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Short Communication

Inheritance of rust resistance in cultivated groundnut (*Arachis hypogaea* L.)

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Abstract

The present investigation was carried out to study the mode of inheritance of rust (*Puccinia arachidis* Speg.) resistance in groundnut (*Arachis hypogaea* L.). Crosses were made between a susceptible (GPBD-5) and three resistant genotypes (GPBD-4,ICGV86699 and ICGV99005). Susceptibility to rust of F_1's in all the three crosses indicated that susceptibility was dominant over resistance. Resistant F_2 plants were further crossed to GPBD-5. The second cycle F_2 populations segregated into susceptible and resistant categories. The observed frequency of plants in each F_2 fitted well into expected ratio of 1 resistant and 3 susceptible with non-significant chi-square values at 5% level indicating that rust resistance in groundnut is determined by a single recessive gene. The F_2 results were confirmed by genetic analysis in F_3 generation.

Key words: Groundnut, rust resistance, inheritance, second cycle F_2

The cultivated groundnut (*Arachis hypogaea* L.) is an important legume grown for the extraction of edible oil and used as a nutritional ingredient of human and animal foods. It is one of the main sources of protein in Africa and Asia [1]. 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 niacine 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 yield is constrained due to infestation by foliar diseases in most of the tropical countries of the world. Rust caused by *Puccinia arachidis* Speg. is an economically important foliar diseases in groundnut. Rust, along with late leaf spot (LLS), cause yield losses higher than 50 to 70 per cent if susceptible cultivars are not protected by chemicals [2]. Besides adversely affecting the pod yield and its quality, they affect the yield and quality of haulm. Though several effective fungicides are available to control the rust disease, 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.

Analysis of the genetic basis of the resistance to rust pathogen would help to know the inheritance pattern to plan and implement appropriate breeding strategy for its incorporation into the cultivars. Resistance to rust in *Arachis hypogaea* L. was reported to be conferred either by a few recessive genes [3] or predominantly controlled by additive, dominance and additive x additive and additive x dominance genetic effects [4] and also digenic mode of inheritance [5], Whereas, Motagi [6] reported that resistance to rust was conferred by duplicate complementary genes. Singh *et al.* [7] observed that rust resistance in diploid species was partially dominant as compared to the recessive nature in cultivated species *Arachis*

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hypogaea L. In order to understand clearly the exact mode of inheritance of resistance to rust disease, three different sources of resistances were investigated.

The experimental material consisted of groundnut genotypes, GPBD-5 (8 on 1-9 scale) used as female parent and three varieties *viz.,* GPBD-4 (4 on 1-9 scale), ICGV 86699 and ICGV 99005 (both recoded 3 on 1-9 scale) were used as pollen parent in crossing programme. GPBD-5 (TG-49 x GPBD-4), a Spanish bunch type high yielding and a bold seeded cultivar but highly susceptible to rust disease. Whereas, GPBD-4 (KRG-1 x ICGV 86855) an improved Spanish bunch groundnut variety a second cycle product of interspecific hybridization with desirable combination of early maturity, high yield, high pod growth rate, desirable pod and kernel features, high oil content and resistance to rust and late leaf spots. Both GPBD-4 and GPBD-5 were developed at University of Agricultural Sciences, Dharwad [8].

ICGV 86699(*Arachis batizocoi* x *A. duranensis)* x *A. hypogaea* (cv. NC 2) and ICGV 99005(TMV2 x (*A. hypogaea*) x (*Arachis batizocoi* x *A. duranensis*) are Virginia Bunch high-yielding interspecific derivatives with multiple resistance/tolerance to diseases like rust, and late leaf spots.

The crosses were made during *kharif* 2009 at Main Agricultural Research Station, Dharwad. The confirmed F_1 hybrids from each cross were harvested to raise F_2 during summer 2010. Rust reactions were recorded on 0-9 scale [9] in 80 F_2 plants from GPBD-5 x GPBD-4; 100 F_2 plants from GPBD-5 x ICGV 86699 and 60 F_2 plants from GPBD-5 x ICGV 99005 crosses. Identified rust resistant F_2 plants from all three crosses were second cycle crossed to recurrent parent, GPBD-5 to produce F_2 generation during same season. The F_1s thus obtained were selfed to produce second cycle F_2 populations. Seeds of identified rust resistant F_2 plants and second cycle F_2 populations from the three crosses were sown during *kharif* 2010. The two parents of respective cross and widely grown cultivar TMV_2 (9 on 1-9 scale), highly susceptible to rust disease were included for evaluation. All the necessary agronomic practices except plant protection against rust disease were followed to raise the crop successfully.

Evaluation of rust resistance

Artificial disease epiphytotic conditions were created in experiments for the rust disease using "Infector row technique" with TMV_2 (infector) planted at every 10^{th} row as well as on border around the field to maintain the effective inoculum load as suggested [10]. In order to encourage disease pressure, artificial inoculation with spraying of spore suspension was also done from 40 days after sowing. Rust urediniospores were isolated by soaking and rubbing of infected leaves in water for 30 minutes The filtered inoculum contained 20,000 urediniospore per ml suspension mixed with tween 8 (0.2 ml per 1.2 litres of water) as mild surfactant and atomized on the plants using Knapsack sprayer in the evening and high humid condition was created by frequent water spraying for three days following inoculation. Besides of this the infected leaf debris collected from the previous season harvests were spread through out the experimental area to serve as additional inoculum.

Statistical analysis was done using Chi-square for goodness of fit and also to confirmation the genetic hypothesis for segregation in F_2, second cycle F_2 and F_3 generations for rust resistance. The significance of chi-square value was tested against table value with (n-1) degrees of freedom, where n is the total number of segregating classes [11].

Inheritance of rust resistance

The total number of 80 F_2 plants of the cross GPBD-5 x GPBD-4 and 100 F_2 plants of GPBD-5 x ICGV 86699 and 60 F_2 plants of GPBD-5 x ICGV 99005 were screened for rust reaction by creating artificial epiphytic condition using same procedure as that for the parental and F_1s screening in Summer 2009-10. Rust reaction was recorded on a 1-9 point scale as suggested Subbarao *et al.* [11].

All the F1 hybrids were susceptible to rust indicating that resistance to rust in recestival in nature. Out of the total 80 F_2 plants GPBD-5 x GPBD-4 cross, 61 were be susceptible and 19 resistant to rust, the proportion of which was closer to the expected frequency of plants with simple monogenic recessive inheritance with 1:3 ratio for susceptible and resistant reaction. The calculated χ^2 value (0.066) was not significant indicating its monogenic recessive mode of inheritance. Similarly in GPBD-5 x ICGV 86699 cross, out of 100 F_2 segregants, 78 were found to be susceptible and 22 resistant and from another cross GPBD-5 x ICGV 99005, 44 were found to be susceptible and 16 plants were resistant to rust disease thus fitting well for monogenic recessive mode of inheritance with non-significant χ^2 (0.48 and 0.08 respectively) value (Table 1).

The data from BC_1F_2 populations [F_2(GPBD-5 x GPBD-4) x GPBD-5], [F_2(GPBD-5 x ICGV 86699) x GPBD-5] and [F_2(GPBD-5 x ICGV 99005) x GPBD-5)] grown during summer 2011 also, indicated that resistance to rust is governed by a single recessive gene (Table 1).

Phenotyping of the F_3 populations for reaction to rust

To confirm the mode of inheritance, all F_3 families of the cross GPBD-5 x CPBD-4, GPBD-5 x ICGV 86699 and GPBD-5 x ICGV 99005 were screened under natural as well as artificial conditions using same procedure as that for the parental screening in *kharif* 2010. Each F_3 family was classified as resistant (homozygous), susceptible (homozygous), and segregating (heterozygous).

In F_3, 20 families breeding true with susceptible reaction, 40 segregating into susceptible and resistant and 17 families bred true for resistance in GPBD-5 x GPBD-4. The number of families screened fit well into theoretically expected ratio of 1:2:1 (Table 2). F_3 breeding behaviour in GPBD-5 x ICGV 86699 indicated that 23 families bred true for susceptible reaction, 55 segregated in (3:1) resistant susceptible plants and 20 families bred true for resistant reaction. Similarly in the cross GPBD-5 x ICGV 99005, 16 families bred true for susceptible reaction, 32 families segregated in 3:1 susceptible: resistant and 13 progenies bred true for resistance confirming goodness of fit with 1:2:1 ratio for single recessive gene governing rust resistance (Table 2). The present results have demonstrated that the resistance to rust is determined by a single recessive gene.

To our knowledge there have been a few reports on inheritance of host plant resistance to rust disease in groundnut. Previous studies considering both qualitative and quantitative genetic models suggested several varying modes of inheritance of rust resistance.

Resistance to rust in cultivated groundnut has been reported to be recessive and also governed by a few genes. One gene [3, 12] and two gene models [13] have been proposed, but there were no definite pattern of segregation in many crosses [14]. Vasanthi and Reddy [15] reported involvement of 2-3 genes acting in duplicate complementary manner for rust resistance.

In another experiment, rust resistance was reported to be governed by 1, 2 or 3 recessive genes as evidenced from the segregation ratios reported by John *et al.,* [16] depending on the genetic constitution of the parents used in the crosses. Kishore [17] proposed trigenic mode of inheritance in a study involving three susceptible and three resistant parents.

These varying reports on mode of inheritance of

Table 1. Segregation for rust resistance in F_2 and F_2BC_1 generations of different crosses in groundnut

Crosses	Generations	Number of plants		Expected ratio	χ^2	P value
		Resistant	Susceptible			
GPBD-5 x GPBD-4	F_2	19	61	3:1	0.66	0.90-0.75
GPBD-5 x ICGV 86699	F_2	22	78	3:1	0.48	0.50-0.25
GPBD-5 x ICGV 99005	F_2	16	44	3:1	0.08	0.90-0.75
F_2(GPBD-5 x GPBD-4) x GPBD-5	Second cycle F_2	47	145	3:1	0.02	0.90-0.75
F_2(GPBD-5 x ICGV 86699) x GPBD-5	Second cycle F_2	30	109	3:1	0.74	0.50-0.25
F_2(GPBD-5 x ICGV 99005) x GPBD-5	Second cycle F_2	44	152	3:1	0.68	0.50-0.25

Table 2. Segregation in F_3 families derived from three different crosses

Crosses	Number of families			Total	Segregation ratio	χ^2	P value
	Resistant	Segregation	Susceptible				
GPBD-5 × GPBD-4	17	40	20	79	1:2:1	0.40	0.90-0.75
GPBD-5 × ICGV 86699	20	55	23	98	1:2:1	1.65	0.50-0.25
GPBD-5 × ICGV 99005	13	32	16	59	1:2:1	0.53	0.90-0.75

rust resistance could be due to the diverse genetic resources and varying genetic backgrounds of the material used for inheritance studies. The present study indicated monogenic recessive mode of inheritance for rust resistance in groundnut and the parent used in the present study differed for this single gene controlling resistance. It can be suggested that simple selection in direct and backcross advanced generations (F_2 onwards) would help the breeders to transfer rust resistance from the genetic sources identified for genetic improvement in respect of rust resistance froundnut.

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