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Annotation and analysis of the genome of *Phycomyces blakesleeanus*, a model photoresponsive zygomycete

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I. Abstract

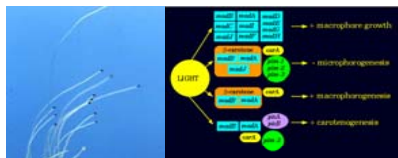
Annotation and analysis of the genome of *Phycomyces blakesleeanus*, a model photoresponsive zygomycete Alan Kuo^{1*}, Asaf Salamov¹, Jasmyn Pangilinan¹, Erika Lindquist¹, Harris Shapiro¹, Scott Baker², Luis Corrochano³, and Igor Grigoriev¹. ¹DOE Joint Genome Institute, Walnut Creek, CA, USA. ²Pacific Northwest National Laboratory, Richland, WA, USA. ³Departamento de Genética, Universidad de Sevilla, Spain. *akuo@lbl.gov

Light induces in *P. blakesleeanus* multiple developmental and biochemical responses (sporangiophore growth and development, beta-carotene synthesis). *P. blakesleeanus* is an intensively studied, experimentally tractable model organism, and whole-genome analysis is expected to further elucidate the signaling pathways underlying its photoregulation. To this end, the genome was sequenced to 7.49X depth and assembled into 475 scaffolds totaling 56Mbp, and 47847 ESTs were assembled from cDNAs of light and dark cultures. We combined into a single annotation pipeline a variety of gene modeling methods (homology-based, EST-based, and *ab initio*), and predicted 14792 protein-coding genes. Many of these gene predictions are supported by homology in nr (68%), by Pfam domains (44%), or by ESTs (35%). We next assigned GO terms to 41% of the proteins and EC numbers to 16%. We then distributed these annotations to the *Phycomyces* consortium, along with tools to curate them manually. We expect that the annotation will provide a solid platform for expression analysis. In addition to its value as a model organism, *P. blakesleeanus* is the second zygomycete with a sequenced genome, after the related *Rhizopus oryzae*. We therefore will present preliminary results of comparative analysis between the two zygomycetes.

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II. Introduction - why sequence this genome?

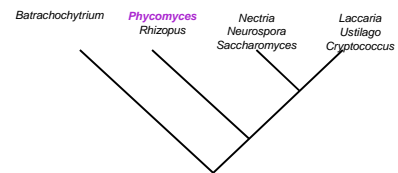
A. It's photoresponsive



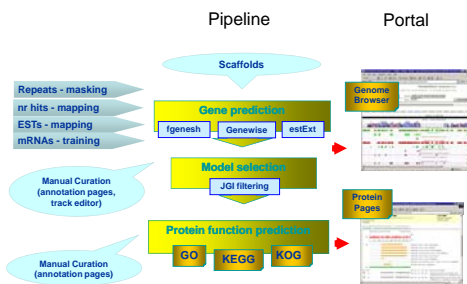
What genes are regulated?

B. It's a zygomycete

Chytridiomycota Zygomycota Ascomycota Basidiomycota



III. Annotation methodology

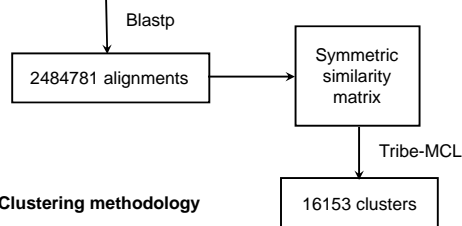


JGI *Phycomyces* Portal available at <http://genome.jgi-psf.org/Phyb1/>

IV. Annotation results

Genome size	55.9 Mbp
Number of scaffolds	475
Number of ESTs	47847
Number of genes	14972
supported by sequence similarity	9993 (68%)
supported by Pfam domains	6576 (44%)
supported by ESTs	5110 (35%)
Average gene length	1759 nt
Average number exons per gene	4.80
Average protein length	392 aa

- 14792 *P. blakesleeanus* proteins
- 17467 *Rhizopus oryzae* proteins from Broad Institute (http://www.broad.mit.edu/annotation/genome/rhizopus_oryzae/)



V. Clustering methodology

VI. Clustering results - *P. blakesleeanus* (Pb) vs. *R. oryzae* (Ro)

Number of Pb gene families	9731
Average number Pb genes / Pb family	1.52
Number families with 1 Pb gene	8169
Number with 1 Pb and 1 Ro gene (orthologs)	2040
Number families with > 1 Pb gene	1562
Number with > 1 Pb gene and 0 Ro	484
Number with both Pb and Ro genes and Pb:Ro >= 3	15

Potentially expanded families (relative to Ro)

Some appear to be real genes: see **Family 17** and **Family 38**

VII. Example of a Family 17 gene as displayed in JGI Portal's Genome Browser

Family 38 protein

Confirmed by ESTs

F-box domain, usually Involved in ubiquitination

VIII. Example of a Family 38 protein as displayed in JGI Portal's Protein Page

Family 38 protein

Extended by ESTs

Similar to conserved fungal protein

IX. Conclusions

1. 14792 genes predicted, most with functional assignments
2. 2040 orthologs with *R. oryzae* predicted
3. 1562 gene families (> 1 gene) predicted, many expanded relative to *R. oryzae*
4. Several expanded families have EST, Pfam, or sequence similarity support