RESEARCH PAPER

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Morphological characterization of induced mutants in groundnut using RAPD Markers

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An experiment was conducted for morphological and molecular characterization of induced mutants. From both morphological and molecular analysis, it was revealed that TMV 2 and its mutant NLM were diverse and placed in different cluster, same holds good for DER and its mutants but for VL 1 and its mutants, there is lack of relationship between morphological and molecular diversity and RAPD failed to differentiate different botanical types of groundnut.

Key words : Groundnut, Mutants, Molecular Diversity, RAPD and TMV-2.

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INTRODUCTION

Groundnut is believed to have originated in the Bolivian region of South America where the greatest diversity is found (Krapovickas, 1969). Though *Arachis monticola* has been identified as the tetraploid progenitor, the A and B genome donors and mode of origin of two subspecies is still controversial (Smartt, 1990). Groundnut (*A. hypogaea*) is classified into two subspecies, *viz.,* ssp. *hypogaea* (Krap. and Rig.) and ssp. *fastigiata* (Wald.) based on variation in morphology. Further, the ssp. *hypogaea* is bifurcated into var. *hypogaea* (Virginia bunch/runner) and var. *hirsuta* (Peruvian runner), and likewise ssp. *fastigiata* into var. *fastigiata* (Valencia), Peruviana, aequatoriana and var. *vulgaris* (Spanish bunch) (Stalker and Simpson, 1995). Groundnut is one of the principle economic crops of the world, which has been exposed extensively to mutagenic treatments for induction of variability. Physical mutagens such as, X-ray, gamma rays, â-rays and fast neutrons (Shivaraj *et al.,* 1962) and chemical mutagens like, ethyl methane sulphonate (EMS), ethidium bromide, acryflavine (Levy, 1976), diethyl methane sulphonate (DES), N- nitroso-N- methyl – urea, N- ethyl–N-nitroso-urea, ethylene imine and sodium azide (Venkatachalam and Jayabalan, 1997) has been used to create genetic variability in groundnut. However, gamma rays and EMS are most widely used and most effective mutagens in groundnut. Mutants have been obtained in groundnut either spontaneously or induced by physical/ chemical mutagens. In cultivated groundnut very low or no polymorphism to abundant polymorphism in wild *Arachis* has been reported (Halward *et al*., 1991; Lanham *et al*., 1992; Paik-Ro *et al*., 1992). However, recent studies revealed polymorphism in cultivated groundnut using amplified length polymorphism (AFLP) (He and Prakash, 1997) randomly amplified polymorphic DNA (RAPD) (Bhagwat *et al*., 1997; Subramanian *et al*., 2000; Dwivedi *et al*., 2001) and simple sequence repeats (SSR) (Hopkins *et al*., 1999). Randomly amplified polymorphic DNA is a convenient, economic and rapid method as compared to other techniques as it requires no probes and prior sequence information. Further, relatively small number of primers can be used to generate a very large number of fragments from different regions of the genome and hence, multiple loci may be examined very quickly. This makes RAPD a powerful technique for screening the germplasm for assessing the genetic diversity. Therefore, this study was carried out to assess genetic diversity among 21 mutants representing four botanical types using RAPD.