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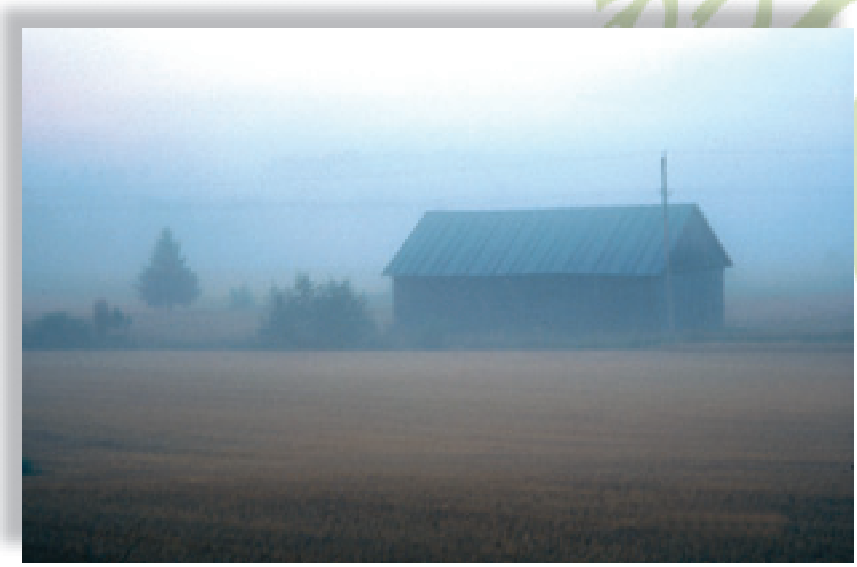
7th International Oat Conference

Pirjo Peltonen-Sainio and Mari Topi-Hulmi (eds.)



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Summary

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At the 6th International Oat Conference, held in New Zealand, in 2000, it was agreed that the next conference would be held in Helsinki, Finland, in 2004. The National Organising Committee of the forthcoming conference gave a warm welcome to the important task devoted to oats.

With the conference theme, *Born to be functional*, the National Organising Committee aspired to emphasise the essence of oat as a crop - the thorough functionality we have experienced in oats in large context. The Conference Program and Proceedings cover the following main areas with titles: Born to be functional; Genetic resources; Breeding and biotechnology (quality, yield and resistance); Markets, products and applications (feed, food and non-food) and Production chain. This proceedings is a compilation of eight short papers written by keynote speakers, and 140 abstracts of oral and poster presentations.

Key words: Avena sp., oat, functionality, processing, feed, food, non-food, genetic resources, plant breeding, biotechnology, quality, yield, resistance, production, agronomy, crop physiology, markets, products, applications

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Acknowledgements

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Born to be functional

Oat – a multifunctional grain

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Abstract
The multifunctional uses of oat include animal feed, human food and raw material for food, health care, and cosmetic products. The major components of oat that contribute to its functions include protein, oil, starch and β-glucan. In addition, there are minor components, including tocols and avenanthramides, that have antioxidant properties and may contribute to human health and well being.

Key words: food, feed, protein, oil, β-glucan, avenanthramides, tocols

Introduction

Like most other grains, oat is used as feed for livestock and pets and food for humans. Oat is considered to be a nutritious source of protein, carbohydrate, fibre, vitamins and minerals, and it contains minor constituents that are believed to contribute to human health and well being. Furthermore, oat has some unique functional properties that make it a useful raw material for a number of products, especially in the food, medical, and cosmetic areas. Some of these products are in the market place, while others are in the research and development phase.

Uses of oat

Animal feed. Livestock feed rations are measured nutritionally and economically against a standard combination of maize and soybean meal. Oat is an important local feed grain in areas where the climate does not allow the production of maize and soybean. The presence of the hull, which comprises about 25% of the grain weight, is well tolerated by ruminant animals although it reduces the energy density of the feed. Whole oat is the preferred grain for horses, because the hull aids in digestion. Oat groats and hulless oat are superior to whole oat for poultry and swine, although oat is inefficiently utilized by young chicks because of the high β-glucan content. Research is underway to utilize oat for aquaculture.

Human food. Oat has long been recognized as a good source of protein and fibre for human food. The protein concentration is relatively high, and the amino acids are well balanced for a cereal grain. The soluble fibre (β-glucan) is known to reduce cholesterol and lower the risk of heart disease. Dietary fibre, consisting of cellulose, nonstarch and noncellulosic polysaccharides, and lignin, has been shown to protect against colorectal cancer. Oat exerts beneficial effects on plasma glucose and insulin response, which is particularly important for the control of diabetes. Oat also contains minor constituents, including tocols and avenanthramides, that may have antioxidant properties and deliver health benefits to consumers. Lignans and phytosterols have anticancer effects. Oat is consumed in several forms, including rolled oats, a component of cold cereals, and as flour, which is blended with wheat flour to make bread.

Raw material. Some of the oat grain constituents are valuable as ingredients or starting materials for several types of products. Oat β-glucan has received the most attention and has a number of uses and potential uses. The lipid fractions are also potentially valuable, especially the polar fraction. The other major components, protein and starch, have received little attention as isolated components, although they contribute to the function of the whole grain. Any fractionation scheme to produce high-value components must also find uses for these lower-valued co-products in order to be economically feasible. Minor constituents of oat are also of interest, especially some of the secondary products that have antioxidant or other health-promoting properties.

Oat chemistry and function

Protein. North American oat typically contains 15-20% protein when measured in the groat, with Scandinavian oat somewhat lower. This is a higher concentration than most other grains. The amino acid balance of oat protein is also superior to that of most other grains, and this is because its primary storage protein is a globulin. Globulins have a higher concentration of lysine and other essential amino acids than do typical cereal storage proteins, the prolamins. “High-lysine” mutants, which in maize, sorghum and barley, are due to reduction in the prolamin fraction, are unlikely to occur in oat because of its already low proportion of prolamin. Researchers have prepared oat protein concentrates by both wet and dry milling techniques and characterized their properties. A US company produces a product containing oat protein with native starch, which is intended primarily for personal care products. For both food and feed, high protein is better. Plant breeders can increase protein concentration through hybridization and selection, although pushing protein higher is not considered to be a high priority of most breeding programs at this time.

Oil. Oat has a higher oil concentration than other cereals, averaging about 7%. This level was increased to 18% through six generations of a recurrent selection scheme, albeit with some loss in yield and other agronomic characteristics. For animal feed, higher oil is better, as it is a denser energy source than carbohydrate. The cultivar, Matilda, from Svalöf Weibull in Sweden, has 10-11% oil and has had some success in the horse feed market. Hulless, high-oil cultivars are being developed in the UK for poultry feed. In contrast, oat millers prefer low oil concentration for food products, because high oil products are more susceptible to develop rancidity and to a shorter product shelf life. Also, a low saturated fat content, along with 0.75 g of soluble fibre (per serving) is part of the requirement for a US Food and Drug Administration health claim on oat products.

Oat oil consists primarily of palmitic (16:0), oleic (18:1) and linoleic (18:2) acids, with variation among genotypes and growing environments in the relative proportions. The high concentration of monounsaturated oleic acid in oat oil is favorable for its use as a food oil. Oat oil is higher in oleic acid than the commonly used soybean and sunflower oils, but it is lower than canola and olive oils, which are considered to be the most healthy vegetable oils. Currently, oat oil is not processed as a food oil, primarily for economic reasons, although it might become feasible if high-oil cultivars with good agronomic characteristics are developed.

Among the oat polar lipids, enriched glycolipid fractions in particular, have functional properties that are useful in pharmaceutical, cosmetic, and food applications. Liposomes formed from non-ionic glycolipids are more stable than similar dispersions made from phospholipids, such as soy or egg lecithin. An emulsion formed from oat glycolipid and palm oil, when mixed into a low-fat yogurt, yields a food product that increases satiety. This product may be useful in a weight-control program. The digalactosyl diacylglycerol (DGDG) fraction is used to produce an oil-in-water emulsion cream that has an extended moisturizing effect for use in topical creams for skin care. Liposomes from oat DGDG are useful as carriers to control the delivery of pharmaceuticals. Companies in Sweden, Canada and the USA are actively engaged in research and development of products based on oat polar lipids.

β-Glucan. Oat, as well as barley, has a high concentration of mixed-linked β-glucan (soluble fibre) as a component of the endosperm cell walls. Many studies with humans and model animals have confirmed that diets containing oat β-glucan will lower LDL-cholesterol in hypercholesterolemic subjects, decreasing their risk for heart disease. These studies formed the basis for the first health claim allowed on a food product by the US Food and Drug Administration. Oat containing β-glucan has also been shown to slow the increase in blood sugar following a meal, an important characteristic for the dietary control of Type II diabetes. Plant breeders are developing oat lines with high β-glucan concentration that may be particularly useful for food or as a raw material for fractionation and processing. For animal feed, however, low β-glucan concentration is desirable, particularly for young poultry.

β-Glucan is concentrated in the bran. Oat bran is prepared by milling, and it is used in many food products. β-Glucan is an important component of Oatrim, a fat replacement developed at the USDA laboratories in Peoria, Illinois. β-Glucan has many other potential uses in the medical field, such as promoting wound healing, stimulating immune cell function, and protecting and moisturizing skin. A Canadian company produces a liquid β-glucan product for use in functional food, personal care, and pharmaceutical products.

Starch. Starch is the most abundant component of the oat grain. Oat starch has about 25-30% amylose, and there are no known waxy or high-amylose mutants. Starch granules occur as compound aggregates and single grains. Oat starches have typical gelatinization characteristics, but have high shear susceptibility and tend to behave like waxy starches. They develop unusually high viscosity upon cooling. Cooled oat starches are clearer, less firm, more elastic, more adhesive and less susceptible to retrogradation than other cereal starches. Oat starch would be a co-product from fractionation of the grain for other, more valuable components. Oat starch could substitute for most other starch applications except those based on waxy maize. Partially hydrolyzed oat starch (soluble amylodextrins) forms the main component of Oatrim (see previous paragraph).

Minor components. The mineral content of oat is typical of other cereals, with minerals concentrated in the bran fraction. Oat contains small but significant quantities of several vitamins: thiamine, niacin, riboflavin, pyridoxine, folacin, biotin and pantothenic acid. In addition to these traditional nutrients, oat contains some secondary products that may affect human health.

Tocols. Oat oil contains α-tocotrienol and α-tocopherol, with trace amounts of other tocols. Collectively, the tocols are known as vitamin E. Their function is not completely understood, but it appears that they assist in the protection of cells against oxidation by free radicals and reduce lipid peroxidation. Other beneficial therapeutic properties of tocols include the ability to reduce serum cholesterol concentration and to inhibit the growth of certain cancer cells. The tocols also help stabilize extracted oat oil. Among a group of North American cultivars, oat grain tocols concentration varied from 20 to 40 mg/kg. Oat and barley contain predominantly α-tocotrienol, in contrast to other grains. The tocotrienols are stronger free radical scavengers than tocopherols, but are not absorbed as readily. In a study with high-oil oat lines, α-tocotrienol was strongly correlated with oil percentage. Tocols are unevenly distributed within the grain, with α-tocotrienol located primarily in the endosperm, whereas α-tocopherol is found in the germ.

Avenanthramides. Novel compounds with antioxidant and possibly other biological activity are found in oat grain and are inducible in oat leaves.

Avenanthramides consist of anthranilic or hydroxyanthranilic acid linked to one of several hydroxycinnamic acids through an amide bond. The three most predominant avenanthramides in oat are formed from hydroxyanthranilic acid and *p*-coumaric, ferulic, or caffeic acids, and have been called **2p**, **2f** and **2c**, respectively. The concentrations of avenanthramides in oat vary greatly according to genotype and growing environment. Avenanthramide **2c** has the greatest antioxidant activity in vitro, which was expected because of its adjacent hydroxyl groups. An experiment where **2c** was fed to rats showed activity in alleviating oxidative stress caused by acute exercise, although the effects were not striking at the dose used. Avenanthramides may be responsible for the anti-irritant properties of oat salves and topical creams. A Canadian company produces a colloidal oat extract, which is a complex mixture of phytochemicals including avenanthramides, flavonoids, saponins and other bioactive compounds. This product relieves itching and sunburned skin, which make it useful for cosmetic and personal care products. The colloidal oat extract may have applications in functional food products in the future.

Phenols, flavonoids, saponins, lignans, and sterols are found in oat grain in small quantities. These substances have antioxidant properties, but their concentrations in the soluble fraction are very low compared to the avenanthramides and tocols. Consequently, they have received less attention from oat researchers.

Conclusions

Aside from protein, oil and β-glucan, very little research has been done on the genetic and environmental variability in the concentrations of the various components that contribute to the functionality of oat. It is technically, if not economically, feasible to develop special oat cultivars by plant breeding or biotechnology that have enhanced attributes for particular uses. The primary obstacle is the relative cost of development in relation to the potential benefit achieved for uses that may require relatively small quantities of oat. Nevertheless, continued research on the functional properties of oat in conjunction with genetics and breeding, should benefit the farmer, processor and consumer through higher value grain.

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Structure-function relationships of cereal β-glucans

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Abstract

There is good evidence that rheological properties play a key role in determining the health benefits of cereal β-glucans. The primary focus of studies has been flow viscosity. Because of the power law relationship between concentration or molecular weight, and viscosity, small differences in solubility or molecular weight can profoundly influence viscosity development in solution (halving concentration may produce a 15 fold decrease in zero shear viscosity). Depolymerisation similarly may have a profound effect on flow viscosity, but as well as reducing the measured flow viscosity, the elasticity, or gel character of the solution may increase. In model clinical studies of glycemic response, using different preparations of β-glucan, about 90% of the differences between different treatments could be accounted for by the flow viscosity of the drinks consumed by the subjects, but the influence of gel formation on glycemic response is unclear. Oats and barley are the primary source of β-glucan but it is also found in rye, wheat and the lichen Icelandic Moss. Structural analysis show that the β-glucan from all sources is composed primarily of β-(1→3)-linked cellotriosyl and cellotetraosyl units, but there are also regions that are more cellulose-like in character, with 4 or more consecutive β-(1→4)-linked glucose units. There are some differences between the structures of these different β-glucans, and these, as well as molecular weight, modify the ability to form gels. Studies of the different gelation characteristics of the β-glucans have allowed conclusions as to the mechanism of gelation.

Böhm N. & Kulicke, W.-M. 1999a. Carbohydrate Research 315: 293-301; Böhm, N. & Kulicke, W.-M. 1999b. Carbohydrate Research 315: 302-311; Tosh, S.M., Wood, P.J., Wang, Q. & Weisz, J. 2003. Carbohydrate Polymers 55: 425–436.

Key words: oats, β-glucan, viscosity, gelation, molecular weight, structure

Variation in the content of nutrients in oats and its relevance for the production of cereal products

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Abstract

Oat for cereal production needs to fulfil several requirements including the processing properties and permissible amounts of residues and contaminants. Recently, requirements regarding the content of nutrients have been added. This study gives an overview over the variation of the content of nutrients in oat and their relevance on the manufacturing of oat products.

Representative samples of commercial oat lots from Germany, Finland, Sweden, Great Britain and Australia harvested between 1995 and 2002 have been investigated. Furthermore, oat samples of variety trials performed by the Agricultural Board of Schleswig-Holstein and Niedersachsen were included. Among others, the content of oat kernels in protein, fat, beta-glucan, vitamin E and thiamine were determined.

The protein content of oat varies between 12 and 17 per cent/dm. In some cases a minimum protein content of oat products of 12 per cent is required. The fat content ranges from 6 to 10 per cent/dm. For the production of rolled oats larger contents are particularly suitable while lower values are advantageous for the production of extruded oat products. The amounts of free fatty acids and peroxides should be low to improve storage life of the oat products.

The beta-glucan content of oat is 3,6 to 5,1 per cent/dm. For the production of oat products with cholesterol reducing activity larger concentrations of beta-glucan are to be prefered. The vitamin E content of the oat samples also varies significantly. The ratio mg alpha-tocopherol-equivalents/g diene acid equivalents is of major relevance in terms of nutritional quality. Low vitamin E contents indicate an exceeding storage time or inappropriate storage conditions (Hampshire 2003). The content of oat in thiamine is influenced by the farming system (conventional or organic farming) used and also by the oat variety and the growing site. For the production of certain dietary foods minimum levels of thiamine have been defined.

Hampshire, J. 2003. Deutsche Lebensmittel-Rundschau 99: 222-231.

Key words: oat quality, protein, fat, beta-glucan, vitamin E, thiamin

Addition of value to low β-glucan oat fraction

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Abstract

Different methods are available for obtaining oat fractions with elevated soluble fibre content. Separation of flour particles based on their size and density gives fractions with maximum around 20 % of β-glucan, whereas higher β-glucan contents can be obtained via various extraction processes. Any of these approaches yields vast amounts of endosperm-rich low β-glucan flour as a side product. The addition of extra value into this side fraction would have a huge impact on the feasibility of whole oat fractionation process.

The composition of low β-glucan oat flour provides no nutritional superiority over other cereal products. Instead, due to high lipid content it has some technological limitations such as a high tendency to stick in elevators, barrels and transporters. Also, when such flour is mixed in water, it will readily form large clumps, which make it difficult to form homogeneous mixtures. Due to these limitations, oat endosperm flour is typically used in low value products such as animal feed.

The purpose of our work was to introduce new technological functionality into low β-glucan oat flour and simultaneously overcome negative aspects associated to this fraction. This was achieved by hydrothermal treatment yielding partially damaged starch (Kiiliäinen et al, 2004). Several desired changes were observed due to this treatment and the hydrothermally treated flour hydrates easily already at room temperature. Concurrently with the starch damage a relocalisation of oat lipids was also noticed, resulting in reduced extractability of the lipids. These changes provide the basics for the use of hydrothermally treated oat flour in baking and ready made food applications where it can offer a cost effective replacement for other water binding agents such as pre-gelatinized starch products.

Kiiliäinen, K. Lehtinen, P., Mikola, M. and Laakso, S. 2004. Journal of Cereal Science, to be submitted 2004.

Key words: oat, water binding, damaged starch, amylose-lipid complex

Nutritional effects of dietary fibre-rich extrudates from oat in rats and man

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Abstract

Cereal products are the most important source of dietary fibre (DF). The objective of this study was to evaluate physiological effects of DF-rich oat-based extrudates from the whole-grain type *in vivo*.

A series of extrudates was prepared from whole-grain oat meal, oat bran and Novelose 330. These products differed in their contents of soluble and insoluble DF as well as of β-glucan and resistant starch. Rats (10 per group) were fed a control diet or test diets containing 50 % of these extrudates for 6 weeks. Further, 12 healthy human subjects consumed 100 g/day of an extrudate from oat meal and Novelose 330 (80/20) additionally to their habitual diet for 4 weeks.

In dependence on the DF composition and concentration, higher formation and absorption of short-chain fatty acids (SCFA) were found in rats as a result of DF fermentation in the caecum and colon. Under the oat-based diets, the composition of the microflora and plasma lipid parameters were slightly changed. Caecum weights and caecal contents were higher in the test groups. In contrast to control, concentrations of bile acids (BA) and neutral sterols (NS) were greater in caecal and colonic contents as well as their excretion. The amount and proportion of secondary BA decreased as a result of lower pH values in intestinal contents of the experimental groups. Weight gain was not changed but rats of test groups consumed more water. The extrudate was well accepted by the human subjects. After 4 weeks of extrudate intake, concentrations of SCFA, including of butyrate, were increased in faeces. The higher DF consumption correlated with higher BA and NS concentrations in faeces. Most of these parameters reached their original levels 2 weeks after the experiment. Administration of DF-rich extrudates from whole-grain oat-based products results in beneficial physiological effects and may be helpful to increase the DF intake in humans.

This work was supported by the FEI (Forschungskreis der Ernährungsindustrie e.V., Bonn), the AiF and the Ministry of Economics and Labour (Project No. 12716 BR).

Key words: Oat extrudate, dietary fibre, physiological effects, humans, rats, steroids, SCFA

Genetic resources

A new approach to locating and utilizing oat genetic resources

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Abstract

Various developments, including the introduction of intellectual property rights (IPR), have changed the ways in which plant genetic resources (PGR) are utilized by agriculture on a global basis. While there have been a number of methods proposed to improve the efficiency of utilization of PGR during this time, any advances have been limited in their success. For example, the core collection method, while enjoying some popularity, has not completely delivered the advantages sought. It is proposed that significant advances can be achieved by focusing on several fundamental parameters associated with identifying PGR whilst employing some modern technologies. Basic passport information that uniquely identifies accessions is one such fundamental parameter. Database and GIS technology can be employed to recognize and more fully exploit the relationship between genotype, environment and evolution to more efficiently identify and utilize desirable genetic variation.

Key words: genetic resources, core collection, utilization, identification, GIS

Introduction

There were around 3.4 million plant genetic resources accessions residing in major gene banks around the world in 1997 which are not being fully utilized, according to FAO. For example, China reports that only 3-5% of conserved accessions are being utilized in breeding programs. The large investment in germplasm conservation, compared to the benefits from its utilization, has not been significantly resolved by traditional and core collection methodologies, and still remains an issue. The unique identification of plant genetic resources is fundamental to the management of gene banks and plant improvement programs. It is also increasingly important in a world where benefit sharing from the utilization of plant genetic resources is a reality. Such identification information should accompany germplasm as it is physically distributed in the same way as humans carry passports for identification purposes as they travel. This same information can also be used in isolation from a specific accession to identify its presence or absence in any gene bank or collection worldwide. This latter application can be employed to develop global inventories of PGR.

Furthermore, it is fundamental to the unique identification of germplasm to know about its origin. In the case of modern cultivars this could be interrupted to include the parentage of an accession. For collected accessions, such as landraces and wild or domesticated relatives, precise information about the collection site is the origin datum. The origin information of accessions, especially for collected germplasm, can be further exploited using modern technologies to enhance the detection of desirable germplasm. For example, GIS and associated database technology provides a platform whereby we can recognize the relationship between genotype, environment and evolution in selecting germplasm for plant improvement.

Thus, an innovative combination of traditional and new methodologies can be employed to 1) identify the wealth of genetic variation contained within global gene banks, 2) to create global inventories and, 3) to increase their use. This will lead to increased knowledge about what is being conserved, the priorities for future collecting, as well as assisting in its management and the sharing of any benefits resulting from its exploitation.

Discussion

The exchange of plant genetic resources and their associated information necessitates the unique identification of the germplasm involved. A list of multi-crop passport descriptors (MCPD) has been suggested to provide international standards to facilitate this exchange of germplasm passport information (Alercia et al, 2001). The proposed MCPD were later tested during the establishment of a global inventory of genetic resources for wheat (GIWGR) (Mackay and Skovmand, 2003) and their applicability were discussed and recommendations for improvement suggested.

The development of an international standard for passport descriptors to accompany germplasm when exchanged, or to serve as a means of identifying germplasm in shared databases (such as inventories), is an obvious advancement. It was found by Mackay and Skovmand that, ideally, such international standards for descriptors should have certain characteristics:

- Individually, or in combination, the descriptors must uniquely identify genotypes,
- The number of descriptors should be kept to a minimum,
- The descriptors should largely include those readily available from most gene banks, breeding institutes etc.,
- Exporting and importing the descriptors into centralized databases should be as transparent as possible.

Present strategies for increasing the utilization of conserved genetic resources have not been particularly useful or efficient in improving the use of these resources. They have been particularly poor in their application to large collection like those found a regional gene bank like the Nordic Gene Bank or in the International Agricultural Research Centers like CIMMYT and ICARDA. The most common strategy, the core collection strategy, is one designed to catch what you can, rather than catch what you need. Here we propose a new strategy that more fully exploits existing information to maximize utilization of genetic resources.

The methodology involved is as follows:

- Exploiting existing PGR accession information:
    - Electronic capture of comprehensive collection site (latitude, longitude, altitude and other locality data).
    - Capture available characterization and evaluation data.

- Capturing novel data:
    - Collection of anecdotal and production constraint information, through surveys, and subsequent inclusion into the system data model

- Locate, obtain, develop and/or derive germplasm identification support information layers:
    - Incorporate a full range of appropriate environmental (climatic and edaphic) information layers that singularly, or in combination, can assist in the identification of germplasm (e.g. temperature, growing degree days, soil types, agro-climatic zones)

- Develop the biological-geographic interface:
    - Utilize GIS to build two-way information flow between the seed and environment domains.

- Conservation management:
    - Collect necessary information on existing *in situ* conservation parks
    - Analyse associated environmental data
    - Build model for *in situ* based conservation using climatic and edaphic data layers to perform environmental analysis.

Summary

If a particular genotype can be uniquely identified by a small set of passport data descriptors, and this set of information accompanies the genotype whenever it is exchanged, then there should never be confusion as to its identity. Similarly, if the same information (without the actual genotype) was shared, or exchanged, then it could be used to identify the same genotype held in any collection or plant improvement program worldwide. Global inventories of plant genetic resources held by national and international gene banks would be useful resources for scientists wishing to utilize them in plant improvement. Such inventories would also be a useful tool in helping understand how and where germplasm is being utilized and conserved.

The large investment in germplasm conservation, through support of traditional and core collection methods, has not provided adequate benefits for utilisation advances to continue unchallenged. Efficient strategies for searching collections still remain a dominant issue. By introducing new technologies, whilst recognising the relationship between genotype, environment and evolution, an innovative combination of traditional and new methodologies can be employed to identify and exploit the wealth of genetic variation contained within global gene banks.

The new technologies suggested here aim to construct a new, objective strategy to identify and utilize germplasm by blending GIS and traditional database technologies. This permits novel, multi-dimensional linkages between biological, genetic resources germplasm and environmental information to be constructed. Such a facility allows us to:

1. investigate novel ways to capture and exploit all kinds of knowledge, such as capturing anecdotal information (or “expert opinions”) of germ collectors, plant breeders, and other germplasm users, and
2. to analyse the applicability of current germplasm management strategies, including *in situ* and *ex situ* methods, in maximising the global community’s conservation and utilization expectations for plant genetic resources.

If such strategies were employed for oats, oat genetic resources will become more accessible and be more fully exploited. At the same time it would provide a tracking system for genetic resources use, which appear to be required under the new international treaty just coming into effect this year.

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Taxonomy and evaluation of genus *Avena* L.

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Abstract

The systematic position of the species in genus *Avena* L. still remains disputable among researchers. Comparative analysis of the whole specific diversity of oats was incited by the profound interest to the use of these forms in taxonomy and breeding practice, enforces by the late development of plant immunological, biochemical and other researches. Further search for taxonomy and utilization of new oat breeding sources is one of the objectives pursued by Vavilov Institute of Plant Industry (VIR) in studying its global germplasm collections (Loskutov 2000; 2001; 2002; 2003; Loskutov et al. 2001). The research presents the field results of studying (1988-2001), about 3000 accessions of 26 oat species with different ploidy level. Complex study of specific diversity and analysis of geographic distribution of the habitats of oat forms and species confirmed that the centre of origin of *Avena* L. lies in the western part of the Mediterranean region, while the secondary centre of formation of *Avena* species and origin of cultivated oat (*A.sativa*) is situated within the Asia Minor centre of crop origin. The analysis of intraspecific diversity helped to identify centres of morphogenesis for all cultivated oat species. The centre for the diploid sp. *A.strigosa* is Spain and Portugal, for the naked forms *A.nuda* L. UK, for the tetraploid species *A.abyssinica* it is Ethiopia, for the hexaploid species *A.byzantina* Algeria and Morocco, for the hulled forms of *A.sativa* Iran, Georgia and Russia (Tatarstan), and for its hull-less forms Mongolia and China. A revised taxonomic system for the species in the genus *Avena* based upon the degree of relationship with hexaploid species has been developed. We have divided this genus into two subgenera, subgen. Avenastrum and a typical subgen. *Avena* which is subdivided into *Aristulatae* Malz. и *Denticulatae* Malz. Such division according to the characters of the lemma tip – biaristulate or *Aristulatae* and bidentate or *Denticulatae*. The study was targeted at morhpological characterization, agronomic traits and resistance to the most widespread diseases: crown and stem rusts, powdery mildew, *Helminthosporium* leaf blotch, *Septoria* blight, *Mirothecium* necrotic mottle and BYDV. Representative collection of all species has been analyzed for groat protein content – amino acid and groat oil content – fatty acid content. The study representative set of accessions of genus *Avena* L. species with different ploidy levels helped to determine intraspecific diversity in all characters. A majority of identified sources may be directly involved in the breeding for disease resistance, agronomic traits and grain quality.

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Key words: taxonomy, agronomic characters, disease resistance, protein, oil

Characterisation of European oat landraces for agronomical, morphological and quality data: Assessment of genetic diversity and link with geographical origin

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Abstract

An evaluation was carried out on a set of European oat landraces issued from European countries with funds from EU through GENRES 99-106 Program. The aim of this evaluation is to get the most complete information on these landraces in order to update the European oat database. Data from years 2001 and 2002 (642 accessions and 18 checks) were collected and showed an important diversity for yield and yield components (mainly 1000 grain weight), tolerance to crown rust (under field and artificial tests) , powdery mildew and lodging. Diversity of these landraces has also been described from the morphological characters. For quality traits, protein content level of the landraces ranged from 9% to over 19%. Correlations have been determined between agronomic traits and protein content. Links between some traits and geographical origin have been examined. Due to the availability of these data, some landraces might be involved in further breeding programs.

Key words: genetic resources, oat, landraces, protein content, agronomical and morphological traits

Genetic diversity of *Avena* landraces accessed by AFLPs

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Abstract

Cultivated oats, *Avena sativa* L. and *A. byzantina* C. Koch, rank fifth among cereals in world production. Most varieties during the 18th, 19th and early 20th centuries were landraces that were heterogeneous mixtures well adapted to the geographical and ecological regions planted (Zeven, 1998). From these landraces a number of modern cultivars have been developed either through the direct selection of single plants or by crosses between the selections. In the present study we try to investigate the genetic relationships among different oat landraces using molecular markers.

Three hundred landraces collected from different parts of Europe were screened. DNA was isolated from young leaves of at least 40 seedlings from each landrace. The Amplified Fragment Length Polymorphism (AFLP), a reproducible and reliable molecular marker generating method, was used (Jones et al. 199). A total of 64 different primer pair combinations were tested and the most informative one was chosen. The AFLP reaction products were separated, scored and analysed using an ABI Prism 310 Genetic Analyser. Genetic similarities were calculated using the DICE algorithm and UPGMA was used for clustering.

Primer pair *Eco*RI-ACA/CAC-*Mse*I produced more than 250 polymorphic markers, discriminating the 300 entries. Groups, containing genetically related accessions, were formed according to the geographical and climatic site of landrace origin.

Zeven, A.C., 1998 Euphytica 104: 127-139; Jones, C.J. et al. 1998. In: Karp, A. et al. (eds.). Molecular tools for screening biodiversity. London: Chapman & Hall. p. 191-192.

Key words: landrace, molecular markers, UPGMA, DICE.

Genetic variation: Wild, cultivated and extra terrestrial

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Abstract

The genetic base from which many of our present day varieties have been derived is quite narrow and frequently, pedigrees trace back to varieties such as Probsteier, Landhafer, Red Algerian, Kherson, Clintland, Bond, Grey Winter and Golden Rain. It has recently been demonstrated that allelic diversity at particular loci, rather than average genetic diversity, is sensitive to oat breeding practices (Fu et al., 2003). Base broadening of the present cultivated genepool by introducing novel germplasm is becoming increasingly important and can be achieved in a number of different ways.

Wild Species. Hexaploid wild oats are the choice for introgressing genes into the cultivated oat *A.sativa*, as hybrids are readily formed between the two species and their chromosome pairing is usually almost complete and depending on genotype, regular. Stable recombinants can usually be recovered quite rapidly. Introgression of characters from tetraploid and diploid species (with the exception of *A.maroccana*, *A.murphyi* and *A.insularis)* is however a protracted and complex affair but have been accomplished.

Cultivated Forms. Though cultivated forms have a lack of diversity at specific loci, there is still a wealth of variation within this genepool. The study of over 1000 landrace accessions under an EU Genetic Resources project (CT99-106) has demonstrated the diversity of genotypes which could be employed to broaden the genetic base of our modern day varieties.

The 'Extra Terestrial'. The mechanisms which release variation not manifest itself in either parent in hybrid combinations, remains largely unclear, but has been attributed to *de novo* mutation induced by hybridity, complementary gene action or the unmasking of recessive genes (transgressive segregation).

Thus although genetic diversity for some traits may be scant, it is nevertheless evident that within the cultivated oat genepool, there is still locked up and hidden variation.

Fu, et al. 2003. Crop Science 43:1989–1995.

Key words: genetic variation, germplasm, introgression ,diversity

Breeding and biotechnology: Quality

New directions in breeding for high quality oats

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Key words: oats, breeding, quality, milling, poultry feed, ruminant feed

Introduction

For all crops - and oats is no exception - the sum of diverse characteristics contribute to the basic qualities required by industry and consumers. These characteristics change and evolve with time in response to industry/consumer ‘pull’ and to new opportunities created by genetic improvement (‘science push’).

Given the length of time that it takes to breed new oat varieties (7-12 years), oat breeders have to predict future requirements based on current trends.

There is general (though not universal) realisation that agriculture needs to be sustainable in terms of protecting scarce resources, minimising pollution, being good for biodiversity and aimed at real markets. This suggests that productivity *per se* will become less important and minimising adverse environmental impacts and achieving high quality products will become more important. In Europe and elsewhere, food scares arising from animal products in feeds underline the need for safe, traceable food and feedstuffs. In the over-fed western world, health enhancing and functional properties present opportunities for capturing high added-value. For intensively-reared animals, nutrient-dense feeds are required in order to fulfil high liveweight gain potential.

Human consumption

In 2000, the British Oat and Barley Millers Association (BOBMA) produced a summary of Oat Millers Requirements for a Breeding Programme. They required varieties that improved mill yield and performance and met consumer expectations. They divided the requirements into List A and B.

List A comprised the traditional needs that the breeder must recognise when developing new varieties. These were high groat content, low screenings, uniformity of size, ease of milling, tight husk enclosure, low breakage and resistance to groat discoloration. High groat content and low screenings were particularly important for the achievement of high milling yield. Other factors affect mill performance and the quality of the end product.

List B constituted end-use requirements with potential to increase the consumption of oats and oat products. The two objectives mentioned were (1) high ß-glucans in order to fully benefit from health claims relating to the soluble fibre in oats, and (2) no increase, or better still, a reduction in fat, provided that there was no effect on oat flavour.

More recently, priorities for milling oats have been identified as high economic competitiveness, high groat content and freedom from pesticide residues. In relation to the last-mentioned, we need to maintain the natural, nutritious, wholesome image of oats with European consumers and meet the requirements of regulations for infant food free of plant growth regulator residues. PGR-free grain can most economically be achieved though genetic improvement of lodging resistance and dwarf straw. These are the priorities of a new project entitled ‘The incorporation of important traits underlying sustainable development of the oat crop through combining 'conventional' phenotypic selection with molecular marker technologies’ (‘OatLink’) in which IGER’s genetic improvement will be taken forward in the next five years. In the future, we may have to consider the scope for increasing levels of antioxidants and whether there needs to be concerted efforts to reduce mycotoxin levels through genetic improvement.

Groat (kernel) content appears to be quantitatively inherited but has been generally demonstrated to be amenable to selection (Wesenberg and Shands, 1973, Stuthman and Granger, 1977) with the highest estimates of heritability observed among populations between diverse parents (Ronald et al., 1999).

Groat percentage determined by hand dehusking, though tedious, is considered to provide the ceiling value for groat percentage (Doehlert et al, 1999). Experimental mechanical de-milling followed by hand sorting of hull and groat fractions is considered to be more practical for larger samples, with impact dehulling probably more akin to what happens in an oat mill than compressed air dehullers.

Minimising differences in size distribution (due to the occurrence of primary and secondary kernels) is also important to maximising milling yield (Ganssmann and Vorwerck, 1995). Doehlert et al., 1999 found significant but incomplete associations between the coefficient of variation (CV) for whole oat area as measured by digital image analysis and groat percentage. Groat percentage may however be related to groat damage; other factors affecting groat damage being mass, hardness and even ß-glucan content (Doehlert and McMullen, 2000, Engleson and Fulcher, 2002).

The complexity and unpredictability of factors affecting groat percentage emphasises the importance of judging each variety individually. In OatLink, millers will undertake their own analyses of milling quality of advanced lines and embrace pilot milling of 100t lots of the most promising varieties.

Premium oats for poultry feed

It has long been known that oats have a number of valuable characteristics for feeding to poultry. These include high levels of essential amino-acids and fatty acids. Oatmeal was the base of the 'FUL-O-PEP' range of feeds marketed by the Quaker Oats Company in the USA 50-80 years ago. Keeping a hopper of whole thin-hulled oats in front of laying hens and chicks was advocated for health, welfare and quality reasons. The demise of oats in poultry rations was probably due to the advent of soyabeans as a source of protein and also to the perceived low metabolisable energy of oats with thick husks.

The recent interest in oats for poultry feed is probably due to the fear of over-reliance on soya and wheat in feed rations, the phasing out of non-plant sources of protein and fats and the breeding of high-yielding agronomically acceptable naked oats.

The Defra/ HGCA/ Industry-funded project Avian Feed Efficiency from Naked Oats (AFENO) (Maunsell *et al*., 2004) has clearly shown that high-yielding naked oats are able to enter least cost formulated feed rations for poultry at acceptable price/t. The high content of oil resulting in increased energy intake that has been the main driver of industry needs. Work at Roslin (Maunsell *et al*., 2004) has also been demonstrated that experimental high oil lines derived from unadapted and low yielding *A. sterilis* derived husked high oil lines from Iowa, containing 14.6- 15.8 % oil DM, had even higher TME_N values (17.78-18.07 kJ/g DM). An intriquing finding has been that moderate levels of husk enhance liveweight gain.

The Poultry Industry has emphasised the needs for oats which are economically competitive and/or have higher oil/energy without jeopardising protein and amino-acid content. Accordingly, we are placing high emphasis in selecting for high oil. We have found this much more tractable than breeding for protein. Good progress has been made since 1991 in transferring this trait from unadapted genetic sources to adapted backgrounds. Possibly, there is ample photosynthate for combining high yield and oil; sink not source may be the limiting factor. In the winter oat breeding programme, we grow F_3 progenies from selected F_2s and accelerated and unselected F_2s in clumps. During the winter, we measure the oil content of every clump using NIR calibrated against the cold Soxhet method. We multiply up the best lines using spring sowing and test lines in yield trials in the autumn. More precise assessments of the oil content of advanced lines are made using acid hydrolysis.

Further genetic improvement of oats for this application is also being taken forward in the OatLink. The project will also seek to validate the use of molecular markers for oil content and other traits. Member companies of the British Poultry Council, including Bernard Matthews Foods Ltd and British United Turkeys Ltd, will validate the performance of new varieties.

This area will be more fully covered by Cark Maunsell in a later paper.

Oats for ruminants

While ruminants can to some extent cope with fibrous feedstuffs, oat husks are a major source of variability in energy content. We have dissected the components of feeding value for ruminants of the oat grain of winter and spring sown oats grown in 2002, including the winter husked oats Gerald, Kingfisher and Millennium, the winter dwarf oats Buffalo (husked) and Hendon (naked), the high yielding winter naked oat Expression and the spring Canadian oat AC Assiniboia on the basis of its reported low husk lignin (Thompson *et al*., 2000). The Thomas *et al.* (1988) prediction equation (Predicted ME for ruminants = 0.14 NCGD + 0.25 oil), as reported by Haigh and Bradshaw (1998), was used as an approximation of the metabolisable energy (ME) of groats and husks. NCGD (neutral cellulase gamanase digestibility) measures cellulase digestible organic matter after neutral detergent extraction (Anon, 1998; Kitcherside et al., 2000).

Groats were highly digestible with NCGD in a relatively narrow range of 94.7 to 95.8 over both years. Predicted MEs of groats were also in a narrow range, from 15.3 (spring-sown AC Assiniboia) to 16.3 mJ/kg.

Apart from predicted MEs of husks being much lower, there was greater variability between genotypes. AC Assiniboia had a predicted ME of 8.3 mJ/kg, compared to 3.0 - 4.3 mJ/kg for the other husked varieties. This was due to lower lignin (3.0%) compared to 9.1 - 11.5% for the other husked varieties, and was also reflected in higher NCGD (58.4 - 59.4% for AC Assiniboia compared to 12.5-28.2% for the other varieties).

We have used the predicted MEs of groat and husk and the proportion of groat (groat%) to determine the predicted ME of whole grain. AC Assiniboia had significantly higher ME (13.8 -14.2) compared to the other husked varieties (12.0 - 13.1 mJ/kg). Moreover, it can be predicted that MEs of up to 14.9 mJ/kg could be obtained by combining the low lignin husk trait with 14% oil and 77% kernel content. This would be a quantum leap in the value of oats to ruminants.

We have now obtained further results from 2003, although Buffalo and AC Assiniboia did not survive the winter in this year. The predicted ME of AC Assiniboia husks were lower (6.8 mJ/kg) than in 2002. A surprisingly close value of 6.4 mJ/kg for spring-sown Buffalo, apparently due to an above-average NCGD (40.8%) and 3.2% oil in the husk suggests that further work is needed to fully understand the determinants of high ME.

Conclusions

Considerable scope exists for making radical improvements in oat quality meeting the needs of human consumption and premium feed for poultry and ruminants. These improvements are essential to meet the modern demands of sustainable agriculture and food production.

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Genomic investigation of oat quality

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Abstract

Both structural genomic and functional genomic approaches increase our understanding of the genetics of quality traits in oats, thereby providing knowledge and tools that accelerate breeding for oat improvement. Initially, we employed the structural genomic approaches of recombination mapping and quantitative trait locus (QTL) analysis to investigate the genetics of a number of quality traits in a Terra x Marion (TM) recombinant inbred population (DeKoeyer et al. 2004). Bi-plot analyses gave complementary insight. These identified genomic regions that play a major role in controlling oil, beta-glucan, and protein content. Comparative marker and QTL mapping with other oat populations increased our understanding of the number and organization of the genes involved and further validated the TM QTLs. Extension to additional elite populations contrasting for these traits helped to complete the analysis. Markers flanking the TM oil and beta-glucan QTLs were converted to sequence characterized amplified region (SCAR) markers (Orr and Molnar 2004). These polymerase chain reaction (PCR)-based markers are robust, rapid, and cost efficient and, therefore, suitable for marker-assisted breeding. Recently, functional genomic approaches have been employed to isolate candidate genes in the biochemical pathways for oil and protein content, to study expression level polymorphisms, and to associate both of these with QTLs in mapping populations (Lybaert 2004). These approaches promise to advance our understanding of the involvement of key enzymes in oil and protein biosynthesis and their regulators.

DeKoeyer, D., et al. 2004, Theoretical and Applied Genetics 108:(in press); Lybaert, A. 2004, PhD Thesis (in preparation), McGill University; Orr, W. & Molnar, S.J. 2004, (submitted).

Key words: oil, beta-glucan, protein, QTL, marker, breeding

AB-QTL analysis for β-glucan content in oats

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Abstract

The advanced-backcross QTL analysis (AB-QTL analysis), as proposed by Tanksley and Nelson (1996), was chosen as an directed approach to introduce QTLs for β-glucan content and other important traits from a genebank accession into cultivar breeding programmes. In this presentation first results from an oat AB-QTL project are presented.

Three BC2S1 populations consisting of 98, 73 and 67 lines, respectively, were derived from the cross 'Iltis' x IA H611-447, the latter of which served as a donor for high β-glucan content. In 2003 the first field nursery was performed with the 237 BC2S4 families at three locations with two replications per location. The most important agronomical and quality traits have been analysed. Segregation between lines was evident in yield components and yield, plant height and quality parameters like β-glucan content. Some transgressive lines for yield and yield components were found and have to be validated in the next generations. The transgressive progenies did not outperform the most recent high-yielding cultivars.

To find useful markers for the QTL analysis, 144 oat SSRs were screened, of which 26 were polymorphic between the parents and 5 showed segregation in the first population. Additionally, 128 *Eco*RI/*Mse*I AFLP primer combinations were detected, of which 32 primer combinations showed 176 polymorphic bands between the parents. The polymorphic AFLP markers, together with STS markers, will be used to genotype the three populations, starting with the first population. This genotyping is on the way.

Tanksley SD, Nelson JC 1996: Theoretical and Applied Genetics 92:191–203

Key words: oats, Avena ssp. β-Glucan, AB-QTL-analysis

Development and use of markers for oil in oats

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Abstract

Understanding and manipulating the genes for oil content are important objectives for breeding modern oat varieties. In particular, naked oats with economically acceptable yields, dwarf straw and significantly higher oil levels are a target for the poultry industry.

Oil and protein content was determined from a range of oat genotypes and microsatellites used to obtain information on their genetic relatedness. A number of candidate crosses were made and these were cytologically screened to check for anomalies of segregation by observing chromosome pairing at meiosis in F_1 hybrids. An F_2 population between a spring high oil source (N327-6, from Iowa) and a dwarf winter naked variety (Hendon) was grown and found to display variation for a number of important characteristics in addition to grain oil content.Interestingly, there were examples of progeny that were naked grained, dwarf, early flowering and with high grain oil content. Use of the dwarf character in breeding programmes has been relatively limited until recently as it has been associated with a number of poor agronomic traits for example late maturity, incomplete extrusion of ears from flag leaves, small grains, poor kernel content and poor resistance to disease. Analysis of this mapping population indicates that we can we can break these apparent linkages and dissect these traits into their components.

We are using a number of approaches to identify and develop markers associated with traits of interest; candidate genes have been identified and used to generate alignments of homologous EST and genomic sequences from the Poaceae entries in Genbank. Primers based on conserved targets flanking one or more introns have then been used in PCRs with our parental lines. Polymorphisms have typically been found at frequencies between 1-5%, allowing us to readily identify single nucleotide polymorphisms (SNPs) in genes in the oil biosynthesis pathway. For genes of particular interest, such as ACCase and KAS, we have then established allele-specific PCRs, further simplifying the screening process. This work holds great promise for the development of rapid and precise marker-assisted selection for oil content.

Key words: oil, dwarf, molecular markers, SNP, genetic mapping

Better feed oat for cattle

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Abstract

Milling and feed grain quality improvement are cornerstones of the Crop Development Centre oat improvement program. Oat quality improvement focuses on food use, but the majority of world production is fed to ruminant livestock, thus feed quality improvement deserves consideration. This is especially true in western Canada where the feed market sets the base price for oat, and without assurance of an alternative feed market, growers cannot economically consider growing oat. While what makes a good food oat generally makes a good feed oat, specific feed value improvements can be made. Breeding to improve feed quality must consider physical and chemical traits, target livestock class and quality of competing grains. This generally means improving oat energy density for ruminants (especially cattle in Canada) versus that from barley, maize or wheat. Oat is considered the poorest grain because of high levels of indigestible fibre (hull) and low energy density.

Improved physical quality, concentrating on increased groat/hull, is a major goal and has greatly improved the feed value of recent CDC varieties. Simultaneous selection for low % hull and greater uniformity, plumpness, bulk density (Test wt.) and size (MKW) resulted in varieties like CDC Dancer with significant genetic improvement in % groat and uniformity resulting in lower ADF, NDF, lignin and crude fibre and increased starch. Combining this improved physical quality with the LLH (low acid detergent hull) trait reported in 2000 (Thompson et al, 2000), where hull digestibility for ruminants is doubled, and increasing energy density by introducing greater groat fat (HOG), the LLH-HOG feed oat project to produce a whole grain oat for cattle with feed value of barley and approaching that of maize has been developed. Initial feed trial results demonstrate that LLH adds 6.5 – 7.5% energy and HOG adds 2.0 – 2.5% versus regular oat, with a total LLH-HOG energy of 84 – 84.5 % TDN versus 82.5% for barley. On an economic basis this translates to LLH-HOG oat valued at $129/tonne in western Canada versus barley at $103 and maize at $110. LLH-HOG selections, entered in the 2004 Western Canadian Co-operative Oat trials, should be considered for registration and release in 2006.

Thompson, R.K., et al. 2000. Canadian Journal of Animal Science 80:377-379.

Key words: oat, ruminant, feed, LLH-HOG, fibre, energy, lignin

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Breeding and biotechnology: Yield

Yield and stability in cereals: past achievements and future progress

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Abstract

Future breeding must be even more efficient than in the recent past to keep increasing cereal productivity at a pace similar to that of population growth. To achieve this objective, breeders may need to complement traditional approaches with the use of new knowledge from crop physiology and new tools from molecular biology. Advances in molecular biology seem auspicious for helping increasing crop productivity; but this hope in the case of complex traits is, at best, doubtful. Recognizing the attributes that were responsible of past success may help identify prospect traits for the future to be used either directly in traditional approaches or through biotechnological tools. Retrospective analyses of physiological bases of yield improvement together with a sound physiological model of yield determination may help identifying promising traits. A short discussion is offered in which these approaches are combined.

Key words: cereal, yield, physiology, components, breeding

Introduction

Improving crop yield appears to be the unique alternative to keep increasing grain production in the future, when the demand is expected to almost double the present figures. This is because expanding the growing area, particularly in a sustainable way, seems unlikely (*e.g.* Cassman 1999). Genetic improvement played a major role in the remarkable yield gains achieved during the 50'-90's (Abeledo *et al*. 2002), but it is expected that its role in the near future will be even more important. This is because the main contribution of management in the past improvements in yield was mainly brought about by increases in use of inputs, such as the doses of N fertilization (Bell *et al*., 1995; Austin, 1999), and it seems likely that further improving yield through crop management in the future would be, if any, much more limited than that produced in the past, due to both economic and environmental restrictions.

Although yield stability is considered an important attribute in breeding and agronomy only limited information is available in the literature on how breeding and management have modified yield stability, and even less has been studied on which attributes may have been responsible for changes in yield stability with improved yields. It seems that yield stability has not been strongly altered during the last century in spite of the fact that yields increased dramatically (Slafer & Kernich 1996; Calderini & Slafer 1998). However, it seems that newer cultivars are more responsive to environmental changes than their predecessors and, therefore, most breeding effects on yield seemed to be accompanied by losses in yield stability that were compensated by improvements in yield stability brought about by modern management (Calderini & Slafer 1999). As yield potential seems positively associated with responsiveness to environmental enhancement (Abeledo *et al.* 2003) it is likely that future increases (or avoidance of losses) in yield stability would remain dependant upon management improvements, if breeding is aimed to further increase yields.

If the apparent leveling off of yields (Calderini & Slafer 1998; Slafer & Peltonen-Sainio 2001) is confirmed, we may need different approaches to further improve cereal yields (Reynolds *et al.* 1996): future breeding should be even more efficient than in the past, this time with cereals that have already a relatively high yield level (particularly wheat and barley), which in turn makes much harder to achieve further genetic gains (Reynolds *et al.* 1996). In this context, I have initially discussed on the need to analyze physiological processes behind the determination of yield to help identifying opportunities for future breeding (by traditional or biotechnological means). Then I recapped briefly the main attributes responsible of past achievements made by cereal breeding and analyzed some traits that may be useful for future progress.

The need to understand better the physiology of crop yield

The impressive advances accomplished by molecular biology during the last decades (Snape 1998) provided tools with the potential to (i) locate particular genes/QTLs related to virtually any trait, including yield and (ii) transfer them into the genome of adapted cultivars (*e.g.* Koebner & Snape 1999; Horvath *et al.* 2002). The literature seems to offer hope for increasing crop productivity from using these genetic factors either by traditional means or by genetic engineering. This hope in the case of simple traits is self-supported as evidenced by the number of successful transgenic cultivars commercially available for different crops. However, when it focuses on complex traits the rationale for the hope is rapidly conflicted with reality (*e.g.* Slafer 2003; Sinclair *et al.* 2004). For instance, although the identification of QTLs for yield is widespread in the literature, expression is usually dependent upon the genetic and environmental backgrounds (Romagosa *et al.* 1999; Stuber *et al.* 1999); making these QTLs of rather little, if any, value in realistic breeding (as the superior genetic value assigned to them in a mapping population line may not be transferred to lines of the elite germplasm of the program; *e.g.* see illustrative example in Reyna & Sneller 2001).

It seems then that biotechnology might only help breeding for further raising yield potential if relatively simple attributes determining yield in a range of environments are identified at the crop level of organization (see untrustworthiness of apparently sound traits at levels of organization much lower than that of the crop canopy in Sinclair *et al*. 2004, and in most failures of plant physiology to contribute with selection criteria in the past). In fact, much of research efforts in crop physiology are related to the objective of identifying relatively simple attributes putatively related to yield in field conditions. Some of these attempts include the retrospective analyses of attributes *de facto* altered when yield was genetically improved in the past.

Past achievements

Understanding the physiological changes associated with past breeding is relevant, at least in part, because understanding the physiological bases of genetic gains in yield would allow the identification of traits that may be potentially useful to boost future progress. This is likely why a large amount of research has been devoted to this issue in cereals (*e.g.* see reviews by Peltonen-Sainio 1994; Calderini *et al*. 1999; Abeledo *et al*. 2002).

In general, summarizing across cereals (see the abovementioned reviews and the papers quoted therein for more details), breeding has increased yield potential chiefly by enhancing biomass partitioning to grains (*i.e.* harvest index), with much smaller (and less generalized) changes in biomass and crop growth attributes. This may have resulted as a consequence of empirical attempts of early breeding to improve resistance to lodging through reductions in plant height. However, as harvest index cannot exceed certain biological limit (as there must be a minimum amount of biomass for assimilation and to provide physical support for the reproductive structures) and actual values in modern cultivars are close to it in most regions without severe terminal drought, it is unlikely that further increases in yield may be brought about by higher harvest index. In addition, modern cultivars would have already a stature close to the optimum and further reductions would be negative for keeping potential yields rising (Slafer *et al.*, 1999).

Thus, by imposing a genetic restriction to stem growth, more assimilates turned out to be available for the growth of the inflorescences (of lower competitive ability than the stems), improving thus the dry matter allocated into reproductive structures at the end of the stem-elongation phase at flowering. This ended up in yield improvements due to the fact that (i) a strong association seems to exist between the number of grains and the dry matter in the inflorescences at flowering, both traits per unit land area (*e.g.* Fischer 1985); and (ii) grain growth seems to by hardly limited by the availability of assimilates during post-flowering (*e.g.* Slafer & Savin 1994) and, therefore, increases in number of grains per m^2 are normally paralleled by increases in yield.

In most conditions breeding has not consistently modified developmental rates to flowering, being old and modern cultivars of similar lifespan (Araus *et al.* 2002). Where breeding has been conducted under terminal stress, modern cultivars tended to have anticipated flowering compared with their predecessors. However, in most regions in which the crops have been traditionally bred during several decades, time to flowering would have been already optimized (as it is normally the first attribute selected for in a breeding program, as it confers general adaptation to the region) and important changes in time to flowering might not be expected as an avenue to keep raising yield potential.

As pointed out above, most and most generalized changes in cereals yields were achieved by changes in harvest index. However, most of the literature in which this assertion is based has focused in wheat and barley. Though less work has been made with oats, there seems that in some cases oat breeding tended to increase biomass more consistently than harvest index, like in Finland (Peltonen-Sainio 1990). This has been likely due to the fact that old Finnish oats seemed to have an already quite high harvest indexes.

All in all, it appears that harvest index, the main attribute changed while yield was empirically improved, would be of little value in breeding for further raising yields in most conditions. Future progress may then depend on gaining more biomass, and particularly during the stem elongation phase when the weight of the inflorescences at flowering is gained (and this trait, in turn, physiologically linked with the number of grains per unit land area and yield whenever grain growth is not strongly limited by the availability of the sources during grain-filling).

Future progress

If genetic gains in yield potential largely require the improvement of biomass accumulation during stem elongation, it will be needed the identification of relatively simple traits putatively related to this trait (biomass accumulation is not much simpler -and then more confidently manipulated- than yield itself) and eventually surrogates of these traits if they are hardly evaluated (Slafer *et al.* 1999). Biomass production during stem elongation may be achieved, at least theoretically, by increasing either the amount of radiation intercepted by the canopy or the efficiency to use the intercepted radiation.

Radiation intercepted by the canopy during stem elongation would depend upon the ability of the crop to intercept the incoming radiation during that phase and on the actual length of the phase (as the longer the phase the higher the amount of accumulated incident radiation). Radiation use efficiency depend on several attributes, the most promising ones include the distribution of incident radiation (and perhaps nitrogen) within the canopy, depending largely on its architecture.

Improving the efficiency of the crop canopy to intercept the incoming radiation may understandably only be valuable in few growing regions, as in most growing areas, when the crop is adequately managed, the canopy has already maximized interception by the onset of stem elongation. Whenever this is not true (*e.g.* some areas of very short growing seasons) improving early vigour may result in improvements in growth during stem elongation. There is genetic variation and breeding for early vigour may be successfully carried out selecting for either attributes of the seedlings determining it (Richards *et al.* 2002) or directly selecting for early differences in ground coverage through the use of vegetation indexes (Araus *et al.* 2001).

Manipulating genetically the length of the stem elongation phase in cereals would be likley as it appears that a certain time from sowing to flowering can be achieved with component phases of different duration (Slafer & Rawson 1994). Thus, it may be hypothesized that manipulating development without greatly modifying the length of the entire growing period could bring about extensions of the stem elongation phase and that this, in turn, would result in an increased number of grains per m2 associated with an improved amount of dry matter accumulated in the inflorescences at flowering (Slafer *et al.* 2001).

Increases in radiation use efficiency can be achieved by improving the distribution of incident radiation by reducing the coefficient of light attenuation, so that each unit of leaf area would intercept less radiation at a higher efficiency, a trai for which genetic variation been reported during the pre-flowering period in wheat (Green, 1989). Emprirically it seems virtually impossible to select for lower attenuation coefficients, but a surrogate may be found in selecting for higher rates of carbon isotope discrimination (Δ) in the absence of water stress (as a higher Δ is related to a higher C_i/C_a ratio due to a larger stomatal conductance and photosynthetic rates; Araus *et al.* 2001).

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What oat breeders really need from biotechnology?

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Abstract

Various aspects of biotechnology have considerable potential to offer the oat improvement community. There are two principal criteria to judge the usefulness of any biotechnological approach: 1) do they address a critical need of oat breeders, and 2) are they cost effective. In the long term these must be satisfied to really make a contribution, novelty is not enough. There is considerable potential in borrowing from other species in terms of comparative genomics and in terms of adapting procedures which function well with other organisms. A complementing strategy among breeders and biotechnologists will best serve the oat improvement community.

Key words: genetic variation, selection, directed variation, transformation, MAS, comparative genomics

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My purpose is to assist/facilitate plant breeders in answering the question posed in the title. Actually, this presentation is an update of one I made in 1997 to the South American Oat Conference. To answer the question I suggest you rephrase it as follows: If only I could do ____________________ to increase my productivity for oat improvement. After finishing that exercise, I suggest that you and the other breeders engage our biotechnology colleagues here at this conference, as well as later and elsewhere, to determine the nature of the interface or intersection between the needs of breeders for more effectiveness and what biotechnology/molecular biology has to offer in the way of new tools to better do the job of oat improvement.

Secondly, engage your colleagues in dialog to learn about information generated by biotechnology in its various forms that will give you greater insight into more efficient modification/improvement of crop plants, specifically for this group, oat. I also challenge you to do these considerations using not only current paradigms, but to “leave the box”, and then imagine what new paradigm possibilities there might be if some of the answers you gave the “what if” question became reality.

According to Sorrells and Wilson (1997), breeding progress depends on (i) discovery and generation of **genetic variation** for agronomic traits and (ii) accurate **selection** of rare genotypes which possess new or improved characteristics due to superior combinations of alleles at multiple loci, or more simply stated (1) genetic variability and (2) selection applied on the phenotypic expression of that variability to advance the more desired genotypes to the next generation.

Regarding the discovery and generation of genetic variability, several things come to mind. First, the new variation should be directed, not random, whenever possible. That direction might be accomplished by (1) the use of specific donor gene(s) to either fix a broken situation or enhance a sub-optimal one. Another possibility (2) is to modify a specific existing gene to produce a better genotype and then phenotype. Further, there are certain gene products that when eliminated by (3) gene suppression might result in a more useful phenotype. Also, as we learn more about interactions among specific loci we may be able (4) to custom design new gene combinations that, as a composite, would produce an improved genotype/phenotype. The use of comparative genomics on other grass species might instruct any or all of these examples.

When some of the advances being discussed at this conference become a reality for oat, successful transformation procedures will provide access to virtually any source of genes that could accomplish any of the four examples of directed genetic variation described above. Further, with more sophisticated means, we can look forward to inserting specific genes into specific sites and, ultimately, to directly replacing existing alleles with more desirable alternatives.

When considering transformation, we might want to first look to donor species and genera whose genomes share many DNA segments/base sequences with oats, because such segments might more easily fit into the recipient DNA. However, depending upon the nature of the desired trait we may have to also look beyond these relatively closely aligned genomes to any organism that contains a gene that could modify a given oat phenotype in a desired manner. Especially as these transfers bridge wider evolutionary distances, isolating the gene of interest and transferring it with a maximum expression potential will increase breeding efficiency. When there is sub-optimum expression, using promoters that provide for tissue-specific expression may effectively enhance/isolate the expression of the desired trait.

If the issue is pest protection, then the elucidation of the genome, functionality, and expression of avirulence/virulence factors in the pest combined with a similar knowledge of host-pest recognition and host response systems would also be quite helpful. A deeper understanding of host recognition and response to a pest might well provide a key to the development of effective non-race specific resistance.

As we learn more about plant response to abiotic stresses, it appears that some stress tolerant genotypes do better when under stress, but not when under more normal conditions. When this is the situation, we would want the reaction to be inducible and function only when the stress is present.

Another major consideration regarding using biotechnology tools to achieve directed or non-random variability is the cost/benefit ratio. Because using most of these procedures will probably be more costly than more conventional breeding, the benefits must be proportionately greater to compensate for the increased costs. Part of that cost consideration includes minimizing the selectivity of genotypes on which the new technology can be effectively used. Said another way, novel procedures that work only on a limited number of recipient genotypes have reduced attractiveness and actually work at cross purposes with expanding genetic variability of the recipient species.

Moving to the second point from Sorrells and Wilson (1997) (selection), it can be summed to say: increase the heritability so that the phenotype better predicts the actual genotype. Remember the simple equation $P=G+E+GE$. We want to highlight/intensify the G term because permanent improvement comes only from retaining and increasing the frequency of superior genotypes. Using transformation to intensify the genetic control of a trait could also elevate the value of G for that phenotype.

For improving selection, the goal is to use better evaluation methods that more effectively identify the actual genotype by reducing the relative E and the GE components in the above equation for phenotype. A better understanding of how the genes within a genotype act singly and, in combination, to produce a given phenotype will obviously contribute to more effective selection, as well as the construction of new directed gene combinations.

Molecular markers, pieces of DNA, whose sequence composition and identity are not influenced by the environment in which they exist, either directly (the E term) or indirectly (the GE term), increase the capacity for more precise prediction of a genotype than those predictions based only on phenotypic observations. Such identification of superior genotypes provides for the continued improved phenotypic expression and is commonly referred to as Marker Assisted Selection (MAS).

MAS is obviously most useful when the marker-trait association exists in many derived populations, i.e., not just in progeny of a specific cross. If the marker trait associations are unique for individual populations, then the investment necessary to determine the idiosyncratic relationship for each breeding population is probably not justified in most breeding situations. Assuming individual associations are operative in multiple populations, those having either tight or flanked linkages can be used to track subtle or minor genes once the association is identified. In other words, QTL’s can be manipulated in the same way as if they were major qualitative loci. The ideal marker, of course, is the gene itself. With more sophisticated mapping, we may be able to localize a QTL to a very small region of the genome. Knowledge of the gene content within that area provides candidate genes. Identification of the correct candidate can be by either transformation or by testing induced mutations in the gene.

Finally, for the near future, it may be that using MAS for parent, rather than progeny, selection will be more cost effective because molecular analyses of 100 parental candidates may be manageable, while analysis of 5,000 to 20,000 progeny may not be.

Another item beyond tools that plant breeders can use from biotechnology is information. Some of this information could come from what I call genetic dissection. This information would tie directly to the directed variability and to the increased heritability, both discussed earlier. Pairs of near isogenic lines (NILs) could assist in estimating the size of the effect of each locus. Currently, when analyzing quantitative data we assume locus effects of equal sizes to make the mathematics manageable, even though we commonly refer to major and minor genes.

Secondly, multiple pairs of NILs could allow detection and estimation of various forms of epistasis in other than aggregated statistical terms such as AxA, AxD, and DxD. That information would facilitate design of selected new gene combinations that, as a composite, would produce new, more desirable phenotypes.

Conclusion

Biotechnology has the potential to assist plant breeders by facilitating or directing the creation of desired variability and, secondly, by providing tools to increase the connection between the observed phenotype and the actual genotype that produced the phenotype, i.e., the heritability. It will also allow differentiating genotypes among individuals with similar phenotypes to increase the chance of exploiting transgressive segregation. The fundamental question that needs to be asked to identify these tools won’t change, but the answer, the tools and therefore the paradigms will change as we learn more over time. Keep an open mind!

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ESTs, cytogenetic stocks, and other tools for oat genomics

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Abstract

The development of tools for structural and functional genomics is essential for the application of these technologies to oat genetics and germplasm improvement. To supplement the fewer than six hundred DNA expressed sequence tags (ESTs) present to date in public data bases for oat, we have sequenced and are annotating for submission to GenBank an additional ~7,700 oat EST sequences. These 5' single pass sequences are derived from random clones isolated from cDNA libraries developed from polyA RNA isolated from 3-week-old green leaf (~2,500 clones), 6-day-old etiolated leaf (~2,600 clones), and 6-day-old root tissue (~2,500 clones) of 'Ogle-C', a reselection of cv. Ogle. About 85% of the oat sequences match Triticeae sequences present in the data base. We have been developing and characterizing cytogenetic stocks to use for relating previously identified oat genetic linkage groups to physical chromosome. Detection of molecular marker deficiencies in monosomic and nullisomic lines, where the missing chromosome or chromosome pair has been identified by C-banding analysis, has allowed assignment of most of the major oat linkage groups to chromosome for the monosomic stocks available. New monosomic stocks are being produced and characterized in an attempt to obtain a complete monosomic series in a single genetic background, cv. Sun II. These are recovered as products of abnormal meiosis in haploid oat plants derived from crosses of oat x maize. The described materials together with genomic tools reported from other labs including a barley DNA gene chip showing about 27% cross detection with oat expressed RNAs (Close et al. 2004), a DNA large fragment library for diploid oat (Bakht et al. 2003), and additional ESTs (e.g. Bräutigm et al., Molnar, this conference) provide opportunities for not only improved understanding of oat genome structure and function but also applications to oat genetic improvement.

Close, T.J. et al. 2004. Plant Physiology 134:960-968; Bakht, S. et al. 2003. http://www.intl-pag.org/11/abstracts/P2a_P82_XI.html.

Key words: EST, cytogenetics, monosomics, genomics

Production and use of anther culture derived DH-lines of oat

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Abstract

Application of DH-lines (doubled haploids) for cultivar breeding saves time and increases selection efficiency. DH-lines are also valuable material for genetic research. Benefits are based on the quick derivation of pure lines from heterogeneous crossing progeny, and the absence of dominance and heterozygosity of these lines. Oat DHs have been produced through anther culture and through wide hybridization (Rines 2003). However, unefficiency of the available methods has limited the use of haploids in oat breeding and research.

Our aim was to increase oat DH production through anther culture to appropriate level. Culture medium and conditions were optimised on the basis of the previously reported protocol (Kiviharju et al. 2000). Also microspore culture was tested, but it was not successful.

Significantly higher plant regeneration rates were got by improved culture medium. Rates up to 30 green regenerants per 100 isolated anthers were obtained, common numbers being around one or less per 100 cultured anthers. Response was genotype-dependent, but crossing progenies of the non-responsive and well-responsive genotypes could be regenerated in several cases. In field conditions, some differences were found when anther culture derived DH-lines were compared with commercial seeds, but in general their quality was in line.

Numerous oat DH-lines produced in the anther culture experiments were tested in field. In the present study we are using anther culture derived DH-population (150 DH-lines) for genetic mapping of oat quality characteristics. As a conclusion, production rates of anther culture derived DH-lines are approaching the numbers needed for practical applications, at least in some genotypes.

Kiviharju, E. et al. 2000. Plant Cell Reports 19:674-679; Rines, H.W. 2003. In: Maluszynski, M. et al. (eds.). Doubled haploid production in crop plants. Kluwer. P. 155-159.

Key words: androgenesis, anther culture, breeding, haploids, oats

Mapping of quantitative trait loci for yield, quality and disease resistance

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Abstract

A genetic map was produced to identify loci contributing to disease resistance, quality and yield of oat. An F8 single-seed descent population of 170 lines was produced from the cross Potoroo x Mortlock. This population segregated for several disease resistances derived from the dwarf feed variety Potoroo and a number of quality traits contributed by the tall milling quality variety Mortlock. The F8 lines were evaluated for 35 agronomic, quality and disease resistance traits at three sites for up to three years.

A genetic map of 24 linkage groups covering 2145 cM was produced using this population. The map currently consists of 45 RFLP, 14 SSR and 381 AFLP markers. Quantitative Trait Loci (QTLs) for cereal cyst nematode resistance and tolerance were identified. A single nucleotide polymorphism assay was developed for one of these loci. Two major QTLs for yield were observed, both contributed by Potoroo. Two major QTLs were found to control the quality characteristics of Mortlock, with one linked in repulsion to a dwarfing gene in Potoroo. A number of QTLs contributed to grain weight, oil content and protein levels.

A summary of the major QTLs, their interactions and the opportunities to combine them to obtain the desired breeding outcomes will be presented.

Key words: molecular markers, genotyping, stem nematode, digital imaging

Breeding oats for subtropical environments

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Abstract

In subtropical environments, Farmers are able to grow two crops per year in the same land, usually under no till system. The two grow season are spring/summer, when farmers cultivated soybean or corn (the cash crops), and winter/spring, when farmers cultivate small grains. Subtropical environments are characterized by a great variation of climatic parameters during the oat growing season (winter/spring), especially over years.

Old oat cultivars (released before 1980) had plant cycles as long as 180 days, hindering the cultivation of a summer crop. Selection for genes for photoperiod insensibility reduced the plant cycle to 125-130 days in the earlier genotypes. Under subtropical conditions, North American oat genotypes (photoperiod sensitive) flower in late spring, when the Brazilian adapted oats are ready or almost ready to harvest. The change in life cycle was possible by conscious crossing and selection of genotypes insensitive to photoperiod. Genetics studies revealed two mechanisms controlling flowering date in oats: 1) temperature dependent; 2) photoperiod dependent (Locatelli, et al. 2002). Plant stature was also reduced from 150-160 cm to 90-120 cm using minor effect genes for plant height. Visual selection of early plant vigour helped to increased harvest index, allowing to increase grain yield at same time that stature was reduced. Test weight was increased from 30-40 kg/100 l to 50-55. Milling yield increased from about 40% to 62%. The most important diseases are crown and stem rust, followed by leaf spots. Resistance to crown rust is based in major effect genes, which have short duration under cultivation conditions. Therefore, oat breeding programs need to release resistant varieties almost every year. Partial resistance has been studied.

Strong selection for broad adaptation to subtropical environments permitted the farmers to obtain grain yields greater than 3 t/ha consistently over the years.

Locatelli, A.B. et al. 2002. 22ª Reunião da Comissão Brasileira de Pesquisa de Aveia, p. 391-393.

Key words: adaptation, selection, flowering date, plant height, grain yield

Oat improvement – *in silico*

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Abstract

Oat improvement is driven by information and ideas. Broadly speaking, bioinformatics is a field dedicated to the exchange and interpretation of information. The purpose of this study was to describe and evaluate various bioinformatics tools (programs and databases) based on their relevance to oat improvement. An inventory of bioinformatics tools was developed, and these were described and evaluated based on their relevance to a "traditional" cycle of oat improvement. This inventory includes tools developed by the authors, as well as many other tools that are freely available on the Internet. The primary components of the "traditional oat improvement cycle" include (1) Parent selection and population development, (2) germplasm selection, and (3) variety evaluation. Tools associated with parent selection include germplasm databases, a newly developed oat pedigree database, databases containing results of screening tests, and databases of marker allele surveys. We report a new tool, "Gelato", for building and maintaining inventories of marker surveys. Tools associated with variety screening are the most numerous, since these include all tools related to molecular marker development and QTL association. We report a new database that allows simple and systematic queries of QTLs identified in oat. Tools associated with variety evaluation include databases that can facilitate detailed studies of cultivar adaptation and end-use quality. We report a new database and query tool that can facilitate assimilation and data mining of multi-trait, multi-environment variety trials.

References: Links to databases described in this study are maintained at: http://gnomad.agr.ca/oat/

Key words: bioinformatics, database, marker, sequence, allele, pedigree, phenotype.

Breeding and biotechnology: Resistance

The applications of biotechnology to disease resistance breeding in oat

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Abstract

Through the use of biotechnology, molecular marker assisted selection and genetic engineering can both contribute to disease resistance breeding. A number of markers for various oat diseases have been identified and some are being used in breeding programs. Genetic engineering of oat is now well established but genetic engineering for disease resistance in any crop is still in its infancy and remains to be proven in the field.

Key words: Biotechnology, disease resistance, markers, genetic engineering

Introduction

In natural ecosystems, plants and the organisms that attack them achieve equilibrium. However in agroecosystems, plants and their predators are not in balance. Large areas of genetically uniform cultivars and species and restricted rotations result in disease epidemics (caused either by fungi, bacteria or viruses) and subsequent losses. Breeding for resistance to diseases is the most cost effective and environmentally sustainable form of control to mitigate these losses. However co-evolution of crop and pathogen results in a continual need for new disease resistance genes to be identified and incorporated into new cultivars. Thus oat breeders, like breeders of all other crops need efficient techniques for incorporating new disease resistance genes into cultivars.

Biotechnology in its broadest sense consists of two types of technology, those that rely on the advances that have occurred over the last thirty years in our ability to manipulate DNA and those that rely on tissue culture. These two forms of biotechnology theoretically offer four ways to help the plant breeder incorporate disease resistance into new cultivars. The ability to manipulate DNA leads to the development and use of molecular markers for disease resistance and to the potential to engineer novel disease resistance genes into plants. Through tissue culture, double haploids and/or interspecific hybridization could be used to more efficiently incorporate novel disease resistance genes from alien species, and in-vitro selection could be used to select for disease resistance. To date tissue culture to produce doubled haploids of oat (through either anther/microspore culture or through corn pollination) has met with limited success. Similarly in-vitro selection for disease resistance in crops, including oat, has not met expectations. Consequently this paper will deal with the use of molecular markers and genetic engineering for improving disease resistance in oat.

Screening for disease resistance

Before the advent of molecular markers, screening for disease resistance in segregating populations could only be performed by exposing members of the population to natural infection or through artificial inoculation in either the field or a controlled environment. While such screening has certainly proved its worth in many cases and continues to be the most common method of disease screening, depending on the particular disease and environment the disadvantages to such procedures may include:

a) the reliance on consistent natural infection for screening
b) the need to develop an artificial inoculation technique and maintain inoculum
c) failure of artificial inoculation
d) the need for significant expertise to properly evaluate the infection
e) the need to introduce a new pathogen into an area from which it is currently absent
f) a significant space (field/greenhouse) requirement for screening
g) the need to screen populations rather than single plants
h) the need for multi-generation work, especially with seed-borne diseases
i) a significant time from seed availability to results
j) masking of multiple alleles/genes

In such cases, a technique that relies on indirect selection for the disease resistance gene through selection for an easily/reliably scored, tightly linked trait (a marker) may have significant advantages and may be economically worthwhile.

Early marker work

Any trait with appropriately close linkage to a gene could serve as a marker for a disease resistance gene. Ideally such a trait should be tightly linked, easily measured, phenotypically neutral and stable over environments. Prior to molecular biology, phenotypic or biochemical markers (e.g. colour, isozymes etc.) tightly linked to disease resistance genes could have been utilized as markers for those disease resistance genes. However very few such markers (and in most cases none) with tight linkage to important traits had been identified and mapping to identify linkage was a much more difficult exercise than after the advent of molecular biology. Genetic maps in some species (but not oat) were relatively well developed (for that time) but did not compare with the high-density maps that have been developed using molecular biology. In addition measurement of the tightly linked trait (such as an isozyme) did not lend itself to the high throughput needed for efficient use in a breeding program. Such markers were also, by definition, not phenotypically neutral and so were either undesirable or not easy to incorporate into a breeding program. Consequently prior to molecular biology only a few markers ever came close to application in a crop-breeding program (e.g. Summers et al. 1988).

Molecular markers

With the advent of Restriction Fragment Length Polymorphism (RFLP) technology and then the development of the Polymerase Chain Reaction (PCR) and related techniques such as Random Amplified Polymorphic DNA (RAPD), Simple Sequence Repeat (SSR) technology, Amplified Fragment Length Polymorphism (AFLP) technology and others, high density genetic maps (and thus potential markers) could be developed relatively quickly and inexpensively. Importantly, these were also phenotypically neutral. Once such maps were developed in a species, then associations between commercially important traits and markers could be identified. With the development of the Bulked Segregant Analysis (BSA) method (Michelmore et al. 1991), markers could be identified without the need for a map of the species. When combined with RAPD technology and more recently AFLP technology this technique has been widely used to discover molecular markers.

As techniques such as RAPD and AFLP may not be highly repeatable, the DNA fragments that represent such markers are now commonly sequenced. Through appropriate primer design, dominant and/or co-dominant Sequence Characterized Amplified Region (SCAR) markers and Allele-Specific Amplicons (ASA) have been developed. Similarly the DNA sequence of RFLP clones and expressed sequence tags (EST) can also be determined and primers designed and developed to produce similar types of markers. These PCR-based markers lend themselves to the high-throughput techniques that need to be utilized if molecular markers are to be economically incorporated into a plant-breeding program.

Once a linked marker is identified, and if a reasonably high-density map of the species has been developed, then markers can be mapped in mapping populations. Thus through the use of high-density maps, BSA developed markers and markers developed through direct mapping may point the way to other markers (RFLP, RAPD, SSR, AFLP) mapped in that region. These may be more closely linked to the trait of interest and so may serve the starting point for a new round of PCR-based user-friendly marker development.

A marker is only as good as the degree of linkage to the trait of interest. The exact degree of linkage needed in order for a marker to be useful depends on the importance of the disease and the needs of the plant breeder. The best marker is of course the gene or allelle itself. With increasing advances in genomics and the cloning of genes of interest to plant breeders, the potential to design primers for use as markers based on the sequence of the gene and its various alleles becomes a reality. In our laboratory we now utilize markers specific for various alleles of the barley stem rust resistance gene Rpg1 (cloned by Brueggerman et al. 2002) based on the sequence of the alleles themselves. But for the time being significantly more work is needed to achieve this end for most crop diseases, particularly for oat diseases. However, cloning of oat disease resistance genes will be helped by the synteny that exists among the genomes of closely related crops, through the very high density maps that exist in some species, through bacterial artificial chromosome (BAC) libraries that have been produced and through knowledge of the complete genome sequence of crops such as rice.

Molecular markers for disease resistance in oat

Penner et al. (1993a) were the first to identify a molecular marker for an oat disease resistance gene (Table 1). This marker was originally developed using BSA as a marker for the stem rust resistance gene Pg3. However Pg3 occurs in a tight cluster with a number of other disease resistance genes, particularly crown rust genes and specifically Pc68. Consequently the Pg3 RAPD fragment has been sequenced from a number of lines and used to develop markers, particularly SCAR markers, for Pc68 (see table 1). In our own laboratory this information was used to develop a SCAR marker for Pc68 that is extensively and routinely used in the oat breeding program.

Table1. DNA markers for oat disease resistance genes

Disease/Gene	**Marker Name/Type**	**Reference**
Stem Rust Pg3 (tight cluster with Pc68, Pc44, Pc46, Pc50, Pc95, PcX, and Pg9)	UBC 195 RAPD	Penner et al (1993a)
Crown Rust Pc68 (tight cluster with Pc44, Pc46, Pc50, Pc95, PcX, Pg3 and Pg9)	SCAR markers based on UBC 195 RAPD (above) SCAR with PAR using Rsa1 SCAR (based on Dumont Pg9 sequence) SCAR with PAR using Rsa1 (based on Rodney 0-Pg3 sequence) Pc68-300 SCAR (ASA) developed by Scoles' lab	See: Orr et al. (1998) Orr et al. (1999) DeKoeyer et al. (2000)
Crown Rust Pc68 (tight cluster with Pc44, Pc46, Pc50, Pc95, PcX, Pg3 and Pg9)	UBC 269 RAPD	Penner et al. (1993b)
Crown Rust Pc38 (tight cluster with Pc62 and Pc63)	RFLPs, ESTs, one SCAR	Wight et al. (2004)
Crown Rust Pc39 (tight cluster with Pc55)	RFLPs, ESTs	Wight et al. (2004)
Crown Rust Pc48	RFLPs, ESTs	Wight et al. (2004)

Crown Rust Pc59	AFLP	Satheeskumar et al. (2002)
Crown Rust Pc71	RFLP	Bush and Wise (1998)
Crown Rust Pc91	RFLP	Rooney et al. (1994)
Crown Rust Pc92	RFLP	Rooney et al. (1994)
Crown Rust Pc94	SCAR94-1 and SCAR94-2	Chong et al. (2004)
Crown Rust - unnamed, from A. strigosa	Pcq1 (QTL)AFLP	Zhu and Kaeppler (2003)
Stem Rust Pg9 (tight cluster with Pc68, Pc44, Pc46, Pc50, Pc95, PcX, and Pg3)	RFLPs, RAPDs, Storage Proteins	O'Donoughue et al. (1996)
Stem Rust Pg9 (tight cluster with Pc68, Pc44, Pc46, Pc50, Pc95, PcX, and Pg3)	Lrk10 Receptor Kinase Sequence	Cheng et al. (2002)
Stem Rust Pg13 (tight cluster with Pg2)	RFLPs, RAPDs, Storage Proteins	O'Donoughue et al. (1996)
Loose Smut (tight cluster of three genes)	Ua300Co SCAR (co-dominant) Ua750SCAR (dominant)	Eckstein et al. (2002)
BYDV	AFLP	Jin et al. (1999)

Penner et al. (1993b) also developed a marker specifically for Pc68 through BSA however attempts to use this to develop other markers for this chromosome region have been less successful than those that have used the Pg3 marker. Many other markers have since been developed for other crown rust genes, stem rust genes and for loose smut and BYDV (Table 1). These have been developed using either BSA or mapped genomic or cDNA clones and some are being utilized in breeding programs. While marker-assisted selection of single genes is the most obvious use for these markers, they are ideally suited for pyramiding of two or more genes for resistance to a particular disease in order to achieve more durable resistance.

Genetic engineering for disease resistance

In order to utilise genetic engineering for disease resistance one must have not only an efficient transformation system but also the appropriate genes and appropriate promoters for them. Genetic engineering of oat to the point of producing stable transformants has now been achieved by a number of groups (Svitashev et al. 2002; Maqbool et al. 2002; Cho et al. 2003; Perret et al. 2003) using particle bombardment of embryogenic callus from either immature embryos or shoot apices. While not as routine as for some crops and probably not routine with all lines, genetic engineering of oat can be regarded as a technology that could be utilized if and when necessary.

Much research has been undertaken to isolate genes that might be candidates for genetic engineering of resistance. To date some success in transferring major disease resistance genes from one species to another has been achieved, at least at an experimental level (Tai et al. 1999). With the hope of genetic engineering for broad-spectrum disease resistance, considerable research is now devoted to understanding the systemic acquired response of plants (SAR) and the role of pathenogenesis related (PR) proteins (Campbell et al. 2002). To date results, even at an experimental level have been limited

(Friederich et al. 2001). Undesirable pleiotropic effects of such manipulation have been reported and need to be addressed (Hammond-Kosack and Parker 2003). Such work will also require appropriate promoters. Although genetic engineering of oat has been limited, Koev et al. (1998) demonstrated some reduction in BYDV infection in oat plants transformed with part of the BYDV genome.

In searching for the "ideal" resistance strategy through genetic engineering we must remember that the co-evolution of crop and pathogen over many years has developed as a finely balanced system. We must be very aware of the selection pressure this (and any other strategy) may put on pathogens and be sure we do not push pathogens to evolve new virulence strategies that traditional breeding approaches cannot handle. With oat in particular, we must also be aware of the ease with which any engineered gene can be transferred to its weedy relatives. This (and consumer acceptance) will be a major issue with any genetically engineered oat, particularly one engineered with a gene (or genes) that may confer some selective advantage.

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Quantitative resistance to crown rust: the role of its components for breeding varieties

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Abstract

Selection of genotypes for quantitative resistance to oat crown rust based on its components needs the knowledge of the association of these components with each other and with the amount of disease in the field, represented by AUDPC. This work aimed to determine these correlations, based on results of previous trials, in which the reaction of 31 white oat genotypes was tested and the resistance components were quantified. Correlations were usually low, among the resistance components with each other as well as the components with the amount of disease in the field. Higher correlations with AUDPC, and consistent among years, were infection frequency in seedlings and latent period and pustule size in adult plants. All other possible correlations were very low. These data suggest that the resistance components mentioned can influence the expression of quantitative resistance in field in a slightly more important manner. Nevertheless, low correlation of resistance components with each other indicates that genotype selection, in this host-pathogen interaction, must not be accomplished on the basis of a single resistance component assessment. The correlation analysis suggests that the expression of quantitative resistance to oat crown rust is not conditioned by a single resistance component only but by the group effect of all of them. In addition, it is possible that different mechanisms are involved in each genotype, in a way that the more important resistance component in one genotype may not be the same in another.

Key words: Puccinia coronata f. sp. avenae, Avena sativa, phenotypic selection for resistance, partial resistance, slow rusting

Single nucleotide polymorphisms as next generation markers for high throughput screening for crown rust resistance in oat

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Abstract

Single nucleotide polymorphisms (SNPs) have rapidly gained popularity as markers of choice because of availability of automated high throughput technologies to genotype them. Direct sequencing of genes and their comparative alignment between genotypes is one approach to SNP discovery. Existing RFLP markers can be used as a source of these genes. The objectives of this study were to discover SNPs in oat using existing RFLPs associated with crown rust resistance, and to determine if such association was retained in the RFLP-derived SNPs so these could be used as markers in genetic studies.

Ten RFLP markers used in this study were sequenced and oligonucleotide primers were designed. One marker (cdo309) was mapped near a cluster containing the crown rust resistance gene *Pc68*. Putative SNP sites between resistant and susceptible plants were identified by direct sequencing and sequence alignment of the PCR products. The Single Base Extension (SBE) assay was used to validate SNPs, using an Applied Biosystems ABI 3100 Genetic Analyzer for capillary electrophoresis of SBE products. Linkage of SNPs to *Pc68* was determined in two populations segregating for this gene.

Ten SNPs between resistant and susceptible plants were validated by SBE. Two, derived from cdo309, were associated with *Pc68*. Linkage to *Pc68* (3.9-4.4cM) was confirmed in two populations. Results showed that SNPs in oat can be derived from RFLPs and applied as markers to genetic studies. The automated ABI 3100 system provided accurate analysis of SNP sites. The throughput is 1,152 samples per 24 hr, with capability to multiplex to 10 SNP sites. Estimated costs are $0.40 per SNP site. The Invader® Operating System requires no prior PCR amplification of genomic DNA to detect SNPs, is quantitative and can detect heterozygosity, making SNPs even more attractive as the next generation markers for high throughput screening.

Key words: SNP markers, high-throughput, single base extension

Analysis of resistance and susceptibility to barley and cereal yellow dwarf virus

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Abstract

Barley yellow dwarf virus and Cereal yellow dwarf virus (YDV) are the most endemic and severe viral diseases in cereal crops and can cause significant yield losses. This study was undertaken to isolate and characterize genes that may be involved in YDV susceptibility in oat and resistance in the wheatgrass, *Thinopyrum intermedium*.

Suppressive subtractive hybridization (SSH, Diatchenko et al. 1996) and mirror orientation selection (MOS, Rebrikov et al. 2000) were combined with differential hybridization to isolate genes whos expression changes when oat and wheatgrass were inoculated with YDV. Expression of these genes was quantified using real-time PCR.

Approximately 90% and 88% of the putative differentially expressed genes selected by differential hybridization from the wheatgrass and oat libraries, respectively were confirmed by real-time PCR. In the resistant wheatgrass-YDV interaction, a number of defense response and basic metabolic genes were up-regulated with fold changes ranging from 2 to 1,782. The expression of these genes either did not change or was suppressed in susceptible inoculated oat. The differences in the wheatgrass and oat gene expression profiles are beginning to delineate the significant variation in plant responses to YDV. Elucidating the function of these differentially expressed genes will provide insights into YDV resistance and susceptibility mechanisms and may lead to novel strategies for protecting small grain crops against YDV.

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Key words: BYDV, CYDV, wheatgrass, virus resistance

Transgenic oat for improved BYDV resistance

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Abstract

Among the cereal crops cultivated in Finland oat (*Avena sativa* L.) ranks second, after barley. Finland is one of the major oat producers in the world and a considerable part of the harvest is exported. The Finnish oat cultivars are generally well adapted to the humid and cool growth conditions in Finland. In order to improve the Finnish oat cultivars better to meet the requirements of the food industry, modern biotechnical methods are being used. Our first aim was to develop oat varieties with resistance to BYDV (Barley Yellow Dwarf Virus) through gene transfer.

Six Finnish oat cultivars were used. The genotypes Kolbu, Rhiannon, GP-1 and *Avena sterilis* were used as controls. Cell cultures were started from mature embryos of all of these cultivars. From two Finnish cultivars leaf bases were also used. Embryogenic tissue cultures or oat leaf bases were used as targets for gene transfer, which was accomplished using particle bombardment. The transformants from the gene transfer experiments with the BYDV resistance gene were regenerated and rooted on selection media and transferred in soil in the greenhouse.

Transgenic plants carrying the BYDV resistance gene were obtained only from those embryogenic cell cultures, which were started from mature embryos of oat. The progeny of these transgenic plants was germinated and screened for the inheritance of the transgene. The germination frequency of the seeds has been good, for example ranging from 92 to 100 % in T1 and in T2, respectively. The progeny carrying the BYDV resistance gene was submitted to viral resistance testing.

Key words: oat, transgenic, BYDV resistance, Avena

Evaluation of frost resistance in oat

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Abstract

Resistance to biotic and abiotic stress is a crucial aspect for cultivar adaptation to agriculture environments. Among winter cereals, oat is the most frost sensitive and its insufficient level of winterhardiness is the main factor limiting sowing of winter oat in Northern Italy and Central Europe. Frost resistance, the most important component of winterhardiness, is an inducible process promoted by cold exposure and associated with a number of biochemical and molecular changes.

We employed field tests and physiological parameters in a set of cultivars released during the last 40 years to explore the genetic variability in frost resistance and identify resistant genotypes. Plants were hardened at +3/+1°C and exposed to freezing temperatures. The efficiency of the excitation capture by open Photosystyem II (PSII) reaction centres was evaluated after freezing, through the chlorophyll fluorescence parameter F_v/F_m, according to Rizza et al. (2001). Different hardening length and pre-hardening temperature (+12/+7°C) were also employed to investigate if a higher level of resistance is associated with the ability to induce early hardening. This capacity is of advantage under field conditions, where temperature falls progressively, because it enables resistant plants to prepare for cold before the susceptible ones. Some significant molecular traits associated to frost resistance such as the accumulation of *cor14* (Cattivelli et al., 1995) were also investigated on selected cultivars.

F_v/F_m analysis appears as an attractive test being rapid, non invasive and able to monitor a trait related to a crucial mechanism of the resistance acquisition. Significant differences in frost resistance were detected within winter cultivars.The most resistant showed a behaviour similar to that of winter barley, suggesting that it should be possible to improve the resistance of winter oat to a level similar to that of winter barley.

Rizza, F. Pagani, D. Cattivelli, C. Stanca, A.M. 2001. Plant Breeding 120: 389-396; Cattivelli, L. Crosatti, C. Rizza, F. 1995 Journal of Genetics & Breeding 49:333-338.

Key words: Avena sativa, frost tolerance, cold hardening, chlorophyll fluorescence, Photosystem II, cor *genes*

Markets, products and applications

Commercialication of value added oat ingredients

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Key words: products, innovation, industry, markets, consumers, commercialication, applications

General

Value added oat ingredients are usually classified as functional food ingredients. The main focus has been in oat soluble fibre, beta-glucan, that has scientifically proven health benefits. However, fractionation of oats produces also other value added ingredients for food industry in the area of technological improvement and nutritional improvement in addition to health benefits. The challenge for value added oat ingredients in terms of commercialisation is that oats are not cultivated as widely as other grains. Commercialisation of oat research and development results to successful food products is challenge for both for R&D and marketing people and top management. Investments are very closely monitored and the commercialisation period has shorten from 3-5 years to 1-3 years. It is crucial for company success that new products and services are launched yearly. The real challenge is to introduce products that are interesting for both consumers and retailers.

Innovation strategy and core competence

The corporate strategy is the framework that gives an organisation its overall directions and impels it to action. The strategy formulation process is continuous process that analysis the threats and opportunities in the environment and understanding the key phenomena underlying demand and competition. Goals, programs, plans, and budgets are formulated to build on the organizations competitive advantages and market opportunities. Competitive advantage reflects the core competence of the company. Core competence has three main characteristics: source of competitive advantage, potential breadth of applications and it is difficult to competitors to imitate. Innovation/ New-product strategy is one part of the overall corporate strategy. It is a means to implement an organizations corporate overall strategy. This means that a new-product strategy depends on the organizations capabilities and its environment. The key to success is the speed that the company can develop and market functional/ value added oat ingredients to the industry. The speed to market, speed versus competitors, speed of consumers evolving changing needs and speed necessary to produce new products to meet the needs of the company bottom line. It is important to note that the story behind the product has to be proven to the consumer.

The food product development process

The food development process consist of four key components:

1. assessing senior management's commitment to new product
2. finding the right idea
3. developing the business case for the product
4. developing and commercialisation of the concept

All the areas of the process has to be completed in order to be successful. The top management commitment and involvement is important for the organization to understand to be successful. From the organizational perspective it has been proven that team approach provides the best scenario for product commercialisation. The key is to create a team and an environment where all of the players feel involved and committed to the overall success of the product. Along with the team it is highly important that the core competencies and unique strengths that the company has and to understand that food/ beverage development begins and ends with the consumer. It is critical to understand the consumer mindset and motivation by studying their values, attitudes, lifestyles, and demographic trends. However, these can be communicated and directed by the corporations, interest groups and authorities.

Any new right idea has both technology and market drivers that must be synergistic for he development process. Technology drivers are research and development, process technology, supply chain and logistics technology, plus distribution, i.e. addition of fibre. Market drivers are consumer segments, functions, product functionality, customer benefits and usage or consumption occasions, i.e. functional high fibre snack products. Cross-functional teams make it easier to generate necessary resources from technology and market drivers that are required to successfully launch a new product.

The product development process is as follows:

Product strategic plan:	Market opportunity assessment
	Product business plan
	Product definition
Product implementation:	Prototype development
	Market strategy and testing
	Scale-up and trial production
Product introduction:	Product introduction
	Product support

High performance team

A team is defined as a group of individuals drawn together toward a common and clearly defined goal. In food research, the high performance team is composed of members who contribute to all aspects of the project of the research, marketing, packing, production and quality assurance. The teams are built around trust, communication and commitment to the final success of the project. The critical factor is that the areas of expertise are present to accomplish the goal. The vertical integration of resources in the development team facilitates the speed and accuracy to get right at the first time.

The model for team research is to have clearly defined goals and teams that include the entire core competencies required to successfully complete the project. If the core competencies are not available to the team they must be obtained from the outside. Outside capabilities may come from partnerships with suppliers, governmental laboratories, university centres, individual consultants, strategic partners and customers. In this model the development includes marketing and sales working team together with technical staff.

High performance team is based on precise communication and trust. The important feature is overcome breakdowns in order to accelerate projects. The individual needs has to be recognised and rewarded. The responsibility of the project champion is to communicate to those who control resources and communicate to them the technical achievements as well as commercial ramifications.

Launching the new product

The target market and positioning strategy are two important elements that are specified early in the development process. Launching the new product includes:

- The introductory marketing program: Target market and positioning
- Financial evaluation of the new product projects: development cost, prototype and pilot plant costs, manufacturing cost, related cost, pricing, anticipated sales, payback measures
- Market testing: Simulated test markets, sell-In tests, controlled testing, sell-in to the trade
- The launch

Summary

Commercialisation of new value added oat ingredients is difficult and time consuming due to competitive circumstances and industry structure. It covers comprehension and incorporation of the benefits of ingredient to consumer needs and ability to enhance teamwork to speed the development phase. As a result the commercialisation period can be reduced and launch success improved.

Adding value to the UK poultry industry

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Abstract

Considerable commercial interest had been expressed in the UK in investigating the use of oats in poultry rations, as birds fed commercially on oat diets appeared to perform better than would have been expected from the nutritional description. Advances in genetic breeding in the UK had led to the establishment of naked oats as a viable break crop option for growers and advanced varieties of ‘high oil’ naked oats offer the potential for significantly enhanced performance in monogastrics diets.

The AFENO project was established to conduct a three year coordinated programme of research to test the advantages of naked oats to the grower as an economic breakcrop, to the poultry industry as an effective ingredient in broiler and turkey rations, and to the consumer in improved meat quality.

The naked oats showed high levels of metabolisable energy when compared to wheat together with a good quality digestible amino acid profile. All other nutritional parameters were established to be satisfactory for poultry. Meat produced on high oat diets was found to have similar taste and texture to conventional diets. A satisfactory predictive energy equation specifically for naked oats was established with the use of a constant.

The research demonstrated the outdated nature of the nutritional information currently available for oats to the animal industry and the positive benefit of the addition of moderate amounts of oat hulls to monogastrics rations. Two commercial collaborators placed a number of experimental short-chain production contracts with growers in order to assess the supply logistics and use of naked oats in commercial operations with the view to a significant increase in the production area if the trials prove to be successful. There is a theoretical demand for approximately 700,000 tonnes of naked oats per year, equivalent to the total current UK annual oat production.

Maunsell C et al. 2003. Avian Feed Efficiency from Naked Oats (AFENO) October 2000 – September 2003. Final report of Defra Project No LS3623

Key words: poultry, naked oats, energy, hull, oil, production

Effect of dehulling on digestibility and nutritive value of oat groats for dogs

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Abstract

Hulls, which dilute the nutritional quality of oats, are perhaps the most important reason why oats has been replaced by other cereals, like rice, corn, wheat and barley, in the nutrition of dogs. The high crude fibre and cellulose contents of hulls have negative effects on the dry matter, organic matter, crude protein, energy and mineral digestibilities (K, Na, Cl) of cereals in dogs (Fahey et al. 1992, Lewis et al. 1994, Kienzle et al. 2001). However, when dehulled, oat groats are superior to other cereals in digestible energy value and digestible crude protein value in dogs (Kempe et al. 2004). Also the digestibility of the main nutrients of oat groats are comparable to those of rice and better than in wheat, barley or corn (Kempe et al. 2004).

The efficiency of dehulling is dependent on rotation speed of the dehuller. It is important that the nutritionally valuable kernels are intact after hulling process. To determine the effect of dehulling on apparent nutrient digestibilities and feed values for dogs, oats was dehulled at three different rotation speeds: 200, 300 and 400 rpm using small laboratory dehuller. The oat groats were heat treated in a flower mill with indirect steam (160°C, 30 min). A digestibility trial was carried out in metabolism cages on eight female Alaskan huskies according to a replicated 4 × 4 Williams square design.

Dehulling the oats at the rotation speed 300 rmp increased the faecal digestibility of dry matter, organic matter, crude fibre, N-free extract, crude carbohydrates and gross energy compared to low rotation speed. High rotation speed 400 rpm did not induce further increase in the nutrient digestibility, except dry matter and crude carbohydrates. Digestibility of crude protein, fat and starch were unaffected by the treatment and were an average 82%, 87% and 99%, respectively. However, the amount of digestible protein (DCP) and energy (DE) increased when dehulling level increased: 121, 134 and and 140 g DCP kg^{-1} DM and 15.1, 16.7 and 17.0 MJ DE kg^{-1} DM, respectively.

Fahey et al.1992. Journal of Animal Science 70: 1169-1174; Lewis et al. 1994. Journal of Nutrition 124: 2716S-2718S; Kienzle et al. 2001. Journal of Animal Physiology and Animal Nutrition 85: 174-185; Kempe, R. et al. 2004. Agricultural and food Science in Finland (in press).

Key words: oats ,dogs, digestibility, dehulling, feeding, nutritive value

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Improved export hay quality characters of oat

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Abstract

Producing oat hay has increased across the southern region of Australia to meet growing export demand over the last five years. More than 500,000 t of oat hay was exported in 2003. Market growth is dependent on producing oat hay that is consistently palatable each year. During this time grading systems have been refined by hay processors to include water soluble carbohydrates (WSC), dry matter digestibility (DMD), neutral detergent fibre (NDF), and acid detergent fibre (ADF).

There is increased emphasis in the breeding program to improve oat varieties for hay production. The outcomes of the breeding program are to release oat varieties with higher hay production, improved disease resistance, and enhanced hay quality. High DMD and WSC with low NDF and ADF combine to provide more consistently palatable oat hay for export markets. The study was conducted to determine if our hay quality evaluation strategy was effective and to assess if there were significant differences between a selected group of varieties and breeding lines for WSC, DMD, NDF, and ADF.

Replicated hay quality data for 12 oat varieties and breeding lines were generated from two sites in South Australia and three replications in 2002. Hay samples were bulked from three replications for 11 varieties and breeding lines at nine sites in 2002. Hay quality was evaluated for 36 entries using three replications at three sites and 14 entries at one site in South Australia in 2003. Hay quality was also evaluated for 18 entries sown at three sites in Western Australia. NIR predictions for the WSC, DMD, NDF, ADF were provided by FEEDTEST® located in Hamilton, Victoria.

Comparison of replicated data from limited sites and bulked samples from several sites showed the sampling error was greatest from the bulked samples. To achieve a sampling error of 5%, two replications were needed for WSC and ADF. Significant variety differences were found for DMD, WSC, NDF, and ADF in the first year. Quality results for 2003 will be presented at the conference.

Key words: hay quality, WSC, DMD, NDF, ADF

Natureal® oat bran instant drink

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Abstract

Dietary fiber in diet is of high importance when trying to fight the global epidemic of overweight and obesity. To obtain viable options for enriching the diet with dietary fiber more applications are needed.

The aim of this research was to study a blood glucose response lowering and dietary fiber giving serving of oat bran. A new oat bran powder was developed and an application model was constructed followed by a clinical study.

High Beta glucan, heat-treated commercial oat bran: Natureal® GI-flour was developed. The aim was an oat bran of high solubility of Beta glucan and a high viscosity in physiological conditions. This was then introduced to a classical drink powder format for measuring the glycemic index. Also the effect of oat bran on glycemic response was measured. The clinical study was done with 12 type 2 diabetic subjects.

This combination of the product and application gives a low postprandial glucose response. The results indicated that oat bran is capable of in an active manner to lower the response of external glucose given simultaneously. It also gives a viable option for introducing in a simple palatable form a substantial amount of daily need of dietary fiber.

This product forms high viscosity in physiological conditions and at the same time introduces substantial amounts of good quality macronutrients. Oat protein is of high value, comparable to that of soy protein and the fat is mostly of unsaturated fat.

Here we have shown a good option for helping the global problem of obesity in a form of natural oat bran giving very high viscosity.

Key words: oat bran, glycemic response, viscosity, obesity

Oat products digestibility studies and their nutritional information

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Abstract

Carbohydrate containing foods can alter blood glucose and insulin levels in markedly different ways depending on the foods fiber content, particle size and method of preparation. Digestibility can be studied using *in vitro* or *in vivo* methods, such as hydrolysis (HI) or glycemic index (GI) measurements (Granfeldt et al. 1992, Jenkins et al. 1981). Recent studies have shown that foods, which have low GI values and maintain normal blood glucose and insulin levels may have metabolic benefits in relation to diabetes and to the reduction of coronary heart disease risk (Jenkins et al. 2002).

Glycemic index and digestibility of oat products has been studied mainly on products which have high β-glucan content. These results show beneficial effects of viscous β-glucan on reduction of glucose absoption. Oat products such as oat porridge or oat pasta have not been widely studied. In this study we examined effects of oat pasta and two different oat porridges on glucose absorption using HI and GI methods.

Results showed that oat pasta, consisting of oat and wheat flours and oat fibers has low GI value and it is digested slowly. Addition of oat fibers, soluble and insoluble, did not lower GI value. Cooked oat porridge gives medium GI values and the glucose curve maintains in moderate levels long time after porridge has been eaten. Results showed, that digestibility of oat pasta is mostly affected by its structure and digestibility of oat porrigde is affected by its processing or cooking method, fiber and β-glucan content.

Granfeldt Y et al. 1992. European Journal of Clinical Nutrition 46:649-60; Jenkins DJ et al. 1981. American Journal of Clinical Nutrition 34:362-366; Jenkins DJ et al. 2002. American Journal of Clinical Nutrition 76:266S-273S.

Key words: oat, processing, porridge, pasta, glycemic index, hydrolysis index, digestibility

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Oats for the production of functional foods in Italy

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Abstract

In this presentation the development of an innovative oat product for the Italian food market was revised. The work was grounded on two aspects: i) the scientific data highlighting the positive role of oat fibre components in reducing the risk of heart diseases and in influencing cholesterol and glucose metabolism; ii) the growing demand of new opportunities to increase human consumption of oats and to promote health through a higher intake of oat soluble fibre.

The project was carried out across different steps. The first step involved the identification of the consumers of interest, together with the most convenient product for them. Children and elders were selected as target consumers, then alimentary pasta, traditional Italian food, was chosen as a suitable product, as both groups could get health benefits from the improvement of its nutritional value through oat enrichment. The second step was focused on the choice of the raw material to be utilised: therefore, genetic variability for the functional compounds of the oat kernel (protein, β-glucan, total dietary fibre) was explored. Both husked and naked oat cultivars were considered in this analysis, the latter resulting the most suited material for pasta production. Finally, low-input agronomical conditions were optimised for seed multiplication, as they favoured the accumulation of functional compounds in the kernel, safeguarding at the same time the environment.

In collaboration with an Italian pasta industry, an innovative oat-enriched food was developed, using natural sources (oat flour and durum wheat semolina). The oat-wheat pasta was then proposed to a panel of consumers: it showed all the qualities to be included in the market of dietetic products, as it preserved the good organoleptic characteristics of natural foods, together with a better nutritional value, due to its higher content of good-quality protein, total dietary fibre and β-glucan.

Key words: oats, functional compounds,health promotion, pasta, Italy

Soy and oats as ingredients for non-dairy products

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Abstract

The market for dairy alternatives represents a rapidly growing sector supported by an increased awareness of milk allergy and by a trend towards a vegetarian lifestyle. Soy dairy alternatives in particular have been expanding. However, recently oat-based products have been developed and are challenging the role of soy-based foods as alternatives to dairy milk and yoghurts.

Soy and oats both have nutritional benefits as food ingredients. Soy has a high content of protein of high nutritional value, and oats are known as a good source of gel-forming dietary fibre. Both can carry an FDA-approved health claim ‘may reduce the risk of heart disease’ in the USA. Amounts justifying the health claim are 6.25 g and 0.75 g of soy protein and of oat beta-glucan per serving, respectively.

There is evidence that diets containing high amounts of soy are associated with lower incidence for certain hormone-related cancers. Proteinase inhibitors, phytic acid, plant sterols and phytoestrogens have been suggested to be responsible for the anti-carcinogenic effect. However, some individuals develop allergic reactions to soy proteins. The beany flavour of soy is rejected by many people and its removal requires costly processing. There has also been consumer concern about genetic modification, which is widely and successfully applied to soybean in the United States.

Oat-based non-dairy alternatives benefit from the anecdotal reputation of oats as being less allergenic than most other foods, including other cereals. During the ten past years clinical evidence has proved oat to be harmless to celiac patients, suggesting that oats should be granted gluten-free status.

The paper deals with the potential and applications of oats in the non-dairy food market making reference in particular to soy-based non-dairy foods.

Key words: oat, soy, non-dairy

Changes in plasma lipids and faecal *Bifidobacterium* spp. in humans after consumption of fermented oat-based products for 5 weeks

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Abstract

In order to obtain milk like products from oats, an industrial process to manufacture a palatable, liquefied oat base has been developed (Lindahl et al 1994). This oat base *per se* has shown to be appreciated as a non-dairy milk alternative in the health market (Anon, 1999). It has also been shown that it is possible to obtain fermented oat milk with texture properties resembling that of traditional yoghurt (Mårtensson et al 2001). In this study we have investigated the effects of fermented oat-based products containing both native and microbial β-glucans, on plasma lipids and on faecal total bacterial count and *Bifidobacterium* ssp. Sixty-two volunteers (free-living subjects) with moderately increased plasma cholesterol levels were recruited. One of the oat products (ropy) was co-fermented with an exopolysaccharide (EPS)-producing strain, *Pediococcus damnosus* 2.6. A significant (p=0.022) reduction in total cholesterol by 6% was observed in volunteers who had eaten the fermented, ropy oat-based product compared to the control group. A significant increase of total bacterial count (p=0.001) and *Bifidobacterium* ssp. (p=0.012) was observed in faecal samples from volunteers in the group who had eaten the fermented, ropy oat-based product. This study shows that a fermented, ropy oat-based product, containing both native and microbial glucans can reduce the cholesterol level and also stimulate the bifidobacteria flora in the gastrointestinal tract.

Anonymous, 1999, in Daily Mail on Sunday, You-magazine March; Lindahl, L.et al. 1997. US Patent 5,686,123; Mårtensson, O. et al. 2001. Journal of the Science of Food and Agriculture 81, 1314-1321.

Key words:Exopolysaccharides, oats, non-dairy, cholesterol, Pediococcus damnosus *2.6, prebiotic*

Probiotic *Bifidobacterium* in a dry oat-based matrix: an *in vivo* study

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Abstract

Probiotics are commonly included in dairy products. These products require cold storage and transportation which limits their use. We have investigated the inclusion of a probiotic *Bifidobacterium lactis* strain in a dry food matrix, an oat-based cereal bar, and its detection in faeces after consumption of this product. From four of the nine subjects whom consumed the cereal bar for a week, *B. lactis* could be identified in the faeces using a culture independent technique (fluorescent *in situ* hybridisation). This detection frequency was not different from earlier reports where *B. lactis* was consumed in fermented or non-fermented dairy products. One week after cessation of *B. lactis* feeding, it could be identified in the faeces of five of the nine subjects. This detection frequency is better than most other studies where *B. lactis* had been included in dairy products. The inclusion of *B. lactis* in an oat-based cereal bar appears to be equally well or better than inclusion in a dairy product and may therefore provide an alternative means of administering probiotics.

Ouwehand, A.C. et al. 2004. International Journal of Food Microbiology. *In press.*

Key words: Probiotic, Bifidobacterium lactis, intestinal colonisation

Xylan from oat spelts: Extraction and possible use

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Abstract

Oat spelts contain high amounts of xylan whereas the lignin content is comparatively low. This raw material is an interesting candidate for the isolation of xylan. Oat spelts are available in large quantities in oat mills with comparatively low price. The xylan content showed a large variation from 22 % to 39 %.During the recent years an emerging interest can be registered for the use of renewable resources as a feedstock for chemicals. New processes have been proposed for the separation and isolation of the individual components of agricultural plant residues: cellulose, lignin and xylan. A wide and cheap access to xylan will open new applications as a polymeric material. A new generation of coatings, hydrogels, paper additives is waiting to be discovered. We are convinced that hemicelluloses and especially xylan will play an important role in future world with decreasing dependency from petrochemical resources to a sustainable economy. Oat spelts from different sources were analysed regarding their chemical composition. In the first stage, separation has been made according to provenance, only, as the wholesalers of grain were collecting green oats from different farmers without differentiating botanical species. Between spelts from oats purchased from Finland, Australia and two German sources major differences have been identified as shown in the table.

	Lignin	Arabinoxylan (Xylose/Arabinose)	Total Glucane	Starch
Origin	% based on starting material			
Finland	23.6	32.6	34.0	0.8
Australia	18.8	33.0	35.4	4.9
Germany-A	22.9	29.6	37.9	10.2
Germany-B	18.5	21.9	46.7	2.6
Raw material for extraction	21.3	32.2	36.5	4.5

The hydrolysis residue is an indication for the lignin content of the spelts.Furthermore, the result of adding up the xylose and arabinose (arabinoxylan) content delievers an indication for the possible quantity and quality of xylan. The part of Peter Koelln in the project was the preparation of oat spelts for the isolation of xylan in order to improve quality and yield of xylan and to reduce the quantity of chemicals for the extraction. Using oat spelts coming from the hulling without other impurities, a yield of 70 % to 75 % of intake oat spelts will be achieved.

Key words: non-food, application, xylan, spelt, lignin

Production chain

Value and functionality capture for oats

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Abstract
The challenge to the oat industry is to create wealth and distribute it fairly along the supply chain in order to encourage reinvestment, production and product innovation and at least maintain, if not improve, competitiveness.

Key words: Functionality, competitiveness, value chain, breeding targets, markets.

Introduction

“Production is for consumption”

In these succinct few words the 18th century economist and philosopher introduced us to the theory of supply chain. His statement precisely defines the reason for production. Ultimately without consumption production will cease.

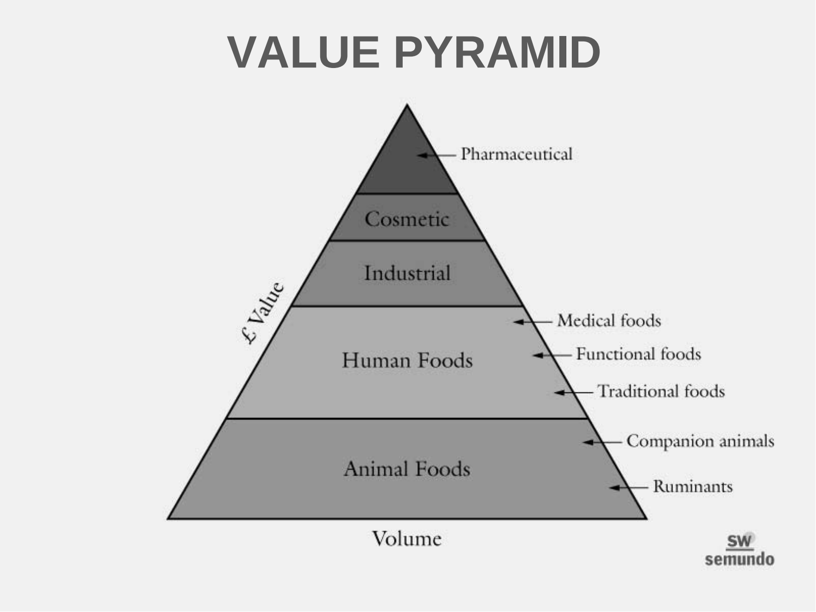
One of the problems of agricultural in the developed world is that it has seen its role as the primary supplier in the supply chain, as opposed to being a strong link in the value chain. In the UK there is much debate about sustainable production. I must point out however that for there to be a sustainable production system wealth and benefit must be created along the chain. Politicians and regulators talk much about sustainable production systems but they consistently avoid the word profit. With profits we employ, reinvest, and pay taxes. So my first message is that wealth and profits must be appropriately apportioned along the value chain. We are of course aware that the profit to one partner represents a cost to another.

The dilemma facing the industry is how can we create wealth and distribute it fairly along the value chain to encourage product innovation to and improving competitiveness.

Where is the value?

In many ways function and value are synonymous; after all it is the functionality of a product that derives its value. The value of a product or component is therefore dependent upon its functional use. However the same product or component may be negatively valued in one market whilst be highly valued in another. For instance beta-glucan is deemed to be an antinutritional factor in monogastric feeds, but the same compound has a high value in human nutrition.

The challenge is to exploit the uniqueness of oats more effectively. In exploiting this unique functionality we need to understand better the value and benefits that we are bringing to the market and consumer.



Value and functionality are inextricably linked. High value is associated with specific functionality where the opportunities for substitution are low. Meanwhile low values occur where quality specifications are less exacting and where opportunity to substitute with another product is more likely. In the value pyramid the lowest functionality is at the base. As with most cereals the volume market and lowest price is as an animal feed grain. However this may change with the emergence of industrial bio fuels market from cereals.

As has been stated value and price is determined by the benefits or bundle of benefits that is delivered to the user or consumer and this in turn is based on functionality. Some benefits may be perceived.

In the supply chain concept the farmer’s role is solely as a producer. Profit is derived from gross output where the grain yield remains the predominant target. Largely they see their produce as a commodity rather than a product. However, as Adam Smith identified nearly three hundred years ago, there is a need for a better connection between production and consumption. In essence this implies a value chain approach.

Value of course does not have to be directly tangible. Environmental issues feature more prominently in agricultural thinking, and reforms are shaped to take this social expectation into account. If we consider the functionality of oats as a crop on the farm then it offers benefits to the environmental consumers. In this instance the consumers can be legislators who want environmental policies for a more benign production such as reduced agrochemical inputs, increased crop diversification, and lower energy demand and pollution. This bundle of benefits is collectively very significant for oats. In terms of crop competitiveness do you feel as an oat industry we promote these environmental functional benefits effectively? Are we underselling the crop politically?

Turning to the more tangible aspects in the value chain, arguably plant breeders we are the first link.

Scandinavia is one of the largest global production areas for oats. Why? The crop is reliable, well adapted to the shorter and harsher growing climate and was readily fed on the farm. This large grain bank has also allowed exploitation for exports. Meeting the demands from North America has increased the quality reputation of Scandinavian oats and helps underpin the base of the value pyramid.

Historically the place for oats was largely as an energy crop namely as a horse feed. Mechanisation was the seismic shock that change the crop’s landscape. Against this scenario there was reduced investment in oat development and accelerated investment in wheat and maize. This prompted new technologies and processes and thus created new market opportunities for those crops. As a consequence oat crop competitiveness and markets declined.

Innovation is the plant breeders business. Grain yield remains a key target, but quality and marketability are now the new drivers. In the instance of a feed oat we are not solely considering grain yield per se but rather to maximise the quality output (protein and energy) per unit of land and to do this in a cost effective manner. Naked oats are a hulless oat which can be seen to be such an innovative step. Weight for weight new naked oat varieties are better than wheat as an animal feed and equal to corn. Despite this it will be a significant challenge to substitute against the readily accepted feed grains especially with genetically modified quality corn and the high yield performance of wheat. Following an integrated industry research programme in the UK we have now a linked agreement between the crop developers and poultry consumers to incorporate naked oats in poultry rations.

As a plant breeder, SW are not only driven by the need to maintain crop competitiveness at the farm level but marketability and alternative emerging value streams now make attractive breeding targets.

In the value pyramid there are many diverse quality platforms but it is totally unrealistic for a single breeding company to successfully attempt to exploit all these sectors.

Moving up the value pyramid there has recently been concern over minimum residue levels especially that of chlormequat which has been commonly used as a straw improver and plant growth regulator. Through selective breeding we have introduced short stiff varieties which do not need a plant growth regulator. Whilst this has met the demands from the market it did not add value to us as breeders. Such situations can not prevail in the longer term.

Within own company programmes we have identified specific traits which have a strong market pull and which we anticipate will provide perceived and unique benefits to the consumer and allow them to exploit and develop value-added products. Beta-glucan is just one example. The danger of course is that over-production could see beta-glucan becoming a commodity.

Those involved in a value chain need to protect their value chain. That means managing it. One approach can be to work in a more integrated way with meaningful consumers who will share both the risks and rewards.

Further up the pyramid we are targeting very high value compounds e.g. antioxidants. As these come to market we will adopt a new production approach. The farm producer will grow to a designated crop protocol designed to optimise production, there will be total traceability and it will be in a close loop contract. This will be a value chain in practice. Risk and reward will be shared.

Conclusions

The challenges facing our industry are massive. Rationalisation and consolidation will lead to a polarised value chain. Within this there will be a power shift. Whilst buyers, (not necessarily consumers) get stronger we must work closer and in better harmony with those engaged in our value chain.

We need to know the value within any given chain. As plant breeders and developers we need to know the wants and desires from those who add value to the primary products, we need to know the process problems, and quality requirements and concerns. We need to understand better the R&D targets of those in our value chain. The food manufacture for instance may have three major themes, namely optimise processing, improve taste, and enhance nutrition. We want to develop, enhance and promote the positive aspects of oats and minimise traits which restrict uptake or consumption. After all this is our business.

We need to be better aware of the problems and issues perceived or real in the value chain i.e. mycotoxins and GM material.

Within the value chain we need to be more open and share the investment risks that each of us have. We need to reduce costs especially where there is no added value. We need focused and cost effective research which is commercially oriented.

In oats we are blessed with having one of God's genetic jewels. We should treasure this dearly, understand its value and never under-estimate its potential.

Reference

Adam Smith "Wealth of Nations."

Effect of environment on oat yield and grain quality

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Abstract

In recent years, little agronomic research has been conducted in Australia on oats. With grain markets becoming more aware of quality traits much can be gained by understanding the response of individual cultivars to growing conditions. The commercial release of new oat cultivars identified the need to determine under what conditions the best yields and quality could be obtained for each cultivar. Nine cultivars were grown in 12 delayed sowing experiments in the wheatbelt region of Western Australia from 1997-2000. Traits assessed included grain yield and quality.

Delayed sowing, reduced grain yield, seed weight and groat oil content. The yield efficiency of converting post sowing rainfall (PSRF) into yield (yield/PSRF) increased with delayed sowing. Delayed sowing also increased groat beta-glucan content and screenings below a 2.0mm screen but decreased groat percent for most cultivars. Whilst grain density and groat protein were not affected by delayed sowing.

As PSRF declined, yield, seed weight, groat percent and groat oil were reduced. Grain density increased as PSRF declined for all cultivars except one. Lower PSRF also resulted in higher screenings, and slightly higher groat protein and beta-glucan content. At lower PSRF levels there was more variation in yield, grain density and screenings because the timing of rain events became more critical at lower rainfall. The difference in groat oil content between the cultivars was much larger than the effect of PSRF.

In the two trials that were waterlogged, yield was reduced by approximately 1.5-1.8 t/ha, grain density was 4 kg/hL lower and protein was reduced by 2%. Under waterlogging oil content increased and yield efficiency decreased with delayed sowing. Where weed competition was observed, yields were reduced by 1.5 t/ha, seed weight by 3-9mg and groat percent by 2-3%.

These findings will provide growers and industry with a greater understanding of environmental effects on oat yield and quality for oats generally and for specific cultivars.

Key words: agronomy, delayed sowing, rainfall, waterlogging, weed competition

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Development of a high-quality oat production chain for human consumption

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Abstract

The European Agricultural Guidance and Guarantee Fund financed a 3-year project ‘The Development of Competence for Oat Production in Satakunta’, in which an integrated cultivation and processing chain for high-quality oats and oat products was developed. The objective was to achieve production of high-β-glucan oats and oat products with minimum levels of toxic compounds. About 150 farmers sent oat samples and cultivation registers including information on soil nutrients, fertilization, sowing, rainfall and harvest data. The β-glucan content and quality of the samples were measured and the toxic compounds cadmium, mycotoxins and pesticides were analysed. In addition, the Falling number of the oat samples, molecular mass of the β-glucan and viscosity of the oat cultivars were determined. The β-glucan level was dependent mostly on cultivar and climate. The Falling number and viscosity behaviour indicated the quality of the β–glucan. In Finnish oat cultivars the differences in molecular mass of the β-glucan were small. The Falling number levels of the good-quality Finnish oat cultivars varied only slightly. The Falling number is considered as one of the most important oat purchasing criteria. The cadmium contents of approved oat cultivars were well below the limit of 100 μg/kg. The mycotoxin levels were very low and no mycotoxins were found to concentrate in any of product fractions during processing. Only one pesticide, clopyralid, was found among the oat samples. The use of clopyralid-containing pesticides is now prohibited during cultivation. The approved oat cultivars were chosen according to their high β–glucan and low cadmium levels. For example, the oat cultivars Salo and Virma are not acceptable for NATUREAL Oat Bran production due to their high levels of cadmium. Cultivation instructions were developed and farmers were educated in the techniques of high-quality oat production using the analysis results of their own samples.

Key words: production chain, oat, Avena sativa L., β-glucan content, cadmium content, pesticides

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Selection for partial resistance to oat crown rust in two recurrent selection populations: a path analysis

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Abstract

Crown rust (*Puccinia coronata*) is the most devastating and widespread disease on oats (*Avena sativa*). Race specific resistance, conferring complete resistance, has proven to be nondurable. Partial resistance has been proposed as a more durable type of resistance. The objective of this work, which is part of a thesis (Pacheco, 2004), was to determine through path analysis which traits were associated with partial resistance to oat crown rust selected in two recurrent selection populations.

The two studied recurrent selection populations are subpopulations derived from the same base population, started in 1968 as a closed system selected for grain yield. A subpopulation was opened twice, in 1988-1989, with introgression of four oat cultivars. Since 1996, six cycles of selection for partial resistance to crown rust were applied on the 'closed system – rust' and four cycles on the 'three-way cross system - rust'. All selected parents from each population, and each selection cycle, were evaluated in two locations, in hill plots, sown with 30 seeds/hill, replicated four times.

Path coefficient analysis revealed that later heading dates were associated with greater partial resistance, especially in the closed system, mainly because of an indirect effect via a longer time to reach 33% of maximum severity (T33-maxsev), which tended to reduce the maximum severity. In the three-way cross system later heading dates also resulted in longer epidemic durations, leading to an increase in the amount of disease in the end of the rust epidemic comparing to genotypes with shorter epidemic duration. Plant height seems to not be associated with partial resistance. Selection of partial resistant genotypes should be based on both AUDPC and maximum severity values and very late flowering genotypes should be avoided.

Pacheco, M.T. 2004. Selection for resistance to oat crown rust in two recurrent selection populations. 133 p. Ph.D. Thesis.

Key words: crown rust, partial resistance, recurrent selection, path analysis

Oat kernel size uniformity

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Abstract

Optimal conditions for dehulling oats with an impact dehuller are affected by kernel size. Oat mills frequently separate oats according to kernel size before dehulling to optimize milling yields. Therefore, oat kernel size uniformity is of concern to oat milling operations. We have evaluated oat kernel size distributions by sequential sieving with slotted sieves and with digital image analysis. The use of slotted sieves is faster, less expensive, and less technically challenging. However, digital image analysis provides more detailed information. Graphical analyses of oat kernel size distributions indicate that they do not resemble normal Gaussian distributions, but rather appear bimodal or multi-modal. A statistical model was developed using likelihood analysis to determine whether a mixture of two subpopulations better describes oat kernel size distributions. The analysis estimates means, variances and numerical proportions of each putative subpopulation and calculates a “bimodal coefficient” which increases with increasing bimodality. Analysis of ten oat cultivars grown in five locations over three years indicated that all samples were better described by a bimodal model than by a normal distribution. The source of the bimodality is likely to be the architecture of the oat spikelet. Most oat spikelets contain two kernels, where the primary kernel is significantly larger than the secondary. Thus, the larger kernel subpopulation appears to be derived from primary kernels of double kernel spikelets and the smaller kernel subpopulation appears derived from the secondary kernels. The presence of single kernel spikelets and triple kernel spikelets tend to make the distributions less distinctly bimodal. Because of the non-uniform nature of the oat spikelet, it appears unlikely that a totally uniformly sized oat can easily be developed. However, selection based on the methods described here potentially could lead to more uniform kernel size distributions. We have found that the application of bimodal analysis to digital image analysis data can reliably estimate the mean sizes of primary and secondary kernels from double kernel spikelets. Significant variation in the bimodal coefficient was also found among the ten cultivars tested thus far, indicating the existence of selectable genetic variation for this trait. Greater kernel size uniformity should therefore be achievable selecting for low size differences between the primary and secondary kernels.

Key words: spikelet, bimodality, digital image analysis, sequential sieving

Oat enzymes – a key to value added oat products

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Abstract

Besides having excellent nutritional value, oat has versatile enzyme machinery. However, the oat enzymes have seldom been utilized to carry out desired reactions in oat or in oat containing materials. Recently, the potential of oat enzymes has been apparent in enhancement of the quality of oat and in upgrading oat for novel food applications.

Lipase activity in oat grain is high even without germination and the inactivation of this enzyme is a common practice for obtaining products with adequate shelf life. However, the existence of the lipase may also be seen as a positive feature and used as an aid in the manufacture of value added oat products. For example, the lipase reaction in crushed oat materials can be adjusted so that almost all fatty acids from storage lipids are hydrolysed to yield a mixture of free fatty acids rich in linoleic acid. This free linoleic acid, unlike its esterified form, is the favoured substrate for the microbial isomerization into the specific health-promoting conjugated linoleic acid isomer (Vahvaselkä et al., 2004).

Native oat grain has also been found to contain an enzyme activity converting the secondary lipid oxidation products into non-volatile form, thus reducing perceived rancidity (Lehto et al., 2003). This heat-labile aldehyde dehydrogenase type activity has been shown to decrease the content of hexanal and other volatile short-chain aldehydes by oxidizing them into corresponding less-volatile carboxylic acids. Native oat flour can thus be used as a supplement in various food formulations to reduce rancid flavour. Consequently, possibilities for utilization of oat in the food industry may be much more abundant than previously thought.

Lehto, S. et al. 2003. Journal of Cereal Science 38: 199-203; Vahvaselkä, M. et al. 2004. Journal of Agricultural and Food Chemistry 52: 1749-1752.

Key words: oat enzymes, lipase, linoleic acid, aldehyde dehydrogenase, lipid oxidation

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Factors affecting the concentration of avenanthramides in oats

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Abstract

The main objective of this study was to get insight on quality related components affecting the end-use properties of different oat cultivars. Combining the harvest data to chemical analyses such as beta-glucan, cadmium and avenanthramides recommendation of most preferable oat cultivars for food applications could be given. In this presentation the focus is on avenanthramides, phenolic compounds which are characteristic to oats. Avenanthramides are of great interest and importance because of their potential utilisation in food and non-food applications.

Avenanthramides of oat varieties cultivated in four different locations were extracted with 80% methanol. Concentrated samples were analysed by high performance liquid chromatograph equipped with diode array detector. Altogether 114 samples were analysed.

The mean concentration of avenanthramides was 23 mg/kg in harvest year 2000 (min. 7 mg/kg, max. 41 mg/kg, n=26), 17 mg/kg in 2001 (min. 8 mg/kg, max. 39 mg/kg, n=33) and 18 mg/kg in 2002 (min. 2 mg/kg, max. 53 mg/kg, n=55). The concentration of avenanthramides was found to be cultivar related. In addition there were remarkable differences in the concentration of avenanthramides of oat cultivars between locations and harvest years. High concentration of avenanthramides can be a result of the attack of certain plant pathogens. Also unfavourable environmental conditions leading to sprouting prior harvest can increase the amount of avenanthramides.

Key words: oats, cultivar, avenanthramide

Assessing the impact of improved crop management on naked oat quality for poultry production

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Abstract

This paper reports findings of field trials carried out on naked oats as part of the Avian Feed Efficiency from Naked Oats (AFENO) project. The project was established to conduct a coordinated research programme into the advantages of naked oats to the grower, poultry producer and consumer alike. The field trials aimed to evaluate how growers could use agronomic techniques to co-optimise grain quality and income.

In each of three seasons (harvest years 2001 – 2003), three fully randomised and replicated field experiments were run at ADAS Rosemaund, Preston Wynne, Hereford. These investigated the effects of variety, seed rate, strobilurin fungicides, applied nitrogen; type, timing and rate on grain yield and quality. Additional sites in Scotland and the East of England were used to further test the interactions and validate results at different sites.

Seed rate experiments carried out on a number of varieties in two years, established that economic optimum were between 82 and 132 plants m^{-2} indicating the possibility to reduce seed rates from current UK commercial practice. However growers have to take into account expected establishment and a degree of insurance before deciding on a seed rate. Plant densities also had a significant effect on grain quality. Reduced plant densities resulted in an increase in thousand grain weight and protein content but a reduction in oil content. Experiments on the effects of nitrogen timing indicated that in the absence of significant lodging the yield was largely unaffected by nitrogen timing. Earlier nitrogen timings tended to have a small positive effect on oil content whilst later nitrogen timings increased protein. Variety, soil fertility, and plant population affected the potential for improved yield from increasing nitrogen applications. On average every 1 kg/ha of applied nitrogen increased grain yield by 13 kg/ha. The project findings were that the quality of naked oats was relatively stable which is appealing to end users but that agronomic techniques can be used to ‘fine tune’ grain quality for poultry production.

This work was supported by the UK Home Grown Cereals Authority (HGCA)

Key words: naked oats, seed rates, nitrogen, grain quality

Nitrogen dynamics and nitrogen use efficiency of old and modern oats

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Abstract

Nitrogen (N) is one of the most important nutrients in crop production. The loss of nitrogen causes environmental pollution as well as economic losses. Therefore, cereal cultivars with more efficient N use are of special interest also in Finland

Three years study with three Finnish oat cultivars under two nitrogen (0 N and 90 N) fertilizer rates were conducted at MTT Agrifood Research Finland in Jokioinen. One landrace and two modern Finnish oat lines were tested. The modern cultivars differed by the plant height and grain protein content. The study investigated N uptake, N utilization and N dynamics of the three oat cultivars with emphasis on N use efficiency. N use was analysed at different growing stages from plants separated to main stem and tillers and further leaves, straw and panicles.

Approximately over 87% of the total aboveground N at maturity was uptaken prior to anthesis in all three years and in both N rates. However, despite the lower grain yields, Aslak (modern cultivar) had highest N use efficiency of 29.3 kg kgN^{-1}. Based on the stepwise regression of different N parameters calculated from anthesis to maturity, high N use efficiency was associated with N uptake efficiency. Instead low N use efficiency was associated with high main shoot straw N concentration and high N gained per cent to vegetative mass during the grain filling. These two latter parameters were particularly high on landrace cultivar released in 1920's.

Key words: Avena sativa, breeding, cultivar, nitrogen uptake efficiency

Posters

Born to be functional

The effect of processing on the extractability and molecular weight of oat beta-glucan

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Abstract

The beneficial physiological effects of oat (1-4)(1-3)- beta-D-glucan are believed to be due to its ability to increase viscosity in the lumen of the small intestine. Viscosity is a function of the solubility and molecular weight (MW) of beta-glucan. Raw materials and processing conditions may affect the physicochemical properties of beta-glucan. The effect processing of raw materials on beta-glucan extractability and MW was studied. Oat groats that had not been heat treated, and rolled oats and bran made from heat treated oat groats were used. Beta-glucan was extracted using two methods; a physiological extraction with digestive tract enzymes at 37 °C and a hot water extraction (ca. 90°C). MW was analysed by HPSEC and extractability was analysed by flow-injection analysis using specific calcofluor binding for detection and anlaysis. The flow behaviour of the extracts was measured by steady shear measurements. The extractability of beta-glucan from oat groats that had not been heat treated was high 75% of the total present at 37 °C and 83% with hot water. Increased extraction temperature increased the amount of solubilised beta-glucan from 50% at 37°C to 72% at 90°C for the heat treated rolled oats and from 42% to 63% for the bran. The MW of beta-glucan extracted from oat groats that had not been heat treated was low (175 200) using extraction at 37 °C, but with hot water extraction MW was 1.6 million. The MW of beta-glucan from rolled oats (2.1±0.1 and 2.4±0.2 million) and from oat bran (2.7±0.2 and 2.2±0.3 million) was high and both extraction methods resulted in similar MW. Raw material processing and extraction temperature greatly affected the extractability and molecular weight of beta-glucan.

Key words: β-glucan, molecular weight, viscosity, processing

Effects of gluten, water and processing conditions on oat bread quality

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Abstract

The aim of our work was to optimise the whole grain oat baking process both in terms of bread quality and physiological functionality of oat β-glucan in bread.

The flour used in baking was whole grain oat (51%) and wheat (49%). A straight dough baking process was used. The effects of gluten, water and processing conditions (mixing time, intermediate proof, proof time, proof temperature, and baking temperature) were investigated using response surface methodology. A central composite design was constructed to study the effects of two ingredients and five processing parameters on baking performance. Response variables measured were: specific volume, instrumental crumb hardness (after 2 and 72 h storage), and sensory texture and flavour of crust and crumb. The concentration (McCleary & Codd 1991) and molecular weight distribution of β–glucan (Suortti, 1993) were analysed from both flours and bread.

The largest specific volume, smallest instrumental hardness of the crumb and best sensory quality was attained by adding 42% water and 7% gluten to the dough and mixing it for 4 min. The intermediate proof of 5 min resulted in the softest bread crumb, but 20 gave enhanced specific volume, crust properties and flavour. Optimal proofing conditions were 40 °C and 75 min. The optimal baking temperature was 210 °C. After optimisation, the specific volume of oat bread was 3.7 cm^3/g, hardness after 2 h was 0.14 kg, and after 72 h 0.3 kg. The sensory quality of the bread was good. The results show that bread containing 51% whole grain oat can be baked and that good taste and texture as well as long shelf life can be attained by optimizing recipe and processing parameters. In straight dough baking about 30% of the β-glucan of the flour was degraded. The possibilities to reduce the degradation of β-glucan during processing will be studied further.

McCleary, B. & Codd, R. 1991. Journal of the Science of Food and Agriculture 55: 55-65; Suortti, T. 1993. Journal of Chromatography 632: 105-110.

Key words: oat, bread, baking, optimisation, whole grain, β-glucan

Effect of processing parameters on the quality of oat flakes

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Abstract

Quality of oat flakes is dependent on end-use. Specific weight is used to steer the flaking process, and is important in ensuring that the correct pack weight is achieved. It is also related to flake thickness. Flake thickness in turn may affect other quality parameters such as water absorption, colour and breakage of the flakes. The aim of this study was to describe the effect of specific weight on the quality parameters of oat flakes.

Oat flakes were prepared from locally grown oats by a commercial mill. Five flake thickness levels were obtained by adjusting the gap between the rolls. According to usual practice, specific weight was used as an indicator of thickness. For determination of moisture content and pasting properties, samples were ground using a pin mill and cyclone mill.

Thickness was measured from 10 randomly selected flakes. Moisture content was determined by air-drying. Water absorption was determined by weighing 50 g of flakes into a beaker and adding 200 ml of water at 24°C. After 5 min the mixture was spread over a pre-weighed 0.85 mm screen, tilted at 28° from the horizontal and allowed to drain. Flake colour was measured with a tri-stimulus instrument. Flake size distribution was measured using 5 and 2.5 mm round-holed sieves, from a representative sample obtained with a sample divider. Pasting properties were measured using a Rapid Viscoanalyzer.

There was a positive correlation between specific weight and flake thickness. Specific weight showed strong negative correlations with water absorption and the peak viscosity of flakes ground in a pin mill, however there were no significant difference between finely ground flakes, which suggests differences in the particle size distribution or extractability of starch. Thin flakes were whiter. The relationship between specific weight and breakage was less clear, although thin flakes were more susceptible to breakage. These results suggest some methods for measuring the quality of oat flakes and show the effect of a milling parameter (specific weight) on these quality parameters.

Key words: flake colour, quality, specific weight, water absorption

Fermented oat vellie from high β-glucan oat bran

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Abstract

Oats have great potential as an ingredient for non-dairy foods and are offering an alternative to soy-based ingredients. Like soy, oats can be used for yoghurt and milk type products. Oat-based ingredients also offer health benefits and technological functionality, and are easy to flavour.

Fermented cereal snacks of yoghurt-type are called vellies. In this study the suitability of various high beta-glucan oat bran products for making oat vellie was tested. Eight commercially available probiotic starters and starter combinations composed of lactobacilli and bifidobacteria were used in fermentation experiments. The vellie was prepared from oat bran concentrate (Natureal) and water. The mixture was cooked and then cooled. After adding the starter the fermentation lasted 15 h at 37ºC.

All oat bran products tested supported fermentation and the growth of bacteria resulting in a final pH of 3.7 to 4.2 depending on the starter. However, there were significant differences in the behaviour of the bacterial strains and starters in this substrate in terms of growth rate, acid production and other parameters. Certain commercially available starters are well suited to vellie fermentation. The colony forming units were 10^6 - 10^7 CFU/g and remained at that level during storage. The combination of a probiotic strain with high beta-glucan in a hydrated product suggests improved health benefits.

Key words: oat, non-dairy, vellie, probiotic

Increasing oat stability through germination and drying

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Abstract

Oat is palatable, beneficial to one's health, it has advantageous lipid composition and valuable technical properties related to forming viscosity. However, due to the high fat content, a rancid and bitter flavour develop easily in oat during storage, and forms thus an obstacle for the use. A germination-drying process has shown nicely to adjust the perceived flavour (Heiniö *et al.* 2001), and was now applied before storing oat, the aim being to increase. the stability.

Changes in sensory attributes determined by descriptive profiling, lipid composition and amounts of volatile and phenolic compounds of native and processed (germinated, dried) crushed oat were followed during a 12 month storage period. The influence of the chemical attributes on the sensory profiles of oats was analysed statistically by PLS regression.

The sensory profiles of the native and processed oat groats changed significantly during the storage period, and chemical changes causing rancidity and bitterness developed more slowly in the processed oat as compared to the native oat (Heiniö *et al.* 2002). The most intensive changes due to deterioration had already occurred after one month of storage in native oat, whereas in processed oat these changes were perceived several months later. Stored, deteriorated oat was assessed as having musty, earthy odour and bitter, rancid flavour. These sensory attributes were closely correlated to free fatty acids and volatile compounds related to lipid oxidation. By contrast, total amount of phenolic compounds and volatile compounds derived mainly from protein degradation were highly related to favourable roasted odour and flavor. Thus, stability of oat groats can be significantly increased through germination and subsequent heat-treatment.

Heiniö, R.-L.*et al.* 2001. Cereal Chemistry 6: 707-714; Heiniö, R.-L.*et al.* 2002. Cereal Chemistry 3: 367-375.

Key words: Oat, germination, storage, rancid & bitter flavour, lipid, volatile

The production of oats lipids by supercritical fluid technologies

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Abstract

The aim of the study was to develop a method suitable for large-scale extraction of oats phospho- and glycolipids. Pilot scale extraction were performed by custom-made SFE-equipment (Chemature Ecoplanning) witch is well suited for research work that requires reliable apparatus with large operation range in both pressure and temperature.

In supercritical state, extraction and separation of different compounds are carried out with changes in pressure and temperature of the medium (fluid). When oat flakes are processed with supercritical carbon dioxide ($SFCO_2$), non-polar lipids are separated from oats. The modification of $SFCO_2$ with alcohol changes the properties of fluid, and slightly polar lipid fractions are separated. By using the supercritical antisolvent technology (SAS), the precipitation of slightly polar lipids, e.g. phospho- and glycolipids, occurs. All these oats lipid fraction are pure and free of organic solvents and, thus, useful in food industry.

$SFCO_2$ showed to be effective in the extraction of fat from oat flakes. The initial oat flakes contains 8-12 % of fat. After extraction with pure CO_2 the oat flakes contains less than 1 % fat. When 4 kg oat flakes was extracted first with pure CO_2 and after that with CO_2 modified with alcohol, and by using the SAS-technology to precipitation we can get 25-35g precipitated fractions.

Key words: oat, supercritical fluid extraction (SFE), phospholipids, glycolipids

Solubility and effective enzymatic hydrolysis of oat globulins

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Abstract

Enzymatic hydrolysis of proteins is used to improve nutritional and functional properties of many foods. The desired degree of hydrolysis (DH) depends on food application. Effective hydrolysis requires optimal hydrolysis conditions for both the enzyme and the substrate protein. This study aimed to hydrolyze the oat globulins (OG) effectively under different conditions. Our first goal was to maximise the OG solubility and then to hydrolyze OG under optimised conditions.

The solubility of isolated OG in Na-phosphate solutions containing 0–1 M NaCl was determined. Globulins were subjected to single-enzyme hydrolysis with either subtilisin, thermolysin or pepsin. In addition, OG were degraded in two-stage hydrolysis first with pepsin and then either with subtilisin or thermolysin. The hydrolysates were analysed by SDS-PAGE and DH was quantified with the OPA method.

The solubility of OG increased when NaCl was added at pH 5–10. Under more acidic conditions the solubility, however, decreased with added NaCl. Solubility of OG was the lowest near its isoelectric point, whereas solubility was the highest at pH 2–3 with no added NaCl and at extremely alkaline conditions in all studied salt concentrations.

The DH varied between 8–20% in single-enzyme hydrolysis. The degradation of OG became more effective in combined hydrolysis with pepsin and subtilisin (DH 42%) or pepsin and thermolysin (DH 30%).

The present study demonstrates that solubility of OG was strongly dependent on pH and NaCl concentration and it was shown that pepsin, subtilisin and thermolysin degraded OG under optimized conditions. Thus, by optimisation of the conditions for both the enzyme and the substrate protein, effective hydrolysis may be obtained.

Key words: oat, globulin, hydrolysis, solubility

Occurrence of ACE-inhibitory di- and tripeptides in oat storage proteins

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Abstract

Angiotensin I-converting enzyme (ACE) regulates blood pressure by its hydrolytic actions. Certain food-derived peptides with appropriate structures inhibit the activity of ACE. This study aimed to show the occurrences and locations of known ACE-inhibitory peptides in the structures of oat storage proteins, globulins and avenins. Liberation of the target peptides is also discussed.

The primary structures of oat globulins and avenins were explored in a protein structure database environment (*i*ProClass) for the known ACE-inhibitory di- and tripeptides (IC50-value 10μM or less). In order to hypothesize, which enzymes could release the target peptides, the structural properties and locations of the found peptide sequences were analysed.

Of the searched ACE-inhibitory peptides, ten occurred in oat storage proteins. Oat 11S globulins contained four dipeptides and three tripeptides, whereas three dipeptides and two tripeptides occurred in avenin structures. Some of the dipeptides had multiple occurrences in avenins and globulins, which make them an interesting target peptide group. Structural analysis revealed that nine of the peptides found in oat storage proteins had an aliphatic amino acid in N-terminus, whereas four of the five tripeptides had proline in their C-terminus. Thus in theory, to liberate these kind of peptides from the structures of oat storage proteins a selective protease that cleaves peptide bonds before aliphatic amino acids could be used together with a proline specific enzyme that cleaves peptide bonds after proline.

The storage proteins of oats thus appeared to be potential sources of ACE-inhibitory peptides. The liberation of these peptides during food processing, however, requires safe and selective enzymes, and suitable hydrolysis conditions for both the enzymes and the substrate proteins.

Key words: ACE, peptides, oat, globulin, avenin, protease

Characterising oil bodies from oats

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Abstract

Oil bodies (0.1 – 2.5 μm in diameter) are present in oilseeds, and their principle role is to store neutral lipids prior to their mobilisation during germination (Huang, 1992; Murphy, 2001). Oats are relatively enriched in oil (3-12% of dry grain mass), but is the oil in-vivo packaged in a similar way to the oil within oilseeds? Although researchers using microscopy have observed spherical droplets of lipid rich material in oat grain no one has analysed these entities ex-vivo.

Oil bodies were recovered from oat bran using an aqueous-based flotation system. Water and urea were used to clean the preparations and SDS-PAGE results confirmed the removal of extraneous proteins. Equivalent oil bodies were recovered from sunflower seeds and comparative studies carried out. Oil body particle size, morphology, intrinsic protein composition and rheology were investigated.

Oil bodies recovered from oats are, in certain aspects, distinct from those recovered from sunflower seeds. This suggests differences between the biosynthesis of oil bodies from cereals and from oilseeds. and would determine any potential applications for oat oil bodies within industry.

Huang, A.H.C. 1992. Annual Review of Plant Physiology and Plant Molecular Biology 43: 177-200; Murphy, D. 2001. Progress in Lipid Research 40 (5): 325-438

Keywords: oilbBodies, oat grain, sunflower seed, rheology

Polyphenolics in milling fractions of grain of covered and naked oat cultivars and their antioxiodant effects in rats

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Abstract

Grain processing is accompanied by losses in dietary fibre and other bioactive compounds. The objective was to study the effect of milling on the levels of total polyphenols in milling fractions of covered and naked cultivars and assess antioxidant potential of these fractions *in vitro* and in rats with induced hypercholesterolemia. The material was whole grain of oats (covered cv. *Kasztan*, dehulled; naked cv. *Akt*) and their milling fractions: flour and bran. Total polyphenols were extracted and determined to measure total radical scavenging activity (RSA%) (Pekarinen et al. 1999). Three groups of Wistar rats (BM 100 ± 3 g), 42 rats each, were used in three 21d consecutive experiments. The animals were fed hypercholesterolemic (1% cholesterol) diets (Pisulewski et al. 2002), formulated with increasing amounts of total dietary fibre (Exp.1: control vs. whole grain – 2, 4, 6%; Exp.2: control vs. flour – 1, 2, 3%; Exp.3: control vs. bran – 2, 4, 6%). The animals were bled to determine serum lipid peroxides using the Kamiya Biomedical assay kit (no CC-004). Processing of oat grain (covered and naked forms) leads to substantial losses of total polyphenols as indicated by their highest concentration in bran. Consequently, bran showed the highest RSA (%) values. At the same time, the flour fraction with a relatively low content of total polyphenols and related low RSA (%) values was most efficient in reducing serum lipid peroxides in hypercholesterolemic rats.

Pekarinen, S.S., et al. 1999. Journal of Agricultural and Food Chemistry 47: 3036-3043; Pisulewski, P.M. et al. 2002. Polish Journal of Food and Nutrition Sciences 52: 63-66.

Key words: oat, polyphenols, DPPH, serum lipid peroxides, rats

Total dietary fibre and beta-glucans in milling fractions of covered and naked oat cultivars and their hypocholesterolemic effects in rats

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Abstract

Grain processing is accompanied by losses in dietary fibre and other bioactive compounds. The objective was to study the effect of milling on the levels of total dietary fibre (TDF) and β-glucans in milling fractions of covered and naked cultivars of oat and assess hypocholesterolemic effects of these fractions in rats with induced hypercholesterolemia. The material was whole grain of oats (covered cv. *Kasztan*, dehulled; naked cv. *Akt*) and their milling fractions: flour and bran. Total dietary fibre (TDF=IDF+SDF) and β-glucans were determined using the Megazyme assay kits. Three groups of Wistar rats (BM 100 ± 3 g), 42 rats each, were used in three 21d consecutive experiments. The animals were fed hypercholesterolemic (1% cholesterol) diets (Pisulewski et al. 2002), formulated with increasing amounts of TDF (Exp.1: control vs. whole grain – 2, 4, 6%; Exp.2: control vs. flour – 1, 2, 3%; Exp.3: control vs. bran – 2, 4, 6%). The animals were bled to determine serum total cholesterol (TC), LDL-cholesterol (LDL-C), HDL-cholesterol (HDL-C) and triacylglycerols (TG). Processing of oat grain (covered and naked forms) results in substantial losses of TDF, including serum cholesterol-lowering β-glucans, thus resulting in TDF- and β-glucan-reach bran and functionally inferior flour. Consequently, only TDF- and β-glucan-reach whole grain and bran exerted hypocholesterolemic effects in rats. No such effects were noted for flour fraction.

Pisulewski, P.M., et al. 2002. Polish Journal of Food and Nutrition Sciences 52: 63-66.

Key words: oat, dietary fibre, β-glucans, serum lipids, rats

A yoghurt with a cereal containing OatWell® betalucan, Primaliv© lowers LDL and total cholesterol

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Abstract

Some earlier work have shown that OatWell® beta-clucan can lower total cholesterol and LDL in healthy volunteers. The aim of the present study was to investigate whether a commercially available product, Primaliv© , consisting of a cup of yoghurt with a lid containing a cereal with a high content of OatWell® beta-glucan could lower cholesterol and other blood parameters and also if glucose tolerance was affected. Volunteers were healthy but chosen from a population with a known slightly increased risk for cardiovascular disease (22 patients, 6 men, 32–68 years). All had first-degree heredity for diabetes type 2. Six had impaired glucose tolerance (IGT), none had diabetes. All had a total p-cholesterol between 5 – 6.5 mmol/l at screening. The study design was a randomized open-labelled crossover model, the volunteers eating either the active product or the control product twice daily. 200 g yoghurt together with 26,5 g of a cereal containing 4 g OatWell® betaglucan and 5 g other plant fibers. The control product consisted of the yoghurt together with bread with an equal amount of carbohydrates as the test product. Test period was four weeks and the wash out period two weeks. All volunteers had a stable weight during the 10-week study period. Slight abdominal discomfort was reported by 8 volunteers but none chose to discontinue the study due to side effects. CRP, fibrinogen and PAI-1 showed no significant change. The glucose tolerance measured from iv glucose challenge with insulin measurements showed no significant change. The study showed that a product containing 4 g of OatWell® beta-glucan, combined with 200 g of yoghurt to constitute a snack, Primaliv© , taken twice daily over a period of four weeks will significantly lower both total cholesterol and LDL when compared to a control product. Glucose tolerance and other blood parameters were unchanged.

Lia Amundsen, Å. et al. 2003. Scandinavian Journal of Nutrition 47(2)68-74; Ripsin, C.M. et al. 1992. The Journal of the American Medical Association 267(24)3317-3325.

Key words: *oat, oat bran, beta-glucan, blood lipids, cholesterol, LDL*

Lowered blood glucose and insulin responses after a mixed breakfast, with Primaliv™ – a yoghurt with a OatWell® beta-glucan enriched müsli

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Abstract

There is convincing documentation, demonstrating positive metabolic effects of a diet containing low GI products in diabetics and hyperlipidemic subjects. Epidemiological data also suggest that a low GI diet may prevent against diabetes type 2, cardiovascular disease, protect against the metabolic syndrome and reduce the prevalence of insulin resistance. Many staple foods, however, cause high blood sugar and insulin responses after meals. In this study the effect of PrimalivTM, a yoghurt containing 4 g of OatWell® beta-glucan, on the subsequent blood sugar and insulin responses in a mixed breakfast meal, was determined in healthy subjects. Thirteen healthy voluntary subjects participated in the study. The test meal and reference meal was served as breakfast in random sequence. Test meal: Primaliv™ (200 g low fat vanilla yoghurt, 27 g müsli), 39.6 g white bread, butter and cheese. Reference meal: 200 g low fat vanilla yoghurt, 66.9 g white bread butter and cheese. The meals were standardised to 50 g digestible carbohydrates. The müsli was based on OatWell® an oat bran rich in beta-glucan and contained 4 g OatWell® beta-glucans per portion. Energy composition of the meals was about 60 E % carbohydrates and 20 E % of both protein and fat, respectively. Before meal, a capillary blood test was taken from each subject to determine fasting value for blood sugar and insulin. After meals blood samples were taken at 15, 30, 45, 70, 95 and 120 minutes. Determination of blood glucose was carried out using glucose oxidase peroxidase reagent. Insulin in serum was analysed using ELISA method. The test meal significantly lowered the glucose 36% and insulin 44% response, compared to the reference meal. The meal with müsli gave significantly lower glucose and insulin responses in the early post-prandial part (0-70 minutes) and a higher glucose level in the later response (95 minutes), which indicates delayed carbohydrate uptake. This quantity is in parity with that used in a study by Tappy et al (1996) in which significant and physiologically meaningful effects were found with 4.0 g OatWell® beta-glucan in a breakfast meal. The conclusion drawn is that the inclusion of a müsli containing 4 g OatWell® beta-glucan from oat moderates the post-prandial blood glucose and insulin response after a mixed breakfast in healthy subjects. The moderation is significant and is considered to be physiologically important, especially for individuals with glucose intolerance.

Tappy, L. et al. 1996. Diabetes Care 19:831-834.

Key words: oat, oat bran, beta-glucan, blood sugar, insulin

Effect of pH on viscosity of oat β-glucan

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Abstract

The aim of our study was to analyze aggregation behaviour of oat β-glucan molecules by measuring pH effects on viscosity of β-glucan solutions.

Commercial oat bran concentrate (Natureal OBC native, Suomen Viljava Oy, Helsinki, Finland) was used as raw material to isolate high molecular weight β-glucan by acid extraction (Suortti et al. 2003). HPLC-SEC was used for analysis of the molecular weight of the isolated β-glucan (Suortti 1993). The viscosities of β-glucan solutions at different pH were measured at shear rates 16.4 - 157 1/s (Autio et al. 1992).

The extraction of oat bran at low pH gave β-glucan solutions where no other polymeric compounds could be detected. The molecular weight of β-glucan was similar to highest molecular weights reported thus indicating that no molecular weight reduction had occurred during the isolation procedure. The molecular weight of the peak representing β-glucan was $1.8\text{-}1.4 * 10^6$ with polydispersity ranging from 1.3-1.5 in all the samples. Lichenase hydrolysis of the acid extracted β-glucan showed that the preparation was pure from other polysaccharides. Viscosity of β-glucan at pH 2 was high. When the pH was adjusted to pH 6 viscosity was decreased by about 20%. When the pH was adjusted to pH 12 the viscosity of the solution was highly decreased, but adjustment of pH back to pH 6 partly restored the viscosity. However, the level was much lower than in the sample where pH was adjusted directly to pH 6 without going by pH 12. The results show that only the change of pH to highly alkaline region reduces viscosity of β-glucan. As this phenomenon is partly reversible the conclusion is that β-glucan is extracted as a network where β-glucan molecules have a strong interaction with each other. Under alkaline conditions this network is dispersed because of the ionization of the hydroxyl groups. The molecular weight of β-glucan is not affected during this change.

Autio et al. 1992. Food Hydrocolloids 5: 513-522; Suortti, T. 1993. Journal of Chromatography 632: 105-110. Suortti et al. 2003. AACC Annual Meeting. Portland, OR, 28 Sept. - 1 Oct. 2003, 109.

Key words:oat, β-glucan, viscosity, molecular weight

Posters
Genetic resources

Genetic diversity among a world collection of spring oat

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Abstract

We have evaluated 116 oat lines cultivars for genetic diversity using the AFLP fingerprinting method. The oat lines originated from breeding programs in Europe (75), North America (30), South America (6), Asia and Oceania (5). Leaf tissue was harvested and genomic DNA was extracted. The DNA was digested with *Mse*I and *Sse8387*I. Two step PCR amplification was applied and eight primer combinations with two selective nucleotides each were used to generate the fingerprints. For fragment detection we used a LI-COR 4200 DNA analyser. We could visually score 87 clear polymorphisms and collected these using a binary code in a spreadsheet. Genetic similarity was calculated according to the Jaccard index. The similarity matrix was further analysed by applying UPGMA cluster analysis and multi-dimensional scaling.

Based on the cluster tree 12 groups were detected, primarily reflecting geographic origin of the lines. Many of the European lines grouped closely together in two main cluster-branches. As expected often lines from the same breeding program and lines related by descent were grouped together, with a few exceptions.

Multi-dimensional scaling showed close clustering of most European lines around the center of the scatterplot. Lines from overseas origin were scattered more widely. This indicates that within the European material the genetic diversity is smaller compared to the diversity in overseas germplasm.

We expect that European oat breeding could benefit from introducing adapted overseas lines in the crossing program because this may increase genetic variation in the breeding populations and thus enhance the potential for selection of improved lines.

Key words: genetic diversity, AFLP fingerprinting

Oat germplasm diversity in the world collection held by Plant Gene Resources of Canada

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Abstract

Plant Gene Resources of Canada (PGRC) maintains a large germplasm collection of the genus *Avena* L. with more than 27,000 accessions. The four major groups are: cultivated hexaploid oat (*Avena sativa* L., including red oat, *A. byzantina* C. Koch), animated oat (*Avena sterilis* L.), slender oat (*A. barbata* Pott ex Link) and wild oat (*A. fatua* L.). A particular strength of the PGRC collection is the representation of 26 species of the genus *Avena*. PGRC initiated in 1998 a project to rejuvenate and agrobotanically characterize the oat collection using morphologic, agronomic, disease resistance and quality characters.

The recent regeneration of 10,991 *A. sativa* accessions and the characterization of these accessions allows plant breeders and other scientists to make efficient use of the germplasm in the PGRC collection. The collected data documents the range of phenotypic diversity for a wide range of characters. All data will be made available via the Internet (http://www.agr.gc.ca/pgrc-rpc).

Different approaches to summarize the characterization data of the hexaploid cultivated oat are presented. Distinct morpho-groups indicating the genetic diversity in the oat collection were defined based on characters which are morphological genetic markers (Rodionova et al. 1994). The genetic diversity in the PGRC oat collection can be quantified by the number of distinct morpho-groups and by the representation of each morpho-group in the collection. It became obvious that certain morpho-groups are dominant in the PGRC collection.

Rodionova, N.A. et al. 1994: Flora of cultivated plants, Vol. 2, Part 3, Oat. Kolos, Moscow.

Key words: Avena sativa, genebank, genetic diversity, morphology, taxonomy

The EUROPEAN AVENA DATABASE (EADB) – towards an expert system for *Avena* genetic resources

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Abstract

The EADB is one of 56 central crop databases initiated within the framework of the European Cooperative Programme for Crop Genetic Resources Networks (ECP/GR). It collects data of more than 30.000 genebank accessions: wild species (2843 accessions), landraces and traditional cultivars (7405 accessions) and advanced cultivars. Some accessions date back to the first half of the nineteenth century, more than 5000 to before 1930. The information system, which started as a list of passport data has been developed as a relational database assisting search of duplication in collections and covering further data: characterisation and evaluation data, marker data and data on identified genes. Most of these data result from an EU-funded collaborative project on European oat land races (GENRES 99-106) and contributions by VIR supported by a ECP/GR funded project. A new online interface allowing combined queries on passport, characterisation and evaluation data has been developed. It provides addresses of holding institutions, passport data, observation data and respective experimental and methodological information. All results can be downloaded and easily imported into MS Excel. It will be available at http://www.genres.de/eccdb/avena/.

Key words: genetic resources, database, information system

Development of an oat database

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Abstract

We have recently built a new database that contains information about oat gene sequences, gene expression profiles, protein structure and activities and primers for cloning and mapping purposes. The database is the property of AvenaGene AB and is denoted AGOD for AvenaGene Oat Database. It is accessible at http://www.agod.org.

The database was built using PostgreSQL, which is an object-relational database management system. It is combined with a web-based user-friendly interface developed with the PHP scripting language. There is also a web-based BLAST engine connected to the database, which gives the user the opportunity to search AGOD with own sequence data.

Our long-term aim is to make AGOD the primary repository for information about oat-related issues and the major part of AGOD will therefore be made publicly available. At present, this database contains more than 10,000 EST sequence entries, full-length cDNA sequences and information about deduced protein activities. OatDB will be continuously updated with new sequence data, as well as with new results derived from various biological experiments, advanced bioinformatics analysis, various protocols, literature references and oat-related web links.

Key words: oat data base, EST sequence

DNA analysis and *Avena* genomes

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Abstract

Molecular analysis and characterization of the four *Avena* genomes (A, B, C and D) is a powerful and promising tool towards understanding species and genome relationships (Katsiotis et al 1997, 2000) which are not yet fully resolved. In a recent study we reported on the resolving power of RAPD (Random Amplified Polymorphic DNA) and AFLP (Amplified Fragment Length Polymorphism) markers in 18 *Avena* taxa (Drossou et al. 2004). In the present study we extend our investigations on several genome and/or taxon-specific RAPD markers and their organisation.

Twelve genome and/or taxon-specific RAPD markers were extracted from agarose gels and cloned. At least five clones per marker were sequenced. These sequences were aligned using CLUSTALW and their similarity homology to other previously characterised sequences was checked by FASTA. For each set of sequences, primer pairs were designed and SCAR (Sequence Characterised Amplified Regions) markers were produced.

Sequencing of the cloned RAPD markers revealed that four RAPD markers contained a single sequence family while the rest were comprised of two or three different families, confirming the co-migration of different sequence families sharing similar sizes in RAPDs. The SCAR markers revealed the presence of certain sequence families in more species and genomes than the RAPD markers indicated. The information from the sequence divergence of the RAPD markers and the SCARs suggests that the modified A genome species are separated mainly due to structural rearrangements, in contrast to the major genetic differences between the A and C genomes.

Drossou, A. et al. 2004. Theoretical and Applied Genetics In Press; Katsiotis, A. et al. 1997. Annals of Botany 79:103-109; Katsiotis, A. et al. 2000. Annals of Botany 86:1135-1142.

Key words: RAPDs, SCARs, cloning, evolution, Avena, genomes,species

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Genetic resources in nordic oat varieties (*Avena sativa* L.) for future breeding purposes

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Abstract

The last hundred years of cultivating nordic oat has led to an array of varieties. It is a common view that intensive breeding leeds to loss of vairation. Through an investigation of genetic diversity found in oat varieties of different ages, ranging from landraces to recent varieties, we evaluate this hypothesis.

Using molecular markers, which are considered neutral in respect of selection (microsatellites), we measure the amount of overall variation found in the varieties and compare these findings with the amount of variation found in six different agronomical characters. This comparison will reveal what happens with the genetic diversity of oat varieties during intensified breeding.

Preliminary results show high levels of among variety diversity when viewing microsatellite data in both old landraces and present varieties, while this seems not to be the case in the results from agronomical characters. This indicates that the overall variation is not declining even if deliberate selection pressure is placed upon the crop, and variation in the genetic resourses connected to the specific agronomical characters is reduced.

Key words: Genetic diversity, microsatellites, agronomical characters, future breeding

Domesticated tetraploid oat *Avena magna* Murph. et Terr. and *A. murphyi* Ladiz. and their potential use in the improvement of moroccan hexaploid oat cultivars of *A. sativa*

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Abstract

In Morocco, oat is a relatively new introduced crop during the 1920s. The area occupied by oat cultivation is extending annually and reaches 70 000 ha. Oat grows in favorable rainfed area in pure stands or as mixture with vetch fod. The hexaploid oat *A. sativa* ($2n = 6x = 42$) is the cultivated species of oat. The National Institute for Agricultural Research (INRA) has registered 14 cultivars of *A. sativa* released from introduced material. In order to improve this material for quality and disease resistance but also to extend oat crop to semi arid area characterized by high temperatures and drought, we initiate a new breeding program using two tetraploid oat species *A. magna* Murphy et Terrel and *A. murphyi* Ladizinsky ($2n = 4x = 28$). These two endemic species are of great economic value, since they have high seed groat protein content (more than 20 %), resistance to diseases and adaptability to the local edaphic and climate conditions. These species were used in interspecific crosses firstly, to improve the hexaploid Moroccan cultivars quality and secondly, to domesticate the tetraploid wild species. Breeding program is currently on F6 generation for both the domesticated tertraploids and the improved hexaploid cultivars.

Key words: hexaploid oat, tetraploid oat, interspecific crosses, domestication

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Posters

Breeding and biotechnology: Quality

Characterisation for functional compounds of Italian oat genotypes

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Abstract

”Functional foods” are defined as foods which give physiological benefits beyond simple nutrition: they enhance overall health, help prevention or treatment of a disease, improve physical and mental performance, *via* an added functional ingredient (Jones 2002). As regards oats, an health claim was advanced in 1997, when FDA recognised the positive role of oat soluble fibre in reducing the risk of coronary heart disease, by lowering the level of serum cholesterol. Due to their high content of unsaturated lipids and protein of good biological value (rich in essential amino acids), oats represent therefore a raw material to be considered for the production of dietetic foods.

An oat-wheat alimentary pasta was recently produced in Italy, using a reduced number of oat genotypes as sources of oat flour. In Italy, oat breeding programs are quite recent, being started about 20 years ago; breeding programs for naked oats are even more recent and rather limited. In addition, the available genetic variability for molecules acting as functional compounds (e.g. oat soluble fibre, β-glucan) has been poorly explored. In this study a group of naked oat cultivars from different countries and Italian breeding lines were characterised in terms of the main compounds related to nutritional quality: protein, soluble and insoluble β-glucan.

Grain protein content ranged from 16.4% (BD126 and BD127, two Italian breeding lines) to 22.7 % d.m. (breeding line Se l84); the mean value was 19.2 ± 1.8 % d.m. The variation of β-glucan content was from 2.67 to 5.40 %d.m. and the mean value was 3,93 ± 0.6 % d.m. Data showed also an high variability in relation to β-glucan composition (soluble and insoluble fraction). The results of two years of multiplication allowed to evidence significant genotype x year interactions for the functional components considered, in particular for total β-glucan. Finally, the water-soluble fraction of protein (albumins and globulins) was quantified in these genotypes.

Jones, P.J. 2002. Clinical nutrition: 7.Functional foods – more than just nutrition. CMAJ 1666(12): 1553-63.

Key words: β-glucan, naked oats, Italian genotypes, functional compounds, variability

Genetic engineering of β-glucan contents of oats

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Abstract

Finland is one of the major oat (*Avena sativa* L.) producers, holding approximately a 20% share of the worldwide oat trade. The health benefits of oats are mainly associated with its mixed β-glucan. Mixed β-glucan is not metabolised by digestive enzymes and lowers the cholesterol levels of blood and balances the glucose and insulin contents of serum after meals. These physiological effects reduce the risks of cardiovascular diseases. Our aim is to increase the β-glucan content of Finnish oats through genetic engineering. The ultimate aim is to use plant-derived genes to elevate the β-glucan content of oats to levels not obtainable through traditional plant breeding methods.

The induction of embryogenic cell cultures from mature embryos of oat cultivars Aslak, Veli and Kolbu was performed according to Somers et al. (1992). Calcofluor staining (Salmenkallio-Marttila et al. 2002) and HPLC-analysis (Suortti 1993) of β-glucan of seeds, apical meristems and cell cultures were carried out. Gene transfer of microbial 1,3-β-glucan synthases (Inoue et al. 1995) was accomplished by using particle bombardment (Bio-Rad, PDS-1000/He) according to Wan & Lemaux (1994).

The β-glucan was mainly localized in subaleurone layers of oat seeds by Calcofluor staining. The molecular weight of oat seed β-glucan was ca. 2 000 000 and the amount varied from 40 to 60 g/kg. In apical meristems trace amounts of β-glucan were observed. In cell cultures the molecular weight of the β-glucan was ca. 200 000 and the amount varied from 2 to 3 g/kg. Gene transfer experiments with microbial 1,3-β-glucan synthase genes have been started in order to evaluate their effect on β-glucan contents of oat cell lines. The cloning of plant β-glucan synthase genes is on the way.

Inoue et al. 1995. Europetan Journal of Biochemistry 231: 845-854; Salmenkallio-Marttila et al. 2002. Cereal Chemistry 78: 429-435.; Somers et al. 1992. Bio/Technology 10: 1589-1594; Suortti 1993. Journal of Chromatography 632: 105-110; Wan & Lemaux 1994. Plant Physiology 104: 37-48.

Key words: oat, β-glucan, β-glucan synthase, transgenic, cell culture

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Low acid detergent lignin oat hull: molecular marker development and chromosome location

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Abstract

Selection for low acid detergent lignin (ADL) hull is one way to significantly improve the feed quality of oat for ruminants. Low ADL hull in the variety AC Assiniboia was reported by Thompson et al. (2000), and subsequent research indicated that the low ADL trait was simply inherited (Williams et al. 2002). The simple inheritance and difficult phenotypic evaluation make this trait an excellent candidate for molecular marker-assisted selection (MMAS).

A population of 103 recombinant inbred lines was created from the cross between AC Assiniboia and the normal ADL breeding line OT775 (from the AAFC Lacombe oat R&D program). The population was grown in replicated field trials at Saskatoon in 2000 and 2001. % ADL was determined using an ANKOM^{200} fiber anaylser. Molecular marker analysis was performed using bulked-segregant DNA and Random Amplified Polymorphic DNA techniques.Random primer OPD15 (CATCCGTGCT) amplified a 1020 bp fragment from DNA of normal ADL lines only and is loosely linked (~ 24 cM) in repulsion with the low ADL trait. The same polymorphic fragment maps to linkage group 24_26_34 (Kanota/Ogle) between loci cdo353a and re2M2_12x. In the test population, low ADL lines were associated with brown hull colour. This relates well with a hull-colour locus located on the same linkage group approximately 30 cM from OPD15. Mapped markers in this region are being tested for tighter linkage with low ADL, and may be converted to PCR-based markers for MMAS. RFLP marker cdo373, which is close to the mapped hull-colour locus and ~25 cM from low ADL, has been isolated and sequenced from both low and normal genotypes. Conversion of this marker, and/or others, to PCR-based markers for MMAS is in progress.

Thompson et al. 2000. Canadian Journal of Animal Science 80:377-379; Williams et al. 2002. In: Proceedings (CD-ROM) of the Soils and Crops Workshop, Univ. of Saskatchewan, Saskatoon, SK, Canada. March 2002.

Key words: oat hull, molecular marker, low lignin, mapping

Cultivation environment affects antioxidants, protein and oil content of oat genotypes differently

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Abstract

Antioxidant compounds, avenanthramides and tocols, in oat (*Avena sativa* L.) may have health-promoting effects on mammals including humans. Content and composition of these substances can be affected by genotype as well as environment. The aim of this study was to determine the differential effect of growth environment on the phenotype composition of oat genotypes adapted to different geographical areas.

Twenty-two genotypes, nine bred in Canada, nine in the USA and four in Sweden, were cultivated in 2003 at four sites, Saskatoon, Canada (S), Madison, USA (M) and Jönköping (J) and Köping (K), Sweden. The harvested grains were dehulled and analysed for content and composition of avenanthramides and tocols, as well as content of oil and protein.

There were significant differences between sites, genotypes and the site x genotype interaction for the major avenanthramides, **2c**, **2p** and **2f**, total avenanthramides, protein and oil content. Significant differences were also found for tocols. Avenanthramide contents of oats grown at sites M and K were significantly higher than from sites J and S. Oats from site J had significantly higher content of avenanthramides than from site S and higher oil content than samples from all other sites. Oats from sites J and M were higher in protein content than those from K and S. The cultivar Belle (USA) and the Canadian line LAO-597-NZ-0544 had significantly higher avenanthramide content than all other genotypes, while the Swedish cultivar Matilda had the highest oil content and together with Gem (USA) the highest protein content. Genotypes when grown in environments to which they are unadapted often had different avenanthramide content than when grown in their adapted location. The significant interactions indicated that genotypes did not respond similarly to different environments and that avenanthramide content may be an expression of genetic adaptation to the environment.

Key words: avenanthramides, tocols , interaction, genotype adaptation

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The influence of genotype and agroecological conditions on aminoacids composition of naked oats

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Abstract

Czech Republic plays important role in both breeding and growing of naked oats. Their proteins have the highest biological value among the cereals proteins with favourable aminoacid composition and a high level of lysine. Main goal of this work was to evaluate influence of genotype and main agroecological conditions on aminoacids contents in naked oats grain. We observed two varieties (Abel, SGK-7555) on four control sites (Nechanice, Kujavy, Hradec nad Svitavou, Krukanice) from 1995 to 1997. The contents of aminoacids was determined by column chromatography. The contents of aminoacids was analogous to the figures reported by Moudrý & Čermák (1995) and Cuddeford (1990), except from the aminoacids glycine and alanine. Moudrý & Čermák (1995) detected approximately double contents of aminoacids glycine and alanine. On the contrary, lower contents of fenylalanine and histidine were found out. No other substantial differences were found. The rate of aminoacids contents in naked oats is mainly influenced by actual season conditions, locality and finally genotype. Statisticaly insignificant differences in aminoacids contents were detected between varieties in most amonoacids. Statisticaly significant differences in aminoacids contents were detected between locality and season conditions (temperature, precipitation. No significant negative correlation was found between the contents of N compounds and aminoacids contents – including lysin. The lower contents of N substances does not automatically lead to worse aminoacids composition.

Cuddeford, D. 1990. In: Oats and triticale – a growing market. National Agricultural Conference, April, Stoneleigh; Moudrý, J. & Čermák, B. 1995. In Czech.

Key words: naked oats, genotype, agroecological conditions, aminoacids.

Influence of genotype and meteorological conditions on grain yield and quality of oat in Estonia

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Abstract

Meteorological conditions are one of the environmental factors that greatly influence the level of oat grain yield and quality. The breeding of oat cultivars well adapted to unfavourable climatic conditions gives a chance to make the oat grain yield and quality more stable. The thorough study of the influence of climatic conditions to oat characteristics plays a key role in breeding for that purpose. The objective of this research was to study the influence of genotype, meteorological conditions, and their interaction on oat grain yield and quality characteristics.

Field studies were carried out at the Jõgeva Plant Breeding Institute during 1998–2002. 101 oat cultivars from Germany, Russia, Sweden, Estonia and other countries were included into this trial. Cultivars were grown in three replicated plots of 5 m², precrop was potato. The plots were sown at 500 seeds/m². The fertilizer level used was $N_{70}P_{16}K_{25}$. Results were subjected to analysis of variance. Grain yield and quality characters such as 1000 grain weight, husk content, volume weight and protein content were evaluated.

The results indicated that both genotype and meteorological conditions strongly affected oat grain yield and quality characteristics. Grain yield was most affected by the meteorological conditions that made up 60% of the variation. Both the drought and lodging lowered the oat grain yield considerably. The differences between the cultivars made up 20% of the variation of the grain yield. The influences of meteorological conditions and varietal differences to the variation of 1000 grain weight and husk content were on the same level. The 1000 grain weight decreased and husk content was high mainly in case of heavy lodging. Volume weight varied mainly (63%) due to the influence of meteorological conditions. The importance of varietal differences in the variation of this trait was small (16%). The variation of protein content was mainly (46%) dependant on varietal differences. The influence of the meteorological conditions on the variation of this trait was only 24% and the interactions of the two factors 25%. The protein content was highest in the case of drought, but remained lower in favourable growing conditions.

Key words: oat, grain yield, quality, genotype, meteorological conditions

Posters

Breeding and biotechnology: Yield

Evaluation of grain yield potential of oat germplasm in Bulgaria

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Abstract

During the last years the interest in oats as a multipurpose crop suitable to production of food and feed grains, forage and bedding for animals increases in Bulgaria. The Institute of Agriculture and Seed Science “Obraztcov chiflik”, Ruse develops and releases improved spring and winter oat varieties for the farmers and the food industry (Panayotova 2004). The objective of this research was to record the progress obtained in the oat breeding program and to evaluate grain yield potential of elite Bulgarian oat germplasm. Oat grain yield is strongly influenced by environmental conditions One of the main objective of oat breeding program is using method of recurrent selection as an effective breeding procedure to produce improved oat germplasm with higher grain yield potential (Holland et al. 2002; Stuthman et al. 1992). A recurrent selection program for adaptation to diverse environments was successful in improving mean oat (*Avena sativa* L.) grain yield within and across testing environments.

Sixty three oat genotypes, result of our program were evaluated from 2000-2003 for his grain yield at the field of the Institute of Agriculture and Seed Science “Obrazcov chiflik”, Ruse (43° 48’ N latitude, 26° 02’ E longitude) in a randomized complete block with three replications.

A number of traits have been evaluated for possible correlated responses. Significant positive correlations were found between grain yield, 1000 seeds mass and seed number. The best ten lines, regardless of their yield potential were used as parents in diallel combinations without reciprocals: p (p-1)/2. Promising yield grain potential was demonstrated in some of cultivars and breeding lines of oat breeding program in Bulgaria. 1000 seeds mass and seed number. The best ten lines, regardless of their yield potential were used as parents in diallel combinations without reciprocals: p (p-1)/2. Promising yield grain potential was demonstrated in some of cultivars and breeding lines of oat breeding program in Bulgaria.

Holland, J.B. et al. 2002. Euphytica 126: 265–274; Panayotova, G. 2004. Proc. of 39 Croatian Symposium on Agriculture Opatija Croatia 1: 251-252; Stuthman, D.D. et al. 1992. Proc. of 4th Intern. Oat Conference Adelaide, South Australia 1: 70-76

Key words: oat, grain, yield

Agronomical characterization of selected oat genotypes

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Abstract

Oats, (*Avena sativa* L.) in pure stand, or associated with vetches are the major grown forages and a main component of crop rotation in Tunisian farming systems. They are mainly grown as a source of harvested fodder (silage or hay) for livestock. Most varieties currently grown in Tunisia are not well adapted to all regions and uses. An oat-breeding program should be able to use the local available and confirmed genetic material in the country. The objective of this study was to evaluate the agronomical characteristics of selected local and introduced oat genotypes.

Nine local genotypes collected from farmers in different regions of northern Tunisia: Bezina, Bni-brahim, Maachar, Blelma, Skhira and Borj-dhab from Bizerte; Nefza from Beja; Fernana from Jendouba and Bni-khiar from Le Kef, the commercial variety Fretissa and two experimental lines (Av-9 and Saia) were evaluated for agronomical characters at the experimental station "Koudia". The experimental design was a randomized complete-block with four replications. Each plot consisted of eight rows, 4 meter long with 0.30 m row spacing within-plot row, and 1.20 m between plot spacing. Sowing was carried out on October 22, 2002. Seed was hand-drilled in rows at the rate of 250 viable seeds/m^2.

Genotypes were ranged in three classes; early heading represented by Fretissa and Av-9 intermediate heading represented by Bni-brahim, Fernana, Nefza, Saia and Bni-khiar while late maturity represented by Blelma, Bezina, Borj-dhab, Maacher and Skhira. There were significant differences among genotypes in the characters reported except dry matter (DM) yield. DM yield varied from 12.44 to 15.56 t/ha. Genotypes Bezina, Borj-dhab, Fernana, Nefza, Saia, Av-9 and Bni-khiar had a DM yield superior to the trial mean. 1000 seed weight ranged from 19.30 to 39.22 g. The flag leaf area varied from 6.19 to 27.78 cm^2. There was less variation among genotypes in reaction to diseases. Promising genetic material exists and this could be introduced in the crossing bloc.

Chakroun, M. & Fathi Gouhis. 1998. Annales de l'INRAT. 71:157-173.

Key word: oat genotype, agronomical characterization, Tunisia

Evaluation of winter-tolerant oat lines for yield and yield components

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Abstract

Food use of oat grain has recently begun to increase mainly in breakfast cereals, snack products, or in bran form. Oat is the most winter tender of the winter cereals. There are not a lot of succes in improvement of winter oats (Veisz et all. 1996). Due to the lack of reliable winter cultivars, the area of oat production in Turkey is relatively small. Therefore, it is necessary to convey winter-tolerant cultivars to farmers.

In this study, one hundred and thirty five oat lines from the Quaker Nursery were sown at Urkutlu experiment location (in Burdur province, Turkey) outside the University campus (37^o 19' N, 30^o 17' E and 850 m from sea level) in the last week of October 1999 and 2001. Twenty three genotypes were selected from this nursery for winter tolerance in the second year of the experiment. The experimental material was sown in a randomised complete blocks design with three replications in a farmers' field at Kızılkaya village (in Burdur province, Turkey) in the fourth week of February 2003 because of the heavy rainfalls, which restrict earlier sowing. Grain yield (g), 1000-grain weight (g), plant height (cm), biomass (g), days to heading and harvest index (%) were recorded in 23 genotypes selected for winter tolerance and a local variety. Data obtained were analyzed using the MINITAB software. There were statistically significant differences among genotypes selected for winter tolerance for grain yield, 1000-grain weight, plant height, biomass and days to heading. Some lines in Quaker nursery showed high agronomic performance over the local check. In case farmers are provided winter tolerant oat varieties for semi dry conditions for fall sowing, it may be expected that oat production will improve.

Veisz, O. B., Bedo, Z., Lang, L., Szunics, L. and Stehli, L. 1996. V. International Oat Conference & VII. International Barley Genetics Symposium, Saskatoon, Canada, July-August 29-06 1996.

Keywords: oat, winter tolerance, yield components

Oats in Argentina: New varieties

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Abstract

In Argentina oat is grown in a large area, about 2.5 million hectares. It is used primarily as forage for cattle, but in our country is possible to obtain pasture, hay and grain. The area production of oat grain has diminished in Argentina in the last years because it is a less profitable crop than wheat and barley and lack of demand.

The main objectives of the Barrow breeding program are the development of new cultivars with higher yield potential (forage and /or grain), better adaptability to different regions, better grain quality, resistance to the most important diseases, such as crown rust (*Puccinia coronata* Cdo.), stem rust (*Puccinia graminis f.sp. avenae)*, tolerance to aphids, tolerance to frost, etc. With the help (collaboration) of the program ¨Breeding Oat Cultivars Suitable for Production in Developing Countries¨ from Quaker Co.and the University Federal of Rio Grande do Sul (UFRGS), Brasil, we can released new varieties. In the last years we released: Bonaerense Payé (1991), Bonaerense INTA Calén (1998), Bonaerense INTA Maja (1998) and Bonaerense INTA Canai (2003).

The most important problem of oat crop are the rusts, crown rust in forage oats and stem rust in grain oats. Both of them cause high damage, lowering yields and quality, and the new varieties are subjected to tremendous rust pressure. Argentina has an excellent environment to grow oats of good quality , new varities and technology (herbicides, fungicides, crop management, etc.) Bonaerense Payé was an excellent material for all purposes, but now is susceptible to both rust. Bonaerense INTA Maja is a good material for forage or double purpose crop. Bonaerense INTA Calén is excellent to forage production in autum seed, and has a large grain production of very good quality in winter seed. Bonaerense INTA Canai has good production for hay, and it is excellent to grain production with good industrial quality. Bonaerense INTA Calén and Bonaerense INTA Canai grain yield was higher than the best varieties. They can produce more than 5.5 ton/ha, with more than 50 PH and groat percentage about 70%. Barrow Breeding Program have lines with good agronomic traits, good grain quality and yield, some of them with possibilities of realizing.

Key words: oat, varieties, forage, grain

Finding AFLP markers associated to panicle weight through bulk segregant analysis

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Abstract

Molecular markers are more and more a part of plant breeding routines, since they allow one to access the genetic variability present in the entire genome without the influence of the environment. However, the application of molecular techniques is limited depending upon the character that is being pursued. The great majority of agronomically important characters are controlled by many genes of small additive effects (QTLs),which are highly influenced by the environment. In the present work, an F_3 population segregating for panicle weight in oat, from the cross UFRGS 14 (High panicle weight) and OR2 (low panicle weight) was conducted up to F_6 under three different methods: hill, full line and spaced plants. Contrasting bulks were formed composed of plants with the average +/- one standard deviation(sd), respectively.These bulks were screened with AFLP markers to detect putative association between marker and character.Up to 145 markers have been analyzed and three presented potential use. More markers are being screened to detect associations at this/these genomic regions.

Key words: oats, molecular markers, panicle weight

Trends of nitrogen use of oat cultivars from 1902 to 2002 in Finland

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Abstract

Plant breeding has improved grain yields of oats in northern growing conditions (Rekunen 1988, Slafer &Peltonen-Sainio 2001).One main contributor to increased yields is harvest index (HI). Cultivars have higher HI and reduced plant height compared to landraces or old cultivars (Peltonen-Sainio 1991). The response of oats to nitrogen fertilizers is also improved (Peltonen-Sainio 1993). The aim of this study was to identify the changes in nitrogen economy caused by plant breeding in northern growing conditions.

In growing season 2003, eighteen oat cultivars (released between 1902 and 2002) were studied in MTT, Jokioinen. Experiment was treated with 70 kg N ha^{-1} and soil N content was measured on spring and autumn. Plant samples were collected at maturity and the plants were divided into main shoots and tillers and further to panicles and vegetative mass. The dry weight was measured and samples were grind for N analyses. Nitrogen harvest index (NHI), N utilization efficiency (UTE), N uptake and N use efficiency were calculated from the dry weights and N contents of the plants.

On the basis of one year results, plant breeding has only changed the N utilization efficiency, not so much N uptake. There were no significant difference between the cultivars in N use efficiency or in N content of the plant (g N m^{-2}). Cultivars did not differ in N uptake either. Instead UTE on new cultivars was 38.4 g g N^{-1} while it was 35.1 g g N^{-1} on old cultivars. There was positive correlation between UTE and NHI and also between NHI and HI. The one year results imply that grain yield is more breed quality than N content or N uptake

Peltonen-Sainio, P. 1991. Journal of Agronomy & Crop Science 166: 90-95; Peltonen-Sainio, P. 1993. Journal of Agronomy & Crop Science 171: 268-273; Rekunen, M. 1988. Journal of Agricultural Science in Finland 60: 307-321; Slafer, G. & Peltonen-Sainio, P. 2001. Agricultural and Food Science in Finland 10: 121-131.

Key words: nitrogen use efficiency, nitrogen harvest index,

Radiation use efficiency of modern and old oat cultivars in Finland

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Abstract

Finnish plant breeding of oats has focused on improving stability as well as productivity in northern growing conditions. Breeding for short stature and early maturing oat lines has increased harvest index (HI) close to 55% (Peltonen-Sainio 1991) and grain yields by 0.3% year^{-1} (Slafer & Peltonen–Sainio 2001). However to further increase grain yield, the biomass production should still be augment (Peltonen-Sainio 1991). Since radiation use efficiency (RUE) and accumulated intercepted radiation ($\sum$Ri) are major elements of crop growth and biomass production (Gallagher and Biscoe 1978), the aim of this study was to identify how they have changed by plant breeding in northern growing conditions.

On growing seasons 2002 and 2003 the crop radiation interception was calculated from spot measurements of incident and transmitted radiation. Above ground dry matter was determined at particular stages of development of the cultivars and green leaf area was measured at the same time. The plots were fertilised with 90 kg and 0 kg N ha^{-1}. Irrigation was practised in 2002. RUE, $\sum$Ri, light extinction coefficient k, green leaf area and biomass accumulation were calculated for each cultivar for pre-anthesis.

There was no significant difference between the cultivars on biomass accumulation, radiation accumulation or on RUE ($P = 0.08$) on vegetative period. More total biomass seemed to accumulate on old cultivar even though the difference was not significant. There were also no significant difference between the cultivars on light interception or on light extinction coefficient. Only the 0 kg N ha^{-1} fertilizer rate resulted in some reduction in light interception during the year 2002. The RUE values at pre-anthesis were higher during the growing season 2002 than on 2003, (means were 2.02 g MJ^{-1} and 1.78 g MJ^{-1}). The fertilizer rate of 90 kg N ha^{-1} resulted in higher RUE values than 0 kg N ha^{-1} on both years.

Gallagher, J. and Biscoe, P. 1978. Journal of Agricultural Science 91: 47-60; Peltonen-Sainio, P. 1991. Journal of Agronomy & Crop Science 166: 90-95; Slafer, G. & Peltonen-Sainio, P. 2001. Agricultural and Food Science in Finland 10: 121-131.

Key words: radiation use efficiency light, extinction coefficient

Apical development of oat

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Abstract

Development of cereal plants progress through set of orderly timed development phases. Rate and timing of these phases and single growth stages are strongly controlled by day length, accumulated temperature and genotype. Awareness of development phases and their potential association with crop responses to management practices (e.g. nitrogen, pesticide applications) and to external stresses, are elemental for understanding their importance to formation of yield potential (Kirby & Appleyard 1984).

Oat cultivar *Belinda* was grown in the greenhouse to visualize the apical development stages and phases described by Åfors et al. (1988). The apical development was monitored frequently and digital images of apex were photographed under stereomicroscope. Accelerated development is characteristics for oat grown in long days. Particularly oat transfers from vegetative to generative phase when only two fully opened leaves are apparent and no tillers have yet emerged. Therefore, main shoot apex is at much more advanced development stage when compared to tiller apices. Hierarchy is also evident within the inflorescence. The development of the oat inflorescence proceeds from the uppermost terminal spikelet downwards to the base of the inflorescence. Within the spikelet, development and cell division of primary grain dominates the development over the secondary grain (Rajala & Peltonen-Sainio 2004). Certain critical apical development phases of oat will be illustrated in the poster.

Kirby, E.J.M & Appleyard, M. 1984. Cereal development guide; Rajala, A. & Peltonen-Sainio, P. 2004. Agricultural and Food Science in Finland, in press; Åfors, M. et al. 1988. Stråsädens utveckling I.

Key words: apical development, inflorescence, oat

Duration of apical development phases and their coincidence with growth rate in oat grown at high latitudes

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Abstract

The growth cycle of oat can be divided into different main phases. Duration of these are dependent on genotype and environment. In this study, apical development and growth of 20 oat cultivars and lines released since 1920’s were monitored in two years. Pre-anthesis developmental phases were split into seven sub-phases: vegetative, pre-fertile, pre-abortion, generative, fertile pre-abortion, fertile, and abortion. Coincidence of apical development with leaf and tiller appearance and growth was studied and association of duration of main developmental phases with yield components analysed.

Cultivar differences in duration of pre-anthesis sub-phases were not attributable to year of release though some tendencies appeared when four oldest cultivars were compared with four latest ones. The most marked change was prolonged duration of generative phase at the expense of duration of grain-filling period in modern cultivars. This was not, however, due to marked differences in cumulated degree days for generative phase, but shorter post-anthesis period. Even though generative phase was not much changed by plant breeding, relative durations of sub-phases were somewhat: e.g. pre-abortion and fertile pre-abortion phases tended to be slightly shorter in modern cultivars in both years. Regarding measured growth parameters, modern cultivars had slightly lower number of leaves and higher Cdd °C demand for maximum leaf number, but lower demand for maximum tiller number. No constant effect of year of cultivar release were found on phyllochron, maximum green leaf number and maximum tiller number. Tillers tended to reach their peak value earlier compared to maximum leaf number in modern cultivars when compared to old ones. Relative elongation rate of the apex, uppermost node and uppermost stipule correlated negatively with duration of many of the pre-anthesis sub-phases.

Key words: anthesis, apex, development phase, grain-filling, growth, leaf number, phyllochron, oat, tiller

Dw6 dwarfing gene enhances shoot elongation of CCC treated plants

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Abstract

Dwarf oat cultivars are often stated to be insensitive to antigibberellins. In some cases antigibberellins have, however, even enhanced stem elongation in dwarf oat. Antigibberellin chlormequat chloride (CCC) and an ethylene-releasing ethephon (ETH, Cerone) were applied to long-strawed landrace cultivar and conventional height (Virma), naked (Rhiannon) and dwarf type (Grane and Pal) oats. Field experiments were conducted at Viikki Experimental Farm, University of Helsinki, Finland and growth chamber experiments at the University of Minnesota, St Paul, USA. They were applied at early growth stages (ZGS 13) or at recommended stages (CCC at ZGS 32 and ETH at ZGS 39). Oat cultivars excluding dwarf type responded to CCC and ethephon, effect being more profound in long-strawed cultivars. Cultivars with *Dw6* dwarfing gene expressed, however, enhanced stem elongation. Repeated measures on field grown dwarf cultivars indicated that stem elongation was retarded or unaffected when measured 7 to 14 days after treatment. However, at post-anthesis, stem elongation was enhanced: especially elongation of peduncle was promoted when compared to controls. This could be a consequence of GA precursor accumulation resulting in CCC induced inhibition of GA biosynthesis. Later on, when inhibition effect fades and GA synthesis resumes there are excess amounts of precursors to be used in GA-synthesis resulting higher rates of GA and concurrently enhanced stem elongation in dwarf type. In some *Dw6* lines the dwarfing effect may also be turned off at later stages, resulting in higher elongation rate of the peduncle (Burrows 1986).

Burrows, V.D. 1986. In: Webster, F.H. (ed.). Oats: Chemistry and technology. AACC, St. Paul, Minnesota. p. 13–46.

Key words: dwarf, oat, plant growth regulators, stem elongation

Growth and architecture of dwarf, semidwarf and tall oat lines under northern latitudes

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Abstract

The Finnish particularly short growing season with frequently occurring fluctuations in climate affects crop growth and yield formation and especially quality severely. Dwarfing genes have been effective sources for lodging control that have enabled higher input use, but also known to enhance floret and grain set and survival. The primary effects of the dwarfing genes on growth are demonstrated for wheat, whereas few publications concern oat. We aimed to describe pre- and post-anthesis growth of dwarf and semidwarf oat lines at high latitudes and evaluate their yielding capacity and contribution to differences in tillering, leaf characteristics and source-sink interaction in productivity.

Three experiments (1999-2001) in a randomised complete block design with five replications (10 m^2) were conducted at the Suitia Experimental Farm. Plant material consisted of Grane (dwarf, 73 cm), Pal (dwarf, 70 cm), Hja 76416 (semidwarf, 81 cm), Salo (semidwarf, 80 cm), Veli (tall, 104 cm), and Jalostettu maatiainen (tall, 110 cm). Plants were analysed for leaf area formation and biomass accumulation separately for main stem and tillers, measured for length (cm), and divided into head, leaf laminae, dead leaves, leaf sheaths, peduncle, nodes and the remainder of the stem. Number of plants, tillers, and heads m^{-2}, date of heading and maturity, and lodging-% were recorded. Additional parameters were calculated. Statistical analyses were carried out with the Statistical Analysis System.

Long leaf area duration and high leaf area index were associated with increased grain yield probably due to more persistent and active assimilation. Higher peduncle, straw and node weights associated with increased grain yield which may be due to more abundant assimilate reserves. Longer straw and peduncle, however, resulted in lower grain yield.

Key words: Avena sativa L., dwarfing gene, internode, leaf area, leaf area duration, plant height, plant stand

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The physiological background of dwarf naked oats varieties: The preliminary results

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Abstract

In Poland the first naked oat cultivar Akt was registered in 1997 and the second variety Polar in 2002. Due to the high interest of farmers, the area of cultivation of naked oat quickly increased. To present *ca* 90000 ha. The factor restricting the cultivation of naked oat is a low grain yield. In the field trial conducted in 2003 on good rye complex soil, 23 strains of the dwarf naked oat, 2 traditional polish naked oats varieties (Akt, Polar) and the hulled variety Chwat were tested. The yield, yield components and biomass accumulation were compared with those of hulled oat. Photosynthetic activity was measured and LAI estimated. The traditional naked oat varieties Akt and Polar yielded 80 % of that in hulled Chwat, due to extremely dry conditions during spring and early summer in 2003. The yield of the dwarf strains of naked oat on an average was lower than traditional naked oat varieties. The plant density of the naked oats was lower than standard hulled oats. The higher productive tillering compensated lower plant density, hence the differences in the panicle density were not significant. The lower grain yield of the dwarf strains was caused by the panicle structure, mainly low number of grains per panicle, which was the result of low number of spikelets and the greater amount of fertile spikelets per panicle. Generally, the short stem strains had lower LAI, hence the canopy photosynthesis was lower. We found out the positive correlation between the LAI and the grain yield of dwarf strains. The main factor restricting the grain yield of the dwarf strains was low amount of assimilate partitioning to the grain. The harvest index this forms oscillated on the level ca 25 % and was significantly correlated with the grain yield. At the same term of measurement the dwarf cultivars had lower root biomass than standard cultivars. From that reason in the dry year they could not show their genetic ability for the high yielding.

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Key word: naked oat, dwarf varieties, grain yield, photosynthesis

DNA marker for oat dwarfing gene

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Abstract

Short and stiff straw is one of the principal aims in oat cultivar breeding. Some dwarfing genes are available for backcrossing programmes. Selection efficiency could be improved by marker assisted selection (MAS) especially when the dwarfing gene is dominant, since the recessive allele causing tall phenotype can be hidden and segregate in further generations.

Finnish spring oat cultivar Aslak (Boreal Plant Breeding Ltd.) was crossed with the Dutch cultivar Kontant (bred by Zelder BV. and represented by Wiersum BV.) containing a dwarfing gene. One F_1 seed produced a progeny of 111 plants. Plants heights were measured and DNAs extracted. Bulked segregant analysis was used to find markers linked to the dwarfing gene. About 500 RAPD (randomly amplified polymorphic DNA) primers were first tested in the parents for polymorphisms. Polymorphic primers (60) were tested in the short and the tall bulk, which were constructed from pooled DNAs of 9 of the shortest and 9 of the tallest F_2 plants. Primers, which revealed polymorphism also between the bulks were further analysed in individual plants of the bulks. One polymorphic marker was present in eight of the nine plants of the short bulk but only in one plant of the tall bulk. When this marker was scored in the whole population, it showed significant linkage to height: only 10 plants (9%) were misclassified. This dominant RAPD marker was converted into a more reproducible and codominant SNP (single nucleotide polymorphism) marker.

The SNP marker can be used to facilitate selection for homozygous short individuals in those breeding programmes, which contain lines carrying the dwarfing gene originated from the cultivar Kontant.

Key words: Avena sativa, bulked segregant analysis, height, RAPD, SNP

Genetic diversity among dwarf inbred lines of oats revealed by microsatellites

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Abstract

New dwarfing genes were introduced from five accessions of wild oats, *Avena fatua*, to the cultivated form, *A.byzantina* cv. 'Kanota'. This study determined allelism between recessive dwarfing genes and clarified genetic variation among the dwarf inbred lines by using microsatellite markers. Three dwarf inbred lines 153, 169(AV198 and Av202) and 812 of BC_1F_5 generation were used for allelism test. These three lines have recessive dwarfing genes, but the allelism between them is unknown. Two inbred lines AV198 and AV202, which were selected from the same accession 169 in the different backcross combinations, showed remarkably differences in the plant height components. So, AV198 and AV202 were expected to have different dwarfing genes. Three inbred lines AV202, 153 and 812 were extremely dwarf and the dwarfing genes reduced the plant heights by half of the tall parent. AV198 showed semidwarfness that the height was about 85 cm. In the two crosses AV198 × line153 and AV198 × line812, the F_1 progeny was dwarf and frequency distribution of the height in the F_2 population fitted to the single factor inheritance 3 extreme dwarf (153 and 812 type): 1 semidwarf (AV198 type) ratio. Therefore, the recessive dwarfing genes of AV198, lines 153 and 812 were allelic, and the dwarfing gene of line153 and 812 were dominant for the gene of AV198. In the two crosses AV202 × line153 and AV202 × line812, the F_1 progeny was tall and F_2 progenies were segregated in the ratio of 7 dwarf : 9 tall. The results indicated that the recessive dwarfing gene of AV202 was located independently at the different locus from Av198, lines 153 and 812. Two dominant dwarf inbred lines 288 and 342 of BC_1F_5, AV21 having *Dw8* of BC_4F_5 in *A.byzantina*, NC2469-3 and 96-8 having *Dw7* and *Dw6* in *A.sativa* were used for microsatellite analysis of 20 primers (AM). The AM primers amplified maximum 3 multiple alleles in the ‘Kanota’ inbred lines. Nei’s genetic distance was calculated and cluster analysis was carried out. The dendrogram showed two strongly different groups were apparent, *A.sativa* and *A.byzantina.* Four lines having the recessive dwarfing genes were clustered together. Because three of the four lines share allelic dwarfing genes, it might be presumed that the chromosome region around dwarfing gene could be inherited as a cluster. The AV21, however, having *Dw8* was far away from ‘Kanota’ tall parent and the other inbred lines. These results indicated that the small chromosome segments originated from wild oat still remained in the dwarf inbred lines.

Key words: dwarfing gene, allelism test, genetic diversity, inbred line, microsatellites, oats

Use of biplots in understanding genotype-by-environment interactions to facilitate oat breeding

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Abstract

Multi-environment trials (MET) are essential for genotype evaluation and selection in plant breeding; MET data are expensive and valuable but are often underused. We present a biplot analysis approach that helped in achieving a fuller understanding of MET data in our oat breeding program. This approach is illustrated with data on yield and eight other traits measured on 30 oat lines grown at five locations in Eastern Canada. Three types of biplots were used. (1) GGE biplots for yield, (2) genotype-by-trait biplots, and (3) a covariable-effect biplot, using yield in each of the environments as response variables and genetic values of other traits as interpretative variabes. GGE biplots for yield revealed strong genotype-by-environment (GE) interactions and identified the two locations that contributed most to this interaction. The genotype-by-trait biplots for the two contrasting locations revealed that plant height was most important agronomic parameter related to the GE interaction for yield. It contributed negatively to yield at Woodstock where lodging was an important factor but negatively at Hebertville where it was not. The co-variable-effect biplot involving height, days to heading, days to maturity, lodging, test weight, and protein content as interpretative variables for yield explained 88% of the GGE pattern. This biplot summarize the trait-yield relations at different locations and revealed more comprehensively that plant height, along with two genetically correlated traits (days to heading and days to maturity), had the strongest effects on GE interactions for yield. In contrast, test weight was positively associated with yield at all locations. In conclusion, the combined use of these three types of biplots provided a better understanding of oat performance, GE interactions, and potential strategies for oat improvement. Biplot analysis can be easily performed using the user-friendly GGEbiplot software (www.ggebiplot.com).

Key words: biplots, yield, location, height, lodging

Posters

Breeding and biotechnology: Resistance

Multi-location testing to identify oat germplasm with partial resistance to crown rust

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Abstract

Partial resistance to cereal rusts is characterized by reduction in pathogen reproduction despite a “susceptible infection type” (Parlevliet, 1985). In some pathosystems (e.g. blast in tropical lowland rice) such resistance has proved to be durable (Bonman et al., 1992). To identify oat germplasm with partial resistance to crown rust, caused by *Puccinia coronata*, a multi-location screening trial was initiated in 2002.

Eighty-six entries were tested at 3 locations planted in the fall of 2002 in the southern US and at 5 locations planted in the spring of 2003 in the mid-western US and Canada using at least 2 replications per site. The line MN841804 was the resistant check and cultivars Brooks and Otana were susceptible checks.

The resistant check showed an average disease level of 7.5% relative to the susceptible checks across locations. One entry, the cultivar CDC Boyer, may have a useful level of partial resistance for areas less prone to the disease. In the present study it averaged 24.5% disease relative to the checks across locations. CDC Boyer and 26 other lines showing relative severity values between 3% and 25% and low variation between locations were selected for further testing in 2004. Also, adult plants of CDC Boyer, OT389 (12.1% across locations) and IA98822-2 (17.6% across locations), are undergoing greenhouse tests with compatible races of *P. coronata*. Further field and greenhouse experiments are planned with these and other lines to ascertain if the lower disease level in field trials is correlated with partial resistance assessed in controlled inoculations.

Bonman, J.M. et al. 1992. Annual Review Phytopathology 30:507-528; Parlevliet, J.E. 1985. In: Roelfs, A.P. and W.R. Bushnell (eds.) The Cereal Rusts vol. II. New York, Academic Press, Inc. p. 501-525.

Key words: crown rust, Puccinia coronata, partial resistance

Does partial resistance exert selection on oat crown rust populations?

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Abstract

Partial resistance to plant disease is often assumed to be durable, presumably because it exerts little or no selection pressure on the pathogen population. We tested this assumption in the field using partial resistance to crown rust of oat.

Oat crown rust was collected from field plots of partially resistant oat cultivars MN841801 and Portage (Leonard, 2002), as well as plots of the susceptible cultivar Starter and advanced breeding lines from selected crosses. Plots were inoculated at the boot stage with a diverse bulk population of *P. coronata* collected from the Minnesota buckthorn nursery the previous season. Single pustule isolates from these collections and the original bulk population used to inoculate plots were tested for virulence on differential varieties used in our annual rust surveys (Chong et al, 2000). Virulence frequencies in the collections from the partially resistant cultivars and the breeding selections were compared with those in the original bulk as well the collection from Starter.

In 2002, we saw no selection for increased virulence to any of the Pc genes in the differential set when collections from MN841801, Portage, or Starter were compared with the bulk population. This suggests that the partial resistance does not exert any strong selection on the crown rust population. However, we did see strong selection for increased virulence to Pc 48 and Pc 52 in collections from breeding selections derived from crosses involving the cultivar Leonard, possibly indicating that these genes were present in those breeding materials. Results from experiments conducted in 2003 will also be presented.

Leonard, K.J. 2002. Plant Disease 86:593-598; Chong, J., et al. 2000. Plant Disease 84:580-585.

Key words: Puccinia coronata, partial resistance, crown rust

Oat crown rust in Tunisia in 2003

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Abstract

Crown rust (Cr), caused by *Puccinia coronata* f. sp. *avenae,* is generally considered the most widespread and damaging disease of oat in Tunisia. The most important sources of resistance are based on the *Pc* genes active as race-specific resistance. Sixteen single gene oat lines were sown in 4 sites. Early-seeded planting were shown to increase early Cr development (Allagui et al. 2002). The conditions of these sites ranged from humid (Sejnane), to sub-humid (Lafareg), to semi-arid (Ariana and Bou Rabia). The oat plants were subjected to Cr natural infections during the 2003 to assess with time the most prevalent Cr pathogenic variability. The differential reactions were determined at the maximum Cr attack being in February for Sejnane, in March for Ariana and in April for Lafareg and Bou Rabia. The five lines *Pc*40, *Pc*45, *Pc*46, *Pc*50 and *Pc*54 were heavily infested. Infection types ranged between 3 to 4 for these differentials having on the leaf area medium to large uredinia without chlorosis. Reaction of the seven lines *Pc*48, *Pc*51, *Pc*56, *Pc*58, *Pc*59, *Pc*62 and *Pc*64 varied between site. The four differentials *Pc*38, *Pc*39, *Pc*52 and *Pc*68 were resistant at Bou Rabia and Ariana. Of these only *Pc*39 was susceptible in Sejnane but leaf area covered with large uredinia was small (1 %); at Lafareg both *Pc*52 and *Pc*68 were susceptible but with only few uredinia on the leaves (1 % and 5 % respectively). According to the nomenclature of Chong et al (2000), reaction of the differentials indicate the Cr virulence phenotypes prevalent in Tunisia ranged from TFRT at Lafareg, to TJFR at Sejnane, to TDFL at Ariana to TBLM at Bou Rabia. The *Pc* genes, more resistant to oat Cr in Tunisia, were *Pc*38, *Pc*39, *Pc*52 and *Pc*68. In previous evaluations carried out in 2000-2002, the lines *Pc*38, *Pc*39 and *Pc*68 were equally resistance (Allagui et al. 2002). However, slow rusting with partial resistance is being now more attractive. The most pathogenic variability rendering many genes ineffective was mainly located in Lafareg and Sejnane. These regions are in the neighborhood of the noth-west tunisinan's mountains having different *Rhamnus* species but not *R.cathartica*. Surveys on these *Rhamnus* species, conducted in 2003, showed for the first time in Tunisia that *R.lycioïdes* is the aecial host for the sexual stage of oat Cr (Hemmami and Allagui. 2003). The high genetic variability of the Cr virulence in these regions could be linked to the aecidial form found on this *R.lycioïdes* species.

Allagui, M.B. et al. 2002. Ann. De l'INRAT 75, 205-221; Chong, J. Et al. 2000. Plant Disease 84, 580-585. Hemmami I, Allagui MB, 2003. Proc. of the 10th National Days on Results of Agronomic Research – Nabeul (Tunisia).

Key words: crown rust, Pc genes, Rhamnus lycioïdes, aecial host, Tunisia

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Inheritance of stem rust resistance in an Amagalon-derived oat line

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Abstract

Few effective genes are available that confer resistance to prevalent North American races of oat stem rust incited by *Puccinia graminis* Pers.: Pers. f. sp. *Avenae* Eriks. and E. Henn. Lines derived from Amagalon, a synthetic hexaploid line developed from a cross between *Avena longiglumis* Dur. (2n=14) and *A. magna* Murphy et Terrell (Rothman 1984) express resistance to stem rust race NA67. NA67 has been increasing in prevalence in North America and nearly all cultivars grown in the northern plains of North America are susceptible to this race. A breeding line, ND990232, has good agronomic characteristics and stem rust resistance derived from Amagalon. To determine the inheritance of stem rust resistance we evaluated the F_2 segregation of resistance to NA67 in nine populations derived crosses of ND990232 and one other Amagalon-derived line, crossed with NA67 susceptible genotypes. Adhikari and McIntosh (2001) suggested stem rust resistance derived from Amagalon is very similar to *pg-a.* Seedling resistance to NA67 of F_1 progeny of ND990232 crossed with a line with *pg-a* stem rust resistance was evaluated to determine the allelic relationship of Amagalon-derived stem rust resistance with resistance conferred by *pg-a.* Nine segregating F2 populations of 100 plants each, produced from crosses involving Amagalon-derived NA67 resistant lines with diverse NA67 susceptible lines, were evaluated in the seedling stage after inoculation with NA67. Eight of the populations fit a 3 resistant (R):13 susceptible (S) ratio, but did not fit 1 R:3 S or 1 R:15 S ratios. Homogeneity of error allowed combining the populations and the combined population fit a 3:13 ratio but did not fit other tested ratios. The data suggest the Amagalon resistance is conferred by one dominant and one recessive gene through dominant suppression epistasis. $F_{2:3}$ lines derived from the seedlings evaluated in the greenhouse were evaluated in the field and verified the results obtained in seedling tests. While resistance of *pg-a* is conferred by the presence of at least two homozygous recessive genes (Erpelding 1987), resistance of Amagalon-derived lines appears to involve a dominant gene. The infection type of F_1 plants produced from crosses of ND990232 with a line with the *pg-a* complex, ND873126, was inconclusive in determining the allelic relationship of *pg-a* and Amagalon-derived resistance. The F_2 will be evaluated to clarify the relationship of *pg-a* and Amagalon-derived resistance.

Adhikari, K.N. & R.A. McIntosh. 2001. Australian Journal of Agricultural Research 52:1011-1016; Erpelding, J. 1987. Inheritance of stem rust resistance in ND811386. M.S. thesis. North Dakota State University, Fargo; Rothman, P.G. 1984. Crop Science 24:1217-1218.

Key words: stem rust, Puccinia graminis, oat stem rust resistance, Amagalon

Avenanthramide concentrations in developing oat genotypes as influenced by crown rust

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Abstract

Oat (*Avena sativa* L.) avenanthramides are unique antioxidant compounds found constitutively in mature grain and inducible in seedling leaves by crown rust (*Puccinia coronata* Corda. var. *avenae* W.P. Fraser & Ledingham) spores in incompatible host-parasite reactions. We investigated the pattern of avenanthramide accumulation in developing grain and the effects of natural infestations of crown rust on the concentrations of avenanthramides in leaves and grain.

Nine genotypes that varied from susceptible to resistant for crown rust were grown in the field in Madison, Wisconsin in 2001 and exposed to a substantial natural occurrence of rust spores. Leaves and grain were harvested and analyzed for avenanthramide concentrations at intervals from panicle emergence to maturity. The experiment was repeated in 2002 with six genotypes. An additional variable was treatment with the fungicide, Tilt.

In 2001, avenanthramides accumulated in grain during filling and in leaves between panicle emergence and senescence. Avenanthramide concentrations differed significantly among genotypes in both tissues. The two genotypes most resistant to crown rust, Belle and X7571-1, had the highest leaf avenanthramide concentrations, although crown rust score was not correlated with leaf (or grain) avenanthramide concentration across all nine genotypes. Rust infestation was almost nil in 2002. Belle and X7571-1 had lower leaf avenanthramide concentrations than in 2001, while other less resistant genotypes were similar both years. This suggested that the infestation of crown rust spores in 2001 had induced higher avenanthramide concentrations in the most resistant genotypes. Tilt treatments lowered avenanthramide concentrations in leaves of all genotypes and had no effect on concentrations in the grain. The results suggest that avenanthramides may function as phytoalexins in some genotypes but not in others.

Key words: avenanthramides, crown rust, phytoalexins, leaf, grain

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A molecular marker for, and the organization of, a cluster of loose smut resistance genes in oat

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Abstract

Loose smut (*Ustilago avenae*) resistance breeding is hampered by the many distinct smut races, and the different, poorly characterized resistance genes. Three pathotypes (A13, A60, A617) represent the most common races present in the prairie regions of western Canada (Kibite et al. 2000). Markers linked to a group of smut resistance genes located on linkage group 14 (Kanota/Ogle) have been developed (Eckstein et al. 2002). One co-dominant SCAR marker was used to study the relationship between the marker and the three resistance genes.

Molecular markers and plant populations used were described in Eckstein et al. (2002). Another population (OT369/89Ab4088) segregating for the three genes was also evaluated. All lines were inoculated with separate isolates of A13, A60, and A617 using a vacuum protocol, and grown over several locations and years in western Canada.

SCAR marker Ua300co (co-dominant) was linked (~ 5 cM) to a resistance gene specific for pathotype A13. Two other pathotype specific genes clustered on the same side of the marker at genetic distances of 8 cM (A617) and 18 cM (A60). The genes are linked in coupling and are likely often inherited as a group. Attempts to find a flanking marker for the cluster are in progress.

Eckstein et al. 2002. In: American Oat Workers Conference, Wilmington, NC, USA, May 5-7, 2002. pp33; Kibite et al. 2000. In: Cross, R.J. (ed). Proceedings of the 6th International Oat Conference, Lincoln, NZ. November 13-16 2000. pp298-301.

Key words: oat, loose smut, disease resistance, marker, gene cluster

Resistance to *Ustilago avenae* in European oat lines

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Abstract

Growing of resistant cultivars is the most effective and ecological way to prevent losses due to the loose smut, a disease prevalent in farming without seed treatments. In the present poster, the resistance level to loose smut in some of the European oat cultivars and genebank accessions is described.

For the inoculation of seed a vacuum-based method was used. The inoculum consisted of two loose-smut collections with different virulences. In all resistance screenings, inoculation was done at 800 mbar vacuum pressure and with an aqueous spore suspension of 1g/litre. Resistance evaluations were started with a glasshouse experiment with 216 genebank *A. sativa* accessions and 40 oat breeding lines or differentials, followed by the nursery experiment at two locations examining 100 cultivars and lines, respectively, and were completed with a glasshouse experiment with 60 oat lines.

The resistance screening at two locations and the two glasshouse screenings revealed at least 8 modern cultivars and 11 genebank accessions with very high levels of resistance. A highly significant correlation coefficient between glasshouse and nursery examination was found, whereby the glasshouse conditions were favourable for testing under a high disease pressure. Among the entries suitable for growing under ecological conditions, the smut-resistant cvs. 'Neklan', 'Jumbo', 'Firth', 'Hamel', 'Boxer', 'Auteuil' and 'Chantilly' are recommended.

Key words: oat, Avena ssp. resistance, organic farming, loose smut

First studies on the virulence spectrum of Finnish *Drechslera avenae* isolates

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Abstract

Leaf spot and seedling blight on oat (*Drechslera avenae* (Eidam) Scharif) is an important disease of oat (*Avena sativa* L.) particularly in areas with a cool climate. In Finland, leaf spot is the most significant disease of oat. Breeding oat for improved resistance to leaf spot is therefore a priority in the Finnish oat disease resistance breeding programme. For leaf spot disease breeding strategies to be successful, it is important to have information both on the pathogen population and also on possible resistance sources.

20 *D. avenae* isolates were collected from a total of seven oat genotypes grown at 12 separate locations across Finland. Single spore cultures were made and the aggressiveness and the virulence of the isolates were tested under greenhouse conditions on 20 different oat genotypes. The genotypes were selected based on the results of two hill plot tests conducted under field conditions utilising natural leaf spot infection.

18 of the 20 *D. avenae* isolates were viable enough for spore production and were tested in the greenhouse. All the isolates produced clear leaf spot symptoms on the oat genotypes examined. The isolates showed clear differences both in their aggressiveness and virulence. Genotypes Cc 3678 and Suregrain, which showed the highest resistance in field tests, were also resistant against all of the 18 isolates in the greenhouse test. However, genotype Dal gave a resistant response in the seedling test but was the most susceptible genotype under field conditions. The correlation between the results of the seedling and the adult plant test is discussed.

Key words:oat,leaf spot,Drechslera avenae,virulence,resistance,Avena sativa

Epidemiological aspects of the oat kernel spot, caused by *Pyrenophora chaetomioides*

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Abstract

The expansion in acreage of oats in Brazil, particularly under no till system, has increased the frequency of foliar and kernel spots caused by *Pyrenophora chaetomioides*. As a necrotrophic, this fungus is extremely dependent on crop debris to survive from one crop season to another. Consequently, the susceptibility of the host, the presence of inoculum and favorable environmental conditions have been the chief aspects for the frequent occurrence of epidemics in South Brazil. The objective of this work was to identify the stages of development of the seed that are most susceptible for the establishment of the fungus and to correlate it with the amount of inoculum produced on lower dead leaves as well as with the environmental conditions. Under field conditions oat panicles were exposed to the inoculum for certain periods of time since their extrusion and to different conditions of temperature and water precipitation. Seeds exposed to inoculum at both milk and early dough stages showed the highest frequency of infection of *P. chaetomioides*. The temperature and water precipitation did not influence the percentage of seeds infected. However, environmental conditions such as high temperatures, excess of rain and the presence of other diseases anticipated the senescence of oat basal leaves, favoring a higher production of spores by the pathogen. The use of cultivars that offer resistance or escape to the seed infection, crop rotation and fungicide spray at the right time are some recommended measures to minimize the damage caused by this pathogen.

Key words: Avena sativa, epidemiology, seed infection, kernel spots, panicle susceptibility.

Inheritance of resistance to powdery mildew and agronomical performance of some oat germplasm

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Abstract

Powdery mildew is an endemic disease in northern parts of Germany and reduces yields depending from time and severity of infection (Bartels 1980).

Resistances to powdery mildew derived from *Avena macrostachya* CAV5264 and *A. pilosa* CAV 0128 (Hoppe & Kummer 1991) have been analysed genetically using the detached-leaf tests on benzimidazole-containing agar. Segregation in F2 and BC1 are explainable by one incompletely dominant gene for resistance derived from *A. macrostachya* CAV5264 and one dominant gene from *A. pilosa* CAV 0128.

Avena occidentalis CAV3889 (Herrmann & Roderick 1996), another donor for resistance to powdery mildew, was investigated in a glasshouse test with F2 and BC1F2 seedlings. According to the segregation two recessive genes encode for resistance, which will be validated by detached-leaf tests in advanced backcross generations.

Several progenies derived from crosses with the resistance donors mentioned above have been examined for agronomic performance at two locations. The germplasm displayed genetic variation in yield components, whereby the lowest yields where found in progenies of crosses with *A. occidentalis* CAV3889, due to the low number of backcrosses (BC1) with the high-yielding parent.

Bartels, G., 1980. Arbeiten der DLG, 166: 79-87; Herrmann M. & H. W. Roderick 1996. Euphytica 89: 405-410; Hoppe, H.-D. & M. Kummer, M. 1991. Vortr. Pflanzenzüchtg. 20: 56 – 61.

Key words: oat, Avena ssp. resistance, powdery mildew

Greenbug resistance in local oat samples from East Asia

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Abstract

Genetic uniformity of crops promotes adaptive microevolution in pests and resistant varieties with various genetic bases are to be cultivated. Till now only 4 oat genes for resistance to greenbug (*Schizaphis graminum* Rond.) are identified. Resistance in sample Russian 77 (CI 2898) to greenbug biotype A is controlled by dominant gene *Tg 1* (Gardenhire 1964). Study of inheritance of resistance in 3 oat varieties revealed that lines PI 186270 and CI 1580 had single dominant genes (*Grb1* and *Grb2* respectively) determining resistance to biotype C; line CI 4888 had dominant gene *Grb3* for biotype B resistance. Possible presence of minor genes for resistance in all 3 samples could not be excluded (Boozaya-Angoon et al. 1981).

Experiments were conducted in a climate chamber as described by Starks & Burton (1977). Samples at the seedling stage were infested with Krasnodar population of the aphid. When the control plants (cv. Borrus) died damage in experimental plants was estimated according to the scale: 0 – no damage, 1 – 1-10%, 2 – 11-20 % … 10 – 90-100 % of the leaf surface damaged.

Among 277 oat samples most representing local forms from Primorskii krai (Russia), Mongolia, China and Japan, eighty five were heterogeneous for resistance to the greenbug. Damage ratings of resistant components in 42 samples were 1-4, low level of resistance was identified in 43 forms. Wide range of variation for damage ratings (1-10) was characteristic for some samples; it could be result of low expressiveness of genes for resistance and/or difference in virulence pattern among the aphid clones in used population. It was possible to select lines with high and low level of the resistance from that samples indicating to several genes for the trait in at least some oat forms. Half of samples with high level of resistance originated from Mongolia. As genes *Grb1* – *Grb3* were identified in local oat forms from Argentina, Italy and Scotland, we suppose that selected lines have genes for the aphid resistance nonidentical to that described earlier.

Gardenhire, J.H. 1964. Crop Science 4: 443; Boozaya-Angoon, D. et al. 1981. Environmental Entomology 10: 557-559; Starks, K.J. & Burton, R.L. 1977. USDA Techn. Bull. 1556: 1-12.

Key words: oat, Schizaphis graminum, genes for resistance

A two-component response regulator is involved in cold sensing in oat

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Abstract

Plants have developed a number of different physiological and developmental responses to abiotic stress. One important process is acclimation, where mild stress conditions greatly enhance tolerance to later and more severe conditions. During the acclimation changes in gene expression patterns occur, which leads to a plant response involving the necessary modifications of growth, development and cellular homeostasis.

During the last years, six different cellular signal transduction pathways between the initial cold-stress perception and the gene expression response have been documented. Here we suggest an additional pathway. Two component systems, first described in prokaryotes, have also been identified in yeast and plant systems, but not in animals. They are characterised by a phosphotransfer reaction between two types of signal transducers and involves a sensory histidine kinase receptor and a response regulator. In plants, two-component systems play important roles in ethylene and cytokinin signalling and osmosensing but have not been directly coupled to cold signalling so far.

From a subtractive oat cDNA library enriched in cold induced sequences we isolated a full-length clone, denoted *AsDP5*. Northern and RT-PCR analysis showed that the *AsDP5* was induced at +4^{o}C in less than 1 h. Analysis of the deduced 621 amino acids long protein revealed that it had a N-terminal two component response regulator domain, putative nuclear localisation signals and a zink finger DNA binding domain at the C-terminus. Thus, the AsDP5 protein strongly resembles the response regulator protein of two-component systems. This cold signalling pathway is now carefully analysed in oat and in the model plant *Arabidopsis*, using various knock-out mutants and transgenic systems.

Key words: two component systems, response regulator, cold induction

Development of a Scandinavian winter oat by molecular breeding and tissue culture techniques

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Abstract

During the winter 2002/2003, 174 different oat cultivars were planted in the field of Landskrona, Sweden to identify cold hardy lines. The germplasm represented the best winter hardy oats available in the world, originating from seed collections in the US (USDA-NSGC), the Vavilov Institute in St Petersburg, Lochow-Petkus in Germany and IGER in Great Britain. Spring oat (Belinda) and winter barley (SW Hampus) were also included in the trial as references. Weather data was continuously monitored. In December, triplicates of all field-grown lines were established in the green house from field selections. In January, a second batch of plants of the most promising accessions was collected in the field. Parameters like vigour, time of flowering and height of plants at bolting were recorded. Some of the lines were also established in tissue culture. Due to the severe winter in south Sweden in 2003, all plants except the repeats from one single line died. This surviving line came from the Pennsylvania winter oat-breeding program and was denoted as Pen#65. Pen#65 plants were crossed with German winter oats and segregating F_2 populations will be tested in field trials during the coming winters. During the winter 2003/2004 a second field trial on winter oat was done. In this trial, leaf samples from several individual plants were collected at different time and temperature intervals. Total RNA was extracted, and global expression studies were performed by micro-arrays using an oat biochip of 2866 different genes, developed by us. From these studies key genes up- and down regulated in the field during winter stress conditions are identified. This information will be used to develop new molecular markers for an efficient selection of cold tolerant oat varieties in segregating breeding populations. Work is also in progress to establish an *Agrobacterium* mediated genetic transformation protocol for the Pen#65 line. Key genes, will then be introduced to the Pen#65 line by genetic transformation.

Key words: winter oat, field test

Establishment of highly efficient callus proliferation, plant regeneration and micro-tillering systems in commercial oat cultivars

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Abstract

Different explants (seeds, mature embryos, 3-day and 6-day old leaf/mesocotyl joints) of seven commercial summer oat varieties (Adamo, Belinda, Birgitta, Freja, Matilda, Petra and Stork) and one winter line, Pen #65, were cultivated on 2, 4-D containing callus induction medium. After about 4 weeks, explants were evaluated for callus growth. In all varieties maximum callus growth was obtained from mature embryos. Efficient shoot regeneration could be obtained from Belinda (mature embryos, 3-day and 6-day old leaf/mesocotyl joints), Birgitta (3-day and 6-day old leaf/mesocotyl joints), Freja (seeds), Matilda (3-day old leaf/mesocotyl joints) and Stork (mature embryos, 3-day and 6-day old leaf/mesocotyl joints) and Pen #65 (3-day old leaf/mesocotyl joints) in a medium with a specific auxin/cytokinin combination. Plant regeneration occurred via either organogenesis or somatic embryogenesis. Root initiation and further growth took place in a hormone free medium.

Cultivating 9-day old leaf/mesocotyl joints of winter oat varieties 83-48-CH and Gerald on 2,4-D and BAP containing MS2m medium suppressed apical growth and induced lateral enlargement of the apical domes. This led to the formation of multiple meristems and resulted in vigorous microtiller forming cultures.

These oat tissue culture protocols have now established a base towards development of genetically engineered winter oat for Swedish conditions.

Key words: tissue culture, winter oat, microtillering

Molecular characterization of *CBF* transcription factor genes in oat

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Abstract

By EST sequencing we identified 2866 different genes from a cold induced cDNA library from the British winter oat variety Gerald (see other abstract by Bräutigam et al). Among these there are several genes similar to cold and/or drought-induced genes previously identified in rice, wheat, rye, barley and *Arabidopsis*. More than 100 genes encoded putative transcription factors.

Of particular importance for the regulation of cold acclimation is the *CBF* transcription factor family genes, which have important regulatory roles in the cold signalling pathway. In all CBF proteins analysed so far, a characteristic AP2-binding domain has been found. This interacts with a *DRE/CRT* regulatory element and activates transcription of downstream cold and dehydration responsive genes. Four *CBF* factor sequences were found in the oat EST collection, belonging to at least 2 different gene families. A full-length cDNA clone from one such gene, denoted *AsCBF1*, was isolated and sequenced. This revealed a 909 bp long open reading frame (ORF) encoding a putative protein of 303 aa that contain an AP2-binding domain. By semi-quantitative RT-PCR analysis we showed that expression of the *AsCBF1* gene was induced already 30 minutes after cold induction at +4°C. By chromosomal walking an additional 457 bp upstream of the AsCBF1 translational start codon was isolated. A TATAA-box was then found as well as several other potential regulatory elements including a Myc-recognition site. These elements will now be further characterised both *in vitro* and *in vivo. CBF* genes will also be used as genetic engineering tools to develop more cold tolerant oat.

Key words: transcription factor, cold induction, CBF

Analysis of 9703 expressed sequence tags in cold acclimated oat

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Abstract

Winter oat, Avena sativa cv. Gerald, was cold acclimated at +4°C for 4, 6, 8 and 32 hours. Total RNA was prepared from these plants, pooled and a cDNA library was constructed. From this library 9792 expressed sequence tags (EST) were sequenced. The average sequence length after vector clipping was 626 bp and the longest sequences were over 900 bp. Clustering and assembly of the these 9792 EST sequences resulted in a set of 4543 sequences. Clustering, assembly and filtering of these sequences resulted in a set of 2866 unique transcripts, denoted the “UniGene” set. Homology searches on publicly available sequence data allowed the assignment of a tentative function to 1622 (57.57%) of these transcripts. Out of the remaining 1246 unclassified sequences, 494 appeared to be oat specific since they lacked any significant sequence similarity (E-values > $1e^{-10}$ after BlastX search) to any sequence presently available in the public databases. Genes active in photsynthesis were most commonly found, but genes involved in metabolism, signal transduction and abiotic stress were also well represented. Interestingly, 398 sequences displayed strong homologies (E-values $\leq 1e^{-10}$ after BlastX search) to genes previously reported to be involved in cold stress related processes. Of particular importance for the regulation of cold-acclimation are cold induced transcription factors. We found 47 such genes, including 4 CBF transcription factor sequences, a known cold regulatory gene class (see other abstract by Bräutigam et al). The set of 4543 clustered and assembled sequences (in total 5.3 Mb) was searched for microsatellites (SSRs) and 596 di- to pentanucleotide SSRs were found. 83% of these SSRs occurred in non-coding sequences. Work is now in progress to identify the particular SSRs from this collection that give reliable PCR products and are polymorphic. The best SSR markers will then be mapped to the oat genome and linked to valuable genetic traits like lipid biosynthesis, antioxidant activity and cold hardiness.

Key words: EST, winter oat, cold induced genes, microsatellites

Reaction of oats F2 hybrids on Al^{3+} toxicity

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Abstract

The opportunity of aimed transfer of the level of aluminum resistance from parents to hybrids by different combination of crosses is very important for breeders. For this purpose, it is necessary to consider nature of distribution of plants of hybrid and parent populations by level of resistance and to calculate quotients of heritability of used parameters of selection.

We used oats varieties Colt, Wilma, Charlotte and Argamak as parents and nine different hybrids between them. Estimation of resistance levels was conducted according to Lisitsyn (2000). Degree of dominance and degree of heritability defined under the formulas Pert, Frey (1966).

The research has shown that there were hybrid plants with a level of resistance retiring for limits of variation of parent levels of resistance. The direction of cross had significant influence on obtained results. The significance of influence of a maternal plant indicates a participation of cytoplasmic genes in adaptive process. In most cases, the ratio of an inheritable diversity in the tested populations was very great. The nature of dominance of a level of aluminum resistance for different crosses considerably differed. The hybrid Colt x Argamak displayed full positive dominance, and hybrid Argamak x Colt - positive overdominance. The overdominance was characteristic for hybrid Wilma x Argamak too. In any other crosses given varieties promoted development of negative dominance and overdominance. The nature of distribution of seedlings aluminum resistance not always looks like unimodal curve that can indicate the influence of several genes (genetic systems) on studied index. The data of research pointed out a possibility of deriving of highly resistant plants not only by crossing of parent varieties contrast on studied index, but also parent varieties with similar levels of potential aluminum resistance.

Lisitsyn, E.M. 2000. Journal of Plant Nutrition 23: 793-804; Pert, F.C., Frey, K.J. 1966. Crop Science 6: 259-262.

Key words: aluminium, heredity, hybrids, oats, resistance

Genetics of aluminum tolerance in hexaploid oats

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Abstract

Most of the sub-tropical and tropical regions of Brazil have soils with high levels of toxic aluminum (Al^{3+}), reducing the yield of the non-tolerant crops. Tolerant cultivars are able to develop a healthy root system under aluminum toxic conditions; therefore it is important to identify sources of tolerance and understand its inheritance. The objective of this paper is to report the results obtained from several genetic studies involving tolerant and susceptible oat genotypes.

Identification of susceptible and tolerant genotypes was based on the length of root regrowth in nutritive solution (Polle et al., 1978) after exposure to 20 ppm of aluminum (Sanchez-Chacon et al., 2000). Generations F_2 to F_6 from crosses between susceptible and tolerant genotypes were analyzed in the lab. The susceptible genotypes had very poor root regrowth (zero to 5mm) and the tolerant ones had more than 10mm.

Tolerance to aluminum toxicity in the soil in *Avena sativa* is due to a single gene with dominance for tolerance. Studies from several different crosses demonstrated that there are at least two different alleles for tolerance. High levels of aluminum tolerance was found in many oat genotypes but the most important sources are UFRGS 17 and UPF 91Al100-1-4.

Polle, C.R., et al. 1978. Crop Science 18: 823-827; Sanchez-Chacon et al. 2000. Pesquisa Agropecuária Brasileira 35: 1797-1808 (http://www.sct.embrapa.br/pab/uspab.asp).

Key words: aluminum tolerance, hexaploid oats, Avena sativa, inheritance

Breeding oat for aluminum tolerance

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Abstract

Aluminum toxicity is a growth-limiting factor for crop production in the south brazilian soils. This toxicity can be avoided by raising pH up to 5,5 - 6,0 with aglime or by growing Al tolerant cultivars.

A oat breeding program for aluminum tolerance has been carried out since 1986 at the University of Passo Fundo by using segregating populations from F2 to F5, at acid soils, on field conditions (Floss et al., 1991). Floss et al. (1993) reported results about a screening for Al tolerance where 156 genotypes of oats (*Avena sativa* L.) were grow in nutrient solutions (growth chamber). On of the most Al tolerant genotype obtained in thi screening was the cultivar Steele, from USA.

In field conditions and acidic soils, many tolerant lines were selected and evaluated for other important traits, as grain yield, test weight, disease resistance, plant height, days from emergency to flowering and to maturity, and grain quality.

One line from this segregating populations, line UPF92Al300, introducted in 1992 by Quaker Oat Nursery (cross QR=981=UPF80197/(X2082-2/CI8428)/Steele, made in College Station by Milton McDaniel, was selected as aluminum tolerant and evaluated in test trials from 1998 to 2001. This line was released in 2002, by the University of Passo Fundo (UPF), named UPFA 20-Teixeirinha. The average performance obtained at 14 different fields, from 1998 to 2002 was: yield = 3049 kg ha^{-1}; test weight = 50 kg hL^{-1}; thousand grain weight = 36 g; days to heading =87; days to maturity=131; height =103 cm; % of grains wider than 2mm =84; % of groats =71; and moderate resistance to leaf and stem rust.

Floss,E.L. et al. Primer congreso sudamericano de avena, Tres Arroyos/Argentina, 1991, Resumos. p.15; Floss, E.L. et al. In:V International Oat Conference, 1996. Proceedings. Saskatoon, 1996,p. 623-625.

Key words: oat, Avena sativa L., aluminum tolerance, cultivar

Biochemical parameters of oats edaphic resistance

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Abstract

As the aluminum resistance is multigene character, which defined by action of internal and external resistance mechanisms, it is necessary to know, what biochemical parameters are most suitable for a large-scale evaluation of aluminum-resistance level of oats varieties.

On a set of oats varieties, differed on level of aluminum resistance, dynamics of development of such root indexes, as oxidative activity, activity of acidic phosphatase and acidic lipase, content and ratio of protein fractions during adaptive process was investigated.

At utilized aluminum concentration (1 mM) dynamics of development of response was differed for different varieties. The most resistant variety Chizh has raised the level of root oxidative activity at 5th day of study and sustained it during all time of study. Less resistant varieties Argamak and Rodney E stabilized the index at 6th day of study, hybrid Tarak x Krasnodarsky - only at 7th day, and the most sensitive variety I-2674 during all study displayed vibratory nature of a change of oxidative activity. Under stress condition there was significant modification of a content of protein fractions for all studied varieties, in most cases dynamics of the modification had vibratory nature. On 5th and 8th day of aluminum action, the relative activity of acidic phosphatase of 'Argamak' was significantly higher, but on 6th and 7th day - lower, than for 'Chizh'. The relative activity of an acidic lipase also alternated on days: on 5th and 7th day, it was higher for variety 'Chizh', on 6th and 8th day - for variety 'Argamak'. The variety 'Chizh' exceeded variety 'Argamak' in all studied indexes only at 7th day of study, at remaining days the variety 'Argamak' exceeded variety 'Chizh' in some indexes.

Thus, different biochemical parameters utilized at different phases of adaptive process, can essentially influence on evaluation of a level of plant aluminum resistance. The most informative may be studying the dynamics of development of exact parameter at 5-8 days of study: the earlier biochemical index will return to control level the most resistant variety will be.

Key words: aluminum, biochemical indexes, oats, resistance, varieties

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Diagnostics of oat plants by the method of laser interference auxanometry

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Abstract

The use of a new high sensitive method (accuracy 0.07 µm) – laser interference auxanometry makes it possible to perform rapid diagnostics of oat plants at different growing conditions and selection of genotypes tolerant to stress. Oat plants cv. Horizont of “sand” and “water” cultures were used. The growth rate of plant leaves was measured by laser interference auxanometer with 10 sec or 1 min intervals during few hours every day. NaCl solution was added to the root zone to concentration 50 mM, 80 mM, 130 mM. In some experiments the roots were washed of NaCl with subsequent measurement of leaf growth rate. Antioxidant ambiol was added twice with one day interval to the root zone to concentration 1.7 µM. It was demonstrated that oat plants grown under deficiency of mineral nutrition had a low leaf growth rate. A significant increase was observed after single addition of antioxidant ambiol. In this case the leaf growth rate increased in two stages: rapid and a slower one. The leaf growth rate increased 4-fold when ambiol was added twice. Addition of NaCl to the root zone caused a two phase response reaction of plant leaves: decrease and the following increase in their growth rate. Secondary addition of NaCl led to a more significant decrease in leaf growth rate than at first addition of NaCl. The leaf growth restarted with low rate after less than 1 h during first phase. Restoration of leaf growth rate during the second phase at secondary and following additions of salt was partial (it did not achieve the initial level) and was more prolonged than at single addition of salt. The leaf growth rate increased at decrease in NaCl concentration at the root zone as result of addition of water or washing the roots of NaCl. At prolonged growing of oat plants at increased NaCl concentrations the yellowing and drying of the leaf ends was observed. The growth of this plant was suppressed as compared to control plants. Our results demonstrate the potentiality of laser interference auxanometry for evaluation of the changes in growth under different growing conditions.

Key words: diagnostics, growth rate, oat plants

Posters

Markets, products and applications

Commercialisation of improved hay oat varieties in southern Australia

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Abstract

The South Australian Research and Development Institute (SARDI) and the Rural Industries Research and Development Corporation (RIRDC) are the joint owners of new hay oat varieties emanating from SARDI's oat breeding program.

SARDI was seeking a unique approach to varietal commercialisation. Rather than commercialising each oat hay variety as they become ready for release, SARDI was seeking longer term support from a company or companies closely aligned with the hay industry. Therefore the commercial license was granted for a period of five years rather than on a variety by variety basis. The licensee's role would be to support the development and commercialisation of oat varieties suitable for hay production.

The requirements of the successful licensee were to provide: 1) a national focus or be capable of expanding to become a national body, 2) alignment with the export and domestic hay industry, 3) comment to SARDI's oat hay breeding program from end users and hay producers, 4) unlimited access to the varieties, and establishment of an alliance with a recognised seed producing organisation. The primary objective of this alliance is to provide low cost, quality assured seed, in large volumes to hay producers.

The commercial license was granted to the Australian Export Company (AEXCO) in 2001. This company was initally made up of eight export oaten hay processors, seven from South Australia and one from Victoria. Membership of AEXCO has expanded to 18 and includes new members in Victoria, Western Australia and New South Wales. In 2002 AEXCO signed an alliance with the Australian Field Crop Association (AFCA) whose primary function is to multiply and distribute seed. Wintaroo was the first of the varieties to be released in 2002 and 1392 t of seed was produced despite a national drought. This seed was sown in all four states and produced a total of 60,000 t of export hay. About 3500 t of seed was produced for hay production in 2004. The impact of this commercial strategy has resulted in widespread uptake of Wintaroo representing 25% of national export hay production.

Key words: SARDI,AEXCO, AFCA, Wintaroo, national, alliance

Effect of oat hulls on the digestibility of equine diet

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Abstract

In previous studies we have discovered that hulling of oats considerable improves its digestibility in equine diets (Särkijärvi & Saastamoinen 2003). However, hulling methods are variable and may lead to various outcomes. The more intensive the hulling is, the better the end product, but also the higher is the level of costs. In order to evaluate the appropriate hulling intensity, we wanted to study the effect of oat hulls on the diet digestibility.

Eight mature Finnhorse mares were used in a study where effects of oat hulls on the apparent digestibility of nutrients was studied. Diets were based on dry hay and four different oat feeds (71:29 on dry matter basis). Oat feeds were based on hulled oats where four different amounts of oat hulls were added. The oat hull additions were: 1) 0% hulls, 2) 8% hulls, 3) 16% hulls and 4) 24% hulls. The last treatment represented the hull content of regular oats. Both, hulled oats and oat hulls, were first ground separately to a fine meal and then pressed into pellets, in order to prevent feed selection by horses. Treatments were assigned in a duplicated 4 x 4 Williams square design. A preliminary feeding of 16 days was followed by 5 day collection in each period. Faecal samples were taken twice a day during the collection period. Chromium mordanted straw was a marker for the estimation of digestibility.

The inclusion of oat hulls did not affect digestibilities of diet nutrients statistically significantly. The digestibilities of nitrogen free extract and crude protein were slightly higher at 0% inclusion, and the digestibilities of crude fat and crude fibre were better for 16 and 24% inclusion rates, but as mentioned, the differences were not statistically significant. Probably the fine milling of the grain material has improved the digestibility of fibre of the oat hulls so tremendously, that the impairing effect of fibre did not show in diet digestibilities.

Särkijärvi, S. & Saastamoinen, M. 2003. Feeding value of various prosessed oat grains. In: Ynze van der Honing et al. (eds.). Book of abstracts of the 54th Annual meeting of the EAAP. Wageningen: Wageningen Academic Publishers. p. 417.

Key words: digestibility, horse, oats, oat hulls, hulling

Effect of amount of oats and barley-oats on milk production

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Abstract

Feed tables give lower feed values for oats than for barley, but oats has been shown in many experiments to improve milk production and milk fatty acid composition compared with barley (Moran 1986, Heikkilä et al. 1988, Martin & Thomas 1988, Ekern et al. 2003). Oats has traditionally been used in Finland as a main cereal for dairy cows on farms. Today farmers often use barley-oats mixtures. In this experiment we studied the effects of increasing amounts (0.2, 0.3, 0.4 kg/kg 4-% fat-corrected milk) of oats and barley-oats mixture (1:1) as the only concentrate on the milk yield and composition and feed utilization in a 2 x 3 factorial continuous trial with 36 Finnish Ayrshire cows. Grass silage was fed *ad libitum* with hay 1 kg/d. An experimental period of 24 weeks was preceded by a 2-week covariance period. The digestibility of feeds was measured on sheep. Mean consumption of cereals was 4.8, 7.5 and 10.2 kg/d with respective proportions of 29, 40 and 51% of dietary dry matter (DM). Increasing the amounts of both cereals from 29 to 51% of DM decreased silage DM intake with a substitution rate of 0.438 and 0.264 for oats and barley-oats, respectively, but total DM intake, milk, fat, protein and lactose yields increased linearly. Oats resulted in higher milk yield response than barley-oats (0.966 vs. 0.745 kg milk/kg cereal DM increase), but the difference in energy-corrected milk yield response was smaller (0.846 vs. 0.781) because of a tendency to lower fat and protein content with increase of oats compared with barley-oats. The oleic acid content of milk fat tended to increase with increasing oats, but to decrease with increasing barley-oats. Milk renneting properties improved with increasing cereal amounts, but less with oats than with barley-oats. Milk production parameters did not differ significantly between cereals except the utilization of metabolizable energy and AAT (amino acids absorbed from the small intestine), which were higher with oats than with barley-oats as a concentrate.

Ekern, A. et al. 2003. Acta Agriculturae Scandinavica, Section A, Animal Science 53: 65-73; Heikkilä,T. et al. 1988. Proceedings VI World Conference on Animal Production Helsinki 1988, p. 336; Martin, P.A. & Thomas, P.C. 1988. Journal of the Science Food and Agriculture 43: 145-154; Moran, J.B. 1986. Animal Production 43: 27-36.

Key words: oats, barley, dairy cow, milk production, milk composition

Effect of volume weight of oats and barley on fatty acid content of milk fat

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Abstract

Feeding oats has been shown to cause beneficial changes in milk fatty acid composition characterised as a reduction in saturated and increased monounsaturated fatty acids compared with barley (Kankare & Antila 1984, Martin & Thomas 1988, Tesfa et al. 1992, Ekern et al. 2003). Unfavourable weather conditions during the growing season may cause crop failure leading to low volume weight. The effects of different volume weights of both oats (33, 43, 51, 61 kg/hl) and barley (31, 38, 57, 69 kg/hl) on milk fatty acid composition were studied with 16 Finnish Ayrshire cows in a replicated (n=2) 4x4 Latin square experiments with 4-week periods. Grass-red clover silage was fed *ad libitum* with 8 kg concentrate, which included 86% oats or barley, 10% rapeseed meal and 4% minerals + vitamins. Mean proportion of oats and barley concentrate consumption was 0.39 of dietary dry matter. Crude fat content of oat based concentrates were over twice that of barley containing concentrates (5.9, 5.6, 6.8, 6.6% vs. 2.6, 2.5, 2.6, 2.6%, respectively). Lipid in oats contained approximately 2.8 times higher oleic acid and 1.4 times lower palmitic and linoleic acid and 3.4 times lower linolenic acid relative to barley. Differences in milk fatty acid composition due to variations in volume weight were small, although statistically significant in some cases. Fatty acid content of milk (% of total fatty acids) produced with oats and barley of different volume weights from the lowest to the highest respectively were: palmitic acid 29.3, 29.9, 28,7, 28.5 and 34.7, 34.8, 34.4, 35.4; stearic acid 13.6, 13.3, 13.7, 13.9 and 10.3, 10.0, 9.3, 9.4; oleic acid 23.7, 22.1, 23.4, 23.9 and 18.3, 17.3, 16.3, 16.8; linoleic acid 0.8, 1.2, 1.0, 1.2 and 1.2, 1.2, 1.4, 1.4; linolenic acid 0.7, 0.7, 0.7, 0.7 and 0.6, 0.6 0.8, 0.8. In conclusion, failure of oats or barley crops has little effect on milk fatty acid composition. Oats are recommended for dairy cow feeding due to a more desirable fatty acid composition of milk for human nutrition compared with barley.

Ekern, A. et al. 2003. Acta Agriculturae Scandinavica, Section A, Animal Science 53: 65-73; Kankare, V. & Antila, V. 1984. Journal of Agricultural Science in Finland 56: 33-38; Martin, P.A. & Thomas, P.C. 1988. Journal of the Science Food and Agriculture 43: 145-154; Tesfa, A.T., et al. 1992. Agricultural Science in Finland 1: 255-264.

Key words: oats, barley, volume weight, fatty acids of milk

Bifunctional oat products: Technology and nutritional effects

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Abstract

The nutritional and health related benefits of oats and beta-glucans respectively are well-known. The implemenation of resistant starch into oats results in a bifunctional food containing factors for the reductions of the risk of coronary heart disease and – additionally – the risk of inflammatory diseases of the colon or even colon cancer. Materials included killned oat kernels (grinded), killned and steamed oat kernels (grinded), addition of corn starch, hiami corn starch, waxy corn starch, commercially available resistant starch, selected varieties (Marion, Hecht, Kanton). The investigations were made by small and industrial scale extrusion machines, partly with pre-conditioning. Moisture ranged from 15 to 30 %, temperature from 90 to 170. In contrary to barley and pea, resistant starch was not generated by extrusion of oat. The oil of oat blocks the introduction of effective amounts of mechanic energy during extrusion. Extrusion of variety Kanton, which is below 6 % oil, resulted in substantial resistant starch of 1.1 % d.b. Oat products with substantial contents of resistant starch in the range between 5 to above 10 % d.b. result by enrichment of oat or oat bran with hiami corn starch, optionally with commercially available resistant starch. Evidence was given to the formation of resistant starch at incompletely hydration. Heating of extrusion premix in an autoclav showed, that resistant starch is generated in substantial amounts by temperatures above 130 °C, dependent from heating time. The oil content influences the generation process. Autoclaving cycles enhance the generation of resistant starch. Bifunctional food products can be made by extrusion of mixtures of oat or oat bran (favored) and of hiami maize or other hiami botanical sources. The product properties, the quality characteristics and physiological effects give a good performance of shelf life, chewing properties or consumption preferences, binding of sterols and fermentation to SCFA, especially butyrate (*in-vitro* tests). Another possibility is the manufacturing of a butyrogenic product by co-extrusion.

Key words: Oat product(s), composition, dietary fibre, resistant starch, butyrogeneity, sterol binding

Toxicity differentiation of oat varieties in celiac disease

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Abstract

Celiac disease (CD) is a permanent intolerance to the grain’s storage protein “gluten”: gliadins (wheat), secalins (rye), hordeins (rye) and possibly avenins (oats). The only possible treatment of the CD is the observation of a strict gluten free diet during lifetime. The toxic role of oats is controversial. Recently it was shown that ingestion of moderate amounts of oats does not have a harmful effect in adult patients with CD (Janatuinen at al. 2002) and was suggested that the immunogenetic sequences in gliadin are not present in avenin (Kilmartin at al. 2003). However, a specially grown and tested oat product was used in these studies.

In our study we used ELISA method to compare 8 oat varieties of different origin and to determine whether they can be safely included in a gluten free diet.

It was shown that: a) the proteins of oat varieties are different by the toxicity for celiac patients; b) for composition of individual gluten-free diets the toxicity of oat varieties must be determined; c) by our preliminary data the oat variety Argamak selected in the North – West Agricultural Institute (Russia) is the best one for gluten-free diet of certain types of patients; d) the blood serum of celiac patients have to be characterized both by quantity of antigliadin antibodies and by their ability to react with different types of antigenic determinant of oat proteins; e) in order to determine types of each celiac patient antigluten antibodies it is promising to prepare the prolamine fraction kits.

Janatuinen, E. 2002. Gut 50: 332-335; Kilmartin, C. 2003. Gut 52: 47-52.

Key words: oat varieties, avenin, celiac disease, antibodies

Physical and sensory properties of oat cakes

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Abstract

Oat-based product has long been identified as a highly desirable food. It has a high nutritional profile due to its high concentration of protein, good distribution of amino acids, and rich fiber content when compared to other grains. Puffed oat cakes may appeal to consumers due, in part, to their low fat, low calorie, high fiber, and whole grain properties which fit well with healthy claims, key snacking trends, and the shift in American dietary attitudes. However, their physical and sensory properties have not been reported in the literature.

Oat cakes were produced by a two-step process: 1) extrude oat flour to make pellets and 2) puff oat pellets in a rice cake machine. A 2×3×4×3 factorial design consisting of four variables and with 2 replications was used to study the effects of extrusion, tempering and puffing conditions on the puffed oat cakes. The four independent variables are extrudate moisture content (30 and 34 % wb), tempering moisture content (10, 12, and 14 % wb), heating temperature (238, 243, 249, and 254 °C), and heating time (4, 6, and 8 s). Physical properties of oat cakes (specific volume, color, hardness, and integrity) and descriptive sensory analysis were conducted.

The results showed that extruded oat pellets can be successfully puffed by a rice cake machine to make oat cakes. All the four processing variables (heating time, heating temperature, extrudate moisture content, and tempering moisture content) had significant effects on the oat cake’s physical and sensory properties. Heating time had the most significant effect. Increasing heating time resulted in oat cakes with increased specific volume, integrity, and redness, but lower lightness and yellowness. Also, Pincipal Component Analysis (PCA) showed that high correlations existed between instrumental and sensory descriptive analysis.

Key words: oat cake, physical properties, descriptive sensory analysis, puffing

Acceptability of oat varieties for the brewing process

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Abstract

Despite of a well kept tradition over centuries to use oat as malted raw material for wort and beer production today this brewing cereal has been displaced almost completely. Ten different oat varieties where examined for their acceptability as brewing cereals and malted. The most favourable sample has even been used to brew different types of beer in pilot scale. The pilot maltings of these samples have been done in a 1 kg scale with 45 % moisture content, isotherm at 14,5 °C (8 and 9 d vegetation time) and with a kilning temperature of 80 °C/3 h. The beer was brewed either in a 1,5 kg or a 10 kg pilot plant. In both cases a lauter tun was used for solid-liquid-separation. Hot break was separated with a whirlpool. The wort was pitched at 10 °C with top fermenting wheat beer yeast (< 5 % dead cells, methylenblue-test) which was been cultivated several times in oat wort. After three days of main fermentation a maturation step at 16 °C and a two week storage time at 0 °C followed. The resulting beers have not been stabilised or filtered.

The varieties differed only little. The malt with the extended malting time of one day demonstrated better levels of enzymatic activities and modification. Therefore the batch which was used for the brewing trials was malted with nine day vegetation time. All ten oat varieties had low levels of extract caused by the high level of husk material, which requires quite high proportion of water for mashing. The high portion of fatty acids was degraded only to a small amount. The low foam levels could be explained by the presence of fatty acids since they are not assimilated completely by the yeast. In addition fatty acids have a negative effect on flavour stability. In comparison to barley malt oat malt have considerably lower levels of enzymatic activity. On this account the enzymatic rests during mashing where noticeable laboured. Saccharification and lautering took place in a fast way. Main fermentation, maturation and storage ran smooth and efficient. All three beer types produced (Schank-, Voll- und Starkbier) offered a pleasant top fermenting aroma which still differ from the familiar southern german wheat beer aroma.

The trials demonstrate that the cereal oat does contain a potential to produce a drinkable pleasing beer.

Key words: malt, beer, top fermented, fatty acids

Posters

Production chain

Development of an integrated *pure oats* cultivation and processing chain for patients suffering from coeliac disease

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Abstract

Coeliac disease is caused by the protein gluten found in most monocotyledonous cereal crops e.g. wheat, barley and rye. Rice, maize and sorghum do not contain gluten and thus are suitable for coeliac patients. Many research results also support the suitability of oat products for consumption by coeliac patients. Oats form an acceptable diet of coeliac patients in Finland, Sweden, Norway and UK. Oat products for coeliac patients must be marketed in Finland with the claim: ‘contains oats and gluten-free compounds’. A high number of foreign grains often limits the suitability of oats for consumption by coeliac patients. The objective of the project was to develop an integrated *pure oats* cultivation and processing chain, which meant fewer than 6 seeds of foreign cereal grains per kilogram of oats. The project was financed by European Guidance and Guarantee Fund, local communities and companies. The *pure oats* cultivation chain was controlled at every step: sowing of seed, cultivation, harvesting, transport from fields to farm, drying, storage, and transport of harvested grain from farm to industry. The fields were cleaned of foreign cereals twice during growing season. The number of foreign seeds was counted from farm samples and samples taken from the truck transporting the *pure oats.* The *pure oats* processing chain from receiving, hulling and milling all the way to packing was also tightly controlled. The final gluten (gliadin) contents were analysed from both oat samples and oat products (AOAC 991: 19). All the final gluten contents of both *pure oats* samples and products were below 0.002 g/100 g grains oats. In the first year 7 farmers took part in the project; 42 % of their oat fields were approved during the field inspections. In the second year 4 farmers cultivated pure oats; all their oat fields were approved in the field inspections. The project educated farmers in the techniques for growing and handling *pure oats* and resulted in development of a quality control system for processing *pure oat* products.

Key words: Avena sativa L., coeliac disease, production, gluten, gluten-free

Environmental impacts of production chain of oat flakes

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Abstract

Supply web based Life Cycle Assessment (LCA) was used to assess environmental impacts of Elovena oat flakes, produced by RavintoRaisio in Finland. Data for the system model were acquired from the field, as empirical investigation of the real processes, thus providing a reliable basis to analyse the sources of environmental impacts ("hot spots") and to consider respective improvement possibilities. The assessment took account of all stages of the most important product and distribution systems of oat flakes concerned from the production of farm inputs and raw material to the retail stores and, finally, to the porridge consumed.

The environmental load from farm operations was the primary cause for global warming, eutrophication, acidification and photochemical ozone creation potential in production chain. However, traditional porridge cooking caused multiple carbon dioxide emissions compared to the production chain of flakes. Most of the environmental impacts of the system can be affected by choosing the porridge cooking method. The air emissions of porridge cooked in microwave were essentially smaller than when using traditional electric hot plate.

The study generated knowledge improving the efficiency of production chain, which can be used as a basis for product improvement measures in the long term and according to the goals of sustainable development. Some improvements have been made in the production chain. Biogas has replaced heavy fuel oil in the generation of steam used for producing oat flakes. This change almost halved the volume of sulphur dioxide emissions in the entire production chain.

Katajajuuri, J.-M. et al. 2003. Environmental impacts of oat flakes. Maa- ja elintarviketalous 33. 48 p. In Finnish. http://www.mtt.fi/met/pdf/met33.pdf. ISSN 1458-5081. ISBN 951-729-802-1.

Key words: life cycle analysis, environmental impacts, production chain, oat flakes

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Relationships among agronomic traits and grain composition in oat genotypes grown in different environments

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Abstract

Genotype and environment are major determinants of economically important quantitative traits, which include agronomic characteristics and grain composition. This study examined relationships among agronomic traits and grain composition as influenced by genotype and environment.

Thirty-three oat (*Avena sativa* L.) genotypes were grown in three trials in Idaho in three consecutive years (1999-2001). Yield, heading date, kernel physical characteristics, and groat protein, β-glucan, oil, tocols, and avenanthramides concentrations were measured.

Analysis of the combined data for all environments showed significant genotypic differences for all traits except avenanthramide **2f**. The genotype × trial interaction was significant only for avenanthramides concentration, and the genotype × year interaction was significant for most traits. Most of the variance was associated with genotype for all traits except α-tocopherol and the avenanthramides. Principal component analysis showed several close associations among traits: avenanthramides and yield; the tocols, β-glucan and protein; the kernel physical characteristics; and oil and heading date. Trait associations differed when calculated from genotype averages as compared to all samples. This reflected a strong environmental influence on some traits. The score plot differentiated Aberdeen trials from those at Tetonia and the 2000 trials from those grown in 1999 and 2001. Biplots for each trait showed the genotype by environment interactions, which differed among the various traits. The results show that knowledge of the relationships among traits and environments can assist breeders in optimizing both agronomic traits and grain composition simultaneously.

Key words: genotype, environment, agronomic traits, grain quality traits

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Nutrient management for fodder oats in India - An overview

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Abstract

In India oats can be grown as fodder crops on all soils, apart from alkaline or waterlogged conditions, in all regions where wheat and barley are grown. It is mostly grown as winter crop. In addition, oats are quick growing, palatable, succulent and nutritious and acceptable to all categories of livestock. It can be fed in many forms such as green forage, straw, silage, and grains. With the introduction of new management systems (proper amounts of manure and fertilizers, multicut cultivars, better combinations such as oats + vetch and oats + peas) both commercial dairy farmers and resource-poor farmers have greatly reduced the feed shortage problem during the dry winter months as well as achieving a 30% reduction in the cost of feed. Besides growing fodder oats as sole crop, oats + vetch is the best mixture for high yields and improved soil fertility. For resource-poor farmers, oat cultivars Canadian and Kent are recommended and a combination of oats + vetch. The general nutrient management practice is application of FYM at the rate of 5 ton/ha by broadcast uniformly and another ploughing done. 80:60:40 kg (N: P_2O_5: K_20) is the recommended fertilizer rate, where N was used in three split doses, applied after each cut under irrigated conditions. Otherwise it was applied as one basal dose under rainfed conditions. After sowing, a land leveler was used to ensure good seed contact with soil. To optimize the fertilizer requirement, various trials were conducted under All India Coordinate Fodder Research Project. Application of 120 kg/ha resulted higher green fodder yield of 30 t/ha. To get a maximum possible yield application of 60 kg Sulphur/ha along with recommended dose of fertilizer can be restored. Fodder oats is also cultivated in cropping sequences like Rice-Cowpea-oats and rice-sorghum-oats. Application of 75 % of recommended fertilizer along with FYM (5 t/ha) recorded maximum rice equivalent yield of 40 t/ha in the case of rice-cowpea-oats cropping sequence. So, oats has the potential to serve as an important winter fodder crop in India during winter season. With good nutrient management it can potentially provides more and better fodder from the same unit of land than the traditionally grown winter wheat.

Key words: mixture, vetch, feed, fertilizer, cropping system

Oat production in Georgia

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Abstract

Georgia is a country with an ancient tradition of land cultivation. In the 20th century it became an agro-industrial country. Traditionally Georgia has been a net exporter of food products and a major supplier of vegetables, fruit, tea, essential oils, citrus, wine, mineral waters, cognac, annual crops, cereals, (spring wheat, winter barley, winter rye, spring rye, oats, maize, beans, buckwheat, sugar-beet, sunflower, ground – nut, Soya-bean, tobacco, cotton, potatoes, vegetables, vegetable crops, corn silage, folder root-crops, hay of perennial grass, hay of annual grass and vegetables. During recent years the supply of agricultural products from Georgia to the FSU republics and international markets has been substantially reduced. The country has lost its position on the export markets and as a result Georgia became a net importer of food products. More than 82 percent of GDP was produced by the private sector in 2002, compared to 74 percent in 2001. Today over 80 percent of agricultural production of cereales is in private sector. Georgia is divided into so called vertical zones. There are different physical, geographic and climatic conditions on this relatively small territory. We can come across almost all kinds of soil and climate existing in the world. With a long growing season and some areas of subtropical climate, cereals, (oats) citrus and a variety of deciduous fruits, vegetables and vine crops grow well along with tea, cereals, sunflower and a variety of field crops. With the variety of climates, almost any crop can be raised, giving Georgia one of the most diverse agricultural bases in our Southern Caucasus region. The agriculture industry is concerned primarily with the production of basic foodstuffs on farms but it also includes the supply of inputs for farming such as Oats seeds, cereals, begetables, fertilizers, animal feeds, and machinery. In addition, agriculture is becoming increasingly integrated with other sectors of the food chain such as processing, distribution and retailing to from the agri-food industry oats.

K. Kelenjeridze Cereals Production in Georgia and Radiation factors of climate 1988.09.11 Tbilisi Georgia. G. Talakhadze Topsoils of Georgia 1990.07.11. Tbilisi Georgia. K. Nadiradze Oat Production in Georgia. 1997. 11.02 Tbilisi Georgia - ”Kvali” (Journal of The Ministry of Agrioculture and Food of Georgia). E. Eristavi USAID. 1992.10.05 Tbilisi Georgia Tbilisi Georgia. FAO 2003.11.02 Tbilisi Georgia

Key words: production, climate, crops

Oats yield in drought conditions

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Abstract

The research was undertaken to determine the most appropriate oat varieties and terms of sowing for three very different localities: Banja Luka, Drinic and Novi Sad. Two oat varieties were two from Croatia, four from Serbia and one from Bosnia and Herzegovina. One was naked variety. The trial was set up according to the randomized block method in four repetitions. The trial was sown in three terms at each location. The field research is planned to be conducted in 2003 and 2004. Primary factor in oats production is climate (Coffman 1961). Oats has very porous stem, consequently high transpiration coefficient and increased water demand (Kastori 1995). Vegetation season in the 2003 was the driest and warmest one in the meteorological history of these meteorological stations. In such circumstances, the highest average yield (4528 kgha^{-1}) and the best quality of seed was obtained on the mountain locality Drinic. The strongest effect of drought was registered on Novi Sad causing serious reducement of grain yield (average 2763 kgha^{-1}). Hectoliter mass and 1000 seeds mass did not fail. The grain yield on Banja Luka was significantly higher than grain yield on Novi Sad, but the mass of 1000 grains and hectoliter mass were lower. The first sowing term in Novi Sad provided highest grain yield. The second sowing term in Banja Luka and Drinic provided the highest average yield. The best grain yield at Novi Sad and Banja Luka was obtained with variety Slavuj. All varieties on Drinic provided very similar grain yield. Naked oat gave significantly lower grain yield on all localities and terms in comparison with chaffed ones.

References: Coffman, A. F. 1961. In: Oats and oat improvement. American Society of Agronomy Madison: p. 12; Kastori, R. 1995. Plant Phisiology. Nauka Beograd: p. 110.

Key words: oats, variety, term of sowing, locality, drought

Environmental benefits and impact assessment of oats in the UK

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Abstract

As part of an application for a Sustainable Arable LINK on the incorporation of important traits underlying sustainable development of the oat crop (in which the Government part funds industrially relevant research to further its policy objectives), we undertook a short Environmental Impact Assessment summarising the impact of current practices and expected project outputs for diverse indicators. Results are summarised here.

Oats receive 0.15kgs/ha of fungicides (wheat 0.58); 0.78 herbicides (2.23); 0.01 insecticide (0.05); 0.89 PGR (1.17); 0.01 molluscides (0.12);total 1.84 (4.15) (Garthwaite and Thomas, 2003). Improved lodging resistant dwarf oats would reduce the risk of plant growth regulators residues in oat products. Oats have been shown to be more nitrogen (N) efficient than wheat, with a lower risk of N pollution of watercourses. Typical N balances (Sylvester-Bradley 1993) are 95kg/ha offtake from 100kg/ha applied compared to 135kg/ha offtake from 200kg/ha applied for wheat. Lower inputs and gas emissions are associated with lower number of sprayer rounds with obvious reductions in fuel consumption and greenhouse gas emissions. A return to mixed farming would have a positive effect on populations of farmland birds, rare arable weeds and the brown hare. Within the rural economy, oats are a profitable break crop valuable in rotations, and the rate of progress in national yields of oats is similar to that of wheat and exceed those of barley.

We conclude that the demand for more oats as a result of expanding existing markets or creating new markets would bring impressive benefits to sustainable agriculture.

Garthwaite DG, Thomas MR, Dawson A and Stoddart H. 2002. Pesticide Usage Survey Report 187. Arable Crops in Great Britain, Defra and Seerad. http://www.csl.gov.uk/science/organ/pvm/puskm/arable2002.pdf;Sylvester Bradley R. 1993. Proceedings of the cereals R&D conference. Home Grown Cereals Authority. Robinson College, Cambridge 5,6 January 1993 pp 198-217.

Key words: oats, environment, pesticides, biodiversity, indicators

Effect of nitrogen fertilisation on the phytic acid, mineral and trace element contents of oats

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Abstract

The purpose of the study was to obtain information on the effects of different cultivation practises on the uptake and formation of some chemical components in oats. The effect of nitrogen fertilisation on the phytic acid, mineral and trace element contents of oats were studied during 1997-1999 at 2 locations in Finland. Phytic acid has considered to have an unfavourable effect on the bioavailability of nutrients as it can form complexes with cationic elements.

The nitrogen fertilisation trials employed 5 N rates (0, 40, 80, 120 and 160 kg N ha^{-1}) with four cultivars (Aarre, Katri, Kolbu and Salo). Mineral and trace element contents were determined after wet digestion by inductively coupled plasma emission spectrometry (ICP-AES). Phytic acid was determined after extraction and ferric precipitation procedure using ICP-AES to determine phosphorus (Plaami & Kumpulainen 1991).

The nitrogen fertilisation increased significantly the Cu, Zn and Fe contents of oats at the higher 120 and 160 kg N ha^{-1} ($p < 0.001$) levels. This may be due to the acidification and increased ionic strenghts that can enhance the solubility or desorption of trace elements. Slight increment was also observed in the phytic acid content in dry and warm growing seasons 1997 and 1999, whereas an opposite trend was observed in cold and wet growing season 1998. Mean phytic acid content of oats in the trials was 13.3 mg/g dry weight. Ca, Mg and P contents were not affected; K and Mn contens were slightly decreased at high nitrogen application rates ($p \leq 0.01$). Clear cultivar differences were also detected.

Plaami, S. & Kumpulainen, J. 1991. J. Agric. Food Chem. 51: 2608-2614.

Key words: oat, Avena sativa, nitrogen fertilization, phytic acid, mineral and trace elements, cultivar

Effects of vesicular-arbuscular mycorrhizae on the growth and uptake of some heavy metals by oat

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Abstract

Today, agriculture practices by taking environmental concerns into account are of great importance. This has urged consistent cultivation and production systems to be developed and implemented. The purpose of the agriecosystem is to ensure alternatives with the concern that population of natural species is to be sustained and the likelihood hazardous effects is to be minimized. One of these alternatives is use of soil microorganisms in agriculture (Weissenhorn at al. 1995), specifically mycorrhizal fungi which can be of great importance in heavy metal availability and toxicity (Leyval at al. 1997). Thereby a natural protection management might be promoted. The objective was to investigate the possibilities of utilisation of VAM in mitigating pollution in soil. Uptake of heavy metals by plants, the effects of mycorrhiza on heavy metal absorbed by plants and mycorrhizal tolerance to heavy metals were explained. Soil samples were taken from farmers field at the depth of 0-20 cm. The sieved soil was mixed with sand (3:1) and was sterilised. Oat roots were inoculated with four species of VAM fungus and the rate of infection on the roots was determined, the test plants was local variety of oat. The different metal contents in the soil were obtained by adding aqueous solutions of ZnSO4. 7H2O ,Cu SO4. 5H2O and 3Cd(SO4). 8H2O . All treatments were applied with and without mycorrhizal inoculum and there were four replicates. Heavy metal contents increased in soil, root, stem and leaves, depending on the increased doses of Cu, Zn and Cd in both inoculated and non-inoculated treatments. Infection rate was found 36 % in VAM infected oat roots. As a result of increased heavy metal application (Cu, Zn and Cd) VAM infection rate lessened [Cu (36-21%), Zn (36-15%) and Cd (36-4%)]. Large part of the metals were retained by roots (Gildon & Tinker1983) VA mycorrhiza hindered metal movements to stem and leaves. (Graham & Fardelman 1986). The filtering property of mycorrhiza may contribute to the efforts to mitigate high levels of heavy metals in soils.

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Key words: vesicular-arbuscular mycorrhizae, growth, uptake, heavy metals

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Antioxidant and β-glucan content in oats as affected by soil type and N-level

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Abstract

Avenanthramides, tocols and β-glucans in oats are substances that can positively influence human health. Their content in the oat grain is affected by genotype and environmental factors. This study was initiated to clarify the role of the soil type and N-level on grain antioxidant and β-glucan content.

Two cultivars, Freja (6% oil) and Matilda (10% oil), were grown in 2003 outdoors in boxes containing soils from two Swedish sites, Jönköping (J) and Köping (K), in four replicates. Two levels of N fertiliser were applied, 120 and 240 kg/ha. The soils were analysed for chemical composition. Grain yield and harvest index (HI) were determined. Grains were dehulled and analysed for content of avenanthramides, tocols, β-glucan, oil and protein.

The overall content of avenanthramides in the oat samples was very high. β-Glucan data were not yet analysed at the time of abstract preparation. There were no significant differences in grain composition between soils. Significant differences were found between N-levels for content of the avenanthramides **2c, 2f**, total avenanthramides, and protein. Cultivars differed for content of avenanthramides, **2p**, **2f,** total avenanthramides, α-tocopherol, total tocols, protein, and oil. Moreover, the cultivar x N-level interaction was significant for content of α-tocopherol, α-tocotrienol, total tocols, protein, and oil. Yield and HI were significantly affected by soil, N-level, and cultivar. The results indicate that differences in type and composition of these soils had little effect on content and composition of avenanthramides, tocols and oil in oat grains. However, other soils that may have greater differences in type and composition could affect grain composition as well as yield and HI. From the two studies of 2003 combined, it may be concluded that environmental factors other than soil type, e.g. N-level, climate, are more important in controlling grain composition.

Key words: avenanthramides, tocols, protein, oil, soil composition

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iSeed^{TM} phosphorus coating of oat grains to improve seedling establishment and early growth

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Abstract

The phosphorus (P) is transformed in soil into unavailable forms for plant due to the high content of active iron (Fe) and aluminium (Al) in acid soils, and due to the high content of calcium (Ca) in alkaline soil. The utilization rate of phosphorus in granular fertilizers is about 10-15% in the first year, but only 1-2% per year there after. iSeed™ - “Intelligent seed” is an early growth promoter for the crop. In the “iSeed™ P solution” seeds are coated with high-soluble phosphate and biodegradable fixing agent. Coating the seed with soluble P fertilizer improves the utilization rate of phosphorus, when the key nutrient is “just in place” for the early root and canopy growth.

In 2003 three cultivars of oats (Salo, Fiia, Belinda) were grown on two soil types low in phosphorus (P-values 4 to 8 mg/L soil). Experimental design was split-plot: cultivars in main plots and treatments (untreated control or iSeed™) in sub plots. At planting all plots received 400 kg/ha NPK fertilizer (20-3-8) as deep placement between seed rows. Planting density was 500 viable seeds/m^2. After emergence the density of treatments was monitored two times by counting the plants (one meter in five rows per plot). Early growth of the oats was measured three times by sampling biomass (50 randomly chosen plants per plot) in weekly intervals.

Grain yields of oat cultivars were high ranging from 470 to 595 g m^2 in exp 1 and 550 to 680 g m^2 in exp 2. Cultivar differences were evident, but coating oat grains with iSeed™ did not increase grain yield. The plant stand structure differed, however, greatly between iSeed™ treated and control plants. iSeed™ treatment resulted in higher biomass of oat plants. How this associates with differences in seedling establishment will be further studied in 2004.

Key words: oats, phosphorus, iSeed, growth, biomass, yield

First trials with naked winter oats varieties

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Abstract

Bulgaria is in a zone of marked transition-to-continental climate. Oat cultivation under these conditions is limited by temperature and rainfall. The data over 100 years show that the drought periods in spring and spring-summer are on increase (Cholakov 2003), which makes winter-crop realization more certain. However, temperature conditions in the autumn-winter period can totally compromise a crop, thus disheartening the producers. The average cold-resistance coefficient for the naked varieties of winter oat was found to be к=2, 3 at k=11 for barley, var. “Mirage” (Antonova & Petrova 2002). Winter oat has to have a coefficient of 10 to guarantee its survival. The aim of the research is estimating the basic agronomic parameters of naked oat varieties and lines in order to formulate a selection strategy. Eighteen naked oats varieties and lines after two preliminary frost tests at -10 –12 ^{O}C were evaluated 2000 - 2003 in a randomized block design. We measured cold resistance using coefficient of cold resistance (Antonova & Petrova 2002), resistance to *Puccina gr*. and *P. coronata*, *f. avenae*, yield with its components and seeds characteris. Years were characterized by meteorological parameters. Stable and high yielding code were 48 and Bullion. Promising genotypes as parents in a cross combinations are: Bandicoot and Carma for radically earlier vegetative period, Bandicoot for very short plant height; Cn 91/257/4 for high 1000 grain mass; Neon and КЗ- 32-78 protein and lysine content. Fats were <7% for all genotypes. There were no outstandingly promising samples as to the degree of nakedness and the discolouration is not a problem for Bulgarian conditions. The genotypes from the UK had high yield potential, medium plant height, lodging resistance but not sufficient cold resistance. As a contribution to the breeding process were established very significant positive phenotypic correlations between yield, main panicle grain weight and test weight (Pixlej & Frey 1992). The weight of the grains in the main panicle is determined by the weight of the main panicle and the rate of grain growth (Peltonen-Sainio 1990). The main selection aim remains winter-tolerance combined with high productivity, which requires a broadening of the naked winter oat genetic stock, including the use of spring varieties.

Antonova & Petrova, 2002. Jubilee Session on the 50th Anniversary of the Dobroudja Agricultural Institute “Breeding and Agrotechnics of Field Crops; 191-198; Cholakov 2003. Scientific Session of Jubilee 120 Years Agriculture Science in Sadovo. Scientific Reports. Vol. III; 154–158; Peltonen-Sainio, P. 1990. Plant Breeding 104: 340-354; Pixlej & Frey, K.J. 1992. Euphytica 60: 149-156.

Key words: naked oats, grain yield, cold tolerance, quality

The effect of depth and sowing time on germination, yield and yield components of naked and hulled oat

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Abstract

The first hulless cultivar Akt was taken into regional distribution in Poland in 1997 and the next one Polar in 2002. Earlier results with the naked cultivars showed that in the field conditions the germination was reduced. Our aim was estimate the influence of the agrotechnical factors on the germination dynamics, grain yield and the yield components of the naked oat variety Akt. Field experiments were conducted in Agricultural Experimental Station Lipnik near Stargard Szczecinski, during 2001-2003 using 2 sowing dates (optimal and 2 weeks later), 2 varieties of oat (naked Akt and hulled Bajka), 4 sowing depths (1, 3, 5, 7 cm). Delay of sowing time did not have a significant influence on number of plants after germination, except in 2003. Depending on the vegetation season the field germination of naked cultivar Akt was lower than hulled cultivar Bajka. Both cultivars were more tolerant of too deeper sowing depth than too lower sowing depth. Two weeks delay of sowing time caused significant decrease in grain yield mainly due to lower grain number in panicle and slightly decrease weight of 1000 grains. Number of panicles per square meter were similar independently on sowing time. Like in Budzyński et al. (1999) the changes of the sowing depth in comparison with recommended depth 3cm caused that the grain yield was decrease up to 10% due to lower number of panicles per square meter. The obtained differences were not similar depending on sowing time and depth in each year of researches. Naked cultivar Akt yielded up to 27% lower comparing to hulled cultivar Bajka, but the differences fluctuated from 33 to 24% depending on vegetation season. The yield difference between cultivars resulted from lower weight of 1000 grains of the naked oat. Naked oat has lower panicle number per square meter at optimal sowing time. Naked cultivar obtained higher grain number than hulled Bajka per panicle. Also Peltonen-Sainio (1994) found naked lines to produce less panicles per square meter and increased the number of grains per panicle, Contrary to Cermak & Moudry (1998).

Budzyński, W. et al. 1999. Żywność. 1(18) Suppl.: 99-103; Cermak, B. & Moudry, J. 1998. Acta Acad. Agricult. Tech. Olst. 66: 89-98; Peltonen-Sainio P. 1994. Agronomy Journal 86: 510-513.

Key word: sowing time, sowing depth, hulled and naked oat, yield, yield components

The comparison of production ability of naked and husked oats

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Abstract

The aim of the research work was to assess differences in yield formation of naked and husked oats and to determine the affecting factors. The exact field small-plot experiments with three naked oats varieties (Abel, Izak, and Salomon) and with three husked oats varieties (Auron, Edmund, and Expander) were carried out in two Austrian sites (Lambach and Freistadt) and in two Czech sites (České Budějovice and Humpolec) during 1999-2001. There were determined mainly panicle length (LP), number of whorls (NW)**,** number of branches (NB), number of spikelets (NS), number of grains (NG) and weight of grains per panicle (WG). Mean values of harvest index for husked and naked oats were 45.8 and 39.7 %, respectively, with negative relationship with plant height and in a positive relationship with WG. The husked varieties reached higher mean levels of the all yield components. The stands of the husked varieties had higher harvest densities, panicles per m^2, gains per m^2 and minimum variability of the coefficient of productive tillering. The weight of panicles was affected by number of grains, rather than their weight. Yield variability has been influenced in greater extent by number of formed spikelets than by their productivity as reported by Peltonen-Sainio (1994). The yield was affected not only by the higher panicle productivity, but also by the stand density. The inter-year variability of the panicle productivity was influenced mainly by precipitation rate during the period of spikelets differentiation and grain filling. The effect of genotype on the panicle productivity was 15.5 %. Crude grain yields in our experiments were 5.83 and 4.30 t/ha for husked and naked oats, respectively. The tested naked varieties would produce at the observed output the yield of “oats rice” 4.20 and 4.26 t/ha. However, such high output of husked oats has not been reached in farming practice. Stelzner (1990) reported outputs 46-55 and 86-92.4 % for husked and naked oats, respectively, under German conditions. In our experiments, the production of dehulled grains was 3.21 and 3.83 t/ha at the outputs 55 and 89 % for husked and naked oats, respectively. The “oats rice” production was observed to be for 31.3 % higher in the naked varieties as compared to the husked ones. Such results support the interest in breeding and cultivation of naked oats under the conditions of the Czech Republic.

Burrows, V. D., et al.2001. Canadian Journal of Plant Science 81:727-729; Peltonen-Sainio, P. 1994. Agronomy Journal, 86: 510-513; Stelzner, CH. Bauern Echo, 17, 1990,6

Key words: hulled oat, naked oat, yield, panicle productivity.

Evaluation of selected quality characters in the collection of naked oats in Czech conditions

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Abstract

Based on increasing use of oats for human nutrition and newly developed processing methods, there is a need of more detailed defining its grain quality. Varieties with growing characteristics suitable for the given environment and grain quality acceptable for defined end use are assumed to meet requirements of both growers and the processing industry.

In 2000-2003, 42 hulless varieties from the oat collection were grown in the field in plots of 2.5 m^2 without replications and evaluated for growing characteristics. After harvest with a combine-harvester, basic parameters of the grain (yield estimation, 1000-grain weight, volume weight, screening fractions, percentage of hulled grains) were evaluated and nutritional characteristics (content of nitrogen, starch, fat and fibre) were determined using the NIR technique.

Results confirmed a high variation in all characters examined. The highest difference between maximum and minimum values in absolute values was found in starch (12.1), however due to high starch content the variation coefficient was lowest (4.5 %). The highest variation coefficient was calculated for fibre content (53 %). This value was markedly affected by a generally low fibre content and relatively high occurrence of hulled grains in some materials depending on weather conditions of the year. The nitrogen (respectively starch, fat, and fibre) content in the examined materials varied from 15.7 to 24.7 (from 52.3 to 64.4, from 2.9 to 8.2, and from 0.2 to 3.8, respectively), the maximum difference between years was 2.1 (2.6, 1.1, and 1.0, respectively). Correlation coefficients were calculated.

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Key words: genetic resources, quality, naked oats

Inheritance of nakedness in crosses between naked genotypes

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Abstract

Nakedness in oats is genetically controlled by a dominant major gene, but it is not known if all oat varieties trace back to the same origin. To find out if different sources exist, we made crosses between naked oats. Spelt forms in segregating generations can only be expected in case of different origin of the major genes for nakedness in the parents.

Starting with 75 crosses the segregating F2 generation could be obtained for 41 crosses. While 35 crossed yielded only naked oat plants, some spelt oat plants were detected in the remaining six crosses. Two of these crosses, both with the French accession AVE 2841 contained 1 to 2 % plants with hulled grains. Selfed progenies were raised from selected plants of the six crosses. Spelt oat plants were found, and the progenies of plants with clearly hulled grains were nearly uniform for hulled grains, but also segregating progenies with a varying degree of the expression of nakedness were observed. Phenotypic variation also exists in cross progenies between spelt and naked oat. The genetic basis was not the same in the parental naked genotypes. The French accession AVE 2841 carries a different major gene from the German (AVE 1296) and Finnish (AVE 1582). The small percentage of plants with hulled grains supports the hypothesis, that in all parents a dominant major gene for naked grains is responsible. We also found a small percentage of naked grains in selfed progenies from plants with hulled grains explained by minor genes. Seven microsatellites were used in the cross AVE 1296 x AVE 2841 to verify that spelt oat plants were derived from the cross between two naked oat plants. Only F3 plants were analysed, which themselves yielded hulled grains and had 2-3 florets per spikelet. All F3 plants went back to the cross of the two naked oat parents. Though not impossible, the risk of erratic plants is very low. In the F2 generation of another cross AVE 1287 (Finland) x AVE 2842 (Germany) only a few plants with spelt oat character were found. Also in this case some F3 plants with spelt oat phenotype were analysed with five microsatellite markers. But in this case two out of four plants could not be derived from the cross, since they showed foreign alleles for three or four microsatellites. This shows that even with a small number of plants a few microsatellites can be used efficiently to control the genotypes. There is strong evidence that the genetic basis of the French accession AVE 2841 is different from other accessions.

Key words: naked oat, nakedness, microsatellites

SWOT analysis of producing naked oat in northern growing conditions

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Abstract

Naked oat is an under-utilised crop, which contributes less than 0.1% to the total oat acreage in Finland. Such low area under naked oat compared to conventional indicates, however, the potential for more comprehensive production. Limited interest in growing naked oat more extensively is attributed to its weaknesses, which ironically result from nakedness that is the factor making naked oat also an exceptionally attractive crop. To be able to weight the potentiality of naked oat, an analysis of weaknesses, strengths, opportunities and threats (SWOT) was carried (Peltonen-Sainio et al. 2004).

Based on the relevant literature and our own experiences in growing and handling naked oat we ended up in the following results of SWOT-analysis: Strengths are 1) experience and long traditions in cultivating oat in Finland, 2) adaptation to northern growing conditions, 3) crop management comparable to that in conventional oat, 4) exceptionally high quality grain and 5) storability; Weaknesses are 1) need for compensating the reduced seed vigour by using 10 % higher seeding rate, 2) sensitivity to grain damage caused by mechanical stress and 3) incomplete expression of nakedness; Opportunities are 1) potential substitute for imported energy, 2) potential for specific, high value applications, 3) potential for future breeding success and 4) lack of economic losses related to hulls; Threats are 1) problems in availability regarding modern cultivars for farmers and lot quantities for industry, 2) lack of signs of increasing production intensity and 3) problems in producing high germination seed in northern growing conditions.

After weighting all these SWOT-factors thoroughly, we ended up in concluding that naked oat is particularly attractive as on-farm feed in Finland.

Peltonen-Sainio, P. et al. 2004. Agricultural and Food Science 13: in press.

Key words: grain damage, feed, naked oat, opportunities, quality, strengths, SWOT, threats, weaknesses

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Threshing naked oat in moist conditions

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Abstract

For naked oat the aim is to maximise the yield free from lemma and palea and minimise threshing loss and grain damage. The fatty grains are, however, soft, and harvest at a high moisture content (in Finland usually harvested at 20% moisture content or higher) further increases the softness of the grain. Mechanical injuries also reduce germination through making the grains vulnerable to fungal infections that reduce storability.

Two naked oat cultivars (*Lisbeth* and *Bullion)* and one conventional oat (*Salo*) were harvested at different grain moisture content using three combine harvester settings: the first setting was that recommended for conventional oat, the second used a reduced cylinder speed and the third used a narrow concave clearance. It was investigated whether grain moisture at threshing and combine harvester settings affected germination and hull content.

The greater the grain moisture content of naked oat at harvest, the more damage was caused by threshing. Lower cylinder speeds tended to result in better germination than higher speeds, even under moist conditions. Narrowing the concave clearance did not affect germination. Threshing settings had only limited effects on hull content and degree of hull retention, and the postulated protective nature of hulls was confirmed only for cultivar *Lisbeth*.

Threshing a naked oat crop at a low as possible grain moisture content can reduce harvesting damage. However, if this is not possible, better germination can be ensured by reducing the cylinder speed. Small grains tended to retain hulls more tightly during threshing. This may indicate that the most advanced grains were more completely filled and mature and therefore, also better able to dehull.

Key words: naked oat, germination, grain moisture, harvester settings, hull

Economic comparison of naked vs. conventional oat in Finland

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Abstract

In Finland oat, almost purely conventional oat, has been the second-most cultivated grain after barley in recent decades. Despite naked oats excellent nutritional value, cultivation of naked oat has failed to spread in Finland, partially because of generally outdated concepts according to which naked oat suffer from low yield and reduced germination and seedling emergence.

Production cost calculations conducted by different advisory organisations show that the cultivation of oat, conventional or naked, in Finland is more cost-effective than that of barley and wheat. This is mainly because of need for lower variable costs caused by disease control, liming and fertilisation.

Two thirds of Finnish oat production is directly consumed on farms as livestock feed. In the feed use of grain, the value is based on energy values, nutritional values and digestibility. In terms of energy yield, wheat and naked oat exceed barley. But the hectare-based energy yield of dehulled conventional oat is lower than that of barley aswell owing to the significant loss during dehulling (20%). In terms of nutritive value, naked oat is a competitive cereal even if the yield was moderate.

An economic study accommodating the feed values and yield levels of naked oat proves that naked oat is a competitive alternative for oat, dehulled oat and barley. For pigs and poultry, naked oat is also more economical than wheat in the Finnish conditions. When comparing conventional oat with naked oat, it is necessary to consider the higher processing costs caused by the hulls of conventional oat in various phases of production.

Information centre of the ministry of agriculture and forestry 2000. Yearbook of Farm Statistics 2000. Helsinki 266 p; Valentine, J. 1990. Aspects of Applied Biology 25: 19-27; Welch, R. W. 1995. In: Welch R.W. (ed.), *The Oat Crop*, pp. 279-320, Chapman & Hall, London, UK.

Key words: naked oat, cost, energy value, economic, production, feed

The effect of sowing rates and seed dressing on yield and yield components of naked and hulled oat

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Abstract

In 1997, first hulless cultivar Akt was taken into regional distribution in Poland, and in 2002 the next one Polar. Field experiments were conducted in Agricultural Experimental Station Lipnik near Stargard Szczecinski 2000-2001. Two cultivars of oat (hulless Akt and hulled Bajka), 4 sowing rates (400, 530, 660, 790 seeds per m^2), 3 variants of seed dressing at recommended rate (Sarfun T450 FS – systematical-contact dressing with active substances karbendazym and tiuram, Dithane 455 SC - contact dressing with active substance mankozeb and control. Seed dressings were used. The increasing of sowing rate from 400 to 790 seeds per m^2 in 2000 year caused significant increase of grain yield irrespective of cultivar. In the following year, when weather conditions were favorable for vegetation period, increasing sowing rates did not significantly influence grain yield. Grain yield of Bajka was higher than for hulless Akt. After taking hull in Bajka cultivar under consideration and subtracting it from the yield. Yields of both cultivars were similar, and significant differences were observed only in the first year of the experiment. Together with increasing sowing rate, also number of plants after germination and number of panicels per 1 m^2 increased. Both cultivars reacted on increasing of plant density by reduction of grains in panicle Productive tillering in present experiment decrease together with sowing rate for both cultivars. Number of plants per m^2 and number of panicles per m^2 are significantly diversified for types only during the first year of the experiment. Weight of 1000 grains depends on agronomical and meteorological conditions. It did not change in 2000 at different sowing rate. Significant differences were observed in case of weight of 1000 grains in 2001, only. Seed dressings used in the experiment did not influence investigated features, except in hulless grains in 2000.

Key word: sowing rate, seed dressing hulless oat, yield components

Evaluation of groat breakage during dehulling

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Abstract

Groat breakage is an important factor affecting milling yield. Variation for breakage exists among varieties but it is not clear what physical and/or chemical characteristics are associated with this variation. One hundred and thirteen oat lines were dehulled using a laboratory-scale, constant speed impact dehuller. Breakage was measured as the mass of broken groats in the dehulled sample. Biplot analysis (www.ggebiplot.com) was used to investigate the relationships among groat protein, oil and b-glucan, groat size (mass and length), difference in kernel and groat length and proportion of undehulled kernels. Breakage was most closely associated with kernel size (both mass and length). There was a weak but positive relationship between groat content and breakage. β-glucan and oil content were negatively but weakly associated with breakage. The difference between kernel and groat length was not associated with groat breakage, but was closely associated with the proportion of undehulled kernels. It is clear that the dehuller speed must be adjusted to account for differences in groat mass.

Key words: groat breakage, biplot analysis

Pattern analysis of yield for oats cultivars in Iran

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Abstract

Several statistical methods have been developed to describe the responses of genotypes to variation in the environment. Amongst them, Additive Main effects and Multiplicative Interactions (AMMI) analysis (Zobel 1988) is particularly effective for depicting adaptive responses. Because yield trails frequently have both significant main effects and a significant genotype × environment interaction and traditional statistical analysis are not always effective with this data structures. AMMI analysis was used to evaluate yield stability of nine oats genotypes (4 Canadian cultivars and 5 Turkish breeding lines) and Makoi barley (as check) in 6 environments (3 dates of planting and 3 sowing densities of 300, 375 and 450 seeds / m^2). The experiment was conducted at Research farm of Isfahan University of Technology in 2001. For each environment a randomized complete design with 3 replications was used. The main effects of genotypes, environment and genotype × environment interaction effects were significant ($p<0.01$) and 70% of interaction sum of squares was explained by the first two principal components. Biplot of genotypic and environmental components of the first interaction principal component (IPC1) and mean yields of the genotypes and environments relieved that Boyer and Line 28 were the most stable genotypes and Boyer had the lowest IPC1.Pacer and Lines No. 2 and 17 were the least stable genotypes. Biplot of IPC2 and means of yield also showed that Boyer was the most stable genotypes. Discrimination of genotypes based on stability statistics of AMMI model (EV_2 & SIPC2) showed that Boyer and Calibre were the most stable genotypes. Pattern analysis of the two significant principal components confirmed that Boyer was the most stable genotypes and is suitable cultivar for breeding program or introduction for commercial production. Based on this pattern analysis Lines No.17 and 2 had specific adaptation to first sowing density (300 seed /m^2). Lines No. 32 and 28 showed specific adaptation to fi×rst planting date (12 Oct.) Makoi and Pacer had the specific adaptation to second and third planting date and second sowing density.

Annicchiarico, P., 1997, Theoretical and Applied Genetics, No. 94, PP. 1072 – 1077; Chapman, S.C. et al. 1997, Euphytica, 95:1–9; Zobel, R.W. et al. 1988, Agronomy *Journal* 80:388 – 393.

Key word:G×E Interaction, pattern analysis, AMMI, biplot,

Oat functionality in forage mixtures

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Abstract

In the rainfed arable land of the Mediterranean basin mixtures of oat and common vetch are planted for haymaking (Caballero et al. 1995, Assefa & Ledin 2001), and to improve the nutritive value of the forage (Thomson et al. 1990). The objective of this research was to evaluate the influence of different oat : vetch seeding rates on forage yield and quality. Field experiments were conducted under rainfed conditions in 1996-97 and 1997-98 growing seasons at Policoro, Southern Italy. The oat (O) and vetch (V) monocrops were compared with three O:V (70:30, 50:50; 30:70) seeding rates. Relative yields (RY) were calculated and the RY Total (RYT) was used as criterion for mi-xed stand advantage. N-total was determined to measure the forage quality.

The seasons were different in total rainfall that contributed greatly to the results. Mean forage production (DMY) of mixtures was not significantly affected by increasing seeding rate of oat over the range used. Seeding rates of O did not influence botanical composition of mixtures. Decreasing O seed proportions, O mean contribution to DMY dropped by 20%, RY of O de-creased by 30%, and RY of V increased by 185%. For mixtures with 30% for oat, RYT exceeded unity suggesting a mixed stand advantage at lower oat seeding proportion. Forage quality was not significantly influenced by studied mixture rates. In conclusion, the net effect of oat in the mixture was to increasing competition as oat density increased.

Table 1. Dry matter and relative yields.

O : V	DMY	Oat Contr.	Relative yields		
Seed ratio	(t ha^{-1})	(%)	O	V	Tot.
Mono O	12.47	100.00	1.00	-	1.00
70 : 30	11.16	87.62	0.78	0.20	0.98
50 : 50	11.00	78.48	0.69	0.35	1.04
30 : 70	9.93	70.04	0.55	0.57	1.12
Mono V	6.89	0	-	1.00	1.00
LSD (.05)	1.03	6.12	0.07	0.03	0.05

Assefa, G. & Ledin, I. 2001. Animal Feed Science and Technology 92: 95-111; Caballero et al. 1995. Field Crops Research 41:135-140; Thomson et al. 1990. Experimental Agriculture 26: 49-56.

Key words: oat, vetch, seed ratio, forage mixtures, Mediterranean basin

Evaluation of the effects of green forage clipping on grain yield and its components in double crop of Iranian oat cultivars

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Abstract

In order to study the dual-purpose use of oat and the effects of clipping at different growth stages on grain yield and some other characters of oat and Maquee barley, an experiment was conducted in educational field of Jihad-Keshavarzei Education Center of Shahrekord in 2000-2001. The experimental was split plot in randomized complete block design with three replications. Three clipping treatments; harvest after 5 and 10 cm growth and a non harvest (control) were assigned as factor A in sub plots, and five lines of oats (No: 2, 17, 28, 32 and 36) and Maquee barley (control) as factor B in sub plots. Clipping effects were significant on all traits except number of grain and number of tillers. Delay in harvest decreased straw yield, grain yield, biological yield, plant height, total number of fertile tiller and 1000- weight grain, while duration sowing to maturity and sowing to heading and forage yield increased. There were significant differences among lines in plant heigh, duration sowing to maturity, sowing to heading, forage yield, grain yield, biological yield, number of grains, harvest index and number of tillers. Lines No. 2 and 17 had the highest grain and biological yields and had faster growth, while lines No. 28 and 32 had a low forage yield, grain yield and biological yield and due to their slow growth rate were not suitable for this region. There were significant interaction effects between clipping and line for plant height and grain yield. It was concluded that clipping in 2 and 17 lines could be done in other to supply the forage for livestock without any adverse effects on yield.

Christian, S. et al. 1989. Agronomy Journal 81:145-150; Dunphy, D. J. et al. 1982. Crop Science 22:106-109; Pumphrey, F. V. 1970. Agronomy Journal 62: 641-643, Redmon, L. A. et al. 1995. Agronomy Journal 87: 137-147; Sharrow, S. H. and Motazedian, I. 1987. Agronomy Journal 79: 502-504; Winter, S. R., et al. 1990. Agronomy Journal 14: 415-421.

Key words: clipping, components yield, double crop, grain yield, lines of oat

The yield and grain composition of naked oat grown with spring vetch as an undersown plant

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Abstract

Growing cereal-legume mixtures is associated with N transfer from the legume to the accompanying cereal and offers the potential for reducing the amount of N-fertiliser used in cereal grain production. Cereal crops grown in these mixtures tend to accumulate more protein in their grain. At the same time they extend their growing season. The traditional oat production system in Poland is based on covered oats grown with vetch on poor and damp soils. Our objective was to determine the grain yield and quality of a naked oat cultivar grown as a pure crop and with a spring vetch companion crop. The field experiment was conducted at the Czyrna Experimental Station from 1999 to 2002. The naked oat cv. *Akt* was sown either as a pure crop or with spring vetch determinate cv. *Ina* at two seed rates. The amount of rainfall over the experimental years varied from 737 to 1040 mm, corresponding with the multiannual average of 834 mm. The effect of graded seed rates of spring vetch on yield and gross chemical composition of naked oat grain (AOAC, 1995) and β-glucans content (the Megazyme assay kit no 995.16) were determined. The present results confirm earlier findings indicating that total yields of wheat and triticale grown with legume companion plants were decreased with decreasing cereal seeding rates (Pisulewska, 1997). Cereal grain protein content was increased with increasing seeding rates of legume companions. We confirmed the negative relationship between oat grain protein and fat content, while ash and β-glucans were only little, although significantly affected. In conclusion, the relative changes in grain yield and quality of naked oat grown either as a pure crop or with a spring vetch companion plant, were similar to those observed for wheat and triticale.

AOAC, 1995. „Official Methods of Analysis of AOAC International" (16th ed.), AOAC International: Arlington, Virginia. USA; Pisulewska, E. 1997. D.Sc. Thesis, Agricultural University of Kraków. Poland.

Key words: naked oat, legume companion, grain yield, composition

Effect of variable sowing ratios and sowing rates of bitter vetch on the herbage yield of oat-bitter vetch mixed cropping

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Abstract

Small grain cereals following fallow predominate the rain-fed arable land of the Mediterranean basin (Caballero 1993). Integrating winter annual legumes into crop rotations has been recommended as a means of reducing the use of nonrenewable resources (Papastylianou & Danso 1991). Caballero and Goicoechea (1986) has shown oat to be the most suitable companion crop for common vetch (*Vicia sativa* L.) and hairy vetch (*V. villosa* Roth.). The objectives of the present study were to determine whether mixtures of bitter vetch [*V. ervilia* (L.) Willd.] with oat would change vetch and total yield in a competitive or facilitative way related to sowing proportions based on number of seeds. Field trials were carried out at the Jordan University of Science and Technology in Northern Jordan. Ratios of the number of vetch to oat seed were 100:0; 85:15; 70:30; 65:35 and 40:60 within each mixture, sowing rates of bitter vetch were 85, 100. 115 and 130 kg ha^{-1}. The oat was sown at 150 kg ha^{-1}. Plants were harvested at the pod setting stage of vetch. Mixed cropping produced 90% more dry matter than the sole cropping of vetch, but 70% less than the oat sole cropping. Mixed cropping yields were not simulated by sowing ratio or sowing rate of vetch but proportions of vetch dry matter decreased linearly as the percentage of oat seed in the mixture increased. The data suggested the possibility of greatest vetch yield with oat proportions below 20%. If high herbage yield is the objective, the oat sole crop will be selected. Crude protein content should not be a criterion to define the best sowing rate of oat-vetch mixture. High forage quality of the mixed cropping would require a very low sowing proportion of oat to increase vetch contribution to forage yield

Caballero, R. & Goicoechea, E. L. 1986. In: Barba, F. M. & Abreu, J. M. (eds.). Grasslands facing the energy crisis. Proceeding of the 11th General meeting of the European Grassland Federation, pp.379-384; Caballero, R. 1993. Journal of Sustainable Agriculture, 3: 133-154; Papastylianou, I & Danso, D. K. 1991. Soil, Biology and Biochemistry 23:447-452.

Key words: Sole cropping, mixed cropping, Vicia, Avena

Reducing the effect of grass weed competition

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Abstract

The control of crop grass weeds is a major limitation to the successful production of oats in Southern Australia. This is due to the combination of few registered herbicide options and limited knowledge on their effectiveness, coupled with effects of management, for different cultivars. Five trials with 6 cultivars were conducted between 1997 and 2001 in the southern wheatbelt of Western Australia to examine this problem.

In a herbicide tolerance screen the yields of the cultivars Mortlock, Toodyay and Needilup were not reduced by any herbicide options tested and were therefore more tolerant to the chemical applications. The yields of the cultivar Hotham however, were reduced by all herbicide treatments except the “safest” treatments, indicating this cultivar is more sensitive.

In the presence of weeds, the yields of Hotham and Needilup were not reduced by herbicides but had relatively high in crop weed biomass and therefore, can be regarded as both poor weed competitors and herbicide tolerant. The crop weed biomass of Mortlock and Toodyay was low and yield wasn’t reduced by any of the herbicide options, therefore both were tolerant to the herbicides and competitive with weeds. Needilup had the strongest relationship between weed biomass and grain yield (R^2=0.80) indicating that Needilup is more responsive than the other varieties tested to changes in weed biomass whilst less sensitive to herbicides.

Two management practices to reduce weed competition were assessed, delayed sowing and increasing crop plant density. Utilising the delayed sowing allowed an extra knockdown herbicide to be applied and resulted in an average grain yield increase of 1.5 t/ha and weed biomass reduction of 1 t/ha. When the target plant population was increased in the presence of weeds, weed biomass was reduced and grain yield was increased.

Through the utilisation of alternative herbicides and changes in management, grass weeds can be effectively controlled in oat crops without reliance on a small number of herbicides (e.g. sulfonylureas).

Key words: herbicide tolerance, crop management, weed competition

Controlling perennial weeds in organically grown oats

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Abstract

Perennial weeds are an increasing problem in Finland, particularly in organic farming. Mechanical control by hoeing, stubble cultivation and bare fallowing provides some options for managing these weeds.

Mechanical control of perennial weeds in barley and oats was studied in a field experiment with five replicates, placed in a clay soil (containing 6–12% organic matter) field under organic production. The field was heavily infested with *Sonchus arvensis* and moderately infested with *Cirsium arvense*, *Elymus repens* and *Stachys palustris*. The treatments were (2001–2002) barley–oats, barley–oats with inter-row hoeing, and bare fallow–oats, and additionally stubble cultivation (yes/no) across these treatments. The experiment was analyzed as a strip-plot design with stubble cultivation as a horizontal factor and treatment as a vertical factor. Weed number and dry mass were assessed prior to crop harvest from two 0.5 m × 0.5 m quadrats per plot.

Both stubble cultivation in previous autumn and inter-row hoeing reduced significantly *S. arvensis* biomass in oats, but bare fallowing was the most effective treatment. Bare fallowing also controlled *E. repens* and *S. palustris*, but was not effective against *C. arvense*. Oat yields were slightly higher after bare fallow and slightly lower in hoeing treatment compared to ordinary oats-after-barley crop stand, but the differences were not statistically significant.

The results suggest that *S. arvensis* could be reduced by stubble cultivation in previous autumn, and could even be controlled by inter-row hoeing in oat stands. Bare fallow is an effective way to reduce most perennial weeds. When tackling perennial weeds in oat production, appropriate options for a given field and rotation should be chosen according to dominant weed species.

Key words: perennial weeds, oats, Sonchus arvensis, Cirsium arvense, Elymus repens, Stachys palustris, mechanical control

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Effects of salinity and wild oat (*Avena ludoviciana)* densities on yield and yield components of wheat

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Abstract

Salinity is one of the main constrains for wheat production in south of Khorasan province, Iran. In this region, wild oat (*Avena ludoviciana*) is one of the noxious weeds which compete with wheat crop. In order to study on the effects of salinity and wild oat density on yield and yield components of wheat (Var. Roushan) a field experiment was conducted during the 2000 and 2001 growing season in the Agricultural Research Station of Birjand University. Experimental design was split plot with three replications. Treatments were: Salinity of irrigation water with four levels (1.5, 4.2, 5.5, and 10.5 dS/m in the first year and 1.5, 5.5, 7.5 and 10.5 dS/m in the second year) and five wild oat density (0, 20, 40, 80 and 160 plants /m^2). Wheat density was 400 p/m^2.

Results showed that grain weight, grain yield and relative grain yield decreased significantly by salinity. However, number of spike /m^2 , number of grain in spike and harvest index were not significantly affected by salinity. Grain weight in the second year, grain yield and relative grain yield decreased significantly by wild oat density. Nevertheless, number of spike/m^2, number of grain /spike, grain weight in the first year and harvest index were not affected significantly by wild oat density. Generally, results of this experiment showed that ability of wild oat competition can reduce under high salinity condition.

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Key words: salinity, wild oat, yield, yield component

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