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# THE GENOMIC RELATIONSHIPS OF TRITICUM KOTSCHYI TO THE S-GENOME DIPLOIDS[1]

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## SUMMARY

*New hybrids between Triticum kotschyi and both T. speltoides and T. longissimum were examined cytologically. The presence of an S genome in T. kotschyi is confirmed. The data also corroborate that T. speltoides or any close relative did not donate the B genome to either T. turgidum or T. aestivum.*

## INTRODUCTION

The B genome of *Triticum aestivum* L. (2n=6x=42) was considered in recent years to have been donated by *T. speltoides (Aegilops speltoides)* (SARKER and STEBBINS, 1956; RILEY *et al.*, 1958). Recent work concerning the evolution of polyploid wheat has caused a reconsideration of *T. speltoides* as the proposed donor of the B genome (DVOŘÁK, 1972; KIMBER and ATHWAL, 1972). This work has prompted an investigation of the genomic relationships of the tetraploid species *T. timopheevii* var. *timopheevii* and the hexaploid *T. timopheevii* var. *zhukovskyi* (SHANDS and KIMBER, 1973). It would also seem appropriate to reinvestigate the relationships of the tetraploid species *T. kotschyi* Boiss. *(Ae. variabilis)*, whose genomes are designated $C^{u}S^{1}$ (KIHARA, 1949) to indicate that it is an allotetraploid originating from the hybridization of *T. umbellulatum (Ae. umbellulata)* and *T. longissimum* var. *longissima (Ae. longissima)*.

The purpose of this contribution is to report investigations of the chromosome homology of *T. kotschyi* with various forms of *T. speltoides* and its immediate relatives in what was the *Sitopsis* section of the genus *Aegilops*.

## MATERIALS AND METHODS

*T. kotschyi* was successfully pollinated by *T. speltoides* G-1039, G-366, and G-1316 (University of California-Riverside collection numbers), which are high-, intermediate-, and low-pairing strains, respectively (KIMBER and ATHWAL, 1972); and by *T. longissimum* var. *sharonensis (Ae. sharonensis)* G-1315. No seeds were obtained from *T. kotschyi* x *T. bicorne (Ae. bicornis)* G-365-1.

The $F_1$ plants were grown in a glasshouse, and their PMCs were examined cytologically at meiosis. The frequency and range of the pairing configurations were recorded.

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## RESULTS

Table 1 shows the mean and range of the chromosome associations observed per cell in the hybrids between *T. kotschyi* and three forms of *T. speltoides* and also one form of *T. longissimum*. Since the sibling plants in any one type of hybrid were so similar, the weighted means of these figures for each group are also given.

Table 1. The mean and range of chromosome pairing observed in PMCs of $F_1$'s having *T. kotschyi* as female parent

| | | Chromosome configurations[1] | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | Pl. | I | II | | III | IV | V | No. |
| Male parent | no. | | Rod | Ring | | | | |
| *T. speltoides* | | 6.35 | 4.60 | - | 1.55 | 0.20 | - | 20 |
| (high pairing) | | 3-12 | 3-8 | - | 0-3 | 0-2 | - | |
| *T. speltoides* | 1 | 9.80 | 4.70 | - | 0.60 | - | - | 20 |
| (intermed. pairing) | | 4-15 | 3-7 | - | 0-2 | - | - | |
| | 2 | 9.30 | 4.55 | 0.05 | 0.75 | - | - | 20 |
| | | 3-13 | 3-7 | 0-1 | 0-3 | - | - | |
| | 3 | 10.90 | 3.40 | - | 1.10 | - | - | 10 |
| | | 7-14 | 1-5 | - | 0-2 | - | - | |
| Weighted mean | | 9.82 | 4.38 | 0.02 | 0.76 | - | - | |
| *T. speltoides* | 1 | 7.20 | 4.70 | 0.20 | 1.00 | 0.25 | - | 20 |
| (low pairing) | | 2-11 | 2-8 | 0-1 | 0-3 | 0-1 | - | |
| *T. longissimum* | 1 | 5.50 | 2.15 | 2.40 | 1.50 | 0.35 | 0.10 | 20 |
| var. *sharonensis* | | 2-8 | 1-4 | 1-3 | 0-3 | 0-1 | 0-1 | |
| (low pairing) | | | | | | | | |
| | 2 | 5.45 | 2.35 | 1.90 | 1.45 | 0.55 | 0.10 | 20 |
| | | 3-8 | 0-4 | 0-3 | 0-2 | 0-2 | 0-1 | |
| | 3 | 5.32 | 2.61 | 1.82 | 1.54 | 0.46 | 0.07 | 28 |
| | | 3-8 | 0-6 | 0-3 | 0-4 | 0-2 | 0-1 | |
| Weighted mean | | 5.41 | 2.26 | 2.02 | 1.50 | 0.46 | 0.09 | |

[1] I, univalent; II, bivalent; III, trivalent; IV, quadrivalent; and V, quinquevalent.

Photomicrographs of typical cells of the four types of hybrids are presented in Figure 1.

## DISCUSSION

The geographical distribution of *T. longissimum* and *T. umbellulatum* overlap in Asia Minor (FELDMAN, personal communication), and thus the possibility of hybridization exists. The cytological evidence of KIHARA *(loc. cit.)* is convincing. In the hybrid of *T. longissimum* x *T. kotschyi* he observed a mean of seven bivalents, five of which were rings, and up to one multivalent per cell. However in the footnote to his Table 5 he indicates that the genome of *T. longissimum* was not truly homologous to the S genome of *T. kotschyi*.

The data presented in this paper are interesting in several aspects. First, there is clearly a genome in common between either *T. longissimum* or *T. speltoides* and *T. kotschyi*. Since hybrids between *T. speltoides* and *T. longissimum* show almost complete chromosome pairing (SEARS, 1941; KIHARA, 1949; KIMBER, 1961), their hybrids with *T. kotschyi* should be cytologically similar. The presence of frequent trivalents and occasional quadrivalents and quinquevalents must indicate the presence of considerable structural differentiation. The hybrid between *T. speltoides* and *T. longissimum (Ae. sharonensis)* investigated by Kimber (1961) did not produce multivalents, and thus it is possible that the structural differentiation observed in the present hybrids is a result of chromosomal reorganization in *T. kotschyi*.

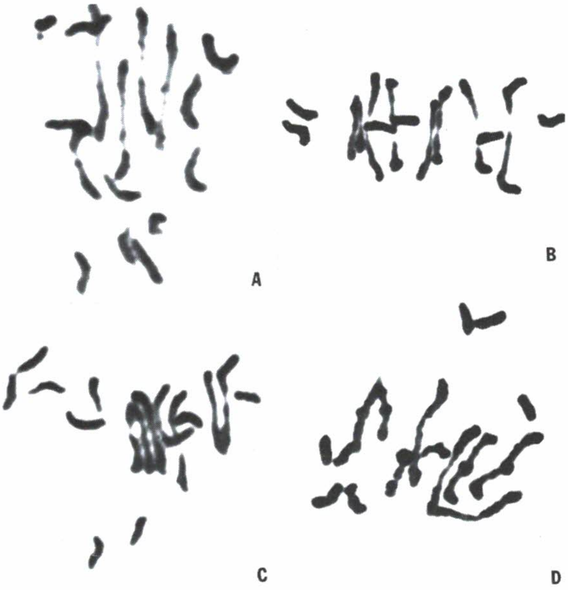

Figure 1. Meiotic metaphase in PMCs in the four types of hybrids of *T. kotschyi* and the S-genome diploids. A,B,C are hybrids of *T. kotschyi* x *T. speltoides*: A, G-1316 low pairing, 11'+5"; B, G-366 intermediate pairing, 6'+6"+1"'; C, G-1039 high pairing, 9'+3"+2"'. D is *T. kotschyi* x *T. longissimum* var. *sharonensis*, G-1315, 6'+6"+1"'. 880X.

A second point is that the genes in *T. speltoides* known to affect chromosome pairing in hybrids with *T. aestivum* (KIMBER and ATHWAL, 1972) seem to have little effect in the various hybrids of *T. speltoides* with *T. kotschyi*. Surprisingly, the hybrid with the intermediate-pairing form has the lowest chromosome association[2] (5.59), while the high- and low-pairing forms are similar to each other (7.33 and 6.90, respectively). The lower frequency of chromosome association may be due to a reduction in chiasma frequency and may not indicate a real difference in homology. Also, since nothing is known of the structural relationships of the various forms of *T. speltoides* at this time, it is possible that the intermediate-pairing form may be differentiated by chromosomal translocations that could affect its pairing in hybrids with *T. kotschyi*.

The three forms of *T. speltoides* are not only similar to each other in their pairing with *T. kotschyi* but are also quite similar to *T. longissimum* in this respect. This lack of variation in behavior is different from the pattern observed by KIMBER and ATHWAL (1972) in hybrids between *T. aestivum* and *T. speltoides* and by SHANDS and KIMBER (1973) in hybrids between *T. timopheevii* and *T. speltoides* (see Table 2). In the low-pairing hybrids with *T. aestivum* they observed almost no chromosome association, while in the low-pairing hybrids with *T. timopheevii* pairing was equivalent to 6.89 bivalents per cell.

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[2] Chromosome association is calculated by dividing the total number of chromosomes less the number of univalents by two. This gives the number of chromosome pairs there would be if all synapsis resulted in only bivalent formation.

This difference is attributed to the lack of a genome in common in the hybrids between *T. aestivum* and *T. speltoides* and the presence of a genome in common in the hybrids between *T. timopheevii* and *T. speltoides*. The rise in the mean chromosome association from the low-pairing to the high-pairing hybrids with both *T. aestivum* and *T. timopheevii* is attributed to an increase in homoeologous pairing between the non-homologous chromosomes unpaired in the low-pairing hybrids. This increase in pairing clearly must be partly dependent on the degree of homoeology between the non-homologous chromosomes. Thus the absence of a similar change in the frequency of chromosome association in the three hybrids between *T. kotschyi* and *T. speltoides* is taken to show a greater dissimilarity between the $C^u$ genome of *T. kotschyi* and the S genome than between the A genome of *T. timopheevii* and the S genome.

Table 2. The mean chromosome association observed in hybrids of *T. aestivum*, *T. timopheevi*, and *T. kotschyi* with the high-, intermediate-, and low-pairing forms of *T. speltoides*

| ♀ parent and genomes of hybrid | Pairing type of ♂ parent, *T. speltoides* High | Interm. | Low |
|---|---|---|---|
| *T. aestivum*[1] ABDS | 10.60 | 5.65 | 0.70 |
| *T. timopheevii*[1] AGS (G=S)[2] | 8.61 | 7.48 | 6.89 |
| *T. kotschyi* $C^uSS$ | 7.33 | 5.59 | 6.90 |

[1] Data for *T. aestivum* and *T. timopheevii* calculated from the data of KIMBER and ATHWAL (1972) and SHANDS and KIMBER (1973), respectively.

[2] SHANDS and KIMBER, 1973.

The similarity of the hybrids of *T. kotschyi* with *T. speltoides* and *T. longissimum* indicates that neither of these species can be singled out as the donor of the S genome to the tetraploid. Clearly the donor must be some diploid similar to these species, but the present evidence does not allow a distinction to be drawn.

Finally, this confirmation of the presence of an S genome in *T. kotschyi* provides additional evidence that a species carrying the S genome could not have been the donor of the B genome to *T. turgidum* and from there to *T. aestivum*, for DRISCOLL and QUINN (1968) have shown that there is not a genome in common between *T. aestivum* and *T. kotschyi*.

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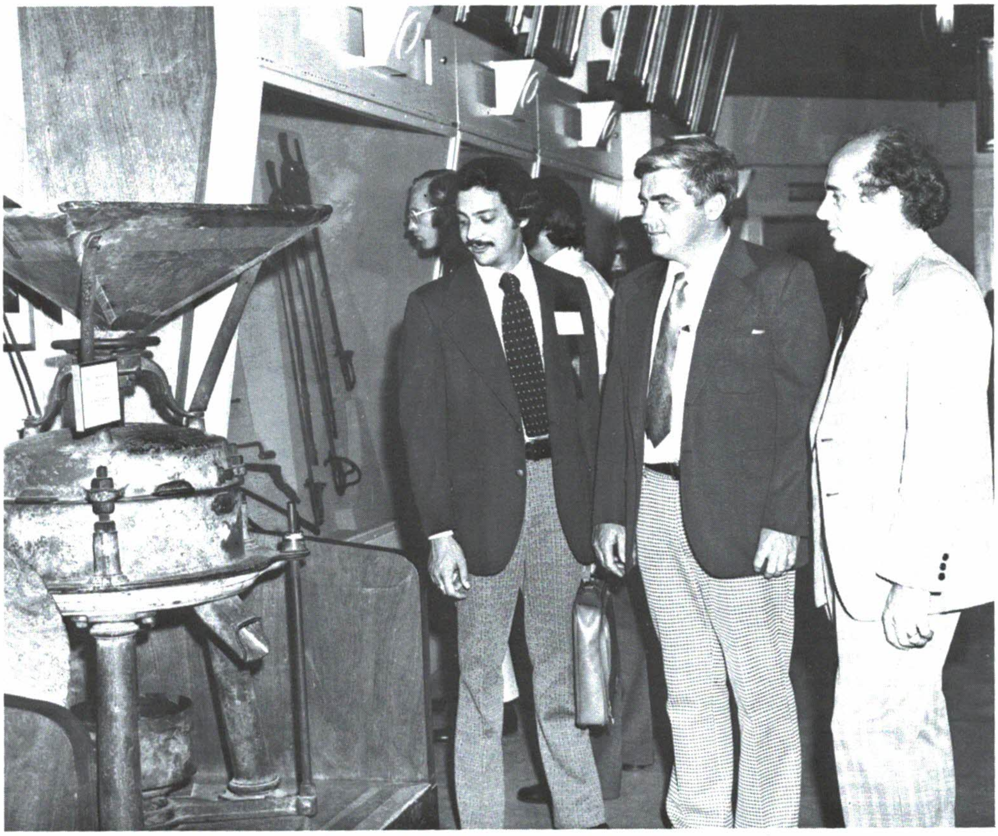

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