

The novel tandem repeat of 646 BP identifies the subtelomeric region of wheat 5BS chromosome

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Motivation and Aim: For study of plant chromosomes the fluorescence *in situ* hybridization with large inserts of genomic DNA cloned in Bacterial Artificial Chromosome (BAC-FISH) is broadly used. Most often the BAC-FISH on wheat chromosomes demonstrates the dispersed pattern because of high mobile elements content [1, 2]. The most specific observed BAC-FISH pattern on wheat chromosomes was the distinct signals on several chromosomal pairs [1]. Our aim was to identify 5B chromosome-specific DNA sequence for study of reorganization of this chromosome during evolution of hexaploid *T. aestivum* and tetraploid *T. dicoccoides* wheats.

Methods and Algorithms: The 20 BAC-clones were randomly selected from 5B chromosome specific BAC-library of *Triticum aestivum* cv. Chinese spring. BAC-FISH on *T. aestivum* (AABBDD, $2n = 6x = 42$) and *T. dicoccoides* (AABB, $2n = 4x = 28$) chromosomes was carried out according to [3]. BAC-end sequences were obtained with Sanger method and used for BLASTn search over the reference genomic sequences: *T. aestivum* cv. CS RefSeq v1.0 (International Wheat Genome Sequencing Consortium repository) and publicly available sequence of *T. dicoccoides* cv. Zavitan. The isolated regions were annotated using BLASTn with TREP and NCBI databases.

Results: The clone 030N24 demonstrated the spot FISH signal in the subtelomeric part of *T. aestivum* and *T. dicoccoides* chromosomes. The BLASTn search with the BAC-end sequences of 443 and 604 bp defined the region of 93,576 bp on the distal part of *T. aestivum* 5BS chromosome. The region contains the cluster of 10,060-bp length formed by 16 units of tandem repeat (unit length is 646 bp). In other regions of the *T. aestivum* genome these repeats were absent. The corresponding region on *T. dicoccoides* chromosome also localized at the distal part and contains the 31 units of 646-bp tandem repeat.

Conclusion: A 5B-chromosome specific region which represents a 10,060 bp cluster formed by 646-bp tandem repeats was identified. The probability of its inheritance from a diploid progenitor or its amplification during the formation of the first allotetraploid of the Emmer group *T. dicoccoides* is discussed.

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References

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