RECOMBINATION RATES IN INTERSPECIFIC AND INTRASPECIFIC COTTON MAPPING POPULATIONS

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Abstract

Recombination is crucial for genome stability by ensuring proper chromosome segregation and can increase genetic diversity by generating novel allele combinations during meiosis. Recombination also allows for the localization of markers, such as single nucleotide polymorphisms (SNPs) and simple sequence repeats (SSRs), through linkage mapping and effects the pattern of linkage disequilibrium between markers and alleles. The rate and distribution of recombination within the genome is important for the creation of novel alleles within cotton hybrids and influences the rate at which the co-inheritance of favorable and non-favorable alleles occurs (linkage drag). In this study, the recombination rates within 2 intra- and 3 inter- specific cotton mapping populations are assessed. Five high-density, SNP-based genetic maps were aligned to the *G. hirsutum* v2 sequence assembly (unpublished) and recombination rates across chromosomes were calculated using linear regressions of 1 mega base (Mb), non-overlapping windows with a minimum of 4 SNPs per window. Significant differences in recombination rates between mapping populations are observed.