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CHANGES IN GENETIC DIVERSITY OF U.S. UPLAND COTTON

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Abstract

There have been events in the history of the cotton industry from 1900 to 1990 that affected cultivar development such as placing a priority on earlier maturing cultivars to combat the boll weevil, developing compact plant architecture to aid in mechanical harvesting, and always strongly emphasizing higher yields even at the expense of other characters. These and other events have placed intense selection pressure on the cotton germplasm which was at the expense of genetic diversity. Using three U.S. Upland breeding programs (MAR, Pee Dee, and a combined CA and NM Acala group) as well as a population of cultivars that were used commercially sometime within this time frame from about 1900 to the mid 1990s, genetic diversity over time was studied using 261 codominant RFLP markers. These groups were separated into three time period relative to their unique history as 'old', 'middle', and 'recent'. UPGMA clustered the time periods of each breeding program cleanly to themselves. It showed that the 'old' and the 'recent' materials were never more closely related to each other than to the 'middle'. This would be expected by a steady change of genetic diversity. Genetic diversity (1-average SS of the allele frequencies) significantly decreased at better than the 0.05 level within the Acala and Pee Dee programs. The cultivar group trended as a slight decrease but was not significant. The MAR program had an increase in genetic diversity that was significant at the 0.10 level. This increase was likely due to a high program priority to release germplasm and a later added stimulation by the program's imminent conclusion. Individual loci were reviewed for each time period and scored as to whether it was fixed (monomorphic) or not. The change from fixed to polymorphic indicates an introduced allele and vice versa indicated the loss of an allele (genetic erosion). These changes can occur both from 'old' to 'middle' and 'middle' to 'recent'. The Acala and Pee Dee programs showed more erosion than introduction for both time interfaces and like the genetic diversity measures, greater loss occurred in the more recent time. Neither the MAR program nor the cultivars showed more alleles lost than gained but there were alleles still being lost. The genetic diversities of the individual loci for the three time periods of the Pee Dee program were charted on a genetic linkage map. The genetic diversity changes from 'old' to 'recent' in this genetic diversity landscape show the loss of specific alleles even to the point of having entire chromosomes fixed.