GENOMIC AFFINITY AMONG *GOSSYPIUM* SUBGENUS *STURTIA* SPECIES BY RAPD ANALYSIS

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Abstract

Gossypium L. is a genus of about 48 species that occurs in relatively arid regions of Africa, Arabia, Australia, and North and South America (Fryxell, 1992). Of the 43 known wild diploid *Gossypium* species, 18 are found in Australia. All Australian species belong to the subgenus *Sturtia* which is divided into three sections, *Sturtia*, *Hibiscoidea* and *Grandicalyx*. The 5 Australian arid zone species possess terpenoid glands in their green tissue but their seeds have rudimentary glands in the embryo. This characteristic is unique in the genus and four of the Australian species, *G. sturtianum, G. australe* and *G. bickii* have been the focus of research to transfer this trait into Upland and/or Old World cotton to achieve insect resistance while maintaining the embryo free of toxic substances that lower its feed or food value (Craven et al., 1995). *Gossypium bickii* was placed in the C genome before Edwards and Mirza (1979) gave it a new genomic designation "G" on the basis of differences in chromosome size and karyotype compared to other Australian *Gossypium* species. Morphologically, *G. bickii* is closely related to the other two Australian species (*G. australe* and *G. nelsonii*) of section *Hibiscoidea* (Fryxell, 1965, 1979; Stewart et al., 1987). Partially fertile hybrids among *G. bickii*, *G. australe* and *G. nelsonii* have been reported and recommendation for the inclusion of these three species in a single genomic group have been made (Stewart and McCombie 1991). In view of the distinctive evolutionary history of *G. bickii* (Wendel et al., 1991), we wished to observe its genomic affinity with other Australian species. *Gossypium australe* and *G. nelsonii* were included because of their taxonomic placement (section *Hibiscoidea*) and morphological similarities. *Gossypium sturtianum*, which belongs to section *Sturtia*, was incorporated because of its cytoplasmic similarity with *G. bickii* (Wendel et al., 1991) and *G. nandewarense* was included because of questions concerning its distinction from *G. sturtianum* (Fryxell, 1992; Craven et al., 1995). Two species from the Australian section *Grandicalyx*, *G. enthyle* and *G. anapoides* (Stewart et al., 1997) were incorporated in the study as representatives of section *Grandicalyx*, and *G. triphyllum* was taken into consideration because of its previous inclusion in section *Hibiscoidea* by Fryxell (1979; 1984) based on morphological similarities. *Gossypium longicalyx* was used as an out group.

The genomic affinity among the selected *Gossypium* species was assessed using Random Amplified Polymorphic DNA (RAPD) analysis. From 30 random decamer primers, 22 produced a total of 569 fragments with a very high level of polymorphism among species. The size of the fragments ranged between 300 and 3000 bp. Pair-wise comparisons of unique and shared polymorphic amplification products were used to generate Jaccard's (1908) similarity coefficients. These were employed to construct a dendrogram using an unweighted pair-group method with arithmetical averages (UPGMA). This study demonstrated that there is a high level of variation and polymorphism among Australian species, compared to the polymorphism within species. The UPGMA analysis showed high intra-specific genetic similarities (0.811 to 0.896) for *G. nelsonii*, *G. australe*, *G. sturtianum* and *G. bickii*. The *G. bickii* clustered between the species of sect. *Hibiscoidea* (*G. australe* and *G. nelsonii*) and *G. sturtianum*. Genetic similarity coefficient of *G. nandewarense* with two accessions of *G. sturtianum* was high (0.812 to 0.890) and median in placement, showing that it should not be considered as a separate species. *G. triphyllum* and *G. longicalyx* were distinct from the Australian species and fell in two separate groups. *G. triphyllum* exhibited very little genetic similarity with Australian species and has been correctly excluded from section *Hibiscoidea.*

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