

Comparative assessment of genetic diversity of peanut (*Arachis hypogaea* L.) genotypes as revealed by RAPD, AFLP and SDS- protein markers

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ABSTRACT

The present work was conducted to evaluate RAPD, AFLP and SDS protein marker systems for their ability to detect genetic diversity among ten peanut (*Arachis hypogaea* L.) genotypes and to compare the efficiency of these marker types in the classification of accessions according to the gene pool of peanut genotypes. The polymorphic fragments were obtained on the basis of 10 differentiating primers using the RAPD method, 2 differentiating primer combinations using the AFLP, and SDS protein. The ten RAPD primers produced 38 polymorphic bands, while AFLP primer combinations produced 30 polymorphic bands, and SDS protein pattern produced 4 polymorphic bands. RAPD data analysis showed that the genetic similarity among ten peanut accessions ranged from 75.3 to 98.7%, while the AFLPs generated data showed that the highest genetic similarity value was 97.8% and the lowest value was 74.7%, and the SDS protein showed that the highest genetic similarity value was 100% and the lowest value was 71.4%. The dendrogram generated with hierarchical UPGMA (Un-weighted Pair Group Method with Arithmetic Averages) cluster analysis of the Jaccard's similarity coefficient matrices revealed two major clusters, which were identified.

Key words: Groundnut accessions, Molecular markers, Polymorphism, Genetic similarity.

INTRODUCTION

Peanut, or groundnut (*Arachis hypogaea* L.) is an important oilseed crop which is widely consumed by humans. Argentina, China and the United States are the largest exporters of peanuts while the European Union and Asia tend to be the largest peanut importers (Revoredo and Fletcher, 2002). Peanut oil, peanut butter and peanut seeds are highly nutritious for human consumption. The seeds contain approximately 45–51% oil and most of their oil content consists of oleic and linoleic acids (Lopez *et al.*, 2000). *Arachis hypogaea* L. is grown

throughout the world as a source of oil and protein. The *Arachis hypogaea* is an allotetraploid (AABB, $2n = 4x = 40$ chromosomes), resulting from duplication of the cross between AA and BB wild type species (Leal-Bertioli *et al.*, 2009).

The classification of groundnut only on the basis of their morphological characteristics is not sufficient, therefore the assessment of variation at gene level during germplasm collections and pedigree construction is necessary. The use of molecular markers will be helpful for the collection of advanced and novel genotypes of groundnut. DNA- based markers provide accurate knowledge at gene