

The *Coprinus Cinereus* Genome Project

A. Gathman*, W. Lilly; J. Stajich; M. Carlson; B. Murphy;
A. Smith; D. Fargo; F. Dietrich; P. J. Pukkila

Coprinus cinereus is an increasingly attractive basidiomycete model system. Its genome has been sequenced and is publicly available; it is readily cultured in the laboratory on defined media, it has highly synchronous meiosis, and numerous laboratory techniques have been adapted for use with it. The 10X shotgun sequence released by the Whitehead Institute comprises 36 Mb of the 37 Mb of the genome, which have been assembled into 106 supercontigs containing 431 contigs. cDNA libraries have been constructed from two meiotic stages, and 1432 candidate genes have been identified from them. Another set of cDNA libraries has been constructed from vegetative *Coprinus cinereus* Okayama 7 grown under different environmental conditions, including heat shock, rapamycin treatment, minimal medium, rich medium, and complex carbon and nitrogen sources. 5000 ESTs are being sequenced from these libraries. The EST sequences have been aligned with the genomic sequence, as have known *C. cinereus* genes from GenBank. Data from known ascomycete gene sequences have been used to train SNAP software to predict a total of 11,340 genes from the remainder of the genome. BlastX and Pfam have been used to assign tentative functions to predicted genes as well as ESTs. tRNA genes have also been identified in the genome. All genomic information is available online via our Gbrowse server.