

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

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Fueling the Future with Fungal Genomics

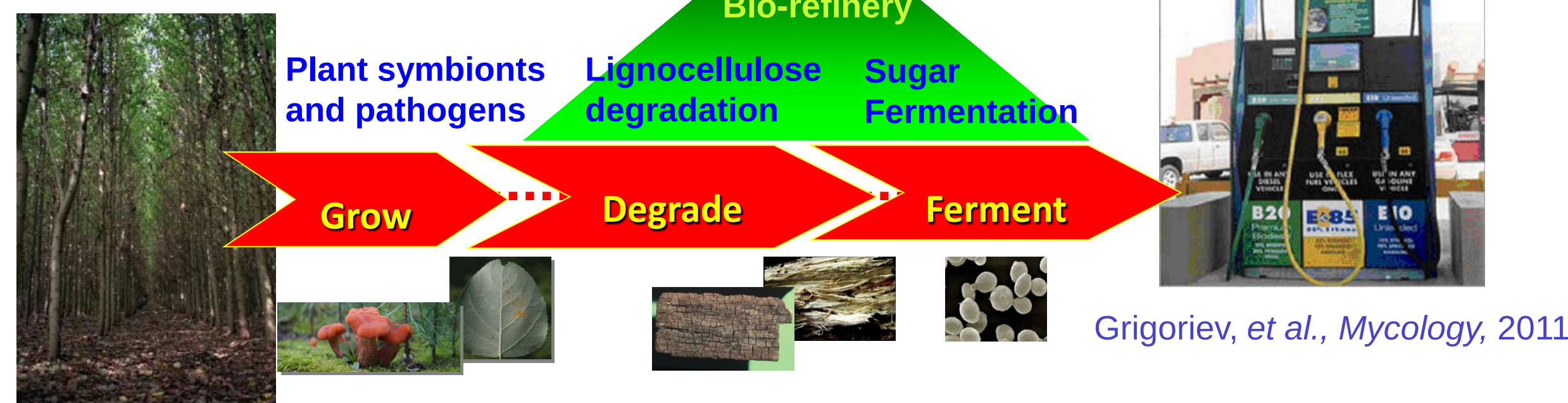
Igor V. Grigoriev, DOE Joint Genome Institute



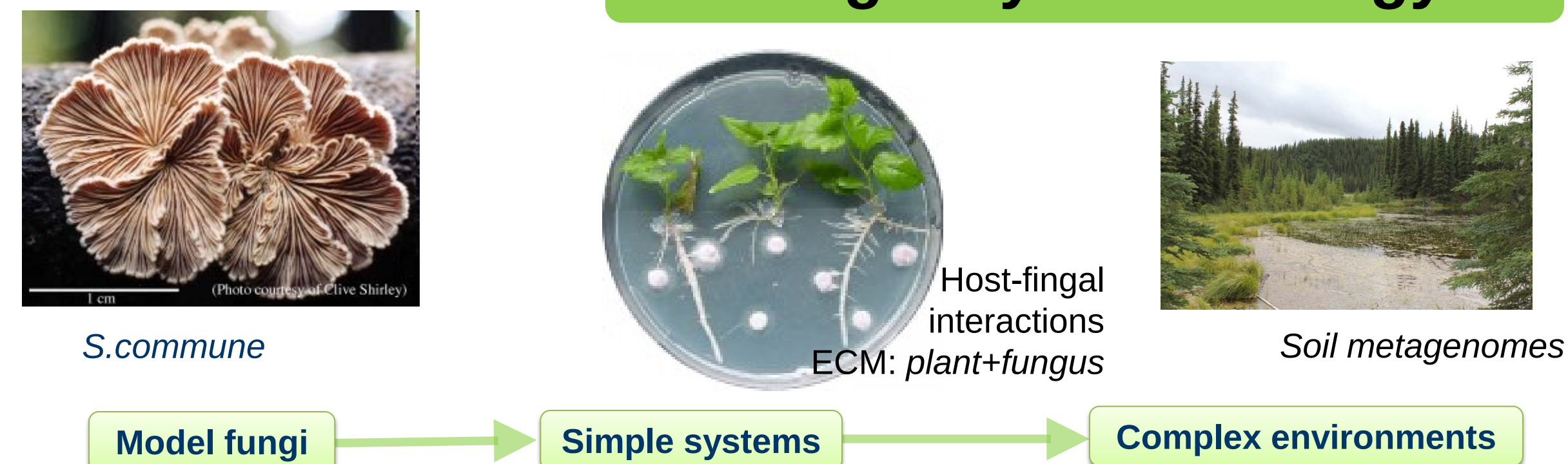
Abstract

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 genomics and functional analysis in these areas are presented here.

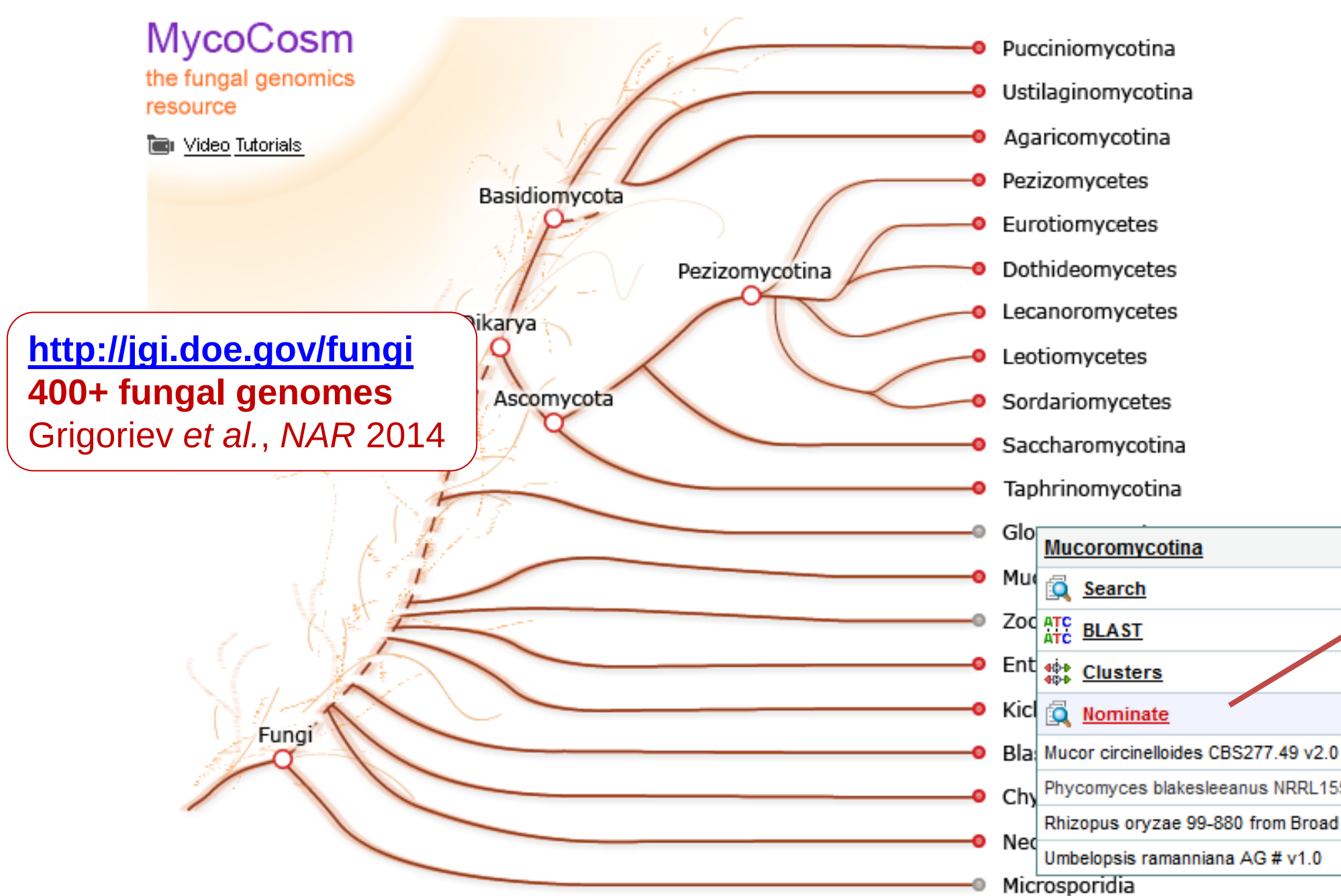
Fungi for Energy



Fungal System Biology

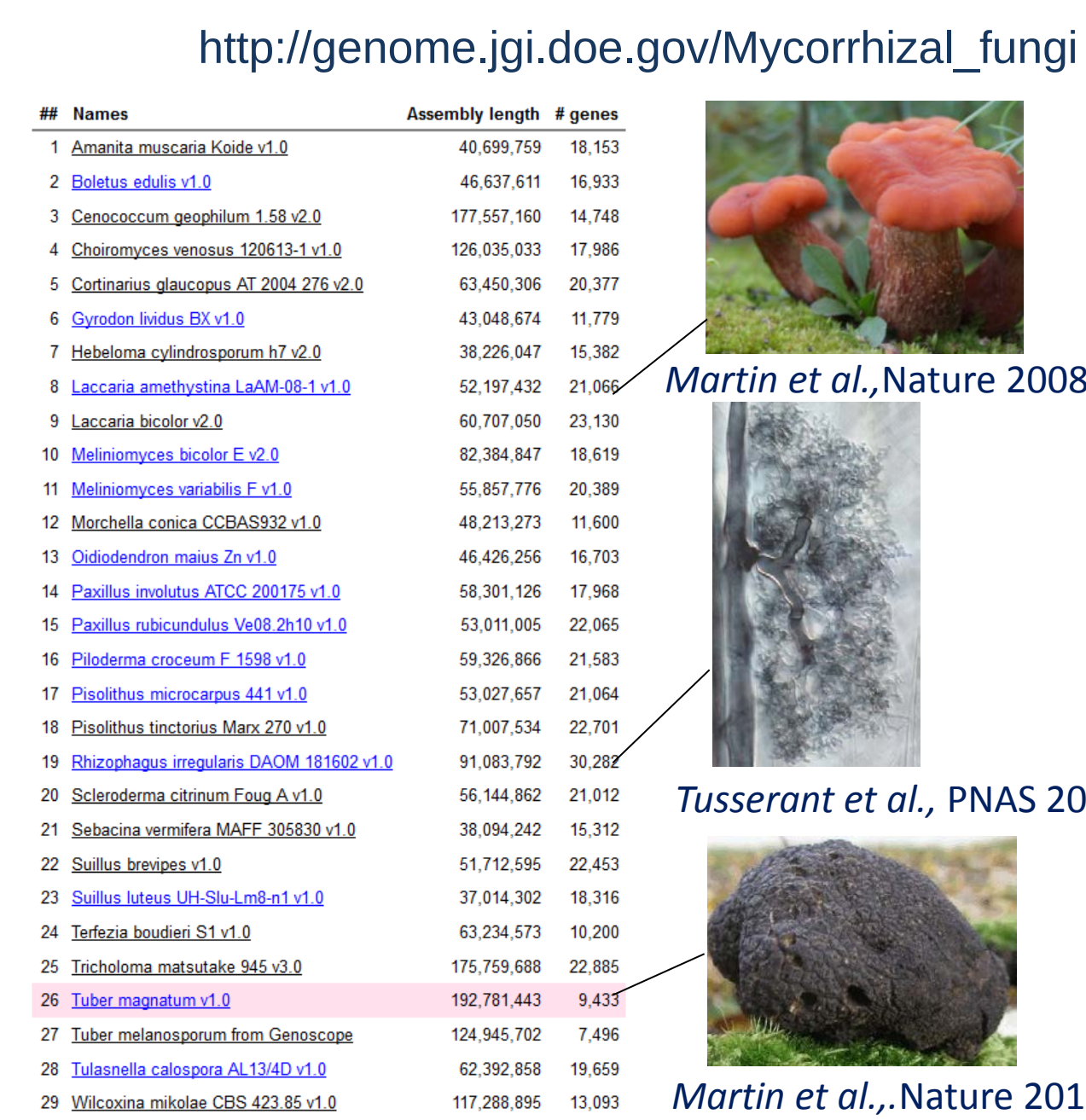


MycoCosm



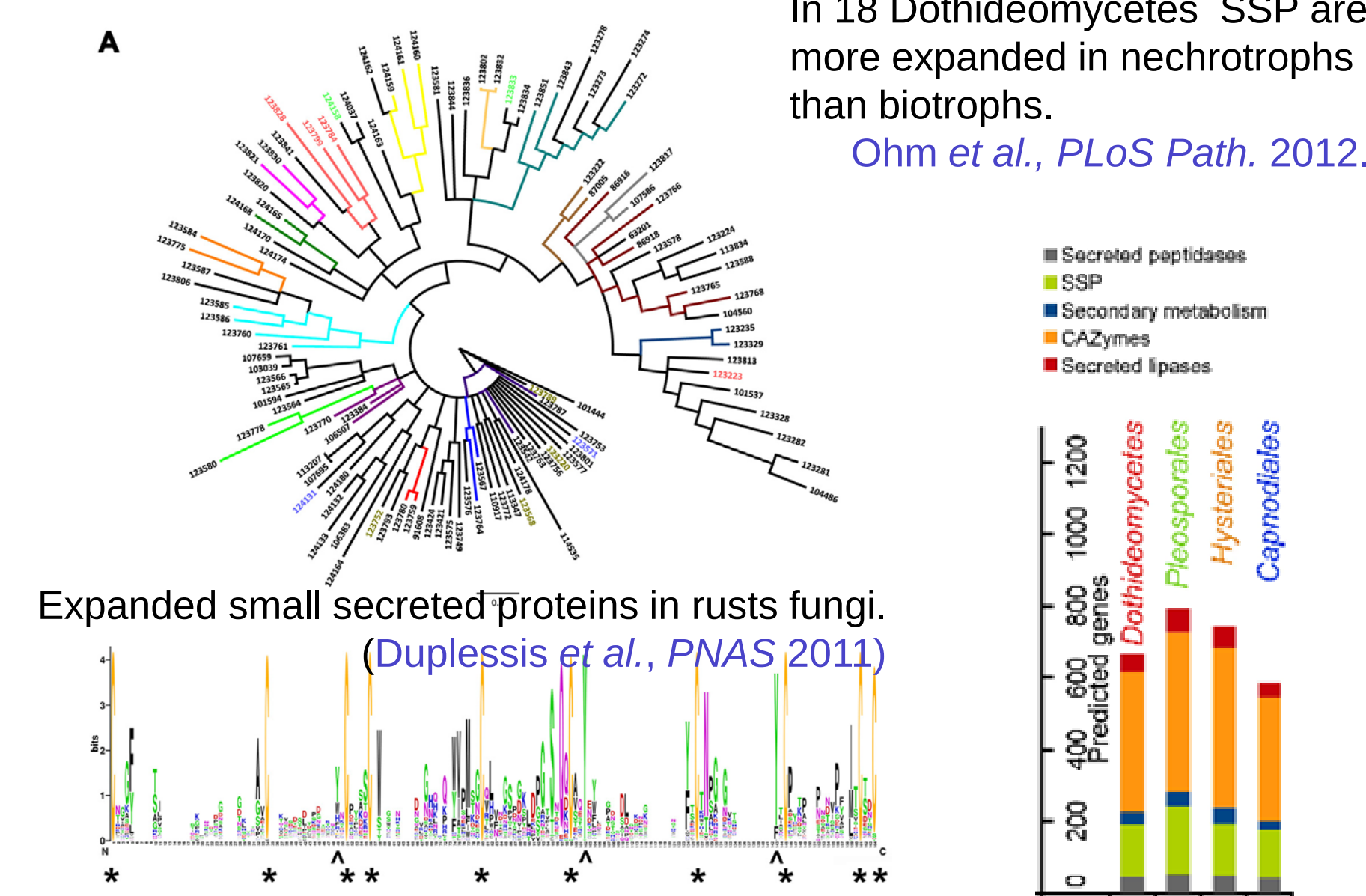
<http://jgi.doe.gov/fungi>
400+ fungal genomes
Grigoriev et al., NAR 2014

Mycorrhizal Symbionts



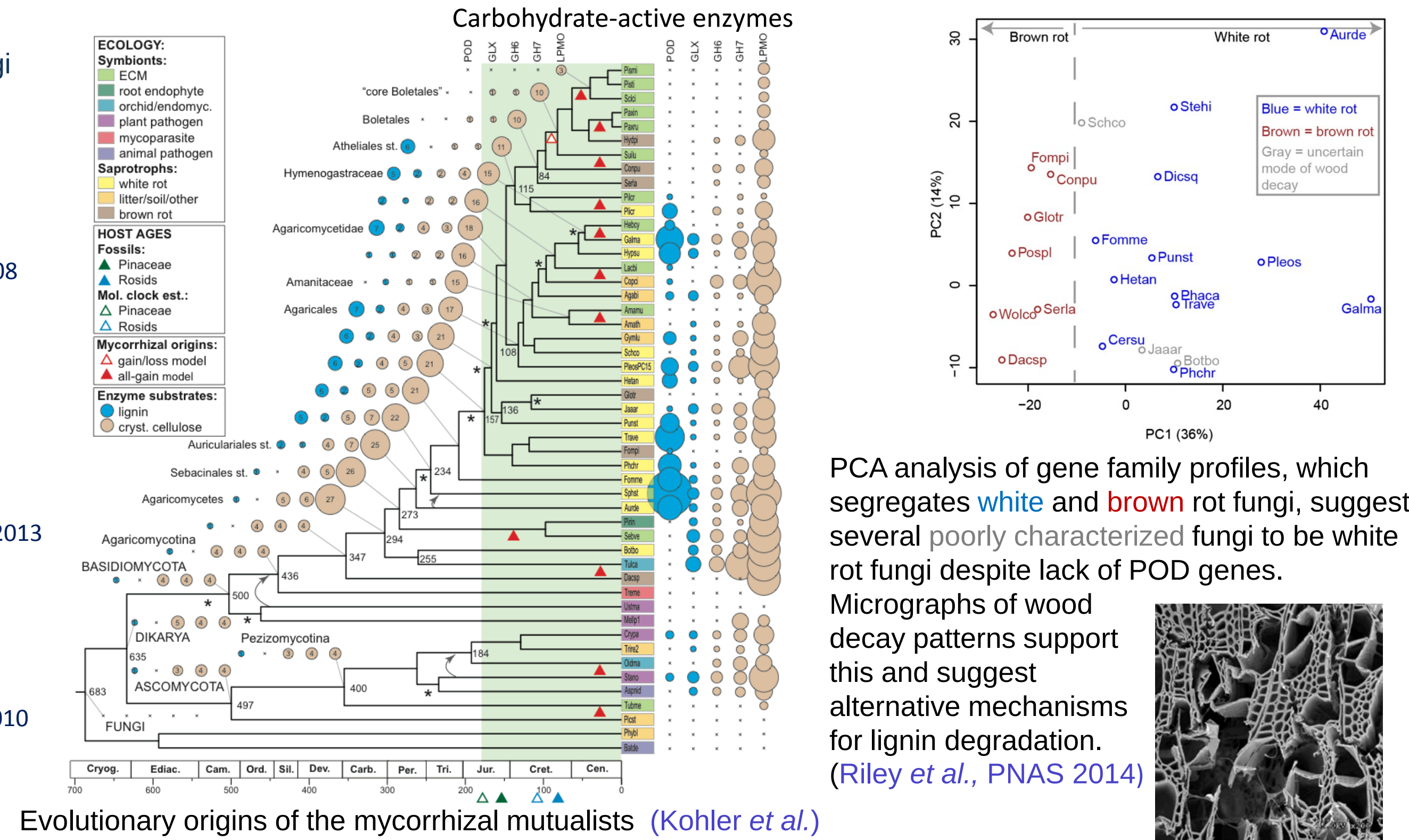
Mycorrhizal Genomics Initiative open doors for analysis of convergent evolution (Martin et al., CSP11)

Plant Pathogens

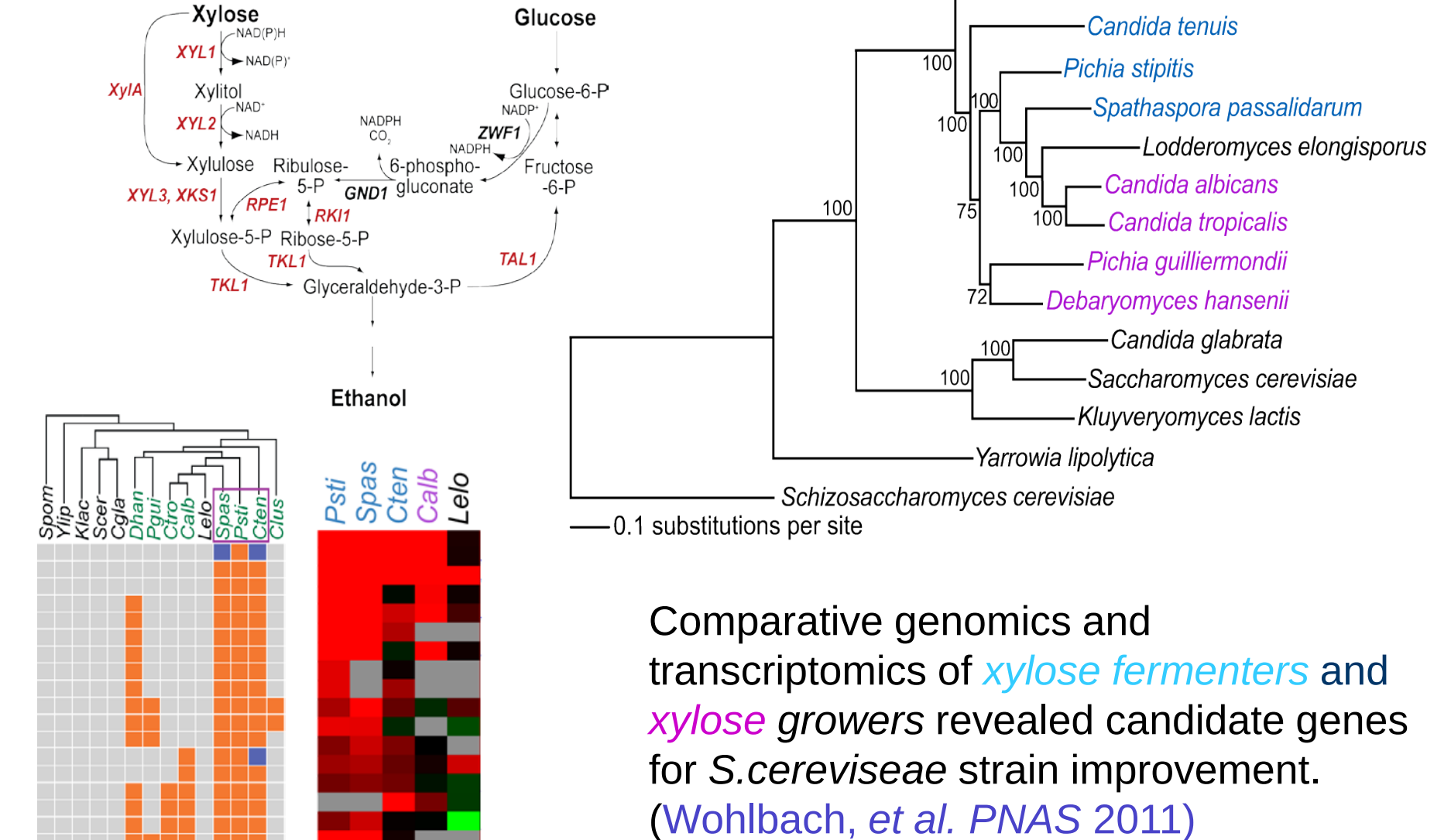


Expanded small secreted proteins in rusts fungi. (Duplessis et al., PNAS 2011)

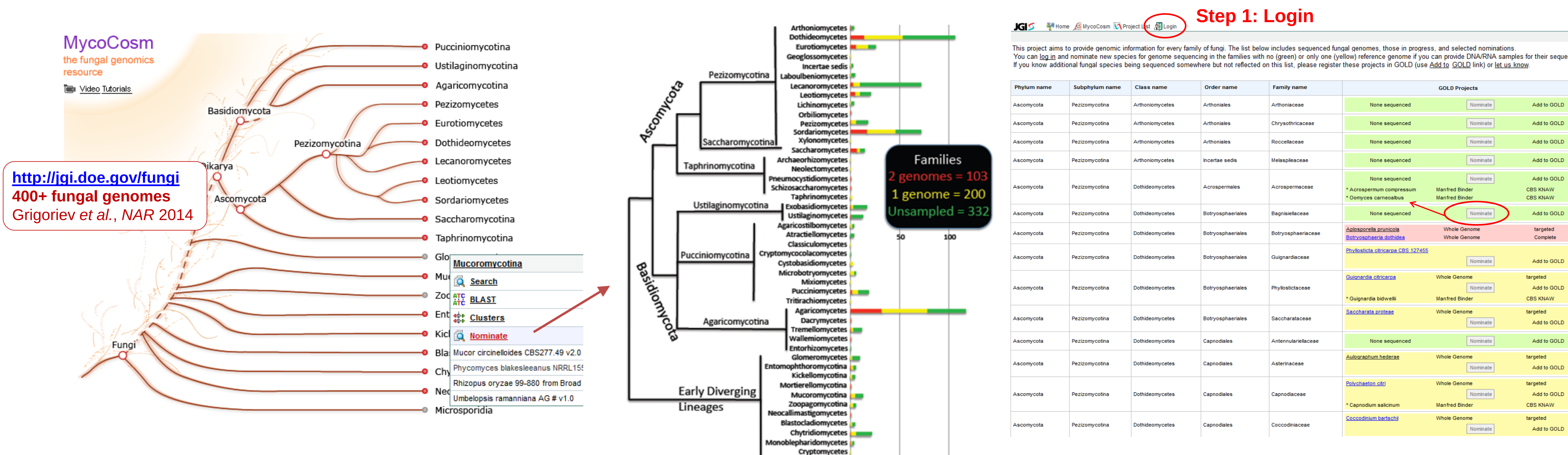
Wood Decayers



Xylose Fermenters



1000 Fungal Genomes Project



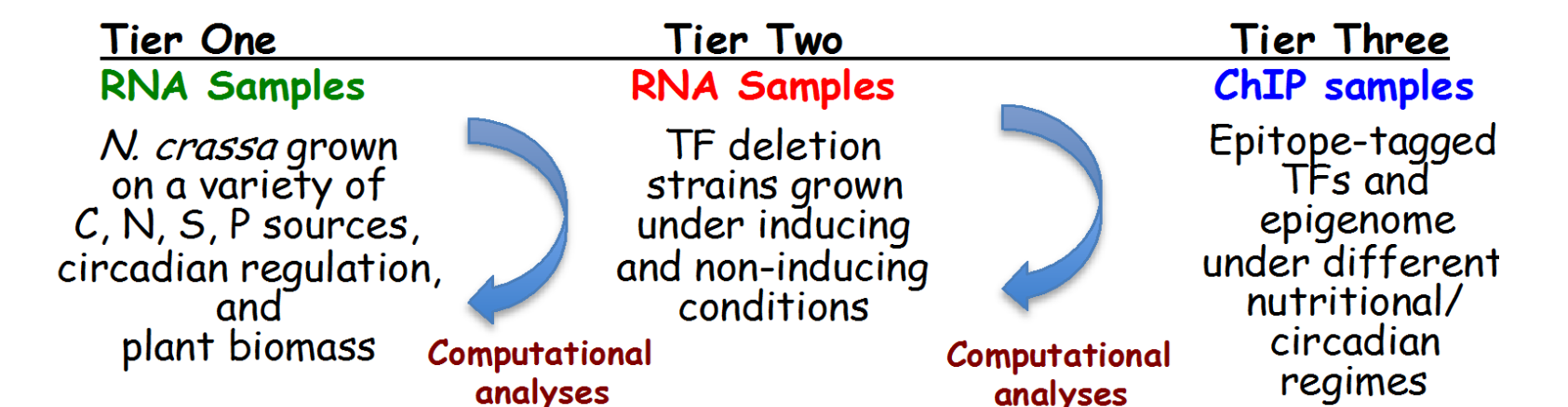
Sequencing 1000 fungal genomes from across the Fungal Tree of Life will provide references for research on plant-microbe interactions and environmental metagenomics. (Spatofora et al., CSP12)

Step 2: Nominate new species

Step 3: Prepare DNA and RNA samples

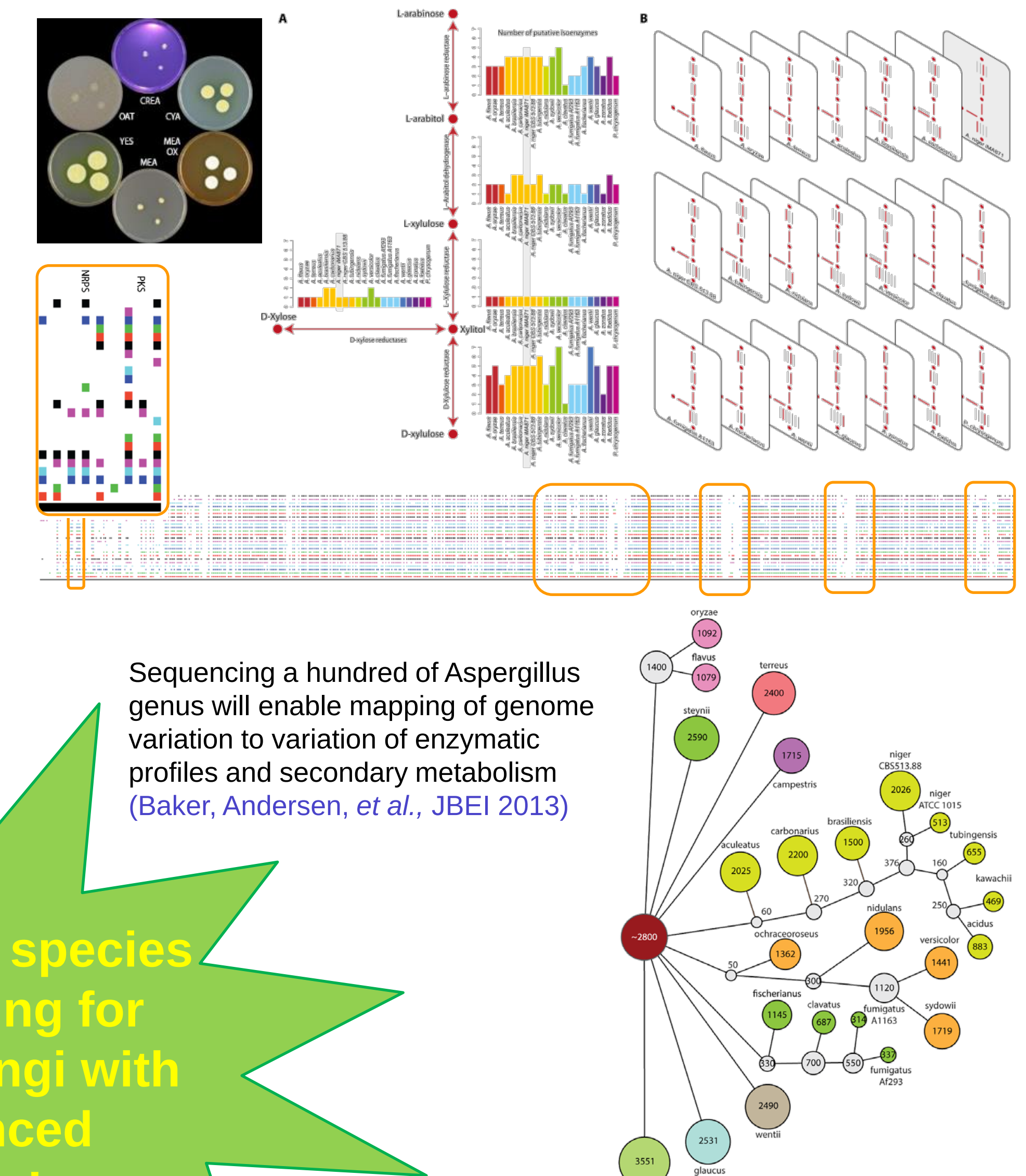
Nominate new species for sequencing for families of Fungi with no sequenced genomes!

Fungal Nutritional ENCODE



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)