Poster 24. High-throughput sequencing to assess the microbial diversity in Hessian fly.

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Recently, oceans and soils have been explored for their large unknown microbial genomic resources. Insects could prove another avenue for genomic innovations as majority of insects are known to harbor the symbionts. The objective of this work was to estimate the microbial diversity associated with the Hessian fly, a serious pest of wheat, using 454 pyrosequencing. Insect fat body and midguts from three different larval stages were dissected out. Following DNA extraction, the V3, the most hypervariable region (corresponding to positions 341-534 in *E. coli*) of the 16S rRNA gene was amplified and sequenced. These 454 tag sequences (total of ~6,000) served as query against reference database (V3RefDB) and the phylotype assignments were made according to V3RefDB sequences that display the minimum distance to the query. The most abundant group associated with Hessian fly is γ-*Proteobacteria* followed by β-*Proteobacteria* and *Bacteroidetes*. For assignment of similarity based operational taxonomic units (OTUs), sequences were aligned and distance matrices were calculated by using ARB software, and clustering was done by DOTUR. At the lowest level of dissimilarity, a total of 951 OTUs were recorded. A relatively large number of different populations dominate all samples, which count for observed phylogenetic diversity.

Poster 25. Recurrent deletions of puroindoline genes at the grain hardness locus in four independent lineages of polyploid wheat.

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Polyploidy is known to induce numerous genetic and epigenetic changes but little is known about their physiological bases. In wheat, grain texture is determined by the hardness (*Ha*) locus consisting of genes *Pina* and *Pinb*. These genes are conserved in diploid progenitors but were deleted from the A and B genomes of tetraploid *T. turgidum* (AB). We now report the recurrent deletions of *Pina-Pinb* in other lineages of polyploid wheat and discuss a physiological basis of this phenomenon. We analyzed the *Ha* haplotype structure in 90 diploid and 300 polyploid accessions of *Triticum* and *Aegilops* species. *Pin* genes were conserved in all diploid species and deletion haplotypes were detected in all polyploid *Triticum* and most of the polyploid *Aegilops* species. Two *Pina-Pinb* deletion haplotypes were found in hexaploid *T. aestivum* (ABD). *Pina* and *Pinb* were eliminated from the G genome, but maintained in the A genome of tetraploid *T. timopheevii* (AG). Subsequently, *Pina* and *Pinb* were deleted from the A genome but retained in the A^m genome of hexaploid *T. zhukovskyi* (A^mAG). Comparison of deletion breakpoints demonstrated that the *Pina-Pinb* deletion occurred independently and recurrently in the four polyploid wheat species. The PIN proteins have α-amylase inhibitor activity and bind to the surface of starch granules in the endosperm. We hypothesize that the sudden gene dosage-driven increase in PIN proteins in a neopolyploid would constrain the embryos obtaining nutrition from the endosperm during seed germination. Therefore, deletions of *Pin* genes would be favored for early stand establishment during polyploid speciation.

Poster 26. The finished genomic sequence of the Septoria tritici blotch pathogen Mycosphaerella graminicola.

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Mycosphaerella graminicola is the haploid ascomycete that causes Septoria tritici blotch, one of the most important diseases of wheat worldwide. This pathogen is phylogenetically distinct from other fungi that have been sequenced and is hemibiotrophic; early infection is biotrophic, followed by a switch to nectrophic growth just prior to symptom expres-