

COMPARISON OF HOMOELOGOUS CHROMOSOMES 1 AND 15 BETWEEN A *GOSSYPIMUM HIRSUTUM* BY *G. MUSTELINUM* MAP AND A MAP OF *G. HIRSUTUM* BY *G. BARBADENSE*

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Abstract

To explore the genome structure of *G. mustelinum* and understand the transmission genetics in crosses between this species and cultivated cotton, a primary *G. hirsutum* x *G. mustelinum* (HM) genetic map was constructed and then compared with a *G. hirsutum* x *G. barbadense* (HB) map. In this study, we compared the structure of homoeologous chromosomes 1 and 15 between the two interspecific maps. The results showed that the arrangements of genetic loci along the chromosomes of HM and HB are identical in most cases; however, a number of significant structural rearrangements were also observed.

Introduction

There are five tetraploid species of *Gossypium* (cotton) designated (AD)1 through (AD)5 for their genome constitutions, namely *G. hirsutum*, *G. barbadense*, *G. tomentosum*, *G. mustelinum*, and *G. darwinii*. To date, genetic maps have been developed from interspecific crosses between *G. hirsutum* x *G. barbadense* (HB) (Rong et al., 2004; Guo et al., 2007), and *G. hirsutum* x *G. tomentosum* (HT) (Waghmare et al., 2005). However, much less is known about transmission genetics and genome organization in the other two naturally occurring allopolyploid cottons. To help understand the evolution of cotton species and extract agriculturally valuable alleles from *G. mustelinum*, it is necessary to reveal the basic transmission genetics in crosses between this species and cultivated cotton. The objective of this research is to explore the genome of *G. mustelinum* by crossing with *G. hirsutum* (HM). A primary HM genetic map was constructed and then compared with the HB map, revealing the similarity and differences in structure of homoeologous chromosomes 1 and 15.

Materials and Methods

An interspecific F₂ population of 92 plants was developed from a cross between *G. hirsutum* (cv. PD94042) and *G. mustelinum*. A genetic linkage map was constructed using microsatellite molecular markers (SSRs) with the MAPMAKER/Exp Version 3.0 software, in which the Kosambi function and LOD=5.0 were used. The assignment of linkage groups to subgenomes and chromosomes was based on information from framework markers on published maps (Rong et al., 2004; Guo et al., 2007).

Results and Discussion

G. mustelinum is a Brazilian endemic cotton representing the first or basal lineage in the polyploid cotton phylogeny. A total of 666 polymorphic marker loci were obtained; 432 were co-dominant, 123 were dominant for the *G. hirsutum* alleles, and 111 were dominant for the *G. mustelinum* alleles. A majority of the loci (94.7%) fit a 1:2:1 (co-dominant) or 3:1 (dominant) ratio. The HM map comprises 582 loci on 26 chromosomes groups, covering 4045.2 cM. Twenty loci were mapped on Chromosome 1 while 37 loci were mapped on its homoeologous chromosome, Chromosome 15. We currently assume that this map underestimates the true recombinational length of the HM map due to the presence of gaps and unlinked markers. The average distance between two adjacent markers was 7.0 cM.

We compared a pair of homoeologous chromosomes 1 and 15 of our HM map with the high density SSR map of HB published by Guo et al. (2007). In most cases, the arrangements of genetic loci along the chromosomes of HM and HB are identical (See Fig1.). However, significant structural rearrangements were also observed (Fig. 1: Chrom15). For example, the rearrangement between anchor loci BNL786 and BNL1667 in HM differs from HB by an inversion appears to differentiate *G. mustelinum* from *G. hirsutum*. The affected region spans about 65.1 cM in HM compared to 7.0 cM in HB. Another significant rearrangement was detected between BNL3902 and BNL2646 with the affected region spanning about only 0.7 cM in HM compared to 12 cM in HB. The incongruity of the gene orders between the HM map and HB map may further help clarify the evolutionary relationships between the tetraploid cottons.

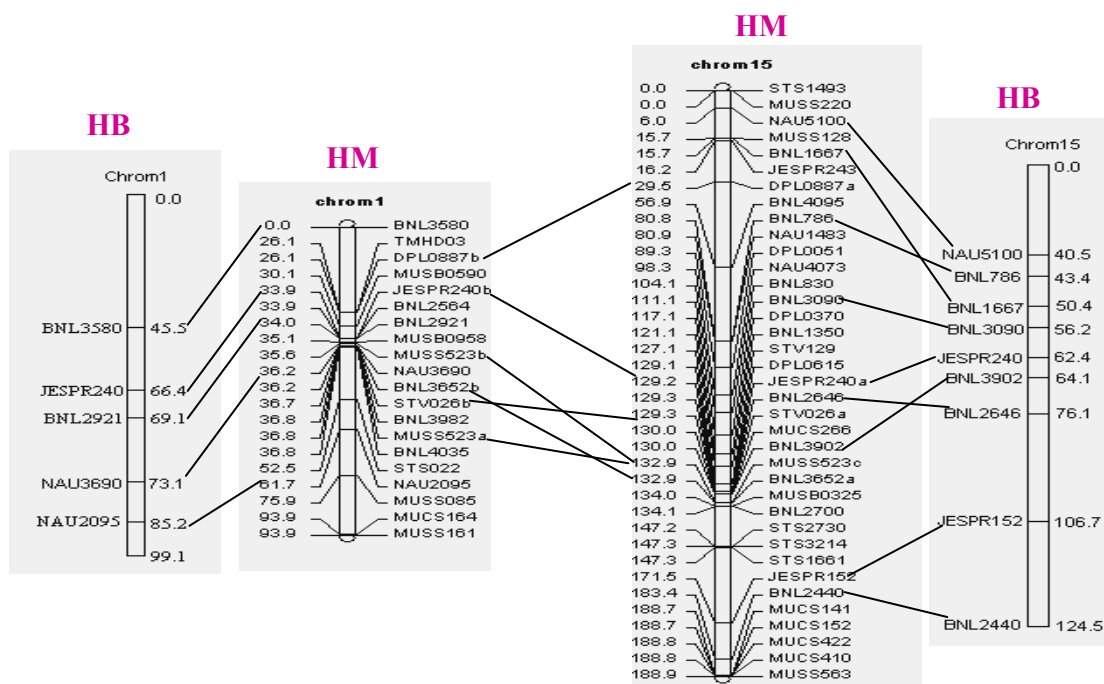


Fig. 1. Homoeologous chromosomes 1 and 15 of *G. hirsutum* × *G. mustelinum* (HM) genetic map and its alignment to the *G. hirsutum* × *G. barbadense* (HB) map.

References

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