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CORRELATION STUDY OF FIBER DENSITY IN COTTON BETWEEN WILDTYPE AND THE N1 NAKED-SEED MUTANT

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Abstract

Fiber density is of great agricultural importance as a critical component of yield and of great biological interest due to the fact that cotton fibers are highly modified cells. Even though fiber density is an important yield component, breeders typically do not select directly for this trait due to the difficulty and cost of doing so on a large scale. In lieu of direct methods, selection for higher fiber density has generally been based on weights of seedcotton (seed plus lint) versus cotton (lint only), which are determined easily and inexpensively. We are exploring an entirely different approach, one based on selection in one or more genetic backgrounds where there is little fiber present on mature seed. In this study, we report on the initial result with the dominant mutation N_1 of *Gossypium hirsutum*, which has long been known to nearly eliminate fiber on mature seed. It is well known that the density and other properties of fibers differ greatly among cotton cultivars and other genotypes, but the technical difficulty of evaluating fiber density has largely precluded efforts to select directly for higher lint density, both in the field and in the lab. We are exploring the feasibility of developing a selection system for fiber density based on fiber development of N_1n_1 mutant hybrid seed. N_1n_1 seed has much lower fiber density and variations in density are much easier to discern visually and digitally. It thus seems possible that some or most genes affecting fiber density on N_1n_1 mutant seed are likely to influence fiber density on non-mutant (n_1n_1) seed. If so, selection for higher fiber density on N_1n_1 mutant seed might be used to increase fiber density in related normal genotypes, e.g., parents, full sibs, or half-sibs. Breeding applications are readily envisioned for line development or population-based allele enrichment, and the concept might be extended to other types of seed and fiber mutants. To be feasible, however, variations in fiber development on normal and mutant types must be genetically related. To determine if such a genetic relationship exists, we have made pair-wise phenotypic comparisons between genetically related mutant and non-mutant genotypes. Based on the analysis of the parental (P) and first filial generations (F_1), respectively, a correlation exists between the fiber density as determined by AFIS data and an equation that was developed. However, a visual scoring process of the F_1 seed failed to correlate to parental (n_1n_1) fiber density. We will continue to assess the prospects of using this approach to develop a selection method and/or investigate developmental genetics of fiber cells.

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