Phenotyping and Molecular Marker Analysis for stem-rot Disease Resistance Using F_2 Mapping Population in Groundnut

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Abstract: Sclerotium rolfsii *is one of the dreaded pathogen which causes stem-rot disease by infecting groundnut from seedling to maturity stages and causes potential yield losses. Molecular markers, linked with stem-rot disease resistance gene/QTLs can facilitate the identification of resistant genotypes. In the present study, a stem-rot susceptible genotype (TG-37A) and a stem-rot resistant genotype (NRCG CS85) were crossed and their F_2 population was used for SSR marker analysis. For the phenotypic data, $F_{2:3}$ progenies were screened for stem-rot disease incidence. Parental polymorphism survey was done using 1266 SSR primer pairs so as to identify the polymorphic markers. Among these SSRs, 52 were found to be polymorphic between the parental combination (TG-37A x NRCG CS85).These markers were further utilized for bulked segregant analysis (BSA). Among the polymorphic SSRs, three primers DGR294, DGR470 and DGR510 were able to distinguish both resistant and susceptible bulks and individual plants constituting the bulks. Further genotyping of whole population using identified markers is under way, which may confirm the linkage of putatively linked markers to with the stem-rot resistance.*

Keywords: Arachishypogaea, Sclerotiumrolfsii, *SSR markers, Bulkedsegregant analysis*

INTRODUCTION

Cultivated groundnut or peanut (*A. hypogaea L.*) is anallotetraploid (2n = 4 x = 40) crop grown extensively in nearly 108 countries. Stem-rot caused by *Sclerotium rolfsii* is one of the most devastating fungal diseases, which imposes huge yield-losses. Although, the search for peanut cultivars resistant to *S. rolfsii* originated way back in 1918 [5], but till date a high degree of resistance has not yet been found. Moreover, no marker(s) has been reported to be associated/ linked with any soil-borne pathogens including stem-rot disease resistance in groundnut [7].

Bulked segregant analysis (BSA) is one of the tools which is used to identify the molecular marker(s) linked with any trait of interest in an organism. This measures the variation present in pools of segregants that have been sorted according to phenotype and uses the correlation between these measurements and the pool phenotype to assign a likely map location. This is an improvement over methods that require individual genotyping, and used increasingly for mapping complex traits including those whose genetic control is unknown [4].

Molecular markers and genetic linkage maps are pre-requisites for molecular breeding in any crop including groundnut. Such tools would speed up the process of introgression of beneficial traits into any preferred genotype. Considering the above advantages, the present study was undertaken to rapidly identify the molecular markers linked with the stem-rot disease resistance gene/ QTLs in groundnut through bulked segregant analysis (BSA).

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