

Our Latest Research Results - October 2010

Genetic Diversity, Population Structure and Linkage Disequilibrium in U.S. Elite Winter Wheat (*Triticum Aestivum* L.)

Authors: D. Zhang, G. Bai, C. Zhu, J. Yu, B. Carver
Submitted to: The Plant Genome

Knowledge of genetic diversity and population structure of elite wheat breeding lines facilitates effective use of limited resources. We analyzed 205 wheat-breeding lines from major winter wheat breeding programs in the U.S.A. using 245 molecular markers across the wheat genome. We found that US winter wheat breeding lines had a high level of genetic diversity. Breeding activities did not reduce the genetic diversity of modern breeding materials due to extensive exchange of materials among breeding programs and introduction of new genes from different sources. All 205 lines can be statistically divided into two major groups, soft verse hard wheat. Hard wheat can be further divided into three subgroups. Hard wheat appeared to be more diverse than soft wheat in this study. The extent of linkage disequilibrium (LD) was highly variable throughout the genomes, but was mainly distributed around centromere regions. Our results on genetic diversity and LD distribution of breeding materials facilitate the effective use of genetic resources for wheat breeding and the choice of markers in gene mapping and marker-assisted breeding.

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Dissection and Fine Mapping of a Major QTL for Preharvest Sprouting Resistance in White Wheat Rio Blanco

Authors: S. Liu, G. Bai

Submitted to: Theoretical and Applied Genetics
Pre-harvest sprouting (PHS) refers to seed germination in a mature wheat spike due to a long period of wet weather. Sprouted wheat grain usually has poor end-use quality. Previously, we identified one quantitative trait locus (QTL), QPhs.pseru-3A, for PHS resistance in white wheat Rio Blanco. This QTL significantly reduced PHS. We found three molecular markers in the QTL region. In this study, we further narrowed down the QTL to a smaller chromosome fragment by developing a new fine-mapping population that segregated only in the chromosome region containing the three markers. The result indicated the QTL in 3A showed single-gene inheritance with partial dominance. Near-isogenic lines (NIL) that differ in having the 3A QTL have been isolated. A high-resolution map in the 3A QTL region was constructed by adding 11 new AFLP markers. This work laid a solid foundation for cloning this gene for

sprouting tolerance. This eventually may lead to future cultivars with higher levels of sprouting tolerance.
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An Experimental Host Range of Triticum Mosaic Virus

Authors: D. Seifers, T.J. Martin, J.P. Fellers
Submitted to: Plant Disease

Triticum mosaic virus (TriMV) was recently discovered in Kansas and isolated from wheat. Prior to this study, it was not known how many different hosts TriMV could infect. It is important to understand the host range for several reasons. First, we need to know what other crops may be at risk of infection and may require breeding efforts to find resistance. Second, if there are other susceptible grass species that reside near fields of wheat, they may act as the source for virus infection and may require control strategies to minimize risk. In this report, TriMV was found to infect barley, oat, rye, and triticale, but not maize or sorghum. It was also found that certain barley and triticale accessions were hosts of TriMV, and not Wheat streak mosaic virus, which is sometimes found to co-infect with TriMV. Many of the grass species were not hosts of TriMV, however, jointed goat grass, three of the brome species, two cupgrasses, green foxtail, and wild oats were susceptible. As some of the species were only susceptible to TriMV and not WSMV, they can be useful in efforts to purify TriMV from a mixed infection.

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Control of Dissected Leaf Morphology by a Cys(2)His(2) Zinc Finger Transcription Factor in the Model Legume *Medicago truncatula*

Authors: J. Chen, J. Yu, L. Ge, H. Wang, A. Berbel, Y. Liu, Y. Chen, G. Li, M. Tadege, J. Wen, V. Cosson, K.S. Mysore, P. Ratet, F. Madueno, G. Bai, R. Chen
Submitted to: Proceedings of the National Academy of Science

As the primary organ for photosynthetic carbon fixation, plant leaves play an important role in plant growth, biomass production and survival in the environment. Plant leaves show great differences in their morphology, which contribute to the diversity of plant types in the natural environment. How different leaf morphologies are determined is not yet understood. *Medicago truncatula* is a legume plant species and its leaf consists of three blades (leaflets). We demonstrate that development of

the leaves with three leaflets is determined by a gene called PALM1 that produces a transcription factor. A plant with nonfunctional PALM1 develops dissected leaves with five leaflets. This basic research could eventually lead to forage crops with higher leaf to stem ratios and thus higher feed value.

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Sequence Analysis of Triticum Mosaic Virus Isolates From Field Surveys of Infected Wheat

Authors: I. Fuentes-Bueno, J. Price, C. Rush, D. Seifers, J.P. Fellers

Submitted to: Phytopathology

In 2006, a new virus was isolated in Western Kansas from the cultivar RonL. The virus was named Triticum mosaic virus (TriMV) and analysis showed that it was a very unique virus. The genome was sequenced, compared to other viruses, and no other virus is like TriMV in nucleotide or amino acid sequence. Since its discovery, TriMV has been found from Wyoming to Texas. This study was undertaken to determine how variable the virus is in terms of its nucleotide sequence. The coat protein gene from fourteen TriMV isolates from Texas, Oklahoma, and Kansas were sequenced and only thirteen changes were found in the gene. As is often the case, Wheat streak mosaic virus (WSMV) was also found in the same plants as TriMV. This study also looked at the coat protein gene of WSMV isolates within the same samples. Sixty-five nucleotide differences were found. This study shows that TriMV appears to be genetically very stable, while WSMV is very variable.

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Variation and Transgression of Aggressiveness among Two *Gibberella zeae* Crosses Developed From Highly Aggressive Parental Isolates

Authors: H.-H. Voss, R.L. Bowden, J.F. Leslie, T. Miedaner

Submitted to: Phytopathology

The fungus *Gibberella zeae* (also known as *Fusarium graminearum*) is the most common cause of Fusarium head blight (FHB) of wheat worldwide. Aggressiveness is the most important fungal trait affecting disease severity and stability of host resistance. We made two genetic crosses between aggressive strains and collected the progeny of the crosses. We found that aggressiveness segregated among the progeny and that some progeny were more aggressive than either parent. This suggests that aggressiveness is controlled by many genes and that *G. zeae* may, therefore, adapt nonspecifically to increased quantitative host resistance.

Breeders and pathologists will need to be vigilant for the possible erosion of current genetic resistance to this disease.

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A Versatile SERS-Based Immunoassay for Immunoglobulin Detection Using Antigen-Coated Gold Nanoparticles and Malachite Green-Conjugated Protein A/G

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Submitted to: Biosensors and Bioelectronics

A novel nanoparticle system was developed for detection of specific antibodies in serum. The system utilizes gold nanoparticles coated with a West Nile virus protein and a specific type of dye bound to a protein A/G molecule that interacts with antibodies. When the specific antibody is present in a solution with the gold nanoparticles and the dye-bound protein A/G then a signal can be detected using a relatively inexpensive instrument that detects the surface enhanced Raman scattering (SERS). The sensitivity and inherent versatility of the assay, which is provided by the binding of pA/G to a broad spectrum of immunoglobulins in different mammalian species, suggests that it could be developed as an alternative immunoassay format to the ELISA.

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