ASSESSMENT OF CROSSABILITY OF TRANSLOCATION LINES FROM A TESTER SET CROSSED WITH HOMOZYGOUS TRANSLOCATION LINES TR2 AND TR20

Norova S.U.

National University of Uzbekistan named after Mirzo Ulugbek,

INTRODUCTION

Crossing translocation lines in cotton (*Gossypium hirsutum* L.) breeding is considered one of the important approaches for combining valuable traits and developing promising genotypes. In particular, the use of translocation lines carrying structural chromosome rearrangements is of great importance for expanding the genetic and cytogenetic resources of cotton. In translocation lines, genetic material is exchanged between two or more chromosomes, and such structural changes may affect chromosome pairing and segregation during meiosis. Therefore, when translocation lines are crossed with each other, the efficiency of hybridization can be assessed depending on the genetic characteristics of the hybrid combination. Determining the crossability between two translocation lines is an important indicator for evaluating their reproductive compatibility. The number of seeds obtained from crosses, seed germination, and the viability of hybrid plants characterize the degree of biological and genetic compatibility between the lines. At the same time, interactions between chromosomes carrying translocations may affect the normal or abnormal progression of meiosis in hybrids and, consequently, the formation of viable gametes. Another important aspect of studying the crossability of translocation lines is that their intercrossing makes it possible to determine the inheritance of structural chromosome rearrangements and their patterns of expression in subsequent generations. In this

regard, evaluating the crossability of translocation lines carrying different chromosomal exchanges is of considerable scientific and practical importance for the effective utilization of the cotton cytogenetic collection, determining the possibility of obtaining hybrid progeny, and selecting promising combinations for further genetic studies.

The aim of this study was to evaluate the crossability of homozygous translocation lines based on their intercrossing**.**

Materials and Methods: The plant materials used in this study were homozygous translocation lines Tr2 and Tr20, which were used as female parents, and chromosome-numbered tester lines, which were used as male parents. A total of 33 homozygous translocation lines were developed by M.F. Sanamyan and her colleagues and are maintained in the Cytogenetic Collection of the National University of Uzbekistan. Among these, two non-homologous chromosomes were involved in the translocations in 31 lines, whereas three non-homologous chromosomes were involved in the translocations in two lines, Tr2 and Tr20.

The Tr2 line was developed by combined treatment of seeds obtained from the F_1 hybrid of the L-500 x L-461 cross with 0.1% colchicine solution and gamma irradiation at a dose of 50 Gy [4;5]. The homozygous translocation line Tr20 was obtained by irradiating seeds of line L-458 with neutrons at a dose of 25 Gy [6;7].

In addition, chromosome-numbered tester lines (Tn2, Tn5, Tn12, Tn13, Tn14, Tn18, Tn21, Tn23, Tn25, Tn28, Tn29, Tn30, Tn37, Tn40, Tn41, Tn50, Tn53, Tn55, and Tn57) from the U.S. Cytogenetic Collection were used. These lines were provided to Prof. M.F. Sanamyan by Prof. David Stelly of Texas A&M University through an exchange program with the Agricultural Research Service of the United States Department of Agriculture (ARS-USDA). The tester lines represent translocation lines of *Gossypium hirsutum* L. that were developed by M.S. Brown and his colleagues over a period of more than 20 years [1].

Results and Discussion: The homozygous translocation line Tr2 was crossed with seven chromosome-numbered tester lines (Tn2, Tn14, Tn18, Tn21, Tn28, Tn29, and Tn50). The highest crossability rate of 100% was recorded in two combinations, Tr2 x Tn14 and Tr2 x Tn28. An intermediate level of crossability, ranging from 60.00% to 75.00%, was observed in three combinations: Tr2 x Tn2, Tr2 x Tn18, and Tr2 x Tn29. When the homozygous translocation line Tr2 was crossed with the chromosome-numbered tester lines Tn21 and Tn50, relatively low crossability rates of 33.33% and 40.00%, respectively, were recorded.

The homozygous translocation line Tr20 was crossed with 14 chromosome-numbered tester lines (Tn5, Tn12, Tn13, Tn21, Tn23, Tn25, Tn30, Tn37, Tn40, Tn41, Tn50, Tn53, Tn55, and Tn57), and the following results were obtained. The highest crossability rate (100.00%) was recorded in four combinations: Tr20 x Tn5, Tr20 x Tn13, Tr20 x Tn40, and Tr20 x Tn50. In addition, when the homozygous translocation line Tr20 was crossed with the tester lines Tn30 and Tn41, the crossability rate was 80.00%. Intermediate crossability rates, ranging from 50.00% to 75.00%, were recorded in six combinations: Tr20 x Tn21, Tr20 x Tn23, Tr20 x Tn25, Tr20 x Tn37, Tr20 x Tn53, and Tr20 x Tn55. In contrast, low crossability rates were observed in the Tr20 x Tn12 (25.00%) and Tr20 x Tn57 (33.33%) combinations.

Comparison of the obtained results with studies of crossability in other plant species, particularly studies on the crossability of wheat with rye and other related species, indicates that interspecific crossability depends not only on gamete formation and fertilization processes but also on reproductive barriers controlled by genetic factors. For example, the crossability of common wheat with rye, wild and cultivated barley species is associated with the Kr gene family**,** and the reproductive barriers caused by these genes reduce the frequency of hybrid seed formation. Molecular genetic studies of wheat–rye crosses have identified a major QTL region controlling crossability on the short arm of wheat chromosome 5B, associated with the Xgwm443 SSR marker**.**

This region was suggested to be associated with the SKr (Suppressor of crossability) locus [2;3]. These findings indicate that the genetic control of crossability may be associated with genes or genomic regions located on specific chromosomes.

In our study, the crossability of translocation lines with different tester lines also varied considerably depending on the cross combination. While a high rate of hybrid seed formation was observed in some combinations, substantially lower rates were recorded in others. This variation suggests that the genetic constitution of the translocation line and the genotype of the tester line may interact and influence crossability.

References

1. Brown M.S. Identification of the chromosomes of *Gossypium hirsutum* L. by means of translocations // Journal of Heredity. - 1980. - V.71. - №4. - P. 266 - 274.
2. Mishina K., Sato H., Manickavelu A., Sassa H., Koba T. Molecular mapping of SKr for crossability in common wheat // Breeding Science. 2009. – V.59. – P.679–684.
3. Rabinovich S.V., Schlegel R., Crespo-Herrera L.A., et al. Genetic control of compatibility in crosses between wheat and its wild or cultivated relatives // Plant Biotechnology Journal. 2022. – V.20.- P.812–832.
4. Sanamyan M.F., Almatov A.S. Cytogenetic characteristics of M_1 plants of an interline cotton hybrid after combined treatment of seeds with colchicine and gamma rays //Uzbek biological journal. - 1985. - №.3. - P.56–59.
5. Sanamyan M.F., Musaev D.A. Production and cytogenetic study of homozygous translocation lines of cotton // Genetika. Moscow. 1992. - V.28. - №11. - P.75–82.
6. Sanamyan M.F., Musaev D.A. Cytogenetic characteristics of new cotton lines with interchromosomal exchanges. Doklady of the academy of sciences of the Republic of Uzbekistan. 2014. - №.5. - P.75–77.

7. Sanamyan M.F., Petlyakova J., Rakhmatullina E.M., Sharipova E. Chapter 10. Cytogenetic collection of Uzbekistan. In: Abdurakhmonov IY. (Ed). World Cotton Germplasm Resources. Croatia: In Tech. - 2014. - P. 247-287