A HAIRY ANTHER MUTANT ISOLATED IN INTERSPECIFIC HYBRIDS BETWEEN UPLAND COTTON AND PIMA COTTON

Jinfa F. Zhang, Gwen Coyle, and James McD. Stewart[1]

RESEARCH PROBLEM

Plant hairs (trichomes) including cotton fiber develop from single epidermal cells on the aerial surfaces of plants. Two main types of trichomes, glandular and nonglandular, can be found playing various functions including protection from insect damage. The development of plant trichomes provides an excellent system for studies of cell developmental biology. Because they are easily observable, simple and easily dissected genetically, qualitative and quantitative genetics of trichomes have been extensively investigated in cotton (*Gossypium hirsutum*). New genes controlling trichomes will provide clues in understanding the molecular basis of fiber development. The objectives of the present studies were to (1) report the discovery of a hairy anther mutant, and (2) conduct genetic studies concerning the inheritance of the hairy anther trait.

BACKGROUND INFORMATION

In the cultivated cotton species, the nonglandular trichomes are normally observed on leaves and stems, petals, bracts, and calyx, but not on carpels. Also, the presence of trichomes on sepals has not been reported. The morphology of trichomes varies from unbranched (simple) to multi-branched (stellate). Genetic variation in cotton trichomes exists in density, distribution, and length. Classic genetic studies have identified five genetic loci (t_1 to t_5) and a total of at least 19 alleles (Lee, 1985). The pilose gene, T_1, on chromosome 6 of the A subgenome, confers heavy pubescence on leaves, stems, and fruits. The second major gene, T_2, on chromosome 25 of the D subgenome, only expresses dense hairs on leaves and stems. The interaction between the two loci was found to affect trichome density (Kloth, 1995). The two loci were confirmed by molecular mapping studies (Wright *et al.*, 1999). Three other quantitative loci (QTL) on chromosome 1, 23, and LGA05 were additionally detected to affect pubescence in cotton.

RESEARCH DESCRIPTION

Hairy anther plants were found in interspecific F_2 populations between T586 (*G. hirsutum*) having the pilose gene (T_1) and Pima 57-4 or Sev7 (*G. barbadense*). Segregation for hairy anther and glabrous anther was recorded. Plants in the F_2 of T582 and 57-4 and 16 other F_2 crosses between four normal upland cotton lines (Hua 101, Emian

[1] Graduate Assistant, Research Specialist, and Professor, Crop, Soil, and Environmental Sciences Department, University of Arkansas, Fayetteville.

18, AC 239, and PD 6520) and four *G. barbadense* lines (designated B1 to B4) were also evaluated for hairy anther in the field.

RESULTS AND DISCUSSION

Interspecific cross-breeding between upland cotton and long staple (*G. barbadense*) cotton has been extensively practiced since the turn of the last century, resulting in the isolation of many new mutants and transgressive segregants. Pronounced genetic variation in trichome density on leaves and stems has been observed in an interspecific F_2 population (Wright *et al.*, 1999). However, the phenomenon of trichomes on the anther surface has not been reported from interspecific crosses.

In our present studies, we made all 16 possible crosses between four upland cotton cultivars and four long staple cotton cultivars including Pima and Egyptian cottons. None of the eight cultivars carried the pilose gene T_1. Among more than 1500 F_2 plants, we found no hairy anther segregants. Surprisingly, when T586 having the T_1 gene was crossed to two Pima cottons (57-4 and Sev7), plants with hairy anthers were observed in the two crosses (Fig. 1). In the F_2 populations, normal pubescent plants and most of the pilose plants did not show the hairy anther phenotype. The segregation ratio fit a 13 glabrous anther to 3 hairy anther ratio. When two of the hairy anther plants were test-crossed onto Sev7, a 1:1 ratio was obtained (Table 1). Obviously, for trichomes to be present on the anther surface in the interspecific crosses, the pilose gene T_1 should be present. The segregation ratios suggest that another dominant gene present in upland cotton inhibits T_1 expression on the anther. We denote this inhibiting gene as I_t. Therefore, T586 has genotype $T_1T_1I_tI_t$, while the Pima cottons are double recessive ($t_1t_1i_ti_t$). The heterozygous F_1 showed the T586 phenotype, as expected. However, among four phenotypes in the F_2, only the phenotype (T_1-i_ti_t) will show hairy anther because the dominant inhibitor gene I_t is absent. The genetic model explaining the results is shown in Fig. 2. According to this model, one-third of the hairy anther plants should be homozygous ($T_1T_1i_ti_t$) and two-thirds heterozygous at the locus T_1 ($T_1t_1i_ti_t$). Since a ratio of one glabrous anther to one hairy anther was obtained in the testcross progeny, the two hairy anther F_2 plants that were chosen for testing were heterozygous at the T_1 locus. A plant homozygous for hairy anther that would produce all hairy anther progeny in a test-cross with Pima cotton was not among the two selected for testing, due in part to the small size of the hairy anther subpopulation.

PRACTICAL APPLICATION

This study first demonstrated that T_1 gene is a universal trichome gene that confers trichomes on the plant body of cotton, but its function on the anther surface is suppressed by a regulatory inhibitor gene in upland cotton. Therefore, trichome gene expression is developmentally regulated. The finding has broadened our knowledge in genetics of trichomes in cotton. It also raises a logical possibility that T_1 might affect fiber development. The physiological and evolutionary importance of hairy anther development will be a very interesting question for further investigations.

LITERATURE CITED

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Table 1. Number of plants segregating for hairy anther: interspecific crosses.

Cross	No. S[z]	No. H	Ratio (S: H)	χ^2
(T586 x 57-4)F_2	25	4	13:3	0.35
(T586 x Sev7)F_2	76	15	13:3	0.23
Hairy anther F_2-1 x Sev7	17	13	1:1	0.53
Hairy anther F_2-2 x Sev7	9	5	1:1	1.14
(T582 x 57-4)F_2	15	0		
(4 GH x 4 GB)F_2	1500	0		

[z] S-glabrous anther; H-hairy anther.

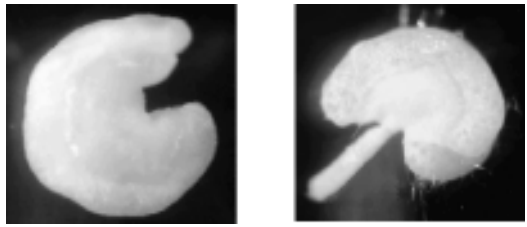

Figure 1. Hairy anther mutant isolated from an interspecific hybrid F_2 population between upland cotton and Pima cotton. *Left:* normal glabrous anther. *Right:* hairy anther.

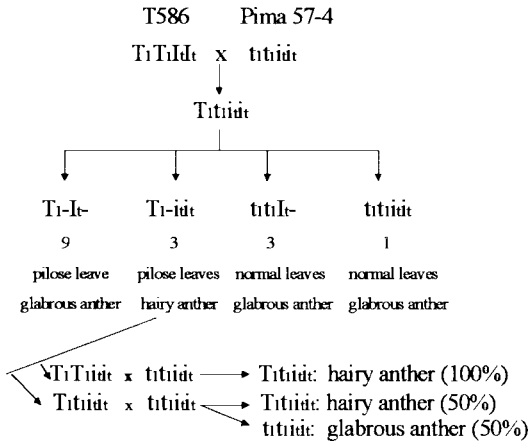

Figure 2. A genetic model explaining the segregation of hairy anther in interspecific F_2 populations.