

Our Latest Research Results - August 2011

Association of Simple Sequence Repeat (SSR) Markers with Submergence Tolerance in Diverse Population of Perennial Ryegrass

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Submitted to: Plant Science

Submergence stress can cause the death of ryegrass. Genetic differences in submergence tolerance were observed among ryegrass germplasm lines. Molecular markers associated with submergence tolerance will facilitate selection of tolerant cultivars for commercial production. After 96 ryegrass lines from different origins were submerged in water for 7 days, their leaf color, chlorophyll fluorescence (Fv/Fm), maximum plant height (HT), and relative growth rate (RGR) were significantly reduced. However, significant variation in these traits was observed among accessions. Marker analysis identified four subpopulations in the collection. Fifteen DNA markers were associated with reduction in green color, Fv/Fm, HT, and RGR. The identified submergence-tolerant germplasm and markers should be useful for genetic improvement of submergence tolerance of perennial ryegrass.

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Quantitative Trait Loci for Resistance to *Fusarium* Head Blight in a Chinese Wheat Landrace Haiyanzhong

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

Submitted to: Theoretical and Applied Genetics
Fusarium head blight (FHB) of wheat, also called scab, can significantly reduce grain yield and end-use quality. Infected grain can be contaminated with mycotoxins that are harmful to human and animal health after consumption of infected grain. Growing resistant cultivars is an effective approach to minimize the FHB damage. The Chinese wheat landrace Haiyanzhong (HYZ) shows a high level of resistance to FHB. We identified four genes for FHB resistance in HYZ with one gene showing a large effect on FHB resistance from chromosome 7D. DNA markers closely linked to the gene were identified. Four other genes having smaller effect on FHB resistance were located on the short arms of chromosome 6B (two genes), 5A and 1A. HYZ carries different resistance genes from those identified in Chinese resistant cultivar Sumai 3 and adds genetic diversity to the Asian FHB resistance gene pool.

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Association Study of Resistance to Soil-Borne Wheat Mosaic Virus (SBWMV) in U.S. Winter Wheat

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Submitted to: Phytopathology

Soil-borne wheat mosaic virus (SBWMV) disease can cause significant yield losses of winter wheat. To identify genes for resistance to the disease in U.S. winter wheat, a selected set of 205 elite U.S. winter wheat experimental lines and cultivars was evaluated for virus symptoms at Manhattan, KS and Stillwater, OK. About 67% of lines showed at least moderately resistant reactions to the disease at the two locations. Association analysis identified one major gene for SBWMV resistance on the long arm of chromosome 5D. We suggested that it is the gene previously reported for soil borne cereal mosaic virus resistance. In addition, a gene on the short arm of chromosome 4D was also associated with disease resistance. Markers linked to the two genes should be useful in marker-assisted selection in U.S. winter wheat.

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Chromosome Size in Diploid Eukaryotic Species Centers on the Average Length with a Conserved Boundary

Authors: X. Li, C. Zhu, Z. Lin, Y. Wu, D. Zhang, G. Bai, W. Song, J. Ma, G. Muehlbauer, M. Scanlon, M. Zhang, J. Yu

Submitted to: Molecular Biology and Evolution

Chromosomes are the basic unit for control of inheritance and evolution of living organisms. Although huge variation in chromosome number and size has been observed among organisms, knowledge of genome and chromosome evolution is important for understanding inheritance and evolution of these organisms. Using available genome sequence information, we show that chromosomes within a species do not change dramatically in their content of mobile genetic elements as the production of these elements increases from unicellular eukaryotes to vertebrates. Actually, variation in chromosome size in diploid eukaryotes with linear chromosomes has an upper limit. A single model can describe the variation in chromosome size for 886 chromosomes of 68 eukaryotic genomes. This model predicts that length (in base pairs) of the majority of chromosomes in a species is expected to range from 0.4035 to 1.8626 times the average chromosome length. This boundary of chromosome size

variation is very conservative and fits a wide taxonomic range with only few exceptions. The results indicate that cellular, molecular, and evolutionary mechanisms, possibly together, confine the chromosome lengths around a species-specific average chromosome length. The research contributes novel knowledge for understanding the role of chromosome size variation in species evolution.

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'Duster' Wheat: A Durable, Dual-Purpose Cultivar Adapted to the Southern Great Plains of the USA

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Submitted to: Journal of Plant Registrations

A new wheat cultivar 'Duster' has been developed. Since its release in 2006, Duster has gained broad acceptance in the US southern Great Plains region with a definitive grain yield advantage and added dough strength. Other important agronomic traits of Duster include aluminum tolerance; effective levels of resistance to diseases including soilborne mosaic, spindle streak mosaic, leaf rust, and stem rust; and high levels of seedling resistance to Hessian fly biotype GP. Duster is susceptible to Fusarium head blight. Duster was selected from a double cross, W0405/NE78488//W7469C/TX81V6187, made in 1987 within the former HRW wheat breeding program of Pioneer Hi-Bred International, Inc. Neither Duster nor its immediate parents are known to have a sib-pair or parent-offspring relationship with cultivars currently in production in the Great Plains.

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Adhesive Performance of Sorghum Protein Extracted from Sorghum DDGS and Flour

Authors: N. Li, Y. Wang, M. Tilley, S. Bean, X. Wu, X. Sun, D. Wang

Submitted to: Journal of Environment and Polymers

About 20 billion pounds of adhesives and resins are used annually in the United States in plywood, particleboard, lamination, and various composites for construction, packaging, furniture, etc. These adhesives are derived mostly from petroleum-based chemicals, however, due to finite petroleum resources, non-uniform distribution of these resources, volatile prices and environmental concerns, the adhesive industry is increasingly interested in bio-based adhesives. We therefore investigated the use of sorghum proteins extracted from distillers dried grains with solubles (DDGS), which is the main co-product from grain-based ethanol production. Our results showed that sorghum

proteins extracted from DDGS using acetic acid had the best adhesion performance. Furthermore, the wet strength of adhesives made from these sorghum proteins was better than that of unmodified soy proteins. These results indicated that sorghum protein has huge potential as an alternative to petroleum-based adhesives.

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Prediction of Kernel Density of Corn using Single-Kernel Near Infrared Spectroscopy

Authors: P. Armstrong, J. Tallada

Submitted to: Computers and Electronics in Agriculture
Corn hardness is an important property for dry and wet-millers, food processors and corn breeders developing hybrids for specific markets. While several methods are used to measure hardness, kernel density provides one of the most repeatable methods to quantify hardness. Near infrared spectroscopy (NIRS) provides an attractive method to measure kernel density as it is non-destructive and can also measure other kernel attributes that may be related to processing the grain or hybrid development. Currently, some commercial NIRS instruments do measure density of bulk samples. Single-seed NIRS, however, may provide additional information and capabilities by measuring single kernels. This has potential applications for breeders or quality control personnel wishing to look at variability within samples and for sorting. This study found that NIRS could roughly determine density of corn samples by averaging single kernel values and that sorting individual samples into high and low density fractions was possible. The latter may be particularly useful for breeders wishing to increase hybrid kernel densities.

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