

Investigation on Evolutionary Relationships of the Subgenomes in Interspecific Triploid Cotton via Meiotic FISH

ZOU Mei-juan¹, PENG Ren-hai^{1,2}, WANG Kun-bo¹, WANG Chun-ying¹,
SONG Guo-li¹, LIU Fang¹, LI Shao-hui¹, ZHANG Xiang-di¹, WANG Yu-hong¹

(1. *Cotton Research Institute, Chinese Academy of Agricultural Sciences; Key Laboratory of Cotton Genetic Improvement, Ministry of Agriculture, Anyang, Henan 455000, China*; 2. *Anyang Institute of Technology, Anyang, Henan 455000, China*)

We report in this paper primary studies on interspecific species of cotton vis GISH (genomic in situ hybridization). We use interspecific triploid hybrids (F_1 from hybridization of allotetraploid cultivated species with diploid A, D, or C genome species) and two cultivated tetraploids to study the chromosome pairing during meiosis of pollen mother cells (PMCs) and to estimate the consequences on synapsis between these three subgenomes after synthetic polyploid formation. PMC-GISH with genomic DNA (gDNA) from the diploid parent species as probes resulted in fragmented signals, and the translocations of the chromosomes in ADC type hybrids were more frequent than in ADD type hybrids, which suggested the more distant relationship between A and C genome. In ADC type hybrids, we observed disperse star-like signals in D and C subgenome chromosomes, which indicated unidirectionally interspecific introgression from A-subgenome into D or C-subgenome chromosomes in the triploid hybrids. Our data enhanced the speculation that integrated events may occur immediately after artificial synthetic polyploidy formation. Different results of tetraploid PMCs were found when using A and D genome DNA as probes, respectively. Signals scattered in the whole cell when probed with gDNA from A genome species, whereas strong star-like signals existed at several chromosomes like the NORs of the PMCs by gDNA from a D genome species probe. Probing the same slide with 45s rDNA, we detected the same signal sites as the GISH results with a D genome gDNA probe, which suggested possible unequal adjustment of subgenomes after polyploidy formation. Possible movement and relationship of the A, D, and C subgenomes in the triploid hybrid are discussed.