

SECONDARY GENE POOL CONTRIBUTIONS IN U.S. UPLAND COTTON

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Abstract

Pedigree analyses have indicated that the Upland cotton gene pool, *Gossypium hirsutum*, has substantial exposure to both secondary and tertiary gene pools. However, the extent of the contribution of these donors is largely unknown. We surveyed about 330 Upland cotton lines/cultivars using 261 evenly spaced RFLP loci to address the amount and genomic locations of introgressed genes in the cotton genome. Preliminary analysis indicated that the cotton genome is largely homogeneous, and that rare alleles, which have likely arisen through introgression, are restricted to only a small group of cultivars. Historical accounts indicate that these few cultivars were clearly developed through interspecific hybridization. These results suggest that the use of secondary and tertiary gene pools remains largely uncaptured in cotton improvement.

Introduction

It is widely accepted that many important phenotypes from wild relatives of cotton have been introgressed into modern Upland germplasm through intentional breeding efforts. For instance, genes from *Gossypium barbadense* have been implicated in the development of many obsolete extra long staple cotton cultivars. It has also been speculated that the increased fiber strength of the Pee Dee material came from tri-species hybrid material that was part of the Pee Dee programs originating germplasm. Furthermore, resistance to cotton rust, caused by *Puccinia cacabata*, was transferred from *G. anomalum* and *G. aboreum* to upland cotton via interspecific hybrids, artificial polyploidization, and backcrossing.

Despite abundant circumstantial evidence, a previous study suggested that retention of genes from interspecific sources has been minimal (Wendel et al. 1992).

The objective of this study is to determine the extent of gene introgression from secondary gene pools into Upland cotton.

Materials And Methods

A collection of 330 cotton lines/cultivars of historical importance were surveyed against a series of almost 300 RFLP loci that were chosen to evenly cover the cotton genome. Two hundred sixty one codominant markers were ascertainable and used to determine the loci diversity using GDA software (Lewis and Zaykin, 2001). Genetic diversity values of individual loci are plotted on the linkage map to reveal genetic diversity landscape of the cotton genome (Figures 1 and 2).

Assumptions

Evidence of putative interspecific introgression into Upland cotton can be detected in loci that are fixed or nearly fixed in secondary gene pools but are rare in Upland cotton germplasm. Putatively introgressant loci would be revealed as low frequency alleles that are restricted to only a few closely related genotypes within a germplasm group. However, shared ancestry or convergence could confound this approach for detecting introgressed alleles. Thus, other supporting evidence such as pedigree analysis showing interspecific hybridization and an occurrence of multiple linked loci carrying a rare allele within the same genotype would provide more definitive evidence for the presence of genes from interspecific sources.

Introgression of *G. barbadense* genes into Upland cotton

Based on the genetic diversity chromosome landscapes in Figures 1 and 2, there are 24 regions (12 each in the A and D subgenomes) that fit our criteria of low diversity, enabling us to detect the presence of introgressed alleles. Although the analysis is still ongoing, we have identified two chromosome regions that fit the further criteria that the rare alleles may indeed be introgressed from the secondary gene pool.

For example in chromosome 5, two adjacent loci indicated a rare allele within a 5 cM region with low genetic diversity (autoradiogram not reproducible in this publication). All of the upland genotypes are fixed for one allele except for Sealand 883 and Wilds 18 which carries an allele that is also found in *G. barbadense*. Pedigree records indicate that both lines were derived from interspecific hybridization between Upland and Sea Island cotton. Sealand 883 is an extra long staple cotton compared to today's commercial cultivars. Retention of these introgressed segments may suggest the presence of favorable alleles for improving upland cotton.

References

Lewis, P.O., and D. Zaykin. 2001. Genetic Data Analysis: Computer program for the analysis of allelic data. Version 1.0 (d16c). Free program distributed by the authors over the internet from <http://lewis.eeb.uconn.edu/lewishome/software.html>

Wendel, J.F., C.L. Brubaker, and A.E. Percival. 1992. Genetic diversity in *Gossypium hirsutum* and the origin of upland cotton. *AmJBot* 79(11):1291-1310.

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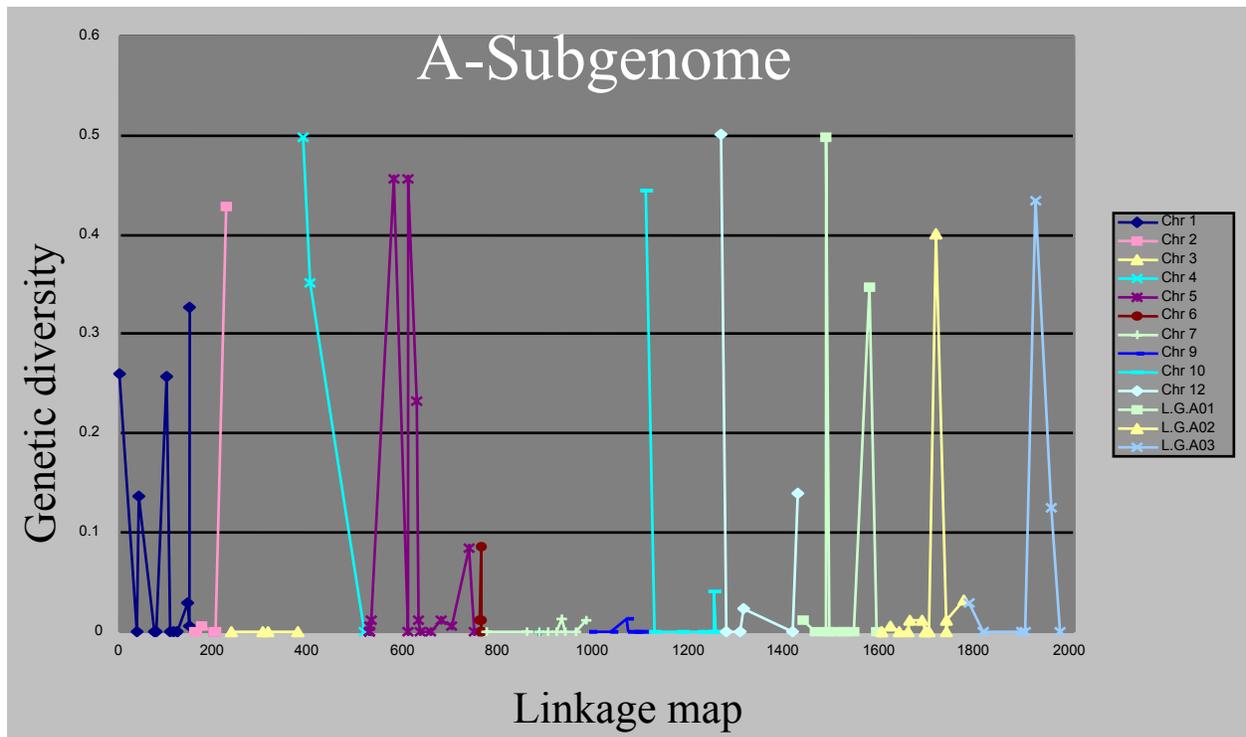


Figure 1. Genetic diversity chromosome landscape of the A-subgenome of *G. hirsutum*.

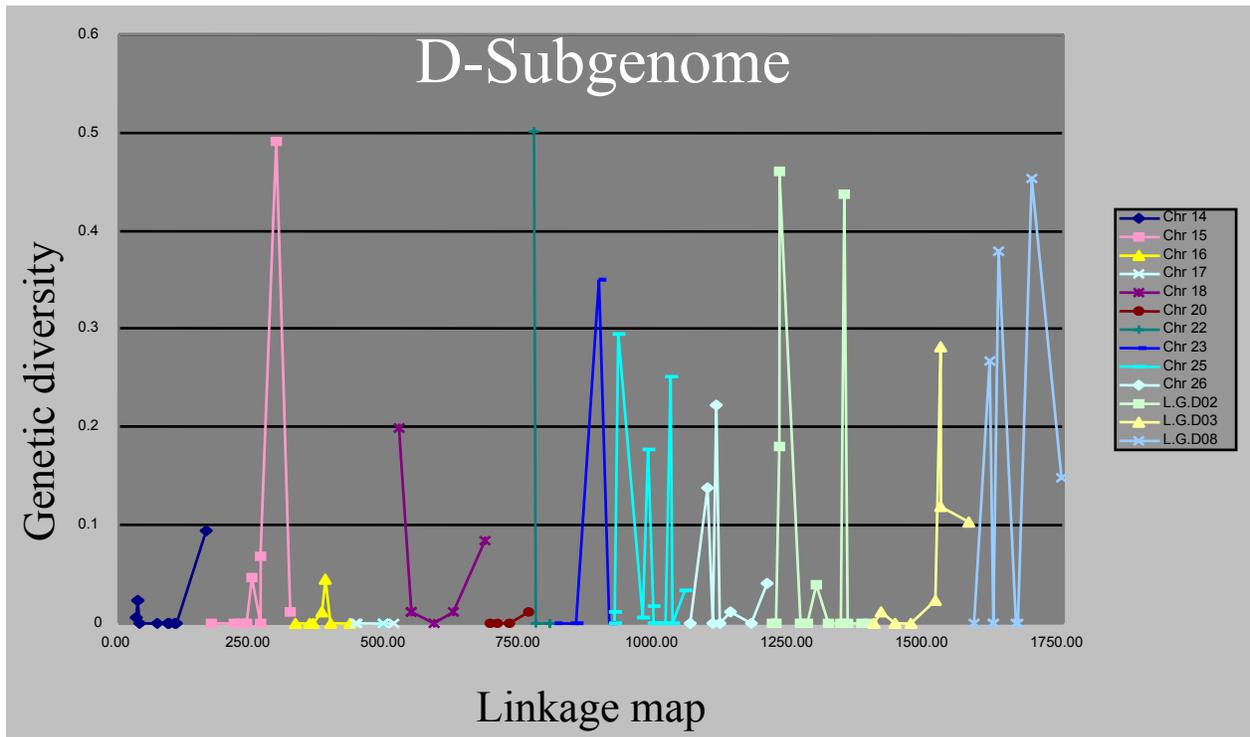


Figure 2. Genetic diversity chromosome landscape of the D-subgenome of *G. hirsutum*.