

Our Latest Research Results - September 2012

Differential Accumulation of Deoxynivalenol in Two Winter Wheat Cultivars Varying in FHB Phenotype Response under Field Conditions

Authors: N.J. Hernandez, P.S. Baenziger, K.M. Eskridge, K.H.S. Peiris, F.E. Dowell, S.D. Harris, S.N. Wegulo

Submitted to: Canadian Journal of Plant Pathology
Fusarium head blight (FHB), or scab, is a destructive disease of small grain cereals. FHB also produces the mycotoxin deoxynivalenol (DON), which accumulates in and lowers the value and quality of grain. Field experiments were conducted from 2007 to 2009 to determine if two winter wheat cultivars accumulated DON differently. We also modeled the relationship between FHB severity and DON accumulation. The moderately resistant cultivar 'Harry' consistently accumulated more DON than the susceptible cultivar '2137'. The relationship between FHB severity and DON was linear and positive for both cultivars in all three years. Environment had a significant effect on DON accumulation in both cultivars, and this effect was attributed to differences in rainfall amount and duration in the months of May and June. DON accumulation was highest in 2008 when there was steady, above-average rainfall in May and June. FDK was highest in 2008 and was higher in 'Harry' than in '2137'. The results from this study suggest that a winter wheat cultivar with a moderately resistant FHB phenotype can be susceptible to FDK and DON accumulation. Based on these results, there is a need to standardize the criteria for characterizing wheat cultivars as resistant or susceptible to FHB.

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Detecting the Antimalarial Artemisinin in Plant Extracts Using Near-Infrared Spectroscopy

Authors: K.M. Dowell, D. Wong, X. Wu, F.E. Dowell
Submitted to: American Journal of Tropical Medicine and Hygiene

Medicinal plants have been used for thousands of years to cure many diseases, including malaria. The antimalarial artemisinin is produced by the plant *Artemisia annua* L. and can be used to cure malaria. Artemisinin is extracted from these plants through a simple tea preparation. The artemisinin content of the tea varies depending on how much of the active ingredient was present in the plant and how much

artemisinin was extracted in the tea. However, there is currently no rapid means of measuring the artemisinin content of the tea. We studied the use of near-infrared spectroscopy (NIRS) to detect artemisinin in tea extracts. Our results showed that NIRS can be used to rapidly predict the artemisinin content in tea, and the scanning procedure is simple and quick. Hundreds of samples can be prepared and scanned per day with relatively little training, and the process requires no consumables. This rapid and simple technique could be used in medical clinics to determine whether tea being prepared for patients contains enough artemisinin to be effective. This technology could also be used to study how the growing conditions of the plant affect its production of artemisinin and how different tea preparation methods affect the amount of artemisinin extracted from the plant.

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Design of a Shear-Thinning Recoverable Peptide Hydrogel from Native Sequences and Application for Influenza H1N1 Vaccine Adjuvant

Authors: H. Huang, J. Shi, J. Laskin, Z. Liu, D.S. McVey, X.S. Sun

Submitted to: Soft Matters

A self-assembling peptide was designed and synthesized by rationally combining two native sequences from an elastic segment of spider silk and a trans-membrane segment of human muscle L-type calcium channel. The peptide forms two distinct hydrogels in Ca²⁺ solution and acidic pH conditions. The shear-thinning, rapid-strength-recovering Ca²⁺ hydrogel has great potential for drug delivery and tissue engineering applications, for example, as an H1N1 influenza vaccine adjuvant.

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Allelic Variations of a Light Harvesting Chlorophyll A/B Protein Gene (Lhcb1) Associated with Agronomic Traits in Barley

Authors: Y. Xia, Z. Ning, G. Bai, R. Li, G. Yan, K. Siddique, M. Baun, P. Guo

Submitted to: PloS One

Light-harvesting chlorophyll-binding proteins (LHCP) are abundant proteins that are important for efficient photosynthesis in plants. Understanding DNA sequence variations of the LHCP genes could facilitate

improvement of barley cultivars. In this study, we analyzed nucleotide variations of a LHCP gene in 292 barley accessions collected from 35 countries. A total of 23 DNA sequence variations were detected. The levels of gene sequence diversity differed among geographic origins and species with the highest diversity in Middle East Asian accessions. Wild barley, *H. spontaneum*, showed greater sequence diversity than cultivated barley, *H. vulgare*. Five DNA sequence variations in Lhcb1 were significantly associated with at least one of the agronomic traits evaluated. The effects of the sequence variants on agronomic performance need to be tested further.

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Quantitative Trait Loci for Resistance to Fusarium Head Blight in the Chinese Wheat Landrace Huangfangzhu

Authors: T. Li, G. Bai, S. Wu, S. Gu

Submitted to: Euphytica

Fusarium head blight (FHB) is a destructive disease of wheat worldwide. The Chinese wheat landrace Huangfangzhu (HFZ) has a high level of resistance to FHB. An experiment was conducted to identify chromosomal regions that are responsible for FHB resistance in HFZ. Two quantitative trait loci (QTL) with major effects were identified in HFZ. One QTL with a large effect was located on the short arm of chromosome 3B and the other was assigned to the long arm of chromosome 7A. In addition, three QTL with small effects on FHB resistance were identified on chromosomes 1AS, 1B and 5AS of HFZ. HFZ carries several QTL for resistance and is a promising source for improving wheat FHB resistance.

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Genotyping-By-Sequencing for Plant Breeding and Genetics

Authors: J.A. Poland T. Rife

Submitted to: The Plant Genome

New DNA sequencing technologies are providing tools to understand not only the human genome but also the genomes of important crop plants. Here we describe how “next-generation sequencing” can be used for plant breeding and genetics research for inexpensive and rapid characterization of various populations of interest. This approach termed “genotyping-by-sequencing” takes advantage of next-generation sequencing capacity and can produce tens to hundreds of thousands of low-cost molecular markers. High-density markers can then be used to connect observed phenotypes (i.e. grain yield) with underlying genetic determinants. Better understanding of the genomes of crop species will lead to improved methods for prediction of important

agronomic traits, increasing the rate of gain in breeding programs.

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Genomic Selection in Wheat Using Genotyping-By-Sequencing

Authors: J.A. Poland, J.B. Endelman, J. Dawson, J. Ruthkoski, S. Wu, Y. Manes, S. Dreisigacker, J. Crossa, H. Sanchez, M. Sorrells, J.L. Jannink

Submitted to: The Plant Genome

Genomic selection (GS) is a new statistical approach that allows plant breeders to select the best breeding lines based on genome-wide DNA (molecular) markers. One important component for applying GS in breeding programs is the availability of low-cost molecular markers. In this study, we show how next-generation sequencing can be applied to a wheat breeding program to produce robust, yet inexpensive, DNA markers in an approach called “genotyping-by-sequencing” (GBS). Relative to other species, the wheat genome is very large and complex, making it difficult to generate molecular markers for breeding and genetics studies. GBS is an excellent tool for breeding purposes and DNA markers can be discovered simultaneously with assaying the whole population of interest. Further, we show that GBS markers can be used to predict the performance of breeding lines for grain yield, heading date, and thousand kernel weight. The low per sample cost of GBS will enable widespread application of GS in breeding programs. This can lead to increasing the rate of genetic gain and rapid development of new cultivars.

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