Title
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Sequencing the Black Aspergilli species complex
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Abstract
The ~15 members of the Aspergillus section Nigri species complex (the "Black Aspergilli") are significant as platforms for bioenergy and bioindustrial technology, as members of soil microbial communities and players in the global carbon cycle, and as food processing and spoilage agents and agricultural pests. Despite their utility and ubiquity, the morphological and metabolic distinctiveness of the complex's members, and thus their taxonomy, is poorly defined. We are using short read pyrosequencing technology (Roche/454 and Illumina/Solexa) to rapidly scale up genomic and transcriptomic analysis of this species complex. To date we predict 11197 genes in Aspergillus niger, 11624 genes in A. carbonarius, and 10845 genes in A. aculeatus. A. aculeatus is our most recent genome, was assembled primarily from 454-sequenced reads and annotated with the aid of > 2 million 454 ESTs and > 300 million Solexa ESTs. To most effectively deploy these very large numbers of ESTs we developed 2 novel methods for clustering the ESTs into assemblies. We have also developed a pipeline to propose orthologies and paralogies among genes in the species complex. In the near future we will apply these methods to additional species of Black Aspergilli that are currently in our sequencing pipeline.