Genet. Res., Camb. (1962), **3**, *pp.* 331–332
Printed in Great Britain

SHORT NOTE

Recessive suppressors in *Aspergillus nidulans* closely linked to an auxotrophic mutant which they suppress

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(*Received* 4 *May* 1962)

Reversion to prototrophy by a further mutation which 'suppresses' an auxotrophic mutant is well-known. The suppressor can be dominant or recessive, site-specific or not, and linked or not to the suppressible site. A recessive suppressor can be used (e.g. Pontecorvo & Käfer, 1956) for mapping by means of mitotic crossing-over since, starting from diploids heterozygous for the suppressor and homozygous for the auxotrophy, segregants homozygous for the suppressor can be selected. Using a recessive suppressor is this way the section of chromosome which can be mapped is that between the centromere and the suppressor. As suppressors are distributed all over the map only few happen to be conveniently distal. A deliberate search was therefore started for such distal suppressors, with the additional working hypothesis that *recessive* suppressors might exist which are either very closely linked to the locus which they 'suppress' or even within that locus, i.e. intra-cistron.

The present note reports: (1) that suppressors of this kind—i.e. recessive and very closely linked to the system which they suppress—do exist; (2) that by choosing an auxotrophic locus distally located, the isolation of suppressors of the type just mentioned offers an easy way of providing distal selectors for genetic analysis *via* mitotic crossing-over.

Isolation of suppressors

The isolation of closely linked, or intra-cistron, suppressors was attempted with two auxotrophs, both located more than 50 map units from their respective centromeres: *meth2* (methionine-requirement) on the left arm of linkage group III (Forbes, 1959), and *paba22* (*p*-aminobenzoic acid-requirement) on the right arm of linkage group IV (Siddiqi, unpublished). Of seven revertants from *meth2*—four dominant and three recessive—isolated by plating large numbers of conidia on methionineless medium, two due to recessive suppressors were located and found not to be closely linked to the *meth2* locus. This locus was investigated no further.

Three revertants of *paba22*—one dominant and two recessive—were obtained by plating 4×10^8 conidia on *p*-aminobenzoicless medium. The two recessives (*su1* and *su4*) were first allocated to their linkage group by mitotic haploidization (Forbes, 1959) after *p*-fluorophenylalanine treatment (Morpurgo, 1961). They were found to be either in the same linkage group (IV) as *paba22*, or in group III. Meiotic analysis by plating ascospores from crosses of the type *su1 paba22* × + + detected no *paba* colonies out of 884 in the case of *su1*, and no *paba* colonies out of 208 in the case of *su4*. Thus, the changes responsible

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for the revertant phenotype map in the same linkage group as, and, at least in the case of *su1*, within less than one map unit from, *paba22* (it is assumed that these are suppressors rather than true back mutations, because they are recessive, as shown below).

Properties of the recessive suppressors

The recessive auxotrophic mutant *paba22*, in haploid or in homozygous condition, was tested in various haploid and diploid combinations with either *su1* or *su4* or both. The results are as follows in respect of growth (+) or no growth (−) in the absence of *p*-aminobenzoic acid:

$$su^{+}\ paba^{+} : (+\ +\ +) \qquad su^{+}\ paba22 : (-)$$
$$su1\ paba22 : (+\ +) \qquad su4\ paba22 : (+\ +)$$

$$\frac{su1\ paba22}{+\ paba22} : (-) \qquad \frac{su4\ paba22}{+\ paba22} : (-) \qquad \frac{su1\ +\ paba22}{+\ su4\ paba22} : (-)$$

The three diploids shown above, inoculated on *p*-aminobenzicoless medium, produce as expected vigorous segregant sectors. The suppressors can, therefore, be used for genetic analysis *via* mitotic crossing-over.

The precise relations, at the fine genetic level, of the suppressors and *paba22* will have to be investigated, and in particular the complementation relations between the two suppressors, indicated by the failure to grow of the diploid carrying the two suppressors in *trans* arrangement.

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