TRANSMISSION RATES OF *GOSSYPIUM MUSTELINUM* AND *GOSSYPIUM TOMENTOSUM* SNP MARKERS OF EARLY-GENERATION BACKCROSSES TO COTTON (*GOSSYPIUM HIRSUTUM*)

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Abstract

The genetic diversity of *G. hirsutum* is considerably restricted, so it is highly desirable to introgress germplasm of related species to expand opportunities for genetic improvement. Successful interspecific introgression efforts require the transmission of alien genes into the cultivated species and homologous recombination. Marker-based analysis of specific chromosome segments and loci during early generations of backcrossing can reveal general and locus-specific features of alien germplasm transmission and recombination with the recurrent parent, and help guide decisions for expanded analysis, subsequent backcrosses and analogous efforts with other donors. Interspecific monosomic hybrids were used to localize pre-validated single nucleotide polymorphism (SNP) markers in six target chromosomes. Eventually, 67 SNPs were used to analyze transmission rates. In the present research, each "breeding situation" was defined as a unique combination of cross direction, backcross generation and cross location. Twelve *G. hirsutum* backcross populations were derived under different breeding situations, six from each of two alien donors, *G. mustelinum* and *G. tomentosum*. KASP analysis of the SNPs revealed the presence or absence of specific donor loci and segments in 784 individuals of the 12 populations, and was used to determine transmission rates. Linkage groups were constructed based on segregation ratios in BC1F1 populations for each donor. Several markers exhibiting strongly distorted transmission rates were discussed. Effects of breeding situations on transmission rate were revealed based on general linear model (GLM) analysis.