A genetic linkage map of the fungus *Phycomyces blakesleeanus*

Suman Chaudhary and Alexander Idnurm

Division of Cell Biology and Biophysics, School of Biological Sciences, University of Missouri-Kansas City, 5100 Rockhill Road, Kansas City, Missouri 64110. chaudharys@umkc.edu

Phycomyces blakesleeanus is a filamentous fungus of research interest because of its ability to sense and respond to its environment. The unicellular sporangiophores show growth responses to light, gravity, wind, chemicals and presence of objects near the growing zone. The mycelium also shows responses by induction of β-carotene synthesis and initiation of sporangiophores. The responses to light have been most carefully analyzed, in part driven by the efforts of Nobel laureate Max Delbrück who tried to develop *Phycomyces* into the "phage of vision". Strains with impaired phototropism (*mad*) were isolated in the 1960s-1980s, as well as mutants affected in other sensory responses or phenotypes. These properties have made *Phycomyces* a model of sensory transduction processes. However, the inability to transform DNA into *Phycomyces* has blocked the identification of genes in this fungus. To identify genes in this fungus, a map-based cloning approach is underway. A genetic map of *Phycomyces* based on mutant phenotypes and tetrad analysis was generated over a 20 year time frame. The new genetic map of *Phycomyces* is constructed largely from amplified fragment length polymorphism of progeny derived from a cross between two wild type strains. 78 markers have been developed and used in PCR analysis to assign alleles from the mapping population. Markers spacing a collective total of 7.1 Mb exhibited a total of 247 map units of recombination (centiMorgans, cM). The average is 1 cM = 29 kb, with a range of 1 cM = 8 kb to 1 cM = 106 kb. With the *Phycomyces* genome comprising an estimated 55 Mb, 190 markers are required for complete coverage with 10 cM resolution. This map has already been used to narrow the search for *mad* genes, with the identification of point mutations in *fur*A and *lys*A genes that flank *madD* and *madE*, respectively. Additionally, using the *carRA* and *carB* genes as a starting point, the DNA regions near the *madI* gene have been found and the adjacent *carS* gene identified.