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Title

Sequencing the Black Aspergilli species complex

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Sequencing the Black *Aspergilli* species complex

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Abstract

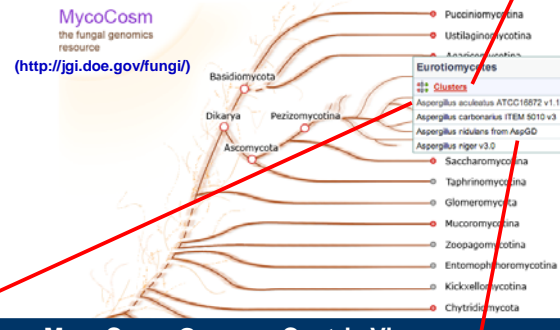
The ~15 members of the *Aspergillus* section *Nigri* species complex (the "Black Aspergilli") are significant as platforms for bioenergy and biotechnological technology, as members of soil microbial communities and players in the global carbon cycle, and as food processing and spoilage agents and agricultural toxigenes. 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, and 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.

Aspergilli in MycoCosm: Genome statistics

| | <i>aculeatus</i> | <i>carbonarius</i> | <i>niger</i> | <i>nidulans</i> (AspGD) |
|----------------------------|------------------|--------------------|--------------|-------------------------|
| Assembly size (Mbp) | 35.4 | 36.3 | 34.9 | 30.5 |
| # of ESTs | 338596947 | 2466582 | 15360 | NA |
| # of genes | 10845 | 11624 | 11197 | 10680 |
| w/ alternative transcripts | 6333 (58%) | ND | ND | ND |
| w/ paralogs | 6758 (62%) | 7032 (59%) | 7045 (63%) | 6182 (58%) |
| # of multigene families | 1561 | 1726 | 1599 | 1461 |

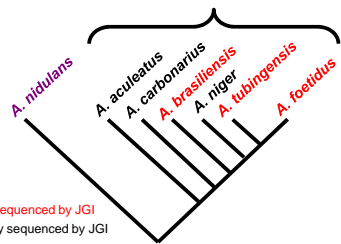
MycoCosm Eurotiomycetes Node

(<http://genome.jgi-psf.org/eurotiomycetes/>)



MycoCosm Genome-Centric Views

The Black Aspergilli (*Nigri* complex)



- to be sequenced by JGI
- already sequenced by JGI
- already sequenced by Broad

non-*Nigri* Eurotiomycetes:
A. sojae
A. wentii
A. versicolor
A. sydowii
A. glaucus
A. zonatus
Penicillium roqueforti

Black Aspergilli are of interest to:
 Bioenergy
 Biotechnological technology
 Soil ecology
 Carbon cycle
 Food processing
 Food spoilage
 Food toxicity

MycoCosm Comparative Genomics View

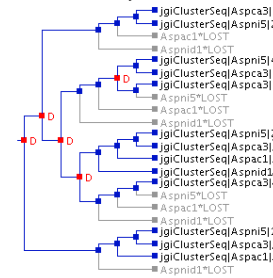
Many *Nigri* complex gene families are expanded relative to *A. nidulans*

Gene families summary view

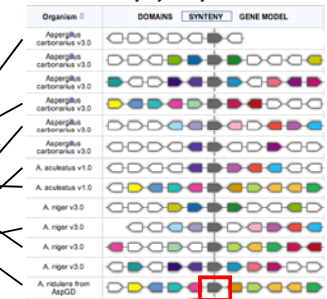
| Cluster | <i>A. aculeatus</i> v1.0 FilteredModels | <i>A. nidulans</i> from AspGD AspGD_genes | <i>A. niger</i> v3.0 FrozenGeneCatalog071608 | <i>Aspergillus carbonarius</i> v3.0 FilteredModels | Total |
|---------|---|---|--|--|-------|
| Totals | 5282 | 4875 | 5433 | 5617 | 21207 |
| 76 | 9 | 1 | | 5 | 25 |
| 144 | 4 | 1 | | 6 | 18 |
| 177 | 5 | 1 | | 6 | 16 |
| 205 | 4 | 1 | | 5 | 15 |
| 207 | 1 | | | 3 | 15 |
| 216 | 3 | | | 6 | 14 |
| 224 | 3 | 1 | | 5 | 14 |
| 229 | 4 | 1 | | 6 | 14 |
| 236 | 4 | 1 | | 4 | 13 |
| 251 | 2 | 1 | | 6 | 13 |
| 256 | 3 | 1 | | 5 | 13 |

Catalase gene family has multiple duplications and losses

Catalase family tree view

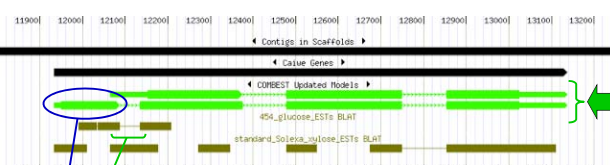


Catalase family synteny view

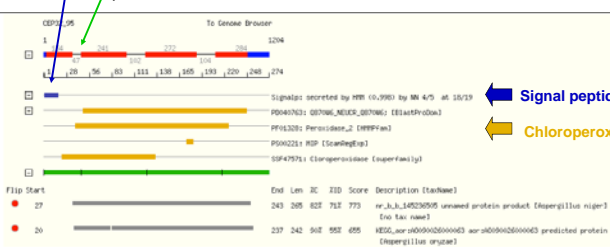


Alternative splicing may affect *A. aculeatus* chloroperoxidase secretion

A. aculeatus locus view

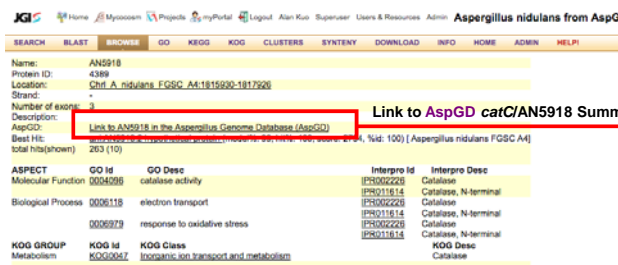


A. aculeatus protein view

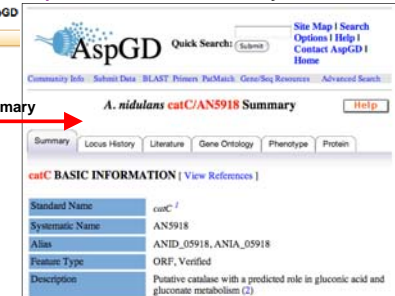


Aspergillus nidulans catalase gene

A. nidulans protein view



AspGD catCAN5918 Summary



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A. carbonarius collaborators: Giancarlo Perrone, Antonia Gallo
A. nidulans genome: Arnaud, MB et al. at AspGD
 (<http://www.aspergillusgenome.org>)