

Molecular Diversity Among Selected Groundnut (*Arachis hypogaea* L.) Genotypes I: RAPD Analysis

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ABSTRACT

The purpose of the present experiment were to study genetic diversity among eighteen selected groundnut genotypes following random amplified polymorphic DNA (RAPD) assay with twenty primers of a 10-mer. The number of amplicons varied from three to ten with an average of 7.5 per primer, of which three were polymorphic. Altogether the primers generated a sum of 150 amplified fragments with 42.32 percent polymorphism. The genetic similarity (S_{ij}) assessed by Dice similarity coefficient was ranged from 86 % to 99 %, with an average of 93 %, indicating very less diversity among genotypes. Clustering technique of unweighted pair group method with arithmetic averages (UPGMA) dendrogram revealed three distinct clusters at S_{ij} of 0.94. Among the genotypes TG 49 and ICG 13787 were found to span the extremes of the entire dendrogram with the remaining types distributed between them, whereas the resistant lines for *Aspergillus* seed colonization are distributed throughout the dendrogram. All germplasm except ICG 14985 (Spanish bunch) clustered distinctly away from cultivars and all the cultivars clustered together indicating narrow genetic diversity among the cultivars and germplasm.

Key words : *Aspergillus* seed colonization, Genetic diversity, Peanut, RAPD.