

The divergence of wheat 5B chromosomes during evolution and its impact on recombination suppression

Salina E.^{1,2*}, Muterko A.¹, Kiseleva A.^{1,2}, Korol A.³

¹ Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia

² Kurchatov Genomic Center of the Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia

³ Siberian Research Institute of Plant Production and Breeding – Branch of the Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia

* salina@bionet.nsc.ru

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Motivation and Aim: Chromosomal rearrangements that lead to recombination suppression can have a significant impact on speciation, and they are also important for breeding. In the present work, we evaluated the key points of chromosome 5B reorganization throughout evolution by identifying regions of recombination suppression in interspecific crosses. Sequence analysis of 5B pseudomolecules of *T. aestivum* ($2n = 6x$) and *T. dicoccoides* ($2n = 4x$) in the studied regions on 5B allowed us to identify possible determinants of recombination suppression.

Methods and Algorithms: Multiple sequence alignment was carried out using MAFFT 7.311 software.

Results: The regions of recombination suppression in wheat chromosome 5B were identified based on comparisons of the 5B map of a cross between the Chinese Spring (CS) variety of hexaploid wheat and CS-5Bdic (genotype CS with 5B substituted with its homologue from tetraploid *Triticum dicoccoides*) with several 5B maps of tetraploid and hexaploid wheat. In total, two regions were selected in which recombination suppression occurred in cross CS x CS-5Bdic when compared with other maps: one on the short arm, 5BS_RS, limited by markers BS0009810/BS00022336, and the second on the long arm, 5BL_RS, between markers Ra_c10633_2155 and BS00087043. The regions marked as 5BS_RS and 5BL_RS, with lengths of 5 and 3.6 Mb respectively, were mined from the 5B pseudomolecule of CS and compared to the homoeologous regions (7.6 and 3.8 Mb respectively) of the 5B pseudomolecule of Zavitan (*T. dicoccoides*). It was shown that, in the case of 5BS_RS, the local heterochromatin islands determined by the satellite DNA (119.2) and transposable element arrays, as well as the dissimilarity caused by large insertions/deletions (chromosome rearrangements) between 5BSs *aestivum/dicoccoides* are likely the key determinants of recombination suppression in the region. Two major and two minor segments with significant loss of similarity were recognized within the 5BL_RS region.

Conclusion: The loss of similarity, which can lead to suppression of recombination is caused by chromosomal rearrangements, driven by the activity of mobile genetic elements (both DNA transposons and long terminal repeat retrotransposons) and their divergence during evolution. The revealed divergence may be a consequence of interspecific hybridization, plant genetic adaptation, or both.

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