

Program Goals

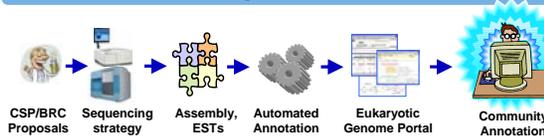
The JGI contributes significantly to worldwide sequencing and analysis of fungal and algal genomes. 68 fungal and 21 algal projects at different stages are currently in JGI pipeline. The DOE mission positions the JGI to sequence a broad range of microbial eukaryotes.

The Eukaryotic Microbial program is built on CSP and BRC proposals, recommendations of advisory boards, and strategic planning for:

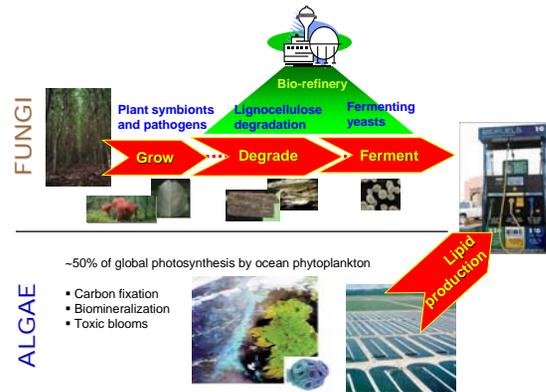
- Sequencing phylogenetic breadth
- Deeper sampling of DOE mission relevant organisms
- Metagenomes (ecological diversity)
- Sequence based science for relevant model systems



Program Tools



Fungi and Algae for DOE Mission

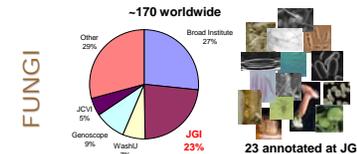


~50% of global photosynthesis by ocean phytoplankton

- Carbon fixation
- Biomining
- Toxic blooms

JGI Leadership in Fungal and Algal Genomics

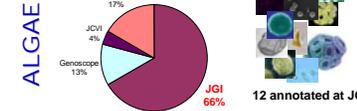
Genomes In Progress



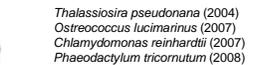
Published Genomes



Genomes In Progress

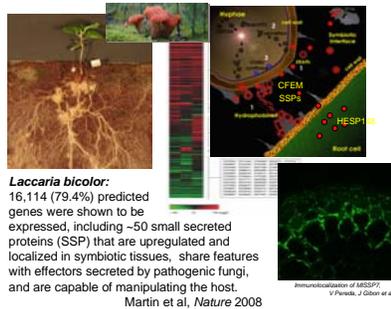


Published Genomes



JGI-enabled Science

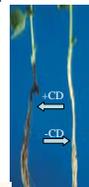
Mycorrhizal Symbiosis



Laccaria bicolor: 16,114 (79.4%) predicted genes were shown to be expressed, including ~50 small secreted proteins (SSP) that are upregulated and localized in symbiotic tissues, share features with effectors secreted by pathogenic fungi, and are capable of manipulating the host. Martin et al., Nature 2008

Plant Pathogens

Nectria haematococca MPVI: Loss of conditionally dispensable (CD) chromosome genes reduces virulence and rhizosphere competency. CD chromosomes show bias in codon usage and significantly lower genome conservation with *Fusarium* sp that other Nectria chromosomes.



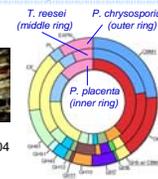
VanEtten et al., in prep.

Lignocellulose Degradation



White rot, Phanerochaete chrysosporium
Martinez et al., Nature Biotech. 2004

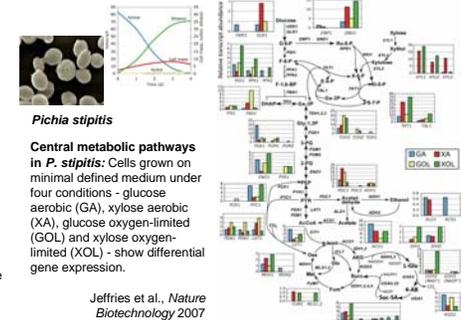
Brown rot, Postia placenta
P. placenta utilizes biodegradative Fenton chemistry to depolymerize cellulose and lost of capacity for efficient lignin depolymerization in comparison with white-rot *P.chrysosporium*.



CAZy composition: unusual repertoire of extracellular glycoside hydrolases in *P.placenta*.

Cullen et al., in prep.

Fermentation

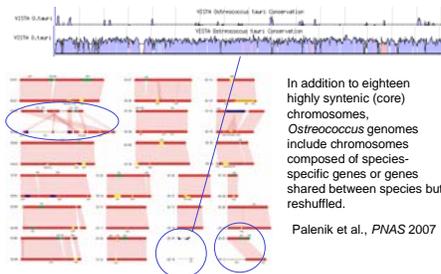


Pichia stipitis

Central metabolic pathways in *P. stipitis*: Cells grown on minimal defined medium under four conditions - glucose aerobic (GA), xylose aerobic (XA), glucose oxygen-limited (GOL) and xylose oxygen-limited (XOL) - show differential gene expression.

Jeffries et al., Nature Biotechnology 2007

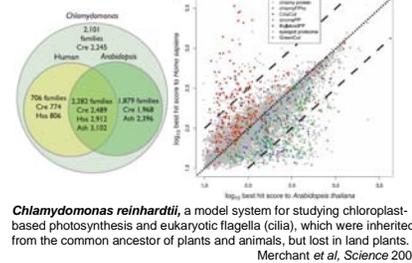
Genome Organization



In addition to eighteen highly syntenic (core) chromosomes, *Ostreococcus* genomes include chromosomes composed of species-specific genes or genes shared between species but reshuffled.

Palenik et al., PNAS 2007

Genome Evolution

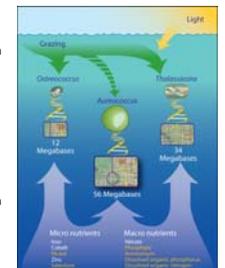


Chlamydomonas reinhardtii, a model system for studying chloroplast-based photosynthesis and eukaryotic flagella (cilia), which were inherited from the common ancestor of plants and animals, but lost in land plants.

Merchant et al., Science 2007

Ecology

Aureococcus anophagefferens, which causes harmful algal blooms, has optimized its genome to enable rapid growth under the widely variable environmental conditions in temperate estuaries and to win competition with co-occurring phytoplankton species.



Gobler et al., in prep

FUNGI

ALGAE