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IDENTIFICATION OF CHROMOSOMES INVOLVED IN TRANSLOCATION LINES OF THE CYTOGENETIC COLLECTION OF COTTON (*GOSSYPIUM HIRSUTUM* L.) IN UZBEKISTAN

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SUMMARY

Cotton (*Gossypium hirsutum* L.) characterization revealed small chromosomes with weak morphological differentiation; therefore, the translocation lines application necessitated its identification. In this study, a unified identification of chromosomes involved in exchanges took place for three translocation lines from the Uzbek cotton cytogenetic collection via translocation tester lines from the USA. Chromosome homology evaluation was according to the meiotic configurations at metaphase-I (MI) in pollen mother cells. Analysis of cotton F_1 hybrids obtained through crosses between translocation lines from two different collections revealed the involvement in translocation of several chromosomes in various lines. These are chromosomes 3 and 6 of the A_t-subgenome of cotton in line Tr8, in line Tr15, chromosome 6 of the A_t-subgenome and chromosome 14 of the D_t-subgenome, and in line Tr16, chromosomes 2 and 3 of the A_t-subgenome. The study also identified the homology of one of the translocated chromosomes in four translocation lines by crossing with tester lines. In two lines, Tr5 and Tr9, the detection of homology was with chromosome 6 of the A_t-subgenome, whereas in two other lines, Tr13 and Tr26, the established homology was with chromosome 3 of the A_t-subgenome.

Keywords: cotton (*G. hirsutum* L.), crossing, Uzbek cotton cytogenetic collection, translocated chromosomes, chromosome identification, translocation tester set

Key findings: Cytogenetic analysis of the cotton (*G. hirsutum* L.) F_1 hybrids revealed that in the Tr8 translocation line, chromosomes 3 and 6 of the A_t-subgenome of cotton showed involvement in the translocation; in the Tr15 line, the involved ones were chromosome 6 of the A_t-subgenome and chromosome 14 of the D_t-subgenome; and in Tr16 line, involved chromosomes were 2 and 3 of the A_t-subgenome.

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INTRODUCTION

In plants' karyological studies with morphologically small and weakly differentiated chromosomes necessitated the development of non-traditional methods for chromosome identification on the exchange basis. Tester sets development with such translocation lines have been successful for six species: maize (Burnham, 1954), barley (Burnham *et al*., 1954), pea (Lamm and Miravalle, 1959), rye (Sybenga and Wolters, 1972), tomato (Gill *et al*., 1980), and cotton (Brown, 1980).

The first induced translocations in upland cotton (*G. hirsutum* L.) were outcomes from seed irradiation during atomic bomb tests carried out at the Bikini Atoll, where exposure to radiation with unknown dose and duration resulted in translocation lines exhibiting several quadrivalents (Brown, 1950). Subsequently, 12 translocations became distinct following X-ray irradiation of germinating seeds at the dose of 1200 R (Menzel and Brown, 1954). Over the 20 years, induction of 53 translocations proceeded via X-ray, gamma radiation, fast-neutron irradiation, and pollen irradiation of cotton cultivars. Meanwhile, obtaining four translocations came from interspecific hybrids between *G. hirsutum* and Asian species, and five hybrids were of spontaneous origin (Brown, 1980). In 58 out of the 62 translocations, two nonhomologous chromosomesv contributed, whereas three nonhomologous chromosomes participated in three translocations, and four in one translocation. Assigning the translocated chromosomes to specific sub-genomes necessitated performing hybridization between the translocation lines and D-subgenome species. As a result, 26 translocations occurred between A-subgenome chromosomes, another 26 between A and D-subgenome chromosomes, and the remaining 10 exchanges occurred between D-subgenome chromosomes (Brown, 1980).

The translocation lines eventual crossing with each other ensued, determining the chromosomes involved in the exchange based on the analysis of chromosome association during meiosis. If two different translocations involved one common chromosome, then in hybrids at MI of meiosis, this formed 23 bivalents and one hexavalent. However, if the two translocations involved two different chromosomes, 22 bivalents and two quadrivalents were evident (Brown, 1980). With this, the A-subgenome chromosomes of *G. hirsutum* L. had numberings from 1 to 13 and the D-subgenome chromosomes received numberings from 14 to 26 as per the genetic nomenclature of cotton (Kohel, 1973). The chromosomes identified in the exchanges reached numbering in the order of determining the chromosomes in the translocations. However, long-term studies have failed to identify the translocation-involving chromosome 26 of the D_t-subgenome; therefore, this chromosome's identification was successful via the exclusion method (Brown, 1980).

Among the 62 cotton translocation lines, a tester set comprising 20 lines obtained its selection, which allows the identification of 25 of the 26 nonhomologous chromosomes of *G. hirsutum* L. (Ray and Endrizzi, 1982).

The development of bacterial artificial chromosomes (BACs) opened a new phase of research in the identification of chromosomes in *G. hirsutum*, enabling the assignment of six linkage groups (A01, A02, A03, D02, D03, and D08) to chromosomes 13, 8, 11, 21, 24, and 19, respectively (Wang *et al*., 2006). The advancement of BAC probes made it possible to distinguish individual chromosomes of the A-genome in *G. arboreum* (2n = 26, AA) (Wang *et al*., 2008). Meanwhile, the physical localization of BAC probes on homoeologous chromosomes A12 and D12 revealed significant differences in genome organization, structure, and size between these homoeologous chromosomes in *G. hirsutum* (Wang *et al*., 2010). The development of oligonucleotide and rDNA probes enabled the identification of 10 chromosomes (Chr. 3, 4, 5, 6, 7, 9, 10, 11, 12, and 13) in the A-subgenome and seven (Chr. 1, 2, 4, 5, 7, 8, and 9) in the D-subgenome of the TM-1 line (Xu *et al*., 2024).

Owing to the need for studies aimed at chromosome identification in cotton, as well as the limited availability of lines from the

American Cytogenetic collection in previous years, the research work commenced at Tashkent State University to develop translocation lines. As a result, 33 homozygous translocation lines of *G. hirsutum* L. were successful in their development. These had the basis of plants' heterozygous for exchange induced by combined treatment of seeds with colchicine and gamma rays (Tr1–Tr11, Tr25, Tr26), gamma-ray irradiation of pollen (Tr12–Tr14, Tr23, Tr24, Tr32), and seed treatment with thermal neutrons (Tr15–Tr22, Tr27–Tr31, Tr33) (Sanamyan and Musaev, 1992; Sanamyan and Rakhmatullina, 2003; Sanamyan and Musaev, 2014; Sanamyan *et al*., 2014; Sanamyan, 2020).

Chromosomes 3 and 6 of the A_t-subgenome of cotton expressed involvement of the translocation line Tr8; in line Tr15, the chromosome 6 of the A_t-subgenome and chromosome 14 of the D_t-subgenome contributed; and in line Tr16, the chromosomes 2 and 3 of the A_t-subgenome were notable. The homology of one of the translocated chromosomes reached detection in four translocation lines of Uzbekistan (Tr5, Tr9, Tr13, and Tr26) compared with tester lines. Based on the above discussion, the consequent study aimed to identify the chromosomes involved in exchanges in translocation lines of the Uzbekistan via translocation lines with identified chromosomes developed in the USA.

MATERIALS AND METHODS

Plant materials

The homozygous translocation line Tr8 came from an initial plant heterozygous for a translocation induced by combined treatments of cotton (*G. hirsutum* L.) hybrid (L-500 × L-461) seeds from the cotton collection of Uzbekistan, with a 0.1% colchicine solution and gamma rays. Two other translocation lines (Tr15 and Tr16) obtained came from two initial forms induced by thermal neutron irradiation of cotton seeds of the line L-458 at the dose of 27 Gy. In obtaining forms that were homozygous for the exchanges and developing new translocation lines on their basis, the study used the previously developed scheme of cytogenetic analysis of the progeny of heterozygous for translocations (Sanamyan and Rakhmatullina, 2003).

Translocation tests

The identification of chromosomes involved in exchanges in accordance with the generally accepted chromosome numbering system necessitated the Uzbek translocation lines' (Tr) crossing with translocation lines of the USA collection with identified chromosomes (TT). Cytogenetic analysis of cotton F_1 hybrids at meiotic MI proceeded according to the scheme proposed by (Yamashita (1951), in which the formation of a hexavalent chromosome association revealed the involvement of common chromosomes in the exchanges participating in the crosses.

Cytological tests

For cytological studies, young flower buds measuring 2–3 mm sustained fixing in an ethanol–acetic acid solution (7:3). Pollen mother cells (PMCs) then incurred staining with iron acetocarmine. Chromosome behavior examination continued in PMCs at meiotic MI. The pattern of chromosome pairing reached assessment in temporary squash preparations. Based on the number and configuration of multivalents at MI of meiosis in F_1 hybrids, the homology of chromosomes involved in the translocation entailed determination as per previously described method (Sanamyan and Norova, 2022).

All the cytological observations performed took place via AxioScope A1 and Laboval microscopes (Carl Zeiss, Germany) and a Biomed microscope (Leica, Switzerland) with objective magnifications of 10× and 100×, a binocular attachment of 1.6×, a GF of 12.5×/120, and a 10× eyepiece. Microphotography, as carried out, used a digital camera (AxioCam ERc 5 s). During the image acquisition, the study utilized a green light filter (3C-11-3).

RESULTS

Analysis of cotton (*G. hirsutum* L.) F_1 hybrids obtained through crosses between three translocation lines of the Uzbek Collection and translocation lines with identified chromosomes from the USA showed two hybrids involving the translocation lines Tr8: Tr8 × TT 3L–19L (E20-7) and Tr8 × TT 3R–5R (8-5Gb). These revealed the formation of 23 bivalents and one hexavalent with different configurations at MI, with a predominance of chain forms and alternate chromosome segregation from translocation rings in 'critical cells' of PMC at meiotic MI. Since chromosome 3 of the A_t-subgenome of *G. hirsutum* L. appeared to be involved in the translocation of both tester lines, with the said chromosome homology confirmed with one of the chromosomes in Tr8 translocation line.

Analysis of three additional F_1 hybrids involving lines Tr8: Tr8 × TT 2L–6R (7-2b), Tr8 × TT 6L–14L (AZ-7), and Tr8 × TT 6L–7L (1048), also enunciated the formation of 23 bivalents and one hexavalent of various configurations. In the first two hybrids, the hexavalents predominantly occurred in chain form, with an alternate type of chromosome segregation from translocation rings. Contrastingly, in the third hybrid, ring-shaped hexavalents with an adjacent type of segregation resulted in 'critical cells' of PMC at MI. This further allowed the homology of the second rearranged chromosome in line Tr8 with chromosome 6 of the A_t-subgenome to reach inference, since all three tester lines showed characteristics of the involvement of this common chromosome in the exchanges (Table 1). Overall, chromosomes 3 and 6 of the A_t-subgenome of *G. hirsutum* L. contributed in the translocation in line Tr8.

However, by crossing the homozygous translocation line Tr8 with nine other translocation lines: Tr8 × TT 1L–7L (5-4c), Tr8 × TT 1L–8L (2780), Tr8 × TT 2R–14R (2B-1), Tr8 × TT 7L–12R (1043), Tr8 × TT 7L–18R (4659), Tr8 × TT 7R–11R (1052), Tr8 × TT 7R–21R (2790), Tr8 × TT 10R–11R (2785), and Tr8 × TT 20L–22R (DP4), 22 bivalents and two quadrivalents were noticeable at MI. The results further revealed that chromosomes 1, 2, 7, 8, 10, 11, 12, 14, 18, 20, 21, and 22

Table 1. Analysis of chromosome configurations at MI in cotton hybrids obtained from crosses between translocation line Tr8 of the Uzbek collection and translocation lines with numbered chromosomes.

Cross combinations	Chromo-somes	Hybrid number	№ PMCs	Frequency of the multivalent	Chromosome Homology	Chromosome configurations at MI in "critical cells"		
						Number of bivalents (II)	Number of quadrivalents (IV)	Number of hexavalents (VI)
Tp8 x TT 1L-7L (5-4c)	1L-7L	265	30	0.2666	Various	22	2	0
Tp8 x TT 1L-8L (2775b)	1L-8L	1069	54	0.2037	Various	22	2	0
Tp8 x TT 2L-6R (7-2b)	2L-6R	985	42	0.1219	Common	23	0	1
Tp8 x TT 2R-14R (2B-1)	2R-14R	881	34	0.1764	Various	22	2	0
Tp8 x TT 3L-6L (4010)	3L-6L	266	41	0.4390	Common	23	0	1
Tp8 x TT 3L-19L (E20-7)	3L-19L	986	35	0.2285	Common	23	0	1
Tp8 x TT 3R-5R (8-5Gb)	3R-5R	987	32	0.2812	Common	23	0	1
Tp8 x TT6L-7L (1048)	6L-7L	268	38	0.1842	Common	23	0	1
Tp8 x TT 6L-14L (AZ-7)	6L-14L	988	43	0.2558	Common	23	0	1
Tp8 x TT 7L-12R (1043)	7L-12R	1028	46	0.2391	Various	22	2	0
Tp8 x TT 7L-18R (4659)	7L-18R	269	35	0.1714	Various	22	2	0
Tp8 x TT 7R-11R (1052)	7R-11R	990	39	0.2564	Various	22	2	0
Tp8 x TT 7R-21R (2790)	7R-21R	991	43	0.2093	Various	22	2	0
Tp8 x TT 10R-11R (2785)	10R-11R	674	47	0.2765	Various	22	2	0
Tp8 x TT 20L- 22R (DP4)	20L- 22R	1071	51	0.1960	Various	22	2	0

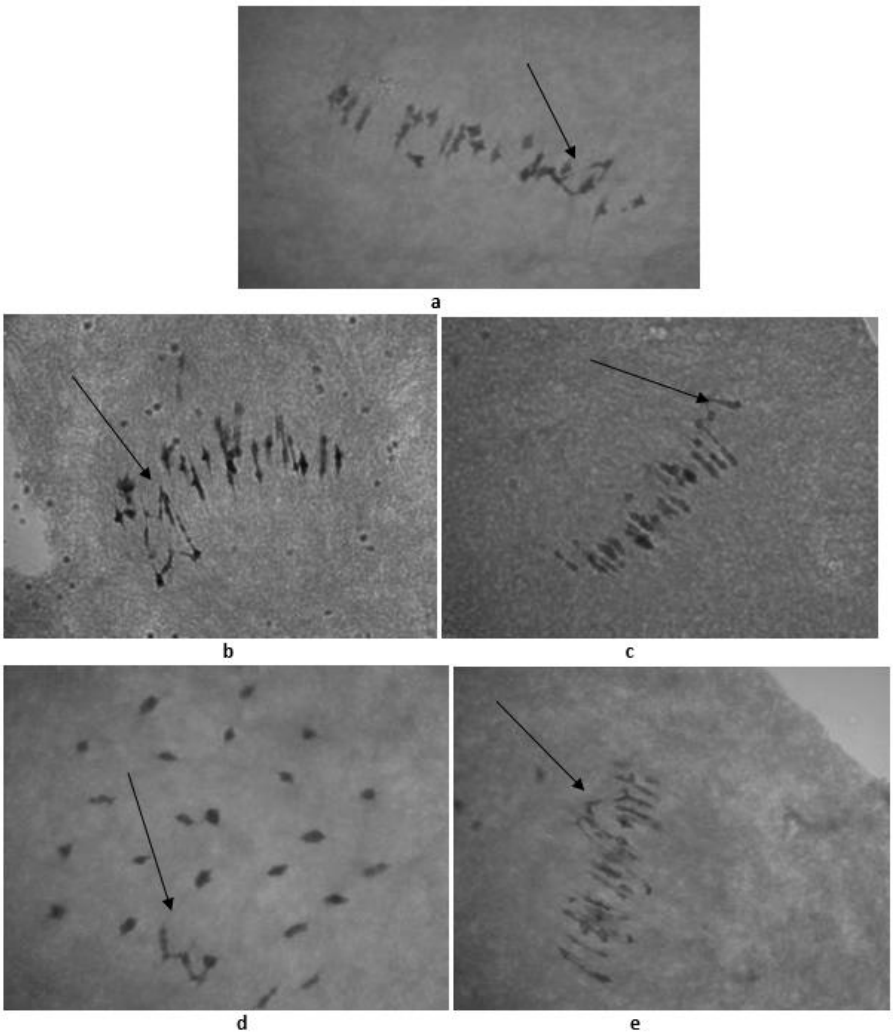

Figure 1. Chromosome configurations at MI in PMC of cotton F_1 hybrids obtained from crosses between translocation lines and tester-set lines: (a) Tr8 × TT6L–7L (1048) ($23^{II}+1^{VI}$); (b) Tr15 × TT 3L–6L (4010) ($23^{II} + 1^{VI}$); (c) Tr15 × TT6L–7L (1048) ($23^{II}+1^{VI}$); (d) Tr16 × TT2-3a (IV_1) ($23^{II}+1^{VI}$); and (e)Tr9 × TT3L–6L(4010) ($23^{II}+1^{VI}$) (Arrows indicate hexavalents).

occurred to be not involved in the translocation in the homozygous translocation line Tr8 (Figure 1).

By crossing the homozygous translocation line Tr15 with 13 lines, chromosome pairing resulted in the formation of 23 bivalents and one hexavalent of various configurations (rings and chains), with adjacent and alternate types of chromosome segregation observed in five F_1 hybrids at MI. Thus, in four F_1 hybrids, Tr15 × TT 3L–6L (4010), Tr15 × TT 6L–7L (1048), Tr15 × TT 6L–10R (Z9-9), and Tr15 × TT 6L–14L (AZ-7), the chromosome 6 of the A_t-subgenome of *G. hirsutum* exhibited involvement. In two other cross combinations, Tr15 × TT 6L–14L (AZ-7) and Tr15 × TT 14R–24R (2781), the hexavalents with a predominance of ring configurations exhibiting an adjacent type of chromosome segregation materialized. Since chromosome 14 of the D_t-subgenome of *G. hirsutum* L. participated in these crosses, one can conclude that chromosome 6 of the A_t-subgenome and chromosome 14 of the D_t-subgenome were considerably involved in the translocation in line Tr15 (Table 2).

Table 2. Analysis of chromosome configurations at MI in cotton hybrids obtained from crosses between the Tr15 translocation line of the Uzbek collection and the translocation lines with numbered chromosomes.

Cross combinations	Chromo-somes	Hybrid number	№ PMSs	Frequency of the multivalents	Chromo-some homology	Chromosome configurations at MI in "critical cells"		
						Number of bivalents (II)	Number of quadrivalents (IV)	Number of hexavalents (VI)
Tp15 x TT1L-8L (2775b)	1L-8L	274	47	0.2340	Various	22	2	0
Tp15 x TT1R-16Rb (4672)	1R-16Rb	688	36	0.2777	Various	22	2	0
Tp15 x TT2-3b (1059)	2-3b	275	31	0.2580	Various	22	2	0
Tp15 x TT3L-6L (4010)	3L-6L	1000	53	0.2452	Common	23	0	1
Tp15 x TT5-9 (C14-3)	5-9	1083	42	0.3333	Various	22	2	0
Tp15 x TT5-12R (SL18)	5-12R	1084	39	0.2820	Various	22	2	0
Tp15 x TT6-7L (1048)	6-7L	1001	28	0.2857	Common	23	0	1
Tp15 x TT6L-10R (Z9-9)	6L-10R	1030	40	0.3250	Common	23	0	1
Tp15 x TT6L-14L (AZ-7)	6L-14L	276	39	0.2307	Common	23	0	1
Tp15 x TT7R-11R (1052)	7R-11R	1154	32	0.2500	Various	22	2	0
Tp15 x TT10R-11R (2785)	10R-11R	1155	28	0.2142	Various	22	2	0
Tp15 x TT12R-19R (9-5H)	12R-19R	1115	35	0.2571	Various	22	2	0
Tp15 x TT14R-24R (2781)	14R-24R	894	30	0.2333	Common	23	0	1

However, by crossing homozygous translocation line Tr15 with eight other translocation lines, namely, Tr15 × TT 1L–8L (2775b), Tr15 × TT 1R–16Rb (4672), Tr15 × TT 2–3b (1059), Tr15 × TT 5L–9L (C14-3), Tr15 × TT 5R–12R (SL18), Tr15 × TT 7R–11R (1052), Tr15 × TT 10R–11R (2785), and Tr15 × TT 12R–19R (9-5H), 22 bivalents and two quadrivalents were evident at the MI. The results further revealed that rearranged chromosomes of these lines (1, 2, 3, 5, 7, 8, 9, 10, 11, 12, 16, and 19) emerged not to be involved in the translocation of the homozygous translocation line Tr15.

Given that crossing translocation line Tr16 with 15 translocation lines, 'critical associations' identified resulted in six F_1 hybrids. Thus, analysis of two cross combinations, Tr16 × TT 2L–3Lb (1059) and Tr16 × TT 2R–8Rb (1058b), revealed chromosome pairing with formation of 23 bivalents and one hexavalent, predominantly in chain configurations with an alternate type of chromosome segregation. Since a common chromosome 2 was a participant in both tester lines, one can conclude that one of the rearranged chromosomes in the Tr16 translocation line was the chromosome 2 of the A_t-subgenome of *G. hirsutum* L.

Analysis of five additional cross combinations also exhibited the presence of hexavalent chromosomes during meiosis, predominantly in chain configurations with alternate types of chromosome segregation: Tr16 × TT 1L–3L (2935), Tr16 × TT 2L–3Lb (1059), Tr16 × TT 3L–19L (E20-7), Tr16 × TT 3R–5R (8-5Gb), and Tr16 × TT 3R–9R (8-30-5). The results confirmed the involvement of another common chromosome 3 of the A_t-subgenome of *G. hirsutum*. Based on these results, chromosomes 2 and 3 of the A_t-subgenome proved involved in the translocation in line Tr16 (Table 3).

By crossing homozygous translocation line Tr16 with nine other translocation lines: Tr16 × TT 1L–8L (2775b), Tr16 × TT 4R–15L (1040), Tr16 × TT 6–7L (1048), Tr16 × TT 7–18R (4659), Tr16 × TT 9R–17Rb (6340), Tr16 × TT 9R–25 (2870), Tr16 × TT 12R–19R (9-5H), Tr16 × TT 13R–19R (2925), and Tr16 × TT 14L–23 (2777), 22 bivalents and two quadrivalents surfaced at MI. The results confirmed that the marked chromosomes of the above-mentioned nine lines (1, 4, 5, 6, 7, 8, 9, 12, 13, 14, 15, 17, 18, 19, 23, and 25) indicated non-involvement in the translocation of the homozygous translocation line Tr16.

Table 3. Analysis of chromosome configurations at meiotic metaphase I in hybrids obtained from crosses between the Tr16 translocation line of the Uzbek collection and the translocation lines with numbered chromosomes.

Cross combinations	Chromo-somes	Hybrid number	№ PMCs	Frequency of the multivalents	Chromo-some homology	Chromosome configurations at MI in "critical cells"		
						Number of bivalents (II)	Number of quadrivalents (IV)	Number of hexavalents (VI)
Tp16 x TT1L-3L (2935)	1L-3L	443	49	0.2448	Common	23	0	1
Tp16 x TT1L-8L (2775b)	1L-8L	278	36	0.2222	Various	22	2	0
Tp16 x TT2L-3Lb (1059)	2L-3Lb	279	26	0.2692	Common	23	0	1
Tp16 xTT2-8Rb (1058b)	2-8Rb	1003	30	0.2333	Common	23	0	1
Tp16 x TT3L-19L (E20-7)	3L-19L	1005	33	0.2727	Common	23	0	1
Tp16 x TT3R-5R (8-5Gb)	3R-5	689	51	0.2745	Common	23	0	1
Tp16 x TT3R-9R (8-30-5)	3R-9R	1006	37	0.2972	Common	23	0	1
Tp16 x TT4R-15L (1040)	4R-15L	1086	32	0.2500	Various	22	2	0
Tp16 x TT6-7L (1048)	6-7L	281	29	0.2413	Various	22	2	0
Tp16 x TT7-18R (4659)	7-18R	282	48	0.2083	Various	22	2	0
Tp16 x TT9R-17Rb (6340)	9R-17Rb	1087	34	0.2647	Various	22	2	0
Tp16 x TT9R-25 (2870)	9R-25	283	36	0.2222	Various	22	2	0
Tp16 x TT12R-19R (9-5H)	12R-19R	1089	27	0.2592	Various	22	2	0
Tp16 x TT13R-19R (2925)	13R-19R	690	33	0.1818	Various	22	2	0
Tp16 x TT14L-23 (2777)	14L-23	1090	29	0.2758	Various	22	2	0

Unfortunately, for four other translocation lines of the Uzbek collection (Tr5, Tr9, Tr13, and Tr26), only one chromosome involved in the exchange is identifiable. Thus, by crossing Tr5 translocation line with 12 lines with identified chromosomes, chromosome pairing in the form of 23 bivalents and one hexavalent succeeded in their detection in four F_1 hybrids. Since TT 2L–6R (7-2b), TT 3L–6L (4010), TT 6L–7L (1048), and TT 6L–10R (Z9-9) in chromosome 6 of the A_t-subgenome of cotton were considerably contributory in the translocation of all four tester lines. Therefore, a conclusion could be that the said chromosome participated in the translocation of the translocation line Tr5.

By crossing Tr9 translocation line with 12 lines with identified chromosomes, two F_1 hybrids showed distinction with the presence of 23 bivalents and one hexavalent during meiosis. However, the results made it possible to infer the homology of one of the chromosomes in line Tr9 with chromosome 6 of the A_t-subgenome of cotton, since this chromosome participated in the translocations of both identified tester lines TT 2L–6R (7-2b) and TT 3L–6L (4010).

Analysis of 14 cross combinations involving line Tr13 and lines with identified chromosomes revealed three cross combinations characterized by the formation of 23 bivalents and one hexavalent during meiosis. The results disclosed the homology of one of the chromosomes in line Tr13 with chromosome 3 of the A_t-subgenome, since this chromosome signified considerable involvement in the translocations of tester lines, TT 2R–3La (IV_1), TT 3L–6L (4010), and TT 3L–19L (E20-7) and in their three cross combinations.

Assessment of 10 hybrids involving line Tr26 and lines with identified chromosomes expressed that in two cross combinations, chromosome pairing with the formation of 23 bivalents and one hexavalent was apparent during meiosis. The results confirmed the homology of one of the chromosomes in line Tr26 with chromosome 3 of the A_t-subgenome, since this chromosome shared in the translocations of tester lines, TT 2R–3La (IV_1)

and TT 3L–6L (4010) and in these two crossing combinations.

DISCUSSION

The classical karyological analysis can be beneficial for chromosome identification in few plant species with large and morphologically well-differentiated chromosomes, characterized by considerable variations in chromosome arms and large and differentially stained C-bands (Vries and Sybenga, 1976). The non-traditional identification methods based on translocation exchanges entailed a crucial requirement for plant species with small and morphologically and poorly differentiated chromosomes, including cotton (Brown, 1965). Through various types of irradiation, the induction of such exchanges made it possible to obtain 62 translocation lines in the USA, 58 of which included two nonhomologous chromosomes. The identification of translocated chromosomes revealed that certain nonhomologous chromosomes appeared to be involved in exchanges more frequently than others were. Overall, A-subgenome chromosomes of cotton (*G. hirsutum* L.) indicated involvement more often than D-subgenome chromosomes. Moreover, only one of the three nucleolus-organizing chromosomes contributed in a translocation.

Although the significance of individual chromosomes involvement in exchanges remains unclear, the large number of induced translocations involving specific chromosomes may exhibit increased sensitivity of certain regions of cotton chromosomes to irradiation. Analysis of translocations in wheat revealed cultivars and lines often considerably differed in the presence of exchanges, and assessment of 466 combinations bared the most frequent involvement of chromosomes 1A, 7B, and 2D in various translocations. Overall, B genome chromosomes occurred to be involved in most exchanges in wheat (Schlegel, 1996).

Overall, the combined data revealed that chromosomes of the A, B, and D genomes of wheat differed substantially in their degree of involvement in different translocations. These indicated the highest number of chromosomal rearrangements recorded was in the B genome (90), followed by the A genome (57) and the D genome (5). Remarkably, the individual wheat chromosomes resulted in chromosomal rearrangements with different frequencies: the highest number of translocations recorded was for the chromosomes 4B, 5B, and 2A (Ali *et al.,* 1994; Kawahara, 1997).

Cytogenetic analysis of hybrid progenies came from various F_1 hybrids among the three homozygous translocation lines (Tr8, Tr15, and Tr16) of the Uzbek collection and American translocation lines with identified chromosomes. These enunciated the involvement of chromosomes 2, 3, and 6 of the A_t-subgenome, as well as chromosome 14 of the D_t-subgenome in exchanges. In two homozygous translocation lines (Tr8 and Tr16), the translocations involved two frequently occurring chromosomes of the A_t-subgenome (3–6 and 2–3, respectively). In contrast, in line Tr15, the translocation involved the chromosomes from two different cotton subgenomes (chromosome 6 of the A_t-subgenome and chromosome 14 of the D_t-subgenome). Additionally, the analysis further revealed homology of one of the translocated chromosomes in four translocation lines of the Uzbek collection (Tr5, Tr9, Tr13, and Tr26) with chromosomes of the tester lines. In Tr5 and Tr9 lines, detected homology was with chromosome 6 of the A_t-subgenome, whereas in two other lines (Tr13 and Tr26), the established homology was with chromosome 3 of the A_t-subgenome. However, all these chromosomes had characteristics of the highest frequency of occurrence in exchanges as per the comparative analysis of translocation lines from the USA collection.

The promising results confirmed past findings revealing the highest degree of involvement of specific cotton chromosomes in exchanges (Brown, 1980), although the homozygous translocation lines of the Uzbek and American Cytogenetic collections differed in the origin and methods used for their induction. Moreover, three translocation lines of the Uzbek collection divulged adequate model objects for conducting comparative cytogenetic studie between translocation lines

from different collections and for elucidating specific features of radiation effects on the cotton karyotype. Further studies aimed at the unified identification of chromosomes involved in exchanges are essential, with more new translocation lines characterized by specific features becoming available. These comprised the *frego*-type bract (Tr10), dense stem pubescence (Tr2), entire leaf margins (Tr12), clustered arrangement of fruiting elements and absence of stigma exertion (Tr18), pale-green leaf coloration due to a cytoplasmic mutation (Tr28), and partial pollen sterility in a homozygous line (Tr21). These result from the considerable involvement of specific chromosomal regions in the exchange, the rearrangement of which led to semi-lethality of gametes (Sanamyan, 2020).

CONCLUSIONS

Cytogenetic analysis of cotton F_1 hybrids obtained through crosses between translocation lines of the Uzbek collection and those with numbered chromosomes from the USA enabled unified identification of translocated chromosomes involved in exchanges. Chromosomes 3 and 6 of the A_t-subgenome of cotton showed involvement in exchange in the Tr8 translocation line; in the Tr15 line, chromosome 6 of the A_t-subgenome and chromosome 14 of the D_t-subgenome proved involved; and in the Tr16 line, chromosomes 2 and 3 of the A_t-subgenome participated. The homology of one of the translocated chromosomes succeeded in its identification in four translocation lines (Tr5, Tr9, Tr13, and Tr26)— in two lines (Tr5 and Tr9), the established homology was with chromosome 6 of the A_t-subgenome, whereas in two other lines (Tr13 and Tr26), the developed homology was with chromosome 3 of the A_t-subgenome.

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REFERENCES

Ali AM, Nakata N, Tomita M, Yasumuro Y (1994). Identification of translocated chromosomes in a Japanese common wheat variety Saitama 27. *Wheat Inf. Serv.* 79: 37–41.

Brown MS (1950). Cotton from Bikini. *Heredity* 41: 115–121. https://doi.org/10.1093/ oxfordjournals.jhered.a106104.

Brown MS (1965). The identification of chromosomes in *Gossypium hirsutum* by means of translocations. *Genetics* 52: 430–431.

Brown MS (1980). Identification of the chromosomes of *Gossypium hirsutum* L. by means of translocations. *Heredity* 71: 266–274. https://doi.org/10.1093/oxfordjournals.jhered.a109361.

Burnham CR (1954). Tester–set of translocations. *Maize Genet. Coop. Newsletter* 28: 59–60.

Burnham CR, White FH, Livers R (1954). Chromosomal interchanges in barley. *Cytology* 19: 191–202. https://doi.org/10.1508/cytologia.19.191.

Gill BS, Burnham CR, Stringam GR, Stout JT, Weinheimer WH (1980). Cytogenetic analysis of chromosomal translocations in the tomato: Preferential breakage in heterochromatin. *Genet. Cytol*. 22: 333–341. https://doi.org/10.1139/g80-041.

Kawahara T (1997). Screening of spontaneous translocations in cultivated emmer wheat. *Wheat Inf. Serv.* 85: 45–46.

Kohel RJ (1973). Genetic nomenclature in cotton. *Heredity* 64: 291–295. https://doi.org/ 10.1093/oxfordjournals.jhered.a108415.

Lamm R, Miravalle RJ (1959). A translocation tester set in *Pisum*. *Hereditas* 45: 417–440. https://doi.org/ 10.1111/j.1601-5223.1959. tb03059.x.

Menzel MY, Brown MS (1954). The significance of multivalent formation in three-species *Gossypium* hybrids. *Genetics* 39: 546–557. https://doi.org/10.1093/genetics/39.4.546.

Ray DT, Endrizzi JE (1982) A tester-set of translocations in *Gossypium hirsutum* L. *Heredity* 73: 429–433. https://doi.org/ 10.1093/oxfordjournals.jhered.a109692.

Sanamyan MF (2020). Cytogenetics of mutations, translocations, monosomy and interspecific

hybridization in cotton. University Tashkent: pp. 384. (In Russian).

Sanamyan MF, Musaev DA (1992). Development and cytogenetic analysis of homozygous translocation lines in cotton. *Genetika* 28: 75–82. (In Russian).

Sanamyan MF, Musaev DA (2014). Cytogenetic peculiarities of the new cotton lines with chromosome interchanges. *Rep. Acad. Sci. Uzbekistan* 5: 75–77.

Sanamyan MF, Norova SU (2022). Some features of chromosome identification in cotton translocation lines using test lines of *G. hirsutum* L. *Bull. Nat. Uni. Uzbekistan* 3: 143–149.

Sanamyan MF, Petlyakova JE, Rakhmatullina EM, Sharipova EA (2014). Cytogenetic Collection of Uzbekistan. In: I.Y. Abdurakhmonov (Ed.), World Cotton Germplasm Resources. IntechOpen: Croatia, Chapter 10: 247–287. https://doi.org/10.5772/58589.

Sanamyan MF, Rakhmatullina EM (2003). Cytogenetic analysis of translocations in cotton. *Plant Breed*. 122: 511–516. https://doi.org/10.1046/j.1439-0523.2003.00887.

Schlegel R (1996). A compendium of reciprocal intervarietal translocations in wheat: 2nd Ed. *Wheat Inf. Serv.* 83: 35–46.

Sybenga J, Wolters AHG (1972). The classification of the chromosomes of rye (*Secale cereale* L.): A translocation tester set. *Genetica* 43: 453–464. https://doi.org/10.1007/BF00122928.

Vries JM, Sybenga J (1976). Identification of rye chromosomes: The Giemsa banding pattern and the translocations tester set. *Theor. Appl. Genet*. 48: 35–43. https://doi.org/10.1007/BF00282408.

Wang K, Guan B, Guo W, Zhou B, Hu Y, Zhu Y, Zhang T (2008). Completely distinguishing individual A-genome chromosomes and their karyotyping analysis by multiple bacterial artificial chromosome—fluorescence in situ hybridization. *Genetics* 178: 1117–1122. https://doi:10.1534/genetics.107.083576.

Wang K, Guo W, Yang Z, Hu Y, Zhang W, Zhou B, Stelly DM, Chen ZJ, Zhang T (2010). Structure and size variations between 12A and 12D homoeologous chromosomes based on high-resolution cytogenetic map in allotetraploid cotton. *Chromosoma* 119: 255–266. https://doi:10.1007/s00412-009-0254-0.

Wang K, Song X, Han Zh, Guo W, John ZY, Sun J, Pan J, Kohel RJ, Zhang T (2006). Complete assignment of the chromosomes of *Gossypium hirsutum* L. by translocation and fluorescence *in situ* hybridization mapping. *Heredity* 113: 73–80. https://doi:10.1007/s00122-006-0273-7.

Xu M, Guo H, Wang Y, Zhou B (2024). Identification of chromosomes by fluorescence in situ hybridization in *Gossypium hirsutum* via developing oligonucleotide probes. *Genome* 67: 64–77. https://doi.org/10.1139/gen-2023-0051.

Yamashita K (1951). Studies on X-ray induced reciprocal translocations in einkorn wheats. III. A newly synthesized ring of 14 chromosomes in complex heterozygotes, *Aegilopoides–monococcum*. *Cytologia* 16: 164–176. https://doi.org/10.1508/cytologia.16.164.