

Exploring the genetic diversity of upland cotton (*Gossypium hirsutum* L.) genotypes using EST-SSR markers

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Cotton is a paramount multi-purpose crop cultivated intensively for the leading source of naturally occurring fiber, animal feeds, and oilseeds. Understanding the genetic diversity of cotton species is necessary for the development of new varieties or cultivars with enhanced yield, fiber quality and disease resistance. EST-SSR markers are widely used for assessing genetic variation owing to their high polymorphism and reproducibility. This investigation used 28 EST-SSR markers to unveil the genetic diversity of 30 upland cotton genotypes collected from Central Cotton Research Institute, Multan, Pakistan. Seven EST-SSR primers out of 28 were found polymorphic at different SSR loci. A total of 37 alleles were ascertained using the 28 EST-SSR primers. The ordinary number of alleles per locus was 1.5, with a range from 1 to 3. The polymorphic information content (PIC) extended from 0.065 to 0.82 with an average of 0.403. Cluster analysis was executed using an un-weighted pair group method with arithmetic. The average algorithm grouped cotton genotypes into four major clusters except DNH-105, Cyto-178 and FH-326, acting as an out-group. Genotypes such as IR-3701, Sitar-008, CIM-598, and CIM-625 exhibited maximum similarity coefficient. Nau-1231 indicated the lowest confusion probability (Cj) value (0.531) along with the greatest PIC (0.82) and discriminating power (Dj) (0.82) values. This study provides valuable information on the genetic diversity of upland cotton, which could be useful for cotton breeders as they evolve strategies for the conservation and implementation of cotton germplasm resources.

Keywords: *Gossypium hirsutum*, Genetic variation, Molecular marker, Similarity coefficient, Cluster analysis