Development of Permanent Mapping Populations RILs in Diploid A Genome

WAGHMARE VIJAY N[1], DONGRE A B[1], GOTMARE Vinita[1], PATIL P G[2],
DESHPANDE L A[1], KHADI B M[1]

(1. *Division of Crop Improvement*, *CICR*, *Nagpur*, *India*; 2. *Ginning and Training Center*, *CIRCOT*, *Nagpur*, *India*)

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 of for fine mapping of complex traits. Cultivated diploid A genome species of cotton holds special significance to dissect complexity of a developing cotton fibers. We have evaluated the interspecifc population (*Gossypium arboreum* var. KWAN-3 × *G. herbaceum* var. Jayadhar) 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 34 mm, strength: 17 to 24.6 cN • tex^{-1} and micronaire: 2.8 to 4.8. The lint proportion (ginning %) has strong negative correlation with fiber length and strength. The F_2 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 F_2 and fine mapping of major QTLs.