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Fueling the Future with Fungal Genomes:

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Fueling the Future with Fungal Genomes

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Fueling the Future with Fungal Genomics

Igor V. Grigoriev, DOE Joint Genome Institute

JGI
JOINT GENOME INSTITUTE
DEPARTMENT OF ENERGY
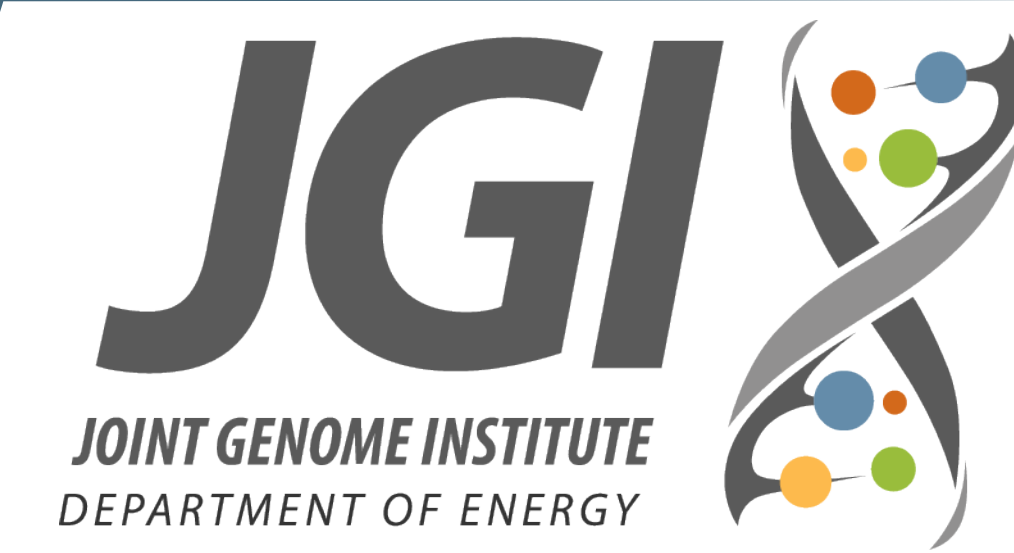
Abstract

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.
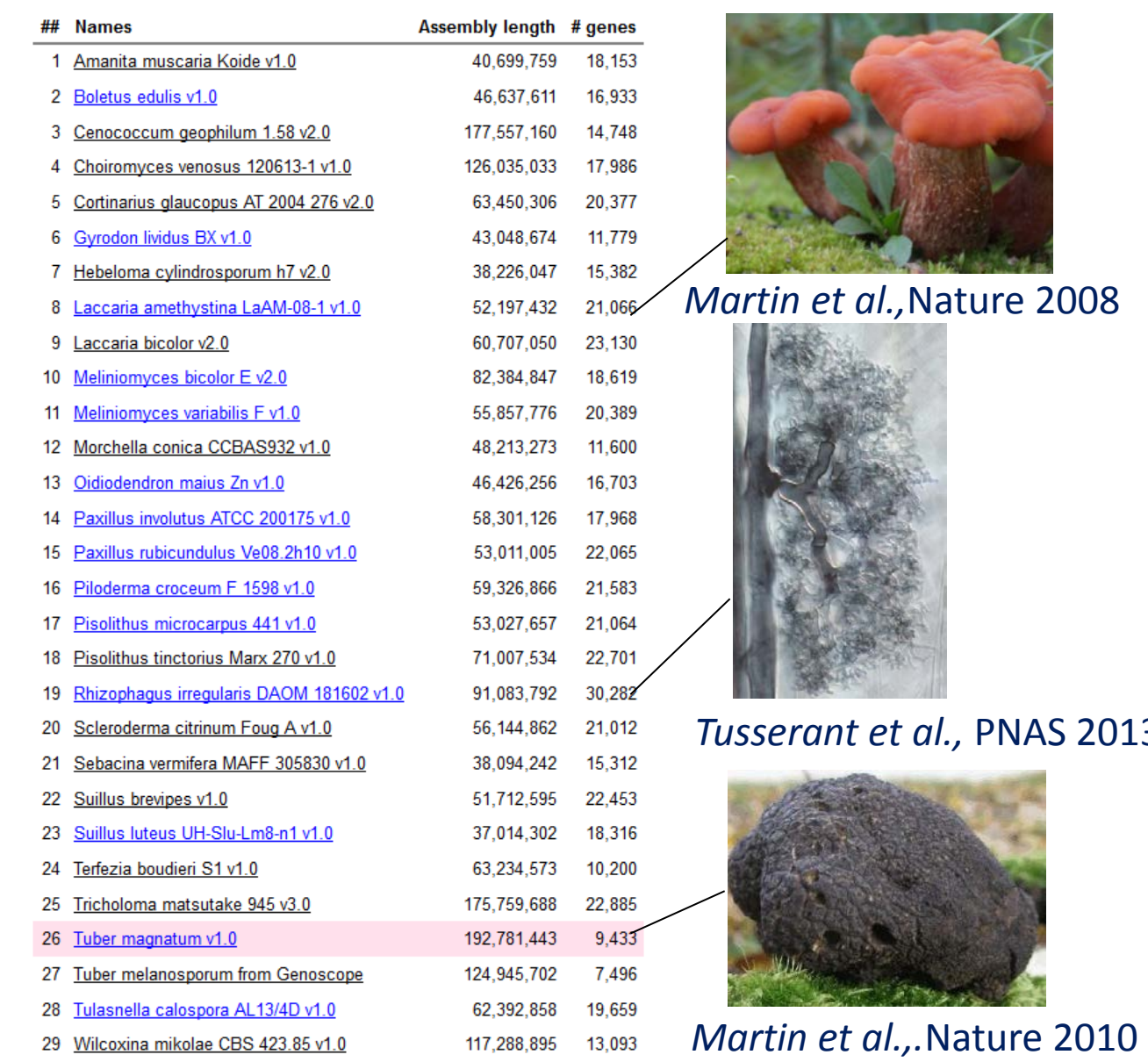
Fungi for Energy

Bio-refinery

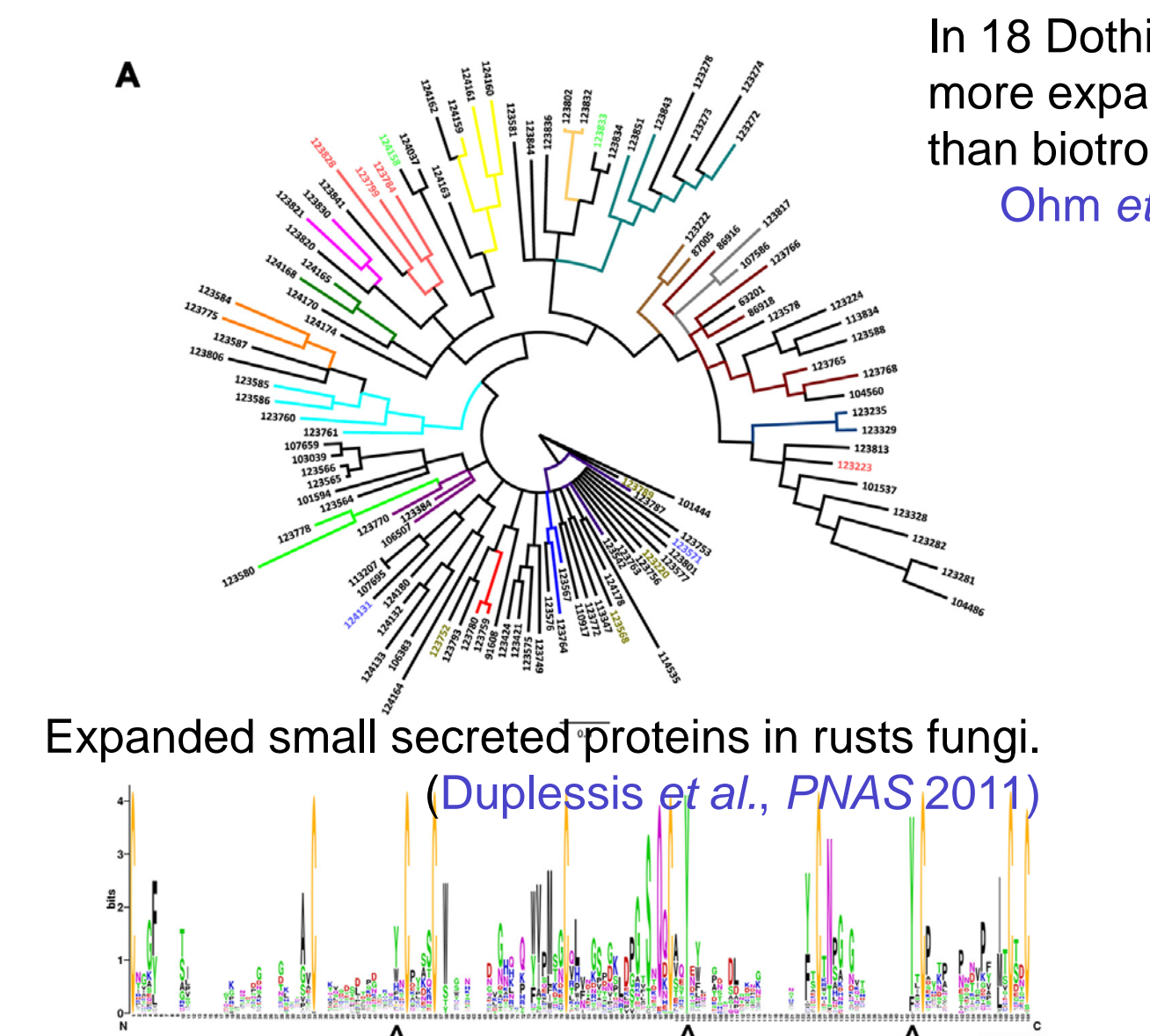Plant symbionts and pathogens → Lignocellulose degradation → Sugar Fermentation

Grow → Degrade → Ferment

Grigoriev, et al., Mycology, 2011

Fungal System Biology

S.commune
ECM: plant+fungus
Soil metagenomes

Host-fungal interactions

Model fungi → Simple systems → Complex environments

The Genomic Encyclopedia of Fungi
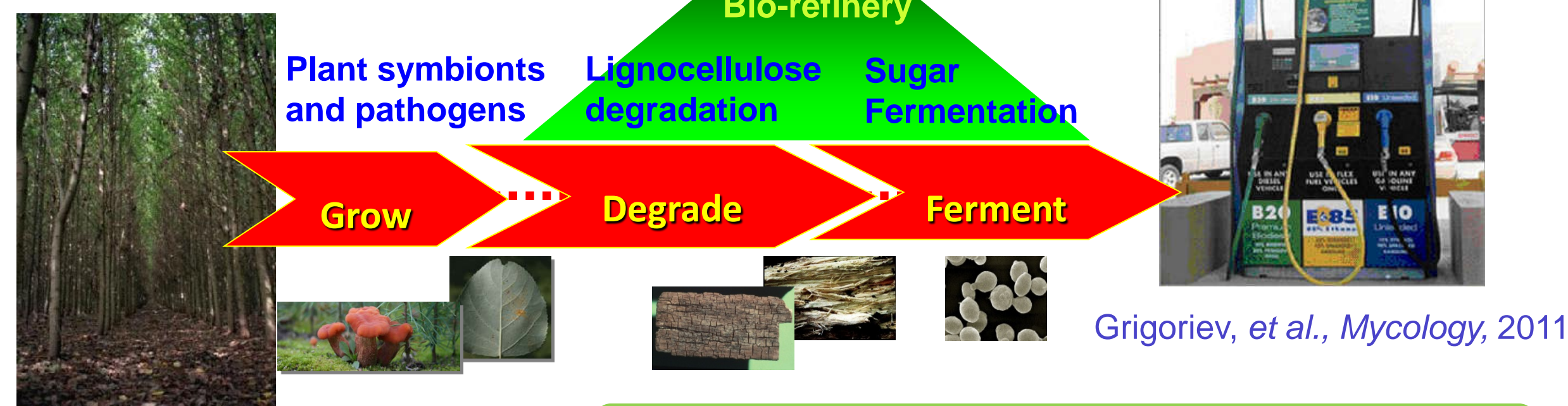
Mycorrhizal Symbionts

http://genome.jgi.doe.gov/Mycorrhizal_fungi

Martin et al., Nature 2008
Tusserant et al., PNAS 2013
Martin et al., Nature 2010

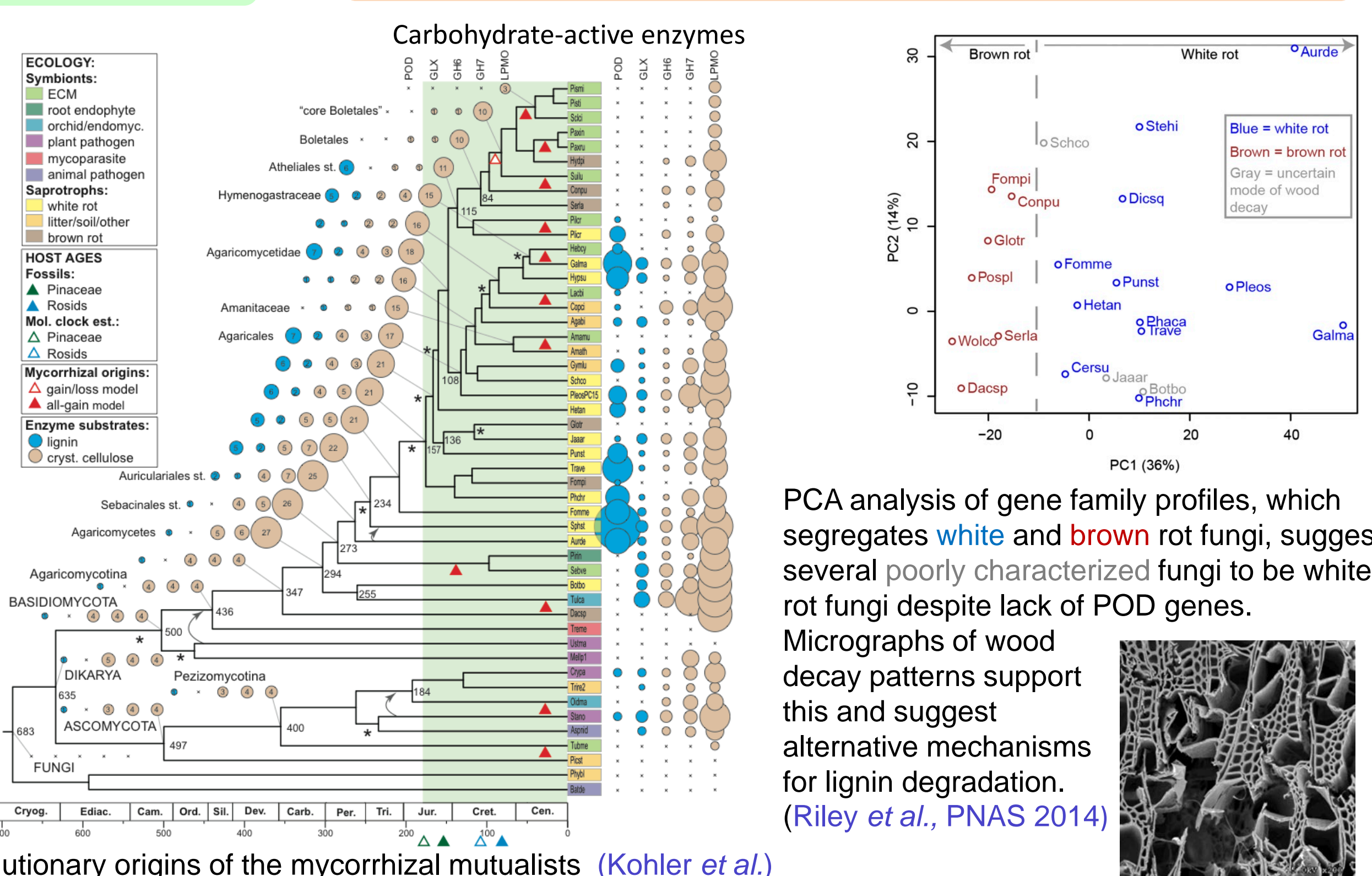Micorrhizal Genomics Initiative open doors for analysis of convergent evolution (Martin et al. CSP11)

Wood Decayers

Carbohydrate-active enzymes

Evolutionary origins of the mycorrhizal mutualists (Kohler et al.)

PCA analysis of gene family profiles, which 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. (Riley et al., PNAS 2014)

Plant Pathogens

In 18 Dothideomycetes SSP are more expanded in nechrotrophs than biotrophs.
Ohm et al., PLoS Path. 2012.

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

Sacreted peptidases
SSP
Secondary metabolism
CAZymes
Sacreted lipases

Xylose Fermenters

Comparative genomics and transcriptomics of xylose fermenters and xylose growers revealed candidate genes for S.cereviseae strain improvement. (Wohlbach, et al. PNAS 2011)

Orthologs   Transcriptomes

Towards Functional Genomics

Fungal Nutritional ENCODE

Tier One
RNA Samples
N. crassa grown on a variety of C, N, S, P sources, circadian regulation, and plant biomass
Computational analyses

Tier Two
RNA Samples
TF deletion strains grown under inducing and non-inducing conditions
Computational analyses

Tier Three
ChIP samples
Epitope-tagged TFs and epigenome under different nutritional/ circadian regimes
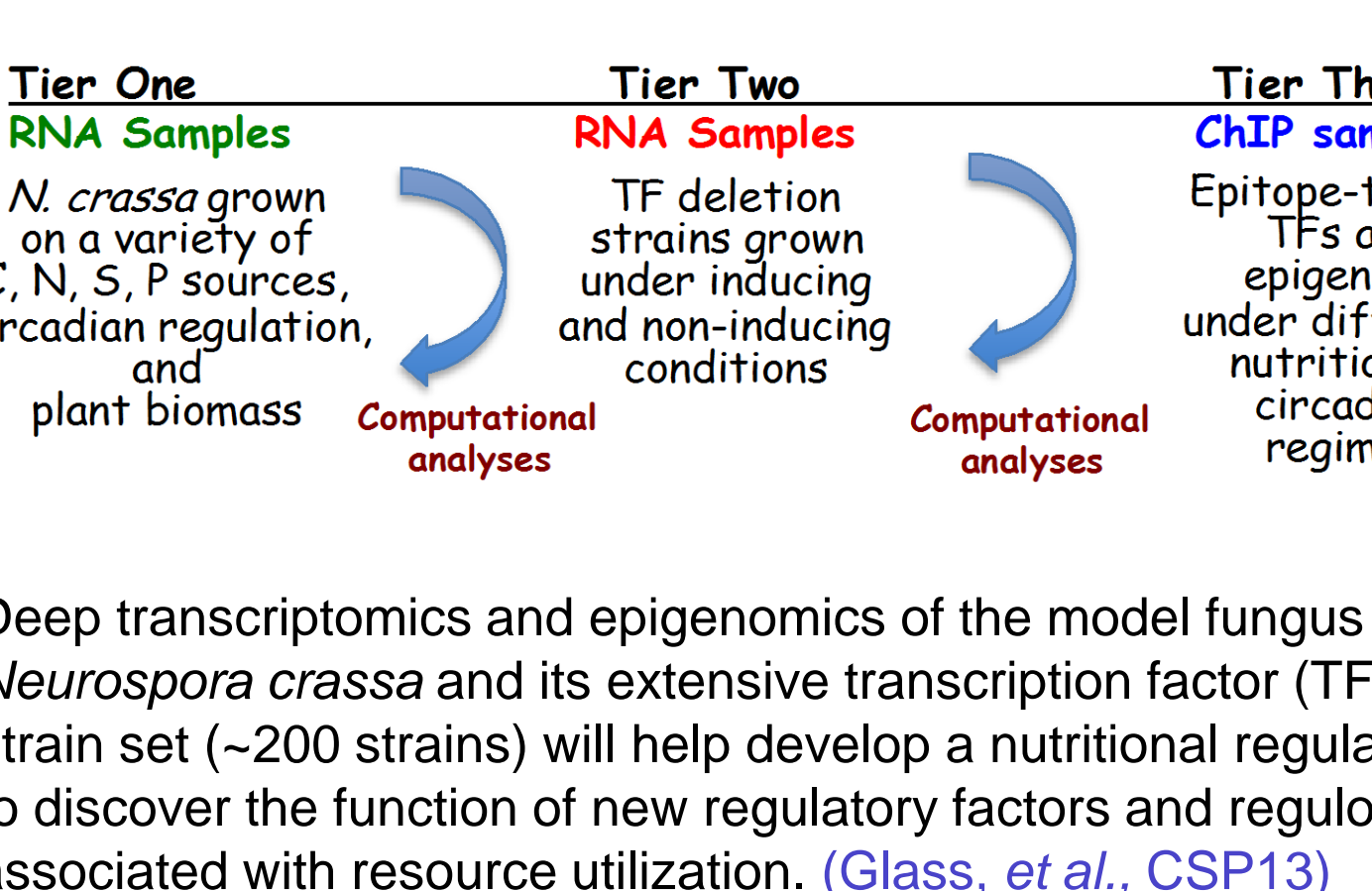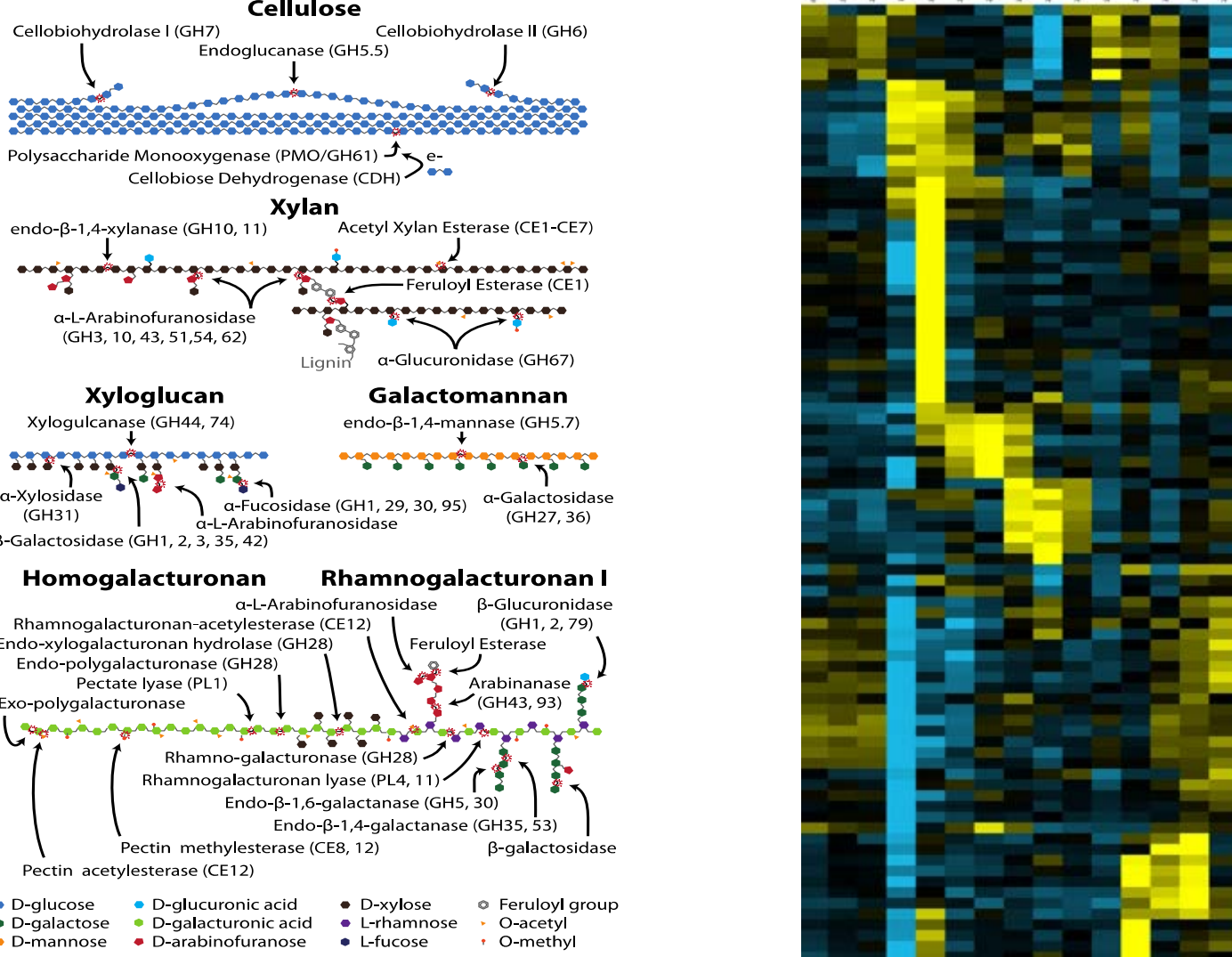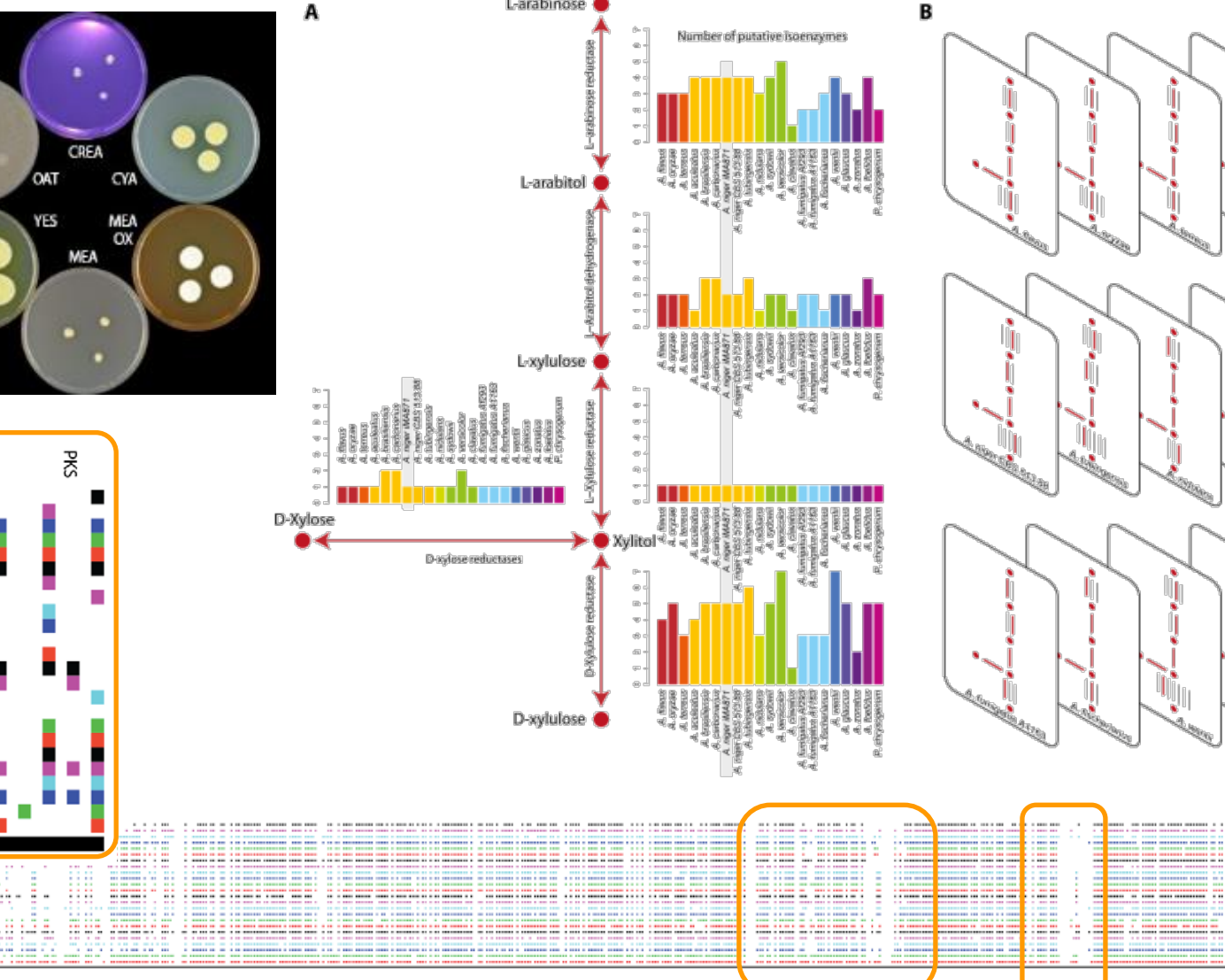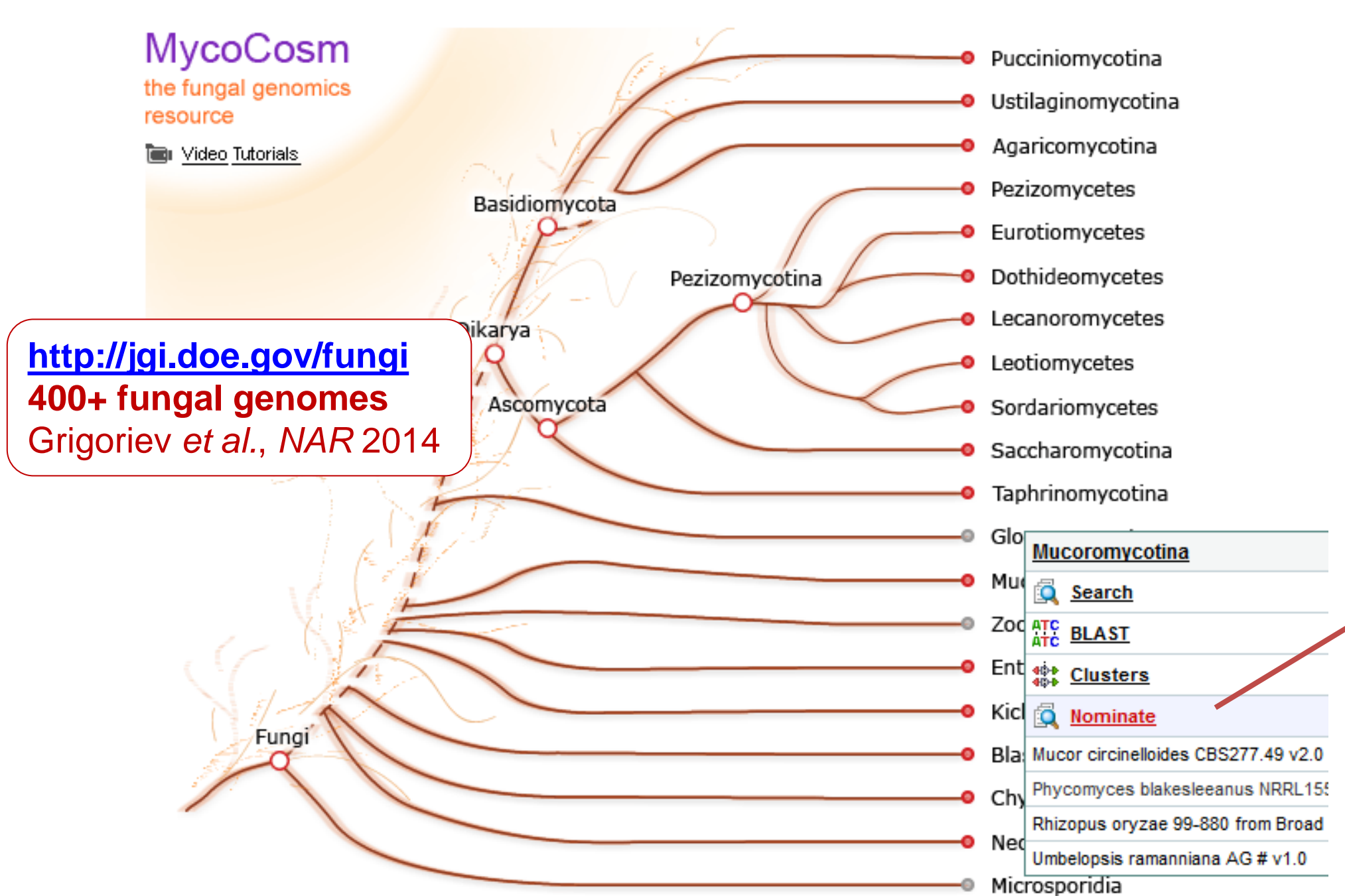
Deep transcriptomics and epigenomics of the model fungus Neurospora crassa and its extensive transcription factor (TF) deletion strain set (~200 strains) will help develop a nutritional regulatory map to discover the function of new regulatory factors and regulons associated with resource utilization. (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)

MycoCosm

MycoCosm
the fungal genomics resource

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

Puccinomycotina
Ustilaginomycotina
Agaricomycotina
Pezizomycotina
Eurotiomycetes
Dothideomycetes
Lecanoromycotina
Leotiomycetes
Sordariomycetes
Saccharomycotina
Taphrinomycotina

Search
BLAST
Clusters
Nominate

1000 Fungal Genomes Project

Step 1: Login

Families
2 genomes = 103
1 genome = 200
Unsampled = 332

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!