JGI Fungal Genomics Program

Igor V. Grigoriev[1]

[1]Lawrence Berkeley National Laboratory

August 2011

The work conducted by the U.S. Department of Energy Joint Genome Institute is supported by the Office of Science of the U.S. Department of Energy under Contract No. DE-AC02-05CH11231

DISCLAIMER

This document was prepared as an account of work sponsored by the United States Government. While this document is believed to contain correct information, neither the United States Government nor any agency thereof, nor The Regents of the University of California, nor any of their employees, makes any warranty, express or implied, or assumes any legal responsibility for the accuracy, completeness, or usefulness of any information, apparatus, product, or process disclosed, or represents that its use would not infringe privately owned rights. Reference herein to any specific commercial product, process, or service by its trade name, trademark, manufacturer, or otherwise, does not necessarily constitute or imply its endorsement, recommendation, or favoring by the United States Government or any agency thereof, or The Regents of the University of California. The views and opinions of authors expressed herein do not necessarily state or reflect those of the United States Government or any agency thereof or The Regents of the University of California.

JGI Fungal Genomics Program

Contact: Igor Grigoriev <ivgrigoriev@lbl.gov>

DOE JOINT GENOME INSTITUTE
US DEPARTMENT OF ENERGY
OFFICE OF SCIENCE

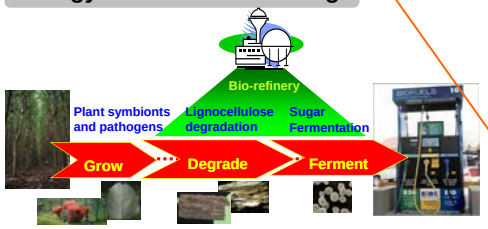
U.S. DEPARTMENT OF ENERGY
Office of Science

Abstract

Genomes of energy and environment fungi are in focus of the Fungal Genomic Program at the US Department of Energy Joint Genome Institute (JGI). Its key project, the Genomics Encyclopedia of Fungi, targets fungi related to plant health (symbionts, pathogens, and biocontrol agents) and biorefinery processes (cellulose degradation, sugar fermentation, industrial hosts), and explores fungal diversity by means of genome sequencing and analysis. Over 60 fungal genomes have been sequenced by JGI to date and released through MycoCosm (www.jgi.doe.gov/fungi), a fungal web-portal, which integrates sequence and functional data with genome analysis tools for user community. Sequence analysis supported by functional genomics leads to developing parts list for complex systems ranging from ecosystems of biofuel crops to biorefineries. Recent examples of such 'parts' suggested by comparative genomics and functional analysis in these areas are presented here.

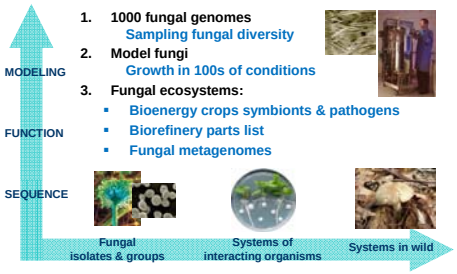
Genomic Encyclopedia of Fungi
- Plant Feedstock Health
- Biorefinery
- Fungal Diversity

Energy & Environment Fungi



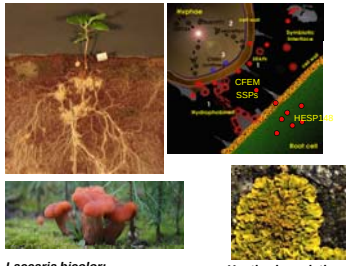
Martin, *et al., New Phytol.* 2011; Grigoriev, *et al., Mycology,* in press

Future Grand Challenges



Plant Health

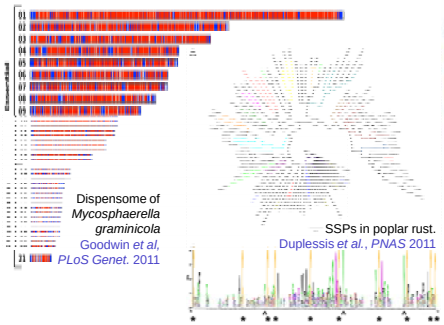
Symbionts



Laccaria bicolor: Ectomycorrhyzal symbiont of poplar. Martin *et al, Nature* 2008

Xanthoria parietina: lichen fungus (PI: Paul Dyer)

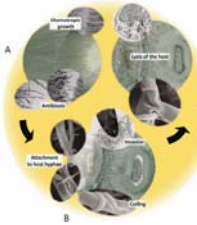
Plant Pathogens



Dispensome of *Mycosphaerella graminicola* Goodwin *et al, PLoS Genet.* 2011

SSPs in poplar rust. Duplessis *et al., PNAS* 2011

Biocontrol

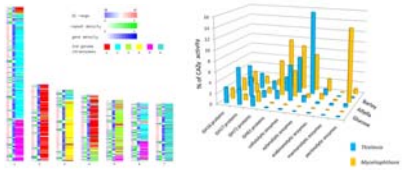


GH family	Chitin/chitosan 18	75	17	55	ß-glucan 64	81	217
Trichoderma atroviride	29	5	5	8	3	2	18
Trichoderma virens	36	5	4	10	3	1	18
Trichoderma reesei	20	3	4	6	3	2	15
Aspergillus nidulans	19	2	5	6	0	1	12
Aspergillus niger	14	2	5	3	0	1	9
Fusarium graminearum	19	1	6	3	2	1	12
Laccaria bicolor	10	0	4	2	0	0	6
Magnaporthe grisea	14	1	7	3	1	2	13
Nectria haematococca	28	2	6	5	2	1	14
Neurospora crassa	12	1	4	6	2	1	13
Penicillium chrysogenum	9	1	5	3	2	1	11
P.chrysosporium	11	0	2	2	0	0	4
Podospora anserina	20	1	4	7	1	1	13
Postia placenta	20	0	4	6	0	0	10
S.cerevisiae	2	0	4	0	0	2	6
S.pombe	1	0	1	0	0	1	2
Tuber melanosporum	5	1	4	2	0	3	9

Integrated genomic and transcriptomic analysis reveals mycoparasitism as the ancestoral life style of *Trichoderma.* Kubicek *et al., Genome Biol.* 2011; Druzhinina *et al., Nature Microbiol Rev.*, in press

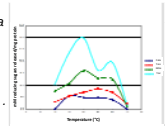
Biorefinery

Thermophiles



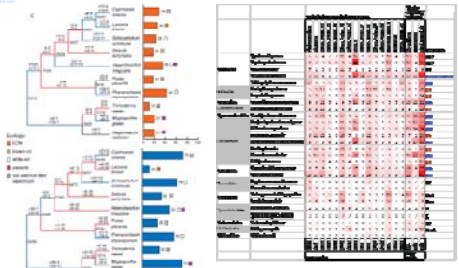
Thermophilic biomass-degrading fungi *Myceliophthora thermophila* and *Thielavia terrestris* are the first with completely finished genomes, new candidate for cell factories with secreted thermostable enzymes.

Berka, Tsang *et al., subm.*



Release of reducing sugars from alfalfa straw by extracellular enzymes

Lignocellulose Degradation

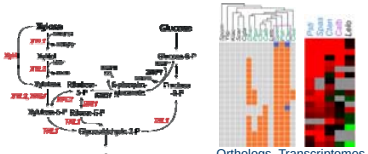


Convergent evolution of brown rot and ECM from white rot ancestor. Eastwood *et al., Science* 2011

CAZy and FOLy in Basidiomycetes

Tandem duplication of peroxidases in *Trametes.* Riley *et al.. in prep.*

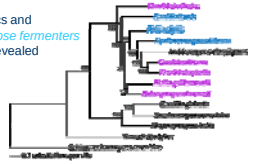
Xylose Fermenters



Orthologs Transcriptomes

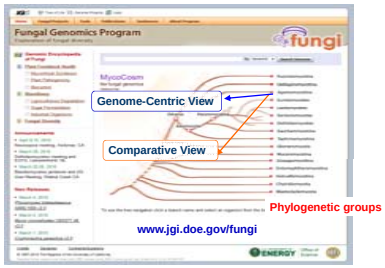
Comparative genomics and transcriptomics of *xylose fermenters* and *xylose growers* revealed candidate genes for *S.cereviseae* strain improvement.

Wohlbach, *et al. PNAS* 2011



Fungal Diversity

MycoCosm: 80+ fungal genomes

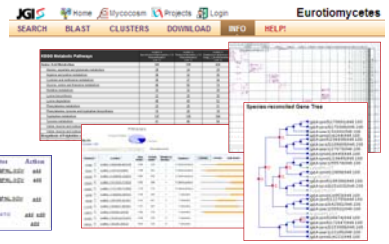


Genome-centric View

Supports genome analysis, functional genomics, user data deposition & curation

Comparative View

Enables analysis of groups of related fungi



The work conducted by the U.S. Department of Energy Joint Genome Institute is supported by the Office of Science of the U.S. Department of Energy under Contract No. DE-AC02-05CH11231.