

Lawrence Berkeley National Laboratory

Recent Work

Title

Whole-Genome gene expression and gene family analyses of *Phycomyces blakesleeanus*, a model photoresponsive zygomycete

Permalink

<https://escholarship.org/uc/item/22w6950s>

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Publication Date

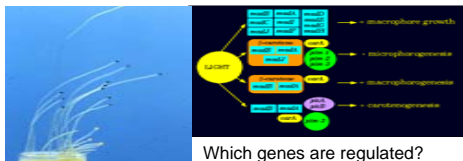
2008-04-06

Abstract

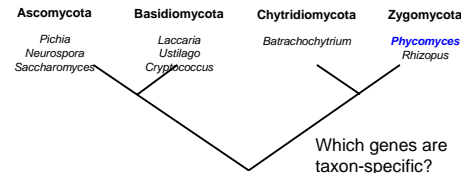
The photoresponsive zygomycete *Phycomyces blakesleeanus* is an experimentally tractable model system for elucidating the signalling pathways underlying photoregulation. Our recent sequencing, assembly, and annotation of the *P. blakesleeanus* genome allows us to complement classical molecular biological studies with genome-wide analyses of gene expression. We sequenced cDNAs from mycelia grown with and without light. The resulting 23410 'light' ESTs and 24437 'dark' ESTs were aligned with the genome and used to identify which of the 14792 genes could be described as transcriptionally active under either condition. We tagged 1538 genes (10%) as potentially light-specific, 1558 genes (11%) as potentially dark-specific, and 2431 genes (16%) as transcribed under both light and dark. In addition to its value as a model organism, *P. blakesleeanus* is one of only 2 zygomycetes with a sequenced genome, providing an opportunity to discover genes that are specific to or missing from zygomycetes, and gene families that are expanded or contracted in zygomycetes relative to the much better-sampled ascomycetes and basidiomycetes. We clustered *P. blakesleeanus* proteins with those of 13 other fungi and so far find 2 zygomycete-specific families of Zn-finger proteins, and a zygomycete-specific expansion of protein kinases. We also confirm the existence of a *Phycomyces*-specific family of F-box domain proteins.

Introduction - why study this genome?

A. It's photoresponsive



B. It's a zygomycote



Annotation results

Number of genes	14972
Genes per Mbp scaffold	264.6
Average gene length	1759 nt
Average number exons per gene	4.80
Average protein length	392 aa

See JGI Portal at <http://www.jgi.doe.gov/Phycomyces/>

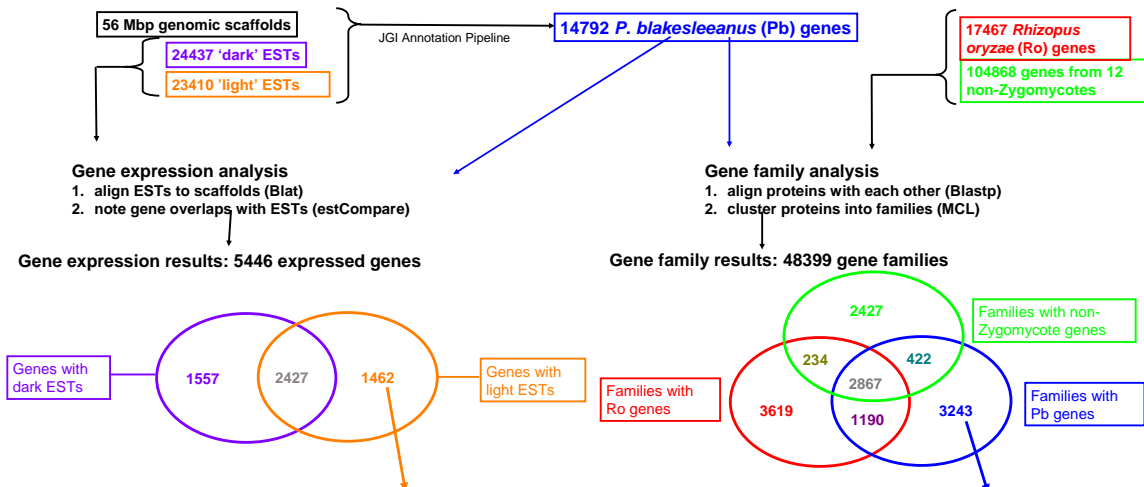
Summary of results

- 14,792 *P. blakesleeanus* genes predicted by JGI Annotation Pipeline.
- Using expression analysis identified light-induced genes including new Zygomycota-specific protease.
- Large number of new genes unique to *Phycomyces* discovered by gene family analysis.

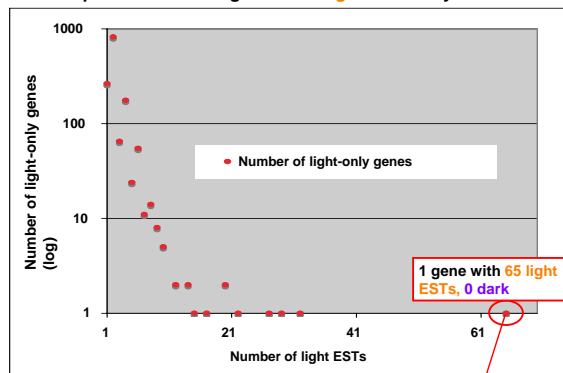
Acknowledgments

Jasmyn Pangilinan at JGI provided the assembly. Erika Lindquist at JGI provided the ESTs. JGI Annotation and Portal teams

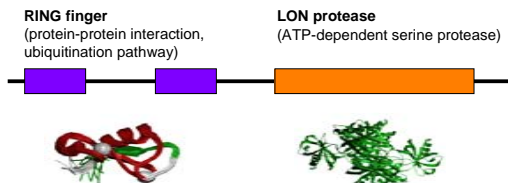
Workflow



Gene expression results: genes with light ESTs only



New gene, found only in Zygomycota



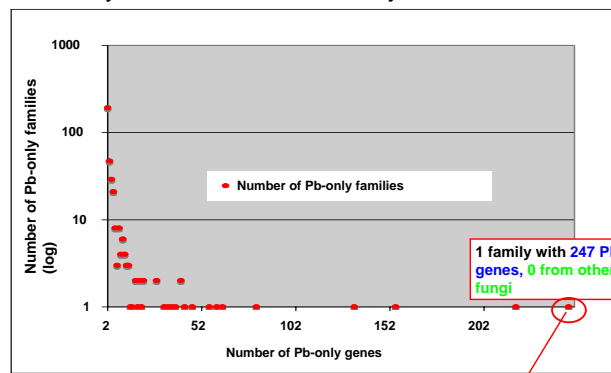
No obvious paralogs in Pb, 3 homologs in *Rhizopus oryzae*.

Remote similarity to light-induced carotenogenesis repressor in *Mucor circinelloides*.

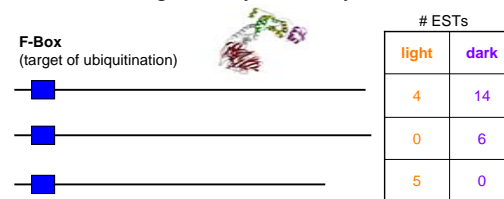
472 aa, 1 exon, 5' and 3' UTR, signal peptide.

Subsequent RT-PCR studies demonstrate 2000-fold induction.

Gene family results: families found in Pb only



New gene family, found only in Pb



Located on 49 different scaffolds.

No homologs in public databases.

Average length = 594 aa.

133 have N-term. F-box, 146 have introns, 45 have ESTs.