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Abstract

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Although Pontecorvo and co-workers demonstrated that parasexual mechanisms occur in Aspergillus niger (Pontecorvo et al. J. Genet. 52:198-210), the genetics of this fungus remained ill-explored despite its biotechnological importance. Lhoas (1967 Genet. Res. 10:45-61) started genetic analysis of A. niger by means of somatic recombination. As it was not possible to acquire the A. niger master strains constructed by Lhoas, we started genetic research on A. niger with a new wild type strain obtained from the Centraal Bureau voor Schimmelcultures (CBS, Baarn, The Netherlands). This strain CBS 120.49 (our collection number N400) is identical with ATCC 9029.

A collection of mutants descending from this strain has been obtained providing useful genetic markers. In order to avoid unrelated genetic damage, we used low doses of mutagen (UV). For the same reason, strains with several markers were made by recombination and not by additional rounds of mutagenic treatment. In this way a preliminary master strain was constructed with markers on six different linkage groups. This test strain and the original strains with single markers are available from the Fungal Genetics Stock Center. Other strains will be added to this collection. The genotype of this test strain with fawn colored conidiospores is:

Linkage group	I	II	III	IV	V	VI
N616	fwnA1	hisD4	lysA7	leuA1	nicA1	pabA1

We are constructing other test strains in which one marker is replaced with another.

The original wild type has black conidiospores on rather long conidiophores. A mutant with low conidiophores was isolated and from this strain (N402) we derived auxotrophic and color mutants. Complementation tests are in progress and different genes are being mapped by haploidization of heterozygous diploids. Strains with low conidiophores (cspA1) are easy to handle and a strain with an additional auxotrophic marker is quite suitable for the isolation of other mutants (e.g. N422 cspA1 metB2; N564 cspA1 fwnA1 heA1). These strains are available to other research groups. Although preliminary results indicate the test strains can be used for genetic analysis of strains descending from other wild type origins, an isogenic background is a prerequisite for a secure genetic analysis. The master strains and mutant collection will be of more general use if other groups use strains of the same origin. - - - Dept. of Genetics, Agricultural University Wageningen, 53 Gen. Foulkesweg, 6703 BM Wageningen, The Netherlands.