

**PHYLOGENOMICS: A NEW APPLICATION OF
MOLECULAR MARKERS TO COTTON RESEARCH**

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Abstract

We have defined “phylogenomics” as the comprehensive integration of DNA-based phenetic and phylogenetic data with genomic data such as linkage maps, physical maps and genomic sequence data. Using a single set of DNA-based markers (including both AFLPs and SSRs) for the assessment of genetic diversity and relationships among cotton taxa, and for the development of linkage maps, we can extract the phylogenetic histories of individual chromosome segments. Genome-wide histories of individual cotton cultivars can be developed with this information, even when there has been extensive cross-hybridization (reticulate evolution). Further, data from different cotton genotypes can be used to uncover relationships between specific genomic regions and phenotypic traits. The objectives of the present study were to identify specific polymorphic marker sets targeted for specific breeding experiments, and 'allele mining' the targeted identified sources of diversity in genomic regions known to control important traits. These methods will have immediate utility in strategies for marker-assisted selection.

By developing linkage-based phylogenetic trees, we can understand the phylogenetic histories of individual cotton accessions that would otherwise be blurred by reticulate evolution due to horizontal gene flow that has occurred by various mechanisms throughout the evolution and development of domesticated cottons. Maps of polymorphic markers for specific breeding objectives can be derived by integrating DNA fingerprinting data from a large number of cultivars, representing much of the world's *Gossypium hirsutum* germplasm, with an existing inter-specific genetic map constructed using the same set of DNA markers (800 AFLPs, 80 SSRs and 2 fiber specific ESTs). The map positions for markers that are polymorphic among 60 *G. hirsutum* germplasm accessions from the USA, Guatemala, India, Mexico, Pakistan, Turkey, and Uzbekistan, including photoperiodic and other primitive accessions, have been derived. Also markers polymorphic among 31 *G. barbadense* germplasm accessions, collected from Egypt, Uzbekistan, USA, and Caribbean Islands are catalogued in the map. The linkage information for these polymorphic markers allows the researcher to readily identify a set of markers that will be useful for any specific breeding objective.

The most important aspect of phylogenomics is trait-based fingerprinting for new allele mining. The SSR markers which are linked to specific traits such as fiber length and strength, and resistance to Verticillium wilt were used for genotyping a diverse *G. hirsutum* germplasm collection for new and divergent alleles that may be useful for the introduction of disease resistance and improved fiber quality. The details of the integrated genetic map, chromosome-specific phylogenies, and various aspects of allele mining are discussed.