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Abstract

Isolation and characterization of deteriorated sectors from duplicate strain A of *A. nidulans*.

Isolation and genetic characterization of deteriorated sectors from duplicate strain A of A. nidulans

The strain A of Aspergillus nidulans has a chromosome segment of linkage group I in duplicate - one in the normal position and the other translocated to linkage group II; the strain is unstable due to the excess of genetic material and produces two broad classes of sectors - improved and deteriorated (Azevedo and Roper 1970 Genet. Res. 16:79-93).

The aim of this work was to isolate deteriorated sectors spontaneously obtained from strain A, to analyze genetically the variants and see if their determinants of deterioration are located at random in the eight linkage groups.

The strain A was inoculated in the center of Petri dishes with Complete medium (Pontecorvo et al. 1953 Adv. in Genetics 5:141-238). Deteriorated variants were isolated and labelled as V53, V54, etc. Crosses were made between these variants and "Master" strains (MSE or MSF) carrying markers on all eight linkage groups (McCully and Forbes 1965 Genet. Res. 6:352-359). Mitotic haploidization was used for the assignment of determinants to their linkage groups. In some cases, further crosses were made to locate determinants more precisely and to test allelism among determinants on the same linkage group.

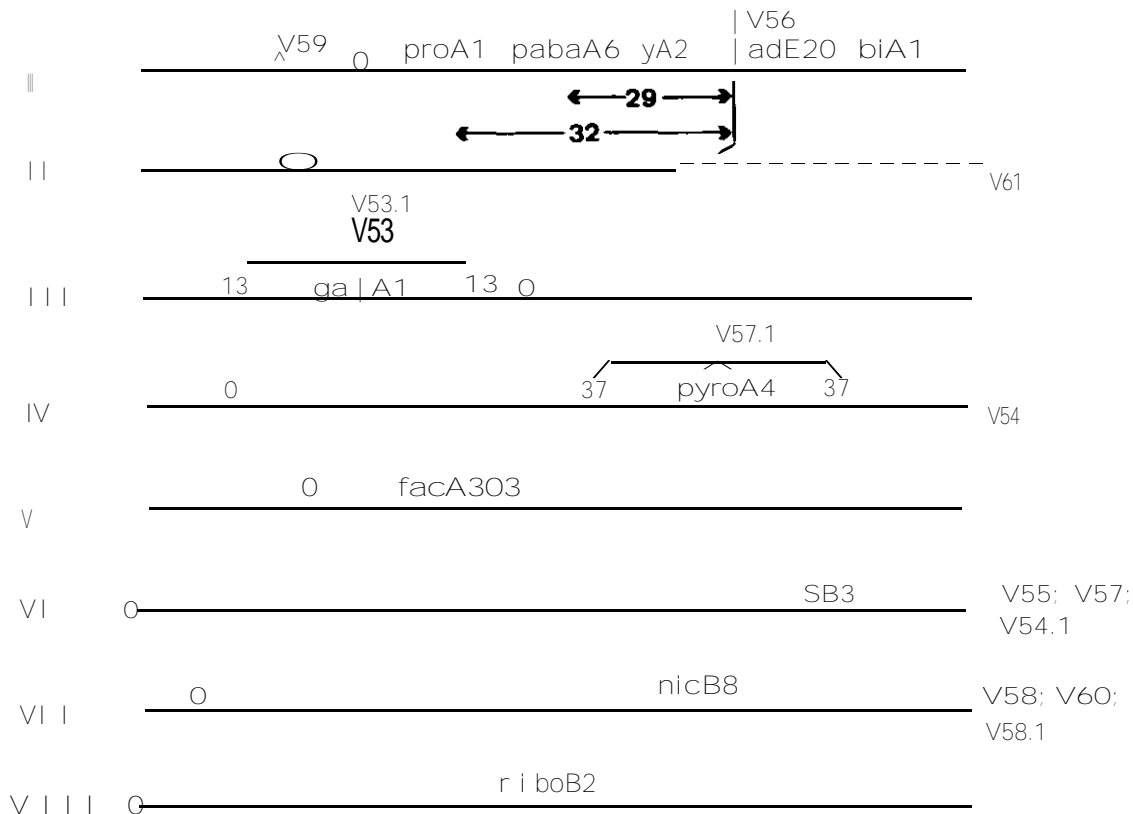


Figure I. Location of the determinants of deterioration in the linkage groups of Aspergillus nidulans.

Nine variants and four derivatives of variants were genetically analysed. The determinants of deterioration acted as single genes; all of them were recessive in the diploid. They were found in all linkage groups, with the exception of groups V and VIII (Figure 1). In Figure 1, linkage maps are not drawn to scale and are approximate. The symbol] designates a deletion. The symbol ^ designates the determinant of deterioration while a square designates the genetic marker of the "Master" strain. The broken line represents the duplicate segment of linkage group I terminally attached to linkage group II. Variants allocated only to their linkage group are shown at the right. Centromeres are represented by open circles. The symbol /---\ indicates that the determinant of deterioration of the variant is linked to the genetic marker and may be located in any of the sides.

To perform the allelism tests, besides the variants isolated in this work, some deteriorated variants obtained by other authors were used. When the two determinants of deterioration are not alleles, we find normal and deteriorated colonies. If the determinants are alleles we find only deteriorated colonies. The determinants of deterioration were alleles in only two out of sixteen crosses performed. These results indicate that the determinants of deterioration must be located at random in the linkage groups, although there are spots in certain linkage groups in which an expressive number of determinants of deterioration is located. Supported by PIG/CNPq. - - - ^1 Dept. de Genetica, I.B., UFRJ, Caixa Postal 68.011, Rio de Janeiro, Brazil; ^2Inst. de Genetica, ESALQ/USP, Caixa Postal 83, Sao Paula, Brazil