

## Genetic Relationships among Wild Cotton Species Analyzed by Molecular Markers

AMUDHA J, Balasubramani G

(Biotechnology Section, Central Institute for Cotton Research, Nagar, Nagpur 440010, India)

**Abstract:** The genetic relationships among wild cotton species has been analysed by randomly amplified polymorphic DNA (RAPD) technique. A total of 758 amplified bands were observed using 45 random sequence decamer primers. The genetic distances, which reveal genetic diversity among the species, were estimated from the binary data matrix. The dendrogram produced by Unweighted paired group method of arithmetic means (UPGMA) clustering method assigned the 16 wild species in to five groups. Group I consisted of 4 species with *G. anomalum* and *G. triphyllum* are closely placed in the dendrogram as they have similarity index of 0.96 since they are also similar in most of the morpholog-

ical characters. The other two are *G. barbosum* and *G. capitis-viridis*. Within the group II *G. davidsonii* and *G. raimondii* were clustered together and showed a very reasonable relationship with *G. thurberi*, *G. harknessi* and *G. aridum*. *G. Klotzschianum* and *G. davidsonii* are closely related but varies in the nature of the stem tip, which is glabrous whereas *G. davidsonii* has light, hairy stem tip and petal spot. *G. longicalyx* (F genome) is a perennial crawling shrub and *G. bickii* (G genome) spreading shrub was apart from each other in the dendrogram and form the IV and V group. Group III in the dendrogram of the species studied was clustered together in which *G. sturtianum* and *G. australe* differ in flower colour.

**Key words:** *Gossypium*; species; molecular markers; UPGMA

**CLC number:** S562.035.3 **Document code:** A

**Article ID:** 1002-7807(2004)06-0360-08