

Abstract:

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

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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