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A GENETIC MODEL OF INHERITANCE OF RESISTANCE TO LATE LEAFSPOT IN F_2 GENERATION OF GROUNDNUT (*ARACHIS HYPOGAEA* L.)

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ABSTRACT

The study was based on F_2 generation of 15 crosses for inheritance of resistance to late leafspot (LLS) disease in groundnut. Resistance to LLS was found to be governed by duplicate recessive genes wherein susceptibility being dominant to resistance. The F_2 plants were susceptible to LLS in all the 15 crosses showing that susceptibility is dominant over resistance in these crosses. The analysis of the inheritance of late leafspot had a good fit to phenotype ratio of 15 (susceptible): 1 (resistance) plants in F_2 segregation in all the crosses. The study revealed that resistance to LLS disease is governed by two to three duplicate recessive genes.

INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is one of the main oilseed and food legume crop in India. 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. The treatments of metaflumizone (16.71%) and lufeneuron (17.51%) proved inferior in checking the H. armigera infestation on groundnut crop (Gadhiya *et al.,* 2014). Late leafspot can cause yield losses up to 80 per cent (Grichar *et al*., 1998). Spraying of Carbendazim + Mancozeb (0.25%) followed by its lower dosage (0.2%) and hexaconazole (0.1%) was found significantly superior in the management of late leafspot and rust of groundnut (Sunkad, 2012**)**. Fungicide application is an effective method to control the disease, but the production cost would be increased by 10% (Coffelt and Porter, 1986). Sources of resistance against them have been identified in some genotypes of cultivated groundnuts. Transfer of resistance in cultivated varieties is thus the cheapest method of disease control as there won't be any need of extra inputs to the farmer. Thus, it is necessary to ascertain the pattern of inheritance of this disease for 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 F_2 generations. Study on the inheritance of late leafspot on groundnut was also performed by earlier workers (Montagi *et al*., 2000. Nevill, 1980). The present study was conducted to understand the mode of inheritance of resistance to LLS in F_2 generation of 15 crosses.

MATERIALS AND METHODS

The experimental material comprising of 15 F_2 crossed populations *viz.*, TPT-4 × GPBD-4, TPT-4 × ICG-13919, TPT-4 x ICG-15234, TCGS-888 × GPBD-4, TCGS-888 × ICG-13919, TCGS-888 × ICG-15234, TCGS-913 × GPBD-4, TCGS-913 × ICG-13919, TCGS-913 × ICG-15234, ICGV91114 × GPBD-4, ICGV91114 × ICG-13919, ICGV91114 × ICG-15234, TG-47 × GPBD-4, TG-47 × ICG-13919 and TG-47 x ICG-15234 were studied in unreplicated design during *Kharif*, 2012 at S.V. Agricultural College Farm, Tirupati. Genotypes TPT-4, TCGS-888, TCGS-913, ICGV-91114 and TG-47 are good performing genotypes based on yield but are susceptible to LLS disease. While, genotypes GPBD-4, ICG-13919 and ICG-15234 are poor performer but have considerable resistance to LLS disease. F_2 progenies of 15 crosses with a population size of 90 plants each 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 (Fig 1). 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

The F_2 plants were susceptible to LLS in all the crosses showing that susceptibility is dominant over resistance in these crosses. The F_2 segregation had a good fit to a phenotypic ratio of 15 susceptible : 1 resistance plants in all the crosses. The proposed genotypic constitution of the F_2 segregation ratios are presented in the Table 1.

From these results it is clear that resistance to LLS is governed by duplicate recessive genes wherein susceptibility being dominant to resistance. Five pairs of duplicate recessive genes appear to be involved in LLS resistance. Resistance to LLS is reported to be controlled by a combination of both, nuclear and maternal gene effects. And among nuclear gene effects, additive effects regulate most of the variation (Pasupuleti *et al*., 2013).

The female parents *viz*., TPT-4, TCGS-888, TCGS-913, ICGV91114 and TG-47 are proposed to possess all genes in dominant condition Lr_1Lr_1 Lr_2Lr_2 Lr_3Lr_3 Lr_4Lr_4 Lr_5Lr_5, while the male parents GPBD-4, ICG-13919 and ICG-15234 have one pair of gene in recessive condition lr_1lr_1 lr_2lr_2 lr_3lr_3 lr_4lr_4 lr_5lr_5. These findings were in accordance with the earlier report (Vasanthi *et al*., 1997), wherein they proposed that resistance is controlled by five pairs of genes in female parent, three pairs of genes were involved to resistance in late leafspot in male parent. Genes at three of four loci controlled the leaf spot resistance based on studies in F_2 of a cross between Robust 33-1 and Krapovickas-16 (Nevill, 1980). Later on a genetic system was proposed involving five loci from his studies on

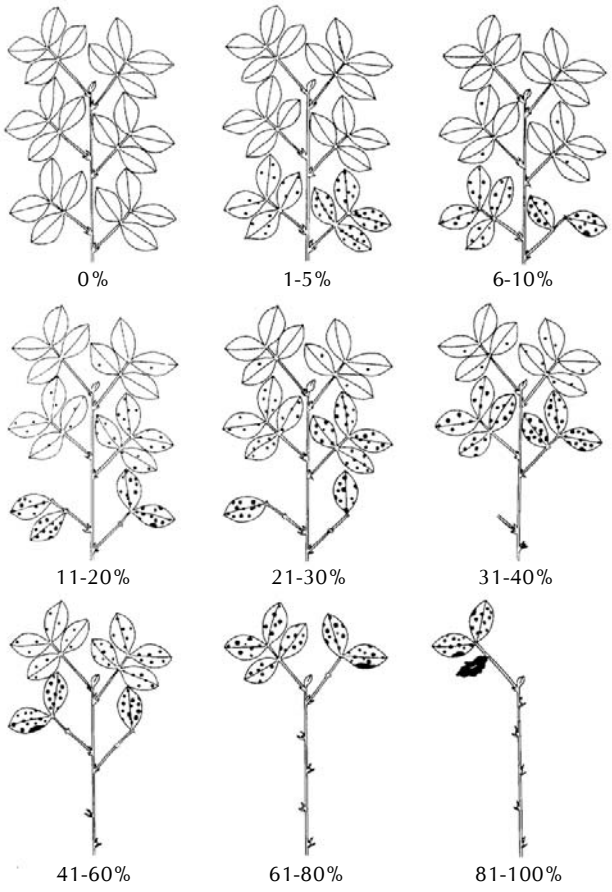

Figure 1: The modified 9-point scale for field evaluation of late leafspot

five F_2 populations from crosses between three resistant lines in which the susceptible parents were used as females (Nevill, 1982). Resistant material is proposed to be homozygous recessive at loci 1, 2, 3 and 4 while susceptibility in Robust 33-1 is homozygous recessive at loci 3, 4 and 5. It was also concluded that susceptible TMV2 has no resistance genes. It

Table 1: Inheritance of resistance to late leafspot in F_2 population of 15 crosses of groundnut.

Sl. no.	F_2 population	Observed value		Expected ratios	Expected value		Chi-square		Total
		NS	NR		NS	NR	NS	NR	
1.	TPT-4 ´GPBD-4	80	10	15 : 1	84.4	5.63	0.23	3.39	3.62
2.	TPT-4 ´ICG-13919	86	4	15 : 1	84.4	5.63	0.03	0.47	0.50
3.	TPT-4 ´ICG-15234	81	9	15 : 1	84.4	5.63	0.14	2.02	2.16
4.	TCGS-888´ GPBD-4	82	8	15 : 1	84.4	5.63	0.07	1.00	1.07
5.	TCGS-888 ´ ICG-13919	85	5	15 : 1	84.4	5.63	0.00	0.07	0.07
6.	TCGS-888 ´ ICG-15234	81	9	15 : 1	84.4	5.63	0.14	2.02	2.16
7.	TCGS-913 ´ GPBD-4	80	10	15 : 1	84.4	5.63	0.23	3.39	3.62
8.	TCGS-913 ´ ICG-13919	88	2	15 : 1	84.4	5.63	0.15	2.34	2.49
9.	TCGS-913 ´ ICG-15234	84	6	15 : 1	84.4	5.63	0.00	0.02	0.02
10.	ICGV-91114 ´ GPBD-4	80	10	15 : 1	84.4	5.63	0.23	3.39	3.62
11.	ICGV-91114 ´ ICG-1391986		4	15 : 1	84.4	5.63	0.03	0.47	0.50
12.	ICGV-91114 ´ ICG-15234 85		5	15 : 1	84.4	5.63	0.00	0.07	0.07
13.	TG47 ´ GPBD-4	80	10	15 : 1	84.4	5.63	0.23	3.39	3.62
14.	TG47 ´ ICG-13919	81	9	15 : 1	84.4	5.63	0.14	2.02	2.16
15.	TG47 ´ ICG-15234	82	8	15 : 1	84.4	5.63	0.07	1.00	1.07

Chi square table value for 1 df = 3.84 at 5 % level. , NS = number of susceptible plants: NR = Number of resistant plant

is to conclude that the resistance in the three testers is under the influence of duplicate recessive genes needs to be further confirmed by test cross procedure for further utilization in resistance breeding programme of development LLS resistant genotypes. The F_2 plants were susceptible to LLS in all the crosses showing that susceptibility is dominant over resistance in these crosses. The F_1 generation of all the crosses also showed susceptibility reaction. It was earlier reported that the F_1 generation of all the crosses also showed susceptible reaction (Srivalli, 2012). Resistance to LLS disease is governed by two to three duplicate recessive genes.

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