

Lawrence Berkeley National Laboratory

Recent Work

Title

Comparative Genomics Tools for analysis of Six Dothideomycete Genomes

Permalink

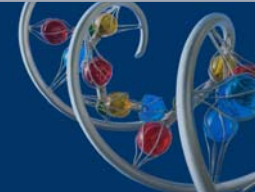
<https://escholarship.org/uc/item/6tp259s3>

Authors

Aerts, Andrea
Minovitsky, Simon
Cantor, Michael
[et al.](#)

Publication Date

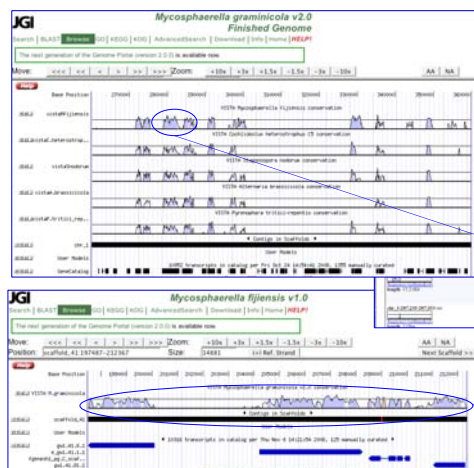
2009-03-17



Abstract

Comparative genomics is a powerful tool for genome annotation and analysis. We recently initiated analysis of six of the *Dothideomycete* genomes that are publicly available: *Mycosphaerella graminicola*, *Mycosphaerella fijiensis* and *Cochliobolus heterostrophus C5* all sequenced and annotated at the DOE Joint Genome Institute as well as *Alternaria brassicicola* sequenced at the Washington University School of Medicine, Genome Sequencing Center and annotated by the Christopher Lawrence Lab at Virginia Bioinformatics Institute, Virginia Tech, *Pyrenophora tritici-repentis* and *Stagonospora nodorum*, both sequenced and annotated by the Broad Institute, MIT. We placed these genomes into a comparative framework equipped with tools to facilitate genome analysis: VISTA genome conservation curves linking genome browsers, gene cluster browser and protein links to homologs in all six genomes, side-by-side comparisons of KEGG pathways and KOG functions, and synteny viewer. JGI community annotation brought biologists behind each of these genomes together to explore common mechanisms of plant pathogenicity and host interactions.

VISTA Conservation Analysis



VISTA tracks show regions of conservation at the genome level between two genomes. The VISTA peak highlighted on the *M.graminicola* browser represents conservation between a coding region in *M.graminicola* and an orthologous region in *M.fijiensis*. By clicking on the VISTA track the user is able to browse orthologous regions in a related genome via an intermediate page.

Genome Statistics

	Genome size (Mbp)	# of genes predicted
<i>Mycosphaerella graminicola</i>	39.7	10,952
<i>Mycosphaerella fijiensis</i>	73.4	10,327
<i>Cochliobolus heterostrophus C5</i>	34.9	9,633
<i>Alternaria brassicicola</i>	30.3	10,688
<i>Pyrenophora tritici-repentis</i>	37.8	12,141
<i>Stagonospora nodorum SN15</i>	37.1	15,983

www.jgi.doe.gov/Mgraminicola
www.jgi.doe.gov/Mfijiensis
www.jgi.doe.gov/Cochliobolus
www.jgi.doe.gov/Abassicicola
www.jgi.doe.gov/Pyrenophora
www.jgi.doe.gov/Snodorum

Clustering Tool

This clustering example demonstrates how the clustering tool can be effectively used to annotate individual genes. The domain view, Fig. 1, shows that the *A.brassicicola* genes are most likely one gene that has been split. The browser viewer, Fig. 2, shows a gap in the assembly (the red section of the longer black bar) which created a split in this gene.

Fig. 2



Proteins included in cluster 1284



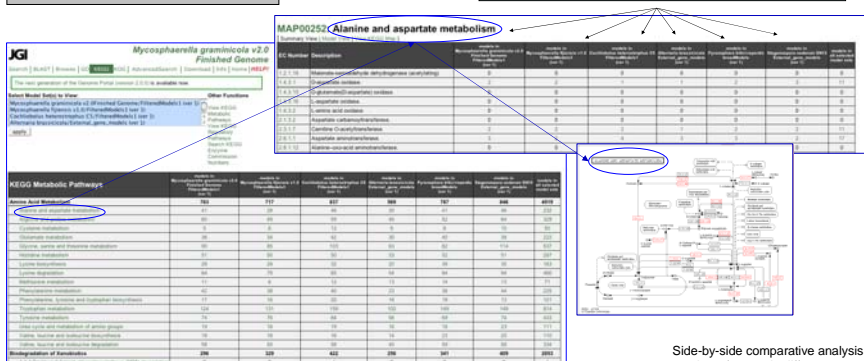
Fig. 1

Homolog Links between Portals

When clicking on the description of the *M.fijiensis* protein aligned to the *M.graminicola* protein the user can then jump to the protein analysis page of the *M.fijiensis* protein thus enabling comparative analysis at the gene level.

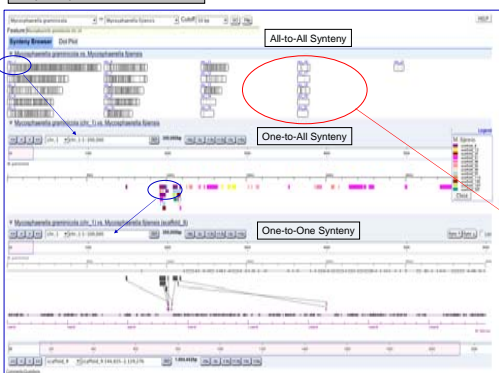


KEGG Functional Annotation Browser

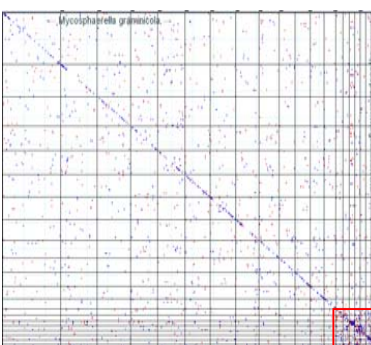


Side-by-side comparative analysis of number of genes in different genomes belonging to the same KOG function or KEGG pathway helps to find gene family expansions or possible annotation errors

Synteny Viewer



Dot Plot Viewer



Smaller chromosomes of *M.graminicola* have higher repeat content, lower gene density, and mostly novel genes indicative of potentially dispensable chromosomes.

<i>M.graminicola</i> v2.0	chr1-chr13	chr14-chr21
fraction of repeats (%)	17 +/- 4	31 +/- 6
gene density (1 per kb)	3.5 +/- 0.2	7.1 +/- 0.8
fraction of gene models with plam domain (%)	55 +/- 4	3 +/- 3

KOG Functional Annotation Browser

