

Spontaneous chromosome substitutions in hybrids of *Triticum aestivum* with *T. araraticum* detected by C-banding technique

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Abstract

One hundred thirty-one plants representing twenty-nine families of *Triticum aestivum* cv. Wichita X *T. araraticum* hybrids were analyzed by the C-banding technique. Transfer of genetic material involved whole chromosome(s) or chromosome arms. Nine different types of chromosome substitution were found. The mean number of substitutions per karyotype was 1.86 (range 1-3). Substitutions involving G-genome chromosomes occurred more frequently than A' genome chromosomes. Individual chromosomes also differed in the frequency of substitution. The most frequently substituted chromosome was 6G, while substitutions with 1A^t, 2A^t, 4A^t, 6A^t, 7A^t, 3G, and 7G were not recovered. A recombinant (rec) 7AS-7A^tL chromosome was identified. The spectrum of substitutions was different from those in other *T. aestivum* x *T. timopheevii* hybrids, indicating that the genotype of the parental species determines the pattern of substitutions in their hybrids.

Introduction

Triticum araraticum Jakubz. is a wild tetraploid wheat with the genome formula A^tA^tGG. Morphologically similar to *T. dicoccoides*, *T. araraticum* differs from it in karyotype structure (Badaeva et al. 1986; Gill and Chen 1987; Jiang and Gill 1994). At present, there is no consensus opinion on the origin of these two wheat species. According to one hypothesis, *T. dicoccoides* and *T. araraticum* were derived from the common ancestor by introgressive hybridization with unknown diploid species (Gill and Chen 1987). On the other hand, there is much evidence that these species had independent origins (Jiang and Gill 1994).

Analysis of substitution types in common wheat x *T. araraticum* hybrids may provide an insight into genetic interrelationships between the A and B genomes of *T. dicoccoides* and the A^t and G genomes of *T. araraticum*. In addition, *T. araraticum* has agronomically valuable traits such as pest resistance and restorer genes for cytoplasmic male sterility and, as a consequence, may be used as a donor of these properties. The determination of chromosomal substitution patterns in the karyotypes of hybrids may be also useful in breeding work.

Materials and methods

Thirty families, consisting of one hundred thirty-six plants, were derived from two independent crosses of *Triticum aestivum* L. em Thell. cvs. Wichita (WI) and Newton (NWT) with *T. araraticum* (Fig. 1). The used accession of *T. araraticum*., TA 39 from Iraq, is maintained at the Wheat Genetics Resource Center, Kansas State University, Manhattan, Kansas, USA. From two to 13 plants were analyzed in each family. A

modified C-banding technique was used for karyotype analysis (Badaeva et al. 1994). Chromosomes of common wheat, *T. aestivum*, and *T. araraticum* were classified according to genetic nomenclature (Gill et al. 1991; Badaeva et al. 1991).

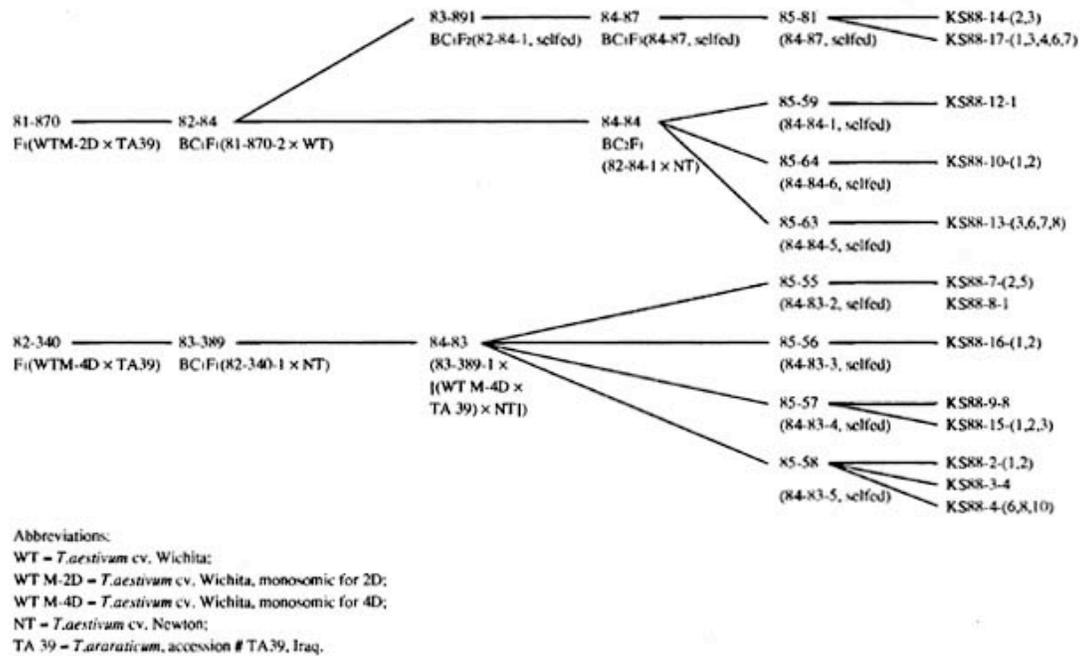


Fig. 1. A pedigree of the studied families.

Results and discussion

Cytogenetic analysis of hybrid lines showed that the majority of plants had a chromosome number of $2n=42$ (Fig. 2a). Two plants were exceptional. Plant #4 of KS88-9-8 with $2n=43$ had a 5G(5B) 6G(6B) double disomic substitution and 4G monosomic addition. Plant #3 of KS88-14-3 with $2n=41$ was monosomic for 1 G(1B) and had a double disomic 5A¹(5A) 6G(6B) substitution.

Twenty-six plants from eight families shared the common chromosome *rec 7AS-7A¹L*. Two plants of KS88-16-2 had one 6B and one 6G chromosome. Telocentric 5BL chromosome in homozygous or heterozygous state was discovered in 11 plants of six families. Twenty-eight plants belonging to nine families had a terminal deletion of 1 BL (Fig. 2b). The modified 1 B chromosome was present in homozygous condition in all plants of KS88-17-1 and KS88-17-6, and was found in homozygous or heterozygous condition in a few plants of the other families. The number of substitutions per karyotype ranged from 0 to 3, and nine different substitution types were recovered (Table 1).

The first type was found only in the KS88-2-2 family, where six plants were homozygous and one plant was heterozygous for *rec 7AS-7A¹L* chromosome. This chromosome had telomeric and subtelomeric bands in the short and a faint proximal band near the centromere in the long arm which were typical of normal chromosome 7A. A large intercalary C-band in the distal half of the 7At long arm indicates that the cross-over site was probably located in the proximal part of the long arms of 7A and 7A¹. Two types of single disomic substitutions were found. Single 2G(2B) disomic substitutions were identified in five families. In four of these families the *rec 7A-7A¹* chromosome was also present. Single disomic 6G(6B) substitution was found in six families. In KS88-16-2, one plant was heterozygous for the *rec 7A-7A¹* chromosome.

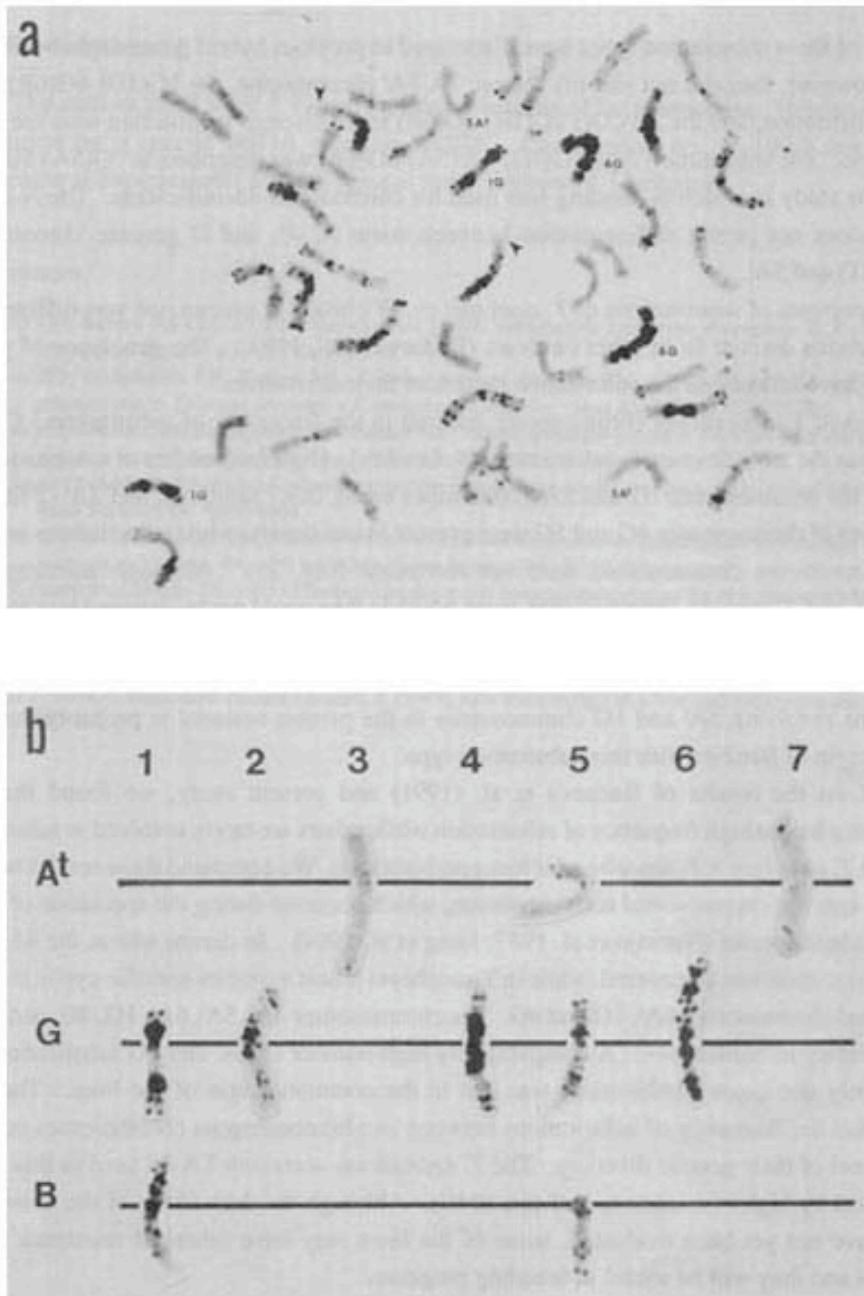


Fig. 2. a: A metaphase cell of KS88-17-6. Only the chromosomes of *T. araraticum* are indicated, and the 1B chromosomes with telomeric deletion are arrowed; b: The A^t- and G-genome chromosomes of *T. araraticum* and modified B-genome chromosomes of *T. aestivum*, which were present in different hybrid families.

Table 1. Types of chromosome substitution in *T. aestivum* cv. Wichita × *T. araraticum* TA 39 hybrid families

Type of substitution	Families
rec 7A-7A ^t	KS88-2-2
<i>Single substitutions:</i>	
2G(2B)	KS88-2-1, KS88-3-4, KS88-4-(6, 8, 10)
2G(2B) and rec 7A-7A ^t	
6G(6B)	KS88-10-2, KS88-12-1, KS88-13-(3, 6, 7, 8), KS88-16-2
<i>Double substitutions:</i>	
3A ^t (3A), 6G(6B)	KS88-7-2
1G(1D), 6G(6B)	KS88-14-3, plant #4; KS88-17-6, plant#3
<i>Triple substitutions:</i>	
4G(4D), 5G(5B), 6G(6B)	KS88-9-8
3A ^t (3A), 2G(2B), 6G(6B)	KS88-7-5, KS88-8-1
with rec 7A-7A ^t	
1G(1D), 5A ^t (5A), 6G(6B)	KS88-14-(2, 3), KS88-15-(1, 2,3), KS88-17-(1, 3, 4, 6, 7)

There were two types of double disomic substitution. Double disomic substitution 3At(3A) 6G(6B) was found in all plants of KS88-7-2 family. One plant of KS88-14-3 and one plant of KS88-17-6 had a 1G(1D) 6G(6B) double disomic substitution.

Three types of triple disomic substitution differed in their frequency of distribution. Triple disomic substitution 4G(4D) 5G(5B) 6G(6B) was only found in KS88-9-8. The 3At(3A) 2G(2B) 6G(6B) triple disomic substitution with rec 7A-7At chromosome was represented by two families. Triple disomic substitution 1G(1D) 5At(5A) 6G(6B) (Fig. 2a) was the most frequent, and was present in ten families (Table 1).

Some of these substitution types were discovered in previous hybrid generations by Gill et al. (1988). However, they did not identify the rec 7A-7A^t chromosome, the 1G(1D) 6G(6B) double disomic substitution, and the 3A^t(3A) 2G(2B) 6G(6B) triple disomic substitution with rec 7A-7A^t chromosome. The substitution type 1G(1D) 5A^t(5A) 6G(6B) was described as ?G(5A) 6G(6B) in the previous study in which N-banding was used for chromosome identification. The N-banding technique does not permit differentiation between some A, A^t, and D genome chromosomes, including 1D and 5A^t.

The spectrum of substitutions of *T. aestivum* cv. Wichita × *T. araraticum* was different from those in hybrids derived from other cultivars (Badaeva et al. 1991). The genotypes of parental forms may have influenced the substitution pattern of their derivatives.

Individual *T. araraticum* chromosomes differed in the frequency of substitution. Chromosome 6G was the most frequently substituted (24 families). High frequencies of substitution were also found for chromosomes 1G and 5A^t (10 families each), 2G(7 families), and 3A^t (3 families). Substitutions of chromosomes 4G and 5G were present in one family, while substitutions involving other *T. araraticum* chromosomes were not recovered (Fig. 2b). Although rearrangements, involving A and A^t genome chromosomes, were possible they could not be detected by cytological methods due to the absence of marker bands. These results are in agreement with data on substitutions in *T. aestivum* × *T. timopheevii* hybrids (Badaeva et al. 1991). The high frequency of substitutions involving 5A^t and 1G chromosomes in the present material is probably due to the common origin of families with this substitution type.

Based on the results of Badaeva et al. (1991) and present study, we found that some chromosomes have a high frequency of substitution while others are rarely involved in substitutions in different *T. aestivum* x *T. timopheevii* cross combinations. We compared these results with data on species-specific chromosomal rearrangements, which occurred during the speciation of the two tetraploid wheat species (Naranjo et al. 1987; Jiang et al. 1994). In durum wheat, the 4A-5A-7B cyclic translocation was discovered, while in Timopheevi wheat a species-specific cyclic translocation included chromosomes 6A^t, 1G and 4G. The chromosomes 4A^t, 5A^t, 6A^t, 1G, 4G, and 7G had a low frequency of substitution. A comparatively high number of 5A^t and 1G substitutions were found in only one cross combination, was due to the common origin of the lines. These data indicated that the frequency of substitutions between two homoeologous chromosomes correlates with the level of their genetic diversity. The *T. araraticum* accession TA 39 used in this study is characterized by high resistance to leaf rust (04C). Although the derivatives of the crosses with Wichita have not yet been evaluated, some of the lines may have inherited resistance from *T. araraticum* and they will be useful in breeding programs.

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