

## **CHALLENGES IN WHOLE-GENOME ANNOTATION OF PYROSEQUENCED FUNGAL GENOMES.**

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Pyrosequencing technologies such as 454/Roche and Solexa/Illumina vastly lower the cost of nucleotide sequencing compared to the traditional Sanger method, and thus promise to greatly expand the number of sequenced eukaryotic genomes. However, the new technologies also bring new challenges such as shorter reads and new kinds and higher rates of sequencing errors, which complicate genome assembly and gene prediction. At JGI we are deploying 454 technology for the sequencing and assembly of ever-larger eukaryotic genomes. Here we describe our first whole-genome annotation of a purely 454-sequenced fungal genome that is larger than a yeast (>30 Mbp). The pezizomycotine (filamentous ascomycote) *Aspergillus carbonarius* belongs to the *Aspergillus* section Nigri species complex, members of which are significant as platforms for bioenergy and bioindustrial technology, as members of soil microbial communities and players in the global carbon cycle, and as agricultural toxigens. Application of a modified version of the standard JGI Annotation Pipeline has so far predicted ~10k genes. ~12% of these preliminary annotations suffer a potential frameshift error, which is somewhat higher than the ~9% rate in the Sanger-sequenced and conventionally assembled and annotated genome of fellow *Aspergillus* section Nigri member *A. niger*. Also, >90% of *A. niger* genes have potential homologs in the *A. carbonarius* preliminary annotation. We conclude, and with further annotation and comparative analysis expect to confirm, that 454 sequencing strategies provide a promising substrate for annotation of modestly sized eukaryotic genomes. We will also present results of annotation of a number of other pyrosequenced fungal genomes of bioenergy interest.