. Spring oats had a lower average HT2+T2 content than winter oats and the average HT2+T2 content increased with increasing cereal intensity within a rotation. Subsequent analysis of grain samples from AHDB Recommended List variety trials clearly identified differences in HT2+T2 content between and within winter and spring varieties. Winter varieties tend to have a higher HT2+T2 concentration compared to spring varieties and have a broader range HT2+T2. Studies are on-going to understand the cause of differences observed between varieties (See Abstract/Poster of Stancic et al).

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### **Notes**

## *Cropping factors influencing the occurrence of dominant Fusarium species and mycotoxins in oats from Swiss harvest samples*

T. Schirdewahn<sup>1</sup>, F. Mascher<sup>2</sup>, C. Martin<sup>2</sup>, T.D. Bucheli<sup>1</sup>, M. Bertossa<sup>2</sup>, R. Morisoli<sup>2</sup>, T. Musa<sup>1</sup>, F.E. Wettstein<sup>1</sup>, B. Keller<sup>3</sup>, S. Vogelgsang<sup>1</sup>

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Small-grain cereals provide the major part of calorie intake for the Swiss population. Especially oats can contain interesting levels of health promoting compounds (HPCs). However, cereals must also be safe and therefore free of health threatening substances, such as *Fusarium* mycotoxins. For *Fusarium* head blight in cereals, *F. graminearum* (SCHWABE) is the most prominent species worldwide. Still, cereal types differ in their susceptibility to different *Fusarium* species and various factors, such as weather and cropping measures have an impact on their occurrence.

The main aim of this project is to reduce the contamination of small-grain cereals by *Fusarium* toxins while developing value added varieties containing higher levels of HPCs. In a first step, oat samples from all over Switzerland have been collected in 2013, 2014 and 2015, along with information on respective cropping factors. The incidence of different *Fusarium* species was obtained by using a seed health test. The mycotoxins were quantified by LC-MS/MS.

Based on the current results, the main occurring species and mycotoxins in oats were *F. poae* and T-2/HT-2, respectively. In depth analyses to reveal potential correlations between *Fusarium* species/mycotoxins and cropping factors are presently running.

Results from the monitoring and epidemiological studies will be used to extend the forecasting system FusaProg for wheat towards oats. Thus, a tool for growers to reduce the application of fungicides and to decrease the infection risk will be developed. Several partners along the food chain will contribute to implement the results for an improved safety of healthy Swiss cereals.

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### Notes

## *Reducing DON content in oats through breeding*

*Selamawit Tekle Gobena*

*Norwegian University of Life Sciences*

Mycotoxins in oats has become a major issue in Nordic oat cultivation during the past 15 years. DON is the major toxin, the relative occurrence of HT2+T2 is less, but unclear. Resistance breeding has focused on the infection process to identify the best traits for selection. DON is the best, since it is direct and FHB has much less and more imprecise variation. However, it may be an underestimate due to shrivelled seeds. Germination percentage is also useful, and may reflect later infections in hulls of still viable seeds. Mechanisms of resistance are unknown, but recent experiments concern anther extrusion and flower opening as important factors. Genetic analyses of mapping crosses and the CORE Spring population has shown DON content to be quantitative and depend on many QTLs. A major QTL, accounting for 10-20%, has been detected throughout. Others also reflect lateness favoring low DON. Breeding since 2005 using a disease nursery system has successfully reduced DON content in the released varieties (with desirable phenology) by 40%, from 10-11 ppm to 6-7ppm.

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### **Notes**

# Poster abstracts

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## *Analysis of the genetic and environmental factors influencing grain quality in oats*

Pilar Martinez Martin, Catherine Howarth. Irene Griffiths. Sandy Cowan.

*Institute of Biological Environmental & Rural Sciences (IBERS), Gogerddan, Aberystwyth University, SY23 3EB, Wales, UK*

Grain quality of oats is important to meet the requirements of the milling industry and to enhance the value of the crop for the grower. Developing oat varieties with high milling quality is constrained by a lack of detailed information on how genetic differences and environmental and management conditions impact on grain quality. Focussing on key milling quality characters, i.e. specific weight, kernel content, hullability and thousand grain weight, four winter oat varieties (Gerald, Mascani, Tardis and Balado) were grown under conventional and organic regimes at six geographical locations in 2012-13 and 2013-14. In addition, grain yields and oil, protein and  $\beta$ -glucan content of the groat was determined. The length, width, area, roundness and weight of the grain and groat, were measured using non-destructive methods. The influence of environment, management conditions and genetic differences on grain quality parameters, were determined by statistical analysis. The results were statistically significant for area, length and width between varieties and locations (p-value <0.05). These parameters also showed correlation with kernel content, hullability and thousand grain weight. Further investigations will examine the effect of nitrogen fertilisation on milling quality traits as well as using a mapping population to determine their genetic basis. These results obtained will be used to develop new varieties for the milling industry, by the farmer to assess quality on farm prior to marketing, and by the plant breeder in selection programs, where genetic improvements in milling quality may be made more precisely and rapidly than previously.

This PhD project is part-funded by AHDB-Cereals and Oilseeds (RD 2012-3774)

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### Notes



## *Scalable Non-contact Phenotyping: from Pot to Field*

Catherine J. Howarth, Marie Neal, Roger Boyle, Alan Gay, Fiona Corke, Sandy Cowan, Martin Vickers, Andreu Alcalde Barrios, John H. Doonan,

*National Plant Phenomics Centre, IBERS, Gogerddan, Aberystwyth University, SY23 3EE*

While genotyping becomes ever cheaper and faster, measuring phenotypic variation remains relatively expensive and slow. To address the “Genotype to Phenotype Bottleneck”, the National Plant Phenomics Centre (NPPC) a BBSRC-funded National Facility within IBERS, is developing non-destructive measurement methods that can assess variation in plant performance within genetically defined populations of crop and model plants. Traits, such as flowering time, plant height, number of tillers, biomass and rate of senescence and root depth - and their response to environmental variation - can be quantified using state-of-the-art computer vision approaches.

As an example, we describe the use of the facility to measure the phenotypic variation within an oat mapping population grown on the large plant platform. We compare the results with those collected by conventional manual phenotyping or from reflectance measurements made from UAV’s (unmanned aerial vehicles). A comparison of the quantitative trait loci obtained by the different methods is presented.

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### **Notes**

## *Interaction of Height and Flowering time QTL*

Catherine Howarth, Sandy Cowan, Irene Griffiths, Tim Langdon

*IBERS, Gogerddan, Aberystwyth University, SY23 3EE, Wales, UK*

Transgressive segregation is defined as the appearance of individuals in segregating populations that fall beyond their parental phenotypes and is often observed in breeding programmes. This is a valuable source of genetic variation as individuals identified are novel relative to their parents. The extensively phenotyped winter oat population derived from a cross between the conventional height cultivar Tardis with the dwarf oat Buffalo displays transgressive segregation for both height and flowering time. QTL analysis has revealed how the complementary action of genes from the two parents contributes to these traits. Although plant height in this population is conditioned by the major gene, *dw6*, a strong interaction was observed with flowering time QTL which also influenced extension growth. Three main QTL associated with flowering time were identified which displayed additive gene action. Buffalo and Tardis differ in their response to vernalisation and to photoperiod and distinct QTL for flowering time were obtained depending on the time of year the population was grown.

A set of QTL- near isogenic lines have been developed targeting the introgression of these QTL into either a Buffalo or Tardis background using marker-assisted backcrossing. These are being used to dissect the effect of the genes controlling these traits in more detail and to develop tools to breed for improved adaptation and yield potential. Gaining a better understanding of the genetic basis of wide-cross transgression is not only desirable from an academic view point, but also because of its practical implications.

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### **Notes**

## *Investigating variety response under different fungicide regimes*

Athole Marshall<sup>1</sup>, Catherine J. Howarth<sup>1</sup>, Irene M. Griffiths<sup>1</sup>, Alexander A Cowan<sup>1</sup>, Ron Stobart<sup>2</sup>, Jane Thomas<sup>2</sup>, Alison Barrow<sup>3</sup>, Chris Green<sup>3</sup>

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The powdery mildew and rust fungi are highly successful pathogens that pose a constant threat to UK cereals where infection may drastically reduce grain quality and yield. The fungi are biotrophic, feeding on living plant cells, depriving the plant of nutrients and causing premature leaf senescence. Growing oat varieties with resistance is the most effective and economical method of controlling crown rust and mildew. In this research programme we have examined the yield response and disease expression of a range of spring and winter oat varieties under differing intensities of fungicide regime over 2 years of testing and at 2 geographical locations. Varieties used include current varieties and a range of new potential lines developed at Aberystwyth University using marker assisted selection for both crown rust and mildew resistance. Interactions between variety choice and fungicide programme were apparent in both winter and spring oat trials. In a high disease pressure environment, mean yield across winter varieties increased by around 0.75t/ha in response to fungicide inputs and in spring varieties increased by around 0.5t/ha in response to fungicide inputs. The new lines displayed enhanced disease resistance and their yields out-performed the controls. In low disease pressure environments, the new lines still yielded as well as the controls. An economic analysis of the value of disease resistance and fungicide application will be presented. This project was funded by Innovate UK with support from Senova.

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### **Notes**

## *A Bacterial Artificial Chromosome (BAC) Library of the oat cultivar Ajay.*

Kathy Esvelt Klos<sup>1</sup>, Christopher Saski<sup>2</sup>, Belayneh Admassu Yimer<sup>1</sup>, and J. Michael Bonman<sup>1</sup>

<sup>1</sup>National Small Grains and Potato Germplasm Research Unit, USDA-ARS, 1691 S. 2700 W., Aberdeen, ID 83210; <sup>2</sup>Clemson University Genomics Institute, 310 Biosystems Research Complex, 105 Collings Street, Clemson University, Clemson, NC 29634

Large insert genomic libraries and sub-genomic sequencing have exponentially accelerated our ability and accuracy in capturing and linking genotype to phenotype in complex, repeat-rich plant genomes. For example, map-based cloning of quantitative trait loci can be greatly facilitated by the ability to identify and sequence large-insert Bacterial Artificial Chromosome (BAC) clones, which harbor mapped EST sequences, and surrounding genomic landscape. Here, we constructed a 5-fold redundant *Avena sativa* BAC library using the cultivar 'Ajay'. Ajay is a spring oat variety adapted to irrigated production, which was released by USDA-ARS, Aberdeen, Idaho in 1989. Two independent restriction-derived BAC libraries were prepared by digesting megabase-size DNA with *HindIII* and *BstYI* resulting a >90% potential of genome capture. Fragments  $\geq 150$  kb were ligated to BAC vector and electroporated into *E. coli* DH10B electrocompetent cells. The BAC library consists of 1,245 384-well plates (~478k clones). The BAC clones were arrayed in duplicate onto 25 nitrocellulose filter membranes at a spotting density of ~18.5k clones per filter. Based on a random sample of 384 clones, the average insert size is approximately 140 kb, with <3% of clones containing empty vectors. We screened the library for EST sequences matching those of markers flanking QTL for crown rust resistance mapped in the Ogle x Tam O-301 bi-parental population. Radiolabelled oligonucleotides were found to bind to sequence inserts within clones. A master copy of the Ajay library is available for public distribution to the research community at the Clemson University Genomics Institute (CUGI, [www.genome.clemson.edu](http://www.genome.clemson.edu)).

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### Notes

## *The genetic diversity of modern oat cultivars relative to historic cultivars and landraces held in the National Small Grains Collection (NSGC).*

Louisa Winkler<sup>1</sup>, Harold Bockelman<sup>2</sup>, J. Michael Bonman<sup>2</sup>, and Kathy Esvelt Klos<sup>2</sup>

<sup>1</sup>Department of Crop and Soil Science, PO Box 646420, Washington State University, Pullman, WA 99164-6420; <sup>2</sup>National Small Grains and Potato Germplasm Research Unit, USDA-ARS, 1691 S. 2700 W., Aberdeen, ID 83210

The USDA-ARS National Small Grains Collection (NSGC) has over 9,000 *Avena sativa* accessions available for distribution worldwide to the research community. These accessions represent wide geographical and temporal diversity, offering the opportunity to explore ways in which breeding may have influenced oat germplasm over time in terms of genetic diversity and population structure. An important population of modern oat genotypes is the Collaborative Oat Research Enterprise (CORE) panel, representing oat germplasm used in current breeding programs. For the present study, 481 oat breeding lines or cultivars developed after 1970 were selected from the CORE panel for comparison with 617 accessions from the NSGC which were classified as landraces at the time of collection, and 383 accessions which entered the collection before 1930 and were classified as cultivars or of uncertain improvement status. It was hypothesized that relatively unimproved material would represent a wider and more continuous spectrum of genetic variation than the modern collection and show different phenotypic trait distributions. Also of interest was identification of phenotypic traits defining subpopulations in unimproved versus improved material.

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### Notes

## *Phenotypic Characterisation and Population Structure of an Oat Association Mapping Panel*

Maciej Bisaga, Catherine Howarth, Tim Langdon, Irene Griffiths

*IBERS, Institute of Biological, Environmental & Rural Sciences, Aberystwyth University, SY23 3EE, Wales, UK*

Association mapping is becoming a more and more popular approach to identify genes responsible for quantitative variation of complex traits with agronomical importance. Recent advances in genomic tools such as high-throughput sequencing technologies and high-density single nucleotide polymorphism (SNP) genotyping, allow for development of powerful statistical analysis which make association mapping more available. Association mapping identifies quantitative trait loci (QTLs) through the examination of the differential decay of linkage disequilibrium (LD) between markers and functional polymorphisms across a set of diverse germplasm collection. Since the method was introduced to plant research, an increased effort is observed in assembling various association-mapping populations and initiating experiments through either candidate-gene or genome-wide approaches in different crop species.

This project will use an association mapping population of oats which has been developed at IBERS and primarily represents European genetic variation including landraces, heritage and modern oat varieties along with advanced lines from our own breeding programme. In this study we will demonstrate that genetic association mapping, especially whole genome scan methodology (GWAS) is an effective technique for identifying and mapping QTL in oats. Initially, the panel of 550 hexaploid oat accessions has been fingerprinted with 70 simple sequence repeats (SSR) markers, and evaluated for a number of important agronomic traits. This data will be used to: 1) investigate the genetic and phenotypic diversity; 2) study the dynamics of LD across the oat genome; 2) test the potential of oat association-mapping panel to identify marker-trait associations; 3) determine the relative genetic diversity of modern and older varieties. The knowledge of, access to, and use of diversity in cultivated plants are essential for broadening the genetic base of varieties to sustain improvement.

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### **Notes**

## *Breeding Oats for Future Climates*

Maciej Bisaga, Catherine Howarth and Tim Langdon

*IBERS, Institute of Biological, Environmental & Rural Sciences, Aberystwyth University, SY23 3EE, Wales, UK*

Global mean surface temperature have increased by 0.6°C to 0.9°C between 1906 and 2005 due to the undisturbed emission of the greenhouse gases. Future temperatures are predicted to increase by 1.5°C to 2.2°C by 2030 and by 3.7°C to 4.8°C degrees over the next 100 years. The expected consequences of such warming include major disruption to agriculture, water supplies, bio-diversity and urban systems. Climate change combined with a growing human population, threatens food security everywhere.

Agriculture is extremely susceptible to climate change. Higher temperatures can inhibit photosynthesis, disturb pollination and lead to plant dehydration. Altered rainfall patterns increase the likelihood of crop failures and a decline in food production. Although the increase of greenhouse gases and temperature may be beneficial for some crops in certain parts of the world, it is expected that the overall impacts of climate change on agriculture will be negative.

In our study we are using the PRECIS (*Providing Regional Climates for Impacts Studies*) climate modelling system developed at the Met Office Hadley Centre. For the first time, PRECIS analysis will be engaged to create high resolution climate change scenarios for the United Kingdom using three regional climate models (HadCM3Q0:SRES\_A1B, 1949-2099; HadAM3P:SRES\_A2#1, 2070-2100; ECHAM5:SRES\_A1B, 1950-2100). This will identify predicted climate changes for regions where oats are currently cultivated and potential new locations. The results will be used to develop an oat breeding programme that incorporates climate modelling and ultimately minimise the negative effects of climate change on agriculture, food security and human welfare.

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### **Notes**

## *Development of high protein oat lines for the feed and food industry*

Bindu A Sunilkumar<sup>1, 3</sup>, Yi Ren<sup>3</sup>, Johanna Lethin<sup>2, 3</sup>, Rickard Öste<sup>1</sup>, Olof Olsson<sup>2, 3</sup>

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Oats are an excellent source of high-quality proteins with a favorable amino acid composition. Oat lines with increased protein content would therefore be a very good complement to existing animal and plant protein sources. The aim of this work was to identify and characterize high protein oat lines from a mutagenized oat population (TILLING-population). Seed flour from 1050 different lines was analyzed for nitrogen content using an elemental particle analyzer and total protein content was calculated from the obtained nitrogen values. Altogether 230 lines with a protein value above 15% (w/w) were identified. The amino acid composition for 31 of these lines was determined by various methods and the content of essential amino acids (EAAs according to FAO/WHO) was evaluated. The results showed that the protein content ranged from 17% to 24%, i.e. ca 50 - 100% higher than Belinda. The average value for Belinda, the variety from which the mutagenized population was originally derived, is around 12% protein. In addition, several of the high protein lines contained relatively higher concentrations of EAAs like lysine, threonine, and methionine, i.e. they are not only high in protein but also have a more favorable balance of amino acids. The five best lines were crossed with Belinda to reduce the number of EMS mutations not relevant to the high-protein character. The F1 hybrid seeds were grown in the greenhouse and allowed to self-pollinate. From the F2 offspring single seeds from individual panicles were analyzed for total protein content and it was confirmed that the high-protein character was stable and successively inherited. To further test the stability of the high protein trait, the selected 15 lines were grown in the field after which the seed protein content was quantified again the high-protein character was confirmed. Finally, total dietary fiber (TDF) and  $\beta$ -glucan content was determined in the selected lines. The values for these components were similar to the levels normally seen in Belinda, thus the high-protein character did not negatively influence the other macromolecules. Our results will provide useful information for breeders aiming at increasing the content and nutritional value of oat protein. If successful, it would open ways to develop novel feed and food products based on oat.

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### **Notes**



## *Fusarium langsethiae* genome sequencing

Giorgio Tumino<sup>1</sup>, Valeria Terzi<sup>1</sup>, Luigi Orrù<sup>1</sup>, Antonella Lamontanara<sup>1</sup>, Rasmus J.N. Frandsen<sup>2</sup>, Kristian F. Nielsen<sup>2</sup>, Ulf Thrane<sup>2</sup>, Hege H. Divon<sup>3</sup>, Anna-Karin Kolseth<sup>4</sup>, Erik Lysøe<sup>5</sup>

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*Fusarium langsethiae* has been identified as the main producer of the highly cytotoxic and immunosuppressive type A trichothecenes T-2/ HT-2 (Edwards *et al.*, 2012). Mycotoxin contamination caused by this *Fusarium* species can therefore represent a continuing threat to the harvest and an important food safety hazard. This fungus has a high preference for oats however is now spreading even on barley and durum wheat cultivated in Mediterranean environments (Lattanzio *et al.*, 2015). *F. langsethiae* shows some morphological and metabolic similarities with *F. poae* and *F. sporotrichioides*, but has specific features, like the slow growth, the different response to some fungicides, the fact that the infected plants are rarely showing clear symptoms of infection, and yield is not significantly affected.

Up to now, no studies have been focused on the molecular characterization of *F. langsethiae*. Such data may reveal important information about the biology of the fungus and provide a basis for development of sustainable control practices. Using next generation sequencing technology we have assembled the first draft genome sequence of *F. langsethiae*. In addition, we also made a chemical profile of the secondary metabolites produced on growth media and *in planta*. These results reveals many interesting aspects of its metabolic potential and toxin production.

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## Notes

## *Resistance in UK oats to toxin producing fungi*

Tijana Stancic <sup>1</sup>, Sandy Cowan <sup>2</sup>, Catherine Howarth <sup>2</sup> Simon Edwards <sup>1</sup>

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*Fusarium langsethiae* which produces the toxins HT2 and T2 is the predominant *Fusarium* species found on oats in the UK. In 2013 The European Commission published the recommendation to monitor the combined concentration of *Fusarium* mycotoxins, HT2 and T2 (HT2+T2) in food and feed with an aim to review the need for legislative limits. In studies across the UK between 2002 and 2008 around 16% of oat samples collected at harvest exceeded the proposed indicative levels of 1000 µg/kg HT2+T2 for unprocessed oats. From 2005 - 2011, oats from over 20 winter and 14 spring national Recommended List variety trials were analysed for the presence of HT2+T2 mycotoxins. Winter variety trials were found to have higher levels of HT2+T2 compared to the spring variety trials.

The impact of agronomy on HT2+T2 accumulation on oats, has not been clearly identified. It is not clear whether the difference observed between winter and spring varieties is due to agronomic (i.e. drilling date) or genetic differences. To test the hypothesis that the differences observed were not due to agronomy, six spring and six winter varieties were drilled together in randomised block experiments at three locations in the UK in autumn and spring of two consecutive seasons (2012 and 2013) and HT2+T2 levels determined after harvest.

It was also observed that the mycotoxin concentration of dwarf varieties (which are short-strawed) tended to be higher than that of conventional varieties although the relationship between plant height and mycotoxin levels was not consistent. To test the hypothesis as to whether crop height is a resistance trait, samples from field trials run by Aberystwyth University of a mapping population developed from a cross between short and tall winter oat varieties (Buffalo and Tardis) were analysed for HT2+T2. This population will be used for the identification of QTL for resistance and to determine genetic linkage with agronomic traits such as height and panicle emergence.

This PhD studentship was funded by AHDB- Cereals and Oilseeds (Project RD-2008-3556) as part of the QUOATS project

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### Notes

## *Oat (Avena sativa L.) – technological and chemical properties*

Małgorzata Wronkowska, Henryk Zieliński

*Department of Chemistry and Biodynamics of Food, Institute of Animal Reproduction and Food Research of the Polish Academy of Sciences, 10-748 Olsztyn, Poland*

The single most abundant food, in terms of world production and consumption, are cereals. There are eight cereals of primary economic importance. These cereals listed in a decreasing order of the world production include wheat, corn, rice, barley, sorghum, oats, millet and rye. Oat (*Avena sativa*) has a high nutritional quality and has the beneficial effect of lowering blood pressure for patients with hypertension.

The aims of the study was basic characteristic of technological and chemical properties of Polish oat cv. Slawko.

The analysed cultivar of oat was characterised by: 13.9% d.m. of protein, 2.4% d.m. of ash, 3.1% d.m. of fat. Hull content was about 24% and pericarb with testa content was 5%. The trace elements content was: 29.2 µg/g d.m. of Zn, 2.5 µg/g d.m. of Cu, 48.0 µg/g d.m. of Mn and 0.17 µg/g d.m. of Se.

Cereal grains are one of the major sources of vitamin E for humans. Vitamin E comprises of naturally occurring tocopherols (T) and tocotrienols (T3).  $\alpha$ -T and  $\beta$ -T were the main isomers found among analysed tocopherols in oat. The main tocotrienol found in oat was  $\beta$ -T3. The total amount of tocopherols in oat was 3.7 IU/kg. The total antioxidant activity measured for oat cv. Slawko was 4.3 µmol Trolox/g d.m. and total phenolic compound was 3.3 mg of catechin equiv./g. The content of total glutathione for oat cv. Slawko was 317.7 nmol/g d.m. Two-times higher content of reduced glutathione (GSH) was noticed compared to oxidized (GSSG) glutathione.

The participation in the conference was supported by the grant of KNOW Consortium "Healthy Animal – Safety Food" (MS&HE; Decision No. 05-1/KNOW2/2015)

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### Notes

## *The effect of thermal treatment on the stability of low molecular weight antioxidants in oat*

Henryk Zieliński

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Oats (*Avena sativa* L.) are an important crop widely used in Europe. They are a source of many compounds that exhibit antioxidant activity. These antioxidants are concentrated mainly in the outer layers of the kernel and therefore the impact of oat processing on the antioxidant content is a current issue from the point of view of human nutrition.

The objective of this study was to show the thermal stability of low molecular weight antioxidants (LMWA) in oat when extrusion cooking at 120 and 200°C was applied as a model of hydrothermal processing. Experiment was carried out on a counter-rotating twin-screw extruder. The material was oat cv. Slawko cultivated in Poland, whereas inositol phosphates, phenolic acids, reduced glutathione, melatonin, tocopherols and tocotrienols formed pool of LMWA. The content of LMWA before and after extrusion cooking was compared to provide an information regarding their hydrothermal stability.

Oat kernel contained inositol hexaphosphates and only traces of inositol pentaphosphate. Among phenolic acids, the dominant free phenolic acid was coumaric acid, whereas sinapic acid was the main bound phenolic one. The content ester bound phenolic acids were five-fold higher as compared to free acids pool. The content of both forms of phenolic acids in oat (30,14 µg/g d.m.) was higher than in wheat (10,01 µg/g d.m.) and barley (6,48 µg/g d.m.) In contrast, GSH content in oat was twice lower than in wheat and barley. The oat kernel was proved to be an important source of melatonin and vitamin E.

Extrusion cooking caused degradation of inositol hexaphosphates by 15% and no link was observed between extrusion temperatures and degradation of this compound. The degradation degree of inositol hexaphosphates indicated that this compound was resistant to hydrothermal treatments. The applied hydrothermal process caused significant changes in the phenolic acids content in the extruded oat kernels. A four-fold increase in free phenolic acids and up to 14% in ester-bound ones was found. This finding may be explained by the fact that hydrothermal processing of oat kernels might release phenolic acids and their derivatives from the cell walls due to the changes in the kernel matrix. The hydrothermal process caused a GSH decrease by 32% thus indicating a moderate thermal stability of this antioxidant. The amount of melatonin in extruded oat was reduced two-fold. Extrusion caused a significant decrease in tocopherols and tocotrienols, expressed in term of biological activity of vitamin E, from 38% (120°C) to 89% (120°C). The least resistant for hydrothermal processing was  $\alpha$ -tocopherol and  $\alpha$ -tocotrienol.

The results provided in this study can be a valuable contribution to oat processing for human consumption thanks to its health benefits.

The participation in the conference was supported by the grant of KNOW Consortium "Healthy Animal – Safety Food" (MS&HE; Decision No. 05-1/KNOW2/2015)

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## **Notes**

## *Integration of morphological, physiological and metabolic responses of oat roots for drought tolerance*

Francisco J Canales<sup>1</sup>, Javier Sánchez-Martín<sup>2</sup>, Luis AJ Mur<sup>3</sup>, Nicolas Rispaill<sup>1</sup>, Elena Prats<sup>1</sup>

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Drought is one of the major environmental factors determining plant yield. Tolerance to this abiotic stress is a complex phenomenon comprising a number of physio-biochemical processes including fine sensing of the stress, complex orchestration of signaling pathways, root-shoot communication and reprogramming of metabolite fluxes. In previous work we performed several physiological and metabolomic approaches to identify leaf responses engaged to cope with drought (Sánchez-Martín et al., 2012, 2015). Here, we started to dissect the root responses at several levels to integrate root and aerial responses to drought and hence to reach a better understanding of the complexity of the tolerance mechanisms to this abiotic stress. To this aim we used two oat genotypes, Flega and Patones, previously characterized as highly susceptible and tolerant to drought. During time courses of increasing water deficit, samples were taken to determine in drought-stressed and control plants 1) morphological parameters including changes in root length and diameter, 2) physiological parameters related with water transport and 3) metabolomics changes indicating engagement of particular metabolic pathways as tolerant responses.

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### **Notes**

## *Importance of genetic resources collections for oat improvement - the case of Avena macrostachya Bal. et Durieu in Poland.*

Bogusław Łapiński, Zofia Bulińska-Radomska

National Centre for Plant Genetic Resources, Plant Breeding and Acclimatization Institute (IHAR),  
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The Gene Bank in Radzików (National Centre for Plant Genetic Resources - NCPGR) maintains oat collection of 2523 accessions, including 165 wild ones. The collection contains 240 local cultivars of common oat, mainly from Poland and neighbour countries of Eastern Europe. There are also 31 old Polish cultivars produced before 1960, including 23 ones created before World War II and five before World War I. The marginal and wild oats are represented by *A. fatua*, *A. sterilis*, *A. insularis*, *A. abyssinica*, *A. barbata*, *A. maroccana*, *A. murphyi*, *A. macrostachya*, *A. agadiriana*, *A. atlantica*, *A. damascena*, *A. hirtula*, *A. longiglumis*, and *A. strigosa*. Samples of the oats are on request to breeders, institutes and universities which search for variation useful in improvement of grain quality and resistance to biotic and abiotic stress. The collection delivered 97 objects to the international project AVEQ (Avena Genetic Resources for Quality in Human Consumption 2007 - 2011), which has contributed to better description of botanical, technological and agrotechnical traits. Access to the seed material and data describing our oat collection is possible via the national EGISET database system ([egiset.ihar.edu.pl](http://egiset.ihar.edu.pl)).

The wild and marginal species are known as particularly valuable source of useful variation, however seldom used in breeding projects because of high input of time, labor and skill. The case of *A. macrostachya*, which was brought from the collecting mission in 1989 and delivered by our gene bank to wide crossing and pre-breeding projects (led by the NCPGR) is a fully documented example of successful application of the wild species in oat improvement. The wild perennial outcrossing species *A. macrostachya* is known as a source of resistance to biotic and abiotic stress, including winterhardiness.

The first interspecific crosses, aimed at improvement of winterhardiness, were made in 2002. Currently, the best two winterhardy oat lines are tested in state trials as promising cultivar candidates which are expected to outyield spring oats and stabilize oat production by better avoidance of drought occurring with increasing frequency as a result of climate change. Addition of a doubled *macrostachya* genome to the *A. sativa* chromosome complement is also responsible for extraordinary increase of seed size (TKW up to 70 g) combined with high protein content (18-20%). More than 50 hybrid lines of spring type with the *A. macrostachya* parentage contribution have been delivered via the gene bank to Polish breeding companies.

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### Notes

## *Producing an efficient doubled haploid protocol for Oats*

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Doubled haploid (DH) technology is an important tool in modern plant breeding and genetic studies, and DH breeding has become routine in a number of major cereal crops including wheat and barley. Conventional oat breeding requires multiple generations of inbreeding to produce stable varieties. By using a DH approach, homozygosity could be fixed in a single step. DH oats have been successfully produced by the methods of another culture, isolated microspore culture (IMC) and wide hybridization, however the efficiency is too low for use in breeding programmes and genetic research.

This project aims to improve the efficiency of DH oat production through another culture and IMC, building on previous research by making incremental changes as well as trying novel compound additives which have been successful in other species. The project will also investigate the basis of genotype-specific responses to treatments. Results to date have been encouraging with progress already being made on improving efficiency and regeneration.

This project is funded by the BBSRC in partnership with Senova and Saaten-Union.

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### **Notes**



## *Systems biology approaches to enhance agronomic and nutritional qualities in oat.*

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One of the many health benefits of oats (*Avena sativa*.L) is its antioxidant capacity associated with a high concentration of phenolic compounds called Avenanthramides (Avns). We performed genome wide association studies (GWAS) on Avns using data collected by ultra-performance liquid chromatography mass spectrometry on a 500-member subset of the AFRI Core and the National Small Grains Collection. Genotypes were selected from a 1000-member collection by coefficient of determination method based upon genotype information. Seed multiplication and tissue collection for genotyping by sequencing analysis were carried out in the greenhouse. An incomplete block experimental design with two repetitions was carried out at two locations, and agronomic traits were measured. We applied GWAS for both metabolomic and agronomic traits. A significant correlation between the rust resistance trait and a module containing three identified Avns (A, B and C) and other putative Avns was observed. After GWAS analysis, fifteen markers were associated with the Avns A and B and four of them were significantly associated with both compounds. Eight markers were associated with avenanthramide C, and five of them were also significantly associated with avenanthramide A. No significant markers were associated to both Avns B and C. Our results are consistent with Avn A as the precursor of both Avns B and C, and that abundance of Avns in oat grain is significantly correlated with resistance to crown rust in the mature plant.

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### Notes

*InnovOat: Developing enhanced breeding methodologies for oats for human health and nutrition. Metabolomics for the discovery of biochemical quality markers - method development and quality assurance*

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Within the InnovOat project, traits which may predict yield will be identified by detailed phenomic and field trial analysis of a model winter oat population and an association genetics panel of advanced breeding lines. Metabolic profiling and micro-scale analytical methods will be used to develop further predictive screens for markers associated with key traits concerned with milling quality and with human health and nutrition. Metabolic profiling will be based upon, Gas Chromatography-Mass Spectrometry (GC-MS; Lisec et al. 2006; Allwood et al. 2015), which largely detects amino acids, organic acids, mono-, di- and trisaccharides, amongst other polar metabolite classes, and Liquid Chromatography - MS (de Vos et al. 2007; Jansen et al. 2009), which largely detects secondary metabolites, such as vitamins and their co-factors, as well as phenolic compounds (e.g. flavanoids and glucosinolates), and a smaller number of primary metabolites such as the amino acids. Once a series of metabolic markers that correlate positively with oat nutritional quality,  $\beta$ -glucan content, and milling quality, have been identified, then more targeted and rapid micro-scale analytical approaches will be developed that will allow the high-throughput screening of metabolic quality traits across large scale oat breeding populations, and which are applicable within green tissues at earlier stages during breeding development when assessments of milling quality or  $\beta$ -glucan content within the grain are not yet possible. Therefore, such an approach will permit selection of relevant breeding lines that show the most promise to take forward to later assessments of the grain quality itself and removal of lines that show little promise. As a first step towards the development of appropriate metabolic profiling methods, we must first evaluate a range of extraction methods which are tested with a range of chromatographic method variants, to maximise compound capture and chromatographic resolution. Once extraction and chromatographic methods have been optimised, they must be further quality assured to ensure reproducibility of metabolic profiles and metabolite quantification for a given quality assurance sample. This poster will present the initial work in metabolic profiling method development and method quality assurance that are currently being performed as part of the InnovOat project.

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**Notes**

## *DArTseq markers towards Dw6 dwarfing gene in oats*

Edyta Paczos-Grzęda<sup>1</sup>, Sylwia Róg<sup>1</sup>, Agnieszka Ostrowska<sup>1</sup>, Piotr T. Bednarek<sup>2</sup>

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The principal purpose of cereal breeding programs are creating of new cultivars characterized by high quality and increased yield of seeds as well as tolerant to biotic and abiotic stresses. Cultivation of intensive forms that positively react towards plant protection and increased fertilization enables achieving high yield. Unfortunately efficient plant vegetation could be diminished by lodging. Moreover, lodging exhibits detrimental effects on seed and straw quality. Lodging could be prevented via application of retardants. However, due to lack of sufficient studies and distinct reaction of oat varieties, retardants are usually not recommended. The alternative way that could be considered for lodging prevention is the use of varieties with increased tolerance supported by dwarfness genes.

In Polish breeding programs of oats, dominant dwarfness *Dw6* gene is used to shorten the straw. The forms carrying that gene are usually about 60% shorter, however, without loss of yield.

The primary aim of the study was the identification of putative *Dw6* gene markers by means of DArTseq approach. The F<sub>2</sub> biparental oat mapping population ('Celer' x STH 9210) consisted of 800 plants was used. The STH 9210 is a line with *Dw6* gene that has a short straw whereas 'Celer' is the Polish breeding cultivar growing up to 120 cm high. The height all of the F<sub>2</sub> plants and corresponding F<sub>3</sub> lines were measured. The observed segregation was consistent with monogenic inheritance model. Random sample of 140 plants and parental forms were genotyped using DArTseq technology. The eleven DArTseq sequences were selected for conversion to specific PCR based on segregation mapping studies. Out of converted DArTseq markers only one proved to be polymorphic on DNAs of short and high F<sub>2</sub> plants. Converted marker was located on 18D chromosome of oat (N. Tinker, personal comm.).

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### Notes

## *Breeding Oats for Taiwan: Past and Present*

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Taiwan lies on the Tropics of Cancer (between 21.7° and 25.3°N). Its climate in Northern and Central parts is sub-tropical, Southern part tropical, while the mountainous regions are under temperate condition. In Taiwan, oat was grown as a forage crop since 1930's, introduced from Japan. In the 1980's, a promising forage oat variety has been identified as "off-type" from an accession of Triticale introduced from USDA. Although oats had given rise to enthusiasm among growers and dairy cattle farmers, it didn't last long due to various reasons. Dairy cattle farms in Taiwan depend heavily on the imported oat forage for animal feed. However, the international oat forage trade is becoming unstable and the price increasing. These difficulties that the dairy cattle farms in Taiwan are experiencing are opening opportunities for other forage alternatives. Oat is high on the list because of its popularity and its past success. We have initiated oat germplasm introduction and preliminary phenotypic evaluation. We aim to provide a list of forage oat varieties for local production in near future, as well as milling oats for human consumption. We will also initiate oat research projects to better understand the adaptive dynamics of oats to different growing conditions.

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### **Notes**

## *Composition of health related compounds in Nordic oat varieties grown in contrasting environments.*

Uhlen, Anne Kjersti<sup>1</sup>, Holtekjølen, Ann Katrin<sup>2</sup>, Sahlstrøm, Stefan<sup>2</sup>, Åssveen, Mauritz<sup>3</sup> and Kirkhus, Bente<sup>2</sup>

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The scientific literature documents beneficial effects on human nutrition and health of using oats in diets, and the positive effects have been associated with content and composition of the mixed linked (1→3)(1→4) β-D-glucans (BGs), fat and antioxidants. Thus, the research focus has been on improving the nutritional profile of oat raw material by investigation of genetic variation between varieties as well as effects of environmental factors and management practices. This study was conducted to characterize BGs, fat and antioxidants in oat varieties adapted to the Northern Europe when grown in contrasting environments with respect to temperature, precipitation and day-length. Nine varieties of oats were grown in field trials at different latitudes; Kapp in Norway (60,4°N ) and Wolde in Germany (52,5°N) in 2009. The weather records showed substantial differences in temperature and precipitation between the two locations. Dry and warm conditions were obtained at Wohlde (19,7 °C and 70 mm precipitation during the grain filling period) whereas cool and wet conditions were obtained at Kapp (14,3 °C and 277 mm precipitation). The oat samples analyzed for composition of BGs, fat and phenolic acids. The results are discussed in respect to effects of genotype and environmental factors.

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### **Notes**

## *Recent changes in oat crown rust and mildew populations in the UK and implications for resistance breeding*

<sup>1</sup>Richard Birchmore, <sup>1</sup>Jane E Thomas, <sup>2</sup>Catherine J. Howarth and <sup>2</sup>Athole H. Marshall

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Samples of crown rust and mildew were collected from a number of sites in the UK during 2011 and 2012 as part of a study supporting oat breeding at Aberystwyth University and Senova UK Ltd. Subsets of the isolates were tested on differential cultivars for each disease. There were a number of changes in the virulence structure of crown rust since previous samples were tested in the 1980's and in 2005. For example, virulence for Pc64 had increased to 100% in the most recent isolates tested, but was undetected in 2005, and virulence for Pc45 had decreased to 45% from 100% in previous tests. The resistance in Pc91 remained effective against all the isolates tested. In contrast the powdery mildew population appeared to have remained stable, with no detectable shifts in virulence structure on the differential cultivars used. Isolates of crown rust were further tested on differentials and elite material under two different temperature regimes. In the majority of cases, reaction types were the same in tests carried out at 28°C and 18°C, but a few lines showed a susceptible reaction type at the higher temperature compared to a resistant reaction at the lower temperature. The results suggest that intermittent monitoring of crown rust populations should be carried out in the UK to ensure that oat breeders are testing material with relevant pathotypes. There was also an indication that a few resistances could perform less effectively at high temperatures, and further work is needed to investigate this. However, new breeding material produced during the course of this project remains effective in the field against current crown rust and mildew populations.

This project is funded by Innovate UK with support from Senova Ltd.

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### **Notes**

## *Quantitative genetic parameter for flowering traits in oats*

Matthias Herrmann

*Julius Kuehn Institute, Federal Research Centre for Cultivated Plants, Institute for Breeding Research on Agricultural Crops, Rudolf-Schick-Platz 3a, OT Gross Luesewitz, D-18190 Sanitz, Germany*

In this poster, quantitative genetic parameter for flowering traits like anther extrusion (AE), portion of flowers without anthers (FWA) and open flowering score, assessed on modern and former oat panels, are presented. The AE and FWA are significantly influenced by the oat genotype, the position within the panicle, the environment and the respective interactions. AE and FWA are highly heritable and effective traits for the selection of more cleistogamous oats to reduce infection by pathogens as *Fusarium* and *Ustilago avenae*.

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### **Notes**

## *The Oat Newsletter: satisfying your hunger for information*

Charlene P. Wight<sup>1</sup>, Gerard R. Lazo<sup>2</sup>, Catherine J. Howarth<sup>3</sup>, Jean-Luc Jannink<sup>4</sup>, S. Shea Miller<sup>1</sup>, Marcelo Pacheco<sup>5</sup>, Zongwen Zhang<sup>6</sup>, Pamela Zwer<sup>7</sup>, and Nicholas A. Tinker<sup>1</sup>

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The Oat Newsletter (<http://oatnews.org>) is a dynamic, on-line publication serving the international oat research community and those associated with it. Oat workers are encouraged to submit research reports, community news, and other information to the editor at any time ([curator@oatnews.org](mailto:curator@oatnews.org)). Research reports are reviewed by two members of the international editorial board. In addition to more recent contributions, the Oat Newsletter also provides access to thousands of digitized articles from the first 50 volumes of the original publication.

The website is updated regularly, with notifications sent out by e-mail. Users are also encouraged to follow our Twitter feed (@OatNewsletter). This poster describes the layout of the newsletter and highlights some recent contributions.

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### **Notes**



## *Opti-Oat: Optimising oat yield and quality to deliver sustainable production and economic impact*

S.C. McWilliam<sup>1</sup>, Peter Bright<sup>1</sup>, Pascale Bodevin<sup>2</sup>, Catherine Howarth<sup>3</sup>, Irene Griffiths<sup>3</sup>, Eric Ober<sup>4</sup>, Derek Stewart<sup>5</sup>, Bill Thomas<sup>5</sup>, David Somerville<sup>6</sup>, Hazel Bull<sup>6</sup> and Sarah Clarke<sup>7</sup>

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The demand for high quality oats for food use in UK has risen by over 23% since 2008 and is projected to increase further with forecast growth of 5% p.a. in the breakfast and healthy snack foods category. To maximise this opportunity UK oat production must achieve higher and more stable yields from the same area and deliver improved grain quality. However, the ADAS Harvest Report (2013) identified that the difference between average farm yield of oats (5.9t/ha) and optimal yields (9.5t/ha) is ~3.6t/ha. This indicates that growers do not have the agronomic intelligence to achieve optimal yields (and grain quality) to maximise returns. This project aims to provide UK oat producers with world-leading agronomic 'tools' to maximise grower returns and capitalise on the increasing demand for food grade oats.

This 4 year InnovateUK Agri-Tech Catalyst project started in March 2015. Reference Crops comprising 2 winter oat (Mascani and Balado) and 1 spring oat (Canyon) will be sown in 5 geographically distinct locations over 3 seasons. Detailed measurements will be carried out including: key growth stages, biomass and nitrogen uptake and partitioning, green area development and yield to understand the growth and development of the oat crop and their interaction with the environment. Allied to this are Commercial Crop Monitoring sites from which targeted measurements on winter and spring commercial crops (of the same varieties) will be collected to validate reference crop data and provide a wider range of environments. Harvested grain from all sites will be analysed for milling quality.

The reference crops and a subset of monitoring crops will be assessed throughout the season using a multi-spectral sensor carried on an Unmanned Aerial System (UAS). These data will be related to the crop measurements taken at the same growth stages and bespoke algorithms for translating visual / spectral sensor data into meaningful crop data derived.

Outputs from the project will be

1. Unmanned Aerial Systems (UAS) based crop monitoring capability to quantify crop status to enable growers to optimise management across oat fields
2. An Oat Crop Model and Decision Support Tools to maximise yield and quality in spring and winter oats
3. An Oat Growth Guide which will provide a reference to assess crops status against key development bench-marks to trigger management intervention where crop performance falls short

Industry partners and co-funders: PepsiCo International Ltd, URSULA Agriculture Ltd, James Hutton Ltd

Academic partners: Aberystwyth University, NIAB, The James Hutton Institute

Major subcontractor: ADAS UK Ltd

This project is co-funded by the UK's innovation agency, Innovate UK, and BBSRC

*The views expressed in this abstract are those of the authors and do not necessarily reflect the position or policy of PepsiCo International Ltd*

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## Notes

## *Phenotypic diversity in Avena species*

S. S. Miller, A. Kaka, C. P. Wight and N. A. Tinker

*Agriculture and Agri-Food Canada, Eastern Cereal and Oilseed Research Centre, Ottawa, ON K1A 0C6, Canada*

In addition to the common *Avena sativa*, which is a hexaploid oat, the genus *Avena* includes a variety of non-domesticated diploid, tetraploid, and hexaploid species. Although there are basic similarities in the vegetative and reproductive structures in all of the species, there is a wide range of phenotypic characteristics within and between ploidies and species, and, indeed, within species. At our centre we are interested in mining rare-but-valuable alleles that are present in wild *Avena* relatives. Part of this project involves the phenotypic characterisation of the germplasm available from Plant Gene Resources of Canada and world gene-banks. We have documented differences in plant growth habit in both vegetative and reproductive growth phases. Broad diversity has also been observed in the hull (size, colour, presence and placement of awns, presence, position and colour of trichomes, shape, abscission characteristics, and lemma architecture), as well as in the enclosed groats (size, shape, amount and colour of trichomes, and pericarp integrity). In addition to the molecular characterisation of wild *Avena* relatives, which is also part of this project, awareness of these phenotypic characteristics will assist breeders in making informed choices regarding integration of wild germplasm into breeding programs working to develop new, value-added oat varieties.

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### **Notes**

## *The therapeutic potential of oat bioactive compounds - targeting the most clinically bioactive oat Avenanthramides*

Jennifer Hawkins<sup>1</sup>, Luis Mur<sup>1</sup>, Ifat Parveen<sup>1</sup>, Ben Barnes<sup>1</sup>, Catherine J. Howarth<sup>2</sup>

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Avenanthramides (AVAs) are a group of clinically-relevant phenolic alkaloids found in oats. AVAs have many health promoting properties including anti-microbial, anti-inflammatory and the ability to reduce LDL cholesterol. However, which of the many AVAs are the most clinically relevant has yet to be clearly defined.

Oat extracts were divided into seven separate fractions using Biotage flash chromatography and AVA-rich extracts were obtained. Using a standardised broth microdilution assay the fractions were screened for their ability to suppress the growth of *E. coli*, *P. aeruginosa*, *S. aureus* and *M. smegatis*. Antifungal assays were also used to screen for their ability to reduce the growth of two strains of *C. albicans*. Fractions were screened for antioxidant activities, another attractive feature of oat varieties with elevated AVAs.

Only two fractions were shown be able to significantly suppress bacterial growth. Peak 7 proved to have particularly potent activity against *S. aureus* whilst peaks 5 and 7 displayed activity against *S. aureus* and *M. smegatis*. In the *Candida* screen peaks four; rich in AVAs and peak five were shown to have strong anti-fungal activities. Those fractions with high anti-fungal activities were shown to have very high antioxidant activities.

On-going work is developing a mammalian cell culture system based on macrophages that will allow the anti-inflammatory properties of AVAs to be tested. In addition the AVA flash chromatography-derived fractions are being sub-fractioned using semi-preparative HPLC to confirm that the properties of individual AVAs have been correctly assigned and to identify unknown compounds which may provide leads for novel therapeutics.

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### Notes

# Closing remarks

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*Your notes*

# Conference participants

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# Network access

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## *Connection details*

A free wireless network is available throughout the hotel for Oats2020 delegates. Access details will be provided by hotel staff on check in.

If you have any questions please contact the organisers.

# Emergencies

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## *Health & Safety and emergency contact information*

### *For assistance from hotel staff and the conference team*

Please dial 511 from any hotel telephone to contact a member of the hotel's conference team.

Alternatively, please dial 0 to contact reception staff.

### *To contact the emergency services*

Fire, Police, or Ambulance dial **999** or **112** from any public or mobile phone.

### *In the event of fire*

A fire drill test takes place every Monday morning at 12:00 noon. If you hear a continuous sounding siren at any other time, please leave the building by the nearest available exit.

An event host will advise delegates of the assembly point on the morning of the conference. Under no circumstances should delegates attempt to re-enter the premises until advised that it is safe to do so by the duty manager.

If you discover a fire operate the nearest fire alarm and alert the emergency services. Leave the building by the nearest available exit. Do not use lifts. Proceed to the assembly point.

Do not attempt to fight the fire. Obey the instructions of hotel staff and emergency personnel and do not re-enter the building until told it is safe to do so by the duty manager.

# Taxis

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## *Booking taxis*

If you require transport at the end of the conference it is advisable to book this in advance. Please dial 0 to contact reception staff who will be pleased to assist. Allow for a wait of at least 30 minutes if calling on the day, especially at rush hour.

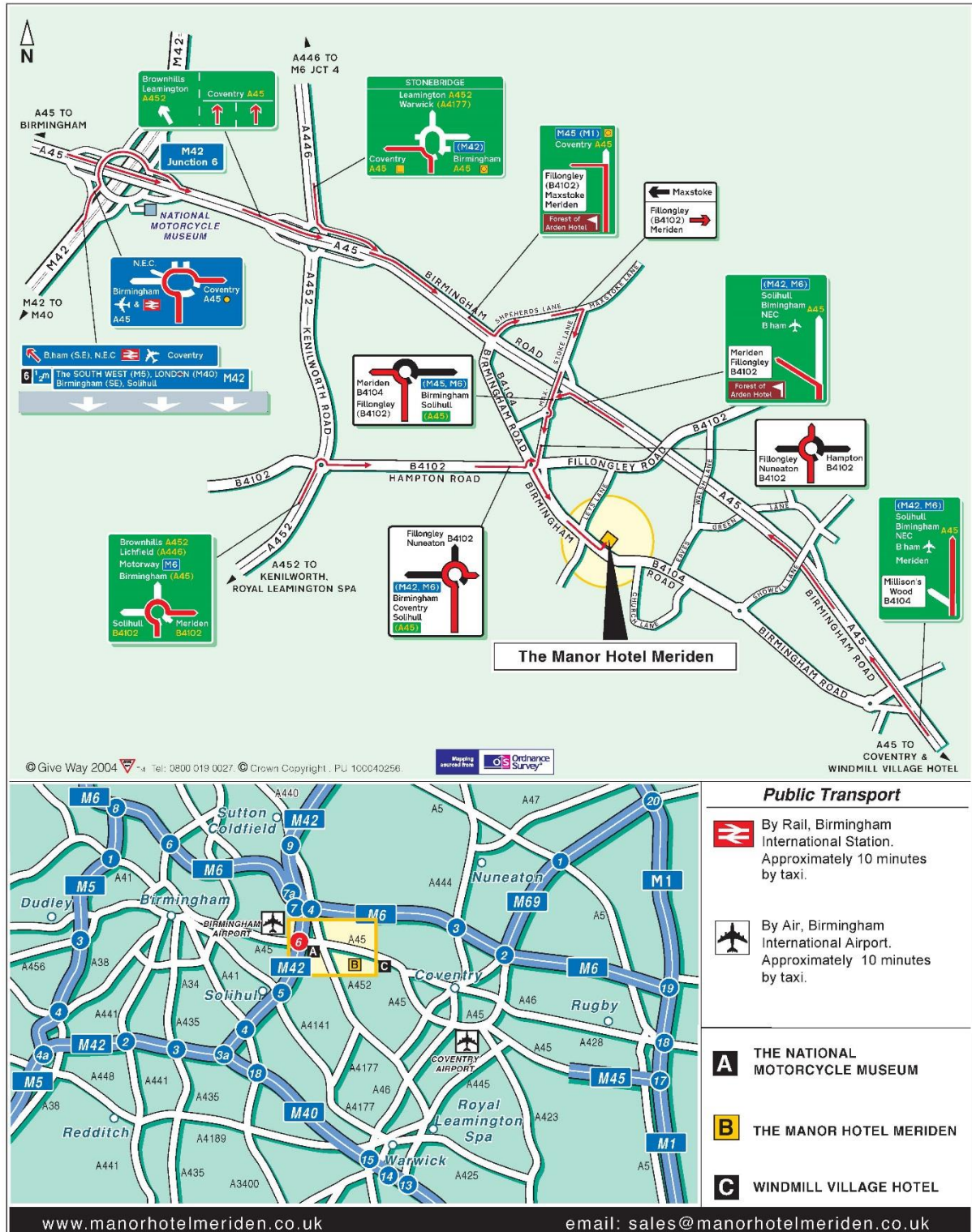
The hotel address is

The Manor Hotel  
Meriden  
West Midlands  
CV7 7NH

Tel. 01676 522735

# Conference location map

## The Manor Hotel, Meriden



The Manor Hotel, Meriden, West Midlands, CV7 7NH | Tel. +44 (0)1676 522735





**Thank you for attending Oats2020**

[www.oats2020.org](http://www.oats2020.org)

[oats2020@aber.ac.uk](mailto:oats2020@aber.ac.uk)

