Variations in patterns of gene expression are central to evolution. A large-scale screen of barley germplasm has identified an alternative de-repressor of lodicule development SV235. The relevant *HvAP2* coding sequence is identical to that of *cly1.b*, so that *HvAP2* down-regulation is not associated with miR172-directed degradation; instead, transcriptional repression appears to be induced by the maintenance of the *HvAP2* promoter in a hyper-methylated state during the period when the vascular tissue in the lodicule would normally develop. The cleistogamous type can also arise in the presence of non-cleistogamous type lodicule development. In certain *Cly1.a* x *cly1.b* hybrids, the spikes remain within the boot during anthesis, and the lodicules remain shrunken even after the emergence of the spike from the boot.

Genetics and molecular evolution of a 3.1-Mb genomic region harboring both wheat prolamin and disease resistance gene families.

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Several important wheat prolamin and disease resistance gene loci have been mapped at similar locations in the short arm of the group-1 chromosomes in wheat. However, genetics and structural organization of genomic regions harboring these important traits have not been well characterized. We therefore sequenced a 3.1-Mb region harboring prolamin multigene families in the genome of *Ae. tauschii*, the D-genome donor of hexaploid bread wheat. The sequence revealed a much higher gene density (98 genes; one gene/31 kb) in the sequenced region than the average value (ca. one gene/112 kb) expected for the wheat D genome. The high gene density is primarily due to the large number of duplicated genes, present either in tandem or interspersed with other genes. In addition to different types of prolamin gene families (γ-gliadin, ω-gliadin, and LMW-glutenin), multiple NBS-LRR disease resistance gene homologues of *Lr21* (resistance to leaf rust) and *Pm3* (resistance to powdery mildew) were identified. Furthermore, leucine-rich receptor protein kinase (LRK) genes, representing a different class of resistance genes, also were highly duplicated in this region. Comparative analyses indicated that the orthologous regions in the rice, *Brachypodium*, and sorghum genomes are highly conserved, whereas in *Ae. tauschii*, only 16 out of 98 genes are syntenic. Most of these highly duplicated genes are unique in the *Ae. tauschii* genome, suggesting rapid evolution in this region. Genetic analysis revealed the sequenced region spanned over 10-cM genetic distance with 13 markers mapped to this region. Recombination rates ranged from ca. 200 to 1,000 kb/cM between two marker intervals. Both co-evolution and independent evolution in different gene families were observed. Mechanisms underlying the molecular evolution of prolamin and resistance gene families in this complex region will be presented.

SESSION V: YOUNG TRITICEAE RESEARCHERS

Genetic provenance and genetic providence in a diverse crop.

Ana M. Gonzales and Peter L. Morrell. Department of Agronomy and Plant Genetics, University of Minnesota, St. Paul, MN, USA.

Multiple factors converge to contribute to high levels of genetic and phenotypic diversity in barley. The progenitor species is ecotopically and genetically diverse, with a large geographic range and large effective population size. Cultivated barley arose from multiple source populations and became adapted to diverse agronomic conditions across much of Eurasia and North Africa over several millennia of human prehistory. Exploiting this diverse adaptive history for barley improvement is challenging if methods are limited to top-down approaches based on genotype-phenotype associations. A new generation of bottom-up approaches provides the opportunity to investigate the genetic differentiation and genetic provenance of adaptive allelic variation and associations between SNPs and ecogeographic variables. Both sets of approaches provide new opportunities for associating genetic variation with phenotypic traits of agronomic importance, including disease resistance and climate adaptation. We make use of genotyping data from 2,417 worldwide barley accessions from the USDA National Small Grains Collection (landraces and cultivars) genotyped with 7,800 SNPs.

We seek to identify the geographic regions that best explain the diversity in domesticated barley and associate genes or genomic regions with diverse environmental conditions.

Molecular tools and genetic resources for eyespot resistance in wheat.

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Eyespot is an important stem base disease of wheat caused by two species of fungi, *Oculimacula yallundae* and *Oculimacula acuformis*, both of which are widespread in northern Europe and the Pacific northwest USA. There are two main sources of resistance available; *Pch1*, a potent resistance gene introduced from *Aegilops ventricosa*, and the moderate resistance of the variety Cappelle Desprez.

Pch1 has not been used widely in European wheat varieties due to linkage between *Pch1* and yield-limiting genes. Breaking this linkage has proven difficult because of a low recombination frequency and a lack of molecular markers that function in both wheat and *Ae. ventricosa*. Utilising the *Brachypodium* genome sequence, we developed co-dominant Conserved Orthologous Sequence (COS) markers targeted to the *Pch1* region. These markers were used to identify recombinants and to locate *Pch1* on chromosome 7DL. By exploiting co-linearity between *Brachypodium*, rice and sorghum, we identified a candidate gene region as a prelude to the map-based cloning of the gene.

Resistance in Cappelle Desprez has been attributed to the partial resistance gene *Pch2*. We mapped *Pch2* resistance to *O. acuformis* as a QTL on the distal end of chromosome 7AL. However, it was not possible identify any resistance to *O. yallundae*. This indicates that *Pch2* operates specifically against *O. acuformis*, and that *Pch2* should not be relied upon as a stand-alone resistance in wheat varieties.

There is previous evidence of an adult-plant resistance on chromosome 5A of Cappelle Desprez. We showed this resistance to also be effective in seedlings and to provide protection against both pathogen species, indicating that it will be useful in commercial varieties. Two chromosome 5A recombinant populations were tested in seedling bioassays and field trials to locate a stable resistance QTL on 5AL and identify linked SSR markers for selection of the resistance.

In addition to characterising existing eyespot resistances, we screened 1,036 hexaploid genotypes from the Watkin's Worldwide Collection for resistance to *O. yallundae*. Some accessions exhibited a high level of resistance. Selected lines will be screened for resistance to *O. acuformis* and the genetic basis of any novel resistances will be determined.

Wheat Zapper, Illumina BSA, and radiation hybrids for synteny analysis of the scs region.

Filippo M. Bassi [1], Yi Wang [2], Monika Michalak de Jimenez [1], Kristin Simons [1], Kerrie L. Forrest [3], Stephan L. Kong [3], Raed Seetan [4], Loai Alnemer [4], Rissa Dizon [1], Hana Simkova [5], Jaroslav Doelzel [5], Farhad Ghavami [1], Anne Denton [4], Jan Dvorak [6], Ming-Cheng Luo [6], Yong Gu [2], Matthew J. Hayden [3], and Shahryar F. Kianian [1].

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Species cytoplasm specific (*scs*) genes are of great evolutionary importance because they guide the precise interaction between nucleus and cytoplasm. Recently, an *scs* gene of wheat (*Triticum* species) was localized to the pericentromere of chromosome 1DL. In an attempt to clone this gene, we generated a radiation hybrid (RH) *in vivo* population of ~1,500 individuals. EST-based markers were developed and used for genotyping the whole 1D chromosome. An online tool was developed to easily and rapidly study the colinearity between wheat and three sequenced plant species (*Sorghum bicolor*, *Brachypodium distachyon*, and *Oryza sativa*), namely the Wheat Zapper (http://wge.ndsu.nodak.edu/wheatzapper/). Employing this tool, together with functional analysis of the RH lines, we determined that the *scs* region corresponds to a region of paleofusion between two ancestral chromosomes corresponding to the modern Sb9-1, Bd3-2, or Os10-5. To