MAPPING HETEROTIC LOCI FOR YIELD AND AGRONOMIC TRAITS USING CHROMOSOME SEGMENT INTROGRESSION LINES IN COTTON

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Abstract

Gossypium hirsutum L. produces high fiber yield while G. barbadense L. possesses excellent fiber quality. The integration of high fiber yield of G. hirsutum and super fiber quality of G. barbedense has always been cotton breeders' dream. But until now, the genetic mechanisms underlining G. hirsutum × G. barbedense interspecific hybrid heterosis remain unclear. In the present study, a set of chromosome segment introgression lines (CSILs) using Gossypium hirsutum L. TM-1 as the recipient parent and G. barbadense Hai7124 as the donor parent were used to explore the genetic basis of heterosis for interspecific hybrids. Two sets of F₁ populations individually derived from CSILs crossing with both parents were configured to investigate heterotic loci (HL) and substitution effect loci (SL) in a 3-year experiment (2010-2012). A total of 58 HLs and 39 SLs were identified in 3 years. One stable HL for lint percentage, hLP-A4-3, could be detected in all 3 years. Three HLs for boll size (hBS-A8-1), lint percentage (hLP-D6-10) and seed index (hSI-D7-11) could be detected in 2 years. Four SLs, sBS-D7-1, sLP-A8-1, sLP-D7-1, and sLP-D12-1, could be detected in 2 years. HL and SL tended to be distributed in some HL-rich chromosome segments with close positions. Compared with QTL detected in a former study, HL showed little overlap with QTL, indicating that trait phenotype and heterosis might be controlled by different sets of loci. All three types of genetic effects (partial-, full-, over-dominant) were identified, while the over-dominant effects made the main contribution to heterosis in yield-related traits. These results may help lay the foundation for clarifying the heredity mechanism of heterosis in cotton.