

## 7.8. *Aspergillus nidulans*

**SIGNIFICANCE:** *Aspergillus nidulans* is one of the critical fungal systems in genetics and cell biology. *Aspergillus nidulans* is important because it is closely related to a large number of other *Aspergillus* species of industrial and medical significance — e.g., *A. niger*, *A. oryzae*, *A. flavus*, and *A. fumigatus* — and serves as a model for their biology. Unlike these other *Aspergilli*, which are asexual, *A. nidulans* has a well-characterized, conventional genetic system. It undergoes DNA-mediated transformation, and genes from other *Aspergilli* as well as some mammalian genes function in *A. nidulans*.

*Aspergillus nidulans* is a particularly useful model organism for studies of cell biology and gene regulation. The initial work on the genetics of tubulin and microtubules was done in *A. nidulans*. Similarly, *A. nidulans* contributes to our understanding of mitosis and the intracellular functions of the mitotic motors kinesin and cytoplasmic dynein. Carbon regulation and nitrogen regulation are also well studied. One useful consequence of these regulatory studies is the characterization and development of the *alcA* alcohol dehydrogenase regulatable promoter (which is induced by alcohol and repressed by glucose) as a useful tool to control gene expression.

**GENERAL DESCRIPTION:** *Aspergillus nidulans* is an ascomycete. It grows rapidly as a filamentous fungus on solid or in liquid media under a variety of nutritional conditions. *Aspergillus nidulans* is homothallic, which means that any two strains can be mated directly. It is normally haploid, but can also be induced to grow as a heterokaryon or a vegetative diploid. It produces both asexual spores (conidia) and sexual spores (ascospores). It undergoes development to produce at least nine different cell types.

**GENOME FACTS:** The size of the *A. nidulans* genome is approximately 31 Mb. It has 8 well-marked chromosomes containing an estimated 11,000–12,000 genes. Approximately 900 genes have been identified in *A. nidulans* by conventional matings; 432 have been mapped to locus, and 254 are cloned and sequenced.

A partial sequence (2–3-fold coverage) of the *A. nidulans* genome was produced by Monsanto. This has been released, but only to academic laboratories under certain restricted conditions that limit genomic investigation. Because of the low coverage, the sequence itself has only relatively small contigs. From this sequence, 29% of the genes have a known function, 23% have a putative function, and 48% are unknown. In addition, although 61% of *S. cerevisiae* ORFs have homologues in *A. nidulans*, 31% of *A. nidulans* ORFs are unrepresented in *S. cerevisiae*.

Plasmid, cosmid, EST, and BAC genomic libraries are publicly available. A physical map is available at <http://gene.genetics.uga.edu/index.html>. Chromosome linkage maps are available at <http://www.gla.ac.uk/Acad/IBLS/molgen/aspergillus/>.

**COMMUNITY:** The well-characterized genetic system of *A. nidulans* and its close relation to medically and industrially significant organisms lend strong support to the sequencing of its genome. Currently, approximately 40 laboratories worldwide focus on the genetics and molecular biology of *A. nidulans*. Nine of these laboratories — representing Australia, England, France, Germany, and the United States — have joined to form a steering group to promote sequencing and annotation of the *A. nidulans* genome. Haploid DNA for *A. nidulans* is available from Ron Morris (UMDNJ–The Robert Wood Johnson Medical Center). The ability to perform comparative analysis of the *A. nidulans* genome with that of the other *Aspergillus* species make this an especially useful data set for computational scientists interested in evolution and comparative genomics.