Development of Permanent Mapping Populations
RILs in Diploid A Genome

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Recombinant inbred lines (RILs) serve as powerful tools for genetic mapping. RILs are obtained by crossing two inbred lines followed by repeated selfing or sib mating to create a set of new inbred lines. The resulting genome in the finally developed RILs is a mosaic of the parental genomes. The fixed variation in RILs is used for fine mapping of complex traits. Cultivated diploid A genome species of cotton holds special significance to dissect complexity of developing cotton fibers. We have evaluated the interspecific population (Gossypium arboreum var. KWAN-5 × G. herbaceum var. Jyotish) for fiber quality attributes such as fiber length, fiber strength, fiber fineness, uniformity, and fiber elongation. The range of variation for the fiber quality traits is tremendous: fiber length, 18 to 31 mm; strength, 17 to 21.6 cN • tex¹ and micronaire, 2.8 to 4.8. The lint proportion (ginning %) has strong negative correlation with fiber length and strength. The F₂ mapping population is being used for developing a linkage map and mapping fiber quality QTLs; substantial progress has already been made. The same population was advanced for development of RILs (a set of 210 inbreds) so as to validate the results of F₂ and fine mapping of major QTLs.