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**OATS  
2016**

**The 10th International  
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**ABSTRACTS**  
of oral and poster presentation

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**11-15 July 2016    St. Petersburg, Russia**





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The 10th  
International Oat Conference  
11-15 July 2016  
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**ABSTRACTS**  
of oral and poster presentation

**Hosted by**

N.I. Vavilov Institute  
of Plant Genetic Resources (VIR)

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# **PLENARY SESSION 1**

## **General reports**

# The Legacy of N. I. Vavilov in XXI Century

Prof. Dr. Nikolai I. Dzyubenko

Federal Research Center N. I. Vavilov Institute of Plant Genetic Resources (VIR),  
St. Petersburg, Russia

E-mail: [n.dzyubenko@vir.nw.ru](mailto:n.dzyubenko@vir.nw.ru)

**Keywords:** *N.I.Vavilov, genebank, plant genetic resources, ex situ and in situ conservation*

Nikolai Vavilov was the first scientist to recognize the utmost importance for the humanity and potential value of world-wide collecting of crop seed, including crop wild relatives, and their conservation in viable conditions. Later his views were shaped into an international scientific concept, while his activities in building up seed collections served as a model. It was Vavilov who showed to the world's scientific community that the vast diversity of genes in populations of wild and weedy species, landraces and improved cultivars is a treasury of promising breeding sources.

By 1901, the collection of cultivated plants in Russia consisted of 301 accessions; in 2015, it has grown to more than 325,000. In the past 90 years, the Vavilov Institute organized and implemented 1558 collecting missions over the ex-USSR territories and 286 to foreign countries.

At present, there are 1750 plant genebanks over the world. Their holdings amount to 7.3 million plant accessions (FAO, 2010), with more than 1.84 million (24.7%) in the five leading national genebanks (USA, China, India, Russia and Japan).

The modern algorithm of crop collecting management comprises the following key components: analysis and assessment of the global plant genetic diversity in nature and in genebanks; systematic inventorying (revision) and assessment of the collected genetic diversity in a national genebank; identification of “gaps” in the genebank's holdings; systematic analysis of national breeding programmes, identification and prognostication of their demands for genetic sources; evaluation of genetic erosion and genetic vulnerability of the accessions for economically important crops and their wild relatives.

The ongoing globalization and international integration processes, rapid development of science and technology, introduction of novel technologies, acceleration of genetic erosion, climate change, and escalation of inter-country competition on the world market call for the need to solve common global problems by cooperative and most effective efforts. The main strategic task for the future is to work out governmental and non-governmental measures aimed at abating negative tendencies and securing the most optimal conditions for safe *ex situ* and *in situ* conservation of plant genetic resources, promotion of fundamental and applied research in the sphere of agricultural biodiversity, avoidance of duplication in such activities, increasing the capacity in collecting valuable genetic diversity, and enrichment of national germplasm holdings through targeted collecting missions all over the world.

# Assessment of *Avena* genepool genetic resources for food and health practical approach\*

Igor G. Loskutov

Federal Research Center N.I. Vavilov Institute of Plant Genetic Resources (VIR), St-Petersburg, Russia  
St-Petersburg State University, St-Petersburg, Russia

E-mail: [i.loskutov@vir.nw.ru](mailto:i.loskutov@vir.nw.ru)

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At present, global PGR collection of VIR is the fourth largest collection in the world and one of the leading ones in terms of significance of genetic materials accumulated in it. Oat VIR collection one of the largest in the whole world, it consists all cultivated species and their wild relatives.

On the bases of analysis of the collecting sites of oat herbarium specimens and genebank accessions of wild *Avena* L. species from the collection maps of distribution areas of the species were produced data base (<http://www.gbif.org/dataset/f875121b-07ae-4b44-a928-9fb793874d54>). A comparison of the climate and soil conditions of the Mediterranean, Southwestern Asiatic and Abyssinian centers of diversity with those of the oat species distribution areas shows that all oat species mostly prefer the moderately hot, semi-arid and dry climate on different types of soil (1). An analysis of the database of geographic distribution on wild oat species showed a full picture of oat species diversity, and a basis to make plans concerning further collecting activities or a basis for selecting potential sources of novel genes that can improve some valuable traits and characters to use them for practical purposes. Complex field and laboratory evaluation of VIR accessions of cultivated and wild species of oat showed valuable results.

Morphological traits used for *Avena* species characterization relate to the vegetative part of a plant: however, the main taxonomic characters are the detailed morphological features related to the structure of generative organs.

An evaluation of diversity of aluminium (Al) tolerance of genebank accessions of cultivated and wild *Avena* species from the VIR collection showed that the accessions with a high degree of aluminium tolerance belonged to the different species (2). A comparison of the data on Al tolerance with the soil conditions demonstrated that most highly tolerance accessions tend to be collected on different type of soils.

A comprehensive phytopathological evaluation of oat species diversity facilitates selection and utilization of new genetic sources and donors of resistance. Sources of resistance to the main *Avena* pathogens including crown and stem rusts, and *Fusarium* fungi, have been found (3). Diseases not only suppress plants, but also deteriorate the yield quality through the accumulation of pathogens waste products. Mycotoxins decrease the cost and consumption properties of oat grain and adversely influence human and animal health.

From the point of view of nutritional qualities, biochemical characteristics of oat grain are of the highest importance (4). The most important biochemical components that increase nutritive value of oat include protein, fats, fatty acid composition,  $\beta$ -glucans, tocopherols, sterols, avenanthramides, micro nutrients, ect.

The metabolomic analysis of *Avena* cultivars and wild species resulted in the identification of metabolites the content of which tends to change along with the 'domestication' process, or differentiates wild oat species from oat cultivars (5). This is to be further examined in detail by metabolomic screening of oat accessions with the identified degree of resistance to *Fusarium* head blight. Positive correlations have been found to reliably exist between the studied kernel quality characters, *Fusarium* head blight resistance and mycotoxins accumulation. It has been also found that the content of saccharose and A fructose inversely correlated with grain affection with *Fusarium* head blight and mycotoxins accumulation.

The analysis of micro nutrient composition in *Avena* species accessions has found genotypes with a high content of paired elements, in particular Fe and Zn, Fe and Mn and Zn and Mn. The identified cultivars may be directly used for the production of micro nutrient-rich dietary foods, or as initial breeding material for creating new productive oat cultivars with an increased micro nutrient composition in the kernel.

A study of accessions of cultivated and wild *Avena* species with differing ploidy levels has shown them to differ much in terms of avenantrominde content in the kernel. It should be noted that the range of avenantrominde values was bigger in wild species than in cultivated one.

It has been established that an improvement of the studied qualitative indicators of the kernel leads to a decrease in avenantromindes; oil content has a more meaningful positive relation with other qualitative indicators (except for avenanthramides), and the same refers to Zn content in the kernel. Besides, a weak link with the avenantromide content increase in the kernel infected with *Fusarium* head blight has been established.

At present, this trend in studies of the cultivated and wild species collection is the most promising one and has resulted in identification of interesting novel initial material for oat breeding.

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# Oats breeding in Russian Federation: results and problems

Galina A. Batalova

North-East Agricultural Research Institute, Kirov, Russia

E-mail: [g.batalova@mail.ru](mailto:g.batalova@mail.ru)

**Keywords:** *oat, Russian Federation, grain yield, varieties, directions of breeding.*

Oats is a traditional crop for Russian Federation. At the beginning of XX century it occupied more than 18 million hectares with total grain yield more than 16 million tons. Decrease in sowing area at second half of XX century leads to significant drop in oats production. At nowadays oats occupies 3-3.25 million ha in Russia and its production is about 4.0-5.33 million tons. In 2015 oats yield was 4.54 million tons at average crop capacity 1.6 t/ha. Basic sowings of oats are in Sibirsky (1.224 million ha), Privolzhsky (0.917 million ha) and Central (0.406 million ha) Federal Districts of the country. They obtain the most grain production of a crop in 2015: 1698.61, 1267.07, and 781.43 thousand tons respectively.

Among territories leading in oats production in 2014-2015 there are Krasnoyarsk territory (389.03-343.76 thousand tons), Republic of Tatarstan (161.36-151.0 thousand tons), Bryansk (121.64-121.78 thousand tons) and Tyumen (242.65-183.01 thousand tons) regions with productivity about 1.84-2.26 t/ha. Productivity level up to 3 t/ha and higher is obtained in Krasnodar territory, Belgorod, Leningrad, Lipetsk, and Kaliningrad regions. Most of Russian regions form oats grain yield at the expense of sowing areas. Some of the reasons for that are drought and dry wind during growing season. Altai territory has the highest oats grain yield – 559.47 thousand tons in 2014, 483.09 thousand tons in 2015 at productivity 1.45 and 1.32 t/ha respectively. Low yields is characteristic in 2015 for Chelyabinsk (1.02-1.29 t/ha) and Samara (1.69-1.26 t/ha) regions with 108.32 and 101.48 thousand tons of grain.

Oats is often considered as a crop which closes crop rotation, so violate technology of its cultivation. This fact in combination with unfavorable regional ecological factors influences negatively on productivity. But use of adaptive assortment and correct technologies allows to get high yield of oats in these territories. For example average oat productivity in Kirov region is 1.6-2.4 t/ha but in enterprises “Krasny Oktyabr” and “Oktyabrsky” productivity of variety Krechet is about 5.6-7.2 t/ha and even under drought conditions is not less than 4.2 t/ha. Variety Krechet occupies 6-th place in rating of oats varieties permitted for cultivation in Russian Federation.

Crop assortment has significant influence on level and stability of production. According to RosselkhozCenter (2016) 706.4 thousand tons of oats were sowing in 2015; only 73.2% of them were varieties of domestic breeding, 1.7% - foreign varieties, but ratio of non-varietal seeds and seeds of varieties non-included in State Register was about 25.1%. There is a stable group of varieties leading in production; it includes varieties bred in leading breeding centers: Rovesnik (Sibirsky Research Institute of Plant Industry and Breeding; Kemerovo Agricultural Research Institute (ARI)); Skakun

(Moscow and Ul'yanovsk ARIs); Sayan (Krasnoyarsk ARI); Krechet (North-East ARI, Falenki Breeding Station); Korifej (Altai ARI). Systematic researches on oat breeding in Russia are spent in 19 breeding centers; 6 of them locate in European part of the country, 3 – in Ural region, and 11 – in Siberia and Far East.

State Register of Russian Federation for 2016 includes 119 oats varieties, 94 of them (78.8%) are domestic varieties. There are 66 varieties permitted for cultivation in Central, North-West, Privolzhsky, Southern, and North-Caucasus federal Districts; most part of these varieties are created by breeders of Moscow, Ul'yanovsk, and North-East ARIs, and Falenki Breeding Station. Since 2016 varieties of covered oats Sapsan and Medved' (North-East ARI, Falenki Breeding Station), Stipler (Moscow and Ul'yanovsk ARIs), Vilensky (Yakutsk ARI), and Kazachok (firm "Klyuchevaya") are permitted for cultivation. There are 58 varieties permitted for cultivation in Ural, Siberia and Far East. Ten varieties of Sibirsky ARI (Orion, Pamyaty Bogachkova, etc) and seven varieties of Kemerovo ARI (including naked varieties Gavrosh and Pomor bred in co-operation with Vavilov's Institute of Plant Industry) occupy most sowing areas in West-Siberian and Ural regions. Investigations of Irkutsk and Siberian ARIs directed at creation of varieties for West-Siberian and East-Siberian regions. Plastic variety Talisman was created in co-operation with ARI of Northern ZaUral'e; it occupies 5-th place in rating and is zoned for 10-th, 11-th, and 12-th regions of Russia. Breeding in these Institutes as well as in Altai ARI directed basically on modernization of assortment for Ural region; 15 varieties of covered and naked oats bred in these Institutions are included in State Register. Among them there is first naked oat Tyumensky golozerny.

Breeding work in Russia is conducted with spring oats as well as with winter oats. It is cultivated in Adygei Republic. State Register for 2016 includes five varieties bred in Adygei ARI, last of them is Oshtain which is zoned in 2014.

Main ecological factors determining effectiveness of oat production are climate and quality of arable soils. Climatic conditions of Russia are different. Significant decrease of solar radiation are observed at moving from south to north; continentality of climate is increases from west to east; annual temperature amplitude rises and amount of precipitation drop from west to east. Frosts in May and June, early frosts in fall, rainy fall are characteristic for significant part of oat-sowing areas. Drought and dry winds are very dangerous too. In some regions productivity of oats is limited by low natural fertility of acid soils which occupies more than 50 million hectares in the country.

All these facts along with demands of manufacturing industry to amount and quality of yield determine direction of oat breeding. Main demands for including of variety into State Register are: high stable productivity and quality, resistance against diseases and pest, manufacturability, claiming for industry.

At detailed of directions of oat breeding in Russia one must draw attention on optimization of growing season, lodging resistance, resistance or tolerance against unfavorable soil factors (acidity, low fertility), resistance to air and soil drought, resistance to diseases (especially to viruses and panicle diseases) and pest. It is necessary to increase effectiveness of action of photosynthetic apparatus of plants by optimization of its architectonics (slope angle and area of flag and second leaves; degree of shading of

downstream leaves; activity of photosynthetic pigments). Upper leaf circle catch most part of solar radiation and converts it during photosynthesis into energy of organic matter. Modernization of panicle from point of view of effectiveness of utilization of solar energy is currently. In spite of relative resistance of oats against soil acidity one must pay attention to traits which determine resistance to edaphic stress in root zone. All of these in combination influence forming of parameters of grain productivity (number of spikelet and grain in panicle; grain mass per panicle; size and fullness of grain; capacity for fruit-bearing shoots) and crop capacity. Another important direction of oat breeding is consumer-aimed and end-product-aimed breeding for forage, food concentrates of total use, dietary and functional products. Oat must be modernized as a fodder crop cultivated for green forage. Main parameters of improvement are plant height, length of panicle, lodging resistance, number of leaves, leaf area, and quality of fodder. We need varieties tolerant to cultivation in mix with grain and legumes crops.

Thus, variety must provide most effective use of favorable natural and technogenic factors at time and space and simultaneously resists to abiotic and biotic stressors at the expense of genetic adaptivity, tolerance, ability to utilize mineral nutrients difficult to access, stress-resistance at critical ontogenetic stages, etc.

# **PLENARY SESSION 2**

**Genetic Resources,  
Diversity and Breeding**



## ORAL PRESENTATIONS

### Changes in utilization of the oat genepool preserved by Plant Gene Resources of Canada

Axel Diederichsen

Plant Gene Resources of Canada, Agriculture and Agri-Food Canada,  
107 Science Place, Saskatoon, SK, S7N0X2, Canada;  
E-mail: [axel.diederichsen@canada.ca](mailto:axel.diederichsen@canada.ca)

**Keywords:** *Avena*, crop wild relatives, genetic resources utilization, paradigm shift, plant breeding;

Oat has remained an important crop in Canada despite a decline in oat cultivation world-wide since the middle of the 20<sup>th</sup> century. This is partly due to the short growing season for agricultural crops in many parts of this country. Canadian plant breeders started in the 1960s to make systematically use of crop wild relatives for utilization in oat improvement. This was possible due to close cooperation between very productive research scientists that dedicated their career to this effort and included plant breeders, plant pathologists, cytologists, taxonomists and genebank curators. As a result, the Canadian national genebank, Plant Gene Resources of Canada (PGRC), maintains the largest collection of oat genetic resources world-wide with nearly 28 thousand accessions of which 55% are crop wild relatives. The collection contains 29 *Avena* species. In 1977, PGRC accepted the task from the International Board for Plant Genetic Resources (IBPGR, today Bioversity International) to preserve the base collection of oat germplasm (Thormann et al. 2015). Many world genebanks deposited back-up duplicates of oat samples at PGRC. During recent years, PGRC has focused on regeneration and characterization of the *Avena* material to ensure that seeds and information about the material are available (Diederichsen 2008). The PGRC website ([www.agr.gc.ca/pgrc-rpc](http://www.agr.gc.ca/pgrc-rpc)) is used to disseminate information about the germplasm holdings. Active utilization of the PGRC oat collection occurs nationally and internationally. From 1998 to 2015, each year about 1000 oat accessions were shipped by PGRC to genebank clients.

The greatest challenge for North American oat breeding is the crown rust disease. Important genetic resources were found in the wild progenitors on all ploidy levels, i.e. the diploid *Avena sterilis*, the tetraploid *A. barbata* and the hexaploid *A. sterilis*. The red oat, *A. sativa* subsp. *byzantina*, has also been an important source of rust resistance. In North America, plant pathologists have been very active in identifying rust resistance genes/alleles and in Canada rust populations were monitored steadily so as to identify new pathotypes and to respond by introducing new resistance alleles in oat cultivars (Fox et al. 1997). As a result, all recent North American oat cultivars have wild progenitor species of the genus *Avena* in their pedigrees. This extremely successful work with crop wild relatives represents in fact a realization of what was envisioned in 1914 by Erwin Baur, who was probably the first to emphasize how important the crop wild relatives are for plant breeding (Baur 1914).

Since the turn to the 21<sup>st</sup> century a paradigm shift manifests itself regarding the relevance and utilization of crop wild relatives. Highly sophisticated molecular methods for germplasm characterization became affordable and phenotyping using advanced technologies complement traditional observations made in the field or greenhouse. Individual researchers pursuing over many years a defined project are becoming a rare concept and the use of technology producing enormous datasets leads to new approaches.

A trend noticed by Plant Gene Resources of Canada is that the requests for species of the secondary and tertiary gene pool of *Avena* have been steadily increasing. The requests for conducting screenings of larger amounts of germplasm of single taxa of the primary gene pool have been decreasing. The germplasm requests by molecular research laboratories are increasing while the requests by plant pathologists and plant breeders are declining. Recently, modern technologies have also been applied to the PGRC oat collection in order to assess the genetic diversity in parts of the collections, enhance the cytological assessments necessary for species identification and to assess the evolutionary relationships among the wild *Avena* taxa (Fu et al. 2003, Yan et al. 2015). Possibly, this will result in a revival of the active utilization of the wild progenitors in oat improvement which Canadian pioneers in breeding and research were already actively involved in the second half of the 20<sup>th</sup> century.

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# Breeding for hybrids – a real option in oats?

Steffen Beuch<sup>1</sup>, Mario Gils<sup>2</sup>, Matthias Herrmann<sup>3</sup>

<sup>1</sup>Nordsaat Saatzeit GmbH, Saatzeit Granskevit, D-18569 Granskevit, Germany;; <sup>2</sup>Nordsaat Saatzeit GmbH, Saatzeit Langenstein, D-38895 Langenstein, Germany; <sup>3</sup>Julius Kühn-Institute (JKI), Institute for Breeding Research on Agricultural Crops, D-18190 Sanitz OT Groß Lüsewitz, Germany  
E-mail: [s.beuch@nordsaat.de](mailto:s.beuch@nordsaat.de)

*Keywords: oat breeding, self-pollinating cereals, heterosis effects, hybrid varieties*

Oats have a long tradition as a healthy food for human consumption. In Europe, the oat area remains under strong pressure due to a lack of economic competitiveness compared to agricultural core crops like winter cereals, maize and oilseed rape. Consequently, in the past oat cropping has been shifted mainly to low input systems on marginal soils and organic farming. In contrast, there is strong increasing interest in oat consumption for human food that requires both, the availability of high quantity and quality oats.

However, environmental impacts (location and year) more strongly affect yield and quality in oats compared to other cereals. Additionally, the ongoing climate change may cause further variation in oat yield and oat quality. Breeding for hybrid varieties is a possible way to overcome this kind of instability. Hybrids use the hybrid effect that results from combining two specific parents for the production of commercial F1-seed. Seeding the F1-generation will result in the so-called heterosis effect. For a long time, this kind of breeding was successfully used in many cross-pollinating crops (i.e. maize, rye, oilseed rape, vegetables) in which the heterotic effect is remarkable. Presently, many European plant breeders state an interest to develop hybrid varieties in self-pollinating cereals like wheat, barley and triticale as well. It is expected that hybrid varieties will have a couple of advantages:

1. More safety to secure global food supply.
2. Better varieties for agricultural farming.
3. Adaptability to environmental impacts caused by climate change.
4. Return on investment for plant breeders.

Interest in wheat hybrids exists for more than 50 years. Compared to conventional varieties it has been proven that hybrid winter wheat can be characterized by i.e. higher yield potential of about 8-10 % to middle of parents, better tolerance to biotic and abiotic stress, higher vigor and better winter hardiness. In oats, there are only a very few studies on heterosis up to now, indicating hybrid effects on a level like in wheat. The optimization of the hybrid breeding process in self-pollinating cereals like wheat or oats requires the consideration of a critical “triangle”: a practical sterility system on the female side, good pollinators on the male side and existence/establishment of heterotic groups.

Comparing former studies and experiences with oats and wheat, we will discuss the potential of the development of hybrid varieties in oats. Based on the introduction of new technologies it seems to be possible to use hybrid varieties in a broader way than in the past – even in self-pollinators. In the end, the commercial success of such process will mainly depend on overcoming the challenges of the above-mentioned “triangle”. Possible ways of solution will be presented as well. A lot of future basic research is still necessary to explore the possible chances of hybrid varieties in oat breeding and growing.

# Genetic Progress in a Subtropical Oat Germplasm

Marcelo Teixeira Pacheco, Daniel Arthur Gaklik Waldow,  
Itamar Cristiano Nava, Luiz Carlos Federizzi

Department of Crop Science, Federal University of Rio Grande do Sul (UFRGS), Av. Bento Gonçalves,  
7712, P.O. Box 15100, Porto Alegre, RS, 91501-970, Brazil.

E-mail: E-mail: [marpac@ufrgs.br](mailto:marpac@ufrgs.br)

***Key words: grain yield, crown rust, plant height, flowering time, harvest index***

The UFRGS Oat Breeding Program, started in 1974, has as its major objective to develop oat cultivars adapted to Southern Brazil environments, with high grain yield and quality potential. The genetic progress of a given trait is a sustained phenotypic change, observed in different genotypes developed along the selection period considered, caused by changes in allele frequencies in the germplasm. This study aimed to estimate the genetic progress of different important agronomic traits in the UFRGS oat germplasm and associate the gains in grain yield with changes in other characteristics. The study was conducted in Eldorado do Sul-RS, Southern Brazil, in two years. We tested 92 UFRGS oat genotypes, developed between 1978 and 2008, and six checks: two old oat cultivars, developed in the U.S.A. and adapted to Southern Brazil conditions, three modern Brazilian wheat cultivars and one modern barley cultivar, also from Brazil. In the first year, the genotypes were evaluated with and without fungicide, while in the second year only with fungicide. The analysis of genetic progress was based on linear regression between the period of three years which the genotype was obtained and the trait evaluated, where the regression coefficient (b) provides an estimate of the genetic gain. The genetic progress of grain yield with fungicide, from 1978 to 2008, was estimated as 38.7 kg.ha<sup>-1</sup>.year in the first year and 25.3 kg.ha<sup>-1</sup>.year in the second year of test. Grain yield without fungicide showed a reduction of 63.8 kg.ha<sup>-1</sup>.year between 1978 and 1990, followed by an increase of 167 kg.ha<sup>-1</sup>.year from 1990 to 2008, this reduction in the early breeding period resulted from the overcome of the resistance genes to leaf rust in the older genotypes of the program. Also, reduction in the number of days from emergence to flowering, plant height and lodging were observed along the 30 years of breeding. Decrease in height, with no change in biomass, resulted in increased harvest index. Number of panicles per square meter and thousand grain weight also increased, without modification of the grain weight of the panicle, resulting in increased grain yield potential. The increase in thousand grain weight and test weight allowed improvement on grain quality. Several variables were associated with grain yield, but weakly, indicating that the increase in grain yield potential was the result of modification of different traits, under different combinations, at different genotypes.



# Oat Researching in China

Changzhong Ren

Jilin Province Baicheng Academy of Agricultural Sciences  
China Oat Breed Improvement Center  
China Oat and Buckwheat Research Center  
E-mail: [13500830080@163.com](mailto:13500830080@163.com)

***Key words: China Oat and Buckwheat Research System; Breeding; Cultivation; Prevention and control of diseases and pests; Processing; Oat industry***

In China the government attaches great importance to the research of oat and buckwheat, specially established the China Oat and Buckwheat Research System. Four departments are included in the Oat and Buckwheat Research System, which are 1) Breeding and seed research department; 2) Cultivation, soil and fertilizer research department; 3) Prevention and control of diseases and pests department; 4) Functional properties and processing department, respectively. It would consist of 15 research scientists and 16 test stations. In the past five years, we obtained outstanding achievements in oat research, 34 oat varieties are wide applied, and achieved remarkable results on demonstration experiment. Now, we formed a complete chain from breeding to processing and promoted the development of oat industry in China.

# Assessment of genetic diversity and adaptation of oat (*Avena sativa* L.) collected from North Africa and Central Europe

Toshinobu Morikawa, Yuka Ishimaru

Graduate School of Life and Environmental Sciences,  
Osaka Prefecture University, Sakai city, Osaka, 599-8531, Japan  
E-mail: [morikawa@plant.osakafu-u.ac.jp](mailto:morikawa@plant.osakafu-u.ac.jp)

**Keywords:** *oat, genetic diversity, adaptation, principal component (PCP) analysis*

The plant expedition team of Gifu University has conducted three exploration surveys (GSEM 1995, 1996, and 1997) of the West Mediterranean and Central European areas during which germplasm of oats was collected. During the expeditions, 116 accessions of cultivated oats (*Avena sativa* L.) were collected directly from agricultural fields in North Africa (Egypt, Tunisia, Morocco, and Southern Spain) and Central Europe (Czech, Hungary, Slovenia, Germany, Austria, and Switzerland). The oat accessions are believed to be an ideal germplasm for comparing genetic diversity and adaptation of cereal crops between the North African and Central European regions as an example of *in situ* conservation. In particular, the number of North African oat germplasms has recently been diminishing. Knowledge about agronomical quantitative and qualitative characteristics is desperately required to effectively utilize plant germplasm in breeding programs.

Isozyme variation is one of the molecular markers based on variation in the enzyme, which is derived from in-del of non-coding regions of the same enzyme. This technique does not involve polymerase chain reaction amplification. The enzyme mobility and activity in the gel are visualized using staining enzymatic products. The tracking of target characteristics over generations could easily be facilitated by the identification of certain critical allele markers.

The main objective of the current study was to estimate genetic diversity of two sets of North African and Central European cultivated oat accessions using quantitative and qualitative agronomical characteristics and isozyme variation. We also attempted to determine whether genetic diversity depended on collection sites and if there was a relationship between isozyme polymorphism and some morphological traits.

According to the days to heading autumn sowing, Central European oats included a much later variety than oats from North African regions. The thousand-grain-weight of the North African oats was higher than that of Central Europe, except for oats from Switzerland. Plant height at maturity of Slovenian (147.8 cm) and Moroccan (144.1 cm) oats was highest among the 10 countries investigated. Czech and Tunisian oats showed the lowest plant heights.

Accessions in Switzerland showed the highest frequency of colored dark brown lemma (0.20). A cline exists showing a north to south distribution of hairiness of the

node. Fifteen accessions of North African oats showed pubescence out of 38 accessions. Merely two Slovenian oat accessions showed pubescence out of a total of 72 European accessions.

Principal component (PCP) analysis was performed to confirm the structure and acquire knowledge about the diversity of 12 quantitative traits in the 38 accessions of North African oats. The scatter diagram showed that Slovenian oats were positively spread along the principal 1<sup>st</sup> axis (2<sup>nd</sup> inter-nod length and days to heading), whereas Czech oats were negatively spread. Austrian, Hungarian, and Swiss oats were located in the center of the scatter diagram. PCP analysis of the frequency of 13 quantitative traits of North African and Central European oats identified two clearly separated areas in the scatter diagram. This was constructed along the principal 1<sup>st</sup> axis (pubescent lemma base and pubescent leaf margin) and the principal 3<sup>rd</sup> axis (waxy frequency in the panicle and leaf), which clearly separated North African oats from Central European oats. The result indicated that a cline exists on the frequency of pubescent lemma base and leaf margin, and a strong awn of common oats from North Africa through Central to East Europe exists.

Isozyme analysis of six enzyme systems revealed 22 variable and 13 non-variable loci and 66 alleles in 116 accessions of oats. This result indicated that North African accessions involved a larger amount of variable loci and heterozygosity than that of Central European oats. Specific relationships were also observed between the adenosine triphosphate (*ATP*) alleles and the mean altitude of collection sites in each country. The oats originating from lowland (<200 m altitude) collection sites of North African countries consistently showed the *N* allele at the *ATP-1* locus and the *F* or *S* alleles at the *ATP-4* locus. On the other hand, Central European accessions from highland areas (>300 m altitude) showed a high frequency of *F* or *S* alleles at the *ATP-1* locus. There was a significantly positive correlation at the 0.05 level between all alleles at all ATP loci and the altitudes of collection sites. Most North African accessions showed the *F* allele at the superoxide dismutase (*SOD*)-1 locus (1.0), except for accessions from Egypt (0.91); however, accessions of Central Europe showed the *S* allele. Central European accessions showed the *S* allele at the *SOD*-3 locus; however, most accessions of North Africa showed a high frequency of the *N* or *F* alleles.

PCP analysis was conducted using morphological traits and isozyme allelic frequencies for clarifying the relationship among oat accessions in the North African, Central European, and Mediterranean coastal regions. The difference in isozyme allelic frequency between North African and Central European accessions indicated that oat varieties of both countries developed separately along the Mediterranean coast.



# **PLENARY SESSION 3**

**Genomics,  
Bioinformatics  
and Molecular Assisted  
Selection**



# ORAL PRESENTATIONS

## Haplotag genotypes: your passport to anywhere in the oat world

Nicholas A. Tinker, Wubishet A. Bekele, Charlene P. Wight, Honghai Yan.

Agriculture & Agri-Food Canada, Ottawa Research and Development Centre,  
Central Experimental Farm, 960 Carling Avenue, Ottawa, Ontario K1A 0C6 Canada.  
E-mail: [nick.tinker@agr.gc.ca](mailto:nick.tinker@agr.gc.ca)

*Keywords: oat, **n**enotyping-by-sequencing, haplotag*

Genotyping-by-sequencing (GBS) generates tens-of-thousands of genetic markers, providing detailed coverage of a complete genome. We have used this technology to construct an improved consensus map in hexaploid oat (Chaffin *et al.* 2016) and to explore patterns of diversity and adaptation in this species (Klos *et al.* 2016). We have also developed new software called ‘Haplotag’, which substantially increases the number of high quality GBS marker genotypes that can be scored (Tinker *et al.* 2016). Haplotag is especially applicable to the large, polyploid genomes of *Avena*, for which reference sequences do not exist. Haplotag is unique in its ability to generate both SNP genotypes as well as tag-level haplotypes, and also in its ability to produce intuitive graphical ‘passports’ that allow detailed inspection and validation of every marker.

In this presentation, we will use Haplotag’s graphical passports to illustrate the power and potential of GBS to a general scientific audience. We will describe new results showing how Haplotag has allowed us to explore the genetic diversity of 25 species of *Avena*, and how this has allowed us to identify the origins of hexaploid chromosomes among these species. We will discuss why tag-level haplotypes can provide increased power for QTL detection in GWAS studies. Finally, we will describe how Haplotag is being applied in the new North American Public Oat Genotyping Initiative to generate data that are available on the T3/Oat database (<https://triticeaetoolbox.org/>).

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## An Oat Nested Association Mapping population

Maciej Bisaga<sup>1</sup>, Alison Bentley<sup>2</sup>, Aigul Abugaliyeva<sup>7</sup>, William Allwood<sup>3</sup>, Sandy Cowan<sup>1</sup>, Debora Giorgi<sup>4</sup>, Irene Griffiths<sup>1</sup>, Catherine Howarth<sup>1</sup>, Yung-Fen Huang<sup>5</sup>, Sergio Lucretti<sup>4</sup>, Ian MacKay<sup>2</sup>, Athole Marshall<sup>1</sup>, Derek Stewart<sup>3</sup>, Nick Tinker<sup>6</sup>,  
Tim Langdon<sup>\*1</sup>

<sup>1</sup>IBERS, Aberystwyth University, SY23 3EE, U.K.

<sup>2</sup>NIAB, Cambridge, CB3 0LE, U.K.

<sup>3</sup>JHI, Craigiebuckler Aberdeen AB15 8QH UK

<sup>4</sup>ENEA, Via Anguillarese, 301, Rome 00123, Italy

<sup>5</sup>NTU, Roosevelt Rd., Taipei 10617, Taiwan

<sup>6</sup>AAFC, Central Experimental Farm, 960 Carling Avenue, Ottawa, Ontario K1A 0C6 Canada.

<sup>7</sup>KazNIIZR, Almalyk, Almaty 040909, Kazakhstan

E-mail: [ttl@aber.ac.uk](mailto:ttl@aber.ac.uk)

***Keywords; oat, Nested Association Mapping, genotyping-by-sequence***

A Nested Association Mapping (NAM) population has been established for hexaploid oat. The common parent is the European elite spring variety Firth, with additional parents representing a broad diversity of germplasm from North American elites through Turkish landraces and *Avena byzantina* accessions to lines containing alien introgressions. 632 lines from twelve sub-populations have been phenotyped at Aberystwyth for standard agronomic traits for two or more years (F8 and F9 generations). Grain morphology, quality and metabolite analyses are underway. In addition the full population has been screened using genotyping-by-sequence (GbS), identifying significant QTLs for characters such as flowering time, height and mildew resistance. The GbS data provides some insights into oat domestication. All parents have been further screened for genetic diversity by RNAseq of developing grain, while the common parent is the target for sequencing of chromosome pools isolated by FISHIS. In conjunction with the IBERS *A. atlantica* diploid oat zipper, candidate genes can be rapidly derived for phenotypes or GbS tags segregating in the NAM population. DNA extracted from F4 plants allows use of the heterogeneous inbred family (HIF) analysis approach to simplify confirmation of candidate genes. The NAM population is being used to develop and test genomic prediction models and for metabolomics analyses as part of the Innovoat LINK project. Future work will include POPSEQ to refine the NAM maps and explore structural variation in parental genomes.

# **Oat adaptation to Mediterranean climate: a critical analysis for association studies**

Nicolas Rispail<sup>1</sup>, Gracia Montilla-Bascón<sup>1</sup>, Javier Sánchez-Martín<sup>1</sup>, Fernando Flores<sup>2</sup>  
Amereo Emeran<sup>3</sup>, Josefina C Sillero<sup>4</sup>, Tim Langdon<sup>5</sup>, Catherine Howarth<sup>5</sup>, Diego  
Rubiales<sup>1</sup>, Elena Prats<sup>1</sup>.

<sup>1</sup>CSIC, Institute of Sustainable Agriculture, Apdo. 4084, 14080 Córdoba, Spain.

<sup>2</sup>E.T.S.I. La Rábida., Univ. Huelva, 21819 Palos de la Frontera, Spain.

<sup>3</sup> Faculty of Agriculture, Kafr El-Sheikh University, 33516-Kafr El-Sheikh, Egypt.

<sup>4</sup> I.F.A.P.A Centro Alameda del Obispo, Apdo. 3092, E-14080 Córdoba, Spain.

<sup>5</sup>Institute of Biological, Environmental and Rural Sciences, University of Aberystwyth, UK

E-mail: [elena.prats@ias.csic.es](mailto:elena.prats@ias.csic.es)

***Keywords: oat, resilience, Mediterranean adaptation, stress resistance, genotype x environment interactions, association studies***

During the last 20 years there has been a steady state increase in the cultivated area of autumn sown oats within the Mediterranean area. However, in this area, the crop face hot and dry weather for which it is not particularly well adapted since traditionally oats has been grown in areas with cool and wet summers, such as Northwest Europe and Canada in which spring sowing is the standard practice. The low adaptation of northern material is reflected in a reduction of almost 3-fold in yield and highlights the need of identification of more resilient plants adapted to Mediterranean environments and crop practices. In this work, we used 141 Spanish landraces, genetically diverse and classified as red and white oats adapted to low and high altitude, and determined its adaptation to autumn sowings under Mediterranean agroecological conditions over 2 crop seasons at 4 contrasting locations in Spain, and Egypt. As expected, genotype  $\times$  environment (GE) interactions was found for all assessed traits, including grain yield, biomass production, H index, flowering and rust resistance, which is the most important disease reducing yield in the Mediterranean area. To test this GE interactions, heritability-adjusted genotype plus genotype  $\times$  environment (HA-GGE), biplot analysis was performed. Resilience of the different genetic clusters was inferred from biplots together with the identification of the best discriminative locations, and those particular landraces with superior and stable characteristic for each assessed trait. Association analysis is a promising approach to overcome the limitations of conventional QTL mapping that has received increasing attention from plant geneticists during the last few years. However, when phenotyping is done under field conditions, the genotype  $\times$  environment interactions may weaken the association found for particular makers. Taking advantage of the detailed genotype  $\times$  environment interaction study performed and through the genotyping of the oat collection by DArT makers, we are performing a critical analysis of association studies for agronomic traits by considering the use of different replications over years, locations, mega-environments, and the use of BLUPs and different models for inferring strong associations.

# **How should I select the individuals of my training population to make selections in GS?**

Julio Isidro Sánchez

Agriculture & Food science, Animal and Crop Section, University College Dublin, Ireland.

E-mail: [j.isidro@ucd.ie](mailto:j.isidro@ucd.ie)

***Keywords: oat, genomic selection, training population set***

The concept of genomic selection (GS) or genome wide selection has brought new expectation and insight for the use of genomic information to make selection in plant breeding. Genomic selection is a newly developed tool in which dense markers covering the whole genome are used to estimate genomic breeding values for quantitative traits of selection candidates. One of the most important questions for implementation of GS is how to select the individuals who will create the training population set (TRS) to make predictions on the candidate sets. This is a key component on the design of the TRS, since it is critical for a better allocation of resources in plant breeding, especially due to the high costs of phenotyping. Our recent research show that this optimization problem depends on the population structure under study, as well as on the phenotypic variance captured by the different algorithm used. Here we will present different methods of optimization of the TRS and its use in different breeding program schemes and highlighting the importance of the use of relationship matrix to improve genetic diversity on your TRS.

## Developing enhanced breeding methodologies for oats

Catherine J. Howarth<sup>\*1</sup>, Maciej Bisaga<sup>1</sup>, Tim Langdon<sup>1</sup>, Irene M. Griffiths<sup>1</sup>, Alexander (Sandy) A Cowan<sup>1</sup>, Athole H. Marshall<sup>1</sup>, Alison R Bentley<sup>2</sup>, Ian J. Mackay<sup>2</sup>

<sup>1</sup>IBERS, Aberystwyth University, SY23 3EE, U.K.

<sup>2</sup>NIAB, Cambridge, CB3 0LE, U.K.

\*E-mail: [Catherine.howarth@aber.ac.uk](mailto:Catherine.howarth@aber.ac.uk)

**Keywords:** *oat, breeding, marker assisted selection*

Traditional plant breeding programs rely mainly on the phenotypes of advanced material being evaluated in a range of environments; selection and recombination are based solely on the resulting data plus pedigree information, when available. Opportunities exist to enhance genetic gain in crop breeding by combining phenotypic selection with faster molecular breeding approaches. Marker assisted selection represents one route to achieve this and is routinely used in the IBERS oat breeding programme, largely based on predictions derived from a few markers linked to large effect quantitative trait loci (QTL). It has been successful for the introgression of major traits controlled by one or a few genes of large effect, but is difficult with more complex traits governed by many genes, each with a small effect. We are developing genomic selection approaches with the aim to improve selection accuracy for quantitative traits by capturing both large and small effect QTL effects with genome-wide marker coverage. Genomic estimated breeding values will be derived from training sets from within the breeding programme that have been subjected to high-throughput genotyping and phenotyping. Initial studies are using a model winter oat population (Buffalo x Tardis) that has been extensively genotyped and phenotyped at IBERS and has recently been genotyped using a Genotype-by-Sequencing approach. We are extending this analysis to other experimental populations within the breeding programme.

In addition, a set of QTL- near isogenic lines (QTL-NILs) have been developed targeting the introgression of a number of large effect QTL into either a Buffalo or Tardis background using marker-assisted backcrossing. QTL analysis has revealed how the complementary action of genes from the two parents contributes to a number of traits including height, flowering time and response to vernalisation. Although plant height in this population is conditioned by the major gene, *dwa6*, 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. These QTL-NILs 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.

# **PLENARY SESSION 4**

**Physiology, Pest,  
Disease Resistance**



# ORAL PRESENTATIONS

## Stress sensitive stages in oat

Pamela Zwer<sup>1</sup>, Mahalakshmi Mahadevan<sup>1</sup>, Daniel Calderini<sup>2</sup>, Victor Sadras<sup>1</sup>

<sup>1</sup> SARDI, Adelaide South Australia, <sup>2</sup> Universidad Austral de Chile, Valdivia, Chile

E-mail: [pamela.zwer@sa.gov.au](mailto:pamela.zwer@sa.gov.au)

***Keywords: yield determination, critical period, yield components, stress***

More than one million hectares of oats in southern Australia have long term average grain yields of less than 1.5 t/ha where shortage of water is a major factor underlying these low yields. With dry conditions experienced at the various growth stages especially at the end of the growing season across southern Australia and the movement of oat production into traditional low rainfall regions, improved adaptation to drought would significantly increase productivity for both grain and hay end uses. This research was conducted to determine the growth stages when stress most affects grain yield and quality. The experiments were conducted at Pinery (2013) and Turretfield (2014) in South Australia and Valdivia (2014) in southern Chile. Three varieties, Mitika, Williams, and Wintaroo, were compared in Australia and two varieties, Mitika, Yallara, in Chile. Stress treatments consisted of eleven 2-week shading periods starting from 14 days after sowing and finishing 167 days after sowing. The assumption is that the effect of stresses such as water or nutrient deficit are partially mediated by reduction in photosynthesis. Grain number per m<sup>2</sup> accounted for yield responses, whereas grain weight was largely unresponsive to stress. The critical period for yield determination in oats was between stem elongation and about 10 days after flowering. Hence, targeting this critical window would be most effective for assessing stress tolerance traits in the breeding program.

# Revealing a polyamine-ethylene regulatory node linked to drought tolerance/susceptibility in oat

Gracia Montilla-Bascón<sup>1</sup>, Francisco José Canales<sup>1</sup>, Luis AJ Mur<sup>2</sup>, Elena Prats<sup>1</sup>.

<sup>1</sup>CSIC, Institute of Sustainable Agriculture, Apdo. 4084, 14080 Córdoba, Spain.

<sup>2</sup>Institute of Biological, Environmental and Rural Sciences, University of Aberystwyth, UK

E-mail: [gmontilla@ias.csic.es](mailto:gmontilla@ias.csic.es)

***Key words:* oat, drought, stress resistance, ethylene, polyamine, nitric oxide.**

Understanding plant tolerance to drought is of fundamental importance in facilitating the breeding of drought tolerant plants. However drought tolerance responses are extremely complex and involve a wide range of processes and intricate signaling events. In a previous work we monitored endogenous nitric oxide (NO) production in drought susceptible and resistant oat cultivars during drought and data suggested lesser production in the resistant genotype. This was confirmed by using transgenic barley lines overexpressing the barley non-symbiotic hemoglobin gene HvHb1 which oxidizes NO to NO<sub>3</sub><sup>-</sup>. Investigation of polyamine metabolism in wild type and HvHb1 transgenic background suggested that NO and ethylene were components in a subtle re-programming of polyamine biosynthetic gene-expression and associated post-transcriptional modification which contribute to either drought tolerance or susceptibility. We are now performing further studies to dissect the role of ethylene and its crosstalk with polyamines during drought resistance in oats. To this aim we are using the oat cultivars Patones and Flega, characterized as drought tolerant and susceptible, respectively. Gene expression analysis through RT-PCR are being carried out to determine the expression of specific genes for polyamine and ethylene pathway, i.e. arginine decarboxylase (ADC), and 1-aminocyclopropane-1-carboxylate oxidase (ACO), respectively, and also for genes that are common nodes for polyamine and ethylene biosynthesis: i.e. methionine adenosyltransferase (MAT), S-adenosylmethionine decarboxylase (AdoMetDC) and 1-aminocyclopropane-1-carboxylate [ACC] synthase (ACS), which catalyzes the first committed step in ethylene biosynthesis diverging from polyamine pathway. Preliminary results showed an increase of more than 20 fold of ACO gene expression in cultivar Flega under drought compared with Patones suggesting an increase of ethylene biosynthesis linked with drought susceptibility. Further work will include the monitoring of *in vivo* ethylene production in Flega and Patones under well-watered and drought conditions.

# Resistance to Fusarium infections in oats: Infection process and parameters in resistance breeding

Selamawit Gobena<sup>1</sup>, Lars Reitan<sup>2</sup>, Trond Buraas<sup>2</sup>, Morten Lillemo<sup>1</sup>,  
Åsmund Bjørnstad<sup>1</sup>

<sup>1</sup> Department of Plant Science, Norwegian University of Life Sciences, N 1430 Ås, Norway

<sup>2</sup> Graminor AS, Hommelstadvn 60, 2322 Ridabu.

E-mail: [asmund.bjornstad@nmbu.no](mailto:asmund.bjornstad@nmbu.no)

**Keywords:** *oat, FHB, mycotoxins, QTL*

Mycotoxins in oats have become 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 trait, since it is directly measured. Scoring FHB in the field is difficult and gives more imprecise variation. However, DON values may be underestimated due to shriveled seeds that would be blown away during harvesting. We have also used germination percentage as an indicator, which is a combined result of dead germ and seedling blight. Anther extrusion and flower opening are possible resistance mechanisms. These traits seem more complex in oats than in wheat due to the extended flowering period in oats. Anther retention is a more accurate trait than open flowering or anther extrusion, since glumes may trap anthers following flowering. Open flowering genotypes which showed higher anther extrusion were more susceptible after spray inoculation in the greenhouse. The opposite was observed after spawn inoculation in the field. Genetic analyses of mapping crosses and the CORE Spring population has shown DON content to be a quantitative trait depending on a number of QTLs. A major QTL on chromosome 13A, accounting for 10-20% first detected by He et al 2013, was confirmed in the CORE study. A number of QTLs show pleiotropy, with lateness and tall stature associated with low DON. However, in practical breeding since 2005, using a spawn-inoculated disease nursery system has successfully reduced DON content in released Norwegian varieties (with desirable phenology and height) by 40%, from 10-11 ppm to 6-7ppm.

# The use of disease resistance alleles in the UK oat breeding programs

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

<sup>1</sup>IBERS, Aberystwyth University, SY23 3EE, U.K.; <sup>2</sup>NIAB, Cambridge CB3 0LE, U.K.;

<sup>3</sup>Senova Ltd, Cambridge CB21 6AS, U.K.

\*E-mail: [igg@aber.ac.uk](mailto:igg@aber.ac.uk)

Keywords: oat, disease resistance, breeding, crown rust, powdery mildew

The crown rust (*Puccinia coronata f.sp. avenae*) and powdery mildew (*Blumeria graminis f. sp. Avenae*) fungi are highly successful pathogens that pose a constant threat to UK cereals where infection drastically reduces both grain quality and yield. Growing oat varieties with resistance is the most effective and economic method of controlling crown rust and mildew. Identifying novel disease resistance alleles and incorporating them into the breeding program is of high importance to maintain disease resistance in the UK oat crop. To aid with the successful incorporation of disease alleles into a UK background marker assisted selection is used.

Bi-parental crosses are devised using a UK adapted line and a line containing a disease resistance allele of interest. In the F<sub>2</sub> generation leaf samples are harvested, DNA extracted and plants containing the alleles of interest are identified. The selected plants go through two generations of single seed decent before entering the field phenotyping system as F<sub>5</sub>s. Many of the novel disease resistance alleles used however are from a non-adapted background and the progeny do not perform well in field trials. One way to mitigate against this is to use marker assisted backcrossing. In this, the F<sub>1</sub> from the original cross between the adapted line and the disease resistant line is used as a parent in the next crossing season. This is crossed again with the UK adapted line and the progeny with the alleles of interest selected and backcrossed again into an adapted background before progressing into the field based selection program. These field experiments test the effectiveness of the resistance and any cost of resistance on yield and grain quality.

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. This enables a comparison to be made between new disease resistant lines against the use of chemical fungicide application. Interactions between variety choice and fungicide programme were apparent in both winter and spring oat trials. 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. In susceptible varieties a 20% incidence of crown

rust resulted in a decrease in yield of 1.7 t/ha and of specific weight by 8%. Crown rust infection also resulted in lower kernel content and in thinner grain. The new lines displayed enhanced disease resistance and their yields out-performed the controls when disease pressure was high. In low disease pressure environments, the new lines still yielded as well as the controls and in all environments had excellent grain quality. The economic return on new resistant lines was significantly greater than using fungicides on susceptible varieties.

## **Pc58a QTL sequence from 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>,  
Tyler Gordon<sup>1</sup>, J. Michael Bonman<sup>1</sup>

<sup>1</sup>USDA-ARS, Aberdeen, ID, USA;

<sup>2</sup>Clemson University Genetics Institute, Clemson, SC, USA.

E-mail: [Kathy.klos@ars.usda.gov](mailto:Kathy.klos@ars.usda.gov)

**Keywords:** *oat, bacterial artificial chromosome, crown rust, QTL*

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 BAC clones, which harbor mapped EST sequences, promoters and regulatory elements, and the surrounding genomic landscape. We constructed a 5-fold redundant *Avena sativa* BAC library using the cultivar ‘Ajay’, 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 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. 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)). We screened the library for EST sequences matching those markers within and flanking the chromosome 9D QTL corresponding to the Pc58a crown rust resistance gene mapped in the Ogle x Tam O-301 population. A total of 115 BAC clones were recruited and fingerprinted to determine a tile path of representative clones for sequencing. DNA sequence was collected using single-molecule technology and consensus sequences were subjected to gene prediction algorithms.





# **PLENARY SESSION 5**

**Agronomy, Nutrition,  
Health Claims and Diets**

## ORAL PRESENTATIONS

### Differential transcription of avenanthramide biosynthesis genes in oat embryos

Jacob Toth, Sudhakar Pandurangan, Santosh Kumar, Jennifer Mitchell Fetch\*

*Agriculture & Agri-Food Canada, Brandon Research and Development Centre,  
Brandon, MB, R7A 5Y3, Canada*

<sup>2</sup>Corresponding Author

\*E-mail: [Jennifer.mitchellfetch@agr.gc.ca](mailto:Jennifer.mitchellfetch@agr.gc.ca)

**Keywords:** *gene expression, qPCR, AsHHT, avenanthramides, oat*

Avenanthramides are polyphenolic phytoalexins in oat (*Avena sativa* L.) well known for their anti-inflammatory, anti-itch, and antioxidant properties. Avenanthramide biosynthesis terminates with the condensation reaction of phenylpropanoids (p-coumaric, ferulic, or caffeic acid) with anthranilic acid or one of its derivatives, catalyzed by the enzyme hydroxyl-cinnamoyl-CoA:hydroxyanthranilate N-hydroxy-cinnamoyltransferase (AsHHT). The isoform AsHHT1 is conditionally expressed in leaf tissue (eg. upon infection with crown rust) and has two closely related isoforms, AsHHT2 and AsHHT3. False malting, a procedure involving steeping dormant seed in water for several days, is known to increase avenanthramide production and shows genetic variability. We hypothesize that this may be due to different levels of AsHHT. In the current work, we examined imbibed embryos and leaf tissue of high (AC Gwen) and low (VAO-22) avenanthramide-producing oat cultivars for differential expression of AsHHT1, AsHHT2, AsHHT3, and total AsHHT using qPCR. Transcript levels of all AsHHT isoforms tended to follow the same expression pattern over a period of 24 hours post imbibition in the two contrasting oat embryos. While the AsHHT levels were initially higher in VAO-22 than in AC Gwen after four hours of imbibition, they were higher in AC Gwen than in VAO-22 at eight to twenty hours of imbibition. Analysis of 10-day-old leaf tissue showed no differences in expression between the two cultivars (AsHHT1,  $p=0.10$ ; AsHHT2,  $p=0.28$ ; AsHHT3,  $p=0.45$ ; AsHHT3,  $p=0.91$ , t-test). These data suggest that AsHHTs are transcribed in oat embryos during imbibition, and the increased embryonic expression at eight to twenty hours of imbibition of AsHHTs in the high avenanthramide producing line might be relevant to the observed difference in avenanthramide levels across cultivars.

# Assessment of important technological parameters of new Moroccan domesticated tetraploid oat lines

Rajae Manzali<sup>1,2</sup>, Ahmed Douaik<sup>2</sup>, Mohamed Bouksaim<sup>2</sup>,  
Gideon Ladizinsky<sup>3</sup>, Nezha Saidi<sup>2\*</sup>

<sup>1</sup>Hassan 1<sup>st</sup> University, Faculty of Sciences and Techniques, Department of Applied Biology and Food Processing, P.O. Box 577, Settat, Morocco.

<sup>2</sup>National Institute for Agricultural Research, Regional Centre of Rabat, P.O. Box 6570, Rabat Institutes, 10101, Rabat, Morocco.

<sup>3</sup>Principal Investigator, USAID, Project No. TAMOU 97-053, Washington, DC 20523, U.S.A

\*E-mail: [nezsaidi@yahoo.fr](mailto:nezsaidi@yahoo.fr)

**Key words:** *Avena magna*, domesticated tetraploid oat lines, oat grains, chemical composition, minerals, proteins, fats, carbohydrates, energy value.

Oat cultivation was introduced to Morocco during the French Protectorate during the 1920s. In Morocco, it is mainly cropped in rained areas and known to be used for animal feed. Due to its high nutritive value, there is an increased demand of oat for human consumption. A breeding programme was launched by the National Institute for Agricultural Research (INRA), aiming the development of new tetraploid oat lines of *A. magna*, having a high nutritive value which can be conceived for human consumption. In the present study, nine domesticated tetraploid oat lines of *A. magna* were assessed for their technological performance. Therefore, the lines were analysed for proximate composition, essential minerals, and energy value. For this purpose, physicochemical analyses were investigated, including moisture, ash, proteins, fibre fractions, lipids, carbohydrates, and minerals. The cultivars were compared using the Analysis of Variance (ANOVA). Statistical analysis revealed a significant difference for the chemical composition between the cultivars. There was a highly significant difference ( $P < 0.001$ ) for groat protein content (11,45-13,92%), fat (3,89-10,15%), carbohydrates (48,99-57,86%), and ash (1,7-3,73%). Analysis of total fibre fractions (NDF, ADF, ADL and CF), showed the presence of significant differences between lines. The highest mean protein contents of 13,62% and 13,92% were noticed for some domesticated lines of *A. magna*. In addition, calcium, phosphorus, and potassium were the most important oat major minerals while iron, manganese, and zinc were the dominant minor minerals.

This study's outcome suggests that Moroccan domesticated tetraploid oat cultivars were in suitable range of nutrients with good estimated energy, and may serve as a good source of beneficial compounds.

## Antioxidant capacity of selected European oat genotypes

Lyudmila Lyubenova<sup>1</sup>, Heinrich Grausgruber<sup>2</sup>, Dagmar Janovská<sup>3</sup>, Marie Chourová<sup>4</sup>,  
Vojtěch Holubec<sup>3</sup>, Ismail Cakmak<sup>1</sup>

<sup>1</sup>Sabanci University, Universite Cd. 27, 34956 Tuzla/Istanbul, Turkey

<sup>2</sup>BOKU, Dept. Crop Sciences, Konrad Lorenz-Str. 24, 3430 Tulln, Austria

<sup>3</sup>Crop Research Institute, Drnovská 507/73, 16106 Praha 6-Ruzyně, Czech Republic

<sup>4</sup>Selgen a.s., Šlechtitelská stanice Krukanice, 330 36 Pernarec, Czech Republic

E-mail: [lyudmila.lyubenova@googlemail.com](mailto:lyudmila.lyubenova@googlemail.com)

**Keywords:** *antioxidants, bioactive compounds, beta-glucan, genotypic variation, minor cereals, nutritional compounds, oat*

The minor cereal species oat (*Avena sativa* L.) is known for its ability to grow well under low input conditions. Nowadays, consumers globally express an increased demand for healthy and nutritious food products. Oat could address these needs. Compared to common wheat, minor cereals generally contain higher amount of nutritional compounds; therefore, they are becoming highly attractive by both producers and consumers. Oats seem to be rich in concentrations of certain bioactive compounds including beta-glucan, phenolics, and antioxidants. Increasing evidence is available showing that oat based foods help to remove cholesterol from the digestive system and exhibit cardio-protective effects.

To our knowledge, studies investigating the nutritional composition and human nutritional impacts of oat are sparse and based on a limited number of genotypes. In the present study, 200 oat genotypes from the FP7 Collaborative **EU project Healthy-MinorCereals** have been investigated for the genotypic variation in mineral nutrients, protein, beta-glucan, phenolics, and antioxidant capacity. Additionally, extracts of the selected oat genotypes were tested for their cell biological effects (e.g. preventing cell death and oxidative cell damage) in human cell cultures. The oat genotypes examined were grown under identical field conditions in the Czech Republic. Among the 200 oat genotypes studied there was a large genetic variation for the measured nutritional compounds, especially in the case of beta-glucan concentrations and total antioxidant activity. A few genotypes were identified having consistently higher amounts of different bioactive compounds which can be exploited in future breeding programs. The most contrasting genotypes are currently used to investigate their role in mitigating oxidative stress and inhibiting apoptotic cell death in human cell cultures.

# Effect of genotype and environment on phenolic compounds and antioxidant activity of naked oats in China

Xin-Zhong Hu, Xiao-ping Li, Mei-yu Li, A-jing Lin, Zhen Ma, Liu Liu

College of Food Engineering and Nutrition Science, Shaanxi Normal University, Xi'an, Shaanxi, China  
710062, China

E-mail: [hxinzhong@snnu.edu.cn](mailto:hxinzhong@snnu.edu.cn)

***Key words: oats; cultivars; environment; year; location; phenolic compounds; antioxidant activity; DPPH***

To investigate the effects of genotype and growing environment on phenolic content and antioxidant activities of naked oats, the total phenolic content (TPC), avenanthramides compositions and antioxidant activity of whole oats from 39 cultivars grown in four location (Inner Mongolia, Qinghai, Shanxi and Gansu) of northwestern China were determine. The results showed environment (E), Genotype (G) and their interaction (E×G) affected significantly the TPC (ranged between 644.9 and 1530.3 mg kg<sup>-1</sup>), the concentration of avenanthramide 2c (2c, varied from 6.2 to 136.2 mg kg<sup>-1</sup>), avenanthramide 2p (2p, from 6.1 to 112.3 mg kg<sup>-1</sup>), avenanthramide 2f (2f, from 7.3 to 222.8 mg kg<sup>-1</sup>) and antioxidant activity (DPPH·scavenging activity from 232.0 to 712.1 μmoles TE/ 100g). The effect of E was considerably higher than the G and E×G. Base on GGE biplots analysis, four locations in northwestern China can be divided to two to three regions. Qinghai was apparently different from other locations. Cultivar Bayou 9 and oats grown in Gansu showed the highest TPC, concentration of 2c, 2p, 2f and antioxidant activity. The results suggested that naked oats enrich in avenanthramides and antioxidant activity might be achieved through selecting appropriate genotype and growth location. Compared with Canadian covered oat varieties, naked oat varieties verities have a higher TPC, the concentration of avenanthramide 2c, 2p, 2f and antioxidant activity in average level.

## Oat – a crop full of possibilities

Olof Olsson<sup>1,2</sup>, Andreas Hansson<sup>1</sup>, Hans Olof Johansson<sup>1</sup>, Johanna Lethin<sup>1</sup>,  
Svetlana Leonova<sup>2</sup>, Yi Ren<sup>1</sup>, Bindu A Sunilkumar<sup>1,3</sup>, Nick Sirijovski<sup>1</sup>,  
Lars Sjögren<sup>1</sup>, Rickard Öste<sup>3,4</sup>

<sup>1</sup>CropTailor AB, c/o Department of Pure and Applied Biochemistry,  
Lund University, Box 124, S-22100 Lund, Sweden;

<sup>2</sup>Department of Pure and Applied Biochemistry, Lund University, Box 124, S-22100 Lund, Sweden,

<sup>3</sup>Food for Health Science Centre, Lund University, Lund, Sweden 22100;

<sup>4</sup>Aventure AB, Scheelevägen 22, 22362 Lund, Sweden;

E-mail: [olof.olsson@tbiokem.lth.se](mailto:olof.olsson@tbiokem.lth.se)

**Keywords:** oat,  $\beta$ -glucane, lipids, breeding

Oat seeds contain many health enhancing bioactive molecules. However, to develop oat as a functional food for the future,  $\beta$ -glucans, protein and avenanthramide contents could be enhanced even further. To facilitate such a development, an increase in the variation of the breeding material would be an advantage. Recently we produced a mutagenized oat population of more 2,500 lines originating from the commercial variety SW Belinda, where more than one million mutations have been introduced into each line. Looking at the whole population, all characters have been modified. Taking advantage of high precision biochemical selection methods, we then identified lines with more than 50% enhanced levels of  $\beta$ -glucans, phytosterols, lipids, proteins, avenanthramides and saponins in the population. By screening seeds from more than 2000 lines of the mutagenized population using an oat-*Fusarium* infection assay, we also identified more than 100 lines displaying an increased *Fusarium* resistance.

Work is now in progress to test the agronomical performance of the best high  $\beta$ -glucan, protein and lipid lines in the field, initiating crossing programs with the most dominant and stable mutations and also to map these mutations on the oat genome. The molecular mechanisms behind several of the modified characters will also be elucidated and molecular markers to facilitate introgression of these characters into elite oat varieties will be developed.

# **PLENARY SESSION 6**

**Production, Processing,  
Products and Consumers**



## ORAL PRESENTATIONS

### Genetic Mapping of Milling Quality Traits in Oat

Gongshe Hu, Sherry Ellberg, Chris Evans, Kathy Satterfield

USDA-ARS, 1691 S 2700 W, Aberdeen, Idaho 83210, USA.

E-mail: [Gongshe.Hu@ars.usda.gov](mailto:Gongshe.Hu@ars.usda.gov)

***Keywords: oat, milling, genetic mapping***

Milling quality of oat is a very important trait of oat varieties and a critical factor for the milling industry to deliver a high quality oat product. Milling quality is measured by the trash weight, groat weight, hull weight and percentage of breakage derived from the CODEMA dehuller process and protein content. To map the genetic factors controlling the milling quality, we have developed a mapping population of 99Ab11717 x CDC Dancer. The population consists of 218 recombinant inbred lines (RILs) in its  $F_{10}$  generation. The whole population was planted at Aberdeen field, Idaho, in 2015. All the lines were harvested and measured for milling quality traits using the CODEMA dehuller with 50 grams of grain samples. Large variation in milling traits among the RILs are detected. Breakage varied from 0.2% to 61.0% with the average of 5%; Protein content varied from 12.1% to 16.1% with the average of 14%; Groat varied from 10.6 to 37.6 grams with the average of 33.1 grams. The large variations of the traits indicated that different genes or alleles have different contributions to the phenotypes. Mapping those loci will help improve milling quality in the breeding programs.

# Oat protein ingredients – processing and applications

Outi E. Mäkinen, Nesli Sozer, Dilek Ercili-Cura, Outi Nivala,  
Emilia Nordlund, Kaisa Poutanen

VTT Technical Research Centre of Finland, Tietotie 2, 02150 Espoo, Finland;  
E-mail: [outi.makinen@vtt.fi](mailto:outi.makinen@vtt.fi)

**Keywords:** *oat, protein, processing*

Oat proteins are unique among cereal proteins because of their nutritional profile and suitability for most celiac patients. Unlike *Triticeae* cereals, the major storage protein is a globulin that contains higher levels of essential amino acids than prolamin storage proteins [1]. Oat protein ingredients have only recently become commercially available, and the selection is still limited. Oat protein ingredients can be manufactured by wet fractionation to produce pure isolates, or by more sustainable dry fractionation technologies to produce protein concentrates. More enriched and functional ingredients can be obtained by fractionating defatted material, as the absence of lipids in the endosperm particles assists separation [2]. The applicability of oat proteins have been demonstrated for high protein pasta and gluten-free bread. Oat protein enrichment of pasta (6-24% protein concentrate) did not affect textural parameters, cooking loss or starch hydrolysis index compared to the semolina control. The use of up to 12% oat protein enrichment in semolina noodles did not significantly affect the sensory characteristics. However, 24% oat protein enrichment decreased elasticity and increased bitterness of semolina noodles. Gluten-free (GF) high protein oat bread was made using oat protein concentrate (35%), corn starch and oat endosperm flour. GF high protein oat bread gave similar loaf volume (2.7 ml/g) but better structural and textural (hardness 4.5 vs 9.5 N at day 3) properties compared to reference bread without protein enrichment. Oat protein ingredients face challenges in liquid and semi-solid applications because of low solubility and poor technological functionality and structure-forming ability of oat proteins at conditions relevant in food processing. Solubility and technological functionality can be improved by enzymatic, thermomechanical and mild chemical treatments. For example, transglutaminase treatment of oat protein isolate has been shown to decrease the zeta potential from -24 mV to -32 mV, improving suspension stability and foaming properties. Another approach is functionalisation with other compounds, e.g. polysaccharides. Electrostatic complexation of oat proteins with anionic polysaccharides increases their suspension stability especially at pH < 5. These methods are a valuable part of a tool kit for tailoring functionalities, required to widen the potential of oat protein ingredients in food industry.

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# **Study on enzymatic processing and soluble $\beta$ -glucan variation of turbid oats beverage**

Xiaosong Hu<sup>1</sup>, Jihong Wu<sup>1</sup>, Qun Shen<sup>1</sup>, Meili Zhang<sup>2</sup>

<sup>1</sup>College of Food Science and Nutritional Engineering, China Agricultural University, Beijing, China

<sup>2</sup>College of Food Science and Engineering, Inner Mongolia Agricultural University, Inner Mongolia, China

E-mail: [644790508@qq.com](mailto:644790508@qq.com)

***Keywords:* oats turbid beverage;  $\alpha$ -amylase; stability; soluble  $\beta$ -glucan**

Oat is of the highest nutritional value cereal in crops, it is in the sixth place of world grain production which is behind wheat, corn, rice, barley, and sorghum. About 500,000 tons of oat is processed in China and the output value is about 6 billion RMB every year. More than 70% of oat is treated as ordinary product, such as oat flour or oatmeal, less than 5% of oat is treated as highly processed products, such as oat beverage or oat noodle. In recent years, oat processing is begun to be paid attention in China, oat beverage is one of research hot spots.

Oat turbid beverage processing method was study in this paper. By determining the stability of the beverage, application of  $\alpha$ -amylase in the processing of oat turbid beverage was studied, and the content variation of  $\beta$ -glucan was determined in method of Congo Red. Results showed that the optimal process conditions of enzymatic hydrolysis, temperature was 55°C, pH was 6.4, enzyme dosage was 91.7 U/100g, hydrolysis time was 180 min, and under this conditions the suspension stability was 93.3%.  $\beta$ -glucan in the oat was 12.8 mg/g, soaking process resulted in loss of  $\beta$ -glucan, while cooking and beating increased the  $\beta$ -glucan content. Enzymolysis of  $\alpha$ -amylase and sterilization had no significant effect on  $\beta$ -glucan content.

## **Food fibers and avenins of grains of perspective naked russian oat cultivars**

<sup>1</sup>Krasilnikov V.N., <sup>2</sup>Gavrilyuk I.P., <sup>3</sup>Batalova G.A., <sup>4</sup>Afonin D.V., <sup>1</sup>Popov V.S.,  
<sup>1</sup>Sergeyeva S.S., <sup>2</sup>Loskutov I.G., <sup>2</sup>Gubareva N.K.

<sup>1</sup>St. Petersburg State University of Trade and Economics

<sup>2</sup>N.I. Vavilov All-Russian Institute of Plant Genetic Resources

<sup>3</sup>N.V. Rudnitsky Zonal Northeast Agricultural Research Institute

<sup>4</sup>Baltika Breweries LLC

E-mail: [protein@peterstar.ru](mailto:protein@peterstar.ru)

***Key words: naked oat, avenin, functional foods, non-starch polysaccharides,  $\beta$ -glucans, arabinoxylans.***

Non-starch polysaccharides ( $\beta$ -glycans and arabinoxylans) of fifteen new and two commercially cultivated naked oat cultivars, as well as one hulled oat cultivar were studied.

A strong correlation and ratio between the content of arabinoxylans and that of  $\beta$ -glucans have been determined. Cultivars with an increased content of these components have been selected.

The studied cultivars demonstrated 11 electrophoretic banding patterns differing in  $\alpha$ - and  $\beta$ -avenin fractions. In most naked oat cultivars were revealed several weak bands of  $\alpha$ -avenin that are the most celiac-toxic peptides. It seems to be promising to assess toxicity of these cultivars from their reaction with celiac patients' sera.

The performed research is of immediate interest from the point of view of engineering functional and special purpose foods.



**PLENARY SESSION 7**  
**Sustainable Farming Systems,  
Commercialization,  
Seed Production, and Royalties**

# ORAL PRESENTATIONS

## Oats, the first 32,000 years and the next 10

Christopher Green

Green Resources Limited  
E-mail: [chris@greenresources.co.uk](mailto:chris@greenresources.co.uk)  
[www.greenresources.co.uk](http://www.greenresources.co.uk)

Last year researchers in Italy identified starch found on stones used in grinding grains to have originated from oats believed to have been grown some 32,000 years ago.

For centuries oats were the mainstay crop and, in feeding horses provided the power for work on the land, harvest and transportation. During the First World War over ten million horses and mules were employed each with an appetite for oats and hay. However, as a result of mechanisation horse numbers declined dramatically and in the absence of alternative markets the area devoted to oats suffered.

We have come a long way in oat innovation with a diversity of products from energy drinks to oat based shampoo for dogs and highly fractionalised products used in the cosmetic and pharmaceutical industries. Our enhanced knowledge has enabled us to promote the nutritional and health benefits of oats to a more discerning consumer. Whilst there is a strong demand from the human food sector and for high value based products this in no compensates for the loss of area as a result of the diminishing role of oats as an animal feed.

Global decline in the area devoted to oats impacts on all of us. In particular the plant breeding industry whose responsibility it is to improve genetic performance through the introduction of new varieties. As a consequence of this decline there has been a continual shift in agricultural investment and research with funds and priorities being directed to the broad acre crops of wheat, maize, rice, soy and cotton. The net result is a continual erosion of oat breeding programmes.

Readers and delegates will be pleased that it is not my intention to review the last 32,000 years. The focus of my presentation is to consider the market as it exists today, to understand the challenges and consider mitigation strategies which can be harnessed at local or regional levels. Our oat community is small. But being present at this 10<sup>th</sup> IOC is a testament that we are motivated and excited by the intrinsic properties that make oats unique. As a researcher, agronomist, breeder, processor or product innovator we each have an input to steer the direction of oats over the next ten years. Grasp the opportunity to network and take forward our individual and collective interests in oats. Harness your quest for knowledge and forge effective and meaningful alliances to deliver research and products that will make a real impact in improving the value and uptake of oats.



# **Commercialisation and end –point royalty collection in Australia**

Peter D. McCormack

South Australian Research & Development Institute, Australia  
[peter.mccormack@sa.gov.au](mailto:peter.mccormack@sa.gov.au)

The Plant Breeders Rights Act (PBR) was introduced in Australia to stimulate private investment in plant breeding. With the introduction of the PBR, breeders were able to confer licensing rights for companies to commercialise varieties and collect a royalty on their behalf.

With the reduction in public/government funding to public breeding programs new initiatives were needed to generate additional financial support.

End point royalties supplement industry funding to maintain breeding program objectives and fund new initiatives and projects.

The development and release of improved milling and hay oat varieties coupled with the increase in demand of oaten hay and more recently milling oat grain in SE Asia, the National Oat Breeding program has enjoyed a sustained period of financial benefit through the ability to collect end point royalties.

The increased adoption of new improved varieties nationally resulted in end point royalty returns being able to fill the gap left by the reduction in public funding.

# **Adaptation strategies of contrasting oat genotypes to planting pattern and population densities**

Bao-Luo Ma<sup>1</sup>, Pu-Fang Li<sup>1,2</sup>, Weikai Yan<sup>1</sup>

<sup>1</sup>Agriculture and Agri-Food Canada, Ottawa Research and Development Centre,  
Ottawa, Ontario, Canada K1A 0C6;

<sup>2</sup>Institute of Soil and Water Conservation, Northwest A & F University, 712100, Yangling, China  
E-mail: [baoluo.ma@canada.ca](mailto:baoluo.ma@canada.ca)

Adjusting planting pattern and population density may be an effective approach to reducing chemical use for weed control in small grain cereal crop production. Such study may also lead to the identification of biological traits for use in plant breeding. Field and controlled growth room studies were conducted to (1) characterize adaptive strategies of contrasting oat genotypes; and (2) determine if there was a difference in oat genotypes representing different growth type on weed suppression in response to planting density and row spacing. The results indicate that under field conditions, oat genotypes with prostrate leaves (OA1256-1) showed significantly lower weed biomass than oat variety with erect leaves (OA1228-1) at high population density, especially under high weed pressure. Greater yield was observed for the prostrate variety at the medium density under high weed pressures, and the opposite was observed at high density cultivation at low weed density. Under the controlled growth room conditions, with increasing plant densities, intensive competition among individuals led to an overall reduction in grain yields for both varieties. However, the erect variety showed reduced aboveground biomass allocation and lower yield, whereas the prostrate variety showed decreased allocation to the roots and increased allocation to the panicles under increasingly competitive environment. Our findings provided a novel rationale for a planting strategy based on plant type selections.

# The effect of 2,4-D butyl ester on percentage of covered grains in naked oat and its residue dynamics in oat plants

Guiqin Zhao, Jikuan Chai, Zeliang Ju, Xudng Song, Liu Huan

Gansu Agricultural University, Lanzhou, China.

E-mail: [zhaogq@gsau.edu.cn](mailto:zhaogq@gsau.edu.cn)

**Key words:** *naked oat; herbicide, 2,4-D butyl ester, covered grains, residues*

**Introduction:** 2,4-D butyl ester is an effective and commonly used herbicide to control broad leaf weeds om oat fields in China, its side-effect of increasing percentage of covered oat grains was also reported. But there is very few reports on variatal and residues of 2,4-D butyl ester. The objectives of this paper is to study the effects different 2,4-DB concentrations on percentage of covered oat grains, and its residu in different oat varieties.

**Material and Methods:** The field experiment was conducted at a farm in Yuzhong County (E104°12', N35°85'), Gansu Province. 5 naked oat varieties were used. A 3×5 factorial experiment, arranged in a completely randomized design with 4 replications, was conducted from March to July 2014. The plot was 20m<sup>2</sup> (4m×5m), oat were seeded in row with 20cm space at 150kg/hm<sup>2</sup> seeding rate. 2,4-DB was applied at 3 concentrations. Five 50cm-long samples for each plot were randomly taken at maturity and harvested. Covered grains were seperated and counted after hand threshing.

To study the residue of 2,4-DB in naked and covered oat, Baiyan No.2 (naked) and Longyan No.3 (covered) were used in another field experiment with completely randomized design in 2015. The seeding was the same as the above experiment, as well as the 2,4-DB dosage and application. 5 spots for each plot, 5 plants for each spot were cut and mixed at 1, 7, 14, 21, 28 days after herbicide application, as well as flowering, milk and maturity (seed) stage, high perforamnce liquid chromatography (HPLC) and ultraviolet fluorescence detector (G1321B, America) were used to detect the residues.

**Results and discussion:** 2,4-DB significantly affected percentage of covered grains from naked oat genotypes (Table 1). With the increasing application dosage, all the naked genotypes increased their covered grains. Compared with the hand weeded check, as much as 4.6, 3.1 and 1.9 times of increase were obtained for the highest, medium and lowest dosage of 2,4-DB, respectively. Significant varietal differences were also observed. Among 5 genotypes, Baiyan No.2 had the highest covered grain number under each treatments. Compared to the control, Jinyan No.17 increased its covered grain percentage by 14.4, 9.4 and 6.6 times under the highest, medium and lowest 2,4-DB treatments, indicating it was the most sensitive variety despite its lower value compared with other genotypes.

Under the same treatments, naked oat had different residue dynamics of 2, 4-DB from that of covered oat (table 2, 3). No residue was detected in the control. With the increasing 2, 4-DB concentration, residues in oats increased significantly at each time of sampling.

At first 5 sampling times, naked oat accumulated much more 2, 4-DB than covered oat. 28 days after 2, 4-DB application, almost 90% of the herbicide was digested. But naked oat still accumulated more 2, 4-DB than covered one, as much as 54.5%, 39.0% and 41.7% more residue were tested in naked oat than in covered ones under the lowest, medium and the highest dosage.

Half-life period of 2, 4-DB in naked and covered oat was also significantly different. Under each herbicide concentration, Baiyan No.2 had much longer half-life period than Longyan No.3.

2,4-DB was hydrolyzed into 2,4-D in plants, table 4 and table 5 showed the residue dynamics of 2,4-D in naked and covered oats. The same results were obtained as the residues of 2,4-DB. Naked oat accumulated significantly more 2,4-D than covered at each sampling times.

The process of 2, 4-DB hydrolyzed into 2, 4-D was affected by pH, lower pH improved hydrolyzation. Naked oat had lower pH than covered oat (5.9 vs. 6.1), which helped 2, 4-DB hydrolyzation and increased its absorption in the plants.

**Conclusion:** significantly affected percentage of covered grains in naked oat genotypes. Baiyan No.2 had the highest covered grain number. Jinyan No.17 was the most sensitive variety. Naked oat accumulated significantly more 2, 4-DB than covered oat; the residue of 2, 4-D in naked oat was also much higher than in covered ones due to its lower pH.

# Different intercropping patterns affecting soil characteristics of intercropped oat with common vetch and alfalfa

Lijun Li, Tingting Zhang, Xiaoting Li, Baoping Zhao, Jinghui Liu

Inner Mongolia Agriculture University, Hohhot, P.R.China, 010018

E-mail: [imaullj@163.com](mailto:imaullj@163.com)

**Keywords:** *Intercropping; Forage; Quality; Soil properties*

In recent years, soil degradation was becoming seriously in the farming-pastoral zone in Inner Mongolia, and grain-forage production structure was becoming imbalanced. In order to promote the coordinated development of grain-forage industry and improve the soil properties, oat intercropped with common vetch and alfalfa was studied in saline land and chernozem. The width of oat was 1.2, 2.4 and 3.6 m, and the width of common vetch and alfalfa was 1.2 m, in other words, the intercropping patterns were 1:1, 2:1 and 3:1. The forage yield and quality, and activities of soil catalase, sucrase, urease enzyme were measured. The results showed that: (1) For oat intercropping with common vetch and alfalfa, the mixed pastures biomass of 2:1 pattern was 3.46%-18.70% and 2.43%-3.45% higher than the other patterns respectively in saline land, and increased by 2.85%-7.06% and 0.71%-20.50% in chernozem soil. Land utilization of 2:1 mode was highest (32%-91%), and oat intercropping with alfalfa was higher than oat intercropping with common vetch. The aggressive ability of oat intercropping with common vetch was different in two years. The aggressive ability of alfalfa has an advantage over oats in 1:1 pattern, but oat was better in the other patterns of oat intercropping with alfalfa. (2) 2:1 and 3:1 mode have higher percentage of crude fat content when oat intercropping with common vetch, but 3:1 mode was significantly higher than that of other patterns when oat intercropping with alfalfa. 2:1 mode could improve the percentage of pastures crude. For oat intercropping with common vetch, the forage RFV of 2:1 and 1:1 pattern were significantly higher than that of other patterns in saline land and chernozem soil, respectively. For oat intercropping with alfalfa, 2:1 was highest in chernozem soil. (3) 2:1 pattern of soil water content of oat intercropping with common vetch increased by 2.26%-38.54% in saline land, and there was no significant difference in chernozem soil. The soil bulk density was decreased 6.19%-11.12% and 6.14%-6.37% of oat intercropping with common vetch and alfalfa respectively in saline land after intercropping, and there was no change in chernozem. The content of >0.25mm soil aggregate structure significantly increased by 2.89%-9.52% and 9.56%-12.56% in saline land and chernozem respectively. (4) The soil microbial biomass carbon content of 2:1 pattern of oat intercropping with common vetch significantly increased by 7.12%-34.44% in saline land, and 1:1 pattern's was lower than other patterns by 6.77%-26.07% and 9.20%-16.13% of oat intercropping with common vetch and alfalfa respectively in chernozem. The soil microbial biomass nitrogen content of 2:1 pattern was significantly higher than that of other patterns, oat intercropping with common vetch and alfalfa increased by 9.97%-49.61% and 3.19%-34.94% in saline land, 11.00%-48.82% and

6.23%-48.82% in chernozem. (5) 2:1 pattern could improve soil catalase and urease activity. The soil sucrase activity of 2:1 pattern increased by 3.33%-4.89% and 0.29%-18.71% of oat intercropping with common vetch and alfalfa respectively in saline land, 2.20%-20.00% and 0.48%-29.62% in chernozem. 3:1 pattern of oat intercropping with common vetch was highest, and 2:1 pattern of oat intercropping with alfalfa was highest for soil alkaline phosphates activity, and respectively increased by 3.33%-32.70%、0.21%-11.02%. (6) 2:1 pattern has more soil organic carbon after intercropping. 3:1 pattern in saline land and 2:1 pattern in chernozem could maintain soil available nitrogen effectively. 3:1 pattern of oat intercropping with common vetch and 1:1 pattern of oat intercropping with alfalfa uses a little of soil total nitrogen. 3:1 pattern in saline land and 2:1 pattern in chernozem consumes least of soil available phosphorus. 2:1 pattern could maintain soil potassium effectively. In one word, 2:1 and 3:1 were both good patterns, but 2:1 pattern of oat intercropping with alfalfa was optimal pattern in saline land, and we could choose both of 2:1 pattern of oat intercropping with common vetch and alfalfa in chernozem.

# **PARALLEL SESSION 1**

**Genetic Resources,  
Diversity and Breeding**



# ORAL PRESENTATIONS

## Oat Genetic Resources in Finland

Elina Kiviharju

Natural Resources Institute Finland, Green Technology, Myllytie 1, FI-31600 Jokioinen, Finland.

E-Mail:[elina.kiviharju@luke.fi](mailto:elina.kiviharju@luke.fi)

**Key words:** *Oat, Avena, genetic resources, breeding, sustainable use*

Oat, *Avena sativa* L., is one of the main cereal crops in Finland. Cultivation area in year 2015 was 306 500 hectares, and total yield 980 million kg. In general, the Finnish oat is known for its high quality, including high protein content, high hectoliter weight, thin cover, purity, and bright pale colour. Earliness, reliability of the yield, and good quality have been important breeding traits.

Until breeding activities started in the beginning of 1900-century, Finnish oat cultivation was based on landraces, of which majority were assumed to be black-covered. First cultivars were mainly selections from the Nordic and Northern-European early cultivars. Early Swedish cv. Kultasade was cultivated in large areas.

Landraces collected around Finland were widely used as crossing parents in cultivar breeding. For example cultivar Kytö, released in 1925, was a cross between Finnish landrace (Ta 091) and Kultasade, where landrace contributed earliness and better yield production in the North (Ulvinen, 2004). Two Finnish landrace can be identified, which have largely affected to the background of the Finnish oat cultivars, bred during the early years of conventional breeding. They originated from Kuopio and Rautalammi regions (Saastamoinen, 2000). Important crossing material has been obtained also from Northern parts of Europe and America, and also Eastern material was used, like Pendek from Siberian origin.

Today, the Finnish national list of plant varieties consists of 46 accepted oat cultivars (*Avena sativa* L.), two of them naked type. Majority of them are cultivars of the Finnish company Boreal Plant Breeding. In addition, also cultivars bred in Sweden, Norway and Germany are in the list. As a landrace, one conservation variety is accepted to the Finnish official list, a black-hulled oat Heljä.

NordGen – the Nordic Genetic Resource Center – conserve seeds of the cultivated plants for food and agriculture for all Nordic countries. Collection includes 142 oat accessions of Finnish origin. Large set of them was recently donated back from the Vavilov Research Institute, showing great importance of co-operation between the gene banks.

Oat is very well adapted to the Northern conditions, and has potential for greater significance in feed and especially in the food sector. Now oat yield is mostly used for animal feed, but different type of food products have been developed and their healthy effects intensively promoted. Targeted breeding for different special aims could potentially increase oat use and productizing.

Breeding research is important to ensure constant improvement in cultivar breeding. In Finland, marked oat research have been done during earlier years, including oat haploid production (Kiviharju et al. 2005), linkage and QTL-mapping (Tanhuanpää et al. 2010), disease resistance and processing studies. Continuous research is essential, in order to get all genetic potential in use.

Nordic oat gene pool is shown to be narrow (He & Bjørnstad, 2012). Due to that, key to go further is an efficient evaluation of existing oat genetic resources, and use in breeding. In addition of oat cultivars, breeding lines and landraces, large gene pool of other *Avena* species is available. Several of them are easily crossed with cultivated oat, like *A. sterilis* known as a source of disease tolerance. Improved genomic tools developed for cereal crops and also for oat, are providing possibilities for identifying valuable alleles and developing identification tools for marker assisted selection of single selected alleles or genome wide.

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## On farm organic oat breeding

Ben Schmehe, Hartmut Spieß, Sabine Martis,  
Lilla Szabo, Stefan Klause, Anjana Pregitzer, Lina Perez

Forschung & Züchtung in der Landbauschule Dottenfelderhof (FZD)  
Dottenfelderhof 1, 61118 Bad Vilbel, Germany  
E-Mail: [ben.schmehe@dottenfelderhof.de](mailto:ben.schmehe@dottenfelderhof.de)

**Keywords:** *on farm, organic agriculture, resistance, loose smut, biodynamic*

In the 1960's the farm 'Dottenfelderhof' in Hesse-Germany was converted from conventional to biodynamic agriculture. Very soon, it became apparent that neither the modern conventional nor old varieties could meet the specific needs of the different practice. In the mid 70's and early '80s on farm breeding programmes for cereals and vegetables were established but it took until 2005 that the first oat (*Avena sativa*) crosses were made. Until then the old cultivars ERBGRAF and PANTHER were used, both of which are susceptible to loose smut (*Ustilago avenae*). Although loose smut does not play a role in the process of variety registration it can be a severe problem for seed certification. Beginning with the year 2007, registered varieties and breeding lines are artificially inoculated with loose smut and selected for resistance in the field.

The breeding scheme follows a pedigree approach. In F3-generation the cultivars are inoculated under partial vacuum at -800 hPa with 5 g spores/litre water for the first time. The percentage of smutted panicles is determined at plant maturity and healthy plants are selected. This process is repeated until F5-generation if necessary. After that the breeding lines are selected in a separate loose-smut-free field but samples of every selected line are still tested for resistance alongside.

Present registered varieties are inoculated for at least two subsequent years up to four years if susceptibility is low. Resistant varieties are incorporated in the breeding programme but also varieties with a higher susceptibility may be incorporated if other agronomic traits are performing well under organic farming conditions. Further important traits for organic breeding among many others are high and stable yield, early-season vigorous growth, good weed suppression, long straw but still good lodging resistance and good dehulling ability.

By the beginning of 2016 there is a dataset of more than 1,400 loose smut tests which contains in total 426 different cultivars. Among these cultivars, recent and old registered varieties, genetic resources from genebanks and breeding lines can be found.

At present, two loose smut resistant cultivars with good characteristics for organic agriculture are in the process of official variety registration at the German Federal Plant Variety Office (Bundessortenamt) for DUS and VCU tests.

Breeding for resistance is important for organic seed propagation, reduction of yield losses and for animal health where oat is used as green fodder. The on farm approach ensures that the breeding process is driven by actual needs and problems of organic farming. In case of loose smut, however, the resistance is limited to the loose

smut race present at the breeding site. More organic oat breeding at other locations is desirable. The screening of registered cultivars is a useful additional information especially for organic farmers because there is no screening for loose smut in the official variety screenings in Germany. In future even conventional farmers may benefit from resistant varieties if the use of seed treatments are further limited due to environmental risks of the chemicals used.

# Breeding oats for grain quality in Southern Brazil

Solange Ferreira da Silveira Silveira; Antonio Costa de Oliveira

Plant Genomics and Breeding Center, Federal University of Pelotas, Pelotas-Brazil,

E-mail: [acostol@terra.com.br](mailto:acostol@terra.com.br)

***Keywords: oat, breeding, grain quality, Brazil***

White oat (*Avena sativa* L.) is a highly adopted cereal for human and animal consumption. Oat breeding programs are constantly challenged by the need of high yield, high grain quality genotypes. In this scenario, breeders need to be efficient in increasing the variability through crosses as well as in using selection methods. This study aimed to evaluate two populations of white oat, through the comparison of different selection strategies, i.e., number of selected plants, heritability measures at different generations and correlation measures, in order to obtain genotypes with high yield and grain quality. Experiments were conducted for segregant populations generated from two different crosses (Albasul x UPF 15 and IAC 7 x UFRGS 19), in the experimental field of Plant Genomics and Breeding Center (CGF / UFPel), located in the municipality of Capão do Leão, Rio Grande do Sul State. The evaluated characters were: height, number of panicles per plant, number of spikelets per panicle, panicle weight, number of grains per panicle, grain mass per plant and thousand grain weight. Concerning the chemical composition of the grains, the following characters were evaluated: protein, lipids, total dietary fiber and  $\beta$ -glucan content. Descriptive, genetic parameters, correlation and selection gain as well as molecular marker analyses were performed. In both populations, it was possible to rescue segregating transgressive genotypes for agronomically important traits. High heritability coefficients were observed for the characters of agronomic performance, enabling selections as early as the  $F_4$  generation. Selection between families are more promising in the generation  $F_5$ . The MSSD selection method (Modified Single Seed Descent) was efficient to obtain genetic gain. The presence of negative correlations make it difficult to select genotypes that are superior in all parameters evaluated in this study. There is a dependency relationship between the performance of agronomic characters and the chemical constituents of oat grains, enabling the indirect selection of grains with higher nutritional quality, however, a strict control of environmental conditions is required.

# Oats in Argentina

Liliana Wehrhahne<sup>1</sup>, Elena Molfese<sup>1</sup>, Federico Moreyra<sup>2</sup>

<sup>1</sup> Chacra Experimental Integrada Barrow (Convenio MAA-INTA)  
Tres Arroyos, C.C. 50 – CP B7500WAA.

<sup>2</sup> EEA INTA Bordenave, Pcia. Buenos Aires- ARGENTINA  
E-mail: [wehrhahne.liliana@inta.gob.ar](mailto:wehrhahne.liliana@inta.gob.ar)

**Key words:** *oat, forage, grain yield, grain quality, cultivars*

The principal characteristic of oats crops (*Avena sativa* L.) in Argentina is the flexibility they offer to the farms systems. The main use is for forage in fall-winter period, either for grazing or to make reservations as rolls or silage. It also constitutes the most relevant double purpose crop (forage or grain) in the whole country. It is used as a cover crop too, before planting soybean. Oat is cultivated in almost 2 million hectares on different soils and climates.

A smaller area is planted for grain harvest only. Oat grain is used for feed, seed and food. It is a good source of protein, fibre and oil. Oat groat for human food is pretended to be high in protein, beta glucan and low in oil, whereas high in oil and protein is desired for livestock feed to maximize the energy. The production of oats for grain presents particular characteristics. The time of sowing is like wheat and barley (May to July) and is differentiated to planting for grazing or hay (February to April) in our region. Some practices like fertilization, weeds and rust control have more importance in grain harvest oats. In some areas such as the influence of the Chacra Experimental Integrada Barrow is a common practice to graze the oats and then let it recover to harvest the grain or eventually to make reserves. This area produces seed for other regions and grain of quality for the industry. Many times the same cultivars are used for different purposes.

The most frequent diseases are crown rust (*Puccinia coronata*) and stem rust (*Puccinia graminis*), but the increase in no till system acreage make leaf spots (*Pyrenophora chaetomioides*) important now.

In the past most of the area was covered with *Avena byzantina*, but in our days it is with *Avena sativa*. The Oat Breeding Programme is done by INTA (National Institute of Livestock and Agricultural Technology) in two different places of Buenos Aires Province, Barrow and Bordenave. We exchange and receive germplasm with the Quaker Oat Program and UFRGS Programme. The main goal of the public programme is the development of forage (Bordenave), forage, and high quality grain cultivars for the food industry (Barrow). For industry it is important full grains, with high test weight, protein, groat percentage and beta glucan content. The climatic conditions and stress in grain filling often does not achieve the desired quality. A potential and special use of oat grain is food for celiac people, and some of our varieties are being tested and could be used for that purpose. In the recent years we released new cultivars Bonaerense INTA Aikén and Bonaerense INTA Sureña (forage and grain), Josefina INTA and Elisabeth INTA (forage) and Bonaerense INTA Yapa (grain).

# A Brazilian overview about oat cultivars for ground cover and grazing

Alfredo do Nascimento Junior\*, Renato Serena Fontaneli, Henrique Pereira dos Santos, Márcio Só e Silva e Eduardo Caierão.

\* Embrapa Wheat, Passo Fundo, Brazil.  
E-mail: [alfredo.nascimento@embrapa.br](mailto:alfredo.nascimento@embrapa.br)

**Keywords:** *oat, Avena strigosa, cultivars, grazing, Brazil*

The food base of the Brazilian meat and milk production is forage, supplied in the form of silage or hay, or directly on planted or natural pastures, which are highly dependent on seasonality and weather. In certain periods, i.e., the dry and cool season, the food supply by pastures is insufficient to meet the animals' needs, which could be circumvented by supplementing grains in high-cost diets, hay or silage.

Oat is one of the main winter crops in southern Brazil. There are no official statistics in relation to the area used for ground cover and grazing. The species *Avena strigosa* Schreb., is the most commonly planted for soil cover as well as incrop-livestock-system. However, most genotypes available are still common oat populations with high genetic variability, without proven genetic origin, used on large-scale farms, because the amount of seed of registered cultivars is insufficient to meet market demands.

In the states of Rio Grande do Sul, Santa Catarina and Paraná, in the 2014/15 growing season, grain was harvested on 19.32 million hectares. Of this total, 3.74 million hectares were used for maize and 11.08 million for soybean, totaling 14.82 million hectares of cultivation in the summer or as second crop. However, of this area occupied in the summer, only 2.64 million hectares were used in the winter for grain crops, and only 0.25 million hectares were used to grain oat production, with *A. sativa* L.. Large areas are available for pasture for meat and milk production, where winter forages could be planted, combining the opportunity with the requirements of the farm enterprise.

There are few diploid oat breeding programs in Brazil, however even diploid and hexaploid species has been using for ground cover and grazing, according the official cultivars register in Brazil, being six of *A. sativa* L., two of *A. brevis* Roth., and fourteen of *Avena strigosa* Schreb..

In spite of, estimating 5.0 million hectares with oats for feed or ground cover, the certified seed production is far to fulfill the market needs. In 2014, only 73,276 hectares were registered for seed production, and the total estimated seed harvested could supplied only 1.83 million hectares, ratifying a low availability of oat seeds in Brazil. To get a worst scenario, 81% of oat area, for certified seed production, were showed with only two old cultivars, 'Embrapa 139 Neblina' (55%) and 'Embrapa 29 Garoa' (26%), both *A. strigosa*, which could result in severe production losses, in case of plant diseases event or adverse weather conditions.



# The ways of oat winterhardiness improvement in Poland

Bogusław Łapiński<sup>1</sup>, Agnieszka Rachwalska<sup>2</sup>

<sup>1</sup>National Centre for Plant Genetic Resources, Plant Breeding  
and Acclimatization Institute (IHAR)- National Research Institute- Radzików, Poland.

<sup>2</sup>Plant Breeding and Acclimatization Institute (IHAR) Experiment Station Grodkowice,  
Poland. PL-05-870 BŁONIE, Radzików – IHAR, KCRZG

E-mail: [b.lapinski@ihar.edu.pl](mailto:b.lapinski@ihar.edu.pl)

**Key words:** *Allopolyploidy, Avena macrostachya, Avena sativa, wide cross, winterhardiness, winter oat, yield*

The Polish program of winter oat breeding started in 2002 from interspecific crossing of foreign winter oats with the accessions of tetraploid perennial wild species *Avena macrostachya* Balan. Single hybrids were obtained in three cross combinations. Large differences were noticed in fertility level and chromosome constitution of progeny of the intensely cloned and colchicine treated  $F_1$  hybrids. The  $B_1F_1$  or  $F_2$  generation consisted of plants with chromosome numbers between 40 and 49, octoploids ( $2n=56$ ) and plants carrying 60 to 70 chromosomes. The quasi-hexaploids of the first group were partly or completely sterile, but their chromosome complement was quickly regulated and fertility restored, usually after additional back-cross to *A. sativa*. A few generations later they produced valuable breeding strains. In field experiments in Radzików (near Warsaw) and Grodkowice (near Krakow), they showed high yielding potential and no negative effects of wild germplasm. In the dry seasons 2009 and 2013 winter oats produced yields nearly 100% higher than the spring cultivar standard. Test weight was also ca. 4kg/hl higher. Two of the husked strains, showing winterhardiness level better than the starting *A. sativa* population, are in the state trials now. They could be recommended for the regions with stable snow cover, because they were not able to survive naked ground surface temperatures below  $-14^{\circ}\text{C}$ , which happened twice in Radzików and once in Grodkowice in the last 8 years of field trials. Especially the last winter (2015/2016) was destructive, even for the octoploids, which were earlier considered the most winter-hardy oats. The octoploids produce healthy green mass and very large plump grain, rich in protein, however they require breeding effort to increase yield (now 50-67% of the best winter hexaploids) and to make ripening uniform. The last severe winter season revealed several new hexaploid strains, transgressive in frost resistance to the octoploids. The 8x or 10x *sativa-macrostachya* allopolyploids proved to be effective sources of winterhardiness for hexaploid oat.





# **PARALLEL SESSION 1**

**Agronomy, Nutrition,  
Health Claims and Diets**

## ORAL PRESENTATIONS

### **Genotypic, phenotypic and FTIR-based metabolic fingerprint diversity in oat landraces in relation to the environment at the place of origin**

Maja Boczkowska<sup>1</sup>, Jacek Zebrowski<sup>2</sup>, Jarosław Nowosielski<sup>1</sup>, Izabela Kordulasińska<sup>1</sup>,  
Dorota Nowosielska<sup>1</sup>, Wiesław Podyma<sup>1</sup>

<sup>1</sup>Plant Breeding and Acclimatization Institute (IHAR) - National Research Institute, Radzików, Poland

<sup>2</sup>Institute of Applied Biotechnology and Basic Plant Sciences, University of Rzeszów, Poland

E-mail: [m.boczkowska@ihar.edu.pl](mailto:m.boczkowska@ihar.edu.pl)

***Keywords: oat, landraces, genotypic, phenotypic, FTIR-based metabolic fingerprint***

Landraces are associated with traditional farming systems and are not the result of premeditated crop improvement (1). They are a dynamic, heterogeneous population of crops that have evolved in response to natural selection for the local environment, mutations, migrations and genetic drift, but also preferences and agricultural practices of local farmers (1–4). Their diversity is the immanent structural attribute among and within landraces (5). As a consequence, they might offer beneficial traits related to yield stability, yield health values, high adaptability to changing environment and the capabilities of reducing or slowing down the expansion of pathogens (6).

Poland was one of the very few European countries that maintained the on-farm cultivation of cereal landraces for a relatively long time due to the considerable fragmentation of farms and, consequently, extensive land use. Such crop management was especially typical for eastern and southern parts of the country. Several expeditions carried out from the beginning of the 1970s (7, 8) confirmed the richness of these regions in cereal landraces, including oats. Currently, cereal landraces are rarely collected during expeditions carried out in Poland. During several expeditions carried out by Polish genebank experts, about 90 indigenous landraces have been gathered. They account for 67% of the oats' accessions described as traditional cultivars or landraces, which are maintained in long-term storage by the National Centre for Plant Genetic Resources of PBAI-NRI i.e. Polish genebank.

We focused on oat landraces developed in the zone of moderate climate attempting to understand their genetic and phenotypic variability in context of the pressure of environmental constraints at the locations where they had evolved. Here we present a comprehensive analysis of the diversity of common oat landraces acquired from different regions of Poland employing multiple phenotypic, genetic and metabolic approaches. The focus was given to establish mutual relationships between germplasm features determined at various description levels and to assess the impact of eco-geographic conditions of landrace place of origin on the descriptor patterns.

Besides ISSR and ALFP molecular markers and diverse phenotypic traits the Fourier transform infrared (FTIR) spectroscopy, enabling throughput metabolic finger-

printing, was used for the description of the germplasm collection. We used sophisticated multivariable analysis to integrate the data for structure analysis and to establish mutual relationships.

We found that the accessions diversity across the eco-geographical variables was manifested differently depending on selected phenotypic, genetic, and metabolic criteria. Grain metabolic fingerprint derived from FTIR spectroscopy revealed the highest degree of germplasm diversity among all of the examined traits, particularly for spectral bands assigned to lipids. The landraces, which were collected in close geographical proximity, showed clear morphological and metabolic resemblances, although they represented quite different genetic backgrounds.

All three levels of analysis ie. genotypic, phenotypic and metabolomic showed the presence of selection resulting from environmental pressures and more specifically from the temperature at the landrace origin site. This research also proved that coupling of genetic polymorphism with the FTIR fingerprinting markedly extended the description of the oat landraces diversity.

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# **Protein markers and metabolomic approach to variety identification, seed control, food and feed utilization of oats**

A.V. Konarev, I.P. Gavriluk, N.K. Gubareva, T.V. Shelenga, I.N. Perchuk, I.G. Loskutov\*

Federal Research Center – The N.I. Vavilov All-Russian Institute of Plant Genetic Resources,  
St. Petersburg, Russia

E-mail: [a.konarev@vir.nw.ru](mailto:a.konarev@vir.nw.ru)

***Keywords: oat, protein markers, metabolomics spectra***

Discussed herein are facts and arguments “in favor of oats”; protein markers in oat gene pool registration; conservation and maintenance of oat genetic diversity and authenticity of its collection; oat seed control (fatuoids, etc.); oats in healthy and medicinal nutrition; and metabolomic approach to oat gene pool analysis. Facts: “Oat is widespread over all continents embracing the whole grain belt of the Globe” (Loskutov, 2007). It is a popular feed for horses. The widest popularity in the world it received as morning oatmeal porridge. The customer market offers a rich diversity of “oat” products, including oatmeal. However, “oat” is in quotes because, unlike the case with bears, there is no guarantee that it is oat we buy and not, for example, barley. According to our data, the popular rolled oats for 40% or more consist of barley. A paramount condition for implementing useful properties of a crop is the compliance of the contents of a sack, package, car, etc. with what is written on them. It is equally valid for the “rolled oats” sold to the population, for seed collections held by genebanks, for breeding centers, for bulk grain (seed) batches, and so on. Methods of crop variety identification according to the spectra of storage proteins developed with VIR’s participation and accepted as international standard techniques make it possible to determine with high accuracy the specific and varietal attribution of plant accessions (Konarev, et al., 1972-1975). In order to justify application of the reference spectrum of Triceae for identification of avenins, the prolamine nature of the storage protein spectrum components was proven for the latter. Prolamine-specific tandem replications have been identified for Triticeae, such as: Gln-Gln-Gln-Pro-Phe (Konarev, Vvedenskaya, 1986). VIR has many years of experience in the use of protein markers to monitor the genetic integrity of its collection. It is especially topical for the accessions of old and local varieties collected 80-100 ago (in N.I. Vavilov’s times), as due to their age they were reproduced many times. Such works has been conducted in many genebanks of the world on different crops, also in cooperation with VIR (Konarev et al., 2005; Perchuk et al., 2016). Protein markers are efficient in seed production and seed control of oat. Avenin spectra help to identify reliably fatuoids in seed batches, i.e. plants with morphological traits of common wild oat. Oat is a unique crop for producing dietary and medicinal food; it has been officially recognized as a functional product. Oat is valuable as a source of forms non-toxic for

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celiac disease. Varieties promising for gluten-free food production have been identified (Gavrilyuk et al., 2012-2014). In recent years VIR has practiced metabolomic approach to the study of wild and cultivated oats. It will help to solve on a new methodological level the problems of quality and resistance to biotic and abiotic stresses. It has been proven that the global oat collection of the Vavilov Institute – a valuable source of forms and carriers of quality traits in a wide range of their expression – serves as a reliable base for the development of varieties which meet the modern requirements of food industry, feed production, healthy and clinical nutrition, etc. Metabolites (compounds) have been identified, whose content changes in the process of “domestication” or which make wild oat species different from cultivated varieties (Shelenga et. al., 2016; Loskutov et al., 2016).

# Nutritional and bioactive properties of hulled and naked genotypes of oat intended for cultivation in Poland

Danuta Boros, Damian Gołębiewski

Institute of Plant Breeding and Acclimatization – National Research Institute

Radzików, 05-870 Błonie, Poland,

E-mail: [d.boros@ihar.edu.pl](mailto:d.boros@ihar.edu.pl)

**Keywords:** *oat, husked, hullless, groat*

The area under oat cultivation is steadily shrinking over the last few decades in Poland, though in 2014 it was grown on nearly 0.460 Mha, constituting 6% of the area applied for all cereals. With the production of 1.460 Mt. Poland is one of the world's biggest producers of this cereal, utilizing about 80% for feed and 5% for human consumption, while the rest for sowing. Each of the end-uses of oat requires grains of specific quality parameters. Selection towards high end-use quality has been adopted as a priority direction in the oat breeding program in Poland. The following quality-related parameters of oat are executing in this program: the weight of grains, grain density and adjustment, content of hull, protein, fat and  $\beta$ -glucan (Nita, 2003; Prażak and Romanowicz, 2014). This breeding program is resulting in 31 cultivars of Polish origin currently admitted to the National List, representing 27 hulled genotypes and 5 naked genotypes and only one hulled cultivar from abroad.

What quality features should distinguish the oat cultivars for two major end-uses? Briefly, beyond general good parameters of agronomic suitability, excellent cultivars for feeding purposes should characterise with a large grain, low content of hull and high content of protein and fat. High hull content of oat is the main determinant of its use in feed for monogastrics (Svihus and Gullord, 2002). Considering the chemical attributes of oat genotypes with grains suitable for human consumption, such cultivars should stand out also in content of  $\beta$ -glucan, main component of dietary fibre, and other bioactive components (Wood, 2007; 2011). Regular eating of foods produced from oat, cereal having the greatest content of soluble  $\beta$ -glucan, which is considered to increase the viscosity of the gastrointestinal contents, leading to slower gastric emptying, enhanced gut fill, and slower absorption of nutrients, reduces the level of blood cholesterol and post-prandial glycaemic responses (Wood, 2007; Granfeldt et al., 2008; Whitehead et al., 2014). Knowledge regarding variability of the chemical composition is therefore of significant importance and help in proper and full utilization of established and newly developing varieties of oat.

The objective of this study was to determine the suitability of advanced breeding materials and varieties of oat currently approved for cultivation in Poland either as sources of high nutritional, bioactive and pro-healthy properties in human food or as valuable feed components for monogastrics. This objective was accomplished through the parallel examination of intact grain and its dehulled counterpart.

Material for the study comprised of 30 genotypes of hulled and 6 genotypes of naked types of oat, including 17 breeding lines and 19 cultivars registered in Poland,

grown in one location in 2014. The following physico-chemical parameters were determined: thousand kernel weight, density, content of gross energy, protein, ash, lipids, starch, free sugars and dietary fibre (TDF) as a sum of water soluble and water insoluble non-starch-polysaccharides (NSP), including  $\beta$ -glucan and Klason lignin. To determine hullability and also for providing material for analyses, 50 g of the grain of each cultivar was dehulled by hand. All analyses were performed in duplicate with standard procedures of AACC, 2011) and the results were expressed in dry matter basis (as % of DM).

On average, hull constituted 28% of the kernel weight and Bingo cv. had the lowest content (23.5%). This cultivar together with Scorpion showed the greatest weight of thousand kernels (40g vs. average value 31.7g). Hullability had the significant impact on chemical characteristics of the grain, negative on content of lipids, starch and soluble fractions of dietary fibre, while highly positive on TDF and its insoluble fractions. It was found a small, although significant variation in content of nutrients among the hulled oat analysed, in range from 3% for mineral, 8% for protein and to nearly 9% for free sugar contents and only lipids had value 11%. Overall, Bingo was the cultivar with the best nutritional characteristics, measured as a sum of protein, lipids, minerals, starch and free sugars content, equal 71%, while the average value was 66%. Three breeding lines set in this respect apart from the others, showing the values exceeding 69%. In the case of dietary fibre oats tested characterised with content of this pro-healthy component in range from 28% in a breeding line to more than 39% in Berdysz cv. The insoluble components made up 89% of the total TDF quantities, specifically 58% I-NSP and 31% lignin.

Removing hulls from oat increased content of these ingredients, which are located in endosperm and germ of the kernel. In this way, content of nutrients has been increased by an average of 25%, with the greatest changes in lipids (by 39%) and protein (by 31%). TDF content dropped by 65% to the level comparable with wheat (12%), although  $\beta$ -glucan increased by 38%. Chemical characteristics of hullless cultivars was similar to that of dehulled grains.

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# The express method of oats genotypes evaluating on $\beta$ -glucan content

Vadim Polonskiy<sup>1</sup>, Igor Loskutov<sup>2</sup>, Alena Sumina<sup>3</sup>

<sup>1</sup>Krasnoyarsk State Agrarian University, Krasnoyarsk, Russia,

<sup>2</sup>Federal Research Center N.I. Vavilov All-Russian Institute of Plant Genetic Resources (VIR),  
St-Petersburg, Russia,

<sup>3</sup>N.F. Katanov Khakass State University, Abakan, Russia

E-mail: [vadim.polonskiy@mail.ru](mailto:vadim.polonskiy@mail.ru)

**Keywords:** grain, oats, beta-glucan content, density, test weight, assessment

Oat (*Avena sativa* L.) is an excellent source of mixed linkage  $\beta$ -glucans, a dietary fibre with cholesterol lowering properties. These polysaccharides are becoming recognized increasingly for their potential to lower the risk of serious diet-related conditions such as type II diabetes, cardiovascular disease, colorectal cancer, and diverticular disease. The positive nutritive values for oat grains make it possible to use them as food for humans and feed for monogastric animals. An increasing of  $\beta$ -glucans content in grain of oat is the most important task of breeding. Known methods of assessing oat grain quality are too time-consuming, complicated, destructive and little avail in breeding process. The aim of our work was to develop indirect method for screening beta-glucans content in grain of oats which is nondestructive, simple and express.

Physical parameters of grain (weight of 1000 grains, test weight, density of hulled and dehulled grain, mass fraction of grain husks) and  $\beta$ -glucans content were studied for 16 hulled oat cultivars. For calculating grain density the oat grain volume was measured by a sand-displacement method (Doehlert and McMullen, 2008). Fine white silica sand was used for oat grain volume measurements. Sea sand collected from a beach (The South China Sea, Vietnam). Test weight was determined by measuring the volume of a measured mass of grain in a graduated cylinder.

The strong positive relation between the density of dehulled grains and  $\beta$ -glucan content was experimentally shown ( $r = 0.811$ ). It was found the low positive correlation between test weight and beta-glucan content; but the middle positive correlation between density of hulled grains and beta-glucan content. It was shown low negative correlation between weight of 1000 grains, mass fraction of grain husks and beta-glucan content. The average value of the dimensionless ratio (the ratio of  $\beta$ -glucans content to dehulled grain density) varied slightly from cultivars of oat. All samples of oats in terms of beta-glucan content were divided into two contrasting groups, which differed significantly from each other not only in terms of beta-glucan content, but the density of dehulled grains.

Indirect method for assessing beta-glucan content in oat was developed. It was proposed to use the criterion of the density of dehulled grains to assess technological qualities of oats. It is assumed that the use of this approach will ensure a simple, speed, and a quantitative assessment of the quality and the undamaged grain oats in respect of its beta-glucan content. Based on the received data the contrasting groups that can be considered as promising forms for oats selection of different directions are singled out.

# **The breeding of high yield high $\beta$ -glucan, disease-resistant naked oat strains - “Bayou 18” by interspecific hybridization**

Junyong Ge\*, Changye Tian, Yunxia Li, Zhanhong Dong, Wenbo Zuo, Shifeng Zhao, Yongzhen Wu, Lixia Cao, Bihong Shi

(Zhangjiakou Academy of Agricultural Sciences, Zhangjiakou, China

\*E-mail: [gejy207@163.com](mailto:gejy207@163.com)

***Keywords: naked oat, interspecific hybridization, breeding,  $\beta$ -glucan, disease-resistant***

“Bayou 18” was bred by Hebei Alpine Crops Research Institute since 1996. Firstly, interspecific hybridization was did using a wild oat (collected on field) as male parent and “Jizhangyou 4”(a naked oat bred variety) as female parent. Drought-resistance, lodging-resistance, disease-resistance and high yield offspring were selected (e.g. 9641-6). Secondly, we take selected offspring 9641-6 as male parent and “Bayou 9” (high  $\beta$ -glucan naked oat variety) as female parent to do sexual hybridization. Then, through early stage phenotypic variation selection, normal desirable traits selection, drought and disease resistance identification, we selected a new naked oat strains, characted by high-yielding, high-quality, disease-resistance, lodging- resistance and drought-resistance, was named “Bayou 18”. The average yield of this new strains reached 6566 kg ha<sup>-1</sup> in Kangbao County farm in 2014. Researches from Institute of Plant Protection, Gansu Academy of Agricultural Sciences also found that the new strains have an immune function to oat covered smut.

# The quality and productivity of All Russian Institute of Plant Genetic Resources (VIR) collections naked oats under Kazakhstan conditions

Aigul Abugaliyeva<sup>1</sup>, Igor Loskutov<sup>2</sup>, Timur Savin<sup>3</sup>

<sup>1</sup>LLP “Kazakh Research Institute of Agriculture and Plant Growing”, Almalyk, Kazakhstan,

<sup>2</sup>N.I.Vavilov Institute of Plant Genetic Resources (VIR), St. Petersburg, Russia,

<sup>3</sup>Kazakh National Agrarian University, Almaty, Kazakhstan

E-mail: [kiz\\_abugaliyeva@mail.ru](mailto:kiz_abugaliyeva@mail.ru)

**Keywords:** *naked oat, grain quality,  $\beta$ -glucan and oil content*

Naked oats compared with filmy characterized with a number of benefits when it is processing. He has a unique biochemical grain composition for food, feed and dietary uses. Comparatively low adaptiveness contain the spread of naked oats, for which demand is growing.

Objective: to test naked oats forms from the All Russian Genetic Resources Institute collection in Kazakhstan and selection the genotypes for quality and yield breeding. The material of the research were 35 samples of collection tested in KazRIAPG conditions near Almaty (43°15' north latitude and 75°54' east longitude, rainfall 450 mm) and under Karabalyk AES near Kostanai, (53°53' north latitude and 62°07' east longitude, rainfall 200 mm).

In the south Kazakhstan conditions with maximum productivity was allocated next samples: Izak> Mozart> Ripon> 87AB5932 (collection trials); Izak> Levsha> Billion = Vitus in breeding block and in the North cultivars was ranged by order Tyumenskiy golozernyi> Anderes> Levsha exceeding filmy cultivar- standard.

The protein content was varied from 15,0% (Sallust, ACT) to 20,0% (Local - Romania), 19,2% - 19,0% (Numbat - James) regarding filmy standard. The most productive form characterized by a relatively high protein content: Izak (16,8-14,4%); Mozart (15,6-16,9%); Ripon (11,2 - 15,3%); Levsha (15,2%); Billion (17,9%), Vitus (16,2%), AV5932 87 (16,0%). The starch content ranged from 54,7% (Pennline 9010), to 60,1% (Local - Mongolia and James).

Grain hardness (SKCS 4100) varied between 29-37 units (Pennline 9010), Local - Mongolia, Local - Romania, Vitus) as a soft grain to 89 units. The  $\beta$ -glucan content in naked oats ranges from 5.2% for Local, Romania to 6.4%, for RA 8098-9033 and Cupon. This two samples were also characterized by maximum values for the phosphorus, iron, magnesium content. The oil content ranged from 6.0% (Vyatskiy golozernyi) to 9.0% (RA 8098-9033).

Cluster analysis of Kazakhstan varieties, VIPGR accessions of a domesticated and wild oats on a content and structure of fat acids allowed to classify the genotypes into two clusters. The first cluster mainly was comprised of Kazakhstan varieties, the second cluster was divided into two subclusters. In turn, the first subcluster combined American oat varieties, having in their pedigree *Avena sterilis* form, and all the studied

samples of hexaploid wild species *A. sterilis*, the second subcluster included- all the other species of wild oats with different levels of ploidy.

Oil quality for oat genotypes determined with content of monounsaturated fatty acids, such as oleic acid, which allows the oil to be stored longer. Its content ranged from 26.1% (cvs James) to 55.8% (cvs Levsha). More than 40.0% of oleic acid is typical for samples from Mongolia VIR-14594 (40.7%) and from Canada AC Baton (45.9%) in addition to a variety Zhorga (41.0%) from Kazakhstan breeding.

The oil biological activity content determines by the ratio of linoleic acid (from 20.5% to 48.7% cvs Izak) to oleic acid, which should approach to unity. The oleic/linoleic acid ratio ranged from 0.4 for cvs AC Baton, Canada and for cvs Levsha 0.6 (OA 504-6) to 1.5-1.7 (Izak, Czech Republic, James, Jung 492, China). The amount of unsaturated fatty acids in naked oats ranges from 58.9% (Beg 3) to 79.7% (Mongolia, VIR-14594). According to the linoleic acid content the cvs Izak, Czech Republic (48,7%), Yung 492, China (46,1%), James, United States (44,6%), Salomon (44.1%), Vyatskiy golozernyi (42.5% ), Romania VIR-14941 (43.7%) cultivars were allocated. Developed the technique of testing for distinctness, uniformity and stability of oats in a south-eastern Kazakhstan. Studied breeding and collection accessions of spring oats on the content and quality of oil to determine the creation prospects of new oat varieties for dietary use.

The ranking of varieties, genetic resources and breeding materials revealed high  $\beta$ -glucan forms with more than 5.0% for following varieties and breeding numbers: Alaman, Nicola, Pegas, Irtysh 15, VIR-14638, VIR-11247, VIR-13587, VIR-13544; VIR-14836.



**PARALLEL SESSION 2**  
**Genomics, Bioinformatics  
and Molecular Assisted Selection**

# ORAL PRESENTATIONS

## Oat Global: Partners in oat research initiatives

Nicholas A. Tinker<sup>1</sup>, the Oat Global Strategy Team<sup>2</sup>

<sup>1</sup>Agriculture & Agri-Food Canada, Ottawa Research and Development Centre, Central Experimental Farm, 960 Carling Avenue, Ottawa, Ontario K1A 0C6 Canada.

<sup>2</sup>Oat Global Strategy Team: (<http://oatglobal.org>)

E-mail: [nick.tinker@agr.gc.ca](mailto:nick.tinker@agr.gc.ca)

***Keywords: Oat Global, T3/Oat, database***

The oat research community is too small to work in isolated units. Many challenges in oat production and processing are global, and transfer of knowledge helps to create economical solutions for everyone. The development of new technologies can be most effective through community-wide consultation and coordinated funding. Reflecting this, Oat Global was formed in 2014 as a strategy forum driven by leaders of the public and private oat community. Oat Global proposes to operate across agencies, institutions, corporations, and national boundaries, in support of all pre-competitive R&D in any research field related to oats. Oat Global is governed by a Strategy Committee representing an open global membership. As needs are identified, Oat Global will engage with potential funding groups, and will co-ordinate or motivate project teams to execute sponsored initiatives.

The first initiative sponsored by Oat Global was the expansion of the T3/Oat database (<https://triticeaetoolbox.org/oat/>) to ensure global access to public genotype and phenotype data. Oat Global then helped to facilitate a USDA-funded effort to genotype a proportion of all public breeding programs in North America, and to make the data available in T3/Oat. Oat Global has also facilitated the formation of a community-wide Oat Rust Initiative that is developing a strategy to address priority research needs and identify funding opportunities in order to manage this devastating oat disease.

Oat Global is closely partnered with the newly revitalized Oat Newsletter (<http://oatnews.org>) and with the GrainGenes Database (<http://wheat.pw.usda.gov>), and works with these partners to foster communication and data sharing through the most appropriate venues. As an official partner to the International Oat Conference (IOC), Oat Global looks forward to helping the IOC maintain an active and connected global oat community between conferences.

# High-throughput SNP genotyping of oat landraces originated from Turkey

Hüseyin Gungor<sup>1</sup>, Ziya Dumlupinar<sup>2\*</sup>, Gönül Comertray<sup>3</sup>,  
Tevrican Dokuyucu<sup>2</sup>, Aydın Akkaya<sup>2</sup>

<sup>1</sup>Duzce University, Turkey

<sup>2</sup>Kahramanmaraş Sutcu Imam University, Turkey

<sup>3</sup>East Mediterranean Agricultural Research Institute, Turkey

\*E-mail: [zdumlupinar@ksu.edu.tr](mailto:zdumlupinar@ksu.edu.tr)

**Keywords:** *oat, landraces, SNP, population structure, diversity*

Genetic resources are essential for oat breeding programs. Cultivated oats *Avena sativa* L. and *Avena byzantina* Coch. are native to Turkey and a plenty of landraces are available throughout the country. Plant breeders have been attempting for many years to improve traits by conventional plant breeding methods. In recent years, these methods have been helped by addition of DNA marker systems which provide genotype information to associate with specific phenotypic traits. The major markers systems have targeted simple sequence repeats (SSRs), amplified fragment length polymorphism (AFLP) and single nucleotide polymorphism (SNP). Markers allow genetic kinship among genotypes and linkage with quantitative trait loci (QTLs) to be estimated and used for selection, and have become standard components of advanced breeding programmes. Most recently, very high throughput characterisation of polymorphisms has become possible with Illumina Infinium 6000 (6K) SNP BeadChip.

In this study a number of 174 oat landraces were genotyped by 6K SNP BeadChip. Genetic similarities were estimated for the oat landraces and population structure analysis was also calculated.

Results indicate that 4599 SNP markers were found polymorphic among the oat landraces. A dendrogram was built with the marker data and oat landraces were separated into four main groups and several sub-groups. Population structure analysis also detected four sub-populations based on allele frequency and showed a similar clustering with dendrogram. In addition, it was determined that TL264 and TL305, TL283 and TL288, TL375 and TL376, TL253, TL254, TL257, TL259 and TL293 were identical.



# A close look at the *Avena ventricosa* populations of Cyprus

Nikolaos Nikoloudakis<sup>1</sup>, Stella Konstantinou<sup>1</sup>, Angelos Kyratzis<sup>2</sup>,  
Andreas Katsiotis<sup>1</sup>

<sup>1</sup> Cyprus University of Technology, Department of Agricultural Science, Biotechnology and Food Science, Limassol, Cyprus

<sup>2</sup> Agricultural Research Institute, Genebank, Nicosia, Cyprus  
E-mail: [andreas.katsiotis@cut.ac.cy](mailto:andreas.katsiotis@cut.ac.cy)

**Keywords:** *oat, species, A. ventricosa, Cyprus*

The genus *Avena* consists of diploid ( $2n=2x=14$ , A and C genome), tetraploid ( $2n=4x=28$ , AB and AC genomes), and hexaploid ( $2n=6x=42$ , ACD genome) species. The major cultivated species belong to the hexaploids *A. sativa* and *A. byzantina*, having the AACCCDD genomic designation. During the last decades a number of diploid species have been proposed to contribute to the evolution of the hexaploid species. Based on cytogenetic and molecular data (Nikoloudakis and Katsiotis, 2008), the most predominant C genome donor as male parent for the hexaploids is considered *A. ventricosa*. This species has limited distribution and it is native to Algeria (Oran), Azerbaidzhan (Baku), Morocco, and Cyprus (Baum, 1977). A restricted number of accessions are available through genebanks (Loskutov and Rines, 2011), and most of them originate from Cyprus, mainly because in 2008 a survey of this species was conducted and a number of populations were collected (Katsiotis and Ladizinsky, 2012). In the present study 69 individual plants from six different populations collected throughout Cyprus were used. In order to assess the genetic diversity of these populations molecular markers have been utilized. Initially ten SSR primer pairs were tested, providing little genetic variability between the accessions, thus AFLPs were used. After screening 56 AFLP primer pairs, four combinations were selected, i.e. *EcoRI*-ACT / *MseI*-CAA, *EcoRI*-ACT / *MseI*-CAC, *EcoRI*-ACA / *MseI*-CAT, and *EcoRI*-ACA / *MseI*-CAC. The *EcoRI* primer was fluorescently labelled and the PCR products were separated in a Genetic Analyser. The total number of peaks were 260 (ranging from 57 to 73), from which 96 in total were polymorphic (ranging from 15 to 35). Based on the polymorphic peaks intra- and inter-population diversity was calculated. Furthermore, a dendrogram indicating the relationships among the accessions was also constructed.

The same material was screened for the production of  $2n$  gametes, since polyploidy is among the most important evolutionary processes in higher plants, including genus *Avena*. The main modes of polyploidization are (i) the somatic chromosome doubling (a rare event in nature) and (ii) the sexual polyploidization through the formation and action of functional  $2n$  gametes (Harlan and DeWet, 1975). Polyploid gamete development in *Avena* has been reported for *A. wiestii* – AsAs genome (Ellison, 1937) and *A. vaviloviana* – AABB genomes (Katsiotis and Forsberg, 1995a), but none of these two species contributed to the evolution of the hexaploids (Nikoloudakis et al., 2008). As a fast method of screening and identifying promising genotypes, a flow cytometer

was used to detect 2C pollen grain nuclei. Entries that were found to contain more than a single peak were further analyzed under the microscope. Size of pollen grains is correlated to the ploidy level of the pollen (Katsiotis and Forsberg, 1995b), and the above mentioned entries were found to contain at a 1% frequency such large pollen grains. Cytogenetic analysis of entries containing large pollen grains remains to be performed in order to identify the mechanism of the  $2n$  pollen formation. The importance of the  $2n$  gametes goes beyond evolutionary studies and can contribute in applied breeding programs (Dewitte et. al, 2012).

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# The origin of few poliploid *Avena* species inferred from an ITS polymorphism study

Alexander V. Rodionov<sup>1,2</sup>, Liubov M. Krainova<sup>2</sup>, Elena S. Kim<sup>1,3</sup>, Natalia B. Tyupa<sup>1</sup>,  
Evgeny E. Andronov<sup>4</sup>, Julia V. Mikhailova<sup>1</sup>, Alexander A. Gnutikov<sup>1,5</sup>,  
Igor G. Loskutov<sup>2,5</sup>

<sup>1</sup>Komarov Botanical Institute, St. Petersburg, Russia;

<sup>2</sup>Department of Botany, St. Petersburg State University, St. Petersburg, Russia;

<sup>3</sup>RASA-Center, Peter the Great St. Petersburg Polytechnic University, St. Petersburg, Russia;

<sup>4</sup>All-Russia Research Institute for Agricultural Microbiology, St. Petersburg, Pushkin, Russia;

<sup>5</sup>N.I. Vavilov Institute of Plant Genetic Resources (VIR), St. Petersburg, Russia.

E-mail: [avrodionov@mail.ru](mailto:avrodionov@mail.ru)

**Keywords:** *Avena* species, genomes, ITS polymorphism

All the diploid *Avena* species contain either an A-genome or a C-genome. According to the results of C-banding staining and the genomic *in situ* hybridization (GISH), both the A- and C- subgenomes can be found in each of the allopolyploid *Avena* species (Leggett, Markhand, 1995; Badaeva et al., 2011). Sanger DNA sequencing of the internal transcribed spacers (ITS) reveals the presence of A-genomes specific 35S rRNA only and it means that there is absolute predominance of the A-genome 35S rDNA in allopolyploid *Avena* species (Rodionov et al., 2005; Nikoloudakis et al. 2008). That corresponds well with the results of physical mapping of 35S rRNA genes in *Avena*: the FISH-painting demonstrates only weak 35S rDNA-positive signal in the C-genome chromosome set in allopolyploid genomes (Fominaya et al. 1995; Shelukhina et al. 2007).

In order to find out which of the diploid species could be a donor of C-genome for polyploid species of *Avena*, we designed C-genome specific primers for internal transcribed spacer regions amplification and therefore sequenced the ITS1 and ITS2 using SCAR-analysis method, based on two specific C-genomes ITS primers created in our laboratory. This approach has yielded the presence of minor quantities of C-genomic rDNA of an ancestor species, that was related to *Avena ventricosa* in the tetraploids *A. magna* and *A. murphyi* as well as in the hexaploids *A. sativa* и *A. occidentalis*. To count a relative quantity of the C-genome specific 35S rRNA genes in allopolyploid oats genomes, we used sequence-tagged Roche 454 pyrosequencing of the ITS1 region of *A. fatua*, *A. sterilis*, *A. insularis* and *A. ludoviciana*. It was showed the presence of 1–4% of ITS sequences derived from C-genome ancestor in all allopolyploid genomes. All of these C-genome specific sequences had already accumulated a lot of different single nucleotide changes, they are polymorphic, but could be divided onto two types. One of them is closer to C-genome of *C. ventricosa*, and the second one having some common traits with the C-genome of *A. macrostachya*.

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## Diversity of oat genetic resources

Leona Leišová-Svobodová<sup>1</sup>, Dagmar Janovská<sup>1</sup>, Günter Backes<sup>2</sup>

<sup>1</sup> Crop Research Institute, Drnovska 507, 161 06 Prague 6, Czech Republic,

<sup>2</sup> Universität of Kassel, Nordbahnhofstr. 1a, 372 13 Witzenhausen, Germany

E-mail: [leisova@vurv.cz](mailto:leisova@vurv.cz)

**Keywords:** *oat, diversity, genetic resources, SSR loci*

The main aim of the study was to evaluate diversity of a file of selected oat genetic resources.

In total, 262 oat genotypes from 26 countries were analysed using microsatellites. Forty-two primer combinations revealed 56 SSR loci, with 323 alleles in total. The average value was 5.77 alleles per locus with the range from 1 to 24 alleles. Polymorphism information content ranged from zero to 0.895. Principal Coordinate Analysis (PCoA) was calculated based on genetic distances between oat genotypes. The first two dimensions represent 16.3 % of total variability in the set of accessions. Results mostly showed no distinct pattern, by the exception of a more distinct group involving accessions from Czech Republic and Austria and another group with accessions from the US and Canada. Clustering based on Bayesian statistics indicated the presence of three genetic sub-populations (cluster) in accessions ( $K = 3$ ). According to their q-values from the Bayesian clustering, all accessions were classified into the three sub-populations. The first sub-population consists of oat accessions mainly from Austria, the Czech Republic and some German accessions, accessions from US and Canada grouped predominantly into the second sub-population and sub-population 3 is formed by the rest of analysed oat accessions. Even though group 2 is the relatively small, it has the highest number of alleles, the highest number of private alleles and the highest gene diversity. The  $F_{ST}$  value for the grouping was relatively small (0.095) and also that these groups, also identified as the best, the data could reveal, were not overly efficient in dividing the accessions. This might be due to the fact that crosses had occurred between the sub-populations. In conclusion, the oat genotypes analysed do not show a very pronounced genetic structure, but that still three different sub-populations can be identified, which also coincide with the geographical source of the accessions.

# Karyosystematics of *Avena* L. based on C-banding and FISH analyses

Ekaterina D. Badaeva<sup>1</sup>, Olga Yu. Shelukhina<sup>1</sup>, Igor G. Loskutov<sup>2</sup>, Vitalyi A. Pukhalskyi<sup>1</sup>

<sup>1</sup>N.I. Vavilov Institute of General Genetics, Russian Academy of Sciences, Moscow, Russia;

<sup>2</sup>N.I. Vavilov Institute of Plant Genetic Resources (VIR), Saint-Petersburg, Russia

E-mail: [katerinabadaeva@gmail.com](mailto:katerinabadaeva@gmail.com)

**Keywords:** *oat, species, karyotypes, C-banding, fluorescence in situ hybridization*

The chromosomal sets of twenty five wild and cultivated *Avena* L. species including 11 diploid, 8 tetraploid and 6 hexaploid with different genomic constitution were analyzed using C-banding and fluorescence *in situ* hybridization (FISH) with 5S and 18S-5.8S-26S rDNA probes. The location of major nucleolar organizer regions (NORs) and 5S rDNA loci on different chromosomes was diagnostic for particular genomic group, although species constituting each genomic group could differ in karyotype structure and the C-banding patterns.

All diploid species of the A-genome group (*A. strigosa*, *A. wiestii*, *A. hirtula*, *A. hispanica*, *A. atlantica*, *A. canariensis*, *A. longiglumis*, *A. damascena*) had relatively symmetric karyotypes lacking the “diffuse” heterochromatin; they all showed similar distribution of C-bands and rDNA probes; and their intraspecific divergence was probably associated with chromosomal rearrangements and amplification/ elimination of repetitive DNA sequences. A group of the C-genome diploid species (*A. ventricosa*, *A. clauda*, *A. pilosa*) was distinct from the A-genome group in highly asymmetric karyotype structure; their chromosomes carried “diffused” heterochromatin and showed different number and location of 45S and 5S rDNA loci. In contrast to the A-genome group, we observed significant karyotypic differences between species with the C-genome type: *A. ventricosa*, from one side, and *A. clauda* and *A. pilosa*, from another side. Differentiation between these sub-groups was probably caused by numerous chromosomal rearrangements, including translocations and inversions, and by accumulation of the “diffused” heterochromatin. Over the course of evolution *A. ventricosa* has lost one of the major nucleolus organizing regions (NORs); in karyotypes of *A. clauda* and *A. pilosa* both 5S rDNA loci have been transferred into one chromosomal arms as a result of pericentric inversion.

Tetraploid *Avena* species are represented by three genomic types, namely CC (*A. macrostachya*), AB (*A. barbata*, *A. vaviloviana*, *A. abyssinica*, and *A. agadiriana*), and AC (*A. murphy*, *A. magna* and *A. insularis*). The location of major NORs and 5S rDNA sites on different chromosomes confirmed the affiliation of *A. macrostachya* with the C-genome group. At the same time, the symmetric karyotype, the absence of “diffuse” heterochromatin and the location of large C-band complexes in proximal chromosomal regions pointed to an isolated position of *A. macrostachya* among other *Avena* species.



Our investigation confirmed that *A. barbata*, *A. vaviloviana*, *A. abyssinica*, and *A. agadiriana* belong to the same AB-genome group, however *A. agadiriana* was distinct from the others. Similarity of karyotype structure and the C-banding patterns, as well as location of NORs and 5S rDNA loci suggested that *A. abyssinica*, *A. vaviloviana*, and *A. barbata* originated from a common tetraploid ancestor, and the divergence of these species was caused by minor chromosomal rearrangements and alterations of the polymorphism system. The results confirmed close relationships of the AB-genome species with the A-genome diploids. An As-genome species is the most probable donor of the A-genome of *A. abyssinica*, *A. vaviloviana* and *A. barbata*. Although their second diploid progenitor has not been identified, most likely it does not belong to the As-genome group. The exact diploid progenitors of *A. agadiriana* have not been determined, however our work suggested that they could be related to *A. damascena*.

Karyotypes of tetraploid oat species of the AC-genome group: *A. magna*, *A. murphyi* and *A. insularis* were similar with respect of morphology and C-patterns of several chromosomes, the number and location of 5S rDNA loci and major NORs. However, the number and distribution of minor 45S rDNA sites, morphology and heterochromatin distribution of some chromosomes were different. Based on the obtained data we assumed, that *A. insularis* is closer to *A. magna*, than to *A. murphyi*. Probably, all three species were originated from one common ancestor, and their divergence was accompanied by different species-specific chromosomal arrangements. It is also possible that evolution of *A. murphyi* occurred independently from the other two species of this group.

Our study revealed similarity of the C-banding patterns and the distribution of ribosomal RNA gene families in karyotypes of all hexaploid oat species, which point to their common origin. *Avena fatua* was characterized by the broadest karyotype diversity; this species possessed chromosomal variants, which were typical for other hexaploid *Avena* species. For example, modification of the chromosome 5C that is marker for *A. occidentalis*, is found in many accessions of *A. fatua*, whereas in other accessions it is similar with the respective chromosome of *A. sterilis*. Specific alterations of the morphology and C-banding patterns of chromosome 2C were detected in *A. fatua* and *A. sativa* only. These facts can be due to either hybrid origin of the *A. fatua*, or to this species is an intermediate evolutionary form of the hexaploid *Avena*. The translocation 7C-17 is present in all studied accessions of wild and weedy oats species (*A. sterilis*, *A. fatua*, *A. ludoviciana*, *A. occidentalis*) and in most *A. sativa* cultivars however it was absent from *A. byzantina* and in two *A. sativa* cultivars. The origin and evolution of *Avena* species are discussed in the light of the obtained results.

## Genotype-environment interaction patterns in oat collection grown in Kazakhstan

Yerlan Turuspekov<sup>1</sup>, Aigul Abugalieva<sup>2</sup>, Tim Langdon<sup>3</sup>, Asem Ashimova<sup>1</sup>, Vladimir Chudinov<sup>4</sup>, Grigoriy Sereda<sup>5</sup>, Boribai Sariev<sup>2</sup>, Saule Abugalieva<sup>1</sup>

<sup>1</sup>Institute of Plant Biology and Biotechnology, Almaty 050040, Kazakhstan

<sup>2</sup>Kazakh Research Institute of Agriculture, Almaty region, Kazakhstan

<sup>3</sup>University of Aberystwyth, Aberystwyth, UK

<sup>4</sup>Karabalyk Breeding station, Kostanai region, Kazakhstan

<sup>5</sup>Karaganda Research Institute of Agriculture, Karaganda region, Kazakhstan

E-mail: [yerlant@yahoo.com](mailto:yerlant@yahoo.com)

**Keywords:** *oat, microsatellite markers, genotype, phenotype, yield traits, adaptability*

Plant adaptation is one of the main aspects influencing yield performance for all crops, including oat. In this study the collection of oat *Avena sativa* and *Avena byzantina* consisting from 163 accessions received from VIR (Sant Petersburg, Russia) and 26 cultivars and promising lines from Kazakhstan were assessed phenotypically in three regions of Kazakhstan. The field trials in Northern, Central and South-eastern regions of Kazakhstan (2012-2015) allowed to assess the patterns of genotype-environment interactions based on evaluation of plant growth stages and yield components. The correlations between yield and plant growth stages were established in all studied sites. The AMMI and BiPlot graphical studies were used to assess the patterns of genotype-environment interaction and relationships between plant growth stages and yield components. In addition, harvested seeds from three regions of Kazakhstan were studied by six grain quality parameters. The relationship among yield components and grain quality parameters were assessed. The results provide important insights into the relationship between genetic and phenotypic patterns in oat collection growing in Kazakhstan.



# Genetic mapping and a new PCR-based marker linked to dwarfing gene in oat (*Avena sativa* L.)

Jun Zhao<sup>1</sup>, Honghai Yan<sup>1</sup>, Changzhong Ren<sup>2</sup>, Yuming Wei<sup>1</sup>, Nicholas A. Tinker<sup>3</sup>,  
Charlene P. Wight<sup>3</sup>, Yuanying Peng<sup>1\*</sup>

<sup>1</sup> Triticeae Research Institute, Sichuan Agricultural University, Wenjiang District, 211 Huimin Road, Chengdu 611130, Sichuan, China

<sup>2</sup> Baicheng Academy of Agricultural Sciences, Baicheng137000, Jilin, China

<sup>3</sup> Agricultural & Agri-Food Canada, Eastern Cereal and Oilseed Research Centre, Ottawa, Ontario, Canada K1A 0C6

\*E-mail: yy.peng@hotmail.com

**Key words:** *Avena sativa*, dwarfing gene, SSR, new codominant marker, marker-assisted selection, molecular breeding.

Short straw is a desired trait in oat (*Avena sativa* L.) for some production environments. Marker-assisted selection, a key tool for achieving this objective, is limited by lack of mapping data and available markers. Here, bulked-segregant analysis was used to identify anonymous PCR-based markers associated with the dwarfing gene in an F<sub>2</sub> population from the cross between *A. sativa* 'WAOAT2132' and *A. sativa* 'Caracas'. Genetic analysis identified a single dominant gene from in WAOAT2132, temporarily designated *DwWA*. A simple sequence repeat (SSR) marker (*AME117*) and a new co-dominant PCR-based marker (*bi17*) developed by homologous cloning in the present study were associated with the dwarfing gene. The two markers were located 21 and 1.2 cM from *DwWA*, respectively. The newly developed markers could find applications in identification of oat germplasm and in fine mapping or positional cloning

# **PARALLEL SESSION 2**

## **Physiology, Pest, Disease Resistance**

## ORAL PRESENTATIONS

### Identification and biological characteristics of *Glomerella graminicola* in oat

XiaoYu Zhang, HongYou Zhou, HuanWen Meng

Agronomy College, Inner Mongolia Agricultural University, Hohhot 010019, China

E-mail: [hongyouzhou2002@aliyun.com](mailto:hongyouzhou2002@aliyun.com)

**Keywords:** *oats anthracnose; Glomerella graminicola; identification; biological characteristics*

Oat anthracnose caused by *Glomerella graminicola* is a major disease affecting yield and quality in Inner Mongolia, Hebei province of China. In order to confirm the pathogen of this disease in Inner Mongolia and Hebei province. The pathogen was isolated with tissues and identified with morphology and molecular biology, pathogenicity was tested in vitro and vivo leaves, and biological characteristics were determined with crossing method. In results, two strains BYH3 and B5 were obtained and both **showed pathogenicity, produced necrosis spots** in vitro and vivo leaves. **The two isolates were both identified as *Glomerella graminicola*** with morphology and sequences of ribosome rDNA-ITS. A lot of conidium plates were observed, and there were abundant black bristles on the conidium plates. Conidia were crescent shape and colorless at  $18.3\sim25.8\times2.7\sim3.69\ \mu\text{m}$ . The two strains could grow in  $5^{\circ}\text{C}\sim30^{\circ}\text{C}$ , and the optimum temperature is  $25^{\circ}\text{C}$ . The pH range of mycelium growth for two strains was 4~11, and the optimal pH was 7. The optimal carbon source for mycelia growth of two isolates was maltose, and the lactose was not suitable. The best nitrogen source was ammonium nitrate, the second was ammonium sulfate, the worst was ammonium carbonate, and two strains almost could not grow in the medium containing ammonium carbonate.

# Effectiveness of fungicides for control of crown rust in forage oat in Australia

Bruce Winter, Richard Uebergang

Department of Agriculture and Fisheries, Toowoomba, Australia.

PO Box 2282, Toowoomba, Qld, 4350, Australia.

E-mail: [bruce.winter@daf.qld.gov.au](mailto:bruce.winter@daf.qld.gov.au)

**Keywords:** *forage oat, fungicides, crown rust, Australia*

Forage oat (*Avena sativa* L.) is the preferred winter forage crop for beef cattle in sub-tropical Australia and is widely grown in coastal and inland areas of central and southern Queensland and northern New South Wales. Crown rust (*Puccinia coronata* f. sp. *avenae*) is the most serious disease of forage oats, reducing forage yield, quality and palatability. Breeding for resistance is the preferred option for control of crown rust; however, the longevity of resistant cultivars has always been a problem. Losses from crown rust can be slightly reduced through appropriate management of the crop but growers often do not notice crown rust infection until the problem is serious.

Fungicides have become a viable means of controlling crown rust infection in forage oat crops because the cost of application has decreased dramatically. However, no information is currently available on the economic thresholds for fungicide application on forage oats in Australian conditions. The purpose of this study was to determine the loss in forage yield from crown rust infection in forage oats, and the response of forage yield to fungicide application. This information was used to develop a set of recommendations for farmers on the circumstances where fungicide application is likely or unlikely to be economically beneficial.

Forage oat cutting trials were planted in 2012 and 2013 at two sites in southern Queensland under irrigated and dryland conditions respectively. A range of foliar and seed fungicides used for leaf rust control in cereals were applied to plots of three forage oat varieties, along with an untreated control. Plots were assessed for crown rust infection and cut multiple times to measure forage yield during the season. A simple model was developed to estimate the correlation between loss of forage yield and loss of live-weight gain in cattle and calculate the economic benefit of fungicide application under different growing conditions and levels of crown rust infection.

The application of fungicide to susceptible forage cultivars in the presence of low levels of crown rust (0 – 10% leaf area infected) did not produce a significant increase in forage yield. However, the application of fungicide in the presence of moderate levels of crown rust (20 – 30% leaf area infected) did produce a significant increase in forage yield, although the size of the response varied according to other factors such as the time of year, seasonal conditions and the length of time between cuts.

Cultivar selection was important in determining the forage yield of a commercial crop, irrespective of the presence of a crown rust infection or the use of fungicide treatments to control rust. Selection of high yielding, late maturity cultivars will help to

overcome the yield loss associated with crown rust, even in the absence of management strategies such as fungicide application.

The fungicides Tilt® (propiconazole) and Folicur® (tebuconazole) were both satisfactory in reducing the level of crown rust infection in susceptible varieties to a level where there was no significant reduction in forage yield. The effects of Tilt and Folicur on crown rust infection or forage yield were not significantly different to each other, suggesting there is no relative advantage to either chemical.

The application of fungicide to control crown rust is most likely to produce a net economic benefit when the crop is grown under irrigated conditions or under good dryland conditions, and unlikely to produce a net benefit under marginal dryland conditions. The application of fungicide to control crown rust is most likely to produce a net economic benefit when the level of crown rust infection is at least moderate, except under marginal dryland conditions. If crown rust infection is low, the application of fungicide is only likely to have an economic benefit under irrigated or very good dryland conditions. However, the use of fungicides should be regarded as only one option in a range of strategies that forage oat growers can use to minimise the effects of crown rust.

# Phenotyping *Fusarium* Head Blight resistance of oat by analysis of morphological and biochemical properties of grains

Charlotte Martin<sup>1</sup>, Torsten Schirdewahn<sup>2</sup>, Romina Morisoli<sup>1</sup>, Susanne Vogelgsang<sup>2</sup>, Mario Bertossa<sup>1</sup>, Brigitte Mauch-Mani<sup>3</sup>, Fabio Mascher<sup>1</sup>

<sup>1</sup>Agroscope, Institute for Plant Production Sciences, Changins/Cadenazzo, Switzerland.

<sup>2</sup>Agroscope, Institute for Sustainability Sciences, Zurich, Switzerland.

<sup>3</sup>University of Neuchâtel, Institute of Biology, Neuchâtel, Switzerland.

E-mail: [charlotte.martin@agroscope.admin.ch](mailto:charlotte.martin@agroscope.admin.ch)

**Keywords:** *oat, FHB, mycotoxins, morphological properties, protein and  $\beta$ -glucans content*

Oats provide elevated quantities of health promoting compounds, such as  $\beta$ -glucans, and become an important component of a healthy diet. Yet, several reports reveal that oat grains are often found contaminated with different mycotoxins of the group of trichothecenes such as deoxynivalenol (DON) and T-2/HT-2 toxins. The contaminations result from cryptic infections caused by various *Fusarium* species that are mostly invisible on the panicle and on the grains. The present study aims at investigating modifications of yield components and biological properties of the grains caused by these infections. For this, 9 modern oat varieties and 6 Swiss landraces, obtained from the Vavilov Institute (VIR), were sown at 3 different sites with and without artificial infections with the DON producing strain of *Fusarium graminearum* FG13. Infections were conducted twice during flowering (BBCH 65-69), in the late afternoon with concomitant overhead irrigation. No symptoms appeared on the artificially infected plants in the field. After harvest, grains of the infected and non-infected plots were examined for thousand kernel weight (TKW), weight ratio of grains compared to their hulls, protein content (using NIRS) and the total  $\beta$ -glucan content (McCleary method). First analyses showed that the  $\beta$ -glucan content increased in grains from infected plots in all environments but at different extents between varieties. Yet, this is so far the only grain characteristic significantly impacted by the infection. As of now, the role of  $\beta$ -glucan in fungal infections in cereals is not clear. We suppose that the increase in  $\beta$ -glucan is part of a defence reaction of the plant. The next steps include the analysis of the DON content and the study of the ability of  $\beta$ -glucan to absorb the mycotoxin. This study, which is part of the project “Healthy and Safe” within the Swiss National Research Programme 69, are in line with a previous work that revealed a significant positive correlation between DON accumulation and  $\beta$ -glucan content in barley kernels.

# Evaluating the *Fusarium* resistance of Nordic oats in greenhouse

Juho Hautsalo<sup>1</sup>, Marja Jalli<sup>2</sup>, Päivi Parikka<sup>2</sup>, Lauri Jauhiainen<sup>2</sup>, Leena Pietilä<sup>3</sup>, Kirsi Peltoniemi<sup>3</sup>, Outi Manninen<sup>3</sup> & Merja Veteläinen<sup>3</sup>

<sup>1</sup>Natural Resources Institute Finland (Luke), Laukaa, Finland,

<sup>2</sup>Natural Resources Institute Finland (Luke), Jokioinen, Finland

<sup>3</sup>Boreal Plant Breeding Ltd., Jokioinen, Finland

E-mail: [juho.hautsalo@luke.fi](mailto:juho.hautsalo@luke.fi)

**Keywords:** *oat, FHB, mycotoxins, greenhouse*

Thirty percentage of the Finnish cereal acreage is covered with oats. Finland is the 2<sup>nd</sup> biggest exporter of oats after Canada with approximately 320 000 tons/year (FAOSTAT 2016). Oats has several positive properties both as animal feed and human food such as favorable fatty acid content, high fibre content and health improving beta-glucans. Oats is also appreciated in crop rotation since it is a relatively healthy crop. The human consumption of oats is growing steadily but it requires that the grain quality will be kept at a high level. This is however threatened by *Fusarium* head blight (FHB) disease (Bjørnstad and Skinnes 2008) which lowers seed germination rate and generates mycotoxins such as deoxynivalenol (DON) in the grains that are infected by this fungus. In cereal trade, this has led to discarding of seed lots that exceed the EU-approved DON content, which has serious economic consequences to the oat producing farmers.

The control of mycotoxin levels with good manufacturing and agricultural practices is limited. However, breeding of resistant cultivars would be an ecological and efficient way to control FHB. In literature, efficient resistance sources have already been reported (Tekauz et al. 2008, Gagkaeva et al. 2013) and also the genetics of resistance has been studied (He et al. 2013), but still the nature of resistance is mostly unknown. Breeding for *Fusarium* resistance has many bottle necks. Current methods for analyzing the amount of *Fusarium* fungus or mycotoxins in the grain are expensive and not always consistent since the levels of infection as well as the toxin formation depend highly on the environmental conditions. There is a need for reliable and cost efficient phenotyping methods to efficiently evaluate new sources of resistance and to bring that to novel cultivars.

The aim of this study was to evaluate the usefulness of greenhouse test method for *Fusarium* resistance screening in oats at Natural Resources Institute Finland (Luke) Jokioinen. In this study, the data from five separate screening experiments has been statistically analyzed.

In these experiments, a total of 52 different oat lines or cultivars were grown in fertilized pots with peat and sand mixture. The experiments were conducted in different greenhouses with controlled temperatures and light conditions. Each experiment included four replicates. Before inoculation the temperature was raised from 18 to 20 °C and the humidity was raised to 100 %. The inoculation was made at full flowering (BBCH 65) with *Fusarium culmorum* suspension that together with *F. graminearum* is the main

DON toxin producer in Finland (Parikka et al .2012) with. Different concentrations of spore suspension were used ranging from  $0.8 \times 10^5$  to  $5.0 \times 10^5$  conidia per ml.

Samples (5 panicles per pot) were harvested at growth stage BBCH 92. Ten seeds from each panicle were placed on selective PCBN plates. Plates were incubated in +23°C for one week in order to obtain clear mycelium growth and then the percentage of *Fusarium* infected kernels was calculated. The tested oat genotypes varied from trial to trial. The statistical model used (a linear mixed model) separated the effects of cultivars and trials. After that estimated means of cultivars were mutually comparable. The distribution of *Fusarium* infected kernels was not normally distributed like the model assumed. Since, the arcsine-square root transformation was done before statistical analysis.

The genotypes with the highest or the lowest infection levels were shown to be statistically different from a genotype with average estimate value. The model gave estimates with high standard deviation and unexplainable variation was also high. Several factors such as general level of infection in the trial and seasonal differences can explain this variation. In the first experiments the infection level was overall high and differences were very small due the high conidia concentration in the inoculation suspension. The main conclusion of this analysis is that the current greenhouse method is able to separate the most resistant and the most susceptible oat accessions from each other, although a wide set of control cultivars should be included to achieve reliable results. Since greenhouse testing is possible around the year it is a good supplement for field testing in the *Fusarium* resistance breeding toolbox for oats.

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# Response of oat genotypes to *Fusarium* infection and mycotoxin accumulation\*

Tatiana Gagkaeva<sup>1</sup>, Olga Gavrilo<sup>1</sup>, Alexandra Orina<sup>1</sup>, Elena Blinova<sup>2</sup>, Igor Loskutov<sup>2</sup>

<sup>1</sup> All-Russian Institute of Plant Protection (VIZR), St-Petersburg, Pushkin, Russia;

<sup>2</sup> Federal Research Center N.I. Vavilov All-Russian Institute of Plant Genetic Resources (VIR)

E-mail: [t.gagkaeva@yahoo.com](mailto:t.gagkaeva@yahoo.com)

**Keywords:** cultivated and wild oats, resistance, *Fusarium* fungi, mycotoxins, DNA.

The genetic potential of *Avena* genus can serve as useful source of material for breeding new resistant cultivars. Earlier the genotypes of cultivated *Avena* species were evaluated for resistance to *Fusarium* infection and accumulation of mycotoxins in grain, and it was found that genotypes of *A. sativa* and *A. strigosa* are less susceptible to *Fusarium* infection, than *A. byzantina* and *A. abyssinica* (Tekauz et al, 2008; Bjørnstad, Skinnies, 2008; Gagkaeva et al, 2013; Loskutov et al., 2016).

Fifty-seven accessions belonged to diploid (16%), tetraploid (32%) and hexaploid (52%) wild *Avena* species from the VIR collection were selected for study the resistance to *Fusarium*: *A. atlantica*, *A. canariensis*, *A. clauda*, *A. damascena*, *A. hirtula*, *A. longiglumis*, *A. wiestii*, *A. agadiriana*, *A. barbata*, *A. insularis*, *A. magna*, *A. murphyi*, *A. vaviloviana*, *A. fatua*, *A. ludoviciana*, *A. occidentalis*, *A. sterilis*. The genotypes were artificially inoculated with *F. culmorum* at the VIR nursery. All grain samples were examined for deoxynivalenol (DON) and zearalenone (ZEN) contents by ELISA. Quantification of the trichothecene-producing *Fusarium* species DNA (TriDNA) was performed by TaqMan PCR (Gagkaeva et al., 2013).

The grains of all analyzed 17 wild oats were infected by *Fusarium*. The mean amounts of DON in grain ranged from 57 to 3862 ppb. Totally, the genotypes belonging to *A. clauda*, *A. damascena*, *A. hirtula* and *A. occidentalis* accumulated less amounts of DON, than genotypes of other analyzed *Avena* species. The maximum amounts of DON were found in grain of *A. canariensis* k-1914 (2188 ppb), *A. barbata* k-9 (2038 ppb), *A. magna* k-1786 (3862 ppb) and k-2100 (2933 ppb), and *A. sterilis* k-140 (2484 ppb). In contrast with DON that which was found in grain of all accessions, ZEN was detected only in three accessions of *A. barbata* k-316, *A. ludoviciana* k-547, and *A. wiestii* k-95 in the amounts 38-237 ppb. The amount of TriDNA showed substantial variation 0.19-5.19 ng/100 ng of total DNA. The tetraploid oats contained in 3.4-4.3 times more TriDNA, then diploid and hexaploid *Avena* species. The tetraploid oats *A. insularis*, *A. magna* and *A. murphyi*, which are related to the C-genome species, were heavy infected by *Fusarium*.

The set of 24 *A. sativa* genotypes was estimated to *Fusarium* resistance by artificial inoculation separately with sum of four *F. culmorum* strains and of five *F. sporotrichioides* strains. The resistance data were based on sum of two parameters: the DNA content of TriDNA and mycotoxin accumulation (DON or T-2 toxin).

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The genotypes that were inoculated with high aggressive *F. culmorum* contained TriDNA from 0.03 to 3.64 pg/g of milled grain, the amount of DON ranged from 20 to 1179 ppb. The quantity of TriDNA in the samples inoculated by relatively weak *F. sporotrichioides* varied from 0.03 to 1.93 pg/g, the amount of T-2 toxin ranged from 0 to 133 ppb.

On the basis of the estimated parameters, all genotypes have been divided into four groups, that are relatively resistant, medium resistant, susceptible and high susceptible. The more resistant genotypes contained considerably less fungal DNA and accumulated less mycotoxins than the group of the more susceptible ones. The high positive correlation between the DNA contents and amounts of DON ( $+0.84$ ,  $p < 0.05$ ) was observed. But the correlation between the DNA contents and T-2 toxin amounts was weak ( $r=+0.26$ ,  $p<0.05$ ).

The group of relatively resistant genotypes to *Fusarium* infection (12.5 %) included varieties Bisuandorodu, Geszty and Gehl. The group of high susceptible genotypes (16.7 %) consisted of Medved, KSI 432/08, Bessin and Hurdal. The resistant to accumulation mycotoxins genotypes were two Russian cultivars Kambulinskiy and Stipler. The most susceptible to accumulation mycotoxins genotypes were Belinda, Bessin, Gere and Numbat.

*Relationship between DNA contents of F. culmorum and F. sporotrichioides in grain of analyzed genotypes was weak* ( $r=+0.21$ ,  $p<0.05$ ). The most reliable results were obtained under inoculation of plant genotypes by the most aggressive pathogen. Apparently a weak pathogen would be unable to penetrate through hull and colonize grain which can leads to higher percentage of *Fusarium* infection at low levels of mycotoxins.

In order to cultivate oats with high quality and safety of grain, breeders should used in crossing the lines or varieties characterized by high resistance to *Fusarium* infection and mycotoxin contamination. A breeding strategy to combine both resistances to pathogen development and mycotoxin accumulation would probably lead to the development of new oats varieties, which able to efficiently limit the problem of mycotoxin in grain.

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# Possibilities to control *Fusarium* infection in oats with fungicide applications

Päivi Parikka<sup>1</sup>, Arja Laitila<sup>2</sup>, Marika Jestoi<sup>3</sup>, Sari Rämö<sup>1</sup>,  
Ari Huttunen<sup>1</sup>, Veli Hietaniemi<sup>1</sup>

<sup>1</sup>Natural Resources Institute Finland (Luke), Helsinki, Finland,

<sup>2</sup>VTT Technical Research Centre of Finland Ltd, Espoo, Finland,

<sup>3</sup>The Finnish Food Safety Authority Evira, Helsinki, Finland

E-mail: [paivi.parikka@luke.fi](mailto:paivi.parikka@luke.fi)

**Keywords:** *oats, cultivation, disease control, mycotoxins*

In the cool and humid climate *Fusarium* infections are common in oat grain. Detected mycotoxin contaminations, however, are mainly low in Finland but their increase has been observed during the recent 15 years. The need to understand infection and survival of mycotoxin producing *Fusarium* species and to control infections has become more important to fulfill the demands set on mycotoxin contents of grain in the European Union.

How *Fusarium* infections develop during the growing season in oat grain and the effects of cultivation practices on infection level and mycotoxin contaminations have been studied during the recent ten years in Finland. Prevalence of infection in the plant residue remaining in the field was also included in the most recent research project in 2010-2012. Part of the work was to study the effects of seed dressing and fungicide applications on mycotoxin producing *Fusarium* fungi. Seed dressing was carried out with fludioxonil (Celest Formula M) and the fungicide application with prothioconazole and trifloxystrobin (Delaro SC325) was made after heading. Observations of *Fusarium* infection were made from heading up to harvested grain. Infection in straw and stubble was also studied as well as the presence of mycotoxin producing *Fusarium* species in overwintered straw.

The weather conditions during the growing seasons had strong influence on *Fusarium* infections in the developing grain. Exceptionally high temperatures and drought in July in 2010 were favorable to *Fusarium poae*, *F. sporotrichioides* and *F. equiseti*, but deoxynivalenol (DON) producing *F. culmorum* and *F. graminearum* were not common in developing oat kernels and harvested grain. In humid and warm conditions in 2011 the situation was different: T-2/HT-2 toxin producer *F. langsethiae* was very common in developing grain. However, despite of high humidity the prevalence of DON producers was low. High humidity but lower temperatures were also favorable to *F. langsethiae*, in 2012, but otherwise *Fusarium* infections in grain were on lower level than in the previous years. Some differences were observed in *Fusarium* infections of oat cultivars in the trials.

The effect of seed dressing on *Fusarium* contamination was restricted to germination and seedling emergence and already four weeks after sowing *F. langsethiae* was observed in seedlings. Fungicide application after heading could slightly reduce *F. gram-*

*inearum* and *F. culmorum* infections but the results varied. No effect on *F. langsethiae* was detected and fungicide treatment did not reduce T-2/HT-2 contaminations of the harvested grain of oat cultivars. This is in accordance to the results of an earlier study in 2004-2006, where fungicide application at flag leaf stage of oats could result in some reduction in DON-producers, especially the prevalence of *F. graminearum* and DON contaminations in harvested grain. However, the analyzed contamination levels both in fungicide-treated and non-treated oats were low. The results were also similar in 2013 and 2014 when timing of fungicide treatment was studied on three oat cultivars in Ylistaro, Ostrobothnia where *Fusarium* infection levels are normally high. The prevalence of DON-producers could be affected with fungicide applications but no significant effect was observed on DON contaminations.

There was also a strong effect of weather conditions on *Fusarium* contamination of oat residue left in the field. The most prevalent *Fusarium* species in straw and stubble has been *F. culmorum*. Humidity and high temperatures could slightly increase *F. graminearum* in plant residue. After a cool season contaminations were lower and the species composition in the straw and stubble were different than in warm conditions. In cool conditions *F. avenaceum* is most prevalent *Fusarium* species in plant residue. Chemical control had no significant effect on *Fusarium* surviving in plant residue. The only observed impacts were on *F. culmorum* and *F. graminearum* contaminations in 2011. As a result, temperature and humidity of the growing season also influenced the *Fusarium* surviving in the field for the following year.

Our studies showed that fungicide application after heading or at flowering could reduce *F. graminearum* infection in grain. Oat cultivars had differences in *Fusarium* infections and in single trials a cultivar could have more effect on DON contamination than fungicide application. No effect on *F. langsethiae* or T-2/HT-2 contaminations in grain were observed. However, the most important factors affecting both *Fusarium* species relations, infections, mycotoxin formation and inoculum in the field are weather conditions during the growing season.

# Elucidating the cropping factors influencing *Fusarium* species and mycotoxin occurrence in Swiss oats

Torsten Schirdewahn<sup>1</sup>, Charlotte Martin<sup>2</sup>, Fabio Mascher<sup>2</sup>, Thomas D. Bucheli<sup>1</sup>, Mario Bertossa<sup>2</sup>, Romina Morisoli<sup>2</sup>, Tomke Musa<sup>1</sup>, Felix E. Wettstein<sup>1</sup>, Beat Keller<sup>3</sup>, Susanne Vogelgsang<sup>1</sup>

<sup>1</sup>Agroscope, Institute for Sustainability Sciences, Zurich, Switzerland

<sup>2</sup>Agroscope, Institute for Plant Production Sciences, Changins/Cadenazzo, Switzerland

<sup>3</sup>University of Zurich, Institute of Plant Biology, Zurich, Switzerland

E-mail: [Torsten.Schirdewahn@agroscope.admin.ch](mailto:Torsten.Schirdewahn@agroscope.admin.ch)

**Keywords:** oat, *FHB*, mycotoxins, health promoting compounds

Small-grain cereals provide the major part of calorie intake of the Swiss population and are important for a balanced diet. In addition, Oats often contain relevant levels of health promoting compounds (HPCs) (Adom et al. 2002). Some of these HPCs (e.g. anthocyanins and flavonoids) possess antioxidant potential and thus can prevent various human diseases such as cancer, cardiovascular diseases and Parkinson's. However, cereals must be safe and therefore free of health threatening substances, such as *Fusarium* mycotoxins. For *Fusarium* head blight in wheat, *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, can influence the species spectrum and subsequent contamination (Schmidt-Heydt et al. 2008).

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 evaluated by utilising a seed health test. Additionally, the quantification of fungal DNA of *F. langsethiae* and *F. poae* by qPCR is presently running. Mycotoxins were detected by LCMS/MS and quantified with matrix-matched calibration. In depth statistical analyses to reveal potential correlations between *Fusarium* species/mycotoxins and cropping factors are presently running and will be discussed. Based on the current results, the main occurring species and mycotoxins were *F. poae* and T-2/HT-2, respectively. Preliminary statistical analyses demonstrated that winter varieties showed an elevated incidence of *F. poae* and *F. langsethiae* and a higher contamination with T-2/HT-2. Furthermore, the risk of a T-2/HT-2 contamination seems to be enhanced by growing oats after other small-grain cereals.

Results from the monitoring and epidemiological studies will be used to extend the forecasting system FusaProg for wheat towards oats. Thus, a system to reduce the application of fungicides and a tool for growers to decrease the infection risk will be developed.

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# **PARALLEL SESSION 3**

**Production, Processing,  
Products and Consumers**



## ORAL PRESENTATIONS

### The study of quality effect on oat-rice processed by new technology of peeling and extrusion

Fang Shan<sup>1,5</sup>, Lijia Zhong<sup>1,5</sup>, Xinzhong Hu<sup>2,5</sup>, Zaigui Li<sup>3,5</sup>, Changzhong Ren<sup>4,5</sup>

<sup>1</sup>Institute of Agricultural Processing, Shanxi Academy of Agricultural Sciences, Taiyuan, China, 030031;

<sup>2</sup>College of Food Engineering and Nutritional Science, Shaanxi Normal University, Xian, China, 710119;

<sup>3</sup>College of Food Science and Nutritional Engineering, China of Agricultural University, Beijing, China, 100083;

<sup>4</sup>Jilin Baicheng Academy of Agricultural Science, Baicheng, China, 137000;

<sup>5</sup>Agricultural Research System (CARS-08-D), Chinese Ministry of Agriculture, Xi'an, China, 710119

E-mail: [shanfang@126.com](mailto:shanfang@126.com); [shanfang@sxagri.ac.cn](mailto:shanfang@sxagri.ac.cn)

**Keywords:** *peeling, extrusion, new technology, oat-rice, quality, study*

Oat-rice is a new kind of product which is suitable for cooking staple food and different from oat meal. It can be cooked into porridge or steamed rice alone or mixed with rice, buckwheat, millet and so on in any proportion. The cooked food tastes smooth, soft, sticky, and very crunchy, also with Low-GI (glycemic index), and high health efficacy.

The characteristic of oat-rice is its high preservation of nutrients and cooking convenience. This study aims on the effect of new peeling and extrusion technology on the nutritional quality and cooking property of oat-rice. The peeling technology includes oat wetting, peeling with brush machine in order to brush away the kernel skin and retain aleurone layer and embryo. The extrusion technology is to maintain the thickness ratio about 0.3, by controlling the extruding strength of roller tablet machine. The standard of product is that the rice can swell and regain the shape of oat grain after cooking and minimize the gelatinization time by controlling the extrusion strength.

The results (dry base) showed that the content of protein (19.1%), lipid (8.64%), crude fiber (4.90%) and  $\beta$ -glucan (4.51%) in oat-rice processed by the new peeling and extrusion technology accounts for 97.3%, 98.5%, 67.8% and 93.5% of the raw material separately. The gelatinization time was reduced from 20.4min to 13.0min, which can meet the requirement of cooking with rice simultaneously. The by-products of this process include awn and epicarp (<5%), peeled broken rice (<0.5%). This technology has reached an advanced level on resource utilization rate and product yield. Clinical evaluation results show that the new oat-rice has the GI value of 51.4, obviously lower than oat meal, suitable for weight loss, postprandial blood glucose control consumer's demand and other aspects.

# Development of short germination malt technology from Vyatsky naked oats

Maria Chekina, Tatiana Meledina

FSAEI of HE “Saint-Petersburg State University of Information Technologies, Mechanics and Optics”, St. Petersburg, Russia

E-mail: [msch18\\_25@mail.ru](mailto:msch18_25@mail.ru); [tatiana.meledina@yandex.ru](mailto:tatiana.meledina@yandex.ru)

***Keywords: naked oats, hulled oats, malting, oat malt, germination, sort germination malt, cytolysis, proteolysis, enzyme activity.***

Nowadays among food belonging to functional nutrition segment syrups made of grains are becoming increasingly common as an additional source of vital nutrients. From the viewpoint of processing grains into syrups and its further using in food production, a great interest arises in thorough studying of naked oat varieties. This issue is closely connected with dietary and curative properties of grains of such culture. Naked oat varieties have several advantages compared with the hulled varieties. The huge interest for elaboration is certainly gluten- free varieties.

There are different approaches to process cereals into syrups: grain handling by enzyme preparations and processing of germinated grains which have their own enzymes. The accumulation of native enzyme is the main task of malting. It should be noted that in the process of malting vitamin content increases in grain, and this in turn increases bioavailability of the food in general.

Usually malting process takes up to 5-7 days. Though, it's known there are technologies of short malt germination from barley with germination duration lasting 3-4 days. In this case, the net cost off end-product reduces alongside with reducing of amylolytic enzymes activity (in the case of using barley). At present days the literature on technology of oat grains germination has general nature, the information about production of short germination malt from oat grains absents. Usually for the production of malt from oat grains it is recommended to use methods for malt production from other grains. Meanwhile, absence of hull can change the process of enzymatic activity accumulation in naked oat grains: it should grow faster than barley, and so - have higher rates characterizing cytolytic and proteolytic dissolution.

**The aim** of this research work is to develop an energy-efficient technology of malt germination from naked oat grains.

The objects of the study were 13 varieties of naked oats created in the Zonal Research Institute of Agriculture of the North-East named after N.V. Rudnicky (Agricultural Research Institute of the North-East, Kirov). Oats grain Vyatsky, Persheron, Pushkinsky (1h07), 857h05, 766h05, 9h09, 12h12o, 9h12o, 12h09, 8h12o, 29h09, 629h09, 21h12o were examined for the presence of allergenic prolamine fraction of wheat - gliadin. According to the results of an ELISA assay, all examined varieties have less than 0.2 mg of gluten per 100 g, that allows to assign them to a gluten-free raw products. Foods, for production of which these grain varieties are used, can be labeled as «gluten-free».



For further research of the impact of malt germination process widely cultivated oat Vyatsky was chosen, containing 0.16 mg of gluten per 100 g. Malt properties, obtained from Vyatsky oat grains were compared with the properties of commercial gluten containing (20 mg / 100 g) oat malt CHÂTEAU OAT (CHATEAU OUT) manufactured by Castle Malting (Belgium). Germination mode of CHÂTEAU OAT is 5-6 days at a temperature of 14-15° C.

Due to the fact that the rate of enzymatic reaction depends primarily on the temperature, we have studied the influence of this parameter on all the indicators characterizing the quality of malt, which are generally used in evaluating malt from barley. There were several variants of grain germination mode under different conditions: 1- three days at 7° C; 2- three days at 10-11° C; 3- three days at 16-17° C; 4- three days at 18-19° C; 5- four days at 18-19° C.

Founded that the organoleptic characteristics such as appearance, smell and taste of Vyatsky oat malt comply with generally accepted standards. Moisture content in samples was  $6 \pm 0,5\%$ . During examination of cytolytic dissolution of oat malt was discovered that the content of  $\beta$ -glucan reduces from 1020 to 757 mg / l under the increasing of germination temperature from 7 to 19° C. While analyzing malt extraction was revealed that extraction of fine grind (Ef) is less than coarse grind extraction (Ec) and in process of germination the difference between the Ef-Ec ( $\Delta E$ ) decreases depending on germination temperature.

Proteolytic indicators (soluble nitrogen, amino-free nitrogen, Kolbah number) in obtained malt exceed the values defined in the industrial sample. Kolbah number increases two times and concentration of amino nitrogen in the wort increases 3,4 times (from 34 to 117 mg/l). Increase in exponent of extract content in wort from coarse grind in congress wort from 57, 1 to 74, 5% indicates the increasing of amylolytic activity of the malt under the increasing of germination temperature.

Thus, revealed that for producing of malt from Vyatsky naked oats a three-day grain germination under the temperature of 18-19° C is enough. The resulting product is referred to a group of short malt germination.

# Functional and technological properties of oat grain and a line of promising food products on its basis

Vitaly Popov, Nataliya Barsukova, Sofiya Sergeyeva, Valery Krasilnikov

«Peter the Great St.Petersburg Polytechnic University»  
50, Novorossiyskaya Str., 194021 St. Petersburg, Russia  
E-mail: [top@spbtei.ru](mailto:top@spbtei.ru)

**Keywords:** *naked oat, non-starch polysaccharides, gluten-free diets, functional foods, wholegrain flour, choux pastry, hydrothermal pre-treatment, profiteroles*

The role of cereal crops in the diet of many peoples is difficult to overestimate, it is great and diverse. Cereal grain can be used for the development of healthy and functional foods as a source of non-starch polysaccharides, nutraceuticals and immunomodulatory agents.

Cultivated oat (*Avena sativa*) is an undemanding to climate and soil, moisture-loving plant with a comparatively short vegetation period. In comparison with other cereals like wheat, rye or barley, oat has lower requirements for the summer heat and a higher resistance to the rain. It is particularly important for the areas with cool and wet summers like in the Northwestern Europe.

Oats – is an amazing crop. It surpasses other crops in the quantity of nutrients. The biochemical composition confirms the high nutritional value of products made from oats and their health-promoting effect.

Epidemiological studies have shown that the consumption of products from whole grain oats rich in beta-glucans and arabinoxylans protects against cardiovascular diseases, type II diabetes, obesity, certain kinds of cancer. In some countries, e.g., in Finland, the United Kingdom and the USA, oats have long been used in gluten-free diets.

The husked oat is widely cultivated in Russia, as well as in the rest of the world. The naked oat (*Avena nudum*) is a new crop and the interest to its cultivation and use has significantly increased in recent years in most countries. The reasons for this are the dietary and health-promoting properties of naked grain.

In comparison with the husked oats, naked oat cultivars differ by high yield and nutritional value. The yield of naked oat groats is 99.2%, while for the husked oats it is only 71.5%. The taste of naked oat groats and flakes is better than that of the same products from the husked oat. Thus, the development of naked oat breeding is advantageous for improving the quality of human nutrition, as well as for developing functional foods.

In our studies we have used the wholegrain flour – one of the products of the naked oat processing, which is the main raw material for manufacturing dough products.

Due to the low gas-retaining capacity of oat flour, the most acceptable types of dough that can be derived from it, are the wafer, biscuit, shortbread and choux pastry.

Oat flour does not form gluten that gives the dough the required visco-elastic properties. At the same time, it contains a large amount of polysaccharides, such as

starch, gums, beta-glucans and other non-starch polysaccharides (NSP) with a limited capacity of swelling in cold water, which results in the formation of a dough that is sticky and does not retain its shape.

When oat flour is brewed, starch gelatinizes, NSP swell, and the dough becomes elastic and flexible. By selecting the required ratio of oat flour, water, and oil on the basis of dough brewing, a technology of profiteroles and crisp breads production has been developed. The products have good organoleptic characteristics, with exception for the taste which was a bit bitter. It was obviously caused by the oat lipid oxidation products. Further studies have shown that hydrothermal pre-treatment (HPT) of oat grain removes lipid oxidation products from grain surface and inactivates enzymes responsible for the oxidative damage to lipids. Therefore, HPT of grain reduces the characteristic taste of oats and bitterness in the finished products, and also extends the shelf life of flour produced from the treated grain.

In earlier studies, we have developed recipes and techniques of preparation of gluten-free gingerbread and wafers on the basis of grain from the celiac non-toxic oat cultivars.

The use of 12% of oat flour in a flour mixture for the production of gluten-free gingerbread makes it soft and crumbly, rich in protein and dietary fibers. Also, the use of oat flour reduces staling of products during their storage, thus extending their shelf life.

The development of oat flour wafers and combinations of sweeteners made it possible to recommend them for the use in diabetic diets. These wafers have good structural, mechanical and organoleptic properties. The studies have yielded the optimal bicomponent mixtures of structural sweeteners which are characterized by a quantitatively synergistic effect associated with a decreased viscosity of wafer dough and increased brittleness of the wafers.

The recipe of a dietary wafer semi-finished product from oat flour that is free from sucrose and wheat gluten, is protected by a patent of the Russian Federation for the invention № 2337550. Commercialization of this invention will broaden the range of health food products available at the domestic market.

# The purification of free radical scavenging peptides from naked oats

Meili Zhang, Sarina Ma, Xiaolan Bao

College of Food Science and Engineering, Inner Mongolia Agricultural University,  
ZhaoWuDa Road, No.306, SaiHan District, Huhhot, 010018 China

E-mail: zhangmeili22@sina.com

***Key words: naked oats; glutelin; enzymatic hydrolysis; purification; free radical***

The present study hydrolysis naked oats glutelin by Alcalase. Sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) result showed that naked oats glutelin molecular weight ranged from 14 to 97 kDa. Ultrafiltration and ion exchange chromatography were used to isolate and purify naked oats glutelin peptide. The results showed hydroxyl radical scavenging activity of component I (molecular weight bigger than 30 kDa) was the strongest among the 5 components separated by ultrafiltration. With the mass concentration of 3 mg mL<sup>-1</sup>, scavenging effect against hydroxyl radical reached higher than 90%. Component I was further purified into 4 fractions by ion exchange chromatography. Fraction D showed higher scavenging effect against hydroxyl radical (IC<sub>50</sub> 1.397 mg mL<sup>-1</sup>), DPPH radical (IC<sub>50</sub> 1.258 mg mL<sup>-1</sup>) than the other 3 fractions. Moreover, fraction D exhibited higher scavenging effect against hydroxyl and DPPH radical than the hydrolysate. Free radical scavenging capacity of naked oats glutelin hydrolysate can be proved by isolation and purification.



**POSTER SESSION**  
**Genetic Resources,  
Diversity and Breeding**

## POSTER PRESENTATIONS

### Identification and characterization of high-protein oat lines from a mutagenized oat population

Bindu A. Similkumar<sup>\*1,2</sup>, Rickard Öste<sup>2,3</sup>, Olof Olsson<sup>1,4</sup>

<sup>1</sup>CropTaio AB, c/o Department of pure and applied biochemistry, Lund University, Lund, Sweden 22100;

<sup>2</sup>Food for Health Science Centre, Lund University, Lund, Sweden 22100;

<sup>3</sup>Adventure AB, Scheelevägen 22, 22362 Lund, Sweden;

<sup>4</sup>Department of pure and applied biochemistry, Lund University, Lund, Sweden 22100

e-mail: [bindu.sunilkumar@food-health-science.lu.se](mailto:bindu.sunilkumar@food-health-science.lu.se)

**Key words-** *oat, high protein, crossing, selection, amplification, field, beta glucan, dietary fiber*

Oat is an excellent source of high-quality protein with favorable amino acids. Normally, the protein content in oat is about 10%. Oat lines with a double protein content, ca 20% would have great potential as an alternative, vegetative protein source.

In this work, more than a thousand individual lines in a mutagenized oat population (TILLING-population) were screened for total protein using an elemental particle analyzer. This identified 230 lines with a seed protein content of 15% protein or higher. The highest line had 24% protein. After this, the 15 highest of these lines were selected for further studies.

First, the protein content in individual seeds was determined. This confirmed the high protein levels and showed that in some lines the high protein character was segregating. Using half-seed technology (see poster by Leonova et al) and single seed descent sublines were raised from the individuals with the highest levels.

Secondly, total protein was extracted and analyzed by SDS-PAGE. This showed that the relative levels of individual proteins were different. A few lines has clearly elevated levels of globular proteins. Total dietary fiber (TDF) and  $\beta$ -glucan levels were also measured in the selected lines. This showed that the values for these components were normally distributed around the original level in Belinda, i.e. there was no positive or negative correlation between fiber content and high protein content.

Crosses were performed between the five lines with the highest protein levels and the original non-mutated Belinda variety from which the mutagenized population was derived. The F1 hybrid seeds were grown in the greenhouse, self-pollinated and individual seeds from the F2 offspring were analysed. This showed that the high-protein character was stably inherited. To further test the stability of high protein content, the 15 highest lines were amplified in the field and protein content was again determined in seeds harvested at the end of the season and the high protein character was confirmed.

# The high quality naked oat cultivars for functional food

Boris L. Ganichev<sup>1</sup>, Olga A. Isachkova<sup>1</sup>, Igor G. Loskutov<sup>2,3</sup>

<sup>1</sup>Kemerovo Agricultural Research Institute, Kemerovo, Russia

<sup>2</sup>Federal Research Center N.I. Vavilov Institute of Plant Genetic Resources (VIR),

<sup>3</sup>St-Petersburg State University, St-Petersburg, Russia

E-mail: [i.loskutov@vir.nw.ru](mailto:i.loskutov@vir.nw.ru)

***Key words: oat, cultivars, breeding, productivity, starch, oil,  $\beta$ -glucans, antioxidants.***

Oat (*Avena sativa* L.) is one of important cereal crops in Russia. The greater part of oat grown in the country is represented by the husked oat cultivars, however, a trend of creating naked cultivars is taking shape.

The cultivars of naked oat differ from the husked ones by the absence of husk and presence of some positive traits. Due to the absence of husk, grain of these cultivars can be directly used by the food and mixed feed industries. Along with high grain productivity, the naked oat cultivars demonstrate high qualities of grain, which transform this crop from grain forage into a source of food, functional and dietary products for humans. In addition to the traditional grain quality indicators as the content of protein, lysine and starch, the content of oil and fatty acids ratio, as well as the content of  $\beta$ -glucans, tocopherols, a complex of vitamins and a wide range of antioxidants (avenanthramides included) become priority indicators of a promising cultivar.

The preliminary study and selection of initial material performed at the N.I. Vavilov Institute, and the breeding carried out at the Kemerovo Agricultural Research Institute using the material selected at the former institution, have resulted in creation of a number of naked oat cultivars.

The jointly bred cultivars of naked oat, that is Levsha, Aldan, Murom, Pomor, Taidon and Gavrosh, possess a series of important agronomical and unique biochemical characteristics. In addition to the traditionally high content of protein, lysine and starch, grain of these cultivars has an increased content of oil with a favorable ratio of individual fatty acids, high content of  $\beta$ -glucans, tocopherols, a complex of vitamins, and a wide range of antioxidants (avenanthramides included) which make the grain a unique raw material for producing functional and dietary products for humans.

By now, six naked oat cultivars have been bred and submitted to State Variety Trials. Author's certificates have been issued for five of them (except for Gavrosh), and three of these cultivars, namely Levsha, Pomor and Taidon, have been patented and recorded in the State Register of Breeding Achievements of the Russian Federation accepted for the cultivation in the country.

All of the named cultivars are no inferior to the husked ones in terms of productivity and considerably surpass them in respect of biochemical parameters. The cultivars Pomor and Taidon have a higher content of protein in the kernel (17-18%); cvs. Murom and Pomor contain up to 60-62% of starch, and cvs. Murom, Pomor and Taidon showed an increased content of oil in the kernel, which is over 8-9%. The content of the oleic



acid (18:1) in oil in kernels of cv. Murom is comparable with that in sunflower oil; cv. Pomor shows the highest content of linoleic acid (18:2), while cv. Taidon has the highest quantity of linolenic acid.

In addition to the determined biochemical substances, the preliminary data show that these cultivars have a higher content of  $\beta$ -glucans and, presumably, an increased content of antioxidants in the kernel. Besides, all of these cultivars are medium resistant to the majority of leaf fungal diseases and are only slightly susceptible to smut, as well as to *Fusarium* head blight and accumulation of mycotoxins in grain.

All of these varieties possess antioxidant and anti-inflammatory functions; they stimulate the immune system and prevent the development of cardiovascular diseases thanks to the high content of  $\beta$ -glucans and antioxidants.

Therefore, all of the presented naked oat cultivars show improved agronomic traits, unique biochemical characters, dietary properties, and can be used by the food industry for producing functional foods.

# **Evaluation of some oat (*Avena sativa* L.) genotypes for yield and selected quality parameters grown under Trakya-Marmara region of Turkey**

Turhan Kahraman<sup>1\*</sup>, Ziya Dumrupinar<sup>2</sup>, Cengiz Kurt<sup>1</sup>

<sup>1</sup> Trakya Agricultural Research Institute, Edirne Turkey

<sup>2</sup> Kahramanmaraş Sutcu Imam University, Kahramanmaraş Turkey

E-mail: [turhankahraman@hotmail.com](mailto:turhankahraman@hotmail.com)

**Key words:** *oat (Avena sativa L.), grain yield, quality.*

In recent years, oat is becoming popular in Turkey according to its health benefit claims and oat production is in increase in Turkey especially in Trakya-Marmara region. This study was carried out in 2013-2014 cropping year in Edirne with 44 oat lines and 5 commercials (Kırklar, Kahraman, Sebat, Yeniçeri and Sebat). The experiment was arranged in an alpha lattice experiment design (7 x 7) with three replications. It is aimed to determine yield and some quality parameter performances of oat lines derived from our breeding program.

In the research, the traits such as grain yield (GY), thousand kernel weight (1000-KW), test weight (TW), protein ratio (PR), plumpness (P, sieved 2.2 mm slotted) and groat percentage (GP) were investigated.

The variation among oat lines for grain yield was significant and differences for 1000-KW, TW, PR, P, and GR were also determined. The GY, 1000-KW, TW, PR, P and GP of oat lines ranged between 306.7-914.5 kg/da, 21.8-40.4 g, 48.3-60.8 kg/hl, 9.92-14.02%, 22.7-93.5% and 60.4-76.7% respectively.

The oat line 49 had the highest GY with 914.5 kg/da and followed by oat line 3 with 867.5 kg/da and oat line 29 with 851.7 kg/da, while the lowest GY was obtained from the oat line 20 with 306.7 kg/da.

The oat lines 49, 3, 29, 44 and 23 were hopeful for GY and the oat lines 5, 13, 10, 8, 1, 36 and 16 were hopeful for investigated quality parameters.

## Oats breeding in the Kuban region

Tamara Kuznetsova, Sergey Levshtanov, Nikolay Serkin.

«Agrostandart» Ltd., Krasnodar, Russia  
350000, Krasnodar, 135/81 Oktyabrskaya st.  
E-mail: [Agrostandart.dr@list.ru](mailto:Agrostandart.dr@list.ru)

***Keywords: oats, collection, variety, line, selection, open blossoming, cross-pollination, recombination, mutation***

Oats is the most important fodder and food crop. Mainly it is valuable due to its wide ecological adaptability, the content of grain protein, carbohydrates, fats, vitamins, trace elements and biologically active substances in the optimum combination necessary for human and animals for normal life and good health. In Russia, spring oats are mainly cultivated in Siberia, Volga and Central Federal Regions. The share of the North Caucasus region in the production of this crop is only 1.5-3.2%, and of the Krasnodar area is even less. In recent years the demand for oats in the sphere of agricultural production has increased dramatically. Released zoned varieties are extremely unstable in yield by years. In 2014 “Agrostandart” Ltd. submitted for the State testing two varieties of spring oats: Desant and Assol. Desant is obtained by individual selection from the Swedish variety Magne. Sort - aristata. Panicle is erect, flattened, its length is average. Plant height is 60-95 cm. The variety is highly resistant to recumbency. Productive tillering is 1,0-1,7 stems. Mid-ripening. The weight of 1000 grains is 27,3-39, 6 g. Its grain quality is better than Valdin 765 for 15 g. The variety has got good field resistance to puccinia coronifera, it's almost resistant to ustilago avenae. The average yield for 4 years is 37.3 t / ha, which is higher than the standard by 11%. Maximum productivity in the competitive testing of varieties is obtained by white mustard predecessor 53, 8 kg / ha. The variety Assol is the result of individual selection from the variety Krasnodarskiy 73. Sort - mutica. By growing season it refers to the mid-ripening varieties, it hoists a panicle and matures similarly to Valdin 765 and one day ahead of the parent variety. The plant height is 68-105 cm, it is resistant to recumbency. Panicle is erect, pyramidal, semi-flattened, loose, with the average length of 20-25 cm. Kharkov type of grain, small, weight of 100 grains is 23,2-34,7, at the standard level. The length of a panicle, number of grains per panicle, grain weight of a panicle and grain nature testifies to the best resistance of the variety to abiotic and biotic stresses. The average yield for 4 years (2012-2015) is 36,6 t / ha, which is higher than Valdin 765 by 2.8 t / ha. The maximum yield obtained is 52, 4 t / ha.

# Half-seeds; an efficient one step method to obtain homozygote lines for a specific trait

Svetlana Leonova<sup>1</sup>, Bindu A Sunilkumar<sup>1,2</sup>, Hans Olof Johansson<sup>3</sup>, Johanna Lethin<sup>3</sup>, Lars Sjögren<sup>3</sup>, Yi Ren<sup>3</sup>, Andreas Hansson<sup>3</sup>, Olof Olsson<sup>2,3</sup>

<sup>1</sup>Department of Pure and Applied Biochemistry, Lund University, Box 124, S-22100 Lund, Sweden;

<sup>2</sup>Food for Health Science Centre, Lund University, Box 124, S-22100 Lund, Sweden,

<sup>3</sup>CropTailor AB, Department of Pure and Applied Biochemistry, Lund University, Box 124, S-22100 Lund, Sweden

Address: Lund University Dept of Pure and Applied Biochemistry Center of Chemistry and Chemical Engineering P.O. Box 124, 221 00 Lund, Sweden

E-mail: [Svetlana.Leonova@tbiokem.lth.se](mailto:Svetlana.Leonova@tbiokem.lth.se)

**Key words:** *Avena sativa*, oat selection and breeding, mutagenesis, homozygotes, single seed descent, half-seed approach

Recently we developed a mutagenized oat population with a very high variation. This variation facilitates screenings both on the genetic level after specific mutations and on the phenotypic level for alterations in macromolecule levels or specific biochemical reactions. Initially the population was screened for characters like high beta-glucan-, protein-, lipid- and avenanthramide levels in the seed and lines modified in the desired trait were identified.

When screening and identifying a specific phenotype, the underlying mutation that give rise to the phenotype is dominant. Upon self-crossing, the mutation will segregate and the offspring show variation in how the trait is expressed. A common challenge with all lines identified for altered phenotypes is therefore to obtain homozygous lines for the respective traits. The classical way to do this is to propagate sublines starting from a single seed (single seed descent) and then quantify the trait a few generations later. The draw back with this strategy is that it is laborious and time consuming.

In this study we utilized an alternative method denoted the half-seed method. In a first step, an assay for the trait, sensitive enough to be applied on a single seed, is developed. In a second step, the single seed assays are further optimized to give reliable and reproducible results on material from only a half seed. Individual seeds can then be cut in two parts in such a way that one part contain the embryo and scutellum plus some endosperm tissue, while the other half only contained endosperm. The embryo-free part is used in the biochemical analyses to quantify the trait.

In a third step, moisture conditions and other growth parameters are optimised for germination and further growth and development of the other, embryo containing part of the half seed. We tested hundreds of half-seed embryos and, as control, intact seeds side by side. In our final protocol the half-seeds were viable as the intact seeds and no other negative effect like i.e. increased pathogen entrances at the cut site could be observed. Thus, no special treatments like fungicide application or pre-sterilization of the seeds were needed for the embryos to develop into mature plants.

The half-seed system was applied on seed pools from lines with elevated levels of protein, beta-glucan, and oil content. After half-seed screening and identification of the individual seeds with the highest levels, the other half was germinated, grown to maturity, self crossed and new seeds collected. From these, single seeds were again measured. The variation between different seeds was then much lower than from the original pools and the average levels of the specific trait were higher. This was true for all traits tested.

## **The latest achievements of Moscow Agricultural Research Institute “Nemchinovka” in oat breeding**

Mikhail I. Maksimenko, Aleksander D. Kabashov, Yakov G. Leibovich

Moscow Agricultural Research Institute “Nemchinovka”, Oat Breeding Laboratory,  
1, Kalinina str., Novoivanovskoye, Moscow region, 143026, Russian Federation

E-mail: [maksimenko.mikhail2014@yandex.ru](mailto:maksimenko.mikhail2014@yandex.ru)

***Keywords: oats, breeding, varieties, crosses, adaptation, diseases, grain yield, quality***

Intensive oat breeding has been carried out at Moscow agricultural institute since the second half of 20th century. The laboratory is currently collaborating with oats breeders from Vladimir Agricultural Research Institute (NIISKh), Kaluga NIISKh, and Kotlas Agricultural Experiment Station, Kursk NIISKh, Tula NIISKh, Ulyanovsk NIISKh, Chuvash NIISKh, Izhevsk State Agricultural Academy, and Aktobe Agricultural Experimental Station (Kazakhstan). Novgorod NIISKh, NIISKh of the Crimea, and Smolensk Agricultural University also estimate gain yield data of our varieties and lines. The laboratory of oats breeding was responsible independently or in co-operation with the other research institution for the introduction of 22 oat varieties. The most successful varieties were Skakun (registered in 1988), Konkur (2008) and Yakov (2010). Now days we together with Ulyanovsk NIISKh and Kursk NIISKh support patents on 11 varieties, or 18% of varieties, which are under patent protection in Russia. Oats breeding objectives of the laboratory are to develop new high-yielding cultivars with wide adaptation based on drought tolerance, resistance to lodging, shattering, as well as to the most harmful diseases such as: loose smut, barley yellow dwarf virus, crown and stem rust of oats which provide stable grain yield and economic competitiveness of oats.

# Finnish Oat Research Breeding and Production

Leena Pietilä, Merja Veteläinen

Boreal Plant Breeding Ltd., Myllytie 10, FI-31600 Jokioinen, Finland

E-mail: [merja.vetelainen@boreal.fi](mailto:merja.vetelainen@boreal.fi)

*Keywords: oat, breeding, production, cultivars, Finland*

Thirty percentage of the Finnish cereal acreage is covered with oats. The total cultivation area has been around 350 000 ha yearly and the oat harvest app. 1 1000 000 tons per year. The crop is used for feed and human food. Export of oats has been considerable for Finland and has been ca. 300 000 tons/year during the 2000's and thus, oats is the fifth important food stuff export product from Finland. Finland is also the second biggest exporting country of oats and the biggest demand comes from Germany with 145 000 tons in 2013. Especially demand of oats for human consumption and food stuff industry is growing and Finnish oats is desired. The value of total pure cereal export from Finland in 2013 was 131 milj € of which oats accounted for 72 milj.€.

Oats has several positive properties both as animal feed and human food. As animal feed oats is used both for ruminants and monogastric animals as oats has characteristics that increase its feed value. Especially, the fatty acid content of oats is more favorable than in the other cereals and fat content is high and rich in oleic and linoleic acids. Compared with other cereals, oats have a more balanced amino acid composition and higher concentration of essential amino acids, such as lysine. For human consumption, especially fibre content is appreciated and valued in morning cereals and other oat based food products. Health claims for beta-glucans and their positive effects to maintain normal blood cholesterol concentrations have been approved by EU.

Oats is also appreciated in crop rotation more than other domestic cereals. It is a relatively healthy crop and requires less pesticide than other cereals. Organic production is thus easier than with other cereals.

In Finland 2/3 of oat area is cultivated with Finnish varieties bred by Boreal Plant Breeding Ltd. In the northern parts of Finland, where early ripening varieties are a requirement, domestic cultivars cover 80-90% of the cultivation area. Boreal's oat breeding programme has been especially successful in producing high-yielding early cultivars.

It can be concluded that oats is an extremely important crop for Finnish farms, feed and food stuff industry, as well as for the oat importing countries that utilise the crop for traditional products and new food and feed innovations. Future prospects for oats to develop to an even more widely grown cereal in Finland are very positive due to its beneficial nutritional qualities and positive environmental impacts. The prerequisite for further growth is that the grain quality can be kept at a high level with respect to food and feed safety.



# White oat cultivar development at IAPAR – Brazil

Carlos Roberto Riede<sup>1</sup>, Klever Márcio Antunes Arruda<sup>1</sup>, Raceli Sandrin<sup>2</sup>

<sup>1</sup>Oat Breeders at the Agricultural Research Institute of Paraná –

P.O. Box 10030, CEP 86047- 902, Londrina-PR-Brazil

<sup>2</sup>Food Chemist at the Research & Development Laboratory of SL Food Company, Mauá da Serra – PR.

E-mail: [crriede@iapar.br](mailto:crriede@iapar.br)

***Key words: Oat breeding, grain yield, industrial quality, disease resistance***

White oat breeding activities started at IAPAR in 1996, with the introduction of advanced lines and cultivars of the breeding programs of UFRGS (Federal University of Rio Grande do Sul), UPF (University of Passo Fundo), FAPA (Agrária Cooperative Research Foundation), and IAC (Agricultural Research of Campinas). The best selected lines sowed at the Londrina Experimental Station of IAPAR, were used to organize the crossing blocks aiming to combine best adaptation traits needed in the new cultivars. The main objectives of the oat breeding program are: a) Grain yield increase; b) Earliness; c) Lodging resistance; d) Resistance to the main diseases; e) Quality improvement; and f) Wide adaptation including the subtropical regions of the Paraná state. The main breeding method used in the program was the Modified Pedigree, in which panicle bulk selections were practiced at the F<sub>2</sub> to F<sub>3</sub> generations followed by individual plants from F<sub>4</sub> to F<sub>6</sub>. In the F<sub>7</sub> generation, most advanced lines would be uniform and ready to participate in the institutional preliminary trials. First year preliminary trials are carried on in Londrina (North of the State), while second year trials are also evaluated at Santa Tereza do Oeste (West of the State) and in Ponta Grossa (South of the State), representing different environments for winter crops adaptation. The major diseases causing damage to the oat crop in the region are leaf rust caused by *Puccinia coronata* f. *sp. avenae*, leaf spot, caused by *Drechslera avenae* and a new disease named Pyricularia blast caused by *Magnaporthe grisea*, which severely damage the oat leaves and panicles. The size of the program has been increasing considerably from 272 yearly average segregating populations in the period 1999-2003, to 548 populations in the period 2004-2010, to 1489 populations in the period 2011-2015. The IAPAR white oat research program is working cooperatively with the SL Food Company Quality Laboratory which has done annual analysis of main cultivars and breeding lines of the interest. The main quality performed analysis are: a) Moisture content; b) Lipids (%); c) Protein (%), d)  $\beta$ -glucan content, Thousand kernel weight (g); Dehulled grains (%), h) Hull (%), i) Losses in the dehulling process (%), and j) Grain hardness. IAPAR has released two white oat cultivars named **IPR Afrodite** in 2012 and **IPR Artemis** in 2016. Seed multiplication has been done in cooperation with Paraná Seeds Company. The VCU (Cultivation and use values) trials are organized every year by the Brazilian Commission for Oats Research and evaluated cooperatively by its members. Advanced lines are evaluated in 10 locations (five in Paraná, four in Rio Grande do Sul, and one in São Paulo States). Released cultivars are evaluated in 20 locations (eight in Paraná, six in Rio Grande do Sul, two in São Paulo and one in Santa Catarina States). There are 23 released cultivars under exploitation in Brazil in 2016. Eleven are from UFRGS, six are from UFPEL, three from UPF, two from IAPAR and one from FAPA.



# Flowering time, yield parameters and grain quality in oat collection harvested in Kazakhstan

Yerlan Turuspekov<sup>1</sup>, Aigul Abugalieva<sup>2</sup>, Asem Ashimova<sup>1</sup>, Vladimir Chudinov<sup>3</sup>, Grigoriy Sereda<sup>4</sup>, Boribai Sariev<sup>2</sup>, Saule Abugalieva<sup>1</sup>

<sup>1</sup> Institute of Plant Biology and Biotechnology, Almaty 050040, Kazakhstan

<sup>2</sup> Kazakh Research Institute of Agriculture, Almaty region, Kazakhstan

<sup>3</sup> Karabalyk Breeding station, Kostanai region, Kazakhstan

<sup>4</sup> Karaganda Research Institute of Agriculture, Karaganda region, Kazakhstan

E-mail: [yerlant@yahoo.com](mailto:yerlant@yahoo.com)

**Keywords:** *oat, collection, flowering time, yield parameters, grain quality*

The collection of oat *Avena sativa* and *Avena byzantina* studied using field trials in three different latitude regions of Kazakhstan and DNA microsatellite markers. The collection consisted from 163 accessions received from VIR (Sant Petersburg, Russia) and 26 cultivars and promising lines from Kazakhstan. In total, 19 SSR markers were found to be polymorphic out of screened 29 markers in our genetic study. Genetic variability of the collection was studied using Nei's index. Most genetic variability index ( $0.521 \pm 0.052$ ) was found in East Europe region. All studied DNA microsatellite marker were ranged by PIC index. Phylogenetic analysis of the collection was performed by using Neighbor Joining method. The grouping of the accessions allowed of identifying 11 separate clusters. The principal coordinate analysis was successfully applied to differentiate the groups of oat within studied collection. It is found that North American and European accessions are genetically close to each other and far from distinct groups in Kazakhstan and South America. Field trials in Northern, Central and South-eastern regions of Kazakhstan (2012-2015) allowed to assess the patterns of genotype-environment interactions based on evaluation of yield components. Pearson's correlations between yield and plant growth stages were established in all studied sites. Harvested seeds from three regions of Kazakhstan were also studied by 6 grain quality parameters. The relationship among yield components and grain quality parameters were assessed. Obtained results can be effectively used in genotyping of commercial cultivars and for improving of oat adaptation, productivity and quality in different regions of Kazakhstan.

**POSTER SESSION**  
**Genomics, Bioinformatics**  
**and Molecular Assisted Selection**

## POSTER PRESENTATIONS

### **The Oat Newsletter: Satisfying your hunger for oat information**

Charlene P. Wight\*, Gerard R. Lazo, Catherine J. Howarth, Jean-Luc Jannink,  
S. Shea Miller, Marcelo Pacheco, Zongwen Zhang, Pamela Zwer, Nicholas A. Tinker

\*E-mail: [curator@oatnews.org](mailto:curator@oatnews.org)

*Keywords: Oat Newsletter*

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. This poster will highlight the various features and sections of the newsletter.

## **All a-Twitter about #oats**

Charlene P. Wight

@OatNewsletter, [curator@oatnews.org](mailto:curator@oatnews.org)

*Keywords: Oat Newsletter*

The social media platform “Twitter” (<https://twitter.com/>) is becoming a valuable tool for anyone interested in communicating more directly with a world-wide audience. The Oat Newsletter’s Twitter account is @OatNewsletter. It can be accessed *via* Twitter itself or from the Oat Newsletter home page (<http://oatnews.org>).

Content is shared by “tweeting” from your account. “Tweets” are limited to 140 characters in length, and can include photos, videos, or web links. You can create your own content, or “retweet” others’ tweets. You can quote or reply publicly to anyone’s tweets, or “DM” (direct message) your followers privately. “Hashtags” (e.g., #oats) can be used to direct your tweets to anyone interested in a particular topic. There is also a very good search feature.

Much of the information posted in the newsletter itself has been found through using hashtags or *via* the 300+ people the account follows. There are 400+ people following @OatNewsletter, very few of whom are involved with the oat research community directly. This gives us an opportunity to reach a much broader audience, including farmers who grow oats, as well as businesses and consumers who use them.

This poster will highlight some examples of how Twitter has been useful for the oat research community. Everyone is encouraged to tweet their own #oat news or send information to [curator@oatnews.org](mailto:curator@oatnews.org) for tweeting by @OatNewsletter.

## **Comparative genetic diversity of cereal crops cultivars in Kazakhstan**

Saule Abugalieva, Kanat Yermekbaev, Shynar Anuarbek, Yerlan Turuspekov

Institute of Plant Biology and Biotechnology, 45 Timiryazev street, Almaty 050040, Kazakhstan  
E-mail: [absaule@yahoo.com](mailto:absaule@yahoo.com)

***Keywords:*** Genetic diversity, cereal crops, DNA markers, microsatellites

The collections of commercial cultivars of oat, rice, barley and wheat from Kazakhstan were screened by different sets of DNA markers. Studied cultivars were officially registered in the Republic of Kazakhstan and allowed to cultivate in designated regions of the country. DNA microsatellite markers were used in order to assess the variability of these four important cereal crops for the country. Most genetic diversity was revealed for barley and oat collections. The Nei's indexes of genetic variability for these crops were 0.54 and 0.52, respectively. The least variable studied crop collection was rice (0.27), which is reflecting narrow region of cultivation in Kazakhstan. As the result of the study genetic passports for all registered cereal cultivars were established. The analysis will help for ongoing important QTL identifications in all four studied crops based on genome wide association mapping approach, as this genetic material is part of a broader set of collections, which were studied phenotypically in Southern, Central and Northern regions of Kazakhstan. Also, this will help local breeders in protection of their intellectual rights.

# **Genetic diversity of oat (*Avena sativa* L.) accessions and identifying of high quality and productive pure lines of oats for breeding**

Aigul Abugaliyeva<sup>1</sup>, Myrzan Nurpeisov<sup>2</sup>, Tim Langdon<sup>3</sup>, Burubai Sariev<sup>1</sup>, Vladimir Chudinov<sup>4</sup>, Kaldarbek Zhundibayev<sup>1</sup>.

<sup>1</sup>LLP “Kazakh Research Institute of Agriculture and Plant Growing”,  
Almalybak, Kazakhstan, [kiz\\_abugaliyeva@mail.ru](mailto:kiz_abugaliyeva@mail.ru)

<sup>2</sup>Kazakh National Agrarian University, Almaty, Kazakhstan, [zhmyrzan@gmail.com](mailto:zhmyrzan@gmail.com)

<sup>3</sup>Aberystwyth University’s Institute of Biological, Environmental and Rural Sciences, Penglais,  
Aberystwyth, Ceredigion, UK, [ttl@aber.ac.uk](mailto:ttl@aber.ac.uk)

<sup>4</sup>Karabalyk Experimental Station, Karabalyk, Kostanai, Kazakhstan, [ch.den@mail.ru](mailto:ch.den@mail.ru)

General screening of oat accessions of Kazakh and foreign selections has been conducted to identify the genetic relationships between the varieties and breeding numbers. Eleven genomic and expressed sequence tags (EST)-derived primer pairs were designed and selected according to their high polymorphism. Thus, the use of eleven SSR primers revealed genetic heterogeneity of all five varieties and 13 breeding numbers, indicating the presence of intracultivar polymorphism of varieties based on one or two loci out of all investigated microsatellite loci. Cluster analysis of the Kazakh and foreign oat accessions, aimed at detection of the genetic relationships between the varieties, allowed classification of the genotypes into two clusters. In turn, the first cluster was divided into two subclusters with the similarity quotient of 0.77-0.89 and 0.93-0.98, respectively. The first subclusters was comprised of seven varieties and breeding accessions of Kazakh selection including two out of five studied varieties, plus one sample of foreign selection. The second subcluster mainly included varieties and breeding numbers of Kazakh selection including the rest of the studied varieties with very close similarity quotient of 0.93-0.98. The second type of cluster combined varieties and breeding numbers of Kazakh selection and five varieties of foreign selection with the similarity quotient of 0.47-0.93.

Studied competitive variety testing (CVT) oat accessions of the forage crops department, the Kazakh Research Institute of Agriculture and Plant Growing (KazRIAPG) by the method of spectral sensing to identify more productive oat accessions. Two genotypes 50/98-12 and 06/03-1 are distinguished with the maximum value in all phases of plant development. The minimum level of biomass accumulation was noted for 23/04-6 and 39/98-12-7 genotypes. The maximum biomass accumulation during the vegetation by two genotypes 50/98-12 and 06/03-1 coincide with grain yield  $7,0 \pm 1,2$  t/ha and  $7,4 \pm 1,5$  t/ha, respectively, with respect to standards Kazakhstanskiy 70 with the yield of 6,3 t/ha. Two accessions 03/05-8 and 50/98-6 with the yield at the level of 6,8-6,9 t/ha, respectively, have a certain interest on productivity.

18 purely lines was allocated (uniform) in Kazakhstan breeding genotypes. They were researched in comparison with a UK collection (Wales) on productivity, NDVI and quality in the north of the Kazakhstan Republic (Karabalyk).

On productivity once again were highlighted the numbers 06/03-1 > 2448 > 30/05-02 with maximum harvest; protein content 06/03-1 (15.0%) and 30/05-2 (14.9%); genotype 06/03-1- distinguished with the highest starch content 57.1% (average for the block 55.2%) and 10.3% amylose.

The maximum content of fat indicated for cultivars Alaman (8.2%), Pegas (8.1%), and breeding number 26 / 05-6, which is also characterized by a maximum value of  $\beta$ -glucan content in grain (5,7-5,9 %), the content of Fe, Mg and P (iron, magnesium, and phosphorus).

# Identification of *Ppd* loci affecting photoperiod response in oat RILs developed from the cross of Chihuahua and Anatolisher varieties\*

Elizaveta Grigoreva, Pavel Ulianich, Vladimir Koshkin,  
Igor Loskutov, Elena Potokina

N.I.Vavilov Institute of Plant Genetic Resources (VIR)  
E-mail: [e.potokina@vir.nw.ru](mailto:e.potokina@vir.nw.ru)

**Keywords:** *oat, photoperiod response, recombinant inbred lines, SNPs*

Besides the large collections of plant genetic resources the VIR genebank accumulates some valuable research material (e.g. Recombinant Inbred Lines, Near Isogenic Lines, hybrid populations) that were created at VIR for many crop species during last two decades and now are accessible for molecular analysis. The created research material could serve as a tool for discovering new valuable alleles since it was singled out by screening of the large worldwide plant germplasm collection.

For hexaploid oats (*Avena sativa* L.) the genes that underlying photoperiodic response (*Ppd*) have not been identified, although the ability to create early-maturing varieties with a weak photoperiodic sensitivity is of great value to domestic breeders. In the most cases the oat varieties with low sensitivity to photoperiod are early maturing. Such oat varieties are required in many regions of Russia, since dominant *Ppd* alleles may affect oat drought tolerance by early flowering allowing escaping high summer temperatures.

In 2007-2009 more than 150 oat accessions from 23 countries were explored for their photoperiod sensitivity in the Pushkin experimental station of VIR (St. Petersburg) (Smirnova, 2011). As a result, 29 valuable oat genotypes with low photoperiod sensitivity were discovered. Among them, cv. Chihuahua (VIR-12230, Mexico) was chosen as a parent to develop oats RILs differing in their photoperiod sensitivity (Koshkin et al., 2013). The parental oat genotypes were contrast in their photoperiod response: for cv. Chihuahua (VIR-12230, Mexico) heading date was recorded 10 days later in short day (SD) conditions comparing to long day (LD); another parent cv. Anatolisher VIR-14668, Turkey) showed heading date 33 days later in SD comparing to LD. As a result of the parents cross followed by self-pollination of progeny during eight generations five RILs were developed: two lines with photoperiod sensitivity as the Chihuahua parent; one line was like Anatolisher parent; two lines were in between.

We employed the developed oat RILs to discover the genetic loci that underlie their difference in photoperiod sensitivity. The oat RILs were grown under conditions of the long (16h) and short (12h) photoperiod, their differences in heading date were recorded. Leaves of the seedlings were collected and a total DNA from each line were

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isolated. For the oat *Ppd* gene identification sequences related to the *Ppd-A1*, *Ppd-B1*, *Ppd-D1* genes in wheat, *Ppd-H1* in barley and other grass species were obtained from GenBank NCBI. An alignments containing genomic sequences from wheat, barley, *Brachypodium* and *Lolium* were produced. Primers anchored in conserved coding regions were designed; PCR products were obtained and subjected to sequencing. The task is to detect any possible SNPs and indels in the target sequences to reveal the causative polymorphism that may underlie the difference in photoperiod sensitivity between the oat RILs.

# Incorporating genotype-by-environment and genomic information into oat breeding programs

Lucia Gutierrez

Department of Agronomy, University of Wisconsin – Madison, 1575 Linden Dr., Madison, WI 53706, USA.  
E-mail: [gutierrezcha@wisc.edu](mailto:gutierrezcha@wisc.edu)

**Keywords:** *oat, genomic selection, genotype by environment Interaction*

Since the advent of agriculture, plant breeding has successfully improved plants for human benefit (Allard 1960; Fehr 1984; Hallauer and Miranda Filho 1988). Modern plant breeding activities consists in evaluating the genetic merit of lines discerning genetic from environment and noise components. To do so, we rely on the genetics foundations derived from Mendel's work and statistical tools (or biometry) generated afterwards (Sprague and Dudley 1988; Lamkey and Lee 2006). Plant breeding activities could be therefore grouped in three categories: traditional, marker assisted (MAS; Tanksley, 1983), and genomic selection (GS; Meuwissen et al. 2001). Traditional plant breeding uses either *per se* phenotypic information, or information from relatives to evaluate their genetic value (Fehr, 1984; Bernardo, 2010). On the other hand, MAS involve the identification of markers linked to genes or quantitative traits loci (QTL) of relevant traits, and then selecting individuals based on their marker scores (Tanksley, 1993; Hospital and Charcosset, 1997). Finally, GS, involves the prediction of the genetic merit of individuals based on their marker scores and a statistical model (Meuwissen et al. 2001; de los Campos, 2012). All of the three strategies require the evaluation of large number of individuals creating massive amounts of data that needs proper analyses.

Furthermore, some of the most relevant traits for agricultural like yield, grain quality and some diseases are quantitative traits that are affected by the environment. Therefore, making phenotyping is crucial in any plant breeding activity. This creates two challenges. First, field trials and experimental designs for large number of genotypes should be carefully chosen to reduce spatial heterogeneity and experimental error and to increase heritability. Second, genotype by Environment Interaction (GEI) is widespread in plants, and affect especially quantitative traits that are of main importance for plant breeding (Mathews et al., 2008). Mixed models have been used for modeling GEI and QTLxEnvironment Interaction (Piepho 2000; Verbyla et al., 2003; Malosetti et al., 2004; van Eeuwijk et al., 2005; Mathews et al., 2008).

Our objective was to present some strategies that are successfully being used in plant breeding programs. We discuss the use of genomic information for genomic selection, and then we discuss how to handle genotype-by-environment interaction with and without genomic information.

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# Screening *Avena ventricosa* populations in Cyprus for the presence of $2n$ gametes

Nikolaos Nikoloudakis<sup>1</sup>, Angelos Kyratzis<sup>2</sup>, Andreas Katsiotis<sup>1</sup>

<sup>1</sup>Cyprus University of Technology, Department of Agricultural Science, Biotechnology and Food Science, Limassol, Cyprus

<sup>2</sup>Agricultural Research Institute, Genebank, Nicosia, Cyprus  
E-mail: [andreas.katsiotis@cut.ac.cy](mailto:andreas.katsiotis@cut.ac.cy)

**Keywords:** *oat, Avena wild species, genomes, Cyprus*

Polyploidy is among the most important evolutionary processes in higher plants, since more than 35% of the plant species possess multiple complements of the basic chromosome number of their genus. Genus *Avena* consists of diploid species either with the AA or the CC genome, tetraploid species either with the AABB or the AACC genomes, and hexaploid species with the AACCCDD genome. The main modes of polyploidization are (i) the somatic chromosome doubling (a rare event in nature) and (ii) the sexual polyploidization through the formation and action of functional  $2n$  gametes (Harlan and DeWet, 1975). Polyploid gamete development in *Avena* has been reported for *A. wiestii* –  $A_s A_s$  genome (Ellison, 1937) and *A. vaviloviana* – AABB genomes (Katsiotis and Forsberg, 1995a), but none of these two species contributed to the evolution of the hexaploids (Nikoloudakis *et. al*, 2008). The most predominant C genome donor to the hexaploids, based on cytogenetic and molecular data, is *A. ventricosa*, serving as the male parent (Nikoloudakis and Katsiotis, 2008). A large number of *A. ventricosa* plants collected in Cyprus were screened for the production of  $2n$  gametes. As a fast method of screening and identifying promising genotypes, a flow cytometer was used to detect 2C pollen grain nuclei. Entries that were found to contain more than a single peak were further analyzed under the microscope. Size of pollen grains is correlated to the ploidy level of the pollen (Katsiotis and Forsberg, 1995b), and the above mentioned entries were found to contain at a 1% frequency such large pollen grains. Cytogenetic analysis of entries containing large pollen grains remains to be performed in order to identify the mechanism of the  $2n$  pollen formation. The importance of the  $2n$  gametes goes beyond evolutionary studies and can contribute in applied breeding programs (Dewitte *et. al*, 2012).

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# Assessing the genetic diversity of *Avena ventricosa* populations in Cyprus using molecular markers

Stella Konstantinou<sup>1</sup>, Nikolaos Nikoloudakis<sup>1</sup>, Angelos Kyratzis<sup>2</sup>, Andreas Katsiotis<sup>1</sup>

<sup>1</sup>Cyprus University of Technology, Department of Agricultural Science, Biotechnology and Food Science, Limassol, Cyprus

<sup>2</sup>Agricultural Research Institute, Genebank, Nicosia, Cyprus  
E-mail: [andreas.katsiotis@cut.ac.cy](mailto:andreas.katsiotis@cut.ac.cy)

**Keywords:** *oat, Avena wild species, population, AFLP*

The genus *Avena* consists of diploid ( $2n=2x=14$ , A and C genome), tetraploid ( $2n=4x=28$ , AB and AC genomes), and hexaploid ( $2n=6x=42$ , ACD genome) species. The major cultivated species belong to the hexaploids *A. sativa* and *A. byzantina*, having the AACCCDD genomic designation. During the last decades a number of diploid species have been proposed to contribute to the evolution of the hexaploid species. Based on cytogenetic and molecular data (Nikoloudakis and Katsiotis, 2008), the most predominant C genome donor for the hexaploids is considered *A. ventricosa*. This species has limited distribution and it is native to Algeria (Oran), Azerbaidzhan (Baku), Morocco, and Cyprus (Baum, 1977). Limited number of accessions are available through genebanks (Loskutov and Rines, 2011), and most of them originate from Cyprus, mainly because in 2008 a survey of this species was conducted and a number of populations were collected (Katsiotis and Ladizinsky, 2012). In the present study 69 individual plants from six different populations collected throughout Cyprus were used. In order to assess the genetic diversity of these populations molecular markers have been utilized. Initially ten SSR primer pairs were used, providing little genetic variability between the accessions, thus AFLPs were used. After screening 56 AFLP primer pairs, four combinations were selected, i.e. *EcoRI*-ACT / *MseI*-CAA, *EcoRI*-ACT / *MseI*-CAC, *EcoRI*-ACA / *MseI*-CAT, and *EcoRI*-ACA / *MseI*-CAC. The *EcoRI* primer was fluorescently labelled and the PCR products were separated in a Genetic Analyser. The total number of bands were 260 (ranging from 57 to 73), from which 96 in total were polymorphic (ranging from 15 to 35). Based on the polymorphic peaks intra- and inter-population diversity was calculated. Furthermore, a dendrogram indicating the relationships among the accessions was also constructed.

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# Genetic and molecular identification of genes required for multiflorous spikelet development in oat

Itamar Cristiano Nava, Cristiano Mathias Zimmer, Itacir de Pierri Ubert,  
Marcelo Teixeira Pacheco, Luiz Carlos Federizzi

Department of Crop Science, Federal University of Rio Grande do Sul (UFRGS),  
Av. Bento Gonçalves, 7712, P.O. Box 15100, Porto Alegre, RS, 91501-970, Brazil.  
E-mail: [itamar.nava@ufrgs.br](mailto:itamar.nava@ufrgs.br)

**Keywords:** *AP2 family genes, indeterminate spikelets, naked oat (Avena sativa subsp. nudisativa), microRNA, SNP markers, quantitative trait loci (QTL)*

The development of multiflorous spikelet is directly associated with the production of naked grains in oats. Genetic and evolutionary mechanisms underlying the formation of multiflorous spikelet in hexaploid oat are not yet fully understood. In several grass species including wheat, barley, rice and maize, genes from the family APETALA2 encoding transcription factors are required for multiflorous spikelet development. Other genes, such as *Vernalization1* (*Vrn1*) and *AGAMOUS-LIKE6* (*AGL6*) can also play an important role in the formation of multiflorous spikelet. *APETALA2* (*AP2*), *Vrn1*, and *AGL6* belong to the ABCDE model of flowering genes and are responsible for the differentiation of floral parts into their characteristic structures and the determination of floral meristem identity. The objectives of this study were to evaluate phenotypically the formation of multiflorous spikelet in oat, to determine the number of genes controlling the trait, to clone regions of candidate loci associated with multiflorous spikelet in oat using sequence information from other grass species, and to identify markers linked to QTL that affect the development of multiflorous spikelet in oat. Two genetic populations of recombinant inbred lines (RILs) developed from the crosses ‘UFRGS 01B7114-1-3 x UFRGS 006013-1’ and ‘URS Taura x UFRGS 017004-2’ were analyzed in this study. The parents UFRGS 01B7114-1-3 and URS Taura are hulled lines presenting panicles with normal spikelet, whereas the parents UFRGS 017004-2 and UFRGS 006013-1 are naked lines presenting panicles with multiflorous spikelet. Parents and RILs from both crosses were evaluated under field conditions in 2013 and in two sowing dates, early and late, in 2014. The expression of multiflorous spikelet was evaluated based on individual whole panicles for each parental line and RIL. Lines showing a determinate growth pattern, with two to three fertile florets per spikelet and grains adhered to well-lignified lemma and palea were grouped as ‘normal spikelet’. Conversely, lines showing an indeterminate growth pattern, varying from four to eight fertile florets per spikelet, elongated rachilla, and grains coated with soft glumes were grouped as ‘multiflorous spikelet’. Lines showing variable expressivity for the trait, with variable number of florets, and with hulled and naked grains in the same spikelet were grouped as ‘mosaic spikelet’. A genetic hypothesis of a single gene controlling the formation of multiflorous spikelet was tested for both genetic populations in the evaluated years and sowing dates. Oat genomic sequences corresponding to the *AP2*, *Vrn1*, and *AGL6* genes were amplified in the parents URS Taura and UFRGS 017004-2, using specific primer pairs developed from multiple alignments. Amplified fragments with the expected



size for each primer pair were cloned and sequenced. In silico analysis were conducted in order to identify genetic polymorphisms among the isolated oat sequences. Parents and RILs of both populations were assayed with 6,000 genome-wide SNP markers. A genetic linkage map for each population was generated using the program JoinMap 4. QTL affecting the formation of multiflorous spikelet were detected by simple interval mapping using the program MQTL. The development of multiflorous spikelet was similar for both populations evaluated in 2013 and 2014. An increased percentage on formation of multiflorous spikelet was observed in the late sowing date in 2014, and this pattern was quite similar for both populations. The increase in the number of multiflorous spikelet may be associated with changes in environmental conditions occurred between the sowing dates. In the late sowing date, higher mean daily maximum temperatures were recorded compared to the early sowing date. Besides variation in temperature, day-lengths were also higher throughout the stages of plant development in the late sowing date. Based on these results, an essential aspect to be noted is that under higher temperature and day-length conditions, as occurred in the late sowing date, variable expressivity of the multiflorous spikelet trait was less pronounced among the evaluated lines for both populations. This phenomenon was demonstrated by the relatively large number of lines expressing 100% multiflorous spikelet in the late sowing date. Genetic analysis revealed the action of a single/major gene controlling the expression of multiflorous spikelet development, regardless of the population, year, and sowing date. Cloned oat sequences corresponding to the *Vrn1* gene revealed the occurrence of a genetic polymorphism in the fourth exon between the parents URS Taura and UFRGS 017004-2. The identified polymorphism altered the amino acid sequence between the parents, suggesting that the *Vrn1* gene may control an important step in the formation of multiflorous spikelet in oat. In this study, we report the first oat cloned sequences corresponding to the *AP2* gene. Sequences isolated from URS Taura and UFRGS 017004-2 showed high nucleotide similarity between them. BLAST analyses of these sequences showed a high nucleotide similarity to *AP2* gene from *Brachypodium distachyon*. Oat sequences for the *AP2* gene showed nucleotide similarity to a non-coding microRNA (miRNA) gene, *miR172a*, from *B. distachyon*. This miRNA regulates the expression of the *AP2* gene in post-transcriptional level and, consequently, regulates the transition between developmental stages and specifies floral organ identity in several grass species. These findings indicate that the expression of multiflorous spikelet trait in oat may be under epigenetic control. Protein modelling demonstrates distinct structural motifs between the predicted polypeptide of each parental line for the *AP2* gene. Sequences derived from the *AGL6*-based primers were also amplified in oat. BLAST analyses of these sequences showed similarity to *AGL6* gene from *Avena strigosa*, *Hordeum vulgare*, *B. distachyon*, *Triticum monococcum* and *Lolium temulentum*. A QTL affecting multiflorous spikelet was detected in both mapping populations, explaining a large fraction of the observed phenotypic variation. Assisted selection using the major QTL identified in this study would provide an efficient strategy for selecting oat plants with a proper genetic constitution for the trait. In this way, marker assisted selection could facilitate the identification of oat genotypes with constant expressivity for multiflorous spikelet. Further studies will confirm the potential of use this QTL in oat breeding programs.

# DArTseq markers towards *Dw7* dwarfing gene in oats

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

<sup>1</sup>University of Life Sciences in Lublin, Institute of Plant Genetics, Breeding and Biotechnology,  
Akademicka Str 15, 20-950 Lublin, Poland

<sup>2</sup>Plant Breeding and Acclimatization Institute – NRI, Radzików, 05-870 Błonie, Poland  
E-mail: [edyta.paczos@up.lublin.pl](mailto:edyta.paczos@up.lublin.pl)

**Keywords:** *dwarf mutant, plant height, DArTseq markers*

Oat (*Avena sativa* L.) has an economically relatively small importance, but is ecologically valuable agricultural crops. It enables the reliable production of feed, food and agricultural biomass even on poor soils. The improvement of lodging resistance is one of the primary breeding goals in the species. Lodging diminishes efficient plant vegetation and exhibits detrimental effects on seed and straw quality. Lodging could be prevented via application of retardants. However, due to lack of sufficient studies and a distinct reaction of oat varieties, retardants are usually not recommended. The key genetic approach to overcome lodging is the reduction of plant height by an introduction of dwarfing genes. Although eight dwarfing genes have been reported in oat, only *Dw6*, *Dw7*, and *Dw8* are readily available where *Dw6* and *Dw8* are dominant, and *Dw7* is partially dominant one. Only *Dw6* and *Dw7* have been used in cultivar development.

The primary aim of the study was to search for new, putatively codominant molecular markers closely linked to *Dw7* locus using DArTseq approach. Such markers, after conversion to convenient PCR, could be used in marker-assisted selection (MAS), as an alternative to phenotyping allowing progeny testing and distinguishing homozygotes and heterozygotes for short straw.

The research material consisted of 200 individuals of the  $F_2$  biparental oat mapping population obtained from the crossing of normal height Polish oat cultivar ‘Bingo’ and dwarf line NC 2469-3 (C.I. 8447). The NC 2469-3 is a line derived from the dwarf mutant identified in the progeny of cross ‘Carolee’ x ‘Fulgrain’. Plants representing this line have very short, stiff straw and a compact panicle. The plant height reduction resulted from a decrease in the number of internodes as well as internodes’ length.

The height all of the  $F_2$  plants were measured. The observed segregation was consistent with monogenic inheritance model. To discriminate between homozygotes and heterozygotes for short straw 50  $F_3$  seeds from each self-pollinated  $F_2$  individual were sown and the height of the plants was measured. Random sample of 140 plants and parental forms were genotyped using DArTseq technology.

Among  $F_2$  plants for which DArTseq analysis was performed homozygous dominant (*Dw7Dw7*) and homozygous recessive (*dw7dw7*), individuals were identified (based on  $F_3$  individuals). DArTseq sequences were selected based on segregation mapping studies and the analysis of the compatibility of DArTseq markers segregation with genotype defined by phenotype were performed. Out of 11784 SNP markers, only 50 DArTseq sequences were selected with segregation corresponding to individ-



ual plants phenotypes. Unfortunately, a perfect correlation was not found in any case. Fifteen DArTseq sequences were selected for conversion to specific PCR. Only one marker proved to be polymorphic on DNAs of short and high F<sub>2</sub> plants. It segregated as a dominant marker, so it is not suitable to distinguish dominant homozygous from heterozygous.

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# Genetic diversity of oat accessions from different countries revealed by SSR markers

Zongwen Zhang<sup>1,2</sup>, Yarvaan Munkhtoya<sup>1,3</sup>, Bin Wu<sup>1</sup>, Qian Zhang<sup>1</sup>

<sup>1</sup>Institute of Crop Science of Chinese Academy of Agricultural Sciences, Beijing 100081, China

<sup>2</sup>Bioversity International, China Office, Beijing 100081, China

<sup>3</sup>Plant Science and Agricultural Research Institute, Darkhan, Mongolia

E-mail: [zhangzongwen@caas.cn](mailto:zhangzongwen@caas.cn)

***Keywords:*** oat accessions; SSR markers; genetic diversity; genetic relation

Oat is a cereal crop widely used for human food and animal feed in the world. A total of 286 oat accessions from four countries, namely Canada, China, Mongolia and USA were arrayed with 83 polymorphic SSR primers in this study. The statistics showed that each SSR locus had a minimum of 2 to a maximum of 8 marker alleles, with average of 3.494 among all the accessions. The allele frequencies of all the population ranged from 0.0035 to 0.9860, averaged 0.4482. The PIC values ranged from 0.0734 to 0.9521, and averaged 0.7012, which indicated the high levels of genetic diversity existing among all the oat populations. The gene diversity computed over all marker loci and accessions was averaged 0.7344, and ranged from a minimum of 0.0747 to a maximum of 0.9540. The Principal coordinate Analysis showed that the first component was positively associated with the accessions from USA and Canada, and negatively associated with accessions from China and Mongolia. The second component was clearly able to discriminate the accession from Canada and those from China and Mongolia. The cluster analysis was based on genetic distances in all possible pair-wise comparisons among the 286 accessions. The hierarchical tree of all the accessions revealed further separation of oat accessions into 6 groups. Accessions from USA were clustered into 3 groups with 1 group including few accessions from Canada. The accessions from Mongolia clearly formed an individual group. The other 2 groups are dominated by Canadian and Chinese accessions, separately. The tree was constructed for the sources of accessions showed a close relation between accessions from Canada and China. Mongolian accessions are most distinct from others. The genetic structure of all the oat accession also gave a similar picture to the cluster analysis.



# **POSTER SESSION**

**Physiology, Pest,  
Disease Resistance**

## POSTER PRESENTATIONS

### Deoxynivalenol in oats from fields in Slovakia during 2013 and 2014

Peter Hozlár<sup>1</sup>, Svetlana Šliková<sup>2</sup>, Sona Gavurníková<sup>2</sup>,  
Martina Mináriková<sup>3</sup>, Edita Gregová<sup>2</sup>

<sup>1</sup>National Agriculture and Food Centre, Research Institute of Plant Production,  
Research and Breeding Station Víglaš-Pstruša 334, 962 12 Detva, Slovak Republic;

<sup>2</sup>National Agriculture and Food Centre, Research Institute of Plant Production,  
Bratislavská cesta 122, 921 68 Piešťany, Slovak Republic;

<sup>3</sup>Department of Theoretical Geodesy, Slovak University of Technology,  
Radlinského 11, 813 68 Bratislava, Slovak Republic

E-mail: [slikova@vurv.sk](mailto:slikova@vurv.sk)

**Keywords:** oat, *FHB*, mycotoxins, *ELISA*, Slovakia

Mycotoxin deoxynivalenol (DON) is formed by different *Fusarium* species infecting the grains already during growth in the field. It is one of the most prevalent mycotoxins in food and feed (EFSA 2013). The main producers of DON are *Fusarium graminearum* and *Fusarium culmorum*. In the Slovak Republic (SR), the data about the occurrence of genus *Fusarium* on oats is not known as much as in wheat where *F. graminearum* Schwabe and *F. culmorum* (W. G. Sm.) Sacc. are the most common. However, *F. poae* or *F. graminearum* have been predominating in the past few years what was connected with climatic conditions (Sudyova and Slikova, 2011). The presence of several *Fusarium* species and their toxins in oat kernels was confirmed by many studies (Gavrilova et al. 2009; Fredlund et al. 2013). DON was found in oat kernels and derived products (EFSA 2013), and its presence is usually a good indicator that other mycotoxins are also present. In the Slovak Republic (SR), the data about the occurrence of genus *Fusarium* and mycotoxins on oats are not known, but survey of these in wheat samples (Slikova et al. 2013) showed that in some years there were very favourable conditions for the development of *Fusarium* head blight in cereals.

The samples of oat grains were obtained during the 2013 and 2014 growing seasons and were collected directly from growers from 18 fields in Slovakia. The incremental samples were mixed and put in paper bags and stored in a cool place (cca. 2000 g). A commercial ELISA kit was used to determine the DON concentration in samples with the limit of detection < 0.2 mg.kg<sup>-1</sup> (ppm) and limit of quantification 0.2 mg.kg<sup>-1</sup> (ppm). The occurrence of samples with DON was 30 % in 2013, with maximum DON content of 0.49 mg.kg<sup>-1</sup>, and 40 % in 2014, with maximum DON content of 0.60 mg.kg<sup>-1</sup>. The limit of 1.75 mg.kg<sup>-1</sup> imposed by the European Union (EU) (setting maximum levels for certain contaminants in foodstuffs by EC No 1881/2006) for DON content was not exceeded in the studied samples. The present results indicated that DON content was at a low level in grains from oats grown during 2013 and 2014.

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# The screening of wild *Avena* species of VIR collection in aluminium tolerance\*

Kosareva I.A.<sup>a</sup>, Blinova E.V.<sup>a</sup>, Bagmet L.V.<sup>a</sup>, Loskutov I.G.<sup>a,b</sup>

<sup>a</sup>N.I. Vavilov Institute of Plant Genetic Resources (VIR), 44 Bolshaya Morskaya str., St-Petersburg, Russia

<sup>b</sup>St-Petersburg State University, 7-9 Universitetskaya emb., St-Petersburg, Russia

E-mail: [irkos2004@yandex.ru](mailto:irkos2004@yandex.ru)

**Keywords:** *aluminium tolerance, Avena wild species, types of soils*

The response of species and genotypes of agricultural plants to soil pH differs and influences the general adaptability of plants. Unfavorable edaphic conditions related to an increased soil acidity and accumulation of toxic aluminium ions are among the limiting environmental factors for productivity of cultivated plants.

One hundred and eighty accessions of nine diploid (43 accessions), six tetraploid (57 accessions) and four hexaploid (80 accessions) wild oat species of different geographical origin were selected for comprehensive field trials which were conducted at the Pushkin Branch of VIR in 2010-2014 together with seed multiplication.

The aluminum tolerance laboratory screening of accessions was performed in the climatic chamber with the controlled daylength and temperature. The aluminum tolerance in cereals was evaluated using the technique developed by A. Aniol (1991b) and modified at VIR (Kosareva and Semenova, 2005). The technique is based on the staining of the aluminum damaged root regions with Eriochrome cyanine R and evaluation of the capability of the plants to restore mitotic activity in roots affected by the mobile aluminum.

The evaluation of genetic diversity of Al tolerance at the species level has shown that the diploid (*A. ventricosa*, *A. clauda*, *A. pilosa*) and tetraploid (*A. magna*, *A. murphyi*, *A. insularis*) species with the C genome were less tolerant than the accessions with a different genomic composition. Wild *Avena* species accessions with a high degree of Al tolerance (on standard level) belonged to the diploids *A. canariensis* from the Canaries (Spain), *A. longiglumis* from Morocco and *A. wiestii* from Egypt, tetraploids *A. barbata* from Azerbaijan, Israel, Tunisia, Turkey and Iran, *A. vaviloviana* from Ethiopia, and hexaploids *A. ludoviciana* from Afghanistan and Ethiopia, *A. sterilis* from Israel, Iraq, Iran, Morocco, Syria, Turkey and Ethiopia.

The comparison of the data on Al tolerance with those on soil conditions has shown that most highly tolerance accessions tend to be collected on mountain cinnamon, chestnut, or mountain forest brown soils. According to the results of the principal component analysis, preliminary screening for Al tolerance can be carried out among hexaploid species with higher degree of plant resistance to pathogens. A search for such wild *Avena* species forms can be carried out in Portugal, Spain and the Canaries, Italy, Azerbaijan, Turkmenistan, Syria, Iraq, Israel, Algeria, Morocco, Tunisia and Ethiopia taking soil differences into account.

# Development of oat lines differing in the genes of photoperiod sensitivity

V.A. Koshkin, I.G. Loskutov, I.I. Matvienko, E.V. Blinova

Federal Research Center – The N.I. Vavilov All-Russian Institute of Plant Genetic Resources,  
St. Petersburg, Russia

E-mail: [koshkin-va@mail.ru](mailto:koshkin-va@mail.ru)

***Keywords:*** oat, photoperiod sensitivity, lines, hybrids

Most of the oat crops in Russia are located in the areas with unfavorable climatic conditions. For these regions, with their short growing season, early-ripening varieties are required. Growth and development processes in early forms are more intense than in late ones, so the duration of their growing period is shorter. Early maturation is a dominant trait if compared with lateness. The total duration of the growing season depends on the lengths of individual interphase periods: germination – ear emergence and ear emergence – ripening. Weak photoperiod sensitivity (PPS) is controlled by the dominant Ppd genes, while the strong one by the recessive rpd [1, 2]. In the hexaploid oat variety Donald PPS is weak due to one dominant gene Di-1 [3]. In most cases, oat varieties with weak PPS are earliness and therefore of great value to many regions of Russia [4, 5].

In 2007, a cross between the weakly photoperiod-sensitive Mexican variety Chihuahua (Mexico) and highly sensitive cultivar Anatolischer (Turkey) was carried out. The hybrids obtained were tested for photoperiod sensitivity. Under the conditions of a short 12-hour day, from the F<sub>2</sub> hybrid population (Chihuahua x Anatolischer) the most early-ripening weakly photoperiod-sensitive plants as well as the most late-ripening photoperiod-sensitive ones were selected. Selection was performed in a manner that allows you to simultaneously isolate such forms [6]. We selected two early-maturing weakly sensitive lines (VIR-15547, Skorospelyi 1, VIR-15548, Skorospelyi 2), two lines with medium sensitivity (VIR-15549, Srednespelyi 1, VIR-15550, Srednespelyi 2), and a late-ripening highly sensitive line (VIR-15551, Pozdnespelyi), differing in photoperiod sensitivity genes.

Experiments on photoperiodic reaction of plants were carried out in the vegetation and photoperiod testing pavilions at the Plant Physiology Department of the Pushkin Branch of VIR (2010-2015) as well as in the field (2014-2015).

Plants were grown on soddy podzolic soil in plastic 5-liter pots under the natural long (17 h 30 – 18 h 52 min) and short (12 h) photoperiod conditions. Short day (SD) was attained by rolling trolley platforms with pots into an opaque photoperiod testing pavilion where they were kept from 9 PM until 9 AM. Long-day plants (LD) were rolled for the same period of time into a glasshouse. PPS was measured according to the delay of ear emergence in SD plants as compared with the LD plants ( $T_2 - T_1$ ) and with the

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help of the PPS coefficient proposed by us ( $C_{PPS}$ ) which is calculated according to the formula ( $C_{PPS} = T_2 / T_1$ ) where  $T_1$  and  $T_2$  mark the duration of the germination – ear emergence phase of oat plants (days) grown respectively under long natural and short 12-hour days [7].

For five years (2011-2015), weakly sensitive early lines 1 and 2 showed a slight delay under the short-day conditions if compared with the long day and had a low  $C_{PPS}$  (1.25 and 1.31), while the medium-ripening sensitive lines 1 and 2 significantly delayed their development under the short day and had a higher  $C_{PPS}$  (1.53 and 1.55). The highest  $C_{PPS}$  (1.84) was observed in the late line.

All lines of oat under the short 12-hour day, if compared with LD, increased their dry weight, length and number of spikelets on the main panicle, whereas the upper internode was shorter. These indicators are influenced by photoperiod and other environmental factors.

In the early lines weakly sensitive to photoperiod the number of grains, grain weight on the panicle, plant weight and economic coefficient ( $C_{ECON}$ ) increased under SD if compared with LD, while in the medium- and late-ripening ones these parameters significantly decreased. Such symptoms are influenced by the genes of photoperiod sensitivity. In weakly sensitive early lines, this effect is produced by dominant alleles of the PPS genes, while in the highly sensitive late line by recessive alleles of the PPS genes.

The greatest differences under the long- and short-day conditions were observed in the late line (VIR-15551, Pozdnespelyi) and the parent form Anatolischer with high PPS. Under the short photoperiod, when compared with the long one, these forms significantly increased the following indicators: the germination – ear emergence phase duration; main stem height; number of main stem nodes; axil length of the flag leaf; dry weight of the plant; panicle length; number of spikelets per panicle. However, other indicators (number of grains and grain weight on the main stem's panicle; weight of 1000 grains;  $C_{ECON}$ ) declined.

Thus, we have developed early-ripening weakly photoperiod-sensitive forms and medium-ripening medium-sensitive ones with dominant alleles of the PPS genes which can be used in oat breeding for earliness without the loss of productivity in new cultivars for different regions of Russia.

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# Main diseases of oats under conditions of the Republic of Belarus

Natalia Poplavskaya, Svetlana Buga, Alexander Zhukovsky

RUC «Institute of plant protection», Priluki, Belarus

E-mail: [n-poplavskaya@list.ru](mailto:n-poplavskaya@list.ru)

**Keywords:** *oat, diseases resistance, Fusarium root rot*

In the Republic of Belarus oats is cultivated on an area of about 146.4 thousand hectares, which is approximately 5.0 % of the sown area of grain crops. In «The State register of varieties» for 2015 17 varieties are included. The average yield of oats in the country is about 3.6 t/ha, in the system of variety trials – 8.5 t/ha.

In oat crops, the most common fungi are *Fusarium* spp., *Drechslera avenae* (Eidam) Scharif, *Puccinia coronifera* Khleb., *Septoria avenae* A. B. Frank, *Ustilago avenae* (Pers.) Rostr, rarely *Scolecotrichum graminis* Fuckel. and *Ascochyta avenae* (Petr.) R. Sprague & Aar. G. Johnson, causing plants damage and reducing crop yield.

The diseases development monitoring was carried out in 2012-2014 in crops of 5 oats varieties (Stralets, Zapavet, Zolak, Fax and Vandrounik), total area of cultivation of which in the Republic is 51.7 %. Studies have shown that the crop studied varieties were infected by red-brown spot, crown rust and root rot.

The oat crop is damaged by *Fusarium* root rot, causing browning of roots and subcrown internodes. The disease severity of root rot over the years studied have been in the range from 11.5 (cv Vandrounik) to 14.7 % (cv Stralets). *Fusarium culmorum* (W.G. Sm) Sacc., *Fusarium avenaceum* (Fr.) Sacc., *Fusarium graminearum* Schwabe, *Fusarium equiseti* (Corda) Sacc., *Fusarium oxysporum* Schltdl., *Fusarium sambucinum* Fuckel, *Fusarium solani* (Mart.) Sacc., *Fusarium poae* (Peck) Wollenw., *Fusarium semitectum* Berk. & Rav., *Fusarium dimerum* Penzigin Sacc., *Fusarium tricinctum* Corda Sacc. and *Gibberella fujikuroi* species complex were isolated from oat roots.

Helminthosporium leaf disease appears annually with different intensities. The first signs of plants infection were observed in crop varieties at the stage of formation 2-3 leaves (BBCH 12-13) in the form of oblong-elliptic or oblong spots of reddish-brown color, sometimes covering the entire lamina and moving to the leaf sheath. By the end of the growing season the disease severity in oat crops can reach 27.9 %.

In the later stages of development oat crops are susceptible to crown rust. The disease usually manifests itself on the leaves at panicles formation stage (BBCH 51-55) in the form of small, oval, yellow-orange pustules. In 2013, on oat crops cv Stralets an edification of the disease severity was noted – 63.0 % (BBCH 85-89). In other years the severity of crown rust was at depressed levels and did not exceed 10.0 %.

Oat panicles are annually affected by red-brown spot and *Fusarium* head blight. Helminthosporium is manifested at milk ripeness stage (BBCH 73). On the spikelet scales an indistinct oval spot is formed, reddish brown in color, with a dark border. For *Fusarium* head blight the hidden manifestations of the disease is characteristic, in which

signs of damage are absent. The intensity of oat panicle damage by red-brown blotch and Fusarium head blight ranges from 6.0 to 38.0 %.

Contamination of oats seeds by *Fusarium* spp. varied from 1.0 to 22.0 %, *Alternaria* spp. – 10.0-69.0 % and the fungus *Dr. avenae* – 5.0-20.0 %. The species composition of pathogens includes 7 species – *F. poae*, *Fusarium sporotrichioides* Sherb., *F. avenaceum*, *F. graminearum*, *F. oxysporum*, *F. culmorum* and *Gibberella fujikuroi* species complex. The fungus *F. poae* is the prevalent species in the pathogenic complex – its proportion makes on the average 62.5 %.

Thus, crops of oat varieties are susceptible to diseases during the whole period of vegetation with different intensity. The most strongly affected crops cv Stralets and Vandrounik (total index of infection by diseases complex is more than 60.0 %).

# Greenbug resistance in oat accessions from Asia

E.E. Radchenko, T.L. Kuznetsova, M.A. Chumakov, I.G. Loskutov

Federal Research Center the N.I. Vavilov All-Russian Institute of Plant Genetic Resources,  
B. Morskaya, 42, 44, St. Petersburg, 190000, Russia  
E-mail: [eugene\\_radchenko@rambler.ru](mailto:eugene_radchenko@rambler.ru)

**Keywords:** *oat, greenbug, resistance, accessions, landraces*

The greenbug *Schizaphis graminum* Rondani is an economically considerable pest of oat and other cereals in southern Russia. Plant breeding for resistance is the drastic and, at the same time, the cheapest and most ecologically safe method of protection from the aphid. The differential interaction with genotypes of the host plant characteristic for *S. graminum* necessitates expanding the genetic diversity of varieties being grown.

Only four oat genes for resistance to greenbug, which are effective against certain biotypes of the insect in the United States, are known. The resistance in the variety Russian 77 (CI 2898) to biotype A of the greenbug is conditioned by one dominant gene *Tg1* (Gardenhire, 1964). The study of resistance inheritance in three oat accessions to two greenbug biotypes demonstrated that PI 186270 and CI 1580 lines each carry one dominant gene (*Grb1* and *Grb2* accordingly) that determine resistance to the biotype C. The line CI 4888 is protected by the dominant gene *Grb3* of resistance to the biotype B. It was found that minor genes for greenbug biotypes reaction may be involved in all three accessions (Boozaya-Angoon et al., 1981). The *Grb2* gene for resistance is effective against biotypes E, I and, in part only, F–H biotypes. It is obvious that the existing stock of resistance genes is not enough for supplying present-day breeding programs.

Landraces of cultivated cereal species often have a high resistance to the pest. Earlier we have found a high frequency of greenbug resistant accessions among barley landraces from East and South Asian countries, and the most resistant to *S. graminum* sorghum forms originating from China. The goal of the present work was to evaluate the hereditary diversity of oats from Asian countries for greenbug resistance.

We studied the resistance of 371 oat accessions (landraces mostly) from Maritime Territory of Russian Federation, Mongolia, China, Japan, North Korea, India, Iran, Afghanistan, and Bhutan. Among these forms 35 were bare-grained oats presumably originated from China and Mongolia.

Experimental accessions and susceptible control (cultivar Borrus) were sown in plastic trays filled with a nonsterile mixture of soil, sand, and peat. Young plants were infested with aphids from Krasnodar population and when the control died, we determined the extent of damage of plants of each accession according to the scale from 0 (no damages) to 10 (91–100% of leaf area damaged, death of plants). Plants with scores 1–4 were assigned to resistant and those with 9–10 to susceptible. Accessions with distinctly expressed resistance were infested with Dagestan population of the aphid.

Clones with different virulence phenotypes (test clones) were used for investigation of the mode of greenbug resistance in some of the selected oat forms. The test clone method allows excluding in the investigated accession the resistance genes effective only against part of the aphid population. If at least one clone virulent to the tester of the given resistance gene damages the cultivar being studied, the cultivar doesn't have a functional allele of the given gene. The experimental accessions and susceptible control (Borrus) were planted in vessels with soil in a circular order and covered with glass isolator cages. In the two leaf stage, the seedlings were infested with aphids of one clone at a rate of five aphids per plant. Upon death of the control, we determined the extent of damage to plants of each accession according to the above mentioned scale.

The 95 accessions heterogeneous for resistance to Krasnodar greenbug population were found. The damage scores of resistant components among 47 accessions constituted 1-4, the moderate resistance (scores 5-7) was revealed in 48 forms being studied. The accessions from Mongolia (46 from the 76 studied or 60.5%), followed by the accessions from China (33.9%), India (19.0%) and Japan were distinguished. The largest number of genotypes (23) with the damage score of which did not exceed 4 value was selected among the accessions from Mongolia. All bare-grained oat accessions were susceptible to phytophage: plant damage was estimated by scores 9-10. For some accessions the wide plant variation in the score range 1-10 was characteristic that can be conditioned by the manifestation of the genes with low expressivity and (or) the presence of clones with varying virulence in the Krasnodar insect population. The majority of the selected forms contained plants resistant to Dagestan greenbug population however the level of the character expression in those plants was usually lower.

The resistant plants of seven accessions were brought to maturity, the seeds were multiplied, and the obtained lines were again estimated for resistance to the greenbug clones. We had 46 clones isolated from Krasnodar and 20 – from Dagestan insect populations. Moreover, in the experiments the accession CI 4888 (Italy) protected by the resistance gene *Grb3* was estimated. All the 66 clones were avirulent to the accession VIR-6688 (India), and frequencies of virulence to the accessions VIR-4074, VIR-12213 and VIR-12214 from Mongolia were very low (0.02, 0.04 and 0.02 correspondingly). Only one clone from the 46 analyzed damaged the accession CI 4888. A little more frequent the clones virulent to the accessions from Mongolia VIR-2490 (0.13) and VIR-2539 (0.28) occurred in the Krasnodar population. Clones severely injuring the accessions VIR-4074 and VIR-1221 were not revealed in the Dagestan population, the virulence to the accession VIR-6688 was very rare. The 30% of the clones in that population possessed virulence to the accessions VIR-12213 and VIR-2499, 50% of the clones heavily damaged the accession CI 4888 and 80% – the accession VIR-2539.

The 7 virulence phenotypes (biotypes) which differentially interact with oat genotypes were found in the Krasnodar population, with the biotype avirulent to all eight oat accessions was dominating (60.9%). In the smaller clone sample from the Dagestan population the 10 virulence phenotypes were revealed among which the phenotype heavily damaging the accession VIR-2539 was dominating (25%). A comparison of resistance of the experimental material to the test clones of *S. graminum* indicates that the

7 selected oat accessions are protected by different alleles of resistance genes which are non-identical to the earlier identified gene *Grb3*. It should be noted that oat accessions from Asian countries are probably protected by earlier unknown genes of phytophage resistance since the genes *Grb1* and *Grb2* were identified in landraces from Argentina and Scotland.

Thus, it was stated that:

- oat accessions resistant to greenbug occur with high frequency among landraces from Asia;

- North Caucasus populations of *S. graminum* significantly differ by the frequencies of virulence to host plant;

- oat accessions VIR-2490, VIR-2539, VIR-4074, VIR-12213, VIR-12214 (Mongolia), VIR-6688 (India) and VIR-13624 (North Korea) are protected by diverse alleles of resistance genes which differ from the earlier identified gene *Grb3*;

- the accession VIR-13624 is protected by the most effective gene (genes) of resistance to the insect populations from North Caucasus;

- the accessions VIR-6688, VIR-4074 and VIR-12214 possess high resistance to Krasnodar and Dagestan greenbug populations.



# Virulence of *Puccinia coronata* f.sp. *avenae* in Poland during 2013-2015

Sylwia Sowa, Edyta Paczos-Grzęda, Agnieszka Ostrowska

University of Life Sciences in Lublin, Institute of Plant Genetics, Breeding and Biotechnology,  
Akademicka Str 15, 20-934 Lublin, Poland

E-mail: [sylwia.rog@up.lublin.pl](mailto:sylwia.rog@up.lublin.pl)

**Keywords:** crown rust, host-pathogen test, resistance genes

Almost every region of oat growing can suffer losses caused by *Puccinia coronata* f. sp. *avenae*. Because of the favorable climatic conditions some regions are most likely to be exposed to the rust fungus. In Poland mild winters, late springs and wet summers support infection, that is why crown rust occurs every year causing high losses in yield and grain quality.

The best way to control crown rust is host genetic resistance. It is beneficial for economic reasons and helps to protect environment. Effectiveness of resistance genes varies because of the diversity of the pathogen populations. Constant evolution of the pathogen imposes monitoring of the crown rust virulence therefore objective of this work was to characterize the virulence of Polish isolates of *P. coronata* f. sp. *avenae* collected over 2013 to 2015.

Multiple samples of *P. coronata* used in the study were collected annually from oat flag leaf both random farm fields and field plots of Polish breeding companies in Poland. Virulence was studied on seedlings of 26 reference lines with different *Pc* genes by means of host-pathogen test under control temperature, humidity and lighting conditions. Assessment of leaf infection was performed using a 0 to 4 scale with ITs of 0 and 1 considered avirulent and 2, 3 and 4 as virulent.

The frequencies of virulence to the different *Pc* genes was relatively stable except for virulence to, *Pc58*, *Pc70* and *Pc103-1* which gradually increased over time, and *Pc59*, which was detected at low frequencies only in 2014 and undetected in 2013 and 2015. Resistance genes *Pc52*, *Pc71* and *Pc91* were the most efficient, although in 2015 resistance covered by *Pc52* and *Pc71* has been slightly overcome.

Due to the lack of resistant Polish oat cultivars virulence of crown rust population stays relatively stable and many sources of resistance are still effective against crown rust races occurring in Poland. However we can already observe overcoming of the most efficient *Pc* genes. To increase durability and broaden the spectrum of resistance it is advisable to cumulate the *Pc* genes in one cultivar and search for new ones in wild oat accessions.

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## Genetic sources of disease resistance in oats

S. V. Svirskova, A. V. Zaushintsena, A. A. Startsev

Kemerovo State University, 6, Krasnaya Str., Kemerovo 650043, Russia

E-mail: [svsvirkova@yandex.ru](mailto:svsvirkova@yandex.ru)

**Keywords:** *oat, disease resistance, yeald*

High and stable oat yields and ecological safety of products are difficult to achieve in Western Siberia due to the diseases that significantly affect cultivars. Along with the smut fungi (*Ustilago avenae* (Pers.) Jens. and *Ustilago kolleri* Wille.), oat is also affected with crown rust (*Puccinia coronata* Corda) and red-brown spottiness (*Drechslera avenae* Eidam.).

The yield of the diseased plants decreases strongly, or may be completely lost. The losses from smut and rust can amount from 10 to 30%, and up to 50% in case of an epidemics. According to the global agricultural information, the distribution of infectious disease agents in oats tends to increase noticeably. An important stage in achieving safe phytosanitary conditions ensuring high economic and ecological effect is the breeding and cultivation of the adapted, disease-resistant oat cultivars, hence is the priority of continuous search for new genetic sources of individual and complex immunity within the global collection of the N.I. Vavilov Institute of Plant Genetic Resources (VIR). Its role as a source of initial material for breeding cultivars with the required properties is high.

Research objective: a study of resistance of oat cultivars from the VIR global gene pool to harmful disease agents in the south of Western Siberia and identification of genetic sources of immunity.

The experimental work was carried out in the south of Western Siberia using natural and artificial infectious backgrounds. The soil was the leached chernozem, hard-loamy granulometrically. The formation of a smut fungi nursery, the recording and monitoring of other oat disease agents development followed the technique developed at VIR [1] and Methodological guidelines for studying barley and oat collections [2]. Six hundred oat cultivars from different countries of the world were studied. Their seeds were treated with a water suspension of *Ustilago avenae* (Pers.) Jens. teliospores.

Epidemics of *Ustilago avenae* (Pers.) Jens and *Ustilago kolleri* Wille in the south of Western Siberia were recorded by the Kemerovo Branch of the State Institution Ros-selkhoztsentr in 1981, 1986, 1990, 1994, 2001 and 2009. The presence of harmful races 40 and 41 in the population of semiloose smut of oat has been confirmed. Fifty-five percent of oat cultivars have been found to be highly resistant to semiloose smut. Among them are cvs. Omikho (Russia), Monarch (France), Scottish chief (Great Britain); OS-6 (India); AV 21/1, AV 17/3/10 (Japan); several cultivars from the USA, such as IL-85-64-67, Belle, Vista, Rodeo, Bentland, Brawn, Bond, Mindo, Benton, Markton, Gopher Oats, Navarro; CDC Baler (Canada); Wandering, Tagra, Toodyay, Numbat, Pallinup, and 69 Q 04 from Australia. Genetic sources of resistance to semiloose smut have been

identified among cultivars of Siberian origin, highly adaptive to local cultivation conditions: these are cvs. Zhuravlyonok, Otrada (Tyumen Province), Boets, Golets, Sayan (Krasnoyarsk Territory), as well as cvs. Mergen and Geser from the Republic of Buryatia.

The genetic sources for breeding smut-immune and highly productive oat cultivars are represented by cvs. Azur (Czech Republic), Navarro, Belle, Rodeo (USA), SDS Baler (Canada), and Pallinup (Australia). Many of them demonstrated high values of productivity elements, namely 422 to 768 productive stems per 1 m<sup>2</sup>, large grain (1000 grains weight of 33-38.5 g), a panicle with a large number of grains (36-78) and productivity at the standard cultivars level, or higher by 74-188 g/m<sup>2</sup>.

Epidemics of crown rust (*Puccinia coronata* Corda) were observed in 1983, 1988, 1996, 2001 and 2010, and cvs. Palini (Greece) and Brawn (USA) have been identified as genetic sources of immunity to the disease. Resistance was also displayed by cvs. Toodyay (Australia) and Vista (USA). Such tolerant cultivars as Azur from the Czech Republic, and Belle, Burt and Navarro from the USA may be used as promising breeding materials. Their productivity was 35-55% higher than that of the best standard cv. Phobos.

The cultivars Palini (Greece) and Brawn (USA) have been identified as genetic sources of complex immunity to semiloose smut and crown rust.

The mass development of symptoms of red-brown spottiness (*Drechslera avenae* Eidam.) on oat leaves across a considerable territory was recorded by the Kemerovo Branch of Rosselkhoztsentr in the south of Western Siberia in 1981, 1989, 1996 and 2003. An assessment under natural conditions has found such Russian cultivars as Drug, Lgovskiy 1026, Mirniy and Isetskiy, as well as cv. Maris Tabard from Great Britain, Astor from the Netherlands and a French cv. Multigrap to be resistant to the agent.

Resistance of oat plants to infectious diseases should be considered as a priority biological property when assessing initial material. Only immune cultivars can fully use the productivity potential and ensure high quality of grain. The genetic sources of resistance have been included in crosses aimed at producing new hybrid pool and selecting immune forms.

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# **Oat response to sowing date, applied nitrogen and plant density in the low rainfall region of Western Australia**

Georgie Troup<sup>1</sup>, Blakely Paynter<sup>1</sup>, Raj Malik<sup>2</sup>

<sup>1</sup>Department of Agriculture and Food, Western Australia, Northam, Australia

<sup>2</sup>Department of Agriculture and Food, Western Australia, Perth, Australia.

E-mail: [georgie.troup@agric.wa.gov.au](mailto:georgie.troup@agric.wa.gov.au)

***Key words: oat, variety, agronomy, plant density, seeding date, hectolitre, screenings***

Oats are traditionally grown in the medium to high rainfall areas in Western Australia (WA). Increasing international demand for WA oats has resulted in the expansion of the oat production area into the less reliable medium to low rainfall areas. New agronomy research is required to optimise the production potential in this lower rainfall area to ensure growers are selecting the appropriate variety and agronomy package to be profitable in their production of high quality milling oats.

The objective of the trial was to examine the influence of seeding date, applied nitrogen, variety selection and plant density on oat grain yield and quality in the lower rainfall part of the oat growing region in Western Australia.

The trial was conducted at three locations during 2015, and built on previous work at these locations in 2014. The trial was sown into sufficient moisture to germinate at all locations; however there was a prolonged dry period during the growing season which shortened the time to maturity.

Seeding date had a greater influence on oat grain yield, oat grain quality and return per hectare (\$/ha) than variety selection, plant density or applied nitrogen (N) in 2015. Early seeding was the key to producing optimal grain quality, high grain yield and maximum return per hectare. When sowing was delayed from early May to early June grain yield reduced by 32% and this was reflected in a 45% reduction in returns per hectare (\$/ha) and a higher proportion of lower grade grain produced.

Plant density did influence hectolitre weight and screenings, but the effects were generally small and often not large enough to change the grade. Achieving a target density between 100 to 200 plants/m<sup>2</sup> maximised return per hectare, which is in line with the suggested target density for grain oats in low rainfall areas of 160 plants/m<sup>2</sup>. Applying more than 20 kg N/ha did not improve the return per hectare (\$/ha); rather, applying 80 kg N/ha consistently reduced return per hectare (\$/ha).

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**POSTER SESSION**  
**Agronomy, Nutrition,**  
**Health Claims and Diets**

## POSTER PRESENTATIONS

### Initial material for development of high protein oat cultivars in northern Trans ural mountain region

Yu. S. Averyasova<sup>1</sup>, M. N. Fomina<sup>2</sup>, I. G. Loskutov<sup>1</sup>

<sup>1</sup>Federal Research Center N.I. Vavilov Institute of Plant Genetic Resources (VIR),  
St-Petersburg, Russia

Agricultural Research Institute Northern Transural,  
Tyumen, Russia

E-mail: [averyasova-uliy@mail.ru](mailto:averyasova-uliy@mail.ru)

**Keywords:** *oat, protein content, productivity, correlations*

Oat is a crop of versatile use. The percentage of protein in oat grain and its yield per unit area often exceed these values in other cereal crops, while the amino acid composition is better balanced. These factors suggest a high nutritional value of this crop. One of the most important directions in oat breeding for quality is the increasing of protein content. Of special interest in this sense are the forms of naked oat capable of accumulating 14-22 % of raw protein in grain. It is obvious now that a rational strategy of crop breeding for the increased protein content in grain should envisage broadening of genetic diversity of cultivated varieties. The task of identifying new sources is quite urgent, and the forms of naked oat play an important role in solving it.

Grain protein content (GPC) has been evaluated under conditions of Northern Transurals in 213 naked oat accessions differing by their ecogeographic origin. The results of evaluation performed in the northern forest-steppe of the Tyumen Province within three years (2012 – 2014) showed that the conditions of cultivation strongly influenced protein formation in grain of naked oat cultivars, this factor amounting up to 75.8 %. The share of genotype influence equaled 11.1 %, and that of the genotype-environment interaction amounted to 13.1 %. The maximum quantity of protein (the experimental average of 20.07 %) was recorded for the severe drought conditions in 2012, while the minimum one (the experimental average of 15.20 %) was noted under the conditions of heat deficiency and excess moisture in 2014. The significant role of the cultivar properties in protein formation was evidenced by the variation of this value within a wide range. For instance, under drought conditions of 2012, GPC varied within grain of accessions from 15.92 % (VIR-14564) up to 23.79 % (VIR-2353, VIR-15225), while in cold and humid 2014 it varied from 11.54% (VIR-14440) up to 18.25% (VIR-14944, VIR-15158). The variation (V) of protein content in grain of accessions was within the 6.5 – 10.3 % range.

The analysis of relations between the GPC and grain productivity of naked oat cultivars has shown it to be strongly negative ( $r = -0.72 - 0.84$ ) in the Northern Transurals. When analyzing the relation between protein content and the structure of yield elements, a negative correlation with panicle productivity ( $r = -0.55 - 0.57$ ) should be

noted. The relation of protein content with the grain mass per one plant, 1000 seeds weight and the grains number per panicle was ambiguous. A positive correlation of productivity per plant with GPC in the naked oat cultivars ( $r = 0.22$ ;  $r = 0.98$ ) was registered under the extreme conditions of cultivation, that is, under severe drought, excess moisture and lack of heat. A positive influence of grain size and ear grain content on protein formation ( $r_1 = 0.57$ ;  $r_2 = 0.76$ ) manifested itself only in conditions of sufficient heat and moisture. An increase in productive tillering had a positive effect on the raw protein content ( $r = 0.76$ ) only under excess moisture and heat deficiency, while in all other cases the correlation was negative.

A positive correlation has been found to exist between GPC and the endosperm quantity in grain ( $r = 0.12 - 0.69$ ); the correlation between protein content and that of fat and starch was not equally linear, as in most cases it was either insignificant, or slightly negative. A positive, medium-size correlation between protein content and that of fat was found to exist under conditions of sufficient heat and moisture ( $r = 0.52$ ). A strong positive correlation between GPC and starch was noted under the conditions of deficient heat and excess moisture ( $r = 0.98$ ). A reliable positive relation between the volume weight of grain and protein content in it ( $r = 0.59$ ) was noted only when both heat and moisture were abundant.

The sources of high GPC that have been identified and recommended for the use in breeding aimed at increasing protein content, are cv. Uspekh (Leningrad Province), cv. Pomor (Kemerovo Province), a local accession from Norway, cv. Polard (Canada), Hull-less (China), etc.

The research has resulted in the identification of high yielding oat accessions which were significantly inferior to the standard cultivar (Tyumensky golozerny) in terms of GPC, but demonstrated a considerable increment in raw protein per 1 m<sup>2</sup> (+11.24 – 29.14 g/m<sup>2</sup>). These include cv. Persheron (Kirov Province), cv. Progress (Omsk Province), Hulless Oats (Canada), etc.

The identified sources combining high GPC with high productivity are cv. Beg (Belarus), MF 9224-106, MF 9224-101 (USA), Brighton (Canada), etc.



# Effect of environment on yield and grain quality parameters of winter oats in different growing seasons in the United Kingdom

Alexander (Sandy) Cowan<sup>1\*</sup>, Pilar Martinez<sup>1</sup>, Irene Griffiths<sup>1</sup>, Athole Marshall<sup>1</sup>,  
Tim Langdon<sup>1</sup>, Sarah Clarke<sup>2</sup>, Nick Fradgley<sup>3</sup>, Catherine Howarth<sup>1</sup>

<sup>1</sup>IBERS, Aberystwyth University, Gogerddan, Aberystwyth, SY23 3EE, U.K.

<sup>2</sup>ADAS Gleadthorpe, Mansfield, NG20 9PD, U.K.

<sup>3</sup>Organic Research Centre, Elm Farm, Hamstead Marshall, Newbury RG20 0HR, U.K.

\*E-mail: [syc@aber.ac.uk](mailto:syc@aber.ac.uk)

***Keywords: winter oat, environment, yield, grain quality***

To understand the effect of growth environment on grain quality parameters, four contrasting winter oat cultivars (Gerald, Mascani, Tardis and Buffalo) were grown at 22 diverse locations in the UK over four harvest years (2011, 2012, 2013 and 2014). Agronomic characteristics including harvested grain yield and physical grain quality parameters of importance to the oat milling industry (specific weight, kernel content and hullability) were recorded. Chemical composition of the grain in terms of oil, protein and beta glucan content was also measured.

Results are presented highlighting the differences between varieties and the effect of environment on grain yield and grain quality parameters. Although the yields of the four varieties were not significantly different there were significant effects of environment on grain yield. There were significant effects of variety and environment on grain quality and differences between varieties in response to environment with some varieties more stable for specific traits than others. Of the four varieties, Mascani had the highest and most stable kernel content, the best and most stable hullability and the highest specific weight. Analysis of the G x E effects on grain quality within an oat breeding programme is discussed.

# Avenins as markers in oat breeding and seed production

N. Gubareva<sup>1</sup>, I. Gavriluk<sup>1</sup>, G. Batalova<sup>2</sup>, I. Loskutov<sup>1</sup>, V. Krasilnikov<sup>3</sup>, A. Konarev<sup>1</sup>

<sup>1</sup>Federal Research Centre – The N.I. Vavilov Institute of Plant Genetic Resources (VIR), St. Petersburg, Russia

<sup>2</sup>Research Institute of Agriculture of the North-East, Kirov, Russia

<sup>3</sup>Institute of Commerce and Economics, St. Petersburg, Russia

E-mail: [ipg1011@mail.ru](mailto:ipg1011@mail.ru)

**Keywords:** *oat, cultivars, hybrids, electrophoresis, avenins*

Grains of all cereals contain storage proteins (prolamins) such as wheat gliadins, barley hordeins, rye secalins, etc. The oat prolamins are avenins consisting of two fractions –  $\alpha$ - and  $\beta$ -avenins. Both fractions are heterogenic and polymorphic. Electrophoresis reveals from 2 to 8 components in them. It is known that the component composition of avenin is variety-specific and can be used successfully for oat cultivar identification and registration. Much less information is available on the nature of inheritance of avenin components in breeding process. Our task is to compare the component composition of avenins in new cultivars and lines of naked oats with their parental forms.

Selection for grain nakedness and valuable agricultural traits from the hybrid population produced by crossing Borrus  $\times$  Mozart resulted in the development of the line 766h05. It consists of two biotypes differing in avenin patterns. Both biotypes include components of the parental cultivars in different combinations. The prevalent biotype (80%) is interesting for the lack of the  $\alpha$ -avenin fraction. The line 735h05 obtained from  $F_3$  of the cross Petra  $\times$  Torchis is homogenic and has one avenin pattern including mainly  $\beta$ -avenins.

Selected from  $F_3$  of the cross Vandrovik  $\times$  Vyatsky was a homogenic line with avenin composition similar to cultivar Vyatsky. In the line obtained from the backcross (Vyatsky  $\times$  Vandrovik) three different avenin patterns were observed. All three contained differently combined avenins of the parental cultivars.

Two lines were selected from the hybrid combination Torch  $\times$  Freya: 2h10 and 668h05. In its avenin composition the line 2h10 is close to cultivar Freya, while 668h05 to cultivar Torch. In  $\beta$ -avenin of the latter line there is a component absent in the avenins of both parental cultivars.

A morphologically homogenic population with 3 different avenin patterns was obtained from the reverse combination Freya  $\times$  Torch. Thirty per cent of this population has avenin patterns identical to the avenin of the line 2h10 from the cross Torch  $\times$  Freya. One of the biotypes, similar to the line 668h05, comprises the  $\beta$ -avenin component which is absent in the avenins of both parental cultivars. This component is typical for cultivar Tyumensky Golozerny. The appearance of this  $\beta$ -avenin component in several lines may probably be explained by the involvement of the hybrid (Torch  $\times$  Freya)  $\times$  Tyumensky Golozerny in one of the stages of the breeding process.

Two stable lines 7h120 and 3h10 were selected from  $F_3$  of the cross (Torch  $\times$  Petra)  $\times$  Tyumensky Golozerny for their grain nakedness and adaptability. Avenins of both

lines comprised all components of the parental cultivars. Only one avenin pattern type was observed in the line 7h120, while the line 3h10 had two types of avenin pattern. One of them is identical to the avenin pattern of the line 7h120 (30% of the population); avenins of the other 70% differ in their composition.

A promising  $F_4$  line was selected from the hybrid population obtained by crossing the covered cultivar Faust with the French naked cultivar Nuprime in 2004. In 2015, it was submitted to the State Variety Trials as the cultivar Bekas. Avenins of 90% grains of this cultivar include intensive  $\beta$ -avenins and very weak  $\alpha$ -avenins. On the contrary, in 10%  $\alpha$ -avenins prevail.

Thus, cultivars and lines involved in breeding programmes differ in the composition of avenin components and can be identified by avenin electrophoresis techniques. More than half of the cultivars and lines studied are homogenic in their avenin patterns. The rest consist of two or three biotypes differing in avenin composition. In morphologically uniform populations with several avenin patterns, latent variability in stress resistance may be present. The same hybrid combinations, depending on the direction of crossing and the method of selection, produced lines differing in their avenins. It means that avenins are useful as markers when parental components for crosses are selected and for making the breeding process more efficient.

Recently, a new trend has taken shape in oat breeding. It is associated with the search for oats without grain proteins toxic for patients with celiac disease. In this context, the most interesting is the composition of  $\alpha$ -avenins. Their molecules have many disulphide bonds and are resistant to proteolysis. It is in these molecules that many peptides toxic for celiac patients have been found. In this respect, oat lines with low content of  $\alpha$ -avenins or without them are very promising for producing functional food for celiac diets. Among the studied breeding forms of oat, prevalent biotypes from the line 766h05 and cultivar Bekas are of interest. Thus, electrophoresis of avenins combined with ELISA may prove useful for the development of oat cultivars required for producing functional foods for celiac diets.

# Genetic diversity in oat genetic resources by seed storage protein polymorphism

Peter Hozlár<sup>1</sup>, Edita Gregová<sup>2</sup>, Svetlana Šliková<sup>2</sup>

<sup>1</sup>National Agriculture and Food Centre, Research Institute of Plant Production, Research and Breeding Station Vígfaš-Pstruša 334, 962 12 Detva, Slovak Republic,

<sup>2</sup>National Agriculture and Food Centre, Research Institute of Plant Production, Bratislavská cesta 122, 921 68 Piešťany, Slovak Republic  
E-mail: [gregova@vurv.sk](mailto:gregova@vurv.sk)

**Keywords:** *genetic resources, genetic diversity, seed storage protein*

Glutelin fractions were prepared from oat seeds (*Avena sativa* L.) using SDS-PAGE (sodium dodecyl sulphate polyacrylamide gel electrophoresis). The protein diversity of 39 genetic resources from 9 countries (USA, Canada, Czech Republic, Germany, Australia, Sweden, Austria, France, and Great Britain) of oat was examined. All samples were obtained from the collection of genetic oat resources of the Gene Bank of the Slovak Republic in Piešťany. Glutelins were extracted by standard referee method ISTA and were performed by discontinuous PAGE based on ISTA methodology (Wrigley, 1992) using the electrophoretic unit Protean II (BioRad). Protein fractions were stained by Coomassie Brilliant Blue R – 250. Similarities between cultivars were estimated using Jaccard's coefficient of similarity. Cluster analyses were conducted on similarity estimates using the unweighted pair- group method for arithmetic averages (UPGMA) and the resulting clusters were expressed as dendrograms. Cluster 1 comprises 37 genotypes where cluster 2 and cluster 3 comprises one genotypes. Genetic similarity coefficients resulted from comparisons by glutelin pattern and they ranged from 0,040 to 0,933. All oat varieties were different from each other. SDS-PAGE result revealed that glutelins presented a higher differentiation power than avenins and could be used as a rapid method for the identification of oat varieties in breeding programmes.

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# Effect of grain development on quality parameters in oats

Pilar Martinez Martin\*, Irene Griffiths, Alexander (Sandy) Cowan, Catherine Howarth

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

\*E-mail: [mjm7@aber.ac.uk](mailto:mjm7@aber.ac.uk)

***Keywords: oat, grain development, quality parameters***

Grain development in oats and its effect on grain quality parameters has not been investigated until now. Panicle architecture in oats influences the size and shape of grain within the panicle and this is reflected by differences in grain development. In order to understand the physiological mechanisms involved in this phenomenon and how grain quality is affected, a field trial was conducted in summer 2015. Three winter oat varieties, Tardis, Mascani and Buffalo were grown and developing grain sampled at five different growth stages (Zadok decimal growth stage, GS). At each GS and from each variety panicles were harvested and divided into individual whorls. From each whorl the primary, secondary and tertiary grain were separated and analysed by image analysis, before and after dehulling. Measurements of area, length, width and moisture content were taken. The results showed differences between the top and the bottom of the panicle in terms of maturity and also the effect of loss of moisture content during maturation. Maximal grain width was reached before maximum grain length with both of them diminishing by final maturity.

These results may allow us to set a benchmark which can be used as a quantitative reference point against the maturity of the grain by which performance can be measured, and at the same time to understand the physical basis of the influence of grain shape and size on grain quality parameters.

# Duplicate accession identification in the VIR (Russia) and NordGen (Sweden) *Avena sativa* L. collections

I. Perchuk<sup>1\*</sup>, A. Konarev<sup>1</sup>, I. Loskutov<sup>1</sup>, E. Blinova<sup>1</sup>, L. Novikova<sup>1</sup>, V. Horeva<sup>1</sup>,  
A. Kolodinska-Brantestam<sup>2</sup>

<sup>1</sup>Federal Research Centre – N.I. Vavilov Institute of Plant Genetic Resources (VIR),  
St. Petersburg, Russia

<sup>2</sup>NordGen, Alnarp, Sweden

\*E-mail: i.perchuk@vir.nw.ru

**Keywords:** *duplication, accession identification, morphological characters, avenin spectra*

One of the important task of plant genebank is to conserve the unique genetic material. As a rule genebank collections have been accumulated over long time, and it is apparent problem of duplicate accessions. To conserve such accessions is neither economic nor technical so there is a need of their identification. Similar passport data are not a guarantee of that the accessions are identical. Their identity cannot be confirmed without comprehensive study of the material. The more information is combination the results of both field evaluation and molecular markers study. This work presents the results of comparative analysis of the same name scandinavian breeding cultivars of oat from the VIR and Nordic genebank collections to ascertain their possible “doublet”. Comparative analysis of the 112 potential duplicate pairs (pair composed of one same name accession from each collection) was carried out on the results of the Pushkin branch VIR field study of the 26 morphological and breeding - valuable characters and using protein markers ( spectra of seed storage protein avenin). As a result of the field trial the authors propose *D summ.* index for evaluation of differences both in qualitative and quantitative plant characters between potential duplicate accessions. *D summ.* index value varied in the range of 0,1 ÷ 8,3. *D summ.* variability structural analysis showed that its distribution is characterized by a pronounced right-sided asymmetry (the asymmetry coefficient was 1.83). These data indicated that the tested oat sample was inhomogeneous and consisted of both duplicate and non-duplicate pair accessions. In accordance with *D summ.* value the accessions were conventionally divided into three groups wherein duplicates could be identified with various degrees of probability.

This time there is no single criterion for evaluating “duplicate accessions”. This may be a “passport”, botanical, genetic duplicate and others. In this work the breeding oat cultivars were studied. Their genotypic composition was formed specifically by breeders. The concept of “cultivar” involves originality genotypic composition along with other characteristics. Therefore cultivar accessions with an identical genotype composition can be considered as duplicates. Comparison of agro-morphological characters allows only indirectly judge the genetic affinity of the compared samples. This is due to the fact that most of these phenotypic traits can vary significantly for the same sample reproduction under different conditions. A more objective evaluation of the degree of genetic identity can be achieved in a comparative analysis of the composition of



seed storage proteins that are genetic markers. Electrophoretic analysis proved that 46% of the 112 pairs may be regarded as duplicates, because each pair accessions had identical composition according to avenin biotypes. Comparison between field and laboratory trials of a group of accessions selected by the authors showed that the lower was the *D summ.* index of differences in the field, the more duplicate pairs were identified in the group with the help of protein markers. The amount of duplicate pairs was about 70% in the group with the lowest *D summ.* index (0.1 – 1.5). The group with the maximum level of differences (3.9 – 8.3) in the field consisted of non-duplicates only. Generally, the sets of duplicate and non-duplicate pairs identified by electrophoresis were significantly different in terms of *D summ.* index according MannWhitneyUTest. ( $p = 0.0001$ ).

Belonging to different collections of gene banks, the same name cultivar samples may differ in any of the characters. To decide which of the samples is a true cultivar representative it is possible by comparing them with the original cultivar. The most reliable in this case is the use of standard laboratory methods, because original cultivar seeds may partially or completely lose germination especially upon prolonged storage. Clear electrophoretic spectra of seed storage proteins can be obtained even of the “century-old” seeds. This approach has been demonstrated by comparing several identified non-duplicate pair accessions with original cultivar samples preserved in the VIR oat collection from the 1920-1960s. For clarity, the same name accessions with avenin biotype composition differed dramatically were selected. According electrophoretic analysis representatives of the original cultivar can be considered accessions of cultivars Gothland, Trifolium, Osmo I I0693, Regent of VIR collection and North Finnish, Stormogult Havre, Nopsa Anos, Gota from Nordic genebank collection. The avenin biotype composition of cultivars mentioned above was identical to that of the corresponding original cultivar samples. Thus in cases of doubt electrophoretic analysis allows to determine the sample cultivar “authenticity” and (or) its “purity.”

The revealed conformity between the results of the field and laboratory tests shows that it is possible to use protein markers (avenin spectra) for identification of duplicate accessions in oat collections even before field trials. Field evaluation of crop accessions is interfaced with phenotypic variability of the majority of characters used in monitoring as well as with its duration. Molecular methods are more objective and reproducible in different laboratories, which is important for coordinating the work of different genebanks.

## Amino acid analysis of high protein oat lines

Yi Ren<sup>1,2</sup>, Bindu A. Similkumar<sup>1,3</sup> Rickard Öste<sup>3,4</sup>, Olof Olsson<sup>1,5</sup>

<sup>1</sup>CropTair AB, c/o Department of pure and applied biochemistry, Lund University, Lund, Sweden 22100;

<sup>2</sup>College of agronomy, Shanxi Agricultural University, Taigu, China 030801; Food for Health Science Centre, Lund University, Lund, Sweden 22100;

<sup>4</sup>Aventure AB, Scheelevägen 22, 22362 Lund, Sweden;

<sup>5</sup>Department of pure and applied biochemistry, Lund University, Lund, Sweden 22100

E-mail: [olof.olsson@tbiokem.lth.se](mailto:olof.olsson@tbiokem.lth.se)

***Key words: oats; amino acid composition; EAA***

Oats possess a protein quality of high nutritional value and, compared to other cereals, a relatively higher amount of limiting amino acids like lysine and threonine. However, in general, the lysine levels in oats are still below the FAO/WHO amino acid reference standard, others like threonine and isoleucine also belong to the limiting amino acids for oats, though the balance between the essential amino acids is much better than the other cereals.

In the present study, the amino acid (AA) composition of protein isolated from 31 high protein oats lines, originally identified from a mutagenized population, were determined. The mean contents (g/kg protein) of each amino acid in these lines were; lysine 37.30, threonine 34.14, phenylalanine 47.32, valine 45.61, histidine 21.36, glutamic acid 180.75, proline 49.23, glycine 46.23, alanine 43.03, cysteine 33.03, methionine 26.96, serine 40.63, tryptophan 10.33, arginine 61.45, aspartic acid 76.43, tyrosine 31.21, isoleucine 35.47 and leucine 69.61. However, there were differences in the levels of individual AA in the different lines. Several of the high protein lines contained, except for lysine, sufficient levels of all the essential amino acids (EAAs) according to the FAO/WHO amino acid recommendations. However, in one high protein line, the lysine level was 46.4 g/kg, which exceeds the recommended FAO reference standard of 45 g/kg protein for adults. Thus, this line both have high total protein level (>20%) and a favorable amino acid composition and has a potential to become a new source of vegetable proteins. An oat with high protein with a complete EAA profile will open new ways to develop novel oat based food products.



# The content of oil and fatty acid composition in 8 cultivars of oat grown in lesser Poland region

Mirosław Krosniak<sup>1</sup>, Anna Zalewska<sup>1</sup>, Renata Francik<sup>2</sup>, Barbara Tatar<sup>1</sup>,  
Elżbieta Kondratowicz-Piertruska<sup>3</sup>, Elżbieta Pisulewska<sup>4</sup>,  
Agnieszka Wojtanowska-Krosniak<sup>1</sup>, Halina Rudd<sup>5</sup>

<sup>1</sup>Department of Food Chemistry and Nutrition, Jagiellonian University, Cracow, Poland,

<sup>2</sup>Department of Bioorganic Chemistry, Jagiellonian University Medical College,  
9 Medyczna Street, 30-688 Cracow, Poland

<sup>3</sup>Department of Chemistry, Faculty of Commodity Science, Cracow University of Economics, Poland

<sup>4</sup>Cracow School of Health Promotion, Poland

<sup>5</sup>Plant Breeding Station, Norway

E-mail: [mfkrosni@cyf-kr.edu.pl](mailto:mfkrosni@cyf-kr.edu.pl)

**Keywords:** *oat, cultivars, content of oil, fatty acid composition*

Oat plant is relatively popular in Poland as a food product. It contains many valuable biologically active compounds. The aim of the present study was to compare the content of oil and fatty acid composition in eight different cultivars of oat (Kasztan, Borowiak, Celer, Ivory, Harnas, Siwek, Nagus and Grajcar) from the agriculture center in Polanowice (Malopolska Plant Breeding - Craków Branch) in Lesser Poland region. In the purified crop, after grain crushing, the total fat content was measured with Soxhlet method. Also, in the obtained oil, the fatty acid composition was analyzed with the use of gas chromatography. The total fat content in dry grain ranged from 3.80 to 7.83%. The IHarnaś cultivar had the lowest total fat content. The largest amount of total fat content was observed in Siwek cultivar. The share of unsaturated fatty acids ranged from 81.60 to 83.82%. The lowest was in Grajcar cultivar and for Siwek cultivar was the highest. The main fatty acids are the following: oleic acid C 18: 1 (cis-9)) - 38.74 - 45.84% and linoleic acid (C18: 2 (cis-9,12)) - 36.20 - 43.08%. The palmitic acid (C16: 0) ranged from 14.62 to 16.60%. The content of stearic acid (C18: 0) ranged from 1.03 to 1.60% and was similar to the content of alpha-linolenic acid (C18: 3 (cis-9,12,15)) - 1.24 - 1.89%. In the tested cultivars, the presence of acids: caproic acid (C6: 0), myristic acid (C14: 0), ceronic acid (C 22: 6 (cis-4,7,10,13,16,19)), docosadienoic acid (C22: 2 (cis-13,16)) and erucic acid (C22: 1 (cis-13)) was detected.

# The metabolomic approach to the analysis of wild and cultivated species of oats\*

T.V. Shelenga<sup>1</sup>, A.V. Konarev<sup>1</sup>, A.L. Shavarda<sup>1,2,3</sup>, E.V. Blinova<sup>1</sup>, N.I. Dzubenko<sup>1</sup>,  
I.G. Loskutov<sup>1,2\*</sup>

<sup>1</sup>«The Federal Research Center All-Russian N.I. Vavilov Institute of Plant Genetic Resources» (VIR),  
St.-Petersburg

<sup>2</sup>St.-Petersburg State University, St.-Petersburg

<sup>3</sup>V.L. Komarov Botanical Institute of the Russian Academy of Sciences, St.-Petersburg

E-mail: [a.konarev@vir.nw.ru](mailto:a.konarev@vir.nw.ru)

**Keywords:** *Avena L.*, wild species, kernels, gas chromatography, mass spectrometry, metabolomics, domestication, adaptability and polymorphism of traits

So far, oat (*Avena L.*) remains one of the most promising and demanded agricultural crops in both this country and abroad. The priorities in *Avena sativa L.* breeding in the 20<sup>th</sup> century have mainly been resistance and yielding ability. As the ‘medical’ biochemistry developed, more and more compounds of importance for the human health have been discovered and identified. From this point of view, the task of conservation and sustainable use of plant genetic resources for providing high qualities of human life that is based on quality nutrition, gains more importance with every decade.

In recent years, a methodologically new approach based on the determination of complete metabolite content and quantity (metabolite profile) of an object has acquired special importance. According to the modern conception, the metabolite profile is the total result of cellular activity at the molecular-genetic and biochemical levels. Such an approach may be used as an effective tool not only for characterizing genotypes, but also for revealing mechanisms of adaptation to stressors, evaluating ontogenetic changes, diagnosing pathologic changes, etc. By analyzing metabolomic profiles, a certain number of biochemical markers of biological processes can be identified.

The present research studied metabolomic profiles in seeds of wild and cultivated forms (cultivars) of oat (*Avena L.*). Seed samples from the VIR collection were used as material for the present research. Metabolomic investigations employed gas-liquid chromatography with mass spectrometry (GLC-MS) using the Agilent 6850 chromatographer (USA). The content and composition of organic and fatty acids, amino acids, polyatomic alcohols and sugars have been analyzed. The range of content fluctuation for the groups of compounds in question in cultivars has narrowed down (significantly in some cases) in comparison with that in the wild species. Along with the sharp increase in the oleic acid content, that of linoleic acid decreased in cultivars. In general, a comparison of the metabolite profiles in seeds of the wild species and cultivars has yielded the following main conclusions. It has been confirmed at a new methodological level that the VIR collection is a valuable source of forms possessing economically

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important breeding traits manifested in a wide range of expression intensity. It makes the collection a reliable basis for creating cultivated forms (cultivars) that meet the most diverse modern requirements of the food and feed industries, of healthy and medicinal nutrition, etc. A series of wild oat species can be recommended as a potential source of biochemical quality traits for breeding. A series of the identified metabolites (compounds) have been found either to change their content along with the ‘domestication’ process, or differentiate wild oat species from oat cultivars. Along with the presence of such widely known chemical components of healthy nutrition as the oleic acid, glucose, fructose, etc., differences concerning MAG (monoacylglycerol) 16:0 and MAG-2-18:2, etc. compounds have been found. A supposition has been made about the possible relation of the MAG compounds to adaptability, in particular, to resistance to diseases and pests, as well as to abiotic environmental factors.

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# Assessment of oat genotypes according to the characteristics determining the nutritional grain quality

Sanita Zute<sup>1</sup>, Igor Loskutov<sup>2</sup>, Zaiga Vicupe<sup>1</sup>

<sup>1</sup>Institute of Agricultural Resources and Economics, Stende Research Centre,  
Dižstende, Lībagi Parish, Talsi District, Latvia,

<sup>2</sup>N.I. Vavilov Institute of Plant Genetic Resources (VIR),  
St. Petersburg, Russia

E-mail: [sanita.zute@stendeselekcija.lv](mailto:sanita.zute@stendeselekcija.lv)

**Key words:** *oat grain, variety, nutritional quality,  $\beta$ -glucan, lipid*

Oat (*Avena sativa* L.) grain has been extensively studied due to its specific chemical composition and nutritional value. Oat grain is valued and assessed by its taste and dietetic properties. The objective of the research was to compare oat varieties to identify genotypes that could be used in oat breeding to obtain new varieties suitable for food production with high nutritional value.

The research was carried out at the State Stende Cereal Breeding Institute (today Institute of Agricultural Resources and Economics) in 2013, 2014 and 2015 including 20 oat varieties from N.I. Vavilov Institute of Plant Genetic Resources (Russia) and two oat varieties bred in Latvia – ‘Laima’ and ‘Stendes Darta’. Growing conditions: sod-podzolic soils (WRB – Eutric Podzovisols), well cultivated moraine loamy sand soil with pH<sub>KCl</sub> of 5.8-6.1 in arable layer, 18 – 24 g kg<sup>-1</sup> organic matter. The mineral fertilizer NPK 15:15:15 was applied before sowing (nitrogen active ingredients 60 kg ha<sup>-1</sup> N). Sowing and harvesting were performed in optimal terms. The following traits were evaluated: crude protein (PC, g kg<sup>-1</sup>), crude lipids (LC, g kg<sup>-1</sup>),  $\beta$ -glucan (BG, g kg<sup>-1</sup>) amount in dry matter by an automatic grain analyser Infratec Analysis 1241.

Oat varieties included in the study differed significantly in their biochemical composition of the grain and in the traits important for grain processing. The value of biochemical composition of oat grain depends on genetic and environmental factors as the method of determination. In this study the most significant differences among characteristics value of oat genotypes were observed in LC and BG (coefficient of variation in the three-year period, respectively 27.4 and 23.7%, in PC – 16.8%). In Latvia the agro-climatic conditions during the vegetation period of cereals usually significantly differ from year to year. As a result it causes the significant variation ( $p < 0.01$ ) of characteristics for oat varieties among testing years. In oat grain PC among varieties ranged from 93 g kg<sup>-1</sup> for variety ‘Auron’ (CZ), in 2013 to 146 g kg<sup>-1</sup> for variety ‘Borot’ (RU) in 2015. The content of LC varied from 44 g kg<sup>-1</sup> for variety ‘Dagny’ (SE) in 2013 to 119 g kg<sup>-1</sup> for ‘Haruoaba’ (JP) in 2015. Oat BG ranged from 24 g kg<sup>-1</sup> for variety ‘Dagny’ in 2013 to 65 g kg<sup>-1</sup> for ‘Matilda’ (SE) and ‘Haruoaba’ in 2015.

The oat lipids have high concentration of monounsaturated oleic acid that is favourable for its use as a food oil (Peterson, 2004, Sterna *et.al.*, 2014). In three years period the highest mean values of LC (more than 85 g kg<sup>-1</sup>) was obtained for oat varieties ‘Matilda’, ‘Haruoaba’ and ‘Borot’. It was observed that the highest oat LC amount in

grains was obtained in 2015 – on the average 81.9 g kg<sup>-1</sup> that was by 19.6 and 14.6 g kg<sup>-1</sup> higher than in 2013 and 2014 respectively. The smallest variation of LC in a three-year period was found for varieties ‘Soku’ (RU), ‘Laima’ (LV) and ‘Stendes Darta’ (LV) showing the coefficient of variation 4.4, 6.4 and 8.1% respectively. Positive phenotypic correlation coefficients between LC and BG content in the grains were high and significant ( $p < 0.05$ ,  $n = 22$ ) for all tree years and ranged from 0.870 - 0.929.

Oats contain a form of soluble fibre called oat BG which is particularly concentrated in the outer layers of the grain. Oats used for human consumption has a breeding target of high  $\beta$ -glucan. (Peterson, 2004; Valentine *et.al.*, 2004). In this study the highest BG on average of three years was obtained for oat varieties ‘Haruaoba’, ‘Matilda’, and ‘Vernij’ (RU) (55.0, 53.3 and 45.3 g kg<sup>-1</sup> respectively). The highest BG amount in grains was found in 2015 – on the average 42.4 g kg<sup>-1</sup> or by 5.6 and 5.7 g kg<sup>-1</sup> higher than it was in 2013 and 2014 respectively. The smallest variation of BG in a three-year period was found for varieties ‘Dagny’, ‘AC Morgan’ (CA), ‘AC Assiniboia’ (CA) (the coefficient of variation <5%), but the value of BG of this varieties was comparatively low (lower than 30 g kg<sup>-1</sup>).

The protein concentration is usually relatively high in oat grain and composition of amino acids are well balanced (Peterson, 2004). In this trial the protein content of oat grains were the most stable characteristic of the analysed (the coefficient of variation PC from 18 varieties was lower than 10%). Oat varieties ‘Borut’, ‘Vernij’, ‘Soku’ (RU) and ‘Haruaoba’ characterized by the highest protein content in the grain on the average of three years (higher than 124 g kg<sup>-1</sup>). The highest PC amount in grains was found in 2014 – on the average 118.4 g kg<sup>-1</sup>.

Oat varieties ‘Haruaoba’, ‘Borut’, ‘Vernij’, ‘Soku’, ‘Matilda’ best met the requirements of grain with high nutritional value according to grain biochemical such as lipid,  $\beta$ -glucan and protein and will be recommended to use as good initial material for breeding of food oat varieties.

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# **POSTER SESSION**

## **Production, Processing, Products and Consumers**

## POSTER PRESENTATIONS

### Evaluation of oat flour quality using MixoLab

Larisa Cato, Jenny Ng

Australian Export Grains Innovation Centre (AEGIC), South Perth, WA 6151, Australia

Email: [larisa.cato@aegic.org.au](mailto:larisa.cato@aegic.org.au)

***Keywords: oat flour, oat noodles, starch quality***

In 2009, China surpassed Mexico as the largest export market for Australian oat grain. The growth in exports to this market has been dramatic with a 16-fold increase since 2007 when only 5,000mt of oats were imported from Australia. With 80% of oats imported by China currently sourced from Australia, this growth represents a significant developing market for food-grade Australian oats. It is anticipated that the demand from China will provide valuable competition with demand for Australian oats from Mexico, Japan and domestic processors that ultimately provides support to both domestic oat production and pricing.

Growth in demand for oat products in China has been driven by increased sophistication in the health market and consumer awareness of their association with lowering of the ‘three health evils’ of high cholesterol, high blood pressure and high blood sugar. Whilst the use of imported oats for oatmeal breakfast remains the largest end-use, growing consumer interest is prompting interest in new Asian food products, with oat based rice, beverages, snack bars and noodles dominating this interest. Whilst the Australian industry already possesses significant information regarding the quality and functionality requirements of oats for oatmeal as a breakfast dish, there is little information regarding the functional requirements of these new oat-based Asian-style products or comparative studies in qualities and processing functionality with competitor Chinese oat varieties. The National Oat Breeding Program has integrated chemical and physical grain quality assessment for 20 years. Linkages with the domestic milling industry have resulted in well-defined end-product quality requirements for traditional oat based food, primarily porridge and muesli bars.

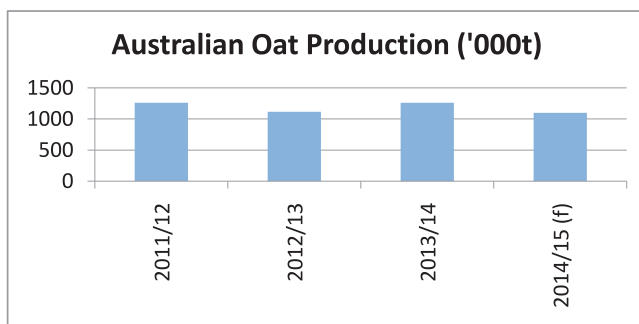
Oat consumption in China has increased recently due to reported health benefits of oats and oat based products. Noodles are popular in China and important part of the diet in many Asian countries. Recently, noodles made from a blend of wheat and oat flour were developed in China. Eating quality preference for these type of noodles seems to be similar to the Japanese Udon.

In this study “MixoLab®” was used to measure both rheological properties of dough and starch gelatinization characteristics of oat flour and wheat / oat blends. Information such as water absorption, dough tolerance, mixing stability, maximum consistency of the gelatinized flour, cooking stability and enzyme activity were determined in a single test.

A key objective of this study was to characterise the rheological properties of oat flour and wheat / oat blends. Main Australian oat varieties have been analysed for starch

and protein quality including weakening of the proteins (C2), starch gelatinisation (C3), gel stability (C4) and starch retrogradation (C5). The general shape of the curve for oats is different from common wheat flour. It is characterized by a low gelatinization and retrogradation of starch. Incorporating oat flour and impact on the starch and noodle quality will be discussed here.

## Results



**Fig. 1.** Australian Oat Production (2011-12 to 2014-15).

Source: ABARES Crop Report Feb 2014 – 3-year average.

**Table 1.** Flour evaluation

Samples	ash %	$\beta$ -glucan %	fat %	moisture %	protein %	TDF %
Wheat Flour 1	0.40	0.40	1.2	12.4	9.2	2.9
Wheat Flour 2	0.44	0.30	1.1	11.9	9.1	2.3
Mitika	0.88	1.50	9.4	8.8	6.8	3.1
Williams	0.73	1.20	8.1	12.3	7.4	2.3
Mitika / Echidna	1.08	2.10	8.3	10.1	10.1	3.5

## Conclusions

- 10 & 20% oat flour addition to the blend showed mixing behavior very similar to 100% wheat flour
- 20, 30 & 40% oat flour addition to the blend showed significant decrease in resistance to mixing
- Noodle firmness decreases with increased addition of oat flour (Mitra et al 2012)
- Noodle cooked yield decreases with increased addition of oat flour

## Future Studies



Further investigations will focus on:

- Perfecting noodle quality as per preferred textural attributes
- Studying the impact of drying process and addition of oat flour
- Improving total fiber content and  $\beta$ -glucan content of oat noodles

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# Size distribution and quality of Australian oat grains

Sabori Mitra, [Larisa Cato](mailto:Larisa.Cato@aegic.org.au)

Australian Export Grains Innovation Centre (AEGIC), South Perth, WA 6151, Australia

E-mail: [Larisa.Cato@aegic.org.au](mailto:Larisa.Cato@aegic.org.au)

**Keywords:** *Oat grains, Dehulling efficiency, Processing*

The interest in oats grain for human food is increasing worldwide mainly because of its nutritional attributes such as those derived from soluble fibre (1→3) (1→4) -  $\beta$ -D-glucan and protein composition (Wang and Ellis 2014). Australian oat grains are known for its bright colour, plump grain and low moisture. Growth in consumption of oat grains driven by increased awareness of its health benefits and continuing expansion of middle class population has made China a key market for Australian oats. The demand for oats depends on many factors, the most important being its suitability for the actual end use. Processing of oats for human consumption involves size separation of cleaned oat grains to improve de hulling efficiency and minimise groat breakage (Girardet and Webster 2011). This is because smaller oat grains require faster impact dehuller rotor speed to obtain similar dehulling efficiency as larger grains (Doehlert and McMullen 1999). Oat grain size segregation also relate to how the oat processor would use them on a production basis relating to the finished product. There is currently lack of knowledge regarding size distribution and value of Australian oats. Such information is of critical importance to the Australian oat industry for both marketing and production issues. Therefore, the objectives of this preliminary study were to understand the variation of selected physical properties among Australian oat cultivars and impact of their size distribution on some grain characteristics.

Eight oat cultivars (Mitika, Yallara, Dunnart, Bannister, Wombat, Williams, 9WA02Q320-9, 03198-18BG) cultivated in 2015, from two locations of Western Australia (Cunderdin and Pingelly) and South Australia (Riverton and Turretfield) were selected for this study. The experiment growing design was a Demonstration Strip Plot. Oat grains were fractionated into size fractions with slotted sieves with a Carter Dockage tester (Simon Day Ltd, Winnipeg Canada) Model C-XT3. Cleaned oat grain samples were initially sieved using a “00” riddle screen to remove immature grains and free groats. Hectolitre weight (using CBH Chondrometer) were analysed for all varieties. The samples were then sieved sequentially on slotted 2.5, 2.2 and 2.0 mm width sieves. All slots were 19.05mm long. Grains held back by these sieves were labelled as large, medium and small respectively. Grains that passed through the 2.0 mm sieve were labelled as under sized. Sieve sizes used for separations were selected to mimic commercial practices. The collected grains weight of each size was determined and expressed as percentages of the total weight. Minolta colour and NIR groat percentage/ lipid/protein were analysed for oat grains pre and post segregation.

For oat cultivars before segregation, Yallara from all locations from both the states had higher brightness and 03198-18BG had lower brightness in comparison to the

other oat cultivars. Hectolitre weight was highest for 9WA02Q320-9 for all locations in both the states. NIR results show that oat cultivars were higher in protein content and lower in lipid content in South Australia in comparison to Western Australia. The largest percentage of segregated oat grains was the medium size grain (2.5 mm to >2.2 mm sieve size) for most of the cultivars. For segregated samples- grain brightness, groat percentage and oil content increased with decrease of oat grain sizes. Protein content of South Australian samples increased with decreasing grain sizes, however for Western Australian samples no such trends were seen for protein.

From this preliminary study variation in oat grain quality was observed among cultivars, growing location and grain sizes. In future, various quality parameters in addition to the ones included for this preliminary study, will be analysed for these Australian oat cultivars over different growing years and compared to oat cultivars from other countries such as, China. The NIR results will also be validated by doing chemical testing on these oat grains.

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# Viscosity of water and buffer extract as a new tool in selection of oat genotypes for specific end-uses

Damian Gołębiewski, Danuta Boros

Institute of Plant Breeding and Acclimatization - National Research Institute

Radzików, 05-870 Błonie, Poland

E-mail: [d.golebiewski@ihar.edu.pl](mailto:d.golebiewski@ihar.edu.pl)

**Keywords:** *oat, viscosity,  $\beta$ -glucan*

Oat is recognized as a beneficial dietary component that protects against cardiovascular diseases, diabetes and obesity. Besides lower content of starch, high amount of valuable protein and lipids, oat is rich source of dietary fibre, especially of  $\beta$ -glucan, in human diet. In epidemiological study it has been proved the lowering effect of  $\beta$ -glucan on blood cholesterol level and postprandial glucose response (Braaten et al., 1995; Jenkins et al., 2002; Queenan et al., 2007; Granfeldt et al., 2008). Oat is also used for livestock feeding, but its amount in the feed is often limited, depending on the animal species, due to a high content of hulls and fibre, that have negative effect on nutrient density and digestibility (Aimonen and Nasi, 1991). Taking into account significant variability in chemical composition, it indicates therefore, that the same cultivars might have different usefulness either for food or feed purposes and the content of  $\beta$ -glucan is crucial in this respect. For these reasons, selection of oat breeding materials with either high or low content of  $\beta$ -glucan, depending on their future use, is a necessity nowadays.

In order to attain better utilization of existing cultivars and also to achieve substantial progress in breeding, it is necessary to provide appropriate tool to facilitate selection of the appropriate genotypes for these two major end-uses of oat. Such tool seems to be a viscosity assay, which needs modification and validation adapted for specificity of oat and conditions of their processing and it was the purpose of our study.

Material for the study comprised of two hulled and one naked oat cultivars, grown at the same location in 2013 harvest year. Optimization of the viscosity assay was performed using intact as well as dehulled grains. Extracts were prepared from finely ground whole grain (a screen with 1.5 mm openings) with distilled water and HCl-KCl buffer of pH 1.5, used as a solvent. The following factors were examined: dilution rate of grain to solvent (1:3w/v, 1:5w/v, 1:10w/v, 1:20w/v), extraction temperature (30°C, 35°C, 40°C, 45°C, 50°C, 60°C), centrifugation speed of resultant suspension (1000 rpm, 6000 rpm). These factors were examined at the same time of extraction (1h) and were measured on Brookfield Cone/Plate Digital Viscometer, with a 0.8° cone spindle and shear rate of 225 sec applied at 30°C. We also determined components which might have a significant influence on the viscosity value, by analyzing content of  $\beta$ -glucan, protein, lipids and starch in both types of extracts.

Extraction of grain with water at a dilution of 1: 5w/v and with acid buffer at a dilution 1:20w/v gave the lowest error between replicates, a very wide variation between samples. In these conditions, the resultant extract was also sufficiently watery,

and seemed to guarantee a maximum extractability of components responsible for viscosity. The optimum temperature of extraction, that gave the best repeating and a high values of viscosity, was 30°C. Higher temperature, in range 35-45°C and 50-60°C, indicated the involvement of endo-enzymes and starch gelatinization on measured viscosity, respectively. Centrifugation speeds did not have any impact on viscosity of both types of extract. Extract produced from every grain sample of oat was very cloudy, thus differed significantly from extract prepared from the other cereals. The overall finding demonstrated that  $\beta$ -glucan provided the major contribution to viscosity of either extract, moreover lipids and protein evidently participated at it. The study will be continuing to validate these two assays on a greater number of oat samples. We assume, that at the end of our study we will be able to propose two viable protocols, appropriate for selecting oat genotypes for food or feed uses.

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# Improving wheat flour quality by addition of fermented oat seeds

Michaela Havrlentová<sup>1,2</sup>, Katarína Naháľková<sup>2</sup>, Tatiana Klempová<sup>3</sup>, Marek Jašurek<sup>3</sup>, Soňa Gavurníková<sup>1</sup>, Milan Čertík<sup>3</sup>, Peter Hozlár<sup>1</sup>

<sup>1</sup>NAFC – Plant Production Research Institute in Piešťany, Research and Breeding Station Vígľaš-Pstruša, VŠS Vígľaš-Pstruša, 962 12 Detva, Slovak Republic, [havrlentova@vurv.sk](mailto:havrlentova@vurv.sk), [gavurnikova@vurv.sk](mailto:gavurnikova@vurv.sk), [hozlar@vurv.sk](mailto:hozlar@vurv.sk)

<sup>2</sup>Department of Biotechnology, Faculty of Natural Sciences, University of SS. Cyril and Methodius, Nám. J. Herdu 2, Trnava, 917 01, Slovak Republic, [lennndy@gmail.com](mailto:lennndy@gmail.com)

<sup>3</sup>Faculty of Chemical and Food Technology, Slovak University of Technology, Radlinského 9, 812 37 Bratislava, Slovak Republic, [klempovat@gmail.com](mailto:klempovat@gmail.com)  
E-mail: [milan.certik@stuba.sk](mailto:milan.certik@stuba.sk)

**Keywords:** *oat, wheat flour, fermented seed*

Cereals cultivated especially for edible grains used in human and animal nutrition are rich source of carbohydrates and proteins, however their added value given by biologically active compounds such as components of dietary fibre, polyunsaturated fatty acids (PUFAs), pigments, etc. is limited. Therefore value-added cereal-derived biomaterials have been prepared by the fungal solid state fermentations that could be attractive in food/feed industry. Seeds of naked (cultivar Tatran) and hulled (cultivar Vavclav) oats were fermented by the fungal strain *Thamnidium elegans* CCF1456 according Čertík *et al.* (2013). Subsequently, dry fermented biomaterial was grinded to flour and in doses of 2.5, 5.0, 7.5, and 10% (w/w) mixed with the control wheat flour (commercially available) to prepare composite flours. Biochemical parameters of nutritional quality as well as rheological and sensory evaluations were obtained in flours, doughs, and breads, respectively. For bread preparation, all necessary ingredients (basic wheat flour, baking yeast, salt, sugar, lard, water) were mixed together and flour from fermented biomaterials was added in the final stage of mixing. After rising, bread loaf (250 g divided into 5 loafs) was baked at 230°C for 20 min. After cooling, analysis of lipid content and fatty acid composition according Klempová *et al.* (2013), starch content according Ewers polarimetric method, and proteins using automatic CNS analyzer were done. Contents of **β-D-glucan** and total dietary fibre were examined using enzymatic kits of Megazyme (Bray, Ireland). The application of fermented biomaterials into bakery products enrich not only final products with new compounds (PUFA, ergosterol, etc.), but also very significantly changes the rheological and nutritional properties of dough and breads such as dough development time and stability, content of starch, proteins, β-D-glucan, dietary fibre and others. In our experiment, sensorial quality of new composite products on the bases of fermented oat seeds was acceptable for customers. In biochemical evaluation, fermentation process increased the amount of total dietary fibre in entry cereals seeds from 18.39% for naked and 21.57% for hulled oats to 24.45% and 26.69%, respectively. Also, there was an increase in total proteins content observed, from 13.06% and 11.81% to 18.54% and 14.59% for naked and hulled seeds. The content of β-D-glucan decreased with fermentation process, in naked oats from 4.73% to 4.07% and in hulled

one from 3.5% to 2.92%. Moreover, prefermented naked and hulled oat contains 0.45 g and 0.32 g g-linolenic acid/kg, respectively. The addition of fermented oat products into wheat flour increased linearly with the added dose the amount of all monitored quality parameters. The content of total dietary fibre was increased from 2.01% in wheat flour to 6.42% for naked oat and to 9.49% for hulled one. In bread, total dietary fibre content was increased from 5.02% to 11.59% for naked and 17.59% for hulled seeds. In control wheat flour the content of proteins was 10.9% and its increase was observed in composite flours and breads linearly with the dose of fermented oat seeds products. Differences between flours and breads were not significant and were in the range 12.38-13.01% for naked and 12.28-12.82% for hulled oats. The amount of <sup>2</sup>-D-glucan was affected by the baking process negatively and a decrease was observed in breads compared to flours. Higher amounts of this parameter were observed in products with naked oat seeds (0.37%-0.51% for flours and 0.28%-0.47% for breads) compared to hulled seeds (0.3%-0.39% in flours and 0.25%-0.34% in breads), however differences were not significant. According to our results it can be confirmed that biotechnologically prepared and enriched cereals are a promising tool for the market of innovative functional cereal food products.

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# **POSTER SESSION**

**Sustainable Farming Systems,  
Commercialization,  
Seed Production, and Royalties**



## POSTER PRESENTATIONS

### Effect of fertilization on important content and quality parameters of common and naked oat

Peter Hozlár<sup>1</sup>, Katarína Matúšková<sup>1</sup>, Michaela Havrlentová<sup>2</sup>, Andrea Lančaričová<sup>2</sup>,  
Svetlana Šliková<sup>2</sup>, Daniela Čemanová<sup>1</sup>

<sup>1</sup>NAFC – Plant Production Research Institute in Piešťany, Research and Breeding Station  
Vígľaš-Pstruša VŠS Vígľaš-Pstruša, 962 12 Detva, Slovak Republic,

<sup>2</sup>NAFC – Plant Production Research Institute in Piešťany, Bratislavská cesta 122,  
921 68 Piešťany, Slovak Republic,  
E-mail: hozlar@vurv.sk

**Keywords:** *oat, fertilization, quality parameters*

Oat was sown in a stationary experiment based on the Research and Breeding Station Vígľaš-Pstruša (hereinafter referred to as RBS) already in 1957. Variants of fertilization were not changed since the establishment of the stationary experiment. This study is focused in the relationship between the examined traits of lines and varieties and fertilization variants with increasing doses of nitrogen, either alone (0 - 40 - 80 - 120 kg N.ha<sup>-1</sup>) (N-nutrition) or combined with P and K nutrition (60 kg P<sub>2</sub>O<sub>5</sub> and 60 kg K<sub>2</sub>O) (NPK-nutrition). The aim of this experiment was to define the effect of fertilization on selected important quality parameters in oat. In the experiment, 12 liming variants of fertilization were used. Five oat genotypes (2 common and 3 naked) were grown on each variant and yield, thousand grain weight (TGW), volume weight (VW), β-glucan, protein, and fat content were analyzed.

In oat yield, statistically highly significant difference between years 2013 and 2014 were observed, when significant higher average yield was recorded in 2014. Similarly, statistically highly significant difference was observed in fertilization, when the highest average yield was recorded at variant 026 (5.99 t.ha<sup>-1</sup>) and the lowest at 011 (2.49 t.ha<sup>-1</sup>). Statistically highly significant difference was observed in yield among genotypes, the lowest average yield (3.79 t.ha<sup>-1</sup>) was recorded in naked oat 100260 CN and the highest (5.28 t.ha<sup>-1</sup>) in common oat Valentin. TGW was not statistically significantly affected by fertilization and year. The highest average value of 32.68 g was found in the fertilization variant 013 and the lowest (28.58 g) in unfertilized variant 011. Variety influenced TGW highly significant, with the highest average of TGW in the variety Valentin (38.57 g) and the lowest (22.57 g) in 100260CN. VW was not significantly affected by fertilization. The highest average VW value (59.3 kg.100 l<sup>-1</sup>) was found in the fertilization variant 023 and the lowest in the unfertilized variant 011 (56.82 kg.100 l<sup>-1</sup>). Variety and year influenced statistically highly significant VW with the highest average of total VW (65.1 kg.100 l<sup>-1</sup>) in the naked oat 100260CN. The lowest average VW had the common variety Valentin (51.71 kg.100 l<sup>-1</sup>). The average β-glucan content was not influenced by fertilization and year. The highest average β-glucan content (3.46%)

was found in the variant 024 and the lowest (2.81%) in the control variant 011. Variety influenced the average  $\beta$ -glucan content statistically highly significant, whereas the highest average content (3.68%) showed 100260CN and the lowest (2.55%) Valentin. The protein content was statistically highly significant influenced by N fertilizer and variety. This was reflected in all variants fertilized with N from the lowest dose of 40 kg.ha<sup>-1</sup> (variants 013, 022) to high dose of N (variant 016 with 150 kg.ha<sup>-1</sup>). Similarly, statistically highly significant differences in protein content were given by genotype. The highest average protein content was found in 100260CN (14.96%) and the lowest in Vaclav (11.04%). The fat content in naked oats was not statistically significantly affected by fertilization and year. The highest average value of fat content (7.60%) was found in the variant 011 and the lowest in 015 (6.57%) and 016 (6.82%), both with the highest dose of NPK. Variety influenced the fat content statistically highly significant and the highest content (7.69%) showed naked oat 100260CN.

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# **The strength of growth and the degree of injury to the seed varieties of oats depending on the ecological conditions of cultivation**

Tazhihan Tleubaeva., Rinat Kassenov

The Kazakh Research Institute of Agriculture and crop production, Almalybak,

The Republic of Kazakhstan

Address: 040909, Republic of Kazakhstan, Almaty region, Karasai District, Almalybak, Erlepesova St.1.,

tel.8 (727) 7153130, 8 (727) 7153057, fax. 388-39-25,

E-mail: [rinat.kasenov.83@mail.ru](mailto:rinat.kasenov.83@mail.ru)

***Keywords: germination, crop quality, vitality, reproduction, seed, the strength of growth, variety, injury seeds***

To create a sustainable food supply for livestock is one of the main places take the oats, grain which is a valuable and nutritious food for farm animals, dietary and therapeutic food for humans.

Oats - one of the most common and important crops. The primary factor in increasing the production of grain oats with high sowing and yield qualities is the genetic potential of varieties. Therefore, the increase in grain production played a major role Seed.

The territory of the South, East and South-East of Kazakhstan is situated in four areas: unsecured and needy bogara, irrigation and mining area in different soil and climatic conditions and the development issues of seed crops in contrasting conditions is of great theoretical and practical importance.

The study on the allocation of ecological zones on the ease of soil and climatic conditions for the production of seeds of grain were carried out in five contrasting agro-ecological zones of the South, South-East and East of Kazakhstan.

The objects of study were promising and approved for use in the production in the Republic of Kazakhstan varieties of crops, in particular, and oats.

The results of the laboratory work showed that all the studied varieties of seeds were viable; vigor and germination of seeds of varieties were within 95-98%.

Depending on the conditions of cultivation, biological characteristics of cultivated varieties and agronomic and soil and climatic conditions of the studied cultures were formed large seeds of varieties of oats Zhorga and Kulan in a foothill zone - and 33,8g 32,6g and less under the medium-area: respectively – 27,5g and 30,4g.

Approved for use oat varieties differ in the number of damaged seeds, depending on the vertical zoning of their cultivation. According to a variety of spring oats was the degree of injury in the zones within the 60,0% - 73,5%. At the same time the varieties of oats fewer injuries had seed grown in a middle mountain zone. Thus, the varieties of oats Jurgen and Kulan in this area of damaged seeds were respectively: 60,0% - 66,5% (from 8.5% macrodamages fetus), while the seeds of the same varieties grown in the foothill region, these figures they were as follows: 69,5% - 73,0% (from 19.5% macrodamages fetus).

Agricultural units are therefore proposed to focus on sowing qualities of seeds and sow the seeds of opportunity with the lowest injury of seeds.

When evaluating the properties of sown seeds (laboratory germination) ignores the value of the seedlings, in particular, the length and number of roots that have a major effect on the germination rate, power and germination.

The most complete sowing qualities of seeds are characterized of growth, i.e. the ability of seeds to germinate faster and focus, as well as the intensive growth of plants in the field. It is determined at germination of seeds under controlled conditions and is expressed as a percentage of strong seedlings to the total number of seeds in the sample.

The intensity of the initial growth of the seed is the main criterion for the viability of seeds, influencing later in the productivity of plants.

In our studies consistently awarded a high initial growth rate in the seeds grown in the conditions of a foothill zone.

The average grades of 10 hours in this region rose seedlings from 88,0% to 92,5%, along with high power growth in seeds during germination the seedlings formed with five roots.

Low levels of growth compared with other zones were at Alaman oat seed varieties and Baige grown in middle zone where the power increase was in the range of 75,5% to 80,0% while in seeds during germination of seedlings are formed with three roots.

Determination of growth of seeds provides more objective assessment of the ability of their seeds for germination and establishment of seedlings, influencing later in the productivity of plants. The value of growth of seeds should be introduced in the calculation formula sowing date and seed it with regard to set the standard of their seeding.

According to a comparative study of germs in the laboratory can predict the level of the crop in the field and to make recommendations on the selection of more productive seed lots.

For the specialization of seed placement is of particular importance in those crops under natural conditions in which the seeds are formed consistently high quality. In our studies, the best yielding properties, high strength growth of the seeds had formed in a second foothill zone.

# **The export oaten hay industry in Australia**

Peter D. McCormack

South Australian Research & Development Institute, Australia  
[peter.mccormack@sa.gov.au](mailto:peter.mccormack@sa.gov.au).

Traditionally oaten hay has been used as a fodder supplement to domestic intensive livestock and dairy industries in Australia. Demand from Japan for premium high quality oaten hay commenced in the early 1990's.

The industry developed a supply chain model that could consistently provide quality oaten hay to the Japanese dairy and Wagyu beef markets. This model was based on sound agronomic benefits to growers, marketing of oat hay varieties, and production of hay with inherent high feed quality traits.

Increased demand for Australian export oaten hay has seen continued growth in the market to a point where export oaten hay is a major agricultural industry in Southern Australia. In the early 1990's exports were at 100,000 tonnes per annum and in 2016 are expected to be around 1,200,000 tonnes. Demand continues to increase at the rate of 50,000 to 100,000 tonnes per annum based on Australian oaten hay being a reliable source of clean green protein.

Export oaten hay has provided a beneficial export industry that has become an important rotation in Australian farmers cropping programs from an agronomic and financial perspective.

# Grain Industry Association of Western Australia (GIWA) Inc.

Will Carrington-Jones<sup>1</sup> Rachel Nash<sup>2</sup>

<sup>1</sup>Chair, GIWA Oat Council, Grain Industry Association of Western Australia Inc (GIWA),  
Perth, Western Australia, Australia.

<sup>2</sup>Marketing and Communications Manager, Grain Industry Association  
of Western Australia (GIWA) Inc., Perth, Western Australia, Australia.  
E-mail: [rnash@giwa.org.au](mailto:rnash@giwa.org.au)

***Keywords: Grain, industry, WA, Western Australia, oats, Perth, Australia, 2020, commercial, scientific, milling, processed, product, international, conference, GIWA, DAFWA, grower, export, trade, supplier, service, processor, value, chain***

## GIWA Background

The Grain Industry Association of Western Australia (GIWA) Inc is a value chain focussed, member-based industry association formed in 2008 after the deregulation of the Australian Wheat Board, to provide a precompetitive industry body to represent Western Australia's export dominated grain industry.

GIWA represents the interests of its members, from researchers to growers to input suppliers and service providers, processors and the trade. GIWA's purpose is to grow the value and profitability of the Western Australian grain industry through:

- Leadership and industry self-regulation, including the setting of standards and grain variety rationalisation
- Precompetitive industry communication and information exchange through its seven Councils
- Providing policy and project solutions for grain value chain issues
- Providing administrative services for a variety of projects

GIWA is a member of Grain Trade Australia and collaborates closely in Western Australia as well as at a national and international level, on grain value chain issues with the Department of Agriculture and Food WA, the Grains Research & Development Council, the Australian Export Grain Innovation Centre, and other representative agri-food and grain industry bodies.

## GIWA Oat Council

The GIWA Oat Council is one of seven GIWA Councils, which meets several times a year. The purpose of the GIWA Oat Council is to:

- Represent the Western Australian oat industry in the area of plant breeding, agronomic development, production, handling and processing of oat varieties in order to promote and safeguard the industry's long term interests
- Encourage sustainable production and marketing of premium quality oats

GIWA Oat Council members include CBH, Quakers Oats, Unigrain, South Australian Research and Development Institute (SARDI), ConsultAg, Department of Agriculture and Food of WA (DAFWA), Grains Research and Development Corporation (GRDC), Australian Export Grains Innovation Centre (AEGIC), Gilmac, AEXCO, growers and researchers.

### GIWA - 2020 International Oat Conference

The GIWA Oat Council is presenting a bid at the 2016 International Oat Conference to host the 2020 International Oat Conference in Perth, Western Australia.

The Western Australian oat industry is a major international exporter of high quality food-grade milling oats and processed oat products. With Australia's proximity to Asia and the end consumers of oats, GIWA believes the global oat arena will benefit from a commercial and scientific perspective from holding the 2020 International Oat Conference in Perth, Western Australia.

GIWA has successfully delivered five annual GRDC Grains Research Updates in WA (formerly Agribusiness Crop Updates), a premier event in the WA grains calendar with over 500 attendees. The events attract international keynote speakers along with attendees, exhibitors and presenters from around Australia. The 2015 and prior events were held at Crown Perth and 2016 was held at Perth Convention and Exhibition Centre in the city centre.

Research Updates is a two day program showcasing the latest research, technology, market development and management innovations to improve the productivity and profitability of the WA grains industry. A number of regional events are also arranged each year.

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# Climate changes influence at oats vegetation in European part of Russia

L. Novikova, I. Loskutov

Federal Research Centre – N.I. Vavilov Institute of Plant Genetic Resources (VIR),  
St. Petersburg, Russia

E-mail: [l.novikova@vir.nw.ru](mailto:l.novikova@vir.nw.ru)

**Keywords:** *oats, varieties, climate changes, temperatures over 15°C*

Climate changes are the important factor of modern crop production. To turn losses from them into the profit, it is necessary to adapt agriculture to changes of a bioclimatic potential of regions. The first purpose at the solution of this problem is identification of the factors influencing plants at climate changes. In this work we analyzed long-term data (1980 – 2011 years) of economic valuable characters of oats varieties. These varieties were used as standards in research of oats collections at four VIR branches: at Pushkin (St.-Petersburg), Moscow, Tambov, Krasnodar regions. In addition vegetation of 16 accessions of wild oats in Pushkin in 1987 – 1999 was analyzed.

At all points from 1980 was observed growth of the sums of active and effective temperatures. The sums of temperatures above 10°C grew with the speed about 150 - 300°C/10 years, above 15°C 190 - 220°C/10 years. Date of transition of temperatures over 10°C moved for earlier dates with a speed of 1 - 5 days/10 years. There were weak tendencies to rainfall increasing, significant for branch in Tambov region (for period with temperatures higher than 10°C with a speed of 54.1 mm/10 years).

Dates of sowing, germination, heading and maturing have moved for earlier time. At Pushkin there were significant shortening of periods from heading to maturity (-4.6 days/10 years), and vegetation at all (-4.0 days/10 years). In other points duration of the vegetative period of standard varieties of oats poorly increased, as has shown the analysis, for various reasons. Regression analysis revealed the main factor of vegetation dynamics is growth of sum of effective temperatures over 15°C ( $\Sigma T_{ef15}$ ), that is temperatures minus 15°C. In Pushkin this factor explained 66% of vegetative period variability between years. At points in Moscow and Krasnodar regions temperature rising was compensated by growth the length of period with temperatures between 10 and 15°C ( $L_{10-15}$ ) in spring. In drought conditions of Tambov region temperature rising, was compensated by growth of rainfall at the time with temperatures over 15°C ( $P_{15}$ ). Such parallel time series (panel data) can be united in one equation for speeds of change of all variables from year to year, so-called equation in differences. For oats varieties in the European part of Russia vegetation duration (L) may be describe by the following united model:

$$\Delta L = -0,06 - 0,04\Delta \sum T_{ef15} + 0,15\Delta L_{10-15} + 0,01\Delta P_{15}$$

Height of a plant and mass of 1000 grains generally had negative tendencies, with exception of Tambov region, where they increased and correlated with rainfall.



The strongest revealed dependence – from the sum of effective temperatures higher ( $\Sigma T_{\text{ef}15}$ ). Height of a plant has shown medium correlations with  $\Sigma T_{\text{ef}15}$ , united model for the studied oats height (H):

$$\Delta H = -0,50 - 0,07 \Delta \Sigma T_{\text{ef}15}$$

For mass of 1000 grains relations with climatic conditions haven't been found that, perhaps, is a consequence of conservatism of this sign and the mediated nature of his formation. Most yield tendencies were positive, but relations with climate factors were not revealed. Yield was determines efficiency by vegetative stage by correlation with high of plant (correlation coefficients was from  $r=0.39$  to  $r=0.72$ ), with mass of 1000 grains ( $r=0,17 \div 0,63$ ).

Wild oats accessions, studied in Pushkin in 1987 – 1999, differed by vegetation duration from 80 to 104 days. All accessions shortened vegetation period on 0,5 to 3,3 days/year. This reduction as well as for the standard variety, was caused by reduction of the period from ear formation to maturing with the speed 0,2 – 3,2 days/year. Regression analysis revealed this reduction was caused by growth the sum of effective temperatures over  $15^{\circ}\text{C}$  ( $\Sigma T_{\text{ef}15}$ ). There was one more factor - mean temperature of 15 days after sewing ( $T_s$ ). Rising of this temperature slowed vegetation. United model for wild oats accessions:

$$\Delta L = -1,82 + 2,92 \Delta T_s - 0,04 \Sigma T_{\text{ef}15}$$

Accessions of wild oats differed by rates of reaction on spring and summer temperatures rising: accessions which the longest vegetative period in the conditions of Pushkin had the largest rate of delay of development at high temperatures after sewing. Standard variety has one of the least rates of reaction on vernalisation and highest for summer temperatures growth.

Thus, the major factor of regulation of vegetation for cultivated and wild oats were sum of temperatures above  $15^{\circ}\text{C}$ . Their rising caused shortening oats vegetation at the most northern point of investigation. At other points rainfall and length of spring with temperatures  $10 - 15^{\circ}\text{C}$  were important factors too. Rainfall growth caused increase in duration of vegetation, plant height, mass of 1000 grains and productivity in droughty conditions of Tambov region. For collection study in such changing conditions became especially important using standard varieties. For adaptation oats cultivation can be used earlier sewing, more late-ripening varieties.

# Transforming Western Australian oat production

Garren Knell<sup>1</sup>, Trent Butcher<sup>1</sup>, Georgie Troup<sup>2</sup>, Robert Loughman<sup>2</sup>

<sup>1</sup> ConsultAg Pty Ltd, Narrogin, Australia

<sup>2</sup> Department of Agriculture and Food, Western Australia, Northam and Perth, Australia.

E-mail: [robert.loughman@agric.wa.gov.au](mailto:robert.loughman@agric.wa.gov.au)

## Background

Western Australian oat producers have developed unique cropping skills to transform traditional oat production to fit oats into the farming system on a large scale.

Oats typically had formed a relatively minor component of Western Australia's (WA's) grain farming systems, receiving low inputs and low management emphasis. Conventional methods of production placed oats late in the sequence of sowing after other crops such as canola, wheat, barley and grain legumes. As a grain or hay crop oats had previously provided seasonal feed reserves for stock, while excess production could saturate traditional markets resulting in low and variable profits.

## Current situation

The growth in Asian demand for oat grain as food, together with the advent of high yielding milling oat varieties, has enabled growers to substantially change oat production.

- Large scale oat producers (1000-3000 ha p.a.) carefully plan oats into their farming system. They identify oat paddocks the year before production so they can be set up in preparation with the preceding crop. Paddock preparation includes harvest weed seed management ahead of the oat crop.

- Large scale oat producers frequently forward contract the production and price of a significant proportion of their crop, through closer relationships with oat manufacturers and traders. In this way prices and production requirements are established prior to seeding, giving all participants in the supply chain confidence in the industry.

- During production, up to 75% of oat area on individual farms is sown ahead of other crops, often sown into dry soil (prior to seasonal rains). Using excellent depth control and seeding implements that form soil furrows to collect early rains. The seeding methods are also adaptable to novel weed control in a system to improved use of pre-emergent herbicide. The resulting crop produces a canopy highly competitive against weeds that is also actively managed for nutrition and disease.

- At harvest weed seed management is again emphasised, with chaff streams collected or concentrated for removal or selective burning, leaving standing stubble for prevention of soil erosion.

Integrating oat production into cropping enterprises helps grain growers reduce environmental, agronomic and financial risks in farming businesses.

- Cropping risks due to the environment are reduced with oats. Early crop establishment, including dry sowing, maximises water use efficiency and reduces the potential for drought stress from dry springs. Oats are relatively tolerant of winter wa-

terlogging and spring frosts. Hence oats can be sown in areas of the landscape where other crops present unacceptable risks.

– Cropping risks due to agronomy can be well managed with oats. Dry sowing at moderate to high seeding rates enhances crop competition against weeds, particularly annual rye grass (*Lolium rigidum*). Oats, including oaten hay, can be a preferred crop for the management of some weed challenges in crop intensive farming systems. Innovative combinations of seeding systems and herbicide can improve pre-emergent herbicide tolerance and enhance the opportunity of low-cost herbicide.

– Cropping risks due to price have improved with the establishment of forward pricing contracts with processors and traders. Fixed or minimum price contracts can be established pre-seeding, incorporating production risk management. Industry reform of oat grades established two milling grades and has simultaneously reduced the production emphasis on feed oats and improved the opportunity to achieve milling grade specifications (1). As a result, risks with oat production have reduced and the area sown to oats is very responsive to the autumn price immediately preceding sowing.

### **Future prospects**

The Western Australian oat industry is now a major international exporter of high quality food-grade milling oats and processed oat products. The future of the industry is underpinned by development of new milling oat varieties, fostered through the close association of the WA and Australian industry with the National Oat Breeding Program (1, 2). Australia also has an effective end point royalty system (3) that protects Plant Breeder's Rights. New oat varieties are also independently tested under a National Variety Trial Program (4), funded by the Grains Research and Development Corporation (5). Up-coming varieties are also streamed into a Regional Agronomy Program (6) to optimise their adoption and utilisation on-farm.

Asia has emerged as a consistent and growing market for food grade oats. Continual development of large scale farming systems is enabling the reliable and consistent production of high quality, clean and sustainably produced oats. Together with well-established market relationships and proximity to key Asian markets, this provides a unique opportunity for the Australian oat industry to grow and develop further in response to international market requirements.

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## Development of an improved single ear/small sample thresher

E. John Stevens, John Hampton, Geoff Gray, Keith Armstrong,  
Dinesh Pariyar, Adrian Russell, Bill Angus

E. John Stevens, Flexiseeder Ltd, Christchurch, New Zealand.

Email: [stevensj@flexiseeder.com](mailto:stevensj@flexiseeder.com)

John Hampton, Lincoln University Seed Research Centre, New Zealand.

Email: [Hamptonj@lincoln.ac.nz](mailto:Hamptonj@lincoln.ac.nz)

Geoff Gray, Geoff Gray Ltd, Christchurch, New Zealand.

Email: [gmlgray@xtra.co.nz](mailto:gmlgray@xtra.co.nz)

Keith Armstrong, Global Oats Ltd, Christchurch, New Zealand. Email: [keith@globaloats.co.nz](mailto:keith@globaloats.co.nz)

Dinesh Pariyar, Nepal Agricultural Research Centre, Kathmandu, Nepal.

Email: [rajbiraje@yahoo.com](mailto:rajbiraje@yahoo.com)

Adrian Russell, Plant Research (NZ) Ltd, Christchurch, New Zealand.

Email: [adrian@plantresearch.co.nz](mailto:adrian@plantresearch.co.nz)

Bill Angus, Email: Global oats (UK) Ltd, Woolpit, Suffolk, United Kingdom.

Email: [bill@anguswheatconsultants.com](mailto:bill@anguswheatconsultants.com)

Participatory varietal selection to offer farmers a choice of varieties suited to their needs is currently being implemented in a cool season crop improvement programme in Nepal focused mainly on forage oats. Head row selection is a useful mechanism for rapidly improving desirable traits, but manual threshing of ears is labour intensive. The need for an efficient single ear small sample thresher was identified, but suitable equipment was not available in Nepal. The Flexiseeder ad hoc Help Group located a small sample thresher built in New Zealand over thirty years ago. In this poster we describe how this machine was modified, built and tested to produce an up-graded version fit-for-purpose, not only in developing (eg, Nepal) but developed (eg, New Zealand and Northern Hemisphere) seed chains.

## **Fodder oats in Nepal: fulfilling farmer needs**

Keith Armstrong, Dinesh Pariyar, John Hampton,  
E. John Stevens, Adrian Russell, Bill Angus

Keith Armstrong, Global Oats Ltd, Christchurch, New Zealand. Email: [keith@globaloats.co.nz](mailto:keith@globaloats.co.nz)

Dinesh Pariyar, Nepal Agricultural Research Centre, Kathmandu, Nepal.

Email: [rajbiraje@yahoo.com](mailto:rajbiraje@yahoo.com)

John Hampton, Lincoln University Seed Research Centre, New Zealand.

Email: [Hamptonj@lincoln.ac.nz](mailto:Hamptonj@lincoln.ac.nz)

E. John Stevens, Flexiseeder Ltd, Christchurch, New Zealand.

Email: [stevensj@flexiseeder.com](mailto:stevensj@flexiseeder.com)

Adrian Russell, Plant Research (NZ) Ltd, Christchurch, New Zealand.

Email: [adrian@plantresearch.co.nz](mailto:adrian@plantresearch.co.nz)

Bill Angus, Email: Global oats (UK) Ltd, Woolpit, Suffolk, United Kingdom.

Email: [bill@anguswheatconsultants.com](mailto:bill@anguswheatconsultants.com)

The introduction of winter fodder production to Nepal, based mainly on fodder oats, has been spectacularly successful as it has allowed improved animal nutrition and health, increased milk production and therefore farmer incomes, and reduced workloads (particularly for women). Seed of improved fodder oat varieties was originally introduced to Nepal in the 1980s, but unfortunately formal maintenance and seed multiplication of the selected varieties was not achieved. Since 2000, a novel New Zealand-based oat improvement initiative, coupled with the winter fodder production programme, has prompted renewed interest in this crop, and since 2004 six new varieties have been released based on parent material originally supplied from Canada, New Zealand and India. Under the new Cool Season Crop Improvement Programme-Nepal, an early generation seed maintenance and production nursery network is being established, linking research, extension and farmers. In this poster we briefly review the history of oat introductions, and provide a framework for the provision of genotypes that fulfill farmer needs for quick growing, high quality dry matter producing, multi-cut varieties.

# **Control weeds integrating agricultural cultivation methods and herbicide in oat field**

XiaoYu Zhang, HongYou Zhou, BaoZhu Dong, HuanWen Meng

Agronomy college, Inner Mongolia Agricultural University, Hohhot, China 010019

E-mail: [zxy2000@126.com](mailto:zxy2000@126.com)

***Keywords: weeds; oat; agricultural cultivation methods; herbicide***

Weeds are major factors affecting production of oat. No effective methods were used for controlling weeds of oat in China. If weeds are sevrer artificial weeding is used, but the cost is higher. 2,4-D Butylate was sometimes used for control dicotyledon weeds, but it is phytotoxicity to oats if using time and concentration are not appropriate. Controlling gramineous weeds of oat is difficult. In 2009 to 2013, in order to control weeds of oat, sowing date and density, watering, ploughing, using low toxicity and residue herbicide were researched. The results showed among the five sowing date of May 2, 9, 16, 23 and 31, the weed density on May 2 was maximum at 50 plants/m<sup>2</sup>, and that of May 31 was minimum at 32.90 plants/m<sup>2</sup>. 7 to 10 days before sowing, watered for quickly germinating of weed seed, and then shallow tallaged 10cm, the germinated weeds would be cut. Among the line space of 10 cm, 15 cm, 20 cm, 25 cm and 30 cm (seed quantity of 150 kg/hm<sup>2</sup>), the 15 cm was the best, had fewest weeds and highest yield. The herbicide 45% Stomp CS (BASF Corporation) of 2250 ml/hm<sup>2</sup> to 2750 ml/hm<sup>2</sup> with water of 900 kg/hm<sup>2</sup> was spraied to siol surface after sowing, could control weeds of 81.41% to 93.45% in different field. The gramineous weeds were controlled 88.97% to 100% in different field, and this herbicide was not phytotoxicity to oats. The yield was increased 20%. In a short, later sowing in sowing period, 7 to 10 days before planting watering, then loughing 10cm befor sowing, reasonable sowing density with line space of 15 cm, applying herbicide of 45% Stomp CS could effectively control the weeds of oat.

# Prediction of some quality parameters of oats by using NIR

Turgay Şanal<sup>1</sup>, Özge Yıldız<sup>2</sup>, Asiye Seis Şubaşı<sup>1</sup>, Tülin Özderen<sup>1</sup>,  
Dilek Özay Sivri

<sup>1</sup>Central Research Institute for Field Crops, Yenimahalle-Ankara, Turkey

<sup>2</sup>Aegean Agricultural Research Institute, Menemen-İzmir, Turkey

<sup>3</sup>Hacettepe University Department of Food Engineering, Beytepe-Ankara, Turkey

E-mail: [turgay.sanal@tarim.gov.tr](mailto:turgay.sanal@tarim.gov.tr)

**Keywords:** Oat,  $\beta$ -Glucan, Protein, Moisture, NIRS

The objective of this study was to test the potential utilization of NIR spectroscopy technique to predict test weight, thousand kernel weight, moisture content, protein content, husk ratio, beta-glucane content, ash content, sieve ratio and flour colour (L,A,B). 64 winter and 49 spring type oats cultivar were grown in two different location (spring type; Edirne and Kırklareli and winter type Menemen and Kırklareli) in 2014-2015 growing session and those samples were used to develop calibration. All the grain samples were scanned by using NIR Systems, Inc 6500. Spectra were obtained by the wavelength scanning instrument using a small ring cup. A scanning range from 400 to 2500 nm and wavelength increments of 2 nm were used. Diffuse reflectance was recorded as  $\log 1/R$ . The samples were hulled by using Codema Laboratory Oat Huller. Hulled samples were scanned and the samples were milled by using ultra centrifugal mill (Retsch mill, ZM 200, Germany) with 0.5 mm sieve then the milling samples scanned again. The wet analysis of the material were done according to AACC and ICC methods analyses. The relationship between the results obtained by classical methods and NIR spectra were investigated by applying various mathematical models MPLS and PC on 0441, 1441, 1661, 1881, 2441, 2661, 2881, 3441, 3661, and 3881 with different scatter correction. The model which had the highest coefficients of determination ( $R^2$ ) value was identified.  $R^2$  and cross-validation (1-VR) values of the MPLS mathematical models obtained from the calibrations were 0.9063 and 0.8203 (3441-None); 0.7408 and 0.6258 (1661-Snv only); 0.8753 and 0.85 (3441\_Snv and detrend), 0.8708 and 0.782 (3441-none), 0.8078 and 0.4184 (3441-None), 0.3821 and 0.1984 (3441-None), 0.8238 and 0.4101 (3661-Snv and detrend), 0.8842 and 0.7646 (3441-None) for test weight, tkw, protein content, moisture content, beta-glucane content, husk, ash content and b value respectively. It can be concluded that NIR spectroscopy technique can be used reliably to predict most of those parameters content in oats samples in breeding material.