

W014: DNA Zoo**DNA Zoo China**

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W015: DNA Zoo**Convergent Evolution of Social Behavior in Sweat Bees**

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Natural variation can help us understand how ecological and evolutionary dynamics shape complex traits. Halictid bees or 'sweat' bees harbor extraordinary variation in social behavior. In this group, eusociality has evolved independently 2-3 times, and variation among species encapsulates nearly all forms of social structure from solitary to eusocial. To identify the genetic factors associated with the evolution of social behavior in this group, we have generated genomic resources for 19 halictid species that encompass all of the well characterized gains and losses of eusociality within this family. This enables an integrative examination of the link between the proximate mechanisms underlying variation in social behavior and the ecological processes driving their evolution. We searched for signatures of convergent evolution in this group using relative evolutionary rates on both coding and non-coding sequence. In general, we find that the evolution of social behavior is primarily associated with changes in non-coding sequence. These putatively regulatory, non-coding elements are highly enriched for proximity to genes involved in behavior and nervous system functioning, including several previously implicated in social evolution in distantly related taxa.

**W016: EBI/IWGSC: Annotation of Gene Families in Animal and Plant Genomes
New Opportunities for Efficiently Studying the Complex Glutenin and Gliadin Genes to Aid the Enhancement of Wheat End-Use Traits**

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Wheat (*Triticum aestivum* L.) is the most widely cultivated staple crop on Earth, and provides about 20% of the food calories and proteins consumed by human. Glutenins, composed of high- and low-molecular weight glutenin subunits (HMW-GSs and LMW-GSs), and gliadins, consisted of alpha-, gamma-, delta- and omega-types, are two major families of storage proteins in wheat seeds. They account for approximately 40% and 50% of the total wheat flour proteins, respectively. Consequently, variations in the quantity and composition of glutenins and gliadin genes have strong impact on the end-use quality and nutritional value of wheat food products, and better understanding and proper manipulation of these genes are critical for developing wheat cultivars with desired end-use traits. However, it has been difficult to precisely and rapidly elucidate the complements of glutenins and gliadin genes, especially those encoding LMW-GSs and various types of gliadins, in desired wheat genotypes. This is because these genes are located in large and complex chromosomal loci, and exhibit strong allelic variations among different wheat genotypes. Copy number changes, single nucleotide polymorphisms and indels of various sizes can all contribute to the allelic variations of glutenin and gliadin genes. Furthermore, there exists transcriptional regulation, which results in differences in mRNA abundance among different glutenin and gliadin genes. Nevertheless, the efficiency in studying glutenin and gliadin genes is expected to rise because of the accumulation of high-quality genomic information for hexaploid wheat, tetraploid wheat and their diploid progenitors since 2017. The availability of rich genomic information, plus the application of complementary functional genomics tools, will stimulate a new phase of molecular studies on glutenin and gliadin genes with the aim to enhance wheat end-use traits. In this presentation, we will report our efforts in dissecting the composition and function of glutenin and gliadin genes in elite Chinese winter wheat cultivars and the application of resultant genetic resources in improving breadmaking quality. We suggest that, although the reference genome sequence information generated for various wheat species is very helpful, genotype-specific efforts are still needed for precisely and efficiently revealing the glutenin and gliadin genes in specific wheat varieties.

**W017: EBI/IWGSC: Annotation of Gene Families in Animal and Plant Genomes
The Gene Networks Involved in Wheat Drought Response**

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Wheat can adapt to most agricultural conditions across temperate regions. Although drought is a major cause of yield and quality losses, the adaptive mechanisms and gene networks underlying drought responses in the field remain largely unknown. Interdisciplinary studies involving field water status phenotyping now provide a basis for interpreting gene expression analyses and show that changes at the transcriptional level were reflected in the remote sensing physiological data from the field. The dehydrin family of genes provided a focus for the study and indicated that the genes located on the group 6 chromosomes were particularly important in drought response.

**W018: EBI/IWGSC: Annotation of Gene Families in Animal and Plant Genomes
Annotation of Animal and Plant Genomes**

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W019: Fruit Trees: Genomics and Molecular Genetics**The Genetic Basis of Domestication and Improvement in Pear**

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Pear is a globally grown fruit, with thousands of cultivars in five domesticated species and dozens of wild species. However, little is known about the evolutionary history of these pear species, and knowledge of the genetic changes that occurred during the domestication and improvement is limited. Recently, we report the genome resequencing of 113 pear accessions from worldwide collections, representing both cultivated and wild pear species. Based on 18,302,883 identified SNPs, we conduct phylogenetics, population structure, gene flow, and selective sweep analyses. Furthermore, we propose a model for the divergence, dissemination, and independent domestication of Asian and European pears. Meanwhile, RNA-seq analysis was used to compare representative sets of wild, landrace, and improved accessions of sand pear (*Pyrus pyrifolia*) to gain insight into the genetic changes associated with domestication and improvement. The expression diversity of selected genes exhibited reduction from the wild group to the landrace group, but a recovery was observed from the landrace to the improved group, showing a distinctly different pattern with variation of DNA sequence diversity. In addition, separate selective sweep signatures, combined with co-localized QTLs and differentially expressed genes, underline distinct phenotypic fruit traits, including fruit size, flesh texture, sugar, acidity, aroma, and stone cells. Thus, our study reveals the specific pattern of domestication and improvement of perennial trees at the DNA and transcriptome level, which provides substantive and valuable genetic resources that will significantly advance pear improvement and molecular breeding efforts.