

EVALUATION OF THE SYNTENY FOR 5AS CHROMOSOME IN *TRITICUM* SPECIES WITH DIFFERENT PLOIDY LEVELS

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Synteny, wheat, genetic maps, evolution

In the frame of the project “Physical mapping of wheat chromosome 5A”, we have undertaken an investigation about the synteny level of the short arm of chromosome 5A (5AS) among different species of *Triticum* genus characterized by a different ploidy level and evolutionarily separated on a time scale in order to get insights into possible chromosomal rearrangements occurred during evolution. The analyzed species were *Triticum aestivum* (AABBDD; 2n=42), *Triticum durum* (AABB; 2n=28) and *Triticum monococcum* (AA; 2n=14). In details, we relied on four mapping populations: [1] Chinese Spring (CS, *T. aestivum*) x Renan (*T. aestivum*); [2] CS x CS disomic substitution line for chr. 5A (*T. turgidum ssp dicoccoides*); [3] Latino (*T. turgidum ssp durum*) x MG5323 (*T. turgidum ssp dicoccum*); [4] DV92 (*T. monococcum*) x G3116 (*T. monococcum*). High density genetic maps have been developed for the short arm of wheat chromosome 5A in these four populations using SSR (simple sequence repeat), SSR-EST (SSR-expressed sequence tags), TE junction (transposable elements) and COS (conserved ortholog set) comparative anchor markers. The specificity of these markers for chromosome 5AS has been assayed using nulli-tetrasomic lines derived from the reference cultivar Chinese Spring. Moreover the physical position of the developed markers has been assigned to deletion bins of 5AS through the utilization of deletion lines. The evaluation of syntenic blocks and non-conserved regions among the homologous segments of different *Triticum* species is reported, while the mapping of EST-based markers allowed identification of syntenic regions in the rice and brachypodium genomes. Identification of possible rearrangements in the different 5AS genetic maps of wheat provide valuable information about the subsequent steps on the BAC contigs anchoring while the consensus map deriving from the integration of these four maps will provide a fundamental tool to link the genetic and physical maps.