

1845 Inferences on Phylogeny and Origin of Polyploid *Gossypium* Genomes from Nuclear Repetitive DNA Sequence Variation

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Variation of nuclear DNA repeated sequences has been successfully used to decipher intractable questions in the genome origin and evolution of several plant species complexes. We have re-examined the genome origin and evolution of the genus *Gossypium* and reconstructed the phylogenetic tree of the genus by using variation of 22 nuclear repeated sequence families. DNA was isolated from 87 accessions of 35 species representing all eight basic genome groups of the genus and analyzed. Fifteen of the repetitive sequences could be detected in all eight diploid genome groups, but five were A-genome-specific and two were detected in some of the non D-genome groups. A total of 642 major restriction bands of repeated sequences were used for phylogenetic analysis of the species. A phylogenetic tree of the species was constructed and shown to be consistent with those existing trees in major clades; however, significantly different branching among some species and low correspondence in the A and D genomes between diploid and polyploid species were observed. These results provide new insights into the phylogeny of the genus.