Permanent mapping population of the cotton genome. (C07-yu160251-Oral)

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Abstract:

Genetic mapping resource developed from an appropriate cross is the foundation for any genome mapping efforts. Lacking in Gossypium has been the availability of a recombinant inbred line (RIL) population that can be shared with the cotton research community. We have developed 191 RILs from the cross of TM-1 x 3-79, the genetic standards for G. hirsutum and G. barbadense, respectively. Extensive genetic and cytogenetic stocks were derived from the two cottons, including a set of aneuploid stocks for rapid localization of genetic markers to cotton chromosomes. The RILs (F7) of the above population were developed via single seed decent (SSD) from the original F2 individuals from which a genetic map was constructed, consisting of approximately 1,000 DNA markers (RFLPs, RAPDs, AFLPs, and SSRs). Characterization of the RILs with a set of the above markers indicates that 95% of genetic loci are fixed in the population and they behave normally in the cotton genome. The RIL population retains the phenotypic variability of the original F2. We are now increasing this permanent mapping population for distribution to the cotton research community for integrated genome mapping.

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