

***Wheat Stem Rust Genome Project: First look under the hood.***

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*Puccinia graminis* f. sp. *tritici*, the casual agent of stem rust of wheat, has caused major epidemics over the last century. Renewed awareness of the threat to wheat production posed by this disease has occurred with the emergence of a new, virulent race (TTKS) in Eastern Africa. *P. graminis* is a dikaryotic fungus with five spore stages and two plant hosts. Whole-genome shotgun coverage (12X) has been generated by paired-end sequencing from three libraries generated by randomly sheared, total genomic libraries. A 6.8 X draft assembly containing 392 supercontigs (N50 911 kb) and covering 89 Mb was constructed. A restriction fingerprint map containing 1,969 contigs (10.8 X) was generated from approximately 22,000 fosmid clones. The restriction fingerprint map and draft sequence assembly are highly similar with 99% of the sequence assembly being placed on the fingerprint map. Annotation of the draft assembly predicted 20,567 genes, with approximately one-half of the gene calls supported by homology to sequence data in public databases and/or *P. graminis* EST database. Approximately 57,000 ESTs were generated from three cDNA libraries (urediniospores, germinated urediniospores, and teliospores), which were assembled into 6,465 synthetic contigs. Thirty-six percent of the EST contigs could be annotated using GO categories. The majority of the EST synthetic contigs were stage-specific, with only 8% common to all three libraries.

***Genomic and metabolic analysis of R gene-mediated defense pathways in wheat.***

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Plant defense involves three major steps: surveillance, signal transduction, and the production of defense chemicals. A great deal of information on signal perception and transduction has been revealed in numerous plant-parasite systems. Here we investigated changes in metabolic pathways that might lead to accumulation of defense chemicals using genomic and metabolic profiling. The wheat-Hessian fly interaction was used in this study. Hessian fly is an insect but shares many features with plant pathogens, being sessile during feeding stages and having avirulence genes that match plant resistance genes in gene-for-gene relationships. Many genes involved in carbon/nitrogen metabolism were differentially regulated during compatible and incompatible interactions. During compatible interactions, the attacking site became a carbon sink. Photoassimilates were transported to the attacking site from other parts of the plant. Part of the transported photoassimilates were converted into amino acids through coordinated activation of key metabolic pathways including glycolysis, the tricarboxylic acid cycle, and amino acid synthesis pathways. In contrast, the attacking site became a nitrogen sink during incompatible interactions. Nitrogen was transported to the attacking site from other parts of the plant in the form of asparagine. The transported nitrogen was likely converted into defensive secondary metabolites. Our data suggested that the formation of a carbon sink and the conversion of C-compounds into N-compounds at the feeding site is a necessary condition for Hessian fly larvae to survive and develop in susceptible plants, whereas the formation of a nitrogen sink and the increase in phenylpropanoids and other secondary metabolites may be part of the resistance mechanism.

***Fine mapping of the Lr46/Yr29 locus in wheat.***

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Rust diseases, including leaf rust (*Puccinia triticina*), stripe rust (*P. striiformis* f. sp. *tritici*), and stem rust (*P. graminis* f. sp. *tritici*) are globally the most important diseases of wheat. Genetic resistance is the best form of control but frequent race changes typically render new varieties susceptible within a few years after release. For typical resistance genes, the