

## Screening of Groundnut Lines in Field and by AhTE Markers for *Sclerotium rolfsii* Resistance

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Groundnut is one of the major economic seed oil crop and is affected by many diseases such as rust, late leaf spot, stem rot etc. Stem rot is caused by *Sclerotium rolfsii* which is becoming a major problem in recent years, causing yield losses up to 80 per cent. Groundnut being the major cultivated crop in northern Karnataka region and any progress made towards improving such a crop will definitely help farming community. In this regard present study was designed to investigate, 94 backcross lines (2 parents and 92 backcross lines) and 44 elite genotypes along with resistant check R9227 and susceptible check TMV-2. Field screening of stem rot resistance with artificial inoculation of mycelium culture having *sclerotial* bodies was carried out during *kharif 2018* at University of Agricultural Sciences (UAS), Dharwad, Karnataka, India. Mycelium was collected from the stems and collar regions of infected groundnut plants, collected from the fields of UAS, Dharwad. Dharwad isolate was confirmed by PCR sequencing of *S. rolfsii* DNA by using ITS (Internal Transcribed Spacer) *S. rolfsii* specific primers. Disease incidence was recorded after inoculation at 30 days interval till harvesting. In addition, productivity traits were also recorded. In field conditions, variability for disease incidence (DI) for all genotype was observed clearly and grouped into different classes like; 11 moderately resistance (10-20 % DI), 73 moderately susceptible (20-30 % DI) and 43 susceptible (>30 % DI) genotypes and only few of them showed partial resistance with 0.1-10 % DI (donor parent of backcross line {derivative of ISATGR 278-18}), 4 backcross lines (2552, 2584, 2854 and 2951) and 4 elite genotypes (ICGV 06420, Mutant III, R 9227 and TG 38). Further back cross lines and elite genotypes were genotyped with AhTE markers, to identify the single marker association (SAM) for the *Sclerotoium* rot resistance/susceptibility. Among 150 markers studied 61 markers showed polymorphism among elite genotypes. Total of 59 Marker Trait Associations (MTA's) were established from backcross lines by 22 markers and 107 MTA's from 61 markers in elite genotypes. Based on PVE per cent (Phenotypic Variance Explained %) 32 markers showed <10 per cent PVE value, 22 markers had 10-20 per cent PVE value and 5 markers showed > 20 per cent PVE value in backcross population. Where as in elite genotypes, 26 markers showed <10 per cent, 68 markers were between 10-20 per cent PVE and 13 markers had > 20 per cent PVE values. P- value (Probability value) ranged between 0.0001 to 0.05 and 0.0001 to 0.07 for the backcross and elite genotypes respectively. Two markers *AhTE0491* and *AhTE0121* which were earlier reported with late leaf spot disease in groundnut were also found SMA with *Sclerotoium* rot in the present study.

Reference for markers Kamble, M. V., 2014, Association analysis for yield related traits and foliar disease resistance using transposon specific markers in a mutant population of groundnut. *M. Sc. Thesis*, Univ. Agric. Sci., Dharwad, Karnataka (India).

