Fueling the Future with Fungal Genomes

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October 2014

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

LBNL- 178363

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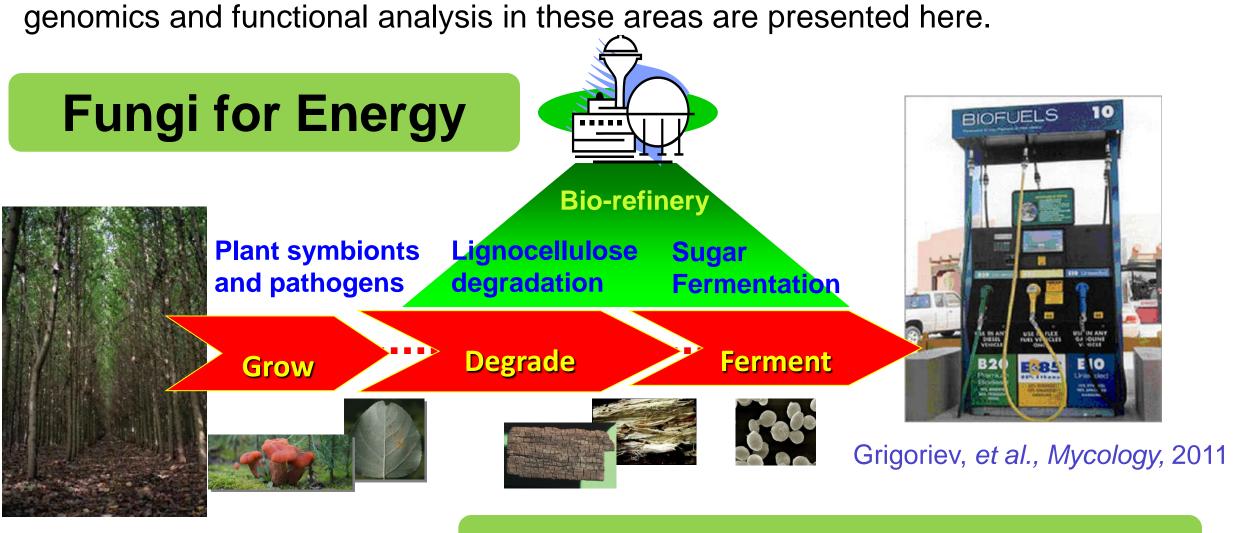
Fueling the Future with Fungal Genomics

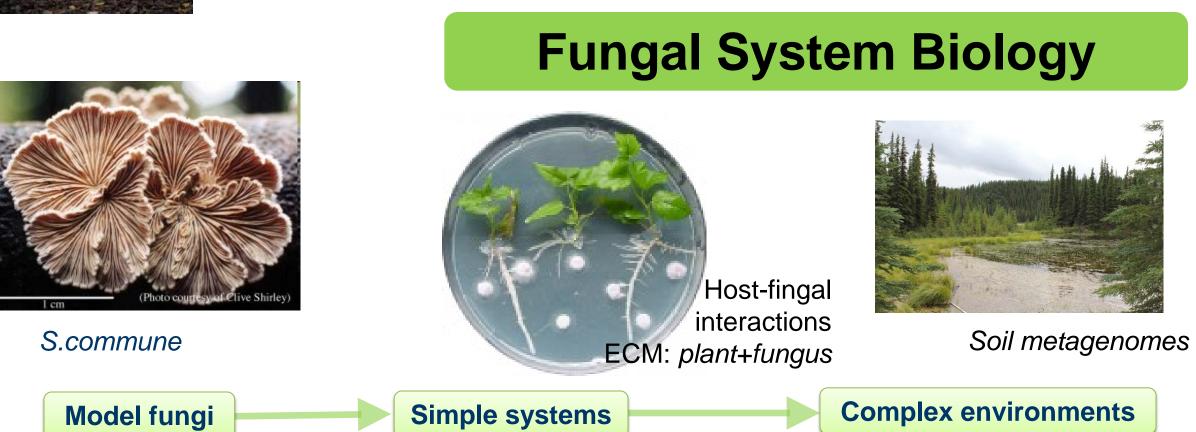
Igor V. Grigoriev, DOE Joint Genome Institute



Abstract

Genomes of fungi relevant to energy and environment are in focus of the JGI Fungal Genomic Program. One of its projects, the Genomics Encyclopedia of Fungi, targets fungi related to plant health (symbionts and pathogens) and biorefinery processes (cellulose degradation and sugar fermentation) by means of genome sequencing and analysis. New chapters of the Encyclopedia can be opened with user proposals to the JGI Community Science Program (CSP). Another JGI project, the 1000 fungal genomes, explores fungal diversity on genome level at scale and is open for users to nominate new species for sequencing. Over 400 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 will lead to developing parts list for complex systems ranging from ecosystems of biofuel crops to biorefineries. Recent examples of such 'parts' suggested by comparative





Pucciniomycotina

Agaricomycotina

Pezizomycetes

Eurotiomycetes

Dothideomycetes

Lecanoromycetes

Leotiomycetes

Sordariomycetes

Saccharomycotina

Taphrinomycotina

Mu Search

Ustilaginomycotina

MycoCosm

Pezizomycotina

MycoCosm

the fungal genomics

http://jgi.doe.gov/fungi

Grigoriev et al., NAR 2014

400+ fungal genomes

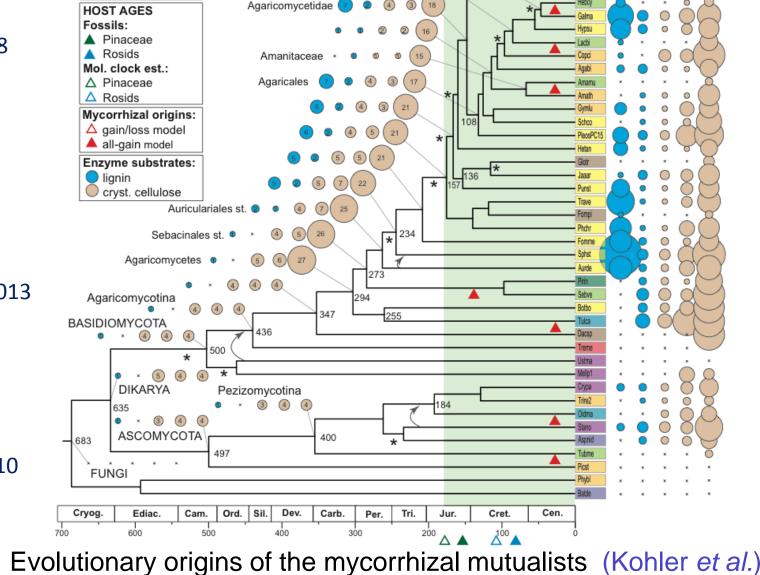
Micorrhizal Genomics Initiative open doors for analysis of convergent evolution (Martin et al.

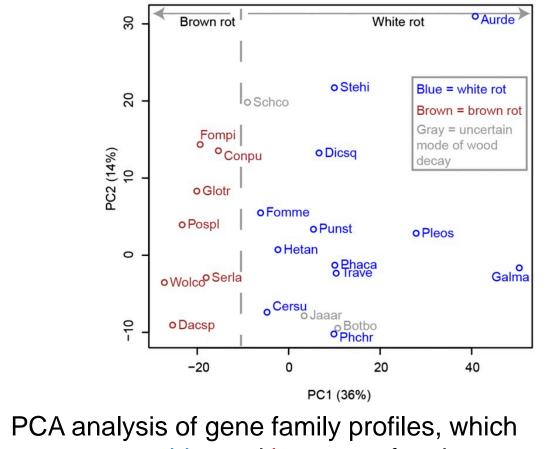
Mycorrhizal Symbionts Carbohydrate-active enzyme http://genome.jgi.doe.gov/Mycorrhizal_fungi root endophyte mycoparasite animal pathoge white rot litter/soil/other brown rot Agaricomycetidae 🕡 🛭 🚯 🧯 **HOST AGES** ▲ Pinaceae Mol. clock est. 60,707,050 23,130 55,857,776 20,389 Mycorrhizal origins 46,426,256 16,703 Tusserant et al., PNAS 2013 BASIDIOMYCOTA • × 4 4 4 175,759,688 22,885 Martin et al.,. Nature 2010 29 Wilcoxina mikolae CBS 423.85 v1.0

Plant Pathogens

Expanded small secreted proteins in rusts fungi.

(Duplessis et al., PNAS 2011)





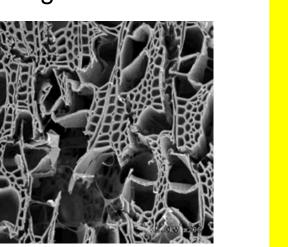
segregates white and brown rot fungi, suggest several poorly characterized fungi to be white rot fungi despite lack of POD genes. Micrographs of wood

decay patterns support this and suggest alternative mechanisms for lignin degradation

Xylose Fermenters

—0.1 substitutions per site

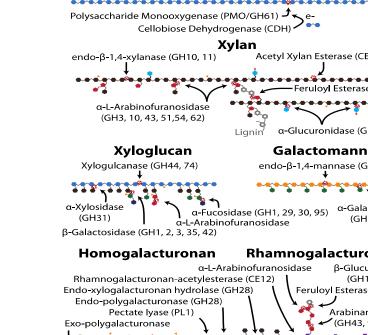
Wood Decayers



Lodderomyces elongisporus

— Debaryomyces hanseni

—Kluyveryomyces lactis



D-glucose
 D-galactose
 D-mannose
 D-glucuronic acid
 D-galacturonic acid
 D-mannose
 D-galacturonic acid
 L-rhamnose
 C-acetyl
 D-methyl



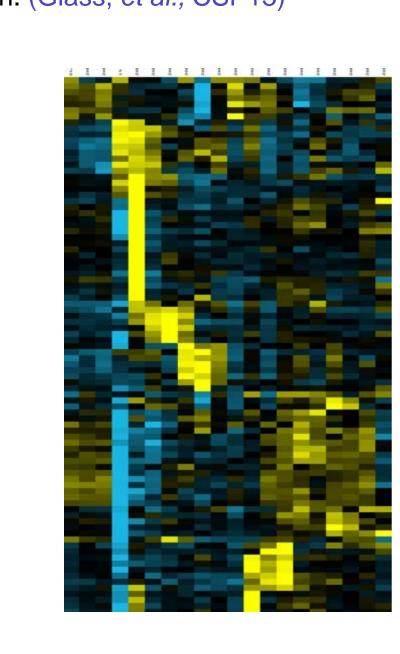
Tier Three ChIP samples

Epitope-tagged TFs and on a variety of strains grown epigenome under different C, N, S, P sources,

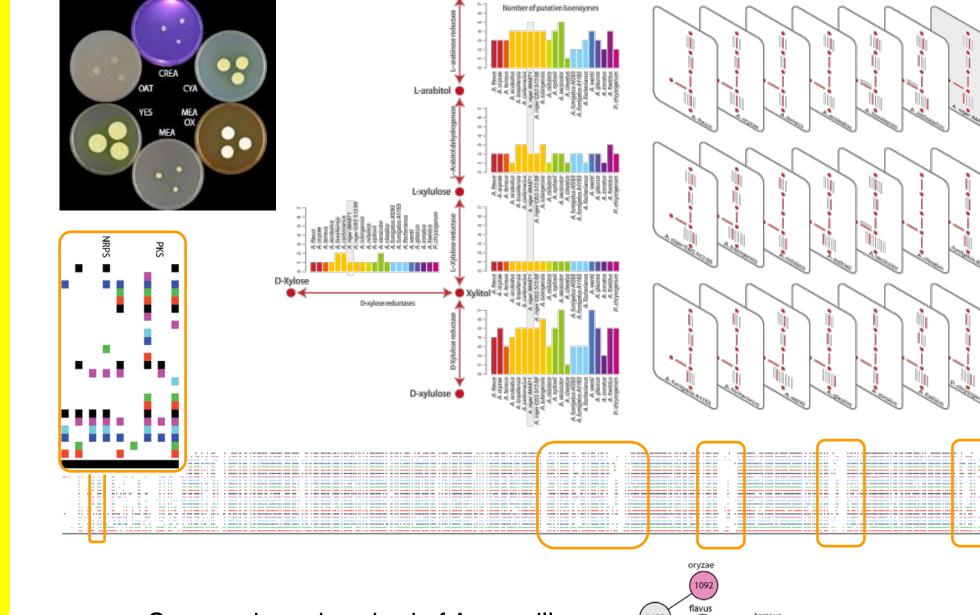
Fungal Nutritional ENCODE

Tier Two

Deep transcriptomics and epigenomics of the model fungus Neurospora crassa and its extensive transcription factor (TF) deletion strain set (~200 strains) will help develop a nutritional regulatory map to discover the function of new regulatory factors and regulons associated with resource utilization. (Glass, et al., CSP13)



Aspergillus Deep Sequencing



Sequencing a hundred of Aspergillus genus will enable mapping of genome variation to variation of enzymatic profiles and secondary metabolism (Baker, Andersen, et al., JBEI 2013)

1000 Fungal Genomes Project

Step 1: Login

In 18 Dothideomycetes SSP are

more expanded in nechrotrophs

Ohm et al., PLoS Path. 2012.

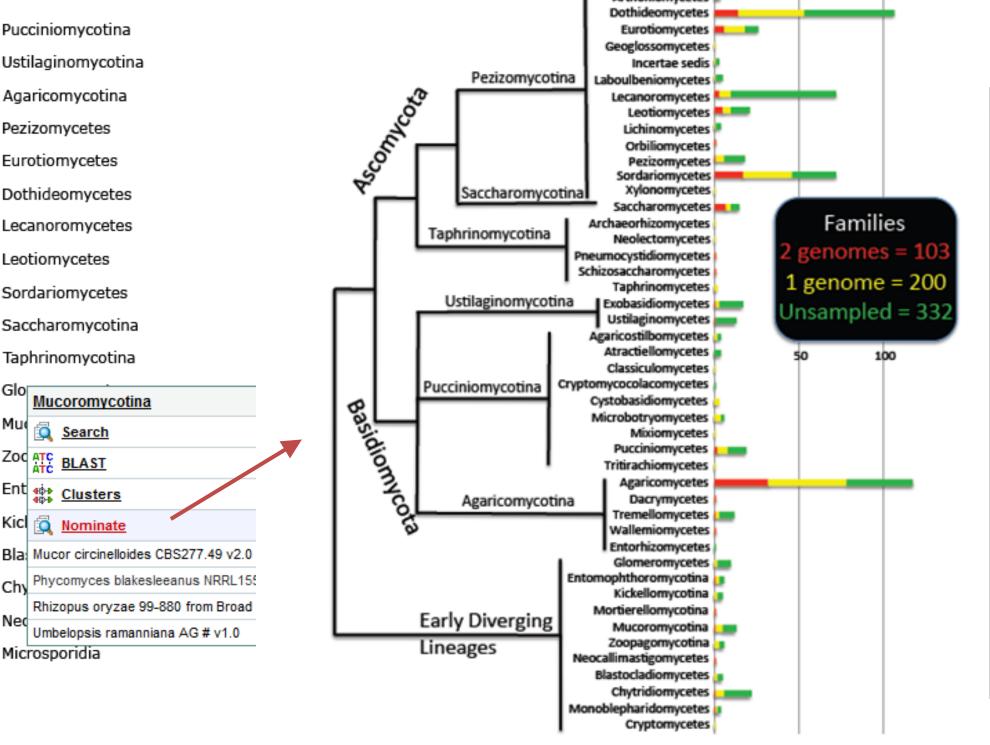
■ Secreted peptidases

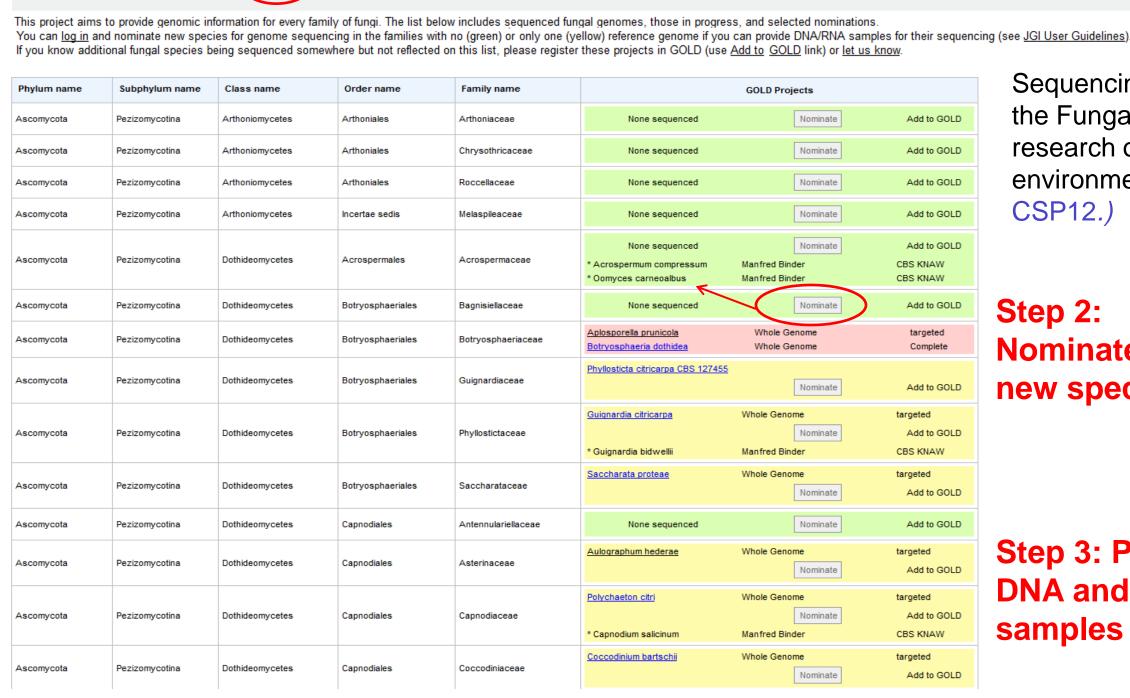
Secondary metabolism

Secreted lipases

800 genes

than biotrophs.





Sequencing 1000 fungal genomes from across the Fungal Tree of Life will provide references for research on plant-microbe interactions and environmental metagenomics. (Spatofora et al., CSP12.)

Schizosaccharomyces cerevisiae

xylose growers revealed candidate genes

for S.cereviseae strain improvement

Comparative genomics and

(Wohlbach, et al. PNAS 2011)

transcriptomics of

Step 3: Prepare DNA and RNA

for sequencing for no sequenced