

Molecular analysis of wheat subtelomeres in the context of chromosome recognition and pairing during meiosis

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Understanding wheat genome organization is essential for geneticists and plant breeders. Particularly, how chromosomes specifically recognize each other to associate in pairs at the beginning of meiosis, the cellular process to produce gametes in sexually reproducing organisms, is important for plant breeding and has an enormous influence on the fertility of wheat plants. Having the knowledge on the molecular bases of chromosome specificity/pairing at the onset of meiosis, we can manipulate interspecific chromosome associations in hybrids or interspecific genetic crosses developed in breeding programs with the aim of introgressing desirable agronomic traits from related species into crops such as wheat.

The terminal regions of chromosomes, which contain telomeres and subtelomeres, participate in chromosome recognition and pairing. We present a molecular analysis of wheat subtelomeres to explore the possible consequences of the variability and plasticity of these regions on homologous chromosome recognition and pairing. We analysed the presence and distribution of genes, transposable elements and less complex repeat sequences (satellites, simple repeats and low complexity DNA). We also studied the localization of multiple sites for DNA-binding proteins putatively involved in chromosome recognition and pairing and the pattern distribution of hot/cold recombination spots. Results showed a high polymorphism in the subtelomeric region among homeologous wheat chromosomes for all the features analysed and suggest the importance of these regions for the specificity of homologous chromosome recognition and pairing at the beginning of meiosis in wheat. The results and their biological implications are discussed in this work.

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