

Inheritance of stem rot resistance in groundnut (*Arachis hypogaea* L)

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Abstract

In the present investigation five crosses out of twenty crosses made in line x tester mating design were utilized for inheritance studies of stem rot resistance. The five crosses were derived from crossing of five susceptible genotypes (TCGS 1694, TCGS 2245, Dheeraj, Kadiri-6 and Narayani) with one stem rot resistant genotype, TCGS 1862 (male parent). F₁s were moderately resistant to stem rot. The segregation pattern in the F₁ generation was good fit to a phenotypic ratio of 1 Susceptible : 2 Moderately resistant : 1 Resistant indicating that resistance to stem rot is governed by incomplete dominance. These F₁ findings were further confirmed by genetic analysis in the F₃ generation.

Introduction

Groundnut (*Arachis hypogaea* L.), an annual, self-pollinated legume crop with a chromosome number of $2n = 4x = 40$, belongs to the family *Fabaceae*. It is native to South America and is now cultivated widely across tropical and subtropical regions of the world, between latitudes 40° N and 40° S. Globally, groundnut is grown over an area of 37.3 million hectares, producing 55.9 million tonnes with an average productivity of 1,656 kg ha⁻¹ (FAOSTAT, 2024). India is one of the major producers of groundnut, with the crop occupying approximately 5.4 million hectares, yielding 11.30 million tones with an average productivity of 2097 kg ha⁻¹. In Andhra Pradesh, groundnut is cultivated on 0.346 million hectares, with a production of 0.360 million tonnes and productivity of 1041 kg ha⁻¹ (INDIASTAT, 2024-2025) which is significantly lower in comparison with productivity at national level. The production of groundnut is threatened by various biotic and abiotic constraints. Among biotic stresses, soil borne pathogens viz., *Aspergillus niger*, *Sclerotium rolfsii* and *Rhizoctonia bataticola* cause severe plant mortality resulting in poor plant stand and reduced yield of 25–40 per cent (Ghewande *et al.*, 2002). Of these, stem rot caused by *S. rolfsii* is particularly destructive, significantly affecting both plant health and yield. The disease, also known as white mold or southern blight, was first reported by Mc Clintock (1917) in Virginia. *Sclerotium rolfsii* is a necrotrophic, soil-borne fungal pathogen with a wide host range, infecting over 500 plant species, including groundnut. Management of soil-borne diseases like stem rot is challenging due to the limited efficacy of fungicides, which must penetrate the plant canopy to reach the soil profile. Persistence of the pathogen in soil and its wide host range often limit the effectiveness of chemical and cultural control of stem and pod rot. Therefore, breeding for genetic resistance is a sustainable and cost-effective strategy for managing stem rot disease in groundnut.

A comprehensive understanding of the genetic basis of resistance to *S. rolfsii* is essential for the development of effective breeding programs. Knowledge of inheritance of resistance helps in selection of appropriate breeding strategies, including crossing and selection schemes, and enable the transfer of resistance genes into high-yielding susceptible cultivars.

Materials and Methods

During the *Rabi* season of 2021–2022, experimental material was developed using a Line × Tester (L × T) mating design. Four stem rot resistant genotypes TCGS 1862, TCGS 2251, ICGR 161930 and NRCG CS 19 were used as testers, while five high-yielding susceptible varieties TCGS 1694, TCGS 2245, Dheeraj, Kadiri-6, and Narayani as lines. A total of 20 crosses were generated through Line x

Tester mating design. Out of these during *Rabi* season (2022–2023), inheritance was studied in five crosses, namely TCGS 1694 × TCGS 1862, TCGS 2245 × TCGS 1862, Dheeraj × TCGS 1862, Kadiri-6 × TCGS 1862 and Narayani × TCGS 1862. All five crosses had a common male parent, TCGS 1862, which resistant to stem rot. Screening of parents and F₁s was done under sick plot condition during *kharif*, 2022 at RARS, Tirupati. The parents (P₁ and P₂), F₁, F₂, and F₃ generations of the selected crosses were screened for stem rot resistance under sick plot conditions during the 2022–2024 period at RARS, Tirupati. Screening for stem rot resistance was done at 70 DAS (days after sowing) and at the time of harvesting. Artificial inoculation was carried out by incorporating *Sclerotium rolfsii* inoculum, multiplied on sorghum grains into the soil between rows followed by mulching with paddy straw to maintain favorable conditions for disease development. To further confirm the mode of inheritance, F₁ progenies were screened under artificially inoculated sick plot conditions during the *Kharif* season of 2023. In each cross, ten plants each from resistant/moderately resistant and susceptible categories were selected from F₁ generation and raised in plant-to-progeny rows in F₁ generation. In F₂ and F₃ generations individual plants were scored for stem rot disease as per the scale of Bera *et al.* (2014). The Chi-square (χ^2) test was employed to test the goodness of fit to Mendelian ratios.

Results and discussion

The total number of 106 F₂ plants of the cross TCGS 1694 × TCGS 1862, 100 F₂ plants of TCGS 2245 × TCGS 1862,106 F₂ plants of the cross Dheeraj × TCGS 1862, 114 F₂ plants of the cross Kadiri-6 × TCGS 1862 and 112 F₂ plants of Narayani × TCGS 1862 were screened for stem rot incidence by creating artificial epiphytic condition using same procedure employed for screening the parents and F₁s. The stem rot disease reaction was scored as per the rating scale given by Ashok *et al.*, (2004) (Table 1a). The stem rot incidence in parents and F₁s is furnished in Table 2.

Table.1(a) Stem rot disease incidence scale of Ashok et al. (2004)

Scale*	Disease reaction
0%	Immune
1–10%	Highly resistant
10 to 20%	Resistant
20 to 50%	Moderately resistant
> 50%	Highly susceptible

***Percent of infected plants per row**

Table.1(b) Stem rot disease incidence scale of Bera et al. (2014)

Disease reaction	Disease intensity	Rating scale
R: Resistant	< 10% drying of plant	1
MR: Moderately Resistant	10 to 25% drying of plant	2
MS: Moderately Susceptible	> 25% to 50% drying of plants	3
S: Susceptible	> 50% drying of plants	4

Table.2 Reaction of parents and F₁s to stem rot disease in groundnut

S.No	Parents / F ₁ s	Stem rot incidence (%)
1	TCGS 1694	23.75
2	TCGS 2245	30.25
3	Dheeraj	32.86
4	Kadiri-6	27.54
5	Narayani	28.01
6	TCGS 1862	3.72
7	TCGS 1694× TCGS 1862	15.81
8	TCGS 2245× TCGS 1862	15.86
9	Dheeraj× TCGS 1862	7.98
10	Kadiri-6× TCGS 1862	10.06
11	Narayani × TCGS 1862	13.24

The F₁ from all five crosses exhibited moderate resistance to stem rot, indicating partial dominance of resistance. Individual plants in the F₁ population were screened for stem rot resistance as per Bera *et al.*, (2014) (Table 1b) and categorized into resistant, moderately resistant and susceptible classes. The segregation data in the F₁ generation fitted a phenotypic ratio of 1 Susceptible : 2 Moderately Resistant : 1 Resistant, suggesting that resistance is incompletely dominant over susceptibility (Table 3). The resistant genotype is assigned the genotype symbol of 'RR', while susceptible genotype as 'rr'. The F₁ is represented as 'Rr' *i.e.*, moderately resistant. The genotypes assigned for parents and F₁s presented in Table 4.

Table.3 Segregation for stem rot resistance in groundnut (*Arachis hypogaea* L) in five F₂ populations

Crosses	F ₁ behaviour	F ₂ behaviour			Ratio	Probability	χ ² Value
		Susceptible	Moderately Resistant	Resistant			
TCGS 1694×TCGS 1862	Moderately Resistant	21	59	26	1:2:1	0.50 – 0.25	1.83
TCGS 2245 ×TCGS 1862	Moderately Resistant	25	49	26	1:2:1	0.99 – 0.95	0.06
Dheeraj× TCGS 1862	Moderately Resistant	19	61	26	1:2:1	0.50 – 0.25	3.34
Kadiri-6× TCGS 1862	Moderately Resistant	25	61	28	1:2:1	0.99 – 0.95	2.527
Narayani× TCGS 1862	Moderately Resistant	22	66	24	1:2:1	0.25 – 0.10	3.643

Table.4 The genotypes assigned for parents and F₁s

Parents/ F ₁ s	Genotype	Phenotype
TCGS 1694, TCGS 2245, Dheeraj, Kadiri-6 and Narayani	rr	Susceptible
TCGS 1862	RR	Resistant
TCGS 2245 × TCGS 1862/TCGS 2251/ ICGR 161930/ NRCG CS19	F ₁ Rr	Moderately resistant

To confirm the mode of inheritance, ten plants each from resistant/moderately resistant and susceptible categories in the F₁ generation were advanced and grown in plant-to-progeny rows in F₂ generation. In F₂ generation, progenies derived from resistant and susceptible F₁ plants bred true, while progenies derived from moderately resistant F₁ plants showed segregation fitting either a 2 Moderately Resistant : 1 Resistant or 1 Resistant : 2 Moderately Resistant : 1 Susceptible ratio (Table 5). These observations support the conclusion that the moderately resistant F₁ plants were heterozygous confirming the incomplete dominance of resistance over susceptibility.

Table:5 Segregation for stem rot resistance in groundnut (*Arachis hypogaea* L) in F₃ populations

Cross	F ₂ phenotype	F ₃ behaviour	Ratio
TCGS 1694 × TCGS 1862	Susceptible	5 S/HS	All bred true
	Resistant/moderately Resistant	1 HR	4(2MR: 1HR)
TCGS 2245 × TCGS 1862	Susceptible	5 S/HS	All bred true
	Resistant/moderately Resistant	-	5(2MR: 1HR)
Dheeraj × TCGS 1862	Susceptible	5 S/HS	All bred true
	Resistant/moderately Resistant	-	5(2MR: 1HR)
Kadiri-6 × TCGS 1862	Susceptible	4 S/HS	All bred true
	Resistant/moderately Resistant	1 HR	4(2MR: 1HR)
Narayani × TCGS 1862	Susceptible	5 S/HS	All bred true
	Resistant/moderately Resistant	-	5(2MR: 1R)

Comparative studies on the inheritance of stem rot resistance in groundnut are limited. Amarnath *et al.* (2022) reported a 3:1 (Resistant: Susceptible) ratio in crosses, Kadiri-6 × NRCG CS 19 and Narayani × J 11 indicating dominant gene action. In contrast, a 15:1 ratio was observed in the crosses ICGV 07262 × TCGS 1862 and ICGV 07262 × TCGS 2149, suggesting the involvement of duplicate dominant genes. Kusmadevi *et al.* (2015) recorded a 13:3 segregation ratio in four crosses, GPBD-4 × AGL-2389, TMV-2 × AGL-168, Dh-86 × AGL-289 and Dh-86 × AGL-63 indicating that stem rot resistance is governed by inhibitory gene interaction.

Stem rot resistance is a complex trait and governed by many genes and expression of resistance is altered by environment. In recent years, many studies attempted to discern the genetic basis of resistance in biparental mating populations. The first QTL linked to stem rot resistance was identified using F₂ population of the cross, TC 37A (Susceptible) x NRCG CS 85(resistant) with SSR markers by Dodia *et al.*(2016). Using the RIL population of the same cross, Dodia *et al.* (2019) identified seven major QTLs with phenotypic variance explained ranging from 5.5 to 8.5 per cent. Luo *et al.* (2020) using RIL population from NC 3033(resistant) and Tifrunner (susceptible) cross reported 33 additive QTLs through SNP and SSR markers and Cui *et al.*(2020) identified another two QTLs linked to stem rot resistance through QTL seq method.

These varying reports on the mode of inheritance may be attributed to differences in the genetic background of the parental materials and the complex nature of the trait. However, in the present study in F₁ populations of 150–200 plants per cross, a clear 1:2:1 segregation pattern was observed indicating the role of a single gene with incomplete dominance in inheritance of stem rot resistance.

There may be involvement of many genes contributing to resistance which could not have been detected at the phenotypic level under field conditions. The case of incomplete dominance could be due to overlapping effect of many minor genes which could not be discerned with naked eye. The ratios that are obtained when characters are governed by additive effects of many genes follow similar pattern. In the present study itself, biometrical analysis revealed additive nature of stem rot resistance *i.e.*, proportion of contribution of lines and testers was greater than line x tester interaction (Suvarna *et al.* 2024), indicating the scope for improvement of stem rot resistance through phenotypic selection.

Declarations

Author Contribution

Conceptualization of research (CS,RPV); Designing of the experiments (RPV,MRS); Contribution of experimental materials (KV,CKKR,YA); Execution of field/lab experiments and data collection (CS,RPV,KV); Analysis of data and interpretation (CS,RPV,KV,YA); Preparation of the manuscript (CS,RPV,KV).

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