

Genetic Variability Analysis in F_3 Populations of Groundnut (*Arachis hypogaea* L.)

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Abstract

Nine crosses involving foliar diseases *viz.*, late leaf spot and rust susceptible (as female) and resistant (as male) parents in F_3 generation were studied for mean performance and variability parameters. Susceptible female parents *viz.*, CO 7, ICGV 00350, TMV 2, TMV Gn 13, VRI 2 and resistant male parents *viz.*, COG 0437, GPBD 4, VRI Gn 6 were involved in these crosses. Among the crosses, the cross VRI 2 \times GPBD 4 recorded higher mean performance for yield characters *viz.*, pod yield per plant (g) and kernel yield per plant (g), and lower mean performance for disease score *viz.*, late leaf spot and rust. It also recorded high PCV and GCV values coupled with high heritability and high genetic advance as per cent of the mean for all the traits studied. Hence based on low performance, variability, heritability and genetic advance (as a per cent of mean) for pod yield, kernel yield and foliar disease resistance, the cross VRI 2 \times GPBD 4 is adjudged as superior. Considering the progeny wise performance, the progeny #1 and #2 of the cross VRI 2 \times GPBD 4 could be selected due to the superior mean performance for yield characters along with disease resistance. These progenies recorded high or moderate coefficient of variation for the entire characters under study. Hence, these progenies need to be advanced further till the attainment of homogeneity to obtain high yield in conjugation with resistance to foliar diseases.

Highlights:

- Groundnut is an important oilseed legume crop grown primarily for high-quality edible oil and easily digestible protein in its seeds.
- Contrain in groundnut yield is due to two foliar fungal diseases *viz.*, late leaf spot and rust that cause considerable loss in most areas of the world.
- The basic key to bring about the genetic upgrading of a crop is to utilize the available genetic variability.
- Nine crosses were made to develop foliar fungal disease resistant lines with acceptable pod and kernel yield in groundnut.
- Based on low performance and variability parameters for pod yield, kernel yield and foliar disease resistance, the cross VRI 2 \times GPBD 4 was adjudged as superior.
- Progeny #1 and #2 of the cross VRI 2 \times GPBD 4 could be selected due to the superior mean for yield characters along with disease resistance.

Keywords: Groundnut, *per se*, genetic variability, pod yield, kernel yield, late leaf spot, rust

Groundnut (*Arachis hypogaea* L.), the king of oilseeds is an important legume grown and consumed predominantly in arid and semi-arid regions of the world. It is a vital food and cash crop for resource-poor farmers in Asia and Africa which offers a rich source of oil, protein, minerals (Ca, Mg, P and K) and vitamins (E, K and B₁). In India, it occupies an area of 47.66 lakh ha with a production of 47.49 lakh tonnes, which accounts

for a productivity of 996 kg/ha (Anonymous, 2014). Even though India ranks first in the cultivated area, its production and productivity are very low due to the major constraints of abiotic and biotic stresses. The low productivity of the crop is ascribed mainly due to two major foliar diseases namely late leaf spot (*Phaeoisariopsis personata*) and rust (*Puccinia arachidis*). Late leaf spot (LLS) and rust are the two most



widely distributed and economically important foliar diseases of groundnut causing severe damage to the crop (Mc Donald *et al.*, 1985 and Kokalis-Burelle *et al.*, 1997). They are commonly present wherever groundnut is grown but their incidence and severity vary between localities and seasons. Each disease alone is capable of causing substantial yield loss, but when they occur together losses are further increased to 50-70%. The undesirable association between resistance, pod and seed characters slows down the progress in groundnut breeding. Mean and variability are the important factors for selection; mean serves as a basis for eliminating undesirable crosses and variability helps to choose a potential cross in the segregating population. Selection for the improvement of quantitative characters can be effective only when the segregating generations possess the potential variability. The probability of obtaining superior lines can be worked out in early generation provided estimates of first and second degree of statistics of genetic variation are available (Jinks and Pooni, 1976). Such information will be of immense use to plant breeders for differentiating crosses (Snape, 1982). In the present investigation, mean and variability of F_3 generation for nine crosses in groundnut are estimated and presented.

Materials and Methods

Study area

The experiment was conducted at Oilseeds Farm, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, during *Rabi* 2013-14.

Experimental material

Crosses were made to develop a foliar disease resistant groundnut lines with acceptable pod and kernel yield using eight groundnut genotypes. Among the eight genotypes, five are susceptible *viz.*, CO 7, ICGV 00350, TMV 2, TMV Gn 13, VRI 2 and three are resistant *viz.*, COG 0437, GPBD 4, VRI Gn 6 to foliar fungal diseases. Nine crosses *viz.*, CO 7 \times VRI Gn 6, ICGV 00350 \times COG 0437, TMV 2 \times GPBD 4, TMV 2 \times VRI Gn 6, TMV Gn 13 \times GPBD 4, TMV Gn 13 \times VRI Gn 6, VRI 2 \times COG 0437, VRI 2 \times GPBD 4, VRI 2 \times VRI Gn 6 were made and utilised for the present study. The selection was done in F_2 generation for pod yield, kernel yield and foliar disease resistance. All the parents and F_3 progenies were evaluated in the non-replicated trial. Recommended cultural practices were followed throughout the crop growing period. The spacing adopted was 30 \times 10 cm.

Observations recorded

Observations were recorded and analyzed in terms of mean and variability parameters on four characters *viz.*, pod yield per plant (g), kernel yield per plant (g), late leaf spot (LLS) and rust diseases. Nine point disease scale suggested by Subrahmanyam *et al.* (1995) was used to screen the lines for sources of resistance to late leaf spot and rust.

Statistical analysis

Standard statistical procedures were adopted for calculating the mean, range and various genetic parameters like phenotypic coefficient of variation (PCV), the genotypic coefficient of variation (GCV), heritability (h^2) in a broad sense and genetic advance as percent of mean (GAM). The range of coefficient of variation (CV) was categorized as per Sivasubramanian and Madhavamenon (1973): below 10% - Low coefficient of variation; 10-20% - Medium coefficient of variation; above 20% - High coefficient of variation. As suggested by Robinson *et al.* (1949), the heritability range was classified as: less than 30% - Low heritability; 30%-60% - Moderate heritability; more than 60% - High heritability. Similarly, the range of genetic advance as per cent of mean (GAM) was grouped as: less than 10% - Low GAM; 10%-20% - Medium GAM; more than 20% - High GAM (Johnson *et al.*, 1955). The significance for mean values was arrived by the critical difference (CD), standard error difference (SE_d) between F_3 progenies and check variety CO 7 as follows, $SE_d = (SE_1^2 + SE_2^2)^{1/2}$; SE_1 = SE of F_3 progeny number 1; SE_2 = SE of CO 7 and $CD = SE_d \times t_{at 5\%}$.

Results and Discussion

Genetic improvement of any crop depends on the magnitude of genetic variability and the extent of heritability. In self-pollinated crop, hybridization stands as one of the methodology by which favorable genes available in different genotypes could be combined into a genotype through genetic recombination. The development of genetic variability with hybridization and selection supplements the natural variability for the crop improvement. Also, it also helps in analyzing and understanding gene action controlling these economic traits. Information on nature and magnitude of variability present in the population due to genetic and non-genetic cause is an essential pre-requisite for a systemic breeding programme.

In the present study, the phenotypic and genotypic coefficient of variation exhibited wide range for all characters. The results on mean and variability parameters such as phenotypic coefficient of variation

**Table 1:** Estimates of variability parameters for yield and foliar diseases in F₃ generations of groundnut

Character	Cross	Mean	PCV (%)	GCV (%)	h ² (BS) (%)	GAM (%)
Pod yield per plant (g)	CO 7 × VRI Gn 6	3.6	74.9	60.7	65.6	101.3
	ICGV 00350 × COG 0437	3.7	80.7	68.5	71.9	119.6
	TMV 2 × GPBD 4	5.3	68.8	62.0	81.1	115.0
	TMV 2 × VRI Gn 6	4.1	100.1	92.2	84.9	175.1
	TMV Gn 13 × GPBD 4	3.4	133.9	125.3	87.6	241.5
	TMV Gn 13 × VRI Gn 6	4.4	95.9	88.8	85.7	169.2
	VRI 2 × GPBD 4	10.6*	50.8	48.5	91.3	95.5
	VRI 2 × COG 0437	6.7	45.6	39.1	73.5	69.0
	VRI 2 × VRI Gn 6	6.0	64.1	58.4	83.0	109.7
	CO 7 (Check variety)	5.79	—	—	—	—
Kernel yield per plant (g)	CO 7 × VRI Gn 6	2.1	85.4	48.7	32.5	57.2
	ICGV 00350 × COG 0437	2.0	86.3	42.8	24.6	43.7
	TMV 2 × GPBD 4	3.3	73.6	57.8	61.8	93.6
	TMV 2 × VRI Gn 6	2.6	103.8	86.9	70.2	150.0
	TMV Gn 13 × GPBD 4	2.2	153.1	137.0	80.1	252.6
	TMV Gn 13 × VRI Gn 6	3.1	104.2	92.3	78.4	168.2
	VRI 2 × GPBD 4	7.0*	56.5	52.5	86.2	100.4
	VRI 2 × COG 0437	4.5	51.4	39.8	59.9	63.4
	VRI 2 × VRI Gn 6	4.1	71.3	61.3	74.0	108.6
	CO 7 (Check variety)	4.22	—	—	—	—
Late leaf spot (score)	CO 7 × VRI Gn 6	2.6*	27.1	—	—	—
	ICGV 00350 × COG 0437	3.2*	32.8	15.3	21.8	14.7
	TMV 2 × GPBD 4	3.1*	35.5	19.5	30.1	22.0
	TMV 2 × VRI Gn 6	2.8*	34.8	8.9	6.5	4.7
	TMV Gn 13 × GPBD 4	2.0*	26.7	—	—	—
	TMV Gn 13 × VRI Gn 6	2.1*	15.1	—	—	—
	VRI 2 × GPBD 4	3.2*	33.3	28.2	71.8	49.3
	VRI 2 × COG 0437	5.6	20.7	12.6	36.8	15.7
	VRI 2 × VRI Gn 6	3.9	27.2	13.0	22.8	12.7
	CO 7 (Check variety)	4.29	—	—	—	—
Rust (score)	CO 7 × VRI Gn 6	5.4	28.9	25.8	79.3	47.3
	ICGV 00350 × COG 0437	6.4	19.7	16.3	68.4	27.8
	TMV 2 × GPBD 4	4.4	45.5	42.5	87.4	81.9
	TMV 2 × VRI Gn 6	5.0	36.5	33.7	85.0	63.9
	TMV Gn 13 × GPBD 4	5.4	35.8	33.3	86.5	63.7
	TMV Gn 13 × VRI Gn 6	5.6	19.2	14.5	56.7	22.4
	VRI 2 × GPBD 4	3.5*	35.1	28.9	67.5	48.9
	VRI 2 × COG 0437	5.0	41.8	39.3	88.5	76.1
	VRI 2 × VRI Gn 6	5.7	25.0	21.7	75.5	38.9
	CO 7 (Check variety)	4.25	—	—	—	—

* Significantly superior to check variety CO 7



(PCV), genotypic coefficient of variation (GCV), heritability (h^2) in broad sense and genetic advance as per cent of mean (GAM) in all the nine crosses for yield and foliar diseases are presented in Table 1 and cross wise progeny performance in Table 2. The outcome of the genetic analysis in F_3 generation for pod yield per plant, kernel yield per plant, late leaf spot and rust disease scores are summarized briefly as follows.

Pod yield per plant (g)

Among the nine crosses, the cross VRI 2 \times GPBD 4 recorded significantly higher mean pod yield per plant whereas, lower mean values were possessed by the cross TMV Gn 13 \times GPBD 4. The average value for pod yield per plant ranged between 10.6 g (VRI 2 \times GPBD 4) and 3.4 g (TMV Gn 13 \times GPBD 4). All the nine crosses exhibited high PCV, GCV values coupled with high heritability and GAM. High PCV, GCV, heritability and GAM values for pod yield per plant were earlier reported by Shinde *et al.* (2010), Dandu *et al.* (2012), Narasimhulu *et al.* (2012), Priyadharsini (2012), Anitha (2013), John *et al.* (2013), Narasimhulu *et al.* (2013), Mukesh *et al.* (2014), Thirumala *et al.* (2014) and Prabhu *et al.* (2015). Thus, the cross VRI 2 \times GPBD 4 can be selected as superior on the basis of mean performance and variability parameters for pod yield per plant.

Kernel yield per plant (g)

The mean value ranged from 2.0 g (ICGV 00350 \times COG 0437) to 7.0 g (VRI 2 \times GPBD 4) for kernel yield per plant. The cross VRI 2 \times GPBD 4 recorded significantly superior mean for kernel yield per plant than other crosses while the cross ICGV 00350 \times COG 0437 exhibited lower mean kernel yield per plant. High PCV and GCV values were recorded by all the crosses. High GCV values indicated the greater extent of variability present in the character and can be improved through selection (Sunil *et al.*, 2015). All the crosses exhibited high heritability and GAM values except CO 7 \times VRI Gn 6, ICGV 00350 \times COG 0437 and VRI 2 \times COG 0437 which recorded moderate heritability and high GAM values. These findings are similar to the findings of Venkataravana and Injeti (2008), Khote *et al.* (2009), Savaliya *et al.* (2009), Dolma *et al.* (2010), Raut *et al.* (2010), Shinde *et al.* (2010), Dandu *et al.* (2012), Narasimhulu *et al.* (2012), Priyadharsini (2012), Anitha (2013), John *et al.* (2013), Narasimhulu *et al.* (2013), Mukesh *et al.* (2014) and Thirumala *et al.* (2014) for the trait kernel yield per plant. Hence, on the basis of kernel yield per plant, the cross VRI 2 \times GPBD 4 can be elected as a best cross among nine crosses.

Late leaf spot score

The range varied from 2.0 (TMV Gn 13 \times GPBD 4) to 5.6 (VRI 2 \times COG 0437) for the trait late leaf spot disease score. The cross TMV Gn 13 \times GPBD 4 (2.0 score) followed by the crosses TMV Gn 13 \times VRI Gn 6 (2.1 score), CO 7 \times VRI Gn 6 (2.6 score), TMV 2 \times VRI Gn 6 (2.8 score), TMV 2 \times GPBD 4 (3.1 score), ICGV 00350 \times COG 0437 (3.2 score) and VRI 2 \times GPBD 4 (3.2 score) recorded significantly lower mean values for leaf spot disease score than the check variety CO 7. The crosses *viz.*, CO 7 \times VRI Gn 6, TMV Gn 13 \times GPBD 4 and TMV Gn 13 \times VRI Gn 6 also exhibited negligible genetic variability; hence, are ignored due to higher environmental influence. The higher mean values were recorded by the cross VRI 2 \times COG 0437 (5.6 score) followed by VRI 2 \times VRI Gn 6 (3.9 scores). The cross VRI 2 \times GPBD 4 recorded high PCV and GCV values coupled with high heritability and GAM values. Similar results were earlier reported by Khedekar (2008), Venkataravana and Injeti (2008), Dolma *et al.* (2010), Narasimhulu *et al.* (2013), Padmaja *et al.* (2013) and Ashish *et al.* (2014). High PCV, medium GCV, moderate heritability and high GAM values were exhibited by the cross TMV 2 \times GPBD 4. All the other crosses possessed high PCV, low to medium GCV, heritability and GAM values. Hence, the cross VRI 2 \times GPBD 4 followed by the cross TMV 2 \times GPBD 4 is best suited for early generation selection with regard to late leaf spot score.

Rust score

For rust severity score, the mean of nine F_3 populations was tested against the standard check CO 7, which in turn revealed desirable mean performance than the check variety. The range of the trait varied between 3.5 (VRI 2 \times GPBD 4) and 6.4 (ICGV 00350 \times COG 0437). Significantly lower mean value for rust disease score was recorded by the cross VRI 2 \times GPBD 4 (3.5 scores). All the crosses recorded high PCV and GCV values, except ICGV 00350 \times COG 0437 and TMV Gn 13 \times VRI Gn 6 which recorded medium PCV and GCV values. All the crosses exhibited high heritability and GAM values while the cross TMV Gn 13 \times VRI Gn 6 alone possessed moderate heritability values. The results are in accordance with John *et al.* (2008), Venkataravana and Injeti (2008), Vishnuvardhan *et al.* (2012), Narasimhulu *et al.* (2013), Ashish *et al.* (2014) and Shridevi *et al.* (2014). Thus with regard to rust disease score, the cross VRI 2 \times GPBD 4 can be opted due to its superior mean performance and the higher values of variability parameters such as PCV, GCV, heritability and GAM.

**Table 2:** Mean performance and coefficient of variation (CV) percentage for yield and foliar diseases in F₃ progenies of groundnut

Char-acter	Progeny #	CO 7 × VRI Gn 6		ICGV 00350 × COG 0437		TMV 2 × GPBD 4		TMV 2 × VRI Gn 6		TMV Gn 13 × GPBD 4		TMV Gn 13 × VRI Gn 6		VRI 2 × GPBD 4		VRI 2 × COG 0437		VRI 2 × VRI Gn 6		CO 7 (Check Variety)
		Mean	CV %	Mean	CV %	Mean	CV %	Mean	CV %	Mean	CV %	Mean	CV %	Mean	CV %	Mean	CV %	Mean	CV %	
Pod yield per plant (g)	1	3.4	69.5	3.0	75.4	4.7	121.1	5.7	97.4	0.8	93.3	7.8*	8.6*	48.1	6.6	39.3	7.9*	51.8		
	2	5.3	120.5	4.1	82.5	4.6	77.0	2.4	117.0	5.9	92.5	2.3	12.3*	20.3	7.3*	32.2	4.4	51.3		
	3					5.6	55.2					3.7	8.9*	58.1	6.6	28.7	3.3	42.1		
	4					8.8*	18.1						11.3*	54.1	5.5	37.7	8.3*	56.4		579
	5					4.8	70.4								7.6*	54.3				
	6					3.7	47.8													
	GM	4.4		3.6		5.4		4.1		3.4		4.6		10.3		6.7		6.0		
Kernel yield per plant (g)	1	2.0	78.6	1.8	75.5	2.8	121.3	3.6	105.2	0.3	123.1	5.6*	5.5*	55.9	4.3	42.9	5.6*	54.0		
	2	3.2	137.1	2.1	93.0	2.6	80.9	1.7	127.0	4.0	102.3	1.5	8.0*	16.5	5.1*	37.8	2.9	60.9		
	3					3.5	62.8					2.6	5.8*	66.0	4.4	28.9	2.0	44.6		422
	4					6.1*	20.6						7.7*	59.8	3.6	40.0	5.7*	64.8		
	5					2.9	75.9								5.2*	61.1				
	6					2.3	61.0													
	GM	2.6		1.9		3.4		2.6		2.2		3.2		6.8		4.5		4.1		
Late leaf spot (score)	1	2.6*	25.7	2.8*	14.4	2.7*	19.4	3.5	20.2	2.0*	0.0	2.3*	3.0*	27.2	5.3	19.2	3.1*	18.7		
	2	3.0*	47.1	3.4*	37.2	2.9*	33.4	2.0*	0.0	40.8	2.0*	2.0*	3.3*	31.0	4.2	10.6	4.1	22.9		
	3					4.0	35.4					2.0*	6.2	24.9	5.4	16.6	3.9	27.1		
	4					3.5*	23.9						5.7	24.5	5.7	23.1	5.1	12.5		429
	5					2.4*	22.0								6.3	16.1				
	6					3.5*	60.6													
	GM	2.8		3.1		3.2		2.8		2.0		2.1		4.5		5.4		4.0		
Rust (score)	1	5.3	29.8	6.0	27.9	3.7	33.0	6.5	10.9	4.0	45.6	5.3	3.6*	38.1	5.2	44.6	5.9	18.9		
	2	6.0	23.6	6.6	14.6	4.4	41.0	3.5	20.2	6.8	7.4	5.3	3.3*	24.5	5.8	30.8	6.1	22.9		
	3					6.1	40.5					6.3	3.2*	36.7	7.0	10.1	4.3	32.6		
	4					2.7*	30.6						4.5	22.2	5.8	37.5	6.1	22.1		425
	5					3.7	37.2								3.7	33.1				
	6					5.5	38.6													
	GM	5.7		6.3		4.3		5.0		5.4		5.6		3.7		5.5		5.6		

Progeny # - Progeny Number, * Significantly superior than check variety CO 7, GM - Grand Mean



Conclusion

Among the nine crosses studied, the cross VRI 2 × GPBD 4 recorded superior mean performance for both pod and kernel yield characters. It also had high PCV and GCV values coupled with high heritability and GAM for all the four traits. Thus, results clearly indicated that there is a presence of wide spectrum of genetic variation and the higher estimates of heritability implied that the environmental effects least influence these characters. High heritability along with high GAM indicated the presence of additive gene effect and these traits are expected to respond to selection with greater efficiency. Hence, based on mean performance and variability parameters for pod yield, kernel yield and foliar disease resistance, the cross VRI 2 × GPBD 4 is adjudged to be the superior cross. Considering the progeny wise performance, the offspring #1 and #2 of the cross VRI 2 × GPBD 4 in the F_3 generation could be selected. Being the F_3 generation, the amount of variability should be low to moderate. However, all the progenies of the cross VRI 2 × GPBD 4 recorded moderate to the high coefficient of variation for all the characters. Hence further selection and advancement of progenies is necessary till the attainment of homogeneity.

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