

Impact of DNA reorganization on recombination suppression of 5b chromosome during wheat evolution

A.A. Kiseleva^{1*}, A.F. Muterko¹, Z. Frenkel², A. Korol², E.A. Salina¹

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

² Institute of Evolution, University of Haifa, Haifa, Israel

* e-mail: antkiseleva@bionet.nsc.ru

Key words: wheat, genetic maps, evolution

Motivation and Aim: A comprehensive study of the evolution of wheat chromosome 5B based on the genetic and physical mapping data and analysis of the primary structure of the chromosome regions that influence the ability of this chromosome to moderate recombination in interspecific *T. aestivum* × *T. dicoccoides* crosses is described.

Methods and Algorithms: Genetic maps were constructed using the MultiPoint UltraDense software. Consensus maps were developed using the “MapFuser” R package. Comparative analysis of DNA was performed using UGENE, “Tandem Repeats Finder” and MAFFT 7.311 software. In order to identify genes and mobile genetic elements, the ENA database of plant protein coding sequences and MIPS Repeat Element Database were used respectively. Similarity searching was performed using BLASTn.

Results: The performed comparative genetic analysis comprises construction of the 5B map using a cross of CS and CS-5Bdic and comparison of the resulting map to the 5B chromosome maps of *T. durum* × *T. dicoccoides*, *T. durum* × *T. durum* and the maps built based on several crosses of common wheat cultivars using the same approaches. The regions of considerable recombination suppression on the 5B chromosome maps of *durum/dicoccoides* and *aestivum/aestivum* have been identified by comparing to CS/CS-5Bdic and can be explained by the divergence between the analyzed tetraploid and hexaploid wheat accessions. The same suppression regions as in CS and CS-5Bdic have been observed in all three studied populations. These regions of the 5B chromosome are actually the sites of rearrangements involved in the tetraploid–hexaploid evolutionary transition. No suppression events have been undetectable in the region of the Ph locus, the emergence of which was associated with the evolutionary stage prior to or during formation of the wild emmer. To unravel the causes of recombination suppression, the primary structure of the detected recombination suppression regions of 5B *T. aestivum* and *T. dicoccoides* chromosomes has been analyzed. In this analysis the inversion, large insertions/deletions, and extended clusters of 119.2 tandem repeats were found, which differ studied homoeologous chromosomal regions of both species.

Conclusion: To study the causes of recombination suppression, the analysis of the primary structure of the discussed regions was performed and the mechanisms underlying their contribution of the detected inversions, large insertions/deletions, and extended clusters of 119.2 tandem repeats to recombination suppression in 5BS are discussed. The results suggest that the detected rearrangements happened during the divergence of tetraploid emmer wheat.

Acknowledgements: This study was supported by the RSF (No. 14-14-00161).