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February 16, 2017

3:45pm

4031 Throckmorton

Application of molecular cytogenetics for studying Triticeae chromosome structure, evolution and chromosome engineering

Abstract: To transfer agronomically important genes from wild relatives to bread wheat (*Triticum aestivum* L., $2n=6x=42$, AABBDD) by induced homoeologous recombination, it is important to know the phylogeny and chromosomal relationships of the species involved. The chromosomes of grasses of the tribe Triticeae are mostly colinear, i.e., composed of homoeoloci located at similar positions, though, several species have rearranged genomes. Fluorescence *in situ* hybridization (FISH) can be used to study chromosome structure, homoeology and evolution. We developed physical map of three wheat genomes using tandem repeats and cDNAs as FISH probes. The cytogenetic map was used to develop molecular markers with known physical position for monitoring the transfer of alien chromosome segments harboring agronomically important genes into bread wheat.

The set of wheat FISH markers was applied to study the chromosome macrostructure, homoeology and evolution of the diploid wild wheat relative *Aegilops markgrafii* ($2n=14$, CC). The genome was found highly rearranged as a result of inter- and intrachromosomal translocations and inversions. To investigate the relationship between chromosomal alterations and the patterns of molecular evolution of the *Ae. markgrafii* chromosomes, we characterized the genome using shallow whole-genome shotgun sequencing and whole exome capture. Comparative analysis of *Ae. markgrafii*, barley and hexaploid wheat orthologous gene sequences revealed rearranged chromosomal blocks with different levels of sequence divergence suggesting their origin from different parental genomes associated with hybrid speciation.