# PLENARY SESSION

Chairperson: Richard W. Ward

# CEREAL GENOME AND GENE SPACE ANALYSIS

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**ABSTRACT**

Cereal genome and gene-space analysis will be discussed with particular reference to wheat and barley of the Triticeae tribe. Both wheat and barley share 12 million years of co-evolutionary history and diverged from a common ancestor of rice about 40 million years ago. Diploid wheat and barley have a basic chromosome number of seven and a genome size of 5,000 Mb. Bread wheat is hexaploid and has a genome size of 16,000 Mb. Classical genome analysis in both crops was facilitated by exploiting the richness of genetic resources, such as mutants, trisomic and translocation stocks in barley and the vast number of aneuploids, such as monosomics, nullisomics and deletion lines, in wheat. Later, wheat-barley addition lines were used to demonstrate the complete conservation of gene synteny between wheat and barley chromosomes. High-resolution RFLP maps were made in the 1990's and anchored to chromosome maps by use of cytogenetic landmarks. Comparative mapping revealed rough conservation of synteny among the major cereal crops and rice, because of its small genome size (420 Mb), was the second plant to be selected for genome sequencing. In order to fully utilize the sequenced genome of rice, EST (expressed sequence tags) resources were developed in both wheat and barley, and EST-based maps were developed. The EST-based maps were compared against the sequenced genome of rice and in silico maps of wheat and barley were constructed. These maps revealed many micro-rearrangements between the Triticeae and rice chromosomes and revealed that there are limits when using the rice genome sequence for gene discovery in barley and wheat. More recently, several laboratories have initiated work on BAC-contig maps of wheat and barley chromosomes anchored to the genetic maps. The goal is to accelerate gene discovery in these two crops by map-based cloning. Both wheat and barley genomes contain more than 90% repetitive DNA and only 5% genes. The emerging concept is to focus only on the analysis of the gene space. The genic portion of the genome can be separated from the repetitive DNA by methylation filtration and Hi Cot analysis. Sequencing the gene-enriched fraction and genic BACs may be the best strategy for analysis of gene space in wheat and barley. For functional genomics, the development of other resources such as chips and mutant populations will be reviewed.

# GENOMICS OF *FUSARIUM GRAMINEARUM*

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## ABSTRACT

We have generated a draft sequence assembly of the *F. graminearum* genome that is available on the web for download and query. The assembly is remarkably complete owing to near lack of repetitive sequences in the genome. After manual editing, the entire assembly currently is contained on 28 scaffolds ranging in size from 3 kb to over 8.8 Mb with an average contig length of over 71 kb. Currently, over 99.8% of the DNA sequence has been anchored to the genetic map by way of 237 genetic markers, 164 of which are sequence-tagged sites. Automated draft gene calls were conducted both at the Broad Institute and at MIPS resulting in >11,000 predicted genes. Improvements to the predicted gene sets are being made by manual annotation by members of GIGI, representing over 25 laboratories world-wide and further EST sequencing at the Broad Institute. MIPS currently is hosting web-access to the manual annotation as well as both the Broad Institute and MIPS gene models. A custom Affymetrix GeneChip microarray designed from gene models derived from the draft assembly is now available. Details of the automated annotation, efforts toward manual annotation, microarray experiments and coordination of functional analysis of the genome will be discussed. The *F. graminearum* sequencing project is funded by the National Research Initiative (NRI), through the USDA/NSF Microbial Genome Sequencing Program. The MIPS *Fusarium graminearum* Genome Database is funded by the Austrian Federal Ministry for Education, Science and Culture and the *Fusarium* microarray is funded by the USDA NRI Integrated Program: Functional Genomics of Microbes.

# HOST-PATHOGEN AND PATHOGEN-PATHOGEN INTERACTIONS IN FHB

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**ABSTRACT**

Globally, *F. graminearum* is the predominant species associated with Fusarium head blight. However, in many situations, several fungi may be involved. These include producers of trichothecene and other mycotoxins as well as species that produce no mycotoxins. Histological studies and, more recently, the use of reporter tagged isolates have revealed how *Fusarium* species colonise host tissues but relatively little is known about the detailed molecular interactions between Fusarium species and the host plant. Within *F. graminearum* and *F. culmorum* both deoxynivalenol (DON) and nivalenol (NIV) producing isolates are present in many areas and cause disease on various cereal hosts. DON has been shown to be a virulence factor but it is not clear how host or environmental factors influence the production of DON. Furthermore, it is not known how DON production, through the loss of the ability to produce NIV, has conferred an apparent selective advantage with respect to pathogenicity towards wheat.

The genetic basis of resistance to FHB is generally complex and may involve a number of mechanisms. Studies are beginning to permit dissection of resistance into component parts and provide some insight into potential mechanisms involved. Differential expression of pathogenesis related proteins has been observed between some resistant and susceptible varieties and reduced accumulation of DON has been found among others. The imminent availability of DNA microarrays for the pathogen and a number of cereal hosts should provide the potential to reveal much about the signalling processes between host and pathogen and identify aspects relating to resistance.

In those regions where toxin-producing and non-toxin producing species form disease complexes the competitive interactions between pathogens has important consequences for disease and subsequent risks to consumers associated with the consumption of contaminated cereals or their products. Molecular diagnostic tools are beginning to shed light on some of these interactions but, as with host-pathogen interaction, much remains to be learned.