these genes in *5AQ* compared to *5AQm* and *5Aq*, demonstrating the role of *Q* in regulating gene networks associated with wheat development. Homoeologous copies of *Q* exist on chromosomes 5B and 5D, but their functions are less understood. Phenotypic analysis of genetic stocks with various combinations of *Q* homoeoalleles indicated that *5Bq* and *5Dq* also contributed to the suppression of speltoid characters and glume toughness, but to a lesser degree than does the *5AQ*. An RQ-PCR study showed that *5Bq* and *5Dq* are transcriptionally active, but *5Bq* is a pseudogene. Combined phenotypic and expression analysis indicated the presence of complex interactions among the homoeoalleles. The evolution of the *Q*/*q* loci in polyploid wheat resulted in the hyperfunctionalization of the master regulator *5AQ*, pseudogenization of *5Bq*, and subfunctionalization of *5Dq*, but all are finely tuned in a coordinated manner to govern domestication and development in polyploid wheat.

Poster 29. Molecular mapping of Brittle rachis (Br-A1) gene in Triticum timopheevii.

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Free shattering at maturity is an important strategy in plants for seed dispersal in nature. Domestication of wheat in the Bronze Age occurred mainly due to two important evolutionary changes, namely the loss of rachis fragility at maturity and evolution of free threshability. The *Brittle rachis* (*Br1*) gene located on homoeologous group-3 chromosomes controls rachis fragility in wheat and barley. In *Triticum timopheevii* subsp. *armeniacum* (A^tA^tGG genomes, 2n=4x=28), characteristic wedge-type disarticulation occurs due to the formation of abscission zone at the base of the spikelets making them spear shaped dispersal units at maturity. Mapping of the A^t-genome, brittle rachis gene (*Br-A^{t}1*) was done in a recombinant inbred line (RIL) population of tetraploid *T. timopheevii* subsp. *armeniacum* and *T. timopheevii* subsp. *timopheevii*. The RIL population segregated 62 brittle and 73 tough rachis, fitting the monogenic segregation ratio of 1:1. Nine out of a total of 72 BAC-end derived markers from wheat 3AS BAC library and 8/24 SSRs from the publically available databases were found to be polymorphic between the parents. The gene was mapped to a 7.4-cM region on short arm of chromosome $3A^t$ flanked by microsatellite markers *Xgwm2* and *Xbem44*. Previously this gene was located in a 35-cM region on chromosome $3A^tS$ between RFLP markers *XksuA6* and *Xpsr1196*. The *T. timopheevii* subsp. *armeniacum Br-A^{t}1* gene may be orthologous to the hexaploid wheat *Br1* locus. Five recombinants were found in the RIL population for these two markers, and 30 recombinants for the closest markers were found in a set of 355 individuals of $F_{2:3}$ families segregating for *Br-A^{t}1*. Heterogenous inbred families from the recombinants for the closest flanking markers are being used for fine mapping. Primers are being designed, tested, and mapped from syntenous regions of rice chromosome 1 and *Brachypodium* chromosome 2. Resources available for chromosome 3A sequencing will be used for the fine mapping and cloning.

Poster 30. Metabolic, physiological, and molecular characterization of cuticular variation in wheat.

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All the aerial organs of land plants are covered with a layer of hydrophobic lipids, termed the cuticle. It plays important roles in development, growth, and defense against biotic and abiotic stresses. Structurally, the cuticle consists of a cutin frame, with intracuticular wax embodied in and an epicuticular wax overlaid on them. A field of densely distributed, epicuticular wax crystals is visible as bloom or glaucousness. In wheat, variation of glaucousness is mainly controlled by wax-production genes *W1* and *W2*, and wax-inhibition genes *Iw1* and *Iw2*. *W1* and *Iw1* are located on the short arm of chromosome 2B (2BS), and *W2* and *Iw2* are on 2DS. Although early field studies showed glaucousness played an important role in drought and heat tolerance, little is known about the molecular mechanisms and metabolic products of these wax genes. We are characterizing a set of six wax near-isogenic lines (NILs) in an S-615 background by combining the genetic, metabolic, physiological, and molecular approaches. Wax profiling by GC-MS indicated that the wax load and composition vary greatly among the NILs. The *Iw2*-NIL has highest wax load, followed by *Iw1*-NIL, S-615, *W2*-NIL, *W1*-NIL, and *w*-NIL. Wax profiles suggested that (1) gene *W2* plays an important role in decarbonylation pathway for n-