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Sequencing The Major Mycosphaerella Pathogens Of Wheat And Banana

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Mycosphaerella is one of the largest genera of plant pathogenic fungi with more than 1,000 named species, many of which are important pathogens causing leaf spotting diseases in a wide variety of crops including cereals, citrus, banana, eucalypts, soft fruits, and horticultural crops. A few species of Mycosphaerella cause disease in humans and other vertebrates. An international project was initiated to sequence the genomes of *M. graminicola* and *M. fijiensis*, two of the most economically important pathogens of wheat and banana, respectively, along with 40,000 ESTs from *M. fijiensis* and the related maize pathogen *Cercospora zeae-maydis*, through the Community Sequencing Program sponsored by the U.S. DOE-Joint Genome Institute. The 9x *M. graminicola* sequencing is complete and was made public November 1, 2006 following automated and manual annotation. Due to the very good assembly statistics as well as a >2000-marker DArT linkage map that was aligned to the genome, JGI decided to finish the *M. graminicola* genome at the Stanford Human Genome Center. The majority of chromosomes have been sequenced completely including both telomeres. These data indicate that *M. graminicola* has both the largest chromosome number and the smallest chromosome sizes recorded among filamentous ascomycetes. The *M. fijiensis* EST sequencing has resulted in more than 30,000 ESTs and the genome sequencing is currently at approximately 2.5x, which enabled us to revise the genome size estimate of *M. fijiensis* to approximately 68 Mb, which is 70% larger than that for *M. graminicola*. The current status of both sequencing projects will be discussed.