



## Genetic diversity analysis of cowpea [*Vigna unguiculata* (L.) Walp] genotypes using RAPD markers

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**Abstract :** Genetic diversity among 21 released varieties of cowpea [*Vigna unguiculata* (L.) Walp] was analysed using RAPD markers. A total of forty primers of two series (OPF01-20 and OPAG01-20) were used to screen the polymorphic primers and the profiles generated by three such primers were used for analysis. The genetic similarity co-efficients among genotypes varied between 0.44 to 0.82. Based on UPGMA and SAHN clustering cowpea genotypes grouped into two main clusters. Cluster II comprised of genotypes CO-7 and GC 3, while other nineteen genotypes were grouped under cluster I. However, the primers OPF 2, OPF 20 and OPAG15 were most polymorphic that can be used to fingerprint cowpea varieties.

**Key Words :** Diversity, Genetic similarity, RAPD markers, Cowpea

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### INTRODUCTION

Cowpea [*Vigna unguiculata* (L.) Walp] is an important multipurpose grain legume extensively cultivated in arid and semiarid regions of Africa and Asia. Whether utilized as a pulse, or green pod vegetable or as a forged crop, it forms an important component of farming systems from semi-arid to the humid tropics. Its grain and leaves are rich of high quality protein and vitamins, which provide an excellent supplement to the lower quality cereal protein (Kitch *et al.*, 1998). Cowpea varieties/ accessions can be distinguished phenotypically from one another by their growth habit, time to maturity, yield and seed size and colour. A clear characterization of accessions is a necessary first step to guide efforts to conserve biodiversity and to facilitate breeding efforts. Data on genetic diversity of Indian cultivars is lacking. The main objective of this study was to determine the pattern and extend RAPD marker variation between cowpea populations from different agro ecological zones, and to determine the degree of genetic

relationships among different varieties released in India. The degree of polymorphism generated by PCR based techniques ensures the higher level of differentiation of plant varieties in comparison to morphological and biochemical markers.

It has been demonstrated that cultivated cowpea had lower genetic diversity than many other crops, especially legume crops (Pasquet, 2000). So far, most characterization data of cowpea accessions in genebanks are based on morphological characters. Knowledge of genetic distance and diversity at the molecular level among landrace materials is important for a more profound characterization and to identify gene flow among populations. While numerous studies have evaluated molecular diversity of common bean, recent reports related to cowpea genetics have focused on linkage map and genome analysis. Information on molecular diversity of cowpea is limited (Nkongolo, 2003) and data on molecular variation at the DNA level of Indian landraces of cowpea is lacking.

The morphological characters have been used both for

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