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IMMATURE FIBER MUTANT OF UPLAND COTTON

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Abstract

The inheritance of a mutant character of Upland cotton, *Gossypium hirsutum* L., that results in abnormal fiber development is described, and the mutant is compared to environmentally induced immature fiber. The phenotype and fiber properties of the mutant resemble those found in bolls that have experienced arrested development due to environmental conditions. Seed of the mutant plants however, showed normal development. The mutant expression was conditioned by homozygous recessive alleles at a single locus and assigned the gene symbol *im*.

A MUTANT PLANT with nonfluffy bolls was found in a field of 'Acala 4-42' cotton by the junior author. Mutant plants were normal in appearance until the bolls started to open. All bolls on the affected plants have the same characteristic appearance in which the fibers remain matted around the seed (Fig. 1), and the bolls do not have the normal fluffy appearance (Fig. 2).

Normal cotton produces bolls with a phenotype similar to the mutant in response to stress. These bolls are commonly referred to as *tight lock* bolls. The source of stress can be moisture, freezing temperatures, or disease, which results in arrested boll and fiber development. For this reason the original mutant stock was called the tight lock mutant, and it was distributed to researchers under that designation. Subsequently, measurement of fiber fineness by either the arealometer or micronaire instruments revealed fibers too fine to measure. The alkali swelling-centrifugation test (Marsh et al., 1953) confirmed the extreme fiber fineness of the mutant.

The unique characteristic of the mutant is its fine weak fiber, typical of immature fiber, and it was assigned the working designation immature fiber. It has been used in investigations under that designation (Kohel et al., 1974; Endrizzi et al., 1985).

Fig. 1. Mutant plant illustrating nonfluffy cotton boll phenotype.

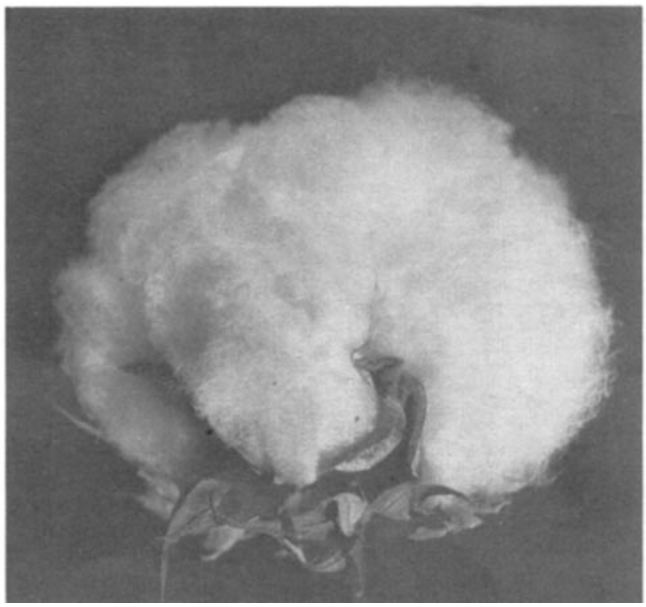

Fig. 2. Normal fluffy boll of 'Acala 4-42' cotton.

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RESULTS AND DISCUSSION

Crosses of the mutant to normal cottons produced F_1 plants with normal bolls and fiber. In the F_2, segregation is for normal and mutant pheotypes (Table 1). Segregation follows that expected for a single recessive gene mutation (3 normal: 1 mutant). None of the F_2 populations deviated significantly from the expected segregation, and there was no significant heterogeneity among the populations. The mutant with immature fiber is controlled by homozygous recessive alleles at a single locus and is assigned the gene symbol *im*.

Table 1. The F_2 segregation data from crosses of the fiber mutant with normal genotypes of cotton.

	No. of plants			χ^2	
Progeny	Normal	Mutant	Total	(3:1)	*P*
1	137	51	188	0.45	0.50–0.70
2	193	69	262	0.25	0.50–0.70
3	216	74	290	0.04	0.80–0.90
4	184	59	243	0.07	0.70–0.80
5	181	59	240	0.02	0.80–0.90
6	178	58	236	0.02	0.80–0.90
7	164	51	215	0.19	0.50–0.70
8	123	31	154	1.95	0.20–0.10
Pooled	1376	452	1828	0.07	0.70–0.80
Heterogeneity (7 df)				2.92	0.80–0.90

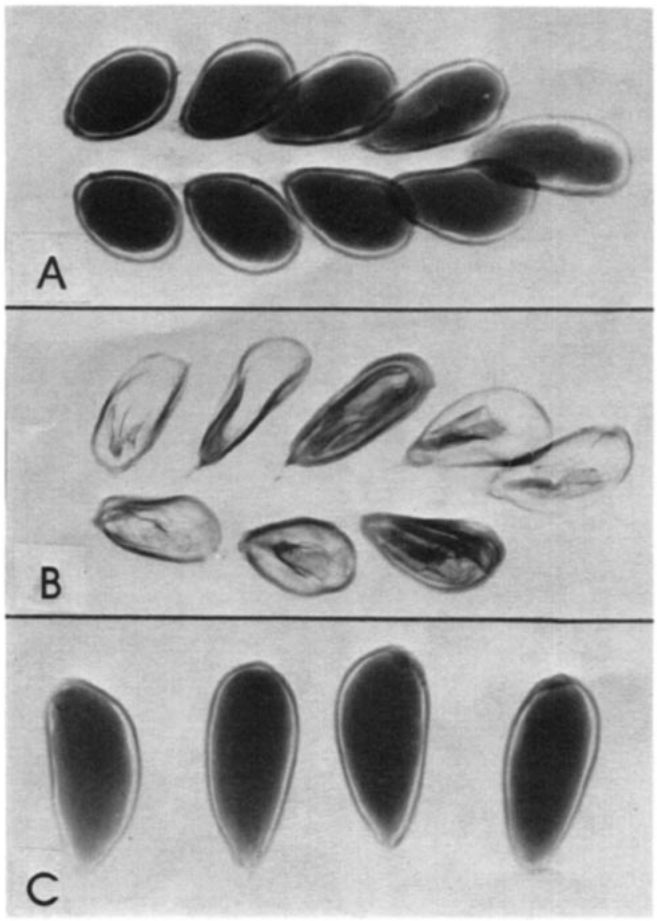

Fig. 3. Radiograph of (A) seeds from mutant, (B) immature seed of Acala 4-42, and (C) normal mature seed of Acala 4-42 cotton.

As part of the program for maintenance of the genetic mutants, the immature fiber mutant was backcrossed to TM-1 (Kohel et al., 1970) to develop an isoline in the TM-1 background. The results through BC_4 substantiated the conclusion that recessive alleles at a single locus control the mutant expression. In each cycle of the mutant backcrossed to TM-1, the F_1 was normal. The backcrossed plants were selfed (SBC_x) to recover the mutant with segregation of 3 normal:1 immature fiber. The combined segregation from these SBC_x populations was 78 normal:16 mutant (Chi-square for 3:1 = 3.19, $P = 0.10$–0.05). Progeny tests of 23 mutant plants in these backcross cycles were all true breeding for the mutant type.

In the course of several years of the backcross program segregants of the *imim* genotype were observed under diverse environmental conditions at College Station, TX. In years with adverse weather conditions such as moisture stress or late season rainy conditions, it was not possible to classify the *imim* phenotype with certainty, and progeny tests were required to verify the mutants. The problem is not one of being able to identify an individual immature fiber plant but rather to accurately classify every plant in a segregating population.

In the review of mutants of the cultivated diploid cottons, *G. arboreum* L. and *G. herbaceum* L., Knight (1954) referenced a report by Balasubrahmanyan et al. (1949) in which an immature lint mutant was identified. This stock is not known in U.S. cotton collections and Knight did not offer a description. However, the report of this mutant in the cultivated diploid cottons that are assigned to the A genome (Beasley, 1940) suggests that the immature fiber mutant of the cultivated tetraploid *G. hirsutum*, $(AD)_1$, might reside in the A subgenome.

Developmental analysis of this mutant compared fiber development to a normal standard. Elongation of fibers was normal, but total dry weight was reduced 40% at maturity (Kohel et al., 1977). The extreme deficiency in dry weight reflects the lack of development resulting in fiber fineness.

Fiber properties were measured for TM-1 and immature fiber grown in a four-replicate test in 1988. Micronaire values of TM-1 were 3.9 but were below measurable values for immature fiber. Both fiber length (2.5% span length, cm) and strength (kN m kg^{-1}) were reduced for the immature mutant compared to TM-1, 2.34 vs. 2.82 ± 0.05 and 164 vs. 204 ± 11.3, respectively.

Because the mutant had the phenotype of bolls resulting from arrested boll development, seed maturation was investigated by x-ray radiography. The radiographs revealed no evidence of major deficiencies in seed development of the mutant (Fig. 3). Bolls of Acala 4-42 were picked prematurely to identify those with the same level of fiber maturity as the mutant. Radiographs of seed from bolls with comparable fiber development revealed poorly developed embryos (Fig. 3).

In the course of genetic analysis no differences in seed germination were noted between mutant and normal genotypes. Seed weight of mutant and normal segregants in BC_2 to TM-1 were 11.4 and 10.8 g/100 seed, respectively.

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The junior author found the mutant described, and shared seed with the senior author. The junior author conducted the preliminary fiber and genetic analyses, and on his retirement, turned over to the senior author a summary of his results to combine with ongoing cooperative studies.

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