

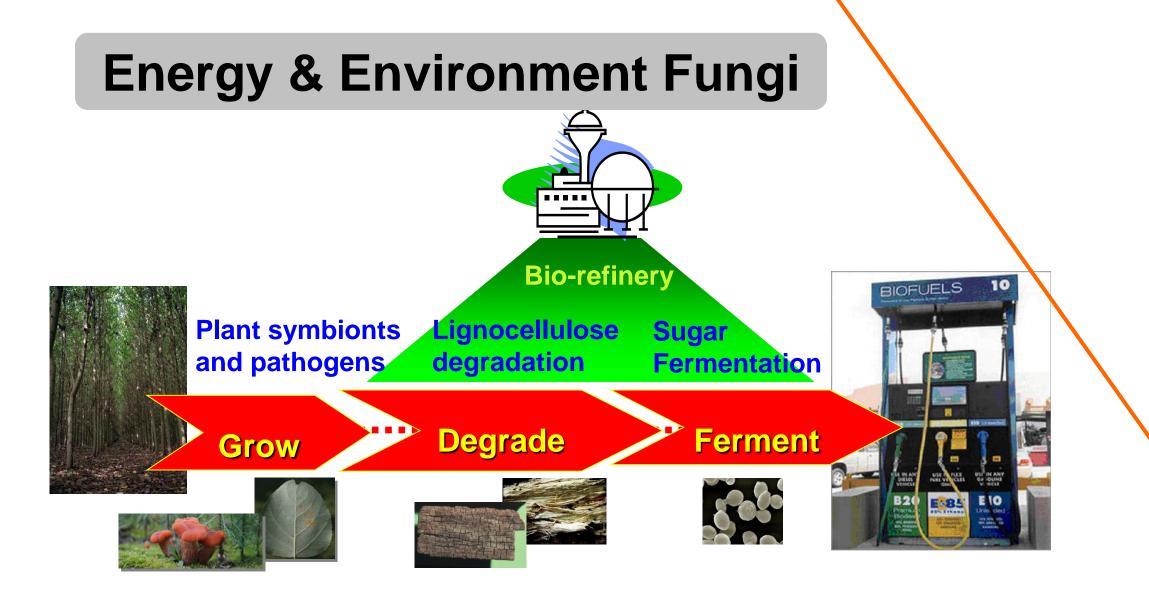
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Abstract

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 50 fungal genomes have been sequenced by JGI to date and released through MycoCosm (www.jgi.doe.gov/fungi), a fungal webportal, 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.





Future Grand Challenges 1000 fungal genomes Sampling fungal diversity Model fungi 2. **Deep sampling over 1000 of conditions** MODELING **Fungal ecosystems: Bioenergy crops symbionts & pathogens Biorefinery parts list FUNCTION** Fungal metagenomes SEQUENCE Systems of Funda Systems in wild isolates & groups interacting organisms

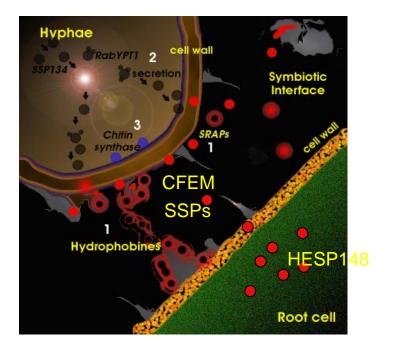
JGI Fungal Genomics Program **Contact:** Igor Grigoriev <ivgrigoriev@lbl.gov>

Symbionts

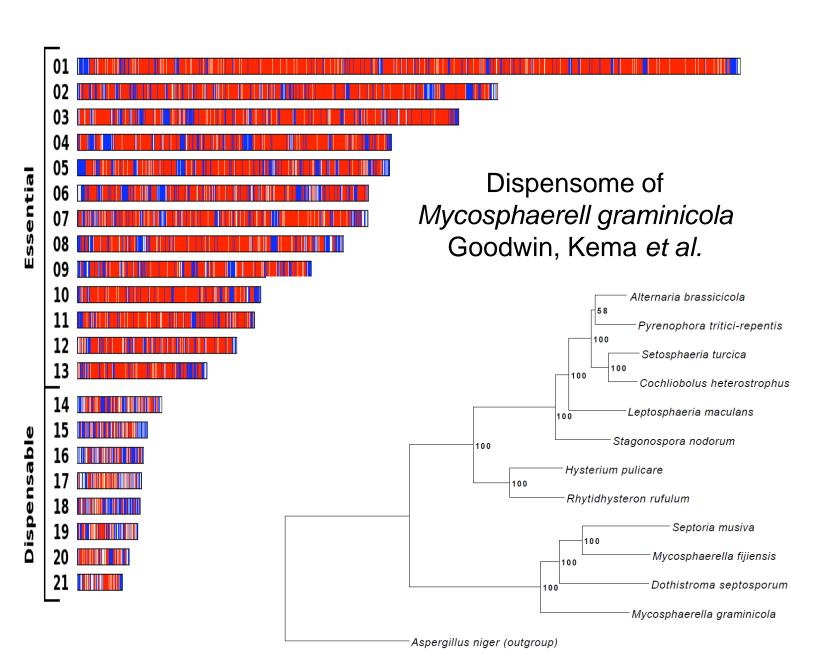


Laccaria bicolor: Ectomycorrhyzal symbiont of poplar. Martin et al, Nature 2008

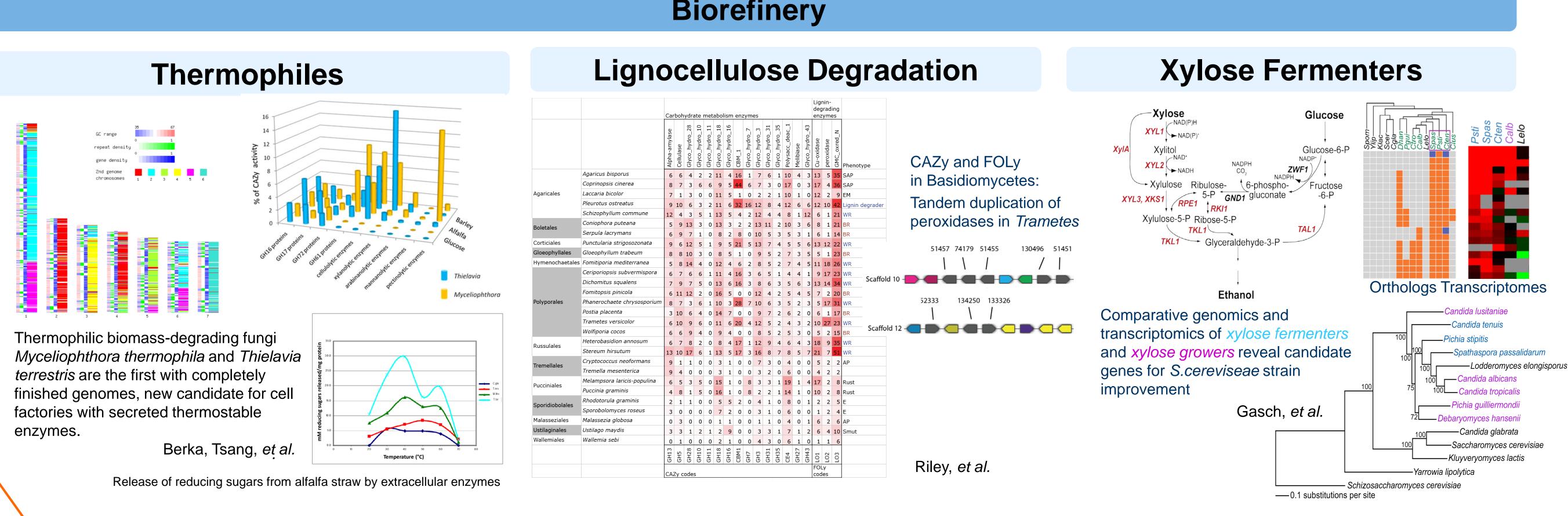




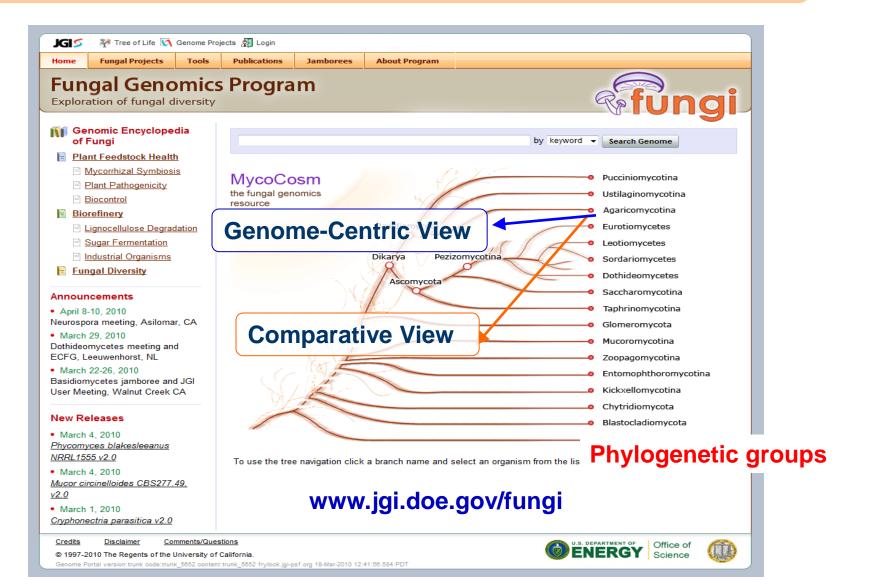
Xanthoria parietina: lichen fungus (PI: Paul Dyer)

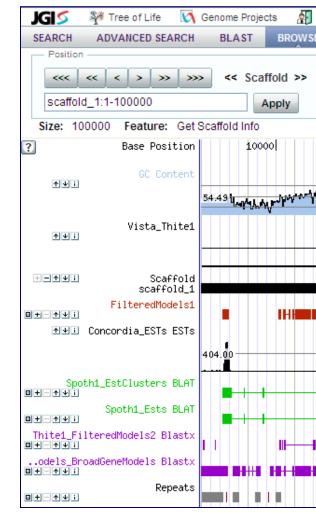


Comparative analysis of 12 Dothideomycetes. Ohm et al., in prep.

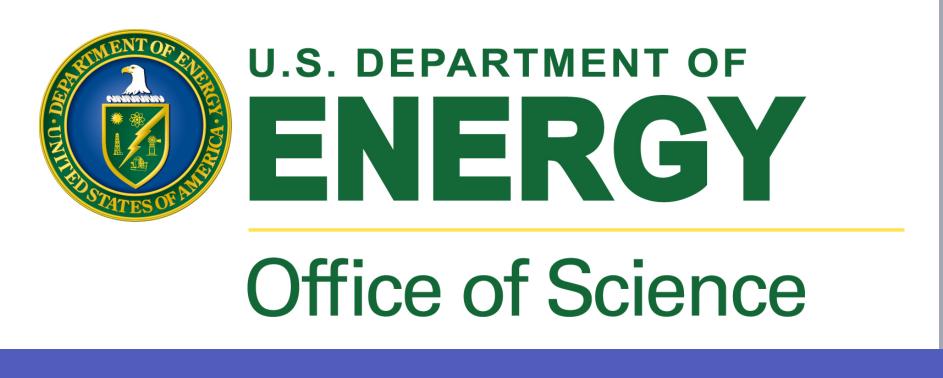


MycoCosm: 60+ fungal genomes





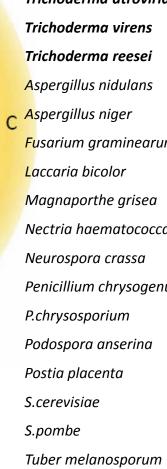




Plant Health

Plant Pathogens

Biocontrol GH family Trichoderma atroviri



Integrated genomic and transcriptomic analysis reveals mycoparasitism as the ancestoral life style of Trichoderma.

Biorefinery

Fungal Diversity

Genome-centric View

Supports functional genomics, user data deposition and curation

Sporotrichum thermophile v1.0 JGI ≶ 🛛 🆓 Home 🖉 Mycocosm 🔯 Projects 🐖 Login KEGG KOG CLUSTERS DOWNLOAD INFO HOME HELP! BLAST CLUSTERS DOWNLOAD Permalink Radd custom tracks Sequence (softmasked length: 17,731 bp nine and proline metabol steine and methionine metabo Vista Browse cine, serine and threonine r ine biosynthesi: ine degradation enylalanine metabolisn henylalanine, tyrosine and t yptophan metabolism osine metabolism Contigs in Scaffolds /aline, leucine and isole PFAM domains /aline, leucine and isoleu nthesis of Polyketides a Concordia ESTs EST Curve Gene Protein length © length © Location = DOMAINS SYNTENY GENE MC Creator Action 51456 Scaffold 5:4062499-4063798 Name SPT97310 SCOTT.BAKER@PNL.GOV add 61641 Scaffold 2:257743-259541 1799 3 03349 Scattold_6:1486938-1488032 1095 3 on-ribosomal peptide SCOTT.BAKER@PNL.GOV 3628 scaffold 6:3119218-3120420 1203 34 synthetase 104062 Scaffold 7:1717709-1718836 1128 31 42750 scaffold 3:1945426-1947615 1190 340 on-ribosomal peptide SCOTT.BAKER@PNL.GOV 28 scattold 3:3572705-3573977 1273 34 12100 Scaffold 2:4899521-4900621 1101 297 135813 Scaffold 6:292593-293938 1346 318 add edi 161591 Scaffold 1:5122124-5123472 1349 338 0 Scattold 7.543391-545033 1643 336 0 T. terrestris Literature add

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.

Chitin/chitosan ß-glucar 18 75 17 55 64 81 217 29 5 5 8 3 2 18 5 4 10 3 1 18 3 2 15 19 2 5 6 0 1 **12** 14 2 5 3 0 1 **9** 1 6 3 2 1 **12** 0 4 2 0 0 **6** 14 1 7 3 1 2 **13** 2 6 5 2 1 **14** 1 4 6 2 1 **13** 2 1 **11** 11 0 2 2 0 0 4 20 0 4 6 0 0 **10** 2 0 4 0 0 2 6 1 0 1 0

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