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Genetic Variability Parameters For Yield Components And Late Leaf Spot Tolerance In BC₁F₂ Population Of Groundnut (*Arachis Hypogaea* L.)

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Abstract

BC₁F₂ population of four crosses was evaluated to assess their genetic parameters. A wide range of variation was observed for the eight traits. High magnitude of PCV and GCV coupled with broadsense heritability and genetic advance as per cent of mean for these characters studied such as mature pods per plant, immature pods per plant, total pods per plant, mature seeds per plant, immature seeds per plant, haulm weight per plant, LLS disease score at 75 DAS and pod yield per plant in all the populations, whereas the direct crosses recorded high heritability coupled with high genetic advance as per cent of mean for LLS disease score at 90 DAS. So the selection may be effective for this trait in these populations. Most of the characters had low value of GCV as compared to the PCV indicating the scope for further genetic improvement. Owing to presence of wide variability, there is scope for yield improvement in these crosses.

Key words: Genetic variability, heritability, genetic advance as per cent of mean, back cross

1.Introduction

Groundnut (*Arachis hypogaea* L.) is one of the most important oilseed crops of India. Even though India ranks first in area, its production and productivity noticed low due to several biotic and abiotic factors. Among the biotic stresses, the two fungal diseases namely late leaf spot (LLS) caused by *Phaeoisariopsis personata* [(Berk. and Curt.) Deighton] and rust caused by *Puccinia arachidis* Speg. Are widespread and economically more important. These diseases often occur together and cause yield loss up to 50-70% in the crop (Subrahmanyam et al., 1985). Therefore, the use of groundnut varieties resistant to leaf spot is considered important and an effective way to manage this disease. It is a highly self pollinated crop and can be grown in tropical and subtropical areas. Genetic variability is the basic requirement for crop improvement as this provides wider scope for selection. Thus, effectiveness of selection is dependent upon the nature, extent and magnitude of genetic variability present in the population and the extent to which it is heritable. To increase yield it is essential to know the extent of genetic variability in the existing population. Knowledge of association among quantitative characters and late leaf spot disease score will enable the breeders to create new variations by effecting crosses between carefully chosen parents and to suggest about the direction and intensity of selection for the matter. The present study was planned to know the knowledge of the magnitude of variability, heritability, genetic advance and genetic advance as per cent of mean in the BC₁F₂ population of groundnut.

2.Materials And Methods

This study was carried out at the ICRISAT, Patancheru, Hyderabad during Kharif 2010. The experimental material for the present study comprised of 4BC₁F₂ back across populations involving susceptible parent, JL 24 and LLS resistant ICRISAT genotypes, ICG

11337 and ICG 13919 were used as parents. The genotypes, ICG 11337 and ICG 13919 are interspecific derivatives bred at ICRISAT after incorporating genes that confer resistance to LLS from wild *Arachis* species, *A. cardenasii* (Singh et al., 1997). Cultivated *A. Hypogaea* was used as female parent while *A. cardenasii* was the pollen parent in developing these interspecific derivatives. JL 24 is a popular short-duration groundnut variety in India, but is highly susceptible to LLS. JL 24 was selected from EC 94943, an introduction from Taiwan, at the Oilseeds Research Station, Jalgaon, Maharashtra and was released for cultivation in 1979. The F_1 's were crossed to the susceptible parent, JL 24 to derive back cross generations and on the same F_1 plants, the F_2 seed was generated by allowing some flowers to self. Artificial disease epiphytotic was created by using "spreader row technique". TMV 2 susceptible to LLS, hence was planted at every 10th row as well as five rows border around the field to maintain the effective inoculum load. Forty five days after sowing, plants were inoculated uniformly in the evening with the inoculum containing 20,000 conidia/ml water and mixed with Tween 80 (0.2 ml/ 1000 ml of water) as a mild surfactant and sprayed on the plants using knapsack sprayer. The weather conditions favoured good development of diseases. High humidity was maintained by irrigating the field in the evening for 30 minutes by sprinkler on rain-free days for 30 days from the day of inoculation. Additional inoculum was provided by placing pots containing diseased plants in the infector row for every 2 m. Rust disease was controlled by spraying calixin 1 ml /litre, while rest of the cultural operations and plant protection measures were followed as per recommended practices ensuring uniform and healthy crop stand. Following observations were recorded from five randomly selected plants viz., days to 50% flowering, days to maturity, mature pods / plant, total pods / plant, mature seeds / plant, haulm weight / plant, 100- seed weight, shelling %, LLS disease score at 75, 90 and 102 DAS and pod yield / plant. The characters of BC_1F_2 population of observations were recorded on each individual plant, for parents randomly selected twenty plants of each parent. Parameters considered in the present study were days to 50% flowering, days to maturity, mature pods per plant, immature pods per plant, total pods per plant, mature seed per plant, immature seed per plant, hundred seed weight, shelling percent, haulm weight per plant, The four segregating populations were planted without replication as it was segregating material. Each entry was planted in 3 meter length with 60 cm spacing between rows and 10 cm between plants within the rows. The size of BC_1F_2 population is presented in Table 1.

The recorded data were analysed as suggested by Falconer (1989) for genotypic and phenotypic coefficients of variation, Hanson et al., (1956) for heritability and Johnson et al., (1955) for genetic advance.

3.Results And Discussion

The mean, range, genotypic and phenotypic coefficient of variation, heritability and genetic advance as percent of mean for all the traits are presented in the Table 2. Days to 50% flowering recorded highest range of 31 to 38 days with a mean of 34 days in the reciprocal cross (ICG 11337 X JL 24) X JL 24. The four crosses recorded low estimates of PCV (3.64-5.34), GCV (2.34-4.55) and genetic advance as per cent of mean (3.09-7.98). High heritability was noticed in two reciprocal crosses, (ICG 11337 X JL24) X JL24 (72.52) and (ICG 13919 X JL24) X JL24 (66.38). The result indicates that non-additive gene effects governing the character. This trait had little scope for further improvement through individual selection. Similar findings were reported by Dolma et al., (2010).

Days to maturity, this is an important character for reducing maturity duration of the crop. The two reciprocal crosses were late in maturity (107 days) than the direct crosses (104 days). The reciprocal cross (ICG 11337 X JL24) X JL 24 recorded highest range (103-125 days). All the four crosses recorded low estimates of PCV (3.55-7.02), GCV (3.50-7.00) and the high heritability (97.00-99.00) moderate genetic advance as per cent of the mean was noticed in reciprocal crosses (ICG 11337 X JL 24) X JL 24 (14.36) and (ICG 13919 X JL 24) JL 24 (10.87). While, direct crosses recorded low genetic advance as per cent of mean (7.09, 7.41). The differences between the direct and their reciprocal crosses are distinct for mean, range and genetic advance as per cent of mean indicating the possibility of maternal effect from the resistant parents for these traits. This trait exhibited low variability with high heritability in all the population. These results are similar with the findings of Sawargaonkar et al., (2010). High heritability coupled with low genetic advances in direct crosses of back cross populations may be ineffective for selection. While reciprocal crosses of back cross populations recorded high heritability coupled with moderate genetic advance indicating that this trait is controlled by both additive and non-additive gene action. These results are similar to the earlier findings (Ahmed, 1995).

Mature pods per plant are directly related to yield enhancement in groundnut. All the populations recorded high estimates of PCV (47.34-52.19), GCV (39.81-44.42), heritability (70.73-75.07) and genetic advance as percent of mean (68.97-78.65). These results are in confirmation with the finding of John et al., (2008) for high PCV and GCV. Mothilal et al.,(2004) reported high estimates of heritability and genetic advance as per cent of mean. The result indicates that this trait is most likely governed by additive genes and the donor parents had contributed some positive alleles for an increase number of mature pods per plant. Hence selection may be effective.

The number of immature pods per plant recorded highest range in reciprocal crosses, (ICG 11337 X JL 24) X JL24 (0-20) and (ICG 13919 X JL 24) X JL 24 (0-25) over direct crosses. The population recorded a mean value of 3 immature pods per plant. The reciprocal crosses recorded the highest value of PCV (107.72, 109.26), GCV (91.51, 91.48), heritability (72.16, 70.10) and genetic advance as per cent of mean (160.13, 157.78) over the direct crosses. This may be due to the maternal effect of resistant parents, ICG 11337 and ICG 13919. All the populations recorded high variability, heritability, genetic advance as per cent of mean except (JL 24 X ICG 13919) X JL 24. Which recorded moderate heritability coupled with high genetic advance that the character is controlled by additive genes. Similar results earlier reported by Shinde et al., (2010).

Total number of pods per plant is directly related to yield enhancement in groundnut. The highest range was observed in the cross (JL 24 X ICG 11337) X JL 24 (4 to 55). All the back cross population recorded high estimates of PCV (43.54-48.02), GCV (36.98-46.27) heritability (72.13-78.96) and genetic advance as per cent of mean (64.70-78.11). The result indicates that this trait is controlled by

additive genes. Hence, selection would be effective for improvement of this trait. The present findings are in agreement with the findings of Yogendra Prasad et al., (2002).

Number of mature seeds per plant is an important yield component and had a positive association with yield. The direct crosses recorded highest range (4-70) over the direct crosses. It indicated that the donor parents contributed positive alleles for increased number of mature seeds per plant. All the crosses recorded high estimates of PCV (47.98-59.75), GCV (40.88-53.83), heritability (72.61-81.15) and genetic advance as per cent of mean (71.76-99.88). The result indicates that their variation is mainly due to additive genes and can be improved through individual plant selection. These results are similar to the findings of Dolma et al., (2010).

The trait, number of immature seeds per plant in the reciprocal cross (ICG 13919 X JL 24) X JL 24 recorded highest mean (5) and range (0-37). All the populations recorded high PCV (107.53-125.44), GCV (75.57-85.65) and genetic advance as per cent of mean (109.22-130.34) coupled with moderate heritability (44.79-54.58) in both direct and reciprocal crosses.

The trait hundred seed weight is an important yield component. The highest range (13.20 to 59.80 g) and mean (31.31) was observed in the cross (JL 24 X ICG 13919) X JL 24. Both direct and reciprocal crosses recorded high estimates of PCV (26.36-31.69), GCV (21.78-29.17), heritability (67.97-84.72) and genetic advance as percent of mean (36.98-55.31). Shoba et al., (2009) reported high estimates of PCV, GCV, heritability and genetic advance as percent of mean estimates for this trait. The difference between PCV and GCV was less influence by environment and selection could lead to a substantial improvement in hundred seed weight. This trait was controlled by additive gene action. Hence, selection based on this trait will be effective in these populations.

Shelling percent is one of the most important yield contributing trait for groundnut. All the populations recorded low estimates of PCV (4.29-4.52), GCV (1.01-1.82), heritability (5.58-16.57) and genetic advance as per cent of mean (0.49-1.53). The result indicating the minor differences between these two estimates indicate the less influence of environment on this character. The results are in accordance with the findings of Savaliya et al., (2009). Low heritability coupled with low genetic advance suggests that the genotypic variation for such character is probably due to non-additive gene action. Similar results were reported by Rosemary and Ramalingam (1996).

Haulm weight per plant ranged from 4.60-49.80g with a mean of 23.39 with high PCV (44.08), GCV (39.82), heritability (81.63) and genetic advance as per cent of mean (74.12). All the crosses recorded high estimates of PCV, GCV, heritability and genetic advance as per cent mean, while the cross (JL 24 X ICG 13919) X JL 24 recorded moderate heritability. These results indicate that this trait was controlled by additive gene effects. Hence, selection for this trait may be effective for improvement of pod yield per plant. These results are similar to the earlier reports of Kavani et al., (2004).

LLS disease score at 75 DAS recorded highest range (1-5), PCV (21.88) and GCV (20.42) in the cross (JL 24 X ICG 11337) X JL 24, while the reciprocal crosses recorded low estimates of PCV and GCV. The difference between GCV and PCV values were smaller indicating low effect of environment on the expression of the character. The findings are in accordance with the findings of Sarvamangala (2009) for LLS disease score at 70 DAS in RIL population. High heritability (65.25) coupled with high genetic advance as per cent of mean (28.29-39.25) in all the populations indicating that additive effects are substantial and environmental effects are small and therefore, selection is effective. The results are similar with the findings of Khedikar (2008) for LLS score at 70 DAS in RIL population.

LLS disease score at 90 DAS of the reciprocal cross, (ICG 11337 X JL 24) X JL 24 recorded lowest range (4-6) with a mean of 5. The direct crosses (JL 24 X ICG 11337) X JL 24 and (JL 24 X ICG 13919) X JL 24 recorded moderate estimates of PCV (13.04, 14.34), and GCV (11.74, 12.56) coupled with high heritability (81.06, 76.69) and genetic advance as per cent of mean (21.78, 22.65). The results indicate that, this trait may be controlled by additive gene action. Hence, improvement of disease resistance could be effective in these populations. These results are in accordance with the findings of Khedikar et al., (2008). The reciprocal crosses recorded low estimates of PCV and GCV with moderate heritability coupled with low to moderate genetic advance. The results revealed that, this trait was controlled by both additive and non-additive gene action. These results are in accordance with the findings of John et al., (2008) for low PCV, GCV, moderate heritability coupled with moderate genetic advance for this trait.

LLS disease score at 102 DAS recorded moderate estimates of PCV (11.56-13.72), GCV (11.23-13.36) with high heritability (94.46-99.96) coupled with high genetic advance as per cent of mean (22.49-26.80). The result indicates that, this trait was controlled by additive gene action. Hence, selection may be effective in these populations. Pod yield per plant is one of the most important trait in groundnut. The reciprocal cross, (ICG 13919 X JL 24) X JL 24 recorded the highest range (3.60-34.60) and mean (10.56). All the populations recorded high estimates of PCV (45.84-51.94), GCV (40.39-48.97), heritability (77.64-88.89) and genetic advance as per cent of mean (73.32-95.10). It indicating that this character is controlled by additive gene action and hence, the selection would be effective for improvement of this trait. Similar results reported by Narasimhulu (2007) for PCV and GCV. Shoba et al., (2009) and Sawargaonkar et al., (2010) reported high heritability coupled with high genetic advance as per cent of mean for this trait.

The relative magnitude of PCV and GCV indicated the presence of environmental influence in the expression of the characters studied. These crosses also had high heritability and genetic advance as per cent of mean in some of the characters viz., mature pods per plant, immature pods per plant, total pods per plant, mature seeds per plant, immature seeds per plant, haulm weight per plant, LLS disease score at 75 DAS and pod yield per plant. High heritability of these traits indicates that whatever variation occurred is mainly genetic and less influenced by the environment (Meghannavar et al. 1998 and Rudra Naik et al. 2009). Therefore, priority should be given for these traits during selection.

Crosses	Mean	Range	PCV	GCV	h^2 (bs)	GA	GAM
				Days to 50% flowering			
C1	32	29-35	4.32	3.16	53.40	1.54	4.76
C2	34	31-38	5.34	4.55	72.52	2.72	7.98
C3	33	32-35	3.64	2.34	41.32	1.01	3.09
C4	33	29-35	4.81	3.92	66.38	2.15	6.58
				Days to maturity			
C1	104	103-117	3.55	3.50	97.00	7.39	7.09
C2	107	103-125	7.02	7.00	99.28	15.42	14.36
C3	104	103-117	3.67	3.63	98.02	7.73	7.41
C4	107	103-117	5.32	5.30	99.10	11.62	10.87
				Mature pods per plant			
C1	14	3-44	47.34	39.81	70.73	9.86	68.97
C2	14	3-43	47.95	40.59	71.65	10.15	70.77
C3	14	4-45	50.86	44.06	75.07	11.34	78.65
C4	13	2-35	52.19	44.42	72.44	10.40	77.88
				Immature pods per plant			
C1	3	0-16	100.50	83.88	69.66	4.45	144.21
C2	3	0-20	107.72	91.51	72.16	4.81	160.13
C3	3	0-30	97.29	67.45	48.07	2.82	96.33
C4	3	0-25	109.26	91.48	70.10	5.41	157.78
				Total pods per plant			
C1	17	4-55	44.48	38.14	73.53	11.70	67.37
C2	17	5-48	43.54	36.98	72.13	11.18	64.70
C3	17	4-47	45.09	39.71	77.54	12.47	72.03
C4	17	4-40	48.02	42.67	78.96	13.12	78.11

Table 1: Mean, Range, Phenotypic And Genotypic Coefficients Of Variation, Heritability (B.S.), Genetic Advance Expressed As Per Cent Of Mean For Different Characters Of Four Back Cross Populations

Crosses	Mean	Range	PCV	GCV	h^2 (bs)	GA	GAM
			Mature seeds per plant				
C1	20	4-70	47.98	40.88	72.61	14.63	71.76
C2	21	5-38	56.98	51.22	80.81	19.46	94.85
C3	22	4-70	59.75	53.83	81.15	22.08	99.88
C4	20	4-57	57.78	49.70	73.98	17.14	88.06
			Immature seeds per plant				
C1	4	0-33	115.93	85.65	54.58	5.39	130.34
C2	4	0-24	121.88	81.95	45.21	4.06	113.51
C3	4	0-32	125.44	83.95	44.79	4.34	115.75
C4	5	0-37	107.53	75.51	49.31	4.99	109.22
			Hundred seed weight				
C1	29.73	12.40-54.40	26.36	22.91	75.51	12.19	41.00
C2	31.31	12.80-59.80	31.69	29.17	84.72	17.32	55.31
C3	30.13	13.20-59.81	31.24	27.36	76.71	14.88	49.37
C4	30.39	16.20-52.50	26.41	21.78	67.97	11.24	36.98
			Shelling %				
C1	65.01	57.00-70.00	4.47	1.82	16.57	0.99	1.53
C2	64.79	60.00-71.00	4.37	1.51	11.97	0.70	1.08
C3	65.19	60.00-72.00	4.52	1.76	15.14	0.92	1.41
C4	65.06	60.00-73.00	4.29	1.01	5.58	0.32	0.49
			Haulm weight per plant				
C1	18.42	4.70-42.60	44.69	37.70	71.17	12.07	65.51
C2	23.39	4.60-49.80	44.08	39.82	81.63	17.34	74.12
C3	21.46	7.20-43.10	34.74	26.62	58.71	9.02	42.01
C4	19.19	7.90-42.90	40.43	31.80	61.88	9.89	51.53
			LLS disease score at 75 days after sowing				
C1	3	1-5	21.88	20.42	87.10	1.32	39.25
C2	3	2-5	18.36	16.31	78.86	0.93	29.83
C3	3	2-5	21.05	17.00	65.25	0.85	28.29
C4	4	3-5	18.55	15.99	74.31	1.13	28.40

Table 2

Crosses	Mean	Range	PCV	GCV	h^2 (bs)	GA	GAM
		LLS disease score at 90 days after sowing					
C1	6	4-8	13.04	11.74	81.06	1.38	21.78
C2	5	4-6	10.75	8.03	55.74	0.62	12.35
C3	6	4-7	14.34	12.56	76.69	1.31	22.65
C4	6	5-8	9.46	6.51	47.39	0.54	9.24
		LLS disease score at 102 days after sowing					
C1	8	4-9	11.99	11.69	94.96	1.95	23.46
C2	7	5-9	13.72	13.36	94.85	1.93	26.80
C3	8	5-9	11.56	11.23	94.46	1.85	22.49
C4	8	7-9	9.18	8.78	91.43	1.44	17.29
		Pod yield per plant					
C1	8.89	2.10-26.30	45.84	40.39	77.64	6.51	73.32
C2	9.13	2.50-31.50	50.79	46.20	82.75	7.90	86.58
C3	9.07	2.30-25.30	45.96	41.32	80.80	6.94	76.51
C4	10.56	3.60-34.60	51.94	48.97	88.89	10.04	95.10

Table 3

C1- (JL 24 × ICG 11337) × JL 24
 C2- (ICG 11337 × JL 24) × JL 24
 C3-(JL 24 × ICG 13919) × JL 24
 C4 -(ICG 13919 × JL 24) × JL 24

PCV - Phenotypic coefficient of variation (%)
 GCV - Genotypic coefficient of variation (%)
 h^2 (bs)- Heritability in broadsense
 GA – Genetic advance
 GAM – Genetic advance as percent of mean

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