EARLY-GENERATION BREEDING RESULTS FROM GENOME-WIDE INTROGRESSION OF G. LONGICALYX AND G. ARMOURIANUM GERMPLASM

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Summary

Wild diploid species of cotton (*Gossypium* spp.) exist in different parts of the tropics, but are not fully exploited for fiber-related traits, mainly due to ploidy barriers in making the crosses with tetraploid cotton (*Gossypium hirsutum* L.), poor meiotic affinities, poor fertility, undesirable linkages, and poor initial agronomic performances. To overcome these barriers, we created a tri-species hybrid and several backcross populations involving wild diploid cottons, *G. longicalyx* Hutchinson & Lee and *G. armourianum* Keraney, and cultivated tetraploid cotton, *G. hirsutum* (HLA). In this experiment, 14 HLA-derived backcrossed generations, including BC_1F_1R1[†], BC_1F_2, BC_1F_2R1, BC_1F_3, BC_1F_3R1, BC_1F_3U1[‡], BC_2F_1, BC_2F_1R1, BC_2F_2, BC_2F_2R1, BC_2F_2U1, BC_3F_1, BC_3F_1R1 and BC_3F_1U1, and four checks, FM-832, PSC-355, Acala NemX and TM-1 were evaluated for fiber quality and yield related traits in a randomized complete block design with four replications for two years, 2005 and 2006, at one location, College Station, Texas. Fiber quality analysis was done by using high volume instrument (HVI) testing method (Zellweger Uster Inc).

Each trait was analyzed with SAS v9.1.3 (SAS Institute, Cary, NC) using mixed model analysis with PROC MIXED method REML (restricted maximum likelihood). Least Square Means (LSMEANS) was used to calculate means for generations. The multiple comparisons were tested for significance using Tukey-Kramer adjusted least significant difference (LSD) and the output was condensed into letter groupings using SAS macro, PDMIX800. To estimate variance for each generation in a year on an individual plant basis as well as computing 95% confidence interval, data sets were analyzed separately for each generation in a year using SAS PROC MIXED method REML with replications and individual plants within a generation, treated as random factors. Variances were considered significantly different if the confidence intervals for different generations did not overlap. Phenotypic correlations among the fiber quality and yield traits were based on individual plant data for each generation, combined across years. Phenotypic correlations were computed by Pearson's product-moment correlations method using PROC CORR procedure of SAS.

Results indicated that most of the introgressed generations had low micronaire readings (fiber fineness) and high fiber strength compared to one or more checks. The most consistent changes in variances after random-mating were observed at BC1 and BC2 levels, where BC1F3R1 and BC2F2R1 had significantly higher variances than their respective generations of origin, BC1F3 and BC2F2, indicating the existence of predominant repulsion phase linkages between the loci associated with yield in the generations of origin.

[†] R1 indicates, one generation of random-mating.

[‡] U1 indicates, generation with uncontrolled pollination, where open-pollinated seed was harvested from a field that has high honey bee population, thus the generation planted would have a mixture of self and open-pollinated seed.

Positive correlation between strength and uniformity index and negative correlations between short fiber content and uniformity index as well as strength and short fiber content ($P \leq 0.05$) were consistent across all the generations. Yield for all the generations was significantly lower than PSC-355, FM-832, Acala NemX and, TM-1, and thus additional backcrossing to high yielding cultivars or lines and selection for yield at each backcross level is needed to increase the yield potential of this germplasm.