



**MOLECULAR DIVERSITY ANALYSIS IN GROUNDNUT USING SIMPLE
SEQUENCE REPEAT (SSR) MARKERS**

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ABSTRACT

In the present investigation eight genotypes of groundnut *viz.*, Tirupati-4, TIR-25, ICGV-91114, TCGS-584, JL-220, ICGV-99029, K-1375 and TCGS-647 have been selected and analyzed with 45 SSR primer pairs to know the variation at DNA level. The results indicated considerable genetic variation among the genotypes. The results also revealed SSRs ability in detecting polymorphism among the genotypes screened. Among 45 SSR primers tested on the eight genotypes, ten primer pairs produced clear polymorphic bands. The results clearly showed that the genotypes have considerable levels of genetic diversity detected by SSR markers. In general, the genotypes analyzed showed wide genetic variation at DNA level.

Keywords: SSR Markers, Polymorphism, Genetic Variations, Tirupati

INTRODUCTION

Cultivated groundnut (*Arachis hypogaea* L.) is an important oilseed crop that is widely grown under rainfed conditions and the crop often suffers yield loss due to prevalence of stresses such as drought, diseases and insect pests. Assessment of genetic diversity and development of genetic linkage maps are important steps in the development of molecular breeding programs. Assessment of molecular diversity should facilitate the identification of agronomically valuable and diverse germplasm for use in linkage mapping and genetic enhancement of

specific traits in groundnut [1]. The identification and understanding of molecular genetic diversity in cultivated groundnut genotypes will help in effective conservation along with efficient breeding programs in this crop. SSR markers were chosen for the study as they are highly polymorphic between species and more importantly between individuals within a species and populations. Thus the specific aim of this study was to evaluate molecular diversity among groundnut genotypes using simple sequence repeats (SSRs).