THE EFFECT OF RECIPROCAL TRANSLOCATIONS ON SEGREGATION AND MULTIVALENT FORMATION IN AUTOTETRAPLOIDS OF RYE, SECALE CEREALE

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Chromosomal segregation, and the frequency of large multivalents in Secale cereale were studied in autotetraploid duplex translocation heterozygotes. Models for estimating expected segregations and frequencies of multivalents were developed incorporating the probabilities of different chromosomal segments being bound by chiasmata. It appeared that the segregation of the two translocations tested fitted quite well the expected corrected segregation ratio of approximately 1:11.5:1, suggesting that induced preferential pairing was not strong enough to enhance preferential segregation resulting from random translocation segregation. Interspecific hybrids with S. montanum carrying the same translocations showed strong preferential pairing, i.e. significant deviation from the expected ratios.

Three translocations tested (two not tested for segregation) showed a decrease in multivalent frequency mainly attributable to preferential pairing, especially in cases where the breakpoint was near one chromosome end. Possible reasons why preferential pairing is expressed here and not in the segregations are discussed.

Introduction

Interchanges in autopolyploids, besides usually having a negative effect on fertility (Ahloowalia, 1963) also have major effects on chromosome pairing and on segregation.

It may be expected (Fig. 1) that chromosome arms of the same structure will attract each other more effectively than chromosome arms of different structure even though these too are at least partly homologous: there is preferential pairing. This, however, is not expected when pairing or even pairing initiation is restricted to small segments situated entirely within the translocated segment: preferential pairing occurs only when the rearrangement disturbs the normal pairing pattern (Sybenga, 1969, 1973).
The effects on segregation are less easily visualized. The basic considerations have been given by LINNERT (1962). The analysis given here to some extent parallels Linnert's but the derivation of the 81 different configuration types is somewhat different. In addition, estimates of the chiasma frequencies in the different association types are used, whereas Linnert assumed 100% association of all essential pairing segments. The model can be used for calculating expected frequencies of specific configuration types and of segregations. It is based on random association of chromosome ends and therefore permits the detection of deviation from randomness of pairing (preferential pairing) by comparing observed with expected distributions.

**THE MODEL**

**Segregations**

Figure 1 shows the eight chromosomes \((2 \times 4)\) of an interchange complex in an autotetraploid in duplex condition. There are two chromosomes of each type, but each segment is present four times. Therefore, for simplicity primarily considering the association of chromosome ends there are four copies of each end segment that can pair in a random manner when there is no preferential pairing. With four homologous segments, the number of combinations is three.

![Diagram showing the eight chromosomes of a duplex reciprocal translocation heterozygote in an autotetraploid. N: the normal sets of chromosomes. T: the translocation sets.](image-url)