

## Phylogenetic relationships of Pigeonpea (*Cajanus cajan*) and its wild relatives based on RAPD markers

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In the present investigation RAPD marker was used for the elucidation of genetic relationships in the genus *Cajanus* and genetic fingerprinting of pigeonpea cultivars as well as wild species of *Cajanus*. RAPD markers utilized for the identification of pigeonpea, *Cajanus cajan* cultivars (DSLRL-17, BDN-2, ICWR-03 and ICWR-12) and ten wild species, including *C. cajanifolius*, *C. lineatus*, *C. sericeus*, *C. acutifolius*, *C. lanceolatus*, *C. reticulatus*, *C. albicans*, *C. scarabaeoides*, *C. volubilis* and *C. platycarpus*, using a set of 10 primers were found to be polymorphic at species level and generated 85 unequivocal scorable polymorphic bands. The size of amplification products ranges from 102 bp to 2854 bp. The present study accentuates upon the utility of RAPD markers for the identification of cultivars of pigeonpea and allied species of *C. cajan*. The inter/ intra specific genetic variability studies based on RAPD marker showed a large amount of genetic variation between the species of *Cajanus* and their clustering pattern partially, supported the sectional classification. It was hypothesised that both *C. cajan* and *C. cajanifolius* might be derived from a common ancestor and experienced minor genomic rearrangement during divergence.

Key words : *Cajanus*, Pigeonpea, RAPD, Proximity matrix analysis

### INTRODUCTION

Pigeonpea, *Cajanus cajan* (L.) Millsp., is an important grain legume crop of the semi-arid tropics. *C. cajan* (L.) Millsp. is the only domesticated species under the subtribe Cajaninae Benth. of the tribe Phaseolae Benth. belonging to the subfamily Papilionoideae under the family Leguminosae (Bentham, 1965). After the inclusion of the Atylosia the genus *Cajanus* comprises 32 species, 18 of which are endemic to Asia, 13 to Australia, and one to West Africa (van der Maesen, 1986). Eleven related genera including *Rhynchosia*, *Dunbaria* and *Flemingia* have been described which can be considered to constitute the tertiary gene pool, while the *Cajanus* species showing crossability with the cultigen, constitute the secondary gene pool of the cultigen (van der Maesen, 1990). The genetic origin of pigeonpea is still not settled. Studies based on morphology (van der Maesen, 1980, 1986, 1990), cytology and crossability (Pundir and Singh, 1985b), isozymes (Krishna and Reddy, 1982) and nuclear RFLPs (Nadimpalli *et al.*, 1993) suggest a monophyletic origin from *C. cajanifolius*. On the other hand, the seeds storage protein profiles (Ladizinsky and Hamel, 1980; Jha and Ohri, 1996) and nuclear DNA amounts (Ohri *et al.*, 1994) suggest a polyphyletic origin of the cultigen. DNA based molecular markers have been used extensively to discern out the putative progenitor species and to depict

phylogenetic relationships in several genera (Nadimpalli *et al.*, 1993; Ishii *et al.*, 1996). Randomly amplified polymorphic DNA (RAPD) is a dominant marker and it follows mendelian fashion. RAPDs are indefinite in number, capable of high level polymorphism and have been used in phylogenetic studies. RAPD has been extensively utilized in the study of genetic relatedness of plant cultivars and plant populations, as well as in the study of inter- and intra-specific genetic relationships between plant species. Within grain legume also crops RAPD markers have been widely used for the identification of genetic relationships among cultivars, among wild forms or between cultivars and wild forms. Ratnaparkhe *et al.* (1995) employed random amplified polymorphic DNA (RAPD) markers for the identification of *C. cajan* cultivars and the wild relatives of *C. cajan* and indicated the immense potential of RAPD marker in the genetic fingerprinting of pigeonpea cultivars and wild accessions. Present study reports here on the utilization of RAPD markers to elucidate the genetic relationships between *C. cajan* and its allied species.

### MATERIALS AND METHODS

#### *Plant materials:*

Seeds of cultivars of pigeonpea (*Cajanus cajan* (L.) Millsp.) BDN-2, DSLRL-17, ICWR-03 and ICWR-12 and ten wild species (*C. cajanifolius*, *C. lineatus*, *C.*