



Research Kernels

Our Latest Research Results • July 2009

A Modified Extensigraph Method for Evaluating Dough Properties of Wheat Breeding Lines

Author: Y.R. Chen

Submitted to: Cereal Chemistry

Wheat flour dough characteristics, such as resistance-to-extension and extensibility, are important traits that predict end-product quality. The selection of wheat breeding lines for development of new wheat varieties is a continuous challenge. There is an ongoing effort to develop better methods to evaluate the dough characteristics because of limitations from the standard extensigraph method in terms of flour sample size, sample throughput, and testing time. A modified extensigraph method was developed to reduce flour size from 300 to 100g and testing time by half with convenient dough preparation compared to the AACC standard method (54-10). Extension measurements determined by the modified method were highly correlated to the standard method. Some dough mixing characteristics and bake tests correlated better with the modified method. The data suggests that the modified method is not only useful for wheat breeding programs, but may be a valuable alternative to the standard method for the milling and baking industries, wheat quality research, and wheat crop quality surveys.

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Manufacture of Gluten-Free Specialty Breads and Confectionery Products

Author: T.J. Schober

Publication: Schober, T.J. Manufacture of gluten-free specialty breads and confectionery products. Chapter 9 in *Gluten-Free Food Science and Technology* (ed E. Gallagher), ISBN: 978-1-4051-5915-9, Wiley-Blackwell, Hoboken, NJ pp. 130–180.

People suffering from celiac disease, wheat allergies or wheat intolerances require breads that do not contain any wheat or related cereals like rye and barley. The manufacture of these so-called gluten-free breads is not well understood. On the other hand, the market for gluten-free breads is growing, as diagnostic tools improve and more people are aware that they have one of the above conditions. This book chapter explains the theoretical and practical aspects of the production of gluten-free breads, cakes and biscuits. Formulations for breads from isolated starches, and from sorghum, rice, maize flours and

flour mixtures are presented and the underlying physicochemical principles explained. Literature from five decades is interpreted and supplemented with the author's own experiments. The chapter provides in-depth explanations for students and scientists with a strong theoretical interest, as well as short summaries of the most relevant facts for practical application. This information will help to spread knowledge of gluten-free bread production and will contribute to improved quality of commercial gluten-free breads, and to new markets for agricultural products such as food-grade sorghum.

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Trypsin-Like Proteins of the Fungi as Possible Markers of Phytopathogenicity

Authors: A.G. Dubovenko, Y.Y. Dunaevsky, M. Belozersky, B.S. Oppert, J.C. Lord, E.N. Elpidina

Submitted to: Mycological Research

Fungal pathogens are often very closely related to benign species that obtain nutrition from non-living material. Distinguishing between these groups is a fundamental requirement for plant protection and selection of biological control agents. From genomic databases, we obtained fungal gene sequences for trypsin, an enzyme that digests proteins. A comparison of fungal species containing trypsin-like sequences revealed that all are pathogens of plants, animals or other fungi. The results support the hypothesis that the expression of trypsins in fungi represents a specific marker of fungal pathogenicity. An evolutionary tree constructed using trypsin-like sequences demonstrated that all sequences have noticeable differences and almost immediately deviate from the common root. Therefore, we conclude that the changes that occurred in trypsins of pathogenic fungi in the course of evolution represent specific adaptations to proteins of their respective hosts, and mutations in trypsin genes permitted association with specific hosts and division into species and genera. This research will aid in selection of targets for plant protection from fungi and agents for biological control of weeds and pest insects.

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Molecular Mapping of Stem Rust Resistance Gene Sr40 in Wheat

Authors: S. Wu, M.O. Pumphrey, G. Bai

Submitted to: Crop Science

Stem rust was historically one of the most destructive diseases of wheat worldwide. Extensive use of

resistant cultivars successfully prevented rust damage over the past several decades. Recently, a new race of the stem rust pathogen called Ug99 has appeared in Africa and has defeated many existing resistance genes. Stem rust resistance gene Sr40 has been transferred from the wild wheat *Triticum timopheevii* ssp. *Armeniacum* and provides resistance against Ug99 stem rust. In this study, we identified several molecular markers for Sr40 that will be useful in marker-assisted selection for resistance.

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NIR Absorbance Characteristics of Deoxynivalenol and of Sound and Fusarium-Damaged Wheat Kernels

Authors: K.H.S. Peiris, M.O. Pumphrey, F.E. Dowell
Submitted to: Near Infrared Spectroscopy Journal

Fusarium head blight is a fungus that causes yield losses in wheat and barley, produces the mycotoxin deoxynivalenol, and affects end-use functionality. Detecting the fungus or toxin in single kernels will help breeders rapidly and objectively evaluate lines for resistance. Also, sorting kernels based on the presence of the fungus or level of toxin may help breeders select for resistance to the fungus or toxin within lines. We measured near-infrared absorption spectra of pure deoxynivalenol, and kernels with and without the toxin or fungus. Specific peaks in the pure toxin were related to those seen in infected kernels. Other differences in infected and uninfected kernels were attributed to changes in the levels of grain food reserves related to the invasion of the fungus. This information will be used to improve near-infrared calibrations used to sort single kernels based on Fusarium infection or DON levels. This work was partially funded by the US Wheat and Barley Scab Initiative and supports work by breeders to develop lines resistant to Fusarium head blight.

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Lesion Mimic Associates with Adult Plant Resistance to Leaf Rust Infection in Wheat

Authors: T. Li and G. Bai

Submitted to: Theoretical and Applied Genetics

Lesion mimics (LM) in wheat are yellowish spots that look similar to plant disease symptoms but without attack from plant pathogens. LM has been reported in many other plant species and demonstrated to increase plant disease resistance to many pathogens. Wheat line Ning7840 has adult plant resistance (APR) to leaf rust (*Puccinia triticina*) and shows LM symptoms. We identified a LM gene (*lm*) in Ning7840 and located it on chromosome 1BL. The data showed that the lines with LM had a higher rust resistance than the non-LM lines. Molecular mapping identified a gene named *Qlr.pser.1BL* for rust resistance on

chromosome 1BL. *Qlr.pser.1BL* and *lm* gene were located at the same chromosome location and showed major effects on leaf rust resistance in two greenhouse experiments, therefore *lm* from Ning7840 may have significant effects on adult plant resistance to leaf rust.

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Mapping Quantitative Trait Loci for Long Coleoptile in Chinese Wheat Landrace Wangshuibai

Authors: J.-B. Yu and G. Bai

Submitted to: Crop Science

In drought environments, longer coleoptile wheat is preferred because it can be sown deeply for better seedling establishment. Wangshuibai, a Chinese landrace, has a long coleoptile. A recombinant inbred population from a cross between Wangshuibai, and the short-coleoptile U.S. wheat cultivar, Wheaton, were used to identify genes for coleoptile length and plant height. Coleoptile length was a highly heritable trait. Six quantitative trait loci (QTL) were identified on chromosomes 1B, 3D, 4D, 5AS, and 5B for coleoptile length; four of them on 3D, 4D and 5AS also affected plant height. One QTL with a major effect on long coleoptile was mapped on the same chromosome location as gene *Rht-D1* (*Rht2*), a gene for reduced height (*Rht*) on chromosome 4DS. Another QTL with a major effect on long coleoptiles was located on chromosome 4DL. The gene *Rht-D1a* from Wangshuibai appeared to affect expression of long coleoptile QTL on 4DL. Other QTL showed only minor effects. To select long coleoptile wheat cultivars with reduced plant height, the *Rht-D1a* from Wangshuibai can be used in combination with other gibberellic acid (GA)-sensitive *Rht* genes.

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