

**GENETIC IMPROVEMENT OF FIBER  
QUALITY IN PIMA COTTON (*GOSSYPIMUM  
BARBADENSE* L.)**

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**Abstract**

Genetic improvement of fiber quality in Pima cotton has been a key component in the successful development of the extra-long staple (ELS) industry in the United States. The objective of this report is to briefly summarize the changes in fiber quality in Pima cotton due to breeding since the turn of the century.

Breeders have created four unique gene pools during the development of Pima cotton in the U.S. The Sacaton, or American-Egyptian, gene pool was created when Egyptian ELS cotton were first introduced into the Southwestern U. S. at the turn of the century. The entire gene pool traces back to 'Ashmouni', a heterogeneous Egyptian variety, and St. Kitts Sea Island (Hathorn, 1951). Breeding efforts focused mainly on re-selecting pure lines from existing varieties or from crosses among lines within the gene pool which resulted in the development of a narrow gene pool with little genetic variability for plant type or fiber quality. Even so, breeders were able to make significant improvements in fiber and yarn strength within this gene pool. The fiber of the Sacaton gene pool is long, strong, and fine, but low in length uniformity. 'Pima 32' was the last cultivar developed solely from this gene pool and was released in 1949. It had an upper half mean length (U.H.M.) of 1.40 in., a mean length of 1.05 in., length uniformity of 75%, fiber strength index of 10.0 (about 30 g/tex), a micronaire of 3.25, and a 60s yarn skein strength of 58 lbs.

Prof. W. Bryan at the University of Arizona created a second gene pool by bringing several different types of cotton together in a series of complex crosses among four types of cotton: Pima, Tanguis, Sea Island (all *G. barbadense* L.), and Stoneville upland (*G. hirsutum* L.). One line from this cross was noticeably earlier, shorter, and more productive than the typical Pimas and was eventually released as 'Pima S-1' in 1951 (Bryan, 1955). Compared to Pima 32, Pima S-1 has shorter U.H.M. lengths (1.32 in.), weaker fiber strength index (9.2, or about 28 g/tex), and higher micronaire (3.70), but better length uniformity (82%) due to longer mean fiber length (1.09 in.). Although Pima S-1 seems to suffer from inferior fiber quality, 60s yarn

skein strength is equal to that of Pima 32 (58 lbs). Breeders recognized Pima S-1 as a novel fiber type and, after industry acceptance, established it as the the new base point for the future development of ELS cottons in the U.S. (Niles and Feaster, 1984).

The Hybrid B gene pool was developed in the mid 1960s from a series of crosses made over time involving Pima S-1, Sacaton Pimas, Coastland type upland, Tanguis, Sea Island, and Egyptian cottons (Young et al., 1976). 'Pima S-3', a cultivar selected from the Hybrid B gene pool, has U.H.M. length similar to the Pima 32, mean fiber length, fiber strength and micronaire similar to Pima S-1, and length uniformity intermediate to Pima S-1 and Pima 32. Again, yarns spun from Pima S-3 are about equal to Pima S-1 and Pima 32 in strength.

Since 1951, breeding efforts have focused on widening the gene pool of Pima cotton through extensive crossing among the best lines from each the three gene pools, followed by rigorous selection and testing of improved types. Each successive cultivar released from this expanded gene pool was significantly better in some aspect of fiber quality than the previous cultivar. 'Pima S-7', a cultivar released in 1991, has approximately equal contributions from each separate gene pool in its parentage (Turcotte et. al., 1992). The fiber of Pima S-7 approaches Pima 32 in staple lengths, and has greater length uniformity, greater fiber strength, and higher micronaire than Pima S-1 or Pima 32. Yarn skein strength of Pima S-7 is better than any variety developed from any of the three separate gene pools.

These advances in fiber quality were made in spite of limited knowledge of the genetic and physiological control of fiber development or fiber quality. Incremental advances in fiber quality are still possible within the current gene pool of Pima, but if history is a guide, future breakthroughs in fiber quality may be dependent on the incorporation of new germplasm into the working gene pool to further expand the range of genetic variability for fiber quality within Pima cotton.

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