

Synthesis of two-chromosome double interchanges in *N. crassa*

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Abstract

Synthesis of two-chromosome double interchanges

Kowles, R. Synthesis of two-chromosome double interchanges in N. crassa.

Two-chromosome double interchanges were synthesized in N. crassa by intercrossing single interchange strains (reciprocal translocations) each with breakpoints that involved the same two chromosomes. Chromosome arrangements that combined both of the single interchanger into the two chromosomes were established presumably by simultaneous crossovers that occurred in the two differential segments.

The scheme to synthesize these strains consisted of crossing the following I-IV single interchange strains with each other in all combinations: T(I;IV) NM119, T(I;IV) NM140, T(I;IV) NM144, T(I;IV) NM164, T(I;IV) NM172, T(I;IV) D304. Block ascospores from these intercrosses were isolated on complete medium in random spore fashion, heat shocked at 60°C for 30 minutes, and incubated at 25°C. All progeny isolated from the intercrosses were subsequently tested by crossing them with each of the two parental single-interchange strains and a standard-normal strain. Those isolates that expressed partial sterility in each of the three testcrosses were deemed to be carrying the desired two-chromosome double interchange. By partial sterility it is meant that defective white ascospores were produced at high percentages. These ascospore abortions ranged from 24% to 62% dependent upon the strain involved.

Linkage **data** were obtained for **each** parental strain to determine the locations of the breakpoints with respect to chromosome arms, and to help in identifying the type of **intercross**. It is a mandatory prerequisite for the production of two-chromosome double interchanges that the **two** single interchanges involved be either the opposite-arms type or the **same-arms** type with both exchanged segments longer in one interchange relative to the exchanged segments in the other interchange.

Five **intercross combinations** resulted in one or more two-chromosome double interchange **strains** as determined by **testcrossing**. This is in agreement with predictions based on the linkage **data**, since the genetic map for the parents in **all** of these crosses **shows** that each **intercross** is of the **same-arms** type with both exchanged segments longer in one interchange relative to the exchanged segments in the other interchange. The combination synthesized are listed in Table 1, column 1. The first **two** numbers indicate the parental interchange strains that were involved in the original **intercross**, the third number is the **isolation** number from the **intercross**, and the **final** letter indicates the mating type.

The suggestion is made that the use of two-chromosome double interchanges for the detection of **linkage** can reduce the number of **strains** required and **at** the same time provides an effective method for this purpose. Although the breakpoints in these **newly**-synthesized strains are not far **apart**, there is little doubt that **two-chromosome** double interchanges with widely **spaced** breakpoints would be extremely effective in linkage detection.

Table 1.

Double interchange	mating type partial sterility	albino-2 partial sterility	osmotic-1 partial sterility
144-119-57a-	-28.3	12.2	12.2
119-164-72A	41.1	25.0	17.8
140-119-23a	32.6	17.7	8.5
144-164-1A	12.7	17.7	12.7
164-172-65A	21.8	12.8	25.7

Recombination **values** involving genetic markers and **partial sterility** (that is, breakpoints) in crosses between **genetic** marker strains for linkage group I and the two-chromosome **double** interchange strains are listed in Table 1. These data were collected from four-point linkage **tests**, but are **presented** in a two-point format. It is difficult to set the **sequence** of **breakpoints** relative to genes with **any great degree** of **certainty** since there are **two** breakpoints in **each** of the **chromosomes** which probably have an overlapping effect upon linkage with marker genes.

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