

Original Research Article

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Genetic Model of Inheritance of Resistance to Late Leaf Spot in F₂ and F₃ Generation of Groundnut (*Arachis hypogaea* L.)

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ABSTRACT

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Late leaf spot caused by *Phaeoisariopsis personata* is the most important disease on groundnut worldwide. Although fungicide treatment is effective, it is uneconomical to use because of high cost, hazardous to environment and insensitivity build up in pathogen. The deployment of resistant cultivars is a better option to control LLS disease in groundnut the investigation was undertaken to determine the mode of genetic inheritance of LLS resistance in two F₂ and F₃ segregating populations of groundnut. F₂ and generation of two cross TG76× GPBD5 and TG76 x ICGV 86699 were sown at MARS, Dharwad in *summer* and *kharif* 2016 were resistant under natural as well as artificial epiphytotic screening conditions. The two populations segregated in 3S:1R ratio in F₂ and 1:2:1 in F₃ generation. Rust resistance. The data had good fit to mendelian inheritance pattern of single recessive gene governing LLS.

Introduction

Groundnut (*Arachis hypogaea* L.) is an important oilseed and food crop grown worldwide with a global production of 42.29 mt from 25.46 mha area. India has the largest groundnut-growing area of 5.50 mha with 6.30 mt production and 1,150 kg/ha productivity (FAO, 2017). It is regarded as “king of oilseed crops” on account of its diversified uses. It is an excellent source of plant protein (25-28%), oil (48-50%), calcium, iron and vitamin B complex like thiamine, riboflavin, niacin and vitamin A. The low productivity of the crop in India is

ascribed to many biotic and abiotic stresses in the cultivation of the crop. Among biotic stresses insects pests and diseases are major factors.

Among oilseed crops, groundnut is unique in consumption pattern that can be consumed directly as an item of food and also utilized in diverse ways. Groundnut seed contains about 26 per cent protein, 48 per cent oil and 3 per cent fiber. It also has high levels of calcium, thiamine and niacin and thus has all the potential to be used as a highly economical food supplement to fight malnutrition that occurs due to deficiencies of these nutrients in

the commonly consumed cereal grains like wheat and rice. Groundnut haulms are used as excellent fodder (Cook and Crosthwaite, 1994) and cake is used for animal feed (Savage and Keenan, 1994). Plant roots left behind after harvest add valuable nutrients to the soil, which is particularly important in the less developed countries where crop is mainly grown under low input condition.

The cultivated tetraploid groundnut ($2n = 4x = 40$) is a member of the genus *Arachis* and belongs to the family *Leguminosae*, subfamily *Fabaceae*, tribe *Aeschynomeneae*, subtribe *Stylosanthenae* (Krapovickas and Gregory, 1994). Based on the differences in the branching pattern and presence of reproductive node on the main stem, the species has been classified into two subspecies, *hypogaea* and *fastigiata* (Krapovickas and Rigoni, 1960). Further each subspecies has been divided into two botanical varieties viz. subsp. *hypogaea* into var. *hypogaea* (virginia) and var. *hirsuta* and subsp. *fastigiata* into var. *fastigiata* (valencia), var. *vulgaris* (spanish), var. *peruviana* and var. *aequatoriana* (Krapovickas and Gregory, 1994).

The cultivated groundnut (*Arachis hypogaea* L.) is an allotetraploid (AABB genome) of recent origin, with low genetic diversity. Groundnut is susceptible to a number of diseases that increases cost of production for chemical control and reduce yields for the farmer. For many of these diseases, good sources of resistance are lacking in cultivated germplasm due to its very narrow genetic base (Kochert *et al.*, 1991). Cultivated groundnut originated from a single allotetraploidization event from a hybrid between two wild diploid species, most probably *A. duranensis* and *A. ipaënsis* (Kochert *et al.*, 1996; Seijo *et al.*, 2004, 2007). The resultant allotetraploid plant would have had hybrid vigour but

reproductively isolated from wild relatives. Therefore, all land races of groundnut are probably derived from one or a few plants and consequently low diversity for traits of agricultural interest exists, resulting in narrow genetic base of the cultivars, constraining progress of the crop by conventional and molecular breeding. Paradoxically, the wild diploid *Arachis* species are genetically very diverse and have been selected during evolution by a range of abiotic and biotic stresses, providing a rich source of variation in agronomically important traits; but sterility barriers have hampered the use of wild species in breeding programmes.

Most commonly grown Spanish bunch type varieties are highly susceptible to foliar fungal diseases like rust (*Puccinia arachidis* Speg.), early leaf spot (*Cercospora arachidicola* Hori) and late leaf spot (LLS) (*Phaeoisariopsis personata* [(Berk. and Curt) Deighton]). In India, LLS and rust generally occur together and cause not only a yield loss up to 70 per cent, but also bring down the quality of the feed and fodder. Though several effective fungicides are available to control the foliar diseases, development of resistant cultivars is considered the best strategy to surmount additional cost of production and hazardous effect of fungicides on the soil and environment.

Breeding for resistant varieties is a preferred means of managing the foliar diseases over chemical control considering the additional cost and biological safety. The success of breeding for foliar disease resistance is influenced by the availability and identification of resistance sources and combining resistance with high productivity and desirable pod features. Identification of resistant lines from the different sources of gene pools is difficult through conventional screening technique because of their co-occurrence and defoliating nature of late leaf

spot. High levels of resistance to these diseases has been transferred from wild species to cultigen (Moss *et al.*, 1997; Nigam *et al.*, 1992; Reddy *et al.*, 1992; Reddy *et al.*, 1996; Stalker and Beute 1993) but the conventional breeding has failed in combining resistance with having good agronomic traits in cultivars. Valencia landraces and wild species of groundnut possess valuable reservoir of genes/high level of resistance to foliar diseases, but the resistance is generally linked to low productivity, late maturity, poor adaptability and undesirable pod features (Singh *et al.*, 1997).

The complex nature of inheritance (Bromfield and Bailey, 1972; Tiwari *et al.*, 1984; Paramasivam *et al.*, 1990) with recessive genes conferring resistance has hindered the progress of disease resistance breeding and interference among these diseases make phenotypic selection less effective.

Thus, it is necessary to ascertain the pattern of inheritance of this disease for formulation of breeding strategy and effective transfer of resistance into cultivated varieties. Genetic studies on LLS and rust resistance suggest that resistance is naturally complex and polygenic and probably governed by several recessive genes (Green and Wynne, 1986; Motagi, 2001; Dwivedi *et al.*, 2002). Jogloy *et al.*, (1987) conducted an experiment to identify the inheritance of late leafspot resistance and agronomic traits in groundnut based on 20 breeding populations in the F₂ generations. Study on the inheritance of late leafspot on groundnut was also performed by earlier workers (Montagi *et al.*, 2000). The present study was conducted to understand the mode of inheritance of resistance to LLS in F₂ and F₃ generation of two crosses.

Materials and Methods

The experimental material comprising of two segregating populations viz., TG76× GPBD5 and TG76 x ICGV 86699 were evaluated in

unreplicated design during Kharif, 2016 at MARS, Dharwad in *summer* 2016. The Spanish bunch groundnut variety GPBD5 and ICGV 86699 is a Virginia Bunch high-yielding interspecific derivative and has multiple resistance/tolerance to diseases like rust, early and late leaf spots that are resistant parents to rust and LLS were used as pollen parent in hybridization with TG76, a bold seeded susceptible cultivar having good agronomic background as female parent.

The F₂ and F₃ progenies of two were sown. Disease severity for LLS was estimated on single plant basis and scoring was done according to 1-9 point field scale (Subramanyam *et al.*, 1982). Plants with lower disease incidence with 1 to 3 LLS score were taken as resistant and 4 to 9 as susceptible. The data were put through chi-square test to determine the goodness of fit of observed ratios (Howell, 2011). It has been reported that the best strategy for obtaining LLS resistant genotypes is selection of the disease score trait in initial inbreeding generations, followed by selection in the following generations with higher inbreeding levels in other crosses (Wambi, 2014).

Results and Discussion

To our knowledge there have been few reports on inheritance of host plant resistance to LLS disease. However previous studies on groundnut using both qualitative and quantitative genetic models suggested that there are several modes of inheritance of LLS disease resistance. The basic knowledge of inheritance and number of genes governing the traits are essential for efficient selection and breeding. Thus the present study was undertaken to know the mode of inheritance and number of genes involved in LLS resistance F₂ population for resistance to LLS and their confirmation in F₃.

Table.1 Inheritance of host plant resistance to LLS disease in F₂ population in two crosses

Cross	Screening condition	Total plants screened	Observed frequency		Ratio	Calculated Chi-square value	Probability
			Susceptible plants	Resistant plants			
TG76 × GPBD5	Field	240	183	57	3:1	0.621	0.900-0.750
TG76 × ICGV86699	Field	300	224	77	3:1	0.057	0.500-0.750

Table.2 Inheritance of host plant resistance to rust disease in F₂ population in two crosses

Cross	Screening condition	Total plants screened	Observed frequency		Ratio	Calculated Chi-square value	Probability
			Susceptible plants	Resistant plants			
TG76 × GPBD5	Field	240	176	64	3:1	1.06	0.900-0.750
TG76 × ICGV86699	Field	300	215	85	3:1	0.057	0.500-0.250

Table.3 Confirmation of inheritance pattern in F₃ generation for resistance to LLS in two crosses

Cross combination		Progenies bred true for susceptible reaction	Progenies segregated for susceptible and resistant reaction	Progenies bred true for Resistant plants	Ratio	Calculated Chi-square value	Probability
TG76 × GPBD5	Observed	60	120	51	1:2:1	1.045	0.900-0.750
	Expected	57.75	115.5	57.75	1:2:1		
TG76 × ICGV86699	Observed	80	146	68	1:2:1	0.966	0.500-0.250
	Expected	73.5	147	73.5	1:2:1		

Table.4 Confirmation of inheritance pattern in F₃ generation for resistance to rust in two crosses

Cross combination		Progenies bred true for susceptible reaction	Progenies segregated for susceptible and resistant reaction	Progenies bred true for Resistant plants	Ratio	Calculated Chi-square value	Probability
TG76 × GPBD5	Observed	52	118	61	1:2:1	0.804	0.900-0.750
	Expected	57.75	115.5	57.75	1:2:1		
TG76 × ICGV86699	Observed	66	150	79	1:2:1	0.528	0.500-0.250
	Expected	73.5	147	73.5	1:2:1		

In the present study, to know the inheritance pattern of LLS resistance, systematic crosses were made and their F₁, F₂ and F₃ generations along with parents were screened under both natural and artificial condition. There was high incidence of LLS disease observed on TG76 (8 on 1-9 scale) compared to the resistant parent GPBD-5 (4 on 1-9 scale) and ICGV 86699 (3 on 1-9 scale). F₁ hybrids involving the susceptible and resistant parents were susceptible to both indicating recessive nature of gene conditioning resistance to LLS.

In F₂ generation, out of the total 240 F₂ segregants, 183 plants were susceptible and 57 plants were resistant in TG76× GPBD5 cross combination, whereas 224 susceptible and 77 resistant plants were observed in TG76 x ICGV 86699 cross. The data had good fit to expected 3:1 (susceptible: resistant) ratio with a single recessive gene governing resistant reaction against LLS (Table 1).

In F₃ 1/3 progenies bred true for susceptibility, 2/3 segregated for susceptible and resistant reaction and 1/3 bred true for resistant reaction as expected in Mendelian inheritance pattern for single recessive gene governing LLS resistance in both the populations, respectively. The proposed genotypic constitution of the F₂ segregation ratios are presented in the Table 2.

From these results it is clear that resistance to LLS is governed by single recessive genes

wherein susceptibility being dominant to resistance. Resistance to LLS in cultivated groundnut was reported to be recessive and appeared to be governed by only few genes. One gene (Paramasivam *et al.*, 1990) and two gene models (Bromfield and Bailey, 1992; Tiwari *et al.*, 1984) have been proposed, but there were no definite pattern of segregation in many crosses (Reddy *et al.*, 1987). In the cross involving in inter-specific derivatives as sources of LLS resistance, it was reported to be governed by partially dominant genes (Singh *et al.*, 1984).

Bromfield and Bailey (1972) reported digenic mode of inheritance with recessive gene conferring resistance from their study on F₂ population of spontaneous cross between rust resistant female PI 298115 and an unknown male parent. In another experiment, Kishore (1981) proposed trigenic mode of inheritance (63 susceptible: 1 resistance) in study involving three susceptible and three recessive parents (Table 3 and 4).

These varying reports on mode of inheritance of rust resistance could be due to the diverse genetic resources and varying genetic backgrounds of the material used for inheritance studies.

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