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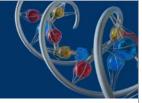
2009-03-17



Comparative Genomics Tools For Analysis of Six **Dothideomycete Genomes**

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*Abstract

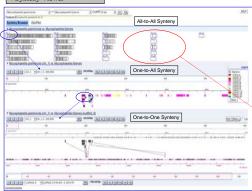
Comparative genomics is a powerful tool for genome annotation and analysis. We recently initiated analysis of six of the Dothideomycete genomes that are publicly available: Mycosphaerella graminicola, Mycosphaerella fijiensis and Cochliobolus heterostropus C5 all sequenced and annotated at the DOE Joint 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 triticirepentis 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

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Synteny Viewer



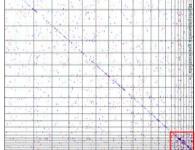
	Genome size (Mbp)	# of genes predicted
Mycosphaerella graminicola	39.7	10,952
Mycosphaerella fijiensis	73.4	10,327
Cochliobolus heterostrophus C5	34.9	9,633
Alternaria brassicicola	30.3	10,688
Pyrenophora tritici-repentis	37.8	12,141
Stagonospora nodorum SN15	37.1	15,983

Genome Statistics

www.jgi.doe.gov/Mgraminicola www.jgi.doe.gov/Mfijiensis www.jgi.doe.gov/Cochliob www.igi.doe.gov/Abrassicicola www.jgi.doe.gov/Pyrenophora www.jgi.doe.gov/Snodorum

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





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

M.graminicola 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 pfam domain (%)	55 +/ 4	3 +/- 3

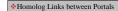


This clustering example demonstrates how the clustering tool can be effectively used to annotate individual genes. The domain view, Fig. 1, shows that the A.brassicicola genes are most likely one gene that has been split. The browser viewer, Fig. 2, shows a gap in the assembly (the red section of bar)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



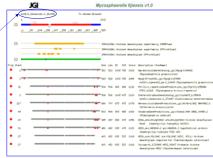
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When clicking on the description of the M.fijiensis protein aligned to the M.graminicola protein the user can then jump to the protein analysis page of the M.fijiensis protein thus enabling comparative analysis at the gene level.

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Side-by-side comparison of KEGG gene function assignments.

*KEGG Functional Annotation Browser

IGI

MAP00252 Alanine and aspartate metabolism

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

*KOG Functional Annotation Browser

function (0)	Function Description	Gene Models in Mycosylumida graninicela 123 Finished Geneme	Gene Models in Wycrogheerstia Tjierwis e1.3	Conte Waters in Contilidatus heterostrophus CS	Gene Models in Abernatis brandicionis	Gene Models in Pyremythers stitui-repetite	Gene Models in Disgenerapers restores EN15
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Side-by-side comparison of KOG gene function assignments.