

Fungal Genomics Program

Igor Grigoriev¹ * (ivgrigoriev@lbl.gov)

¹DOE Joint Genome Institute, Lawrence Berkeley National Laboratory

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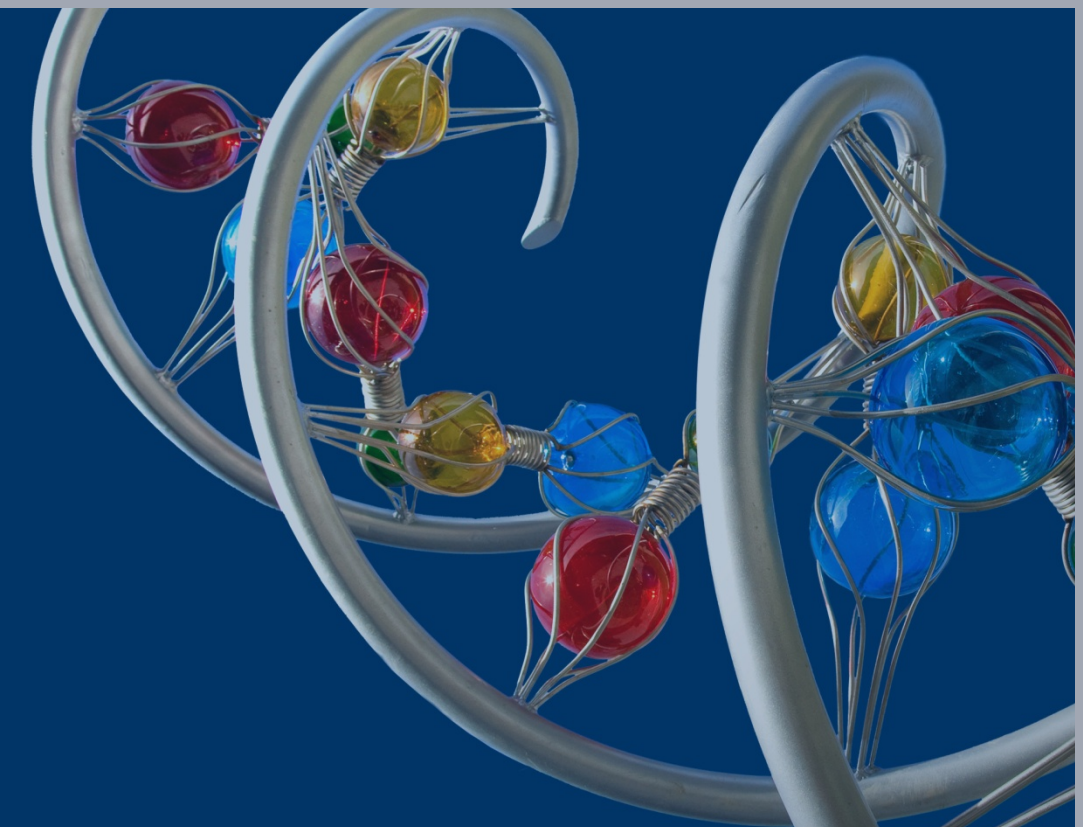
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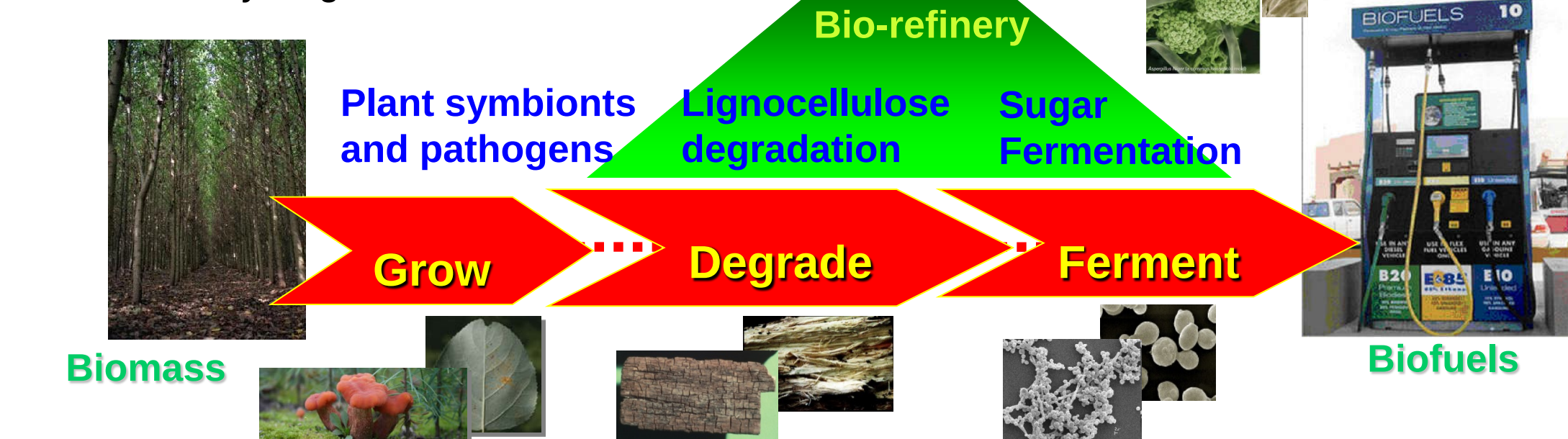
ABSTRACT

Doubling the number of sequenced and annotated genomes every year, the JGI Fungal Program (jgi.doe.gov/fungi) is moving towards the new large scale initiatives aligned with the 2010 Grand Challenges for Biological and Environmental Research: a long term vision. One of the initiatives, the *1000 Fungal Genomes* project, is aimed to explore fungal diversity across the Fungal Tree of Life in order to provide references for research on plant-microbe interactions and environmental metagenomics. Another initiative, the *Genomic Encyclopedia of Fungi*, is focused on diversity among DOE relevant fungi in the areas of plant health and biorefinery parts lists, which will help us to explore the interactions of bioenergy crop species with symbionts and pathogens as well as to catalog industrially relevant genes, pathways, and hosts for biotechnology applications. In addition to broad exploration of fungal diversity, we will also focus on the functional analysis of several *fungal systems* of varying complexity: new model organisms, symbiotic systems such as lichens, and metagenomes of complex communities

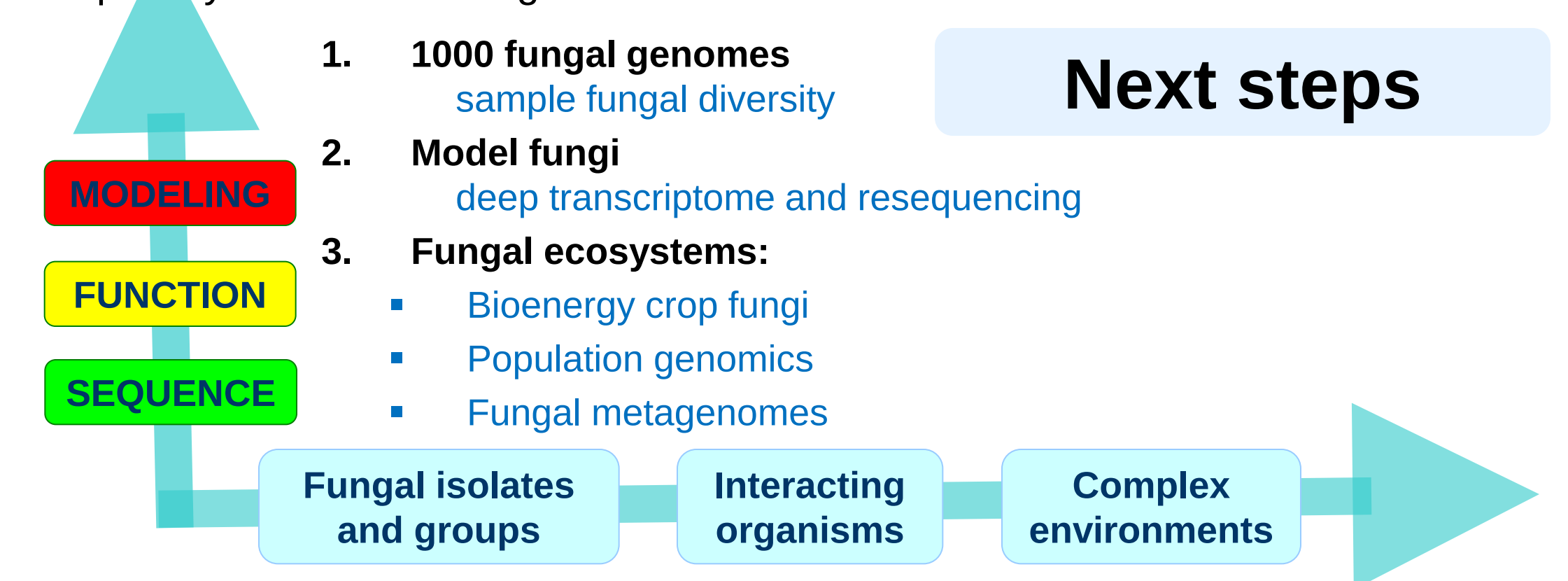


Mission and Strategy

Encoded in the genomes of the organisms of the **Kingdom Fungi** are biological processes with high relevance to the DOE missions in bioenergy production, biogeochemistry, and carbon cycling.

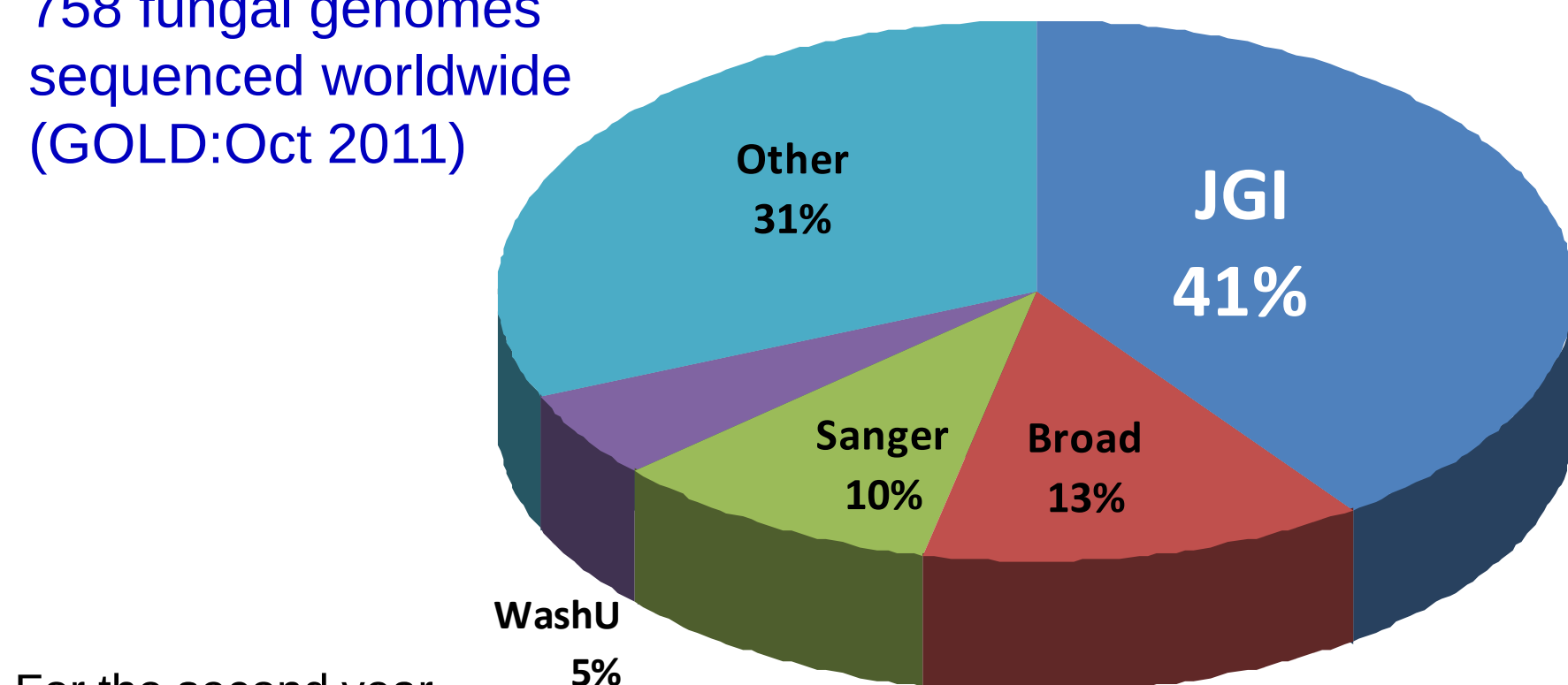


The **JGI Fungal Genomics Program** aims to scale up sequencing and analysis of fungal genomes to explore the diversity of fungi important for energy and the environment, and to promote functional studies on a system level. Combining new sequencing technologies and comparative genomics tools, JGI is now leading the world in fungal genome sequencing and analysis. Over 120 sequenced fungal genomes with analytical tools are available via MycoCosm (www.jgi.doe.gov/fungi), a web-portal for fungal biologists. Our model of interacting with user communities, unique among other sequencing centers, helps organize these communities, improves genome annotation and analysis work, and facilitates new larger-scale genomic projects. This resulted in 20 high-profile papers published in 2011 alone and contributing to the Genomics Encyclopedia of Fungi, which targets fungi related to plant health (symbionts, pathogens, and biocontrol agents) and biorefinery processes (cellulose degradation, sugar fermentation, industrial hosts). Our next grand challenges include larger scale exploration of fungal diversity (1000 fungal genomes), developing molecular tools for DOE-relevant model organisms, and analysis of complex systems and metagenomes.



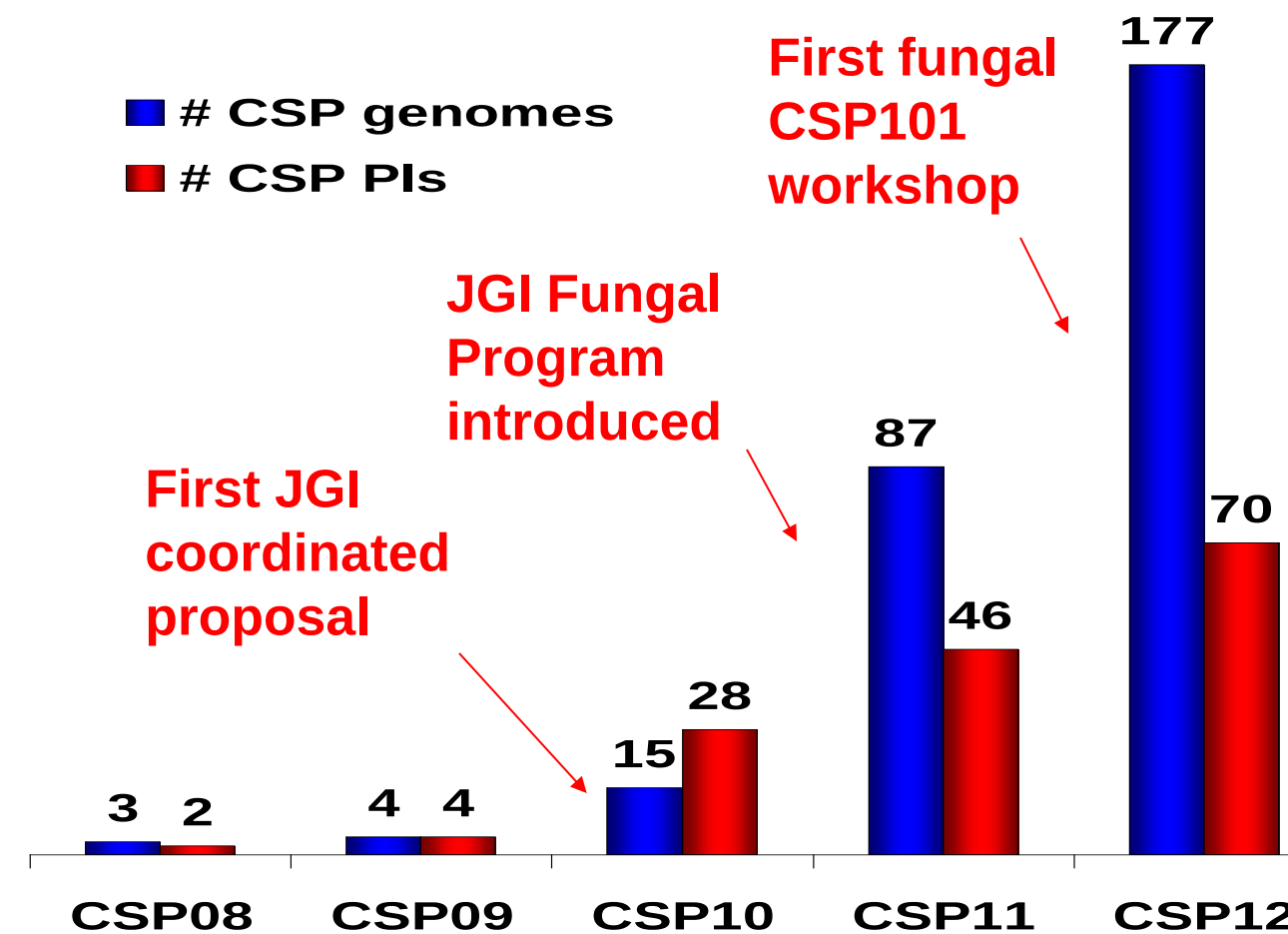
Lead the World in Fungal Genomics

758 fungal genomes sequenced worldwide (GOLD:Oct 2011)

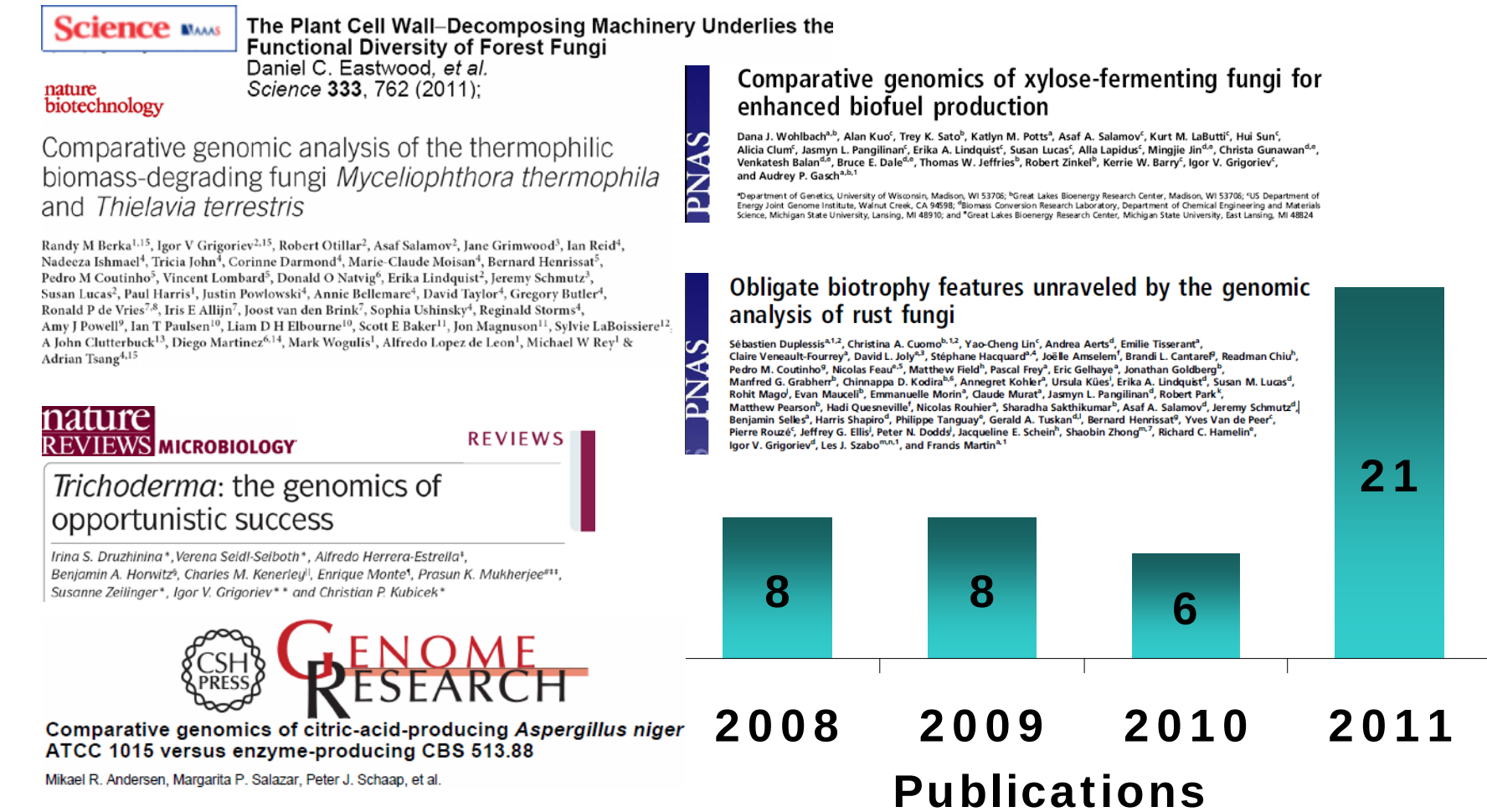


For the second year in a row, we have doubled the number of sequenced and annotated fungal genomes

Organized User Communities



Published High-profile Science



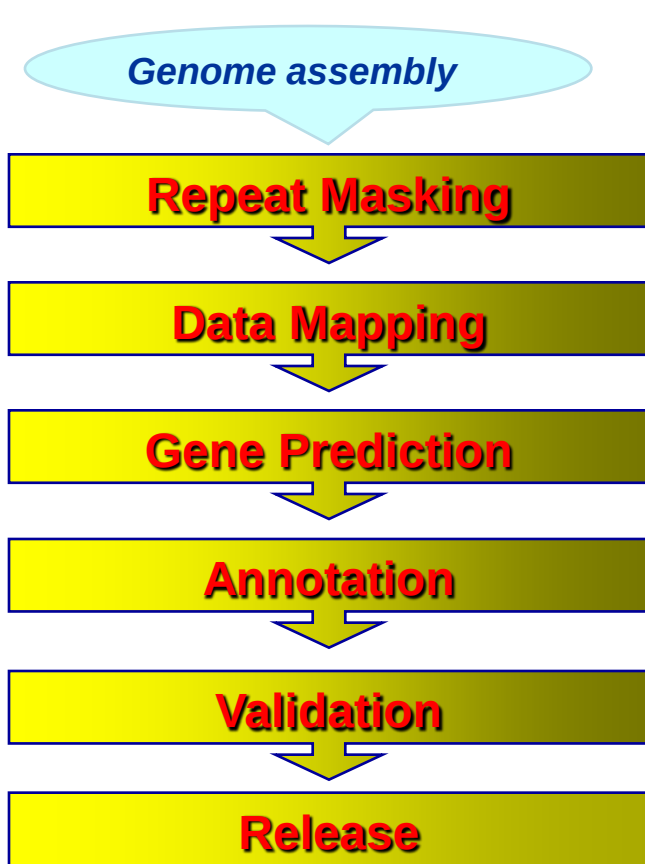
Tools

The Annotation Pipeline

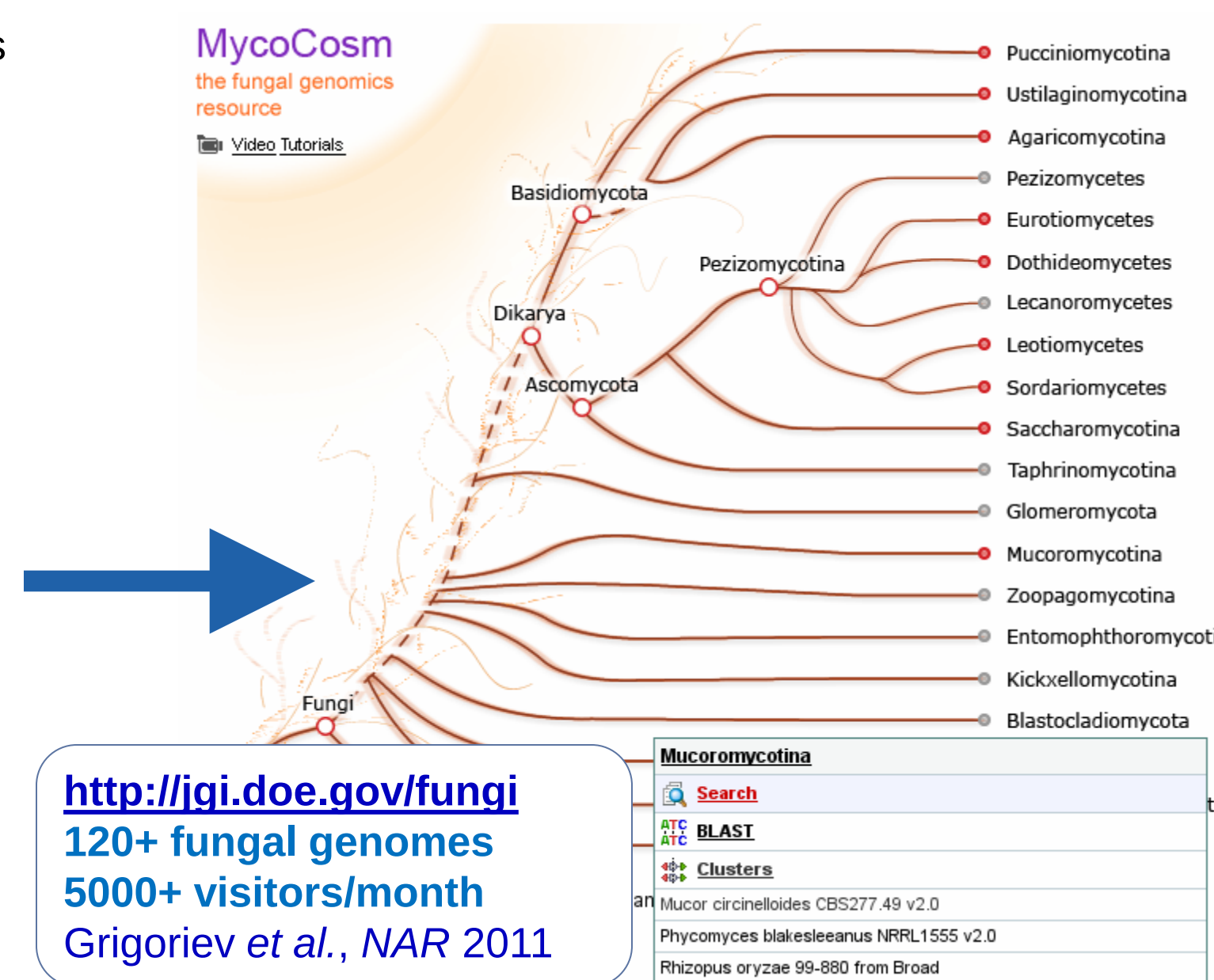
Automated **Annotation Pipeline** tuned for high-throughput annotation of fungal genomes runs on compute clusters at NERSC and is equipped with graphical monitoring tools. **MycoCosm** provides interactive web-based tools for functional and comparative genomics. **Quality assurance** is implemented at every stage of the annotation process: built-in pipeline controls, benchmarked tools, two-tier pre-release data/portal QC, user feedback, and community annotation.

Pipelines Comparison	MAKER	JGI pipeline	JGI R&D
# of predicted gene models	9,940	12,290	12,802
with Swissprot hits	6,521	7,356	7,900
with PFAM domains	5,365	6,010	6,353
with EST support	9,252	10,796	11,105
# of unique PFAM domains	2,207	2,245	2,322
EST coverage per gene	93.0%	93.2%	93.3%
# EST-supported splice sites	99,627	102,200	104,246

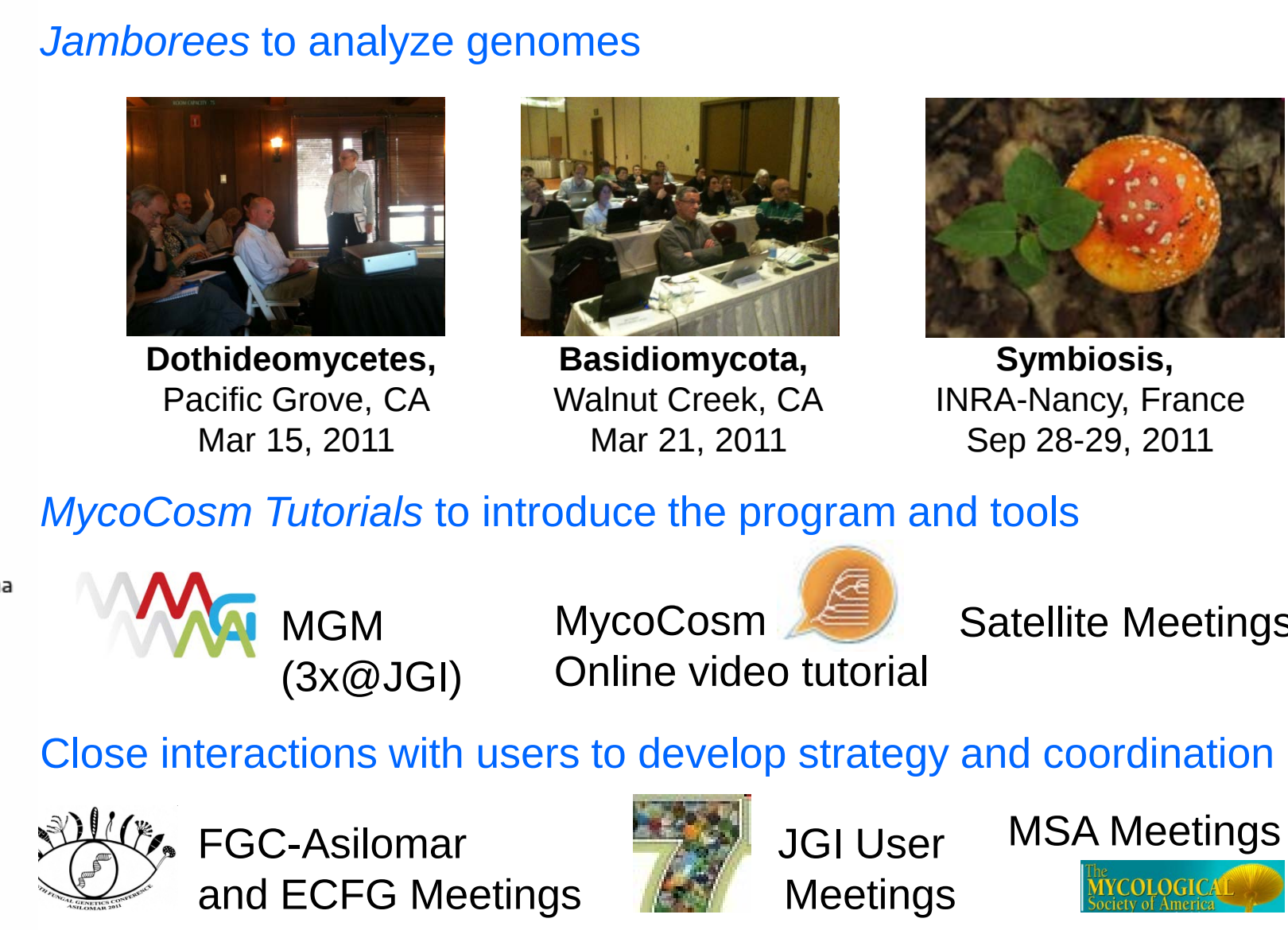
Pipeline benchmarks, development, and release to production



MycoCosm: 100+ fungal genomes

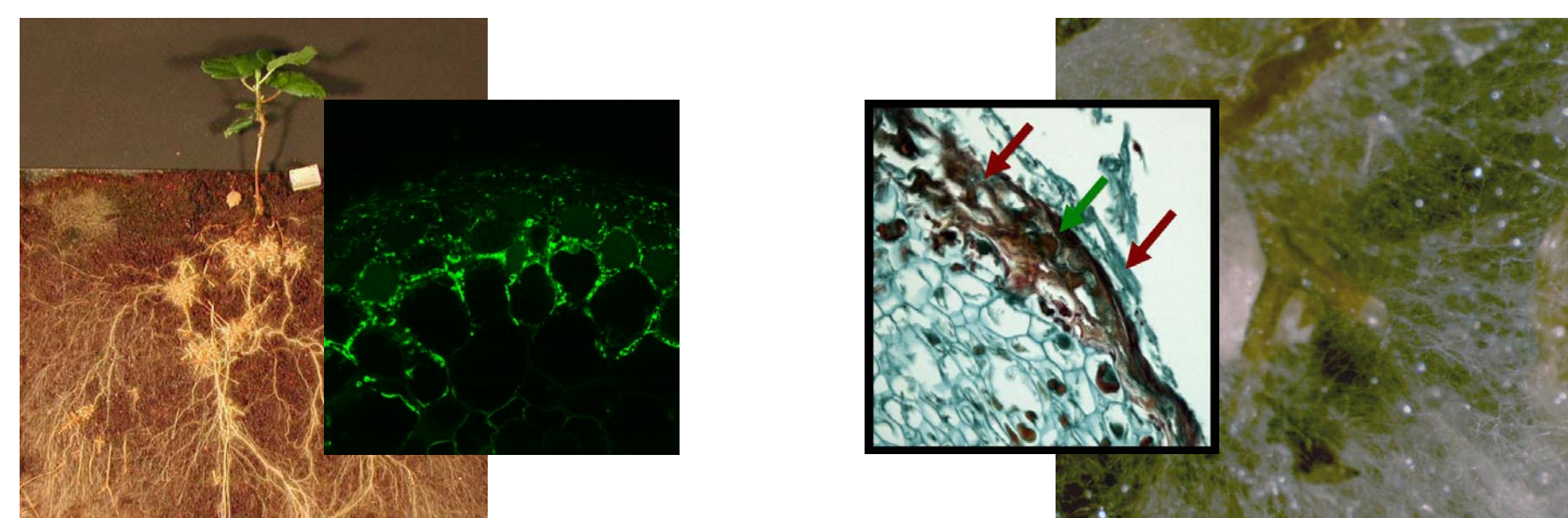


Community Outreach



Science: Genomic Encyclopedia of Fungi

Plant Health: Symbionts



Laccaria bicolor (ECM)

Small secreted proteins are expanded in poplar symbiont and overexpressed in ECM tissue.

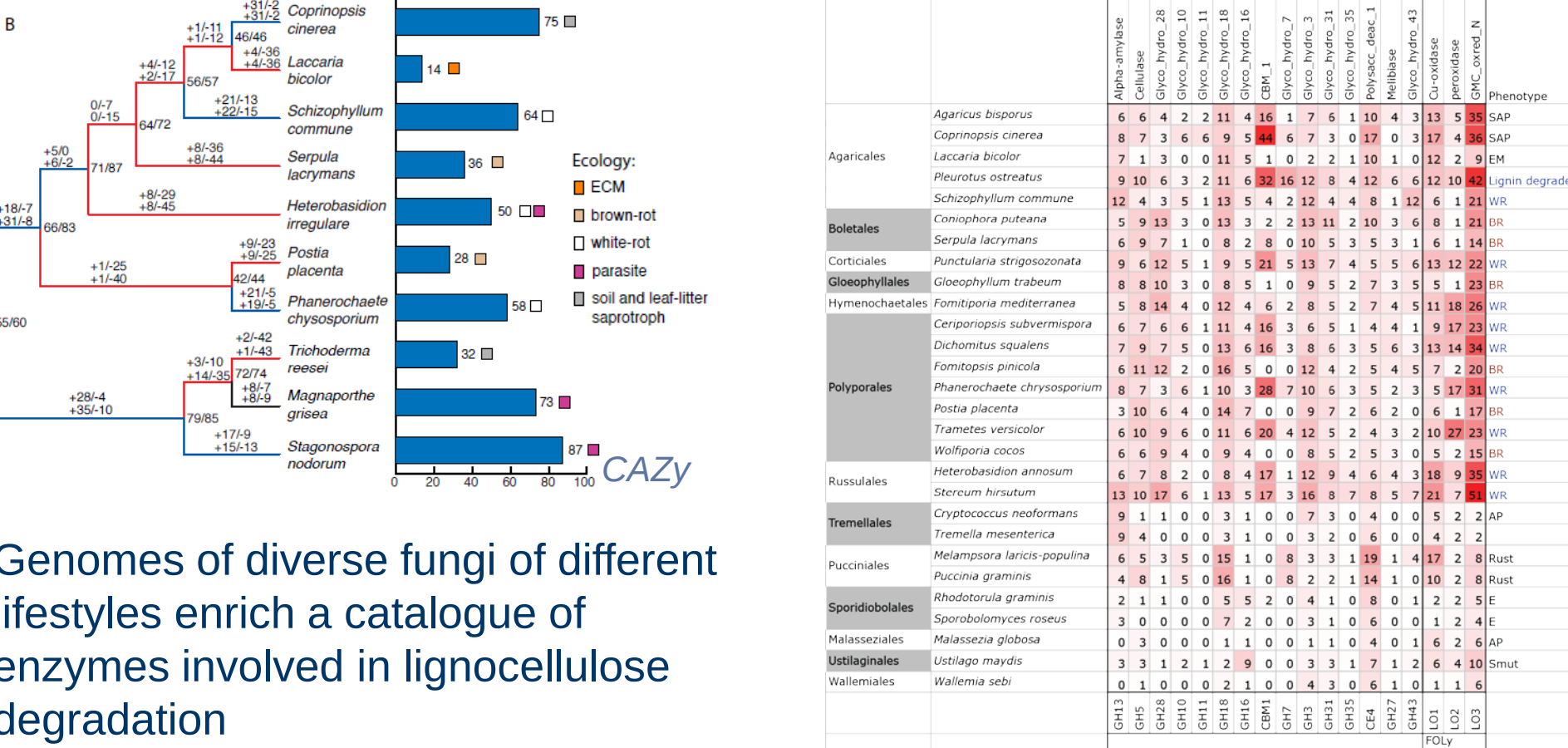
Martin et al., Nature 2008

Serpula lacrymans (brown rot)

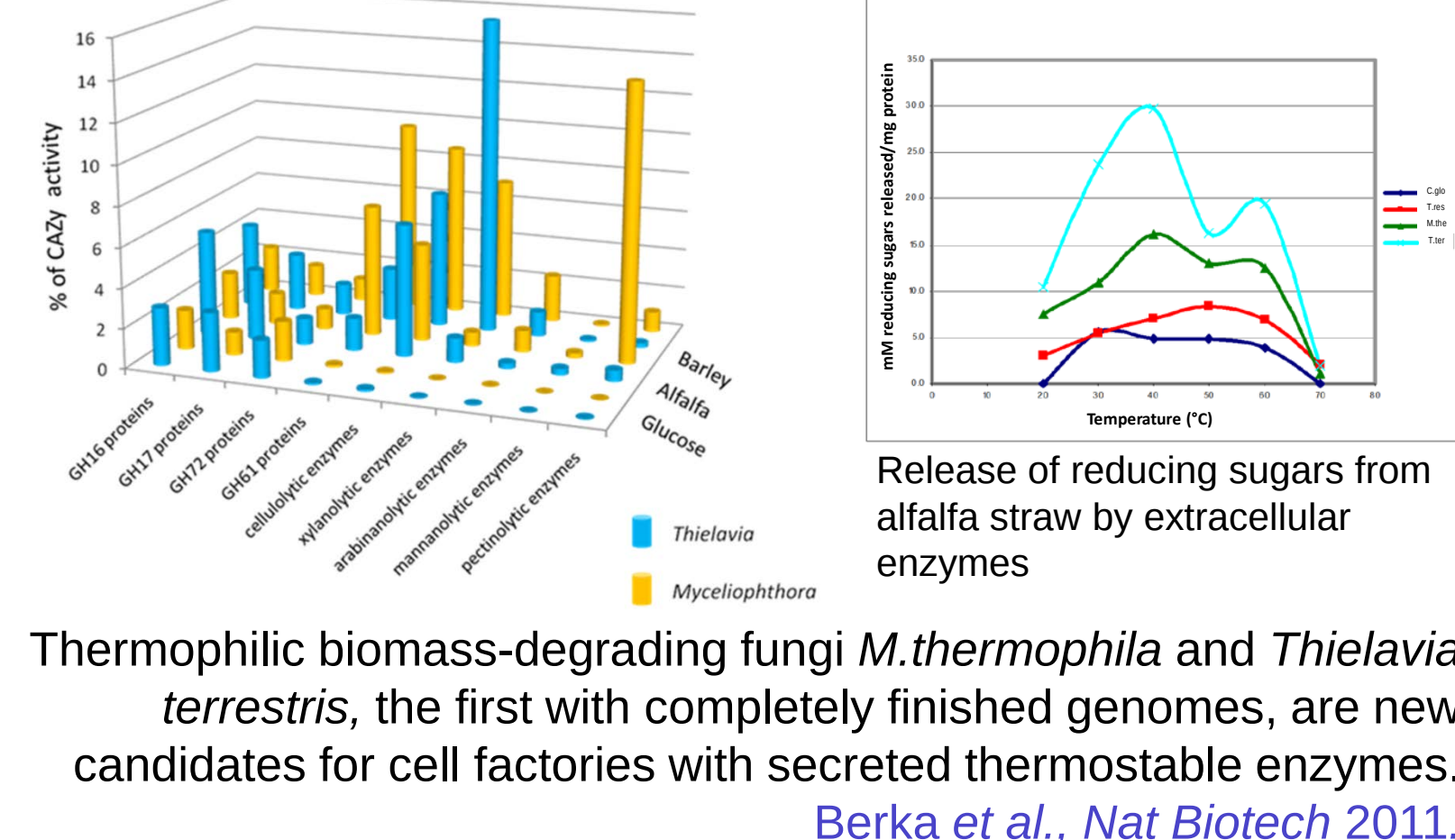
Convergent evolution of brown rot and ECM fungi from white rot ancestor.

Eastwood et al., Science 2011

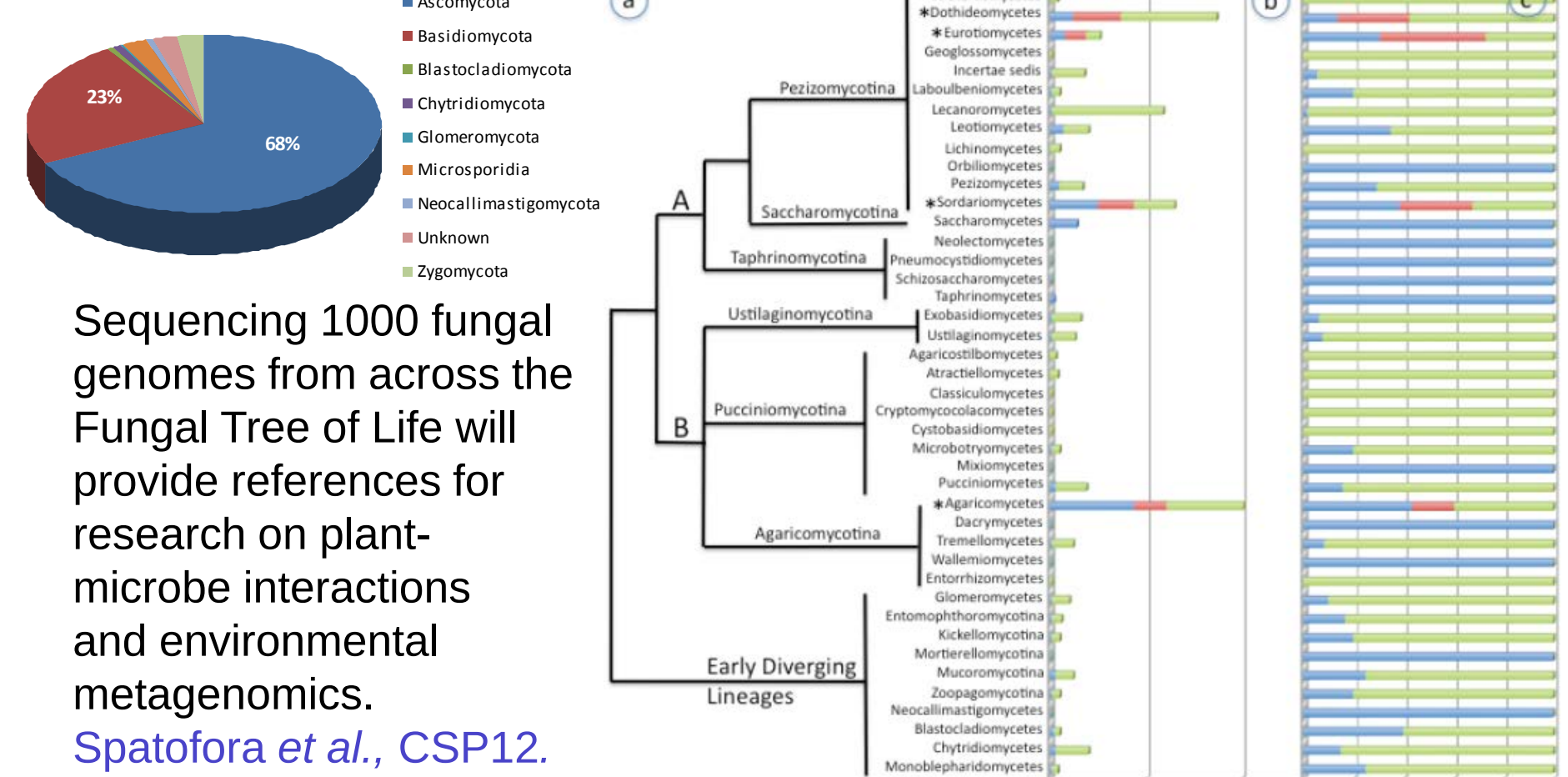
Biorefinery: Lignocellulose Degradation



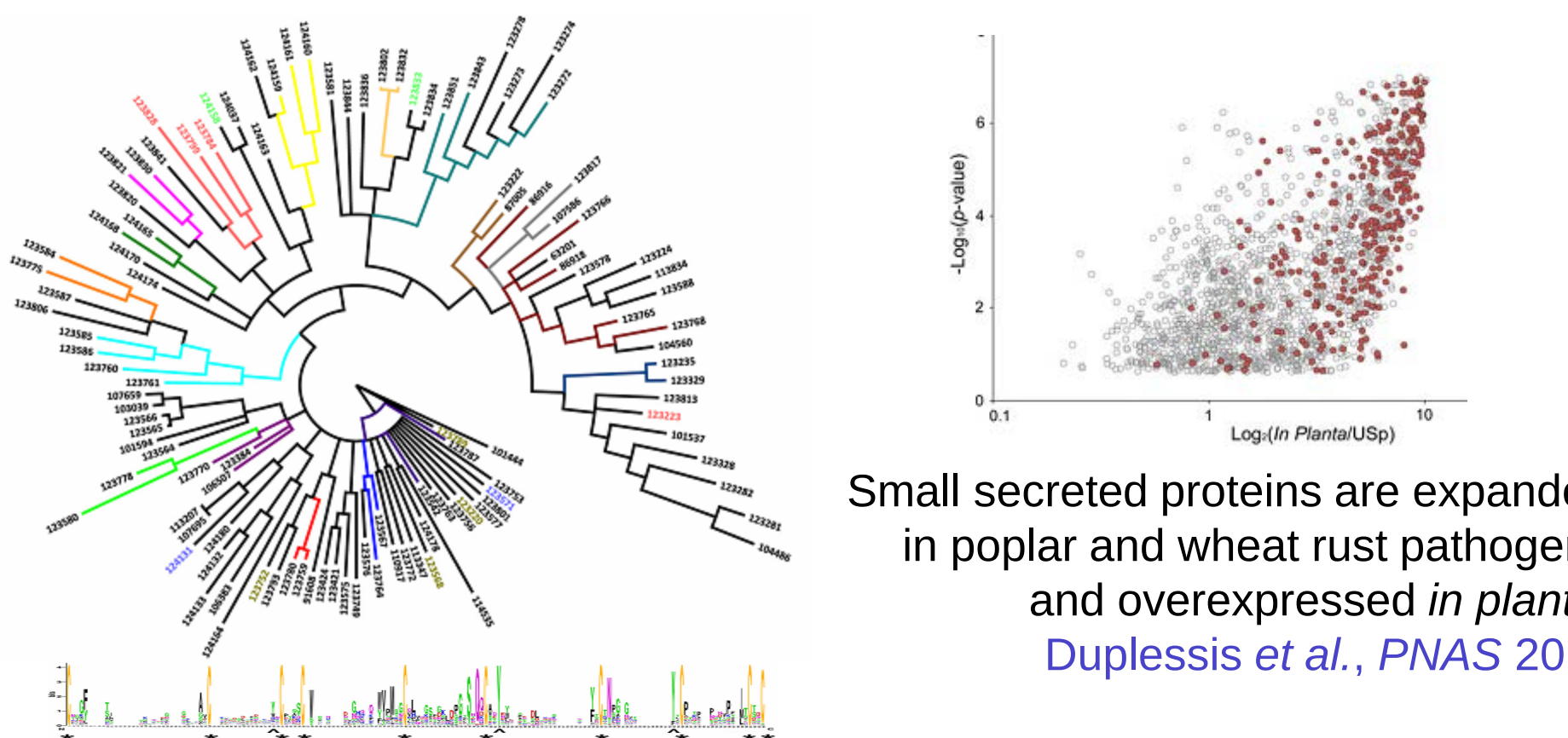
Biorefinery: Thermophiles



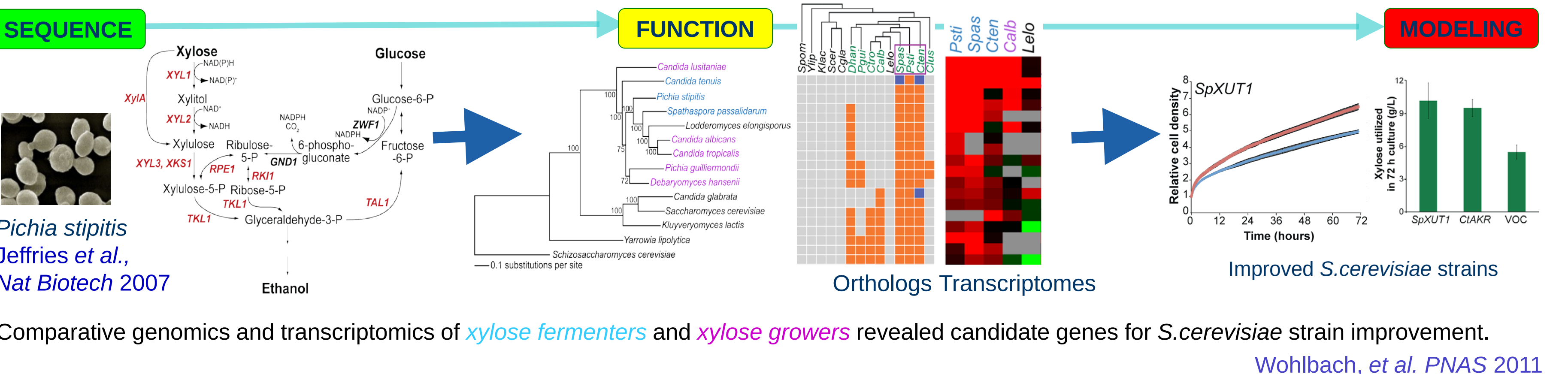
Diversity: 1000 Fungal Genomes



Plant Health: Pathogens



Biorefinery: Engineering Improved Xylose Fermentation



Fungal Systems & Metagenomes

