

Brachypodium distachyon: a new model to study Triticeae genomes.

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Brachypodium distachyon (*Brachypodium*) is being developed as a new model organism for structural and functional genomics of temperate grasses because of its several desirable attributes for plant biology research, such as easy growth requirements, small stature, short generation time, and small genome size. With the recent completion of the *Brachypodium* genome sequence, along with the established *Agrobacterium*-mediated, high-efficiency transformation system for T-DNA insertional mutagenesis and other genomics resources, tools are now available for exploiting the utility of *Brachypodium* in facilitating wheat research. Comparative mapping of several disease resistance genes indicated that wheat retains colinearity of disease gene orthologs with *Brachypodium*. Such colinearity is not present between wheat and rice, suggesting that *Brachypodium* will be more useful in map-based cloning of rapid or recent evolving genes such as wheat resistance genes. Higher colinearity between wheat and *Brachypodium* also is observed in genomic regions harboring wheat prolamin genes. Expression of wheat promoters and genes in *Brachypodium* provides direct evidence supporting the usefulness of *Brachypodium* in functional characterization of important genes or traits of wheat. A collection of over 6,000 T-DNA insertional mutant lines is now available for public access at website <http://brachypodium.pw.usda.gov/TDNA/>. These lines are indexed through flanking sequence tags that facilitate mapping of the T-DNA insertions within the *Brachypodium* genome. Several other useful websites for comparative and functional *Brachypodium* genomics will also be discussed.

SESSION V: EARLY CAREER SCIENTISTS***Identification of a novel QTL for Fusarium head blight resistance on wheat chromosome 7A.***

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Fusarium head blight (FHB), caused by *Fusarium graminearum*, is an important cereal disease worldwide. Resistance to disease spread within a spike (type II) is the more stable type of resistance. A previous study identified a Chinese Spring (CS)–Sumai 3 chromosome 7A substitution line having a high level of type-II resistance, but an associated quantitative trait locus (QTL) on 7A has never been reported. In this study, we developed CS–Sumai 3 7A chromosome recombinant inbred lines (CRIL) from a cross between CS and CS–Sumai 3 7A disomic substitution lines. A genome-wide marker analysis with 72 chromosome-specific simple sequence repeats (SSR) confirmed that entire 7A chromosome and a small fragment from chromosome 3BS were from Sumai 3 and all other chromosomes were from CS. A total of 191 F₅ CRIL were evaluated for type-II, FHB resistance using single-spikelet inoculation in 2009. The proportion of symptomatic spikelets (PSS) for each CRIL was calculated to measure FHB resistance. The frequency distribution of PSS was bimodal, ranging from 6% to 84%. Out of 75 SSR markers screened from chromosome 7A, 33 were polymorphic and only 7 of 30 SSR markers and 30 sequence tagged sites from 3BS chromosome were polymorphic. The linkage maps for chromosome 7A spans a distance of 181.7 cM and for 3BS, over 2 cM. Composite interval mapping feature of QGene software was used for QTL mapping with a LOD score threshold of 2.0 ($P < 0.005$) to claim a significant QTL based on 1,000 simulations. A new, major QTL for type-II FHB resistance was detected on the short arm of chromosome 7A with a LOD score of 11, flanked by markers *Xwmc17* and *Xwmc9*. FHB1, a previously reported major QTL on 3BS, also was detected in this study. Both QTL explained 24% (7A) and 45% (FHB1) of the phenotypic variation. An additive effect was observed between the two QTL. Replacement of both alleles of CS with these of Sumai 3 resulted a 66 % reduction in disease severity. Therefore, the QTL from CS 7A is a new major QTL for FHB resistance and can be used for enhancing FHB resistance in breeding.