IN THIS SECOND 2011 ISSUE of The Plant Genome, we are introducing a new article type called Original Research: Genomic Resources. Genomic Resources articles will report on all forms of resources that further plant genomics research including but not limited to genetic materials (lines, collections, populations), libraries, genomics services, software developments and many others. Please use your imagination to help us expand the types of genomics resources that will significantly advance genomics research by being published in The Plant Genome. The article format, review, and processing will be the same as for Original Research articles. Review and acceptance criteria for Genomic Resources articles will be based on the novelty of the resource, its usefulness and/or impact on genomics research either in a specific area or broadly impactful, and that it is available to other researchers upon request to the corresponding author.

Our first Original Research: Genomic Resources article in this issue is “Cytological and Molecular Characterization of Homoeologous Group-1 Chromosomes in Hybrid Derivatives of a Durum Disomic Alien Addition Line” by Prem P. Jauhar and Terrance S. Peterson. I want to thank Dr. Jauhar for providing a brief description of the context for his work and the potential impact of the resource that was developed. We look forward to receiving more Genomics Resource articles in The Plant Genome.

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Improving Resistance to Scab in Durum Wheat

Allopolyploidy – with multiples of divergent genomes resulting from interspecific or intergeneric hybridization – has played a dominant role in speciation. Several of our crop plants have resulted through this mechanism. Because they contain genomes from related species, a regulatory mechanism is essential for their meiotic and reproductive stability. Durum wheat, *Triticum turgidum* L. (2n = 4x = 28; AABB genomes), the forerunner of bread wheat *Triticum aestivum* L. (2n = 6x = 42; AABBD genomes), offers an excellent example of evolution via allopolyploidy. Because the chromosomes of the A and B genomes are closely related, development of a genetic control of chromosome pairing in the form of the *Ph1* gene in the long arm of chromosome 5B was essential to enforce regular, diploid-like pairing in durum wheat.

The *Ph1*-regulated chromosome pairing also makes chromosome engineering feasible. Diploid wild grasses, for example, are rich reservoirs of useful genes that can be used in the genetic enrichment of polyploid wheats. Diploid wheatgrass, *Lophopyrum elongatum* (Host) Å. Löve (2n = 2x =14; EE), is an excellent source of Fusarium head blight (FHB) resistance. Desirable chromatin of this grass can be fruitfully used in chromosome engineering and genomic reconstruction of durum wheat. And the *Ph1* gene helps in this process.

Crossing this grass with durum wheat followed by a series of backcrosses resulted in a durum disomic addition line, DGE-1, with the grass chromosome 1E added in double dose that conferred enhanced FHB tolerance to DGE-1. The next strategy is to transfer this FHB resistance from the alien chromosome 1E into one of
the durum chromosomes in the homoeologous group-1, i.e., 1A or 1B. It is, therefore, important to have the homoeologous chromosomes 1E, 1A, and 1B in the same cell and then create appropriate conditions for pairing and segmental exchange between 1E and 1A, and 1E and 1B by manipulation of the \( Ph1 \)-system, e.g., by using its mutant allele \( ph1b \) or \( ph1c \).

Such a genomic reconstruction through chromosome engineering brought about by manipulation of the \( Ph1 \) system has far-reaching implications in both basic and applied research in wheat. New genomic resources result from chromosome engineering.