

Control of cotton fiber diameter throughout *Gossypium* evolution and domestication

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Abstract

Modern cotton production, which provides a key renewable resource for the textile industry, is dominated by allotetraploid *Gossypium hirsutum* (commonly grown Upland Cotton, AD1 genome), and a minor contribution from *Gossypium barbadense* (Pima Cotton, AD2 genome). *G. barbadense* has higher quality fiber, including smaller diameter fiber that supports production of premium textiles that are silky yet strong. How the diameter of any plant cell is set is relatively unexplored, and we are analyzing historic and modern *Gossypium* accessions in this context. Specifically, we are examining cotton fiber tip diameter based on our emerging evidence that the diameter of mature fiber is strongly controlled at the tip, with variation between *G. barbadense* and *G. hirsutum*. These two allotetraploid species diversified naturally and then were independently domesticated after the convergence of ancestral A and D diploid genomes. We are using microscopy and measurements of apical diameter to analyze fiber tip morphology in representatives of the diploid genomes and polyploid cultivars throughout the history of cotton domestication and breeding. Pedigree analysis is being conducted in parallel to gain insight into when and how the broader, less desirable, fibers came to exist in the *G. hirsutum* lineage. This information will help to devise strategies to introduce higher quality fiber more like *G. barbadense* into the more agronomically robust *G. hirsutum* species. We thank: Cotton Incorporated, Cary NC for research support; Joe Jareczek and Lori Hinze for contribution of young cotton ovules; Amanda Hulse-Kemp for advice; Ben Graham and Ethan Pierce for teaching techniques; and the U.S. National Cotton Germplasm Collection for supplying seeds.