



Genetic variability studies in F₂ population of Groundnut (*Arachis hypogaea* L.)

¹Padmaja D, ²Eswari K. B., ³Brahmeswara Rao M.V, ⁴Shiva Prasad G.

Department of Genetics and Plant Breeding, College of Agriculture, ANGRAU, Hyderabad

Email: dondapadmaja@yahoo.co.in

Received: 31st Aug 2013, Accepted: 20th Sep 2013, Published: 1st March 2015

Abstract

Present experiment was conducted to study the variability in F₂ population of JL 24 X ICG 11337 and JL 24 X ICG 13919 groundnut. Among these F₂ populations both the crosses showed high variability in the form of PCV, GCV heritability and GAM for mature pods per plant, total pods per plant, mature seeds per plant, haulm weight per plant, LLS disease score at 75 DAS and pod yield per plant. It was observed that selection for these traits would be useful in the genetic improvement of these traits. High heritability coupled with moderate GAM for DS-90 in both the crosses. The cross JL 24 X ICG 11337 recorded high heritability and genetic advance as per cent of mean for DS-102. The result indicates that gains through selection is possible in this cross this may be due to the resistant parent, ICG 11337 may contribute gains through selection for LLS disease score at 102 DAS

Keywords:

PCV, GCV, Heritability and Genetic Advance as percent of mean, Groundnut.

Introduction

Groundnut (*Arachis hypogaea* L.) is an important annual oilseed legume crop, valued as a rich source of protein, minerals and vitamins. is the major oilseed crop in India and in Andhra Pradesh. India ranks second in groundnut production after China with an area of 4.93 million hectares and a production of 5.64 million tons during 2010 (FAOSTAT, 2012). But the average groundnut yield in the country is low (1.14 t/ha) compared to world average and that of China. The productivity is considered to be low because of number of constraints like abiotic (frequent droughts) and biotic stresses (attacks by pests and diseases). The low productivity of the crop is ascribed mainly due to two major foliar diseases namely late leaf spot (causal organism: *Phaeoisariopsis personata* [(Berk. and Curt.) Deighton]) and rust (causal organism: *Puccinia arachidicola* Speg.). These two diseases often occur together and causes up to 50-70% of yield losses in the crop (Subrahmanyam *et al.*, 1985). Development of cultivars resistant/tolerant to late leaf spot could be effective in decreasing the production costs, improving production quality and reducing the

detrimental effects of chemicals on our ecosystem. 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 material and the extent to which it is heritable. In the present study, variability and other genetic parameters were studied.

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 two F₂ populations involving susceptible parent, JL 24 and LLS resistant ICRISAT genotypes, ICG 11337 and ICG 13919 were used as parents. The F₂ seed was generated by allowing some flowers to self. Artificial disease epiphytotics 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. 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. The characters of F₂ population of observations were recorded on each individual plant for parents randomly selected twenty plants of each parent. Parameters considered for the present study were days to 50% flowering, days to maturity, mature pods per plant, immature pods per plant, total pods per plant, mature seeds per plant, immature seeds per plant, hundred seed weight, shelling percent, haulm weight per plant. The two F₂ 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 F₂ population is presented in Table 1. The observation was recorded on individual plants for F₂ population and thirty plants from parents and checks. The recorded data were then analyzed as suggested by Falconer (1989) for coefficient of variance, Hanson *et al.*, (1956) for

heritability and Johnson *et al.*, (1955) for genetic advance.

Results and Discussion

The mean, range, genotypic and phenotypic of variation, heritability and genetic advance as per cent of mean for all the traits are presented in Tables 2&3. Days to 50 per cent flowering of F_2 populations of both the crosses (JL 24 \times ICG 11337 and JL 24 \times ICG 13919) recorded low estimates of PCV (3.46, 4.54), GCV (1.79, 3.56) and genetic advance as per cent of mean (1.90, 5.76). High heritability was noticed in F_2 population of the cross JL 24 \times ICG 13919 (61.62). While, moderate heritability was noticed in the cross JL 24 \times ICG 11337 (43.53). Low estimates of variability indicate limited scope for selection for the trait. Dolma *et al.* (2010) and Shinde *et al.* (2010) also reported low estimates of PCV and GCV for days to 50 per cent flowering. Moderate to high heritability and low genetic advance as per cent of mean in all the populations implies non-additive gene effects governing the character. Dolma *et al.* (2010) reported that non-additive gene effects play an important role in the expression of this trait. Therefore, the results indicate a little scope for further improvement through individual plant selection.

Days to maturity is an important character for reducing maturity duration of the groundnut crop. F_2 populations of the crosses JL 24 \times ICG 11337 and JL 24 \times ICG 13919 recorded low estimates of PCV (4.12, 4.31), GCV (4.07, 4.28) and genetic advance as per cent of mean (8.29, 8.75) coupled with high heritability (97.79, 98.58). These findings are in agreement with Dolma *et al.* (2010). Sawargaonkar *et al.* (2010) for low PCV and GCV.

High heritability with low genetic advance in F_2 populations indicating that selections may be ineffective for these populations. This indicates non additive gene effects playing an important role in the expression of this trait. The findings of Vijayasekhar (2002) support the findings of the present study. Therefore, days to maturity had limited scope for further improvement through individual plant selection.

Mature pods per plant are directly related to yield enhancement in groundnut. F_2 populations (JL 24 \times ICG 11337 and JL 24 \times ICG 13919) recorded high estimates of PCV (51.12, 62.86), GCV (44.97, 57.09), heritability (77.40, 82.51) and genetic advance as per cent of mean (81.51, 106.83). These results are in confirmation with the findings of John

et al. (2007 and 2008b) for high PCV and GCV. Mohitlal *et al.* (2004) who reported high estimates of heritability and genetic advance as per cent of mean. The results indicate that, the trait is most likely governed by additive genes and the donor parents had contributed some positive alleles for increase number of mature pods per plant. Hence, selections may be effective. F_2 populations of the crosses JL 24 \times ICG 11337 and JL 24 \times ICG 13919 showed high estimates of PCV (90.49, 103.30), GCV (79.30, 70.60) and genetic advance as per cent of mean (143.17, 99.40). Heritability was high (76.81) in JL 24 \times ICG 11337 and moderate (46.71) in JL 24 \times ICG 13919 for immature pods per plant. The trait under study was influenced by environmental factors as indicate by large differences among PCV and GCV values. The results are in accordance with the findings of John *et al.* (2008). Moderate to high heritability coupled with high estimates of genetic advance as per cent of mean in all populations. It revealed that the character is governed by additive gene action and hence, selection would be effective for improvement of the trait. The present findings are in agreement with the earlier findings of John *et al.* (2008) and Shinde *et al.* (2010).

Total number of pods per plant is directly related to enhancement of pod yield per plant. It is evident from the results that estimates were higher in F_2 populations (JL 24 \times ICG 11337 and JL 24 \times ICG 13919) for PCV (46.80, 52.79), GCV (41.86, 47.62), heritability (80.01, 81.35) and genetic advance as per cent of mean (77.13, 88.47). High PCV and GCV values were recorded in all the cross derivatives indicating environmental influence on the trait. Similar results were reported by Khote *et al.* (2009) and Shoba *et al.* (2009). These populations exhibited high heritability coupled with high genetic advance indicating that this trait is controlled by additive genes. Azad and Hamid (2000) and Yogendra Prasad *et al.* (2002) also obtained similar results for this trait.

The number of mature seeds per plant is an important yield component and has positive association with pod yield per plant. F_2 populations of two crosses (JL 24 \times ICG 11337 and JL 24 \times ICG 13919) recorded high estimates of PCV (55.04, 56.21), GCV (49.30, 48.68), heritability (80.23, 75.02) and genetic advance as per cent of mean (90.97, 86.86). The results revealed the preponderance of additive type of gene action in expression of this trait. Therefore, the selection of individual plants of this trait would be very effective in improving

pod yield. High heritability and genetic advance for this trait by Dolma *et al.* (2010).

Immature seeds per plant of F_2 populations recorded high estimates of PCV (117.50, 108.62) and GCV (84.09, 36.51) with high genetic advance as per cent of mean (123.99, 25.28). Moderate (51.23) (JL 24 \times ICG 11337) and low heritability (JL 24 \times ICG 13919) were recorded. This trait recorded wide range of variability, low to moderate heritability with high genetic advance as per cent of mean. These results indicate that this trait may be controlled by both additive and non-additive genes. Hence, gains through selection for this trait may not be significant in crop improvement.

Haulm weight per plant of F_2 populations (JL 24 \times ICG 11337 and JL 24 \times ICG 13919) recorded high estimates of PCV (34.97, 40.74), GCV (30.70, 34.04), heritability (77.10, 69.84) and genetic advance as per cent of mean (55.54, 58.61). The difference between PCV and GCV values were high indicating the presence of high variability which is due to environment. Similar findings were reported by John *et al.* (2008), Khote *et al.* (2009) and Shoba *et al.* (2009). High GCV values indicate greater extent of variability for the character and that it can be improved through selection. High heritability coupled with high genetic advance as per cent of mean. 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).

The trait, hundred seed weight recorded high estimates of PCV (22.48), GCV (19.84), heritability (77.83) and genetic advance as per cent of mean (36.05) were observed in F_2 population of the cross (JL 24 \times ICG 11337). Other cross, JL 24 \times ICG 13919 recorded moderate PCV (19.63), GCV (14.31), heritability (53.12) and high genetic advance as per cent of mean (21.48). Shoba *et al.* (2009) reported high PCV and GCV estimates for this trait. The difference between PCV and GCV was less indicating less influence by environment and selection could lead to a substantial improvement in hundred seed weight. Similarly, high heritability coupled with high genetic advance as per cent of mean values was noticed in the cross JL 24 \times ICG 11337 for hundred seed weight. Similar results were reported by Savaliya *et al.* (2009) and Shoba *et al.* (2009) showed that this trait was controlled by additive gene action. Hence, selection based on this trait will be effective in these populations.

Shelling per cent is one of the most important yield contributing trait for groundnut. The character under study exhibited low estimates of PCV (6.22, 5.03), GCV (4.77, 2.90) and genetic advance as per cent of mean (7.54, 3.43) coupled with moderate heritability (58.85, 33.11) in all populations (JL 24 \times ICG 11337 and JL 24 \times ICG 13919). The observed genotypic and phenotypic coefficient of variation were low in both the crosses and the minor differences between these two estimates indicate less influence of environment on this character. The results are in accordance with the findings of Savaliya *et al.* (2009). Moderate heritability coupled with low genetic advance as per cent of mean was in all F_2 populations indicating non-additive gene action governing this trait. These results are in agreement with the findings of Venkateshwarlu (2005).

F_2 populations (JL 24 \times ICG 11337 and JL 24 \times ICG 13919) recorded high magnitude of heritability (90.87, 82.51) and genetic advance as per cent of mean (42.84, 33.26) for DS₇₅. F_2 population of the cross, JL 24 \times ICG 11337 recorded high PCV (22.88) and GCV (21.81), while other cross, JL 24 \times ICG 13919 recorded moderate estimates of PCV (19.57) and GCV (17.77). The differences 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 Venkataravana and Injeti (2008) and Sarvamangala (2009) for LLS disease score at 70 DAS. High heritability coupled with high genetic advance as per cent of mean in all the populations, indicating that additive effects are substantial and environmental effects are small and therefore, selection is effective. The results are in accordance with the findings of Khedikar (2008) reported earlier for LLS score at 70 DAS in RIL population. DS₉₀ recorded moderate estimates of PCV (12.55, 12.93), GCV (10.64, 11.16) and genetic advance as per cent of mean (18.58, 19.82) with high heritability (71.88, 74.41) were noticed in both the crosses (JL 24 \times ICG 11337 and JL 24 \times ICG 13919). Similar results were reported by Sarvamangala (2009) and Dolma *et al.* (2010) for moderate estimates of PCV and GCV values for this trait. Similar findings were reported earlier John *et al.* (2008) for moderate heritability coupled with moderate genetic advance for LLS disease score at 90 DAS. The results revealed that, this trait was controlled by both additive and non additive gene action. The cross JL 24 \times ICG 11337

recorded moderate estimates of PCV (11.80) and GCV (11.46) with high heritability (94.34) coupled with high genetic advance as per cent of mean (22.94), while other cross, JL 24 × ICG 13919 recorded low PCV (9.12), GCV (8.71), high heritability (91.23) and moderate genetic

advance as per cent of mean (17.15) for DS-102. The result indicates that gains through selection is possible in the cross JL 24 × ICG 11337 this may be due to the resistant parent, ICG 11337 may contribute gains through selection for LLS disease score at 102 DAS.

Table 1. Mean, range and genetic parameters in F₂ population of a groundnut cross JL 24 × ICG 11337

Character	Mean	Range	PCV	GCV	Heritability (h ²) (%)	GA	GAM (%)
DFF	32	30-34	3.46	1.79	26.69	0.61	1.90
DM	105	103-117	4.12	4.07	97.79	8.68	8.29
MPD	15	2-40	51.12	44.97	77.40	12.28	81.51
IPD	4	0-15	90.49	79.30	76.81	5.61	143.17
TPD	19	5-48	46.80	41.86	80.01	14.64	77.13
MSD	21	4-58	55.04	49.30	80.23	19.03	90.97
ISD	4	0-25	117.50	84.09	51.23	4.88	123.99
HSW (g)	36.64	22.20-60.50	22.48	19.84	77.83	13.21	36.05
SH (%)	66.56	56.20-75.90	6.22	4.77	58.85	5.02	7.54
HUW (g)	26.41	4.90-45.00	34.97	30.70	77.10	14.67	55.54
DS_75	4	2-5	22.88	21.81	90.87	1.64	42.84
DS_90	5	4-7	12.55	10.64	71.88	1.01	18.58
DS_102	8	6-9	11.80	11.46	94.34	1.83	22.94
PYD (g)	10.95	2.00-31.00	50.78	47.63	88.00	10.08	92.04

DFF - Days to 50 per cent flowering DM - Days to maturity
 MPD - Mature pods per plant IPD - Immature pods per plant TPD - Total pods per plant
 MSD - Mature seeds per plant ISD - Immature seeds per plant HSW - Hundred seed weight
 SH - Shelling per cent HUW - Haulm weight per plant PYD - Pod yield per plant
 DS_75 - LLS disease score at 75 days after sowing
 DS_90 - LLS disease score at 90 days after sowing
 DS_102 - LLS disease score at 102 days after sowing
 PCV - Phenotypic coefficient of variation (%) GCV - Genotypic coefficient of variation (%) GA - Genetic advance GAM - Genetic advance as per cent of mean

Table 2. Mean, range and genetic parameters in F₂ population of a groundnut cross JL 24 × ICG 13919

Character	Mean	Range	PCV	GCV	Heritability (h ²) (%)	GA	GAM (%)
DFF	32	30-35	4.54	3.56	61.62	1.87	5.76
DM	105	103-117	4.31	4.28	98.58	9.17	8.75
MPD	14	3-55	62.86	57.09	82.51	14.87	106.83
IPD	3	0-19	103.3	70.6	46.71	2.70	99.40
TPD	16	4-62	52.79	47.62	81.35	14.35	88.47
MSD	20	7-80	56.21	48.68	75.02	17.73	86.86
ISD	3	0-17	108.62	36.51	11.30	0.86	25.28
HSW(g)	33.80	20.70-54.30	19.63	14.31	53.12	7.26	21.48
SH (%)	65.91	60.00-73.20	5.03	2.90	33.11	2.26	3.43
HUW (g)	21.41	8.80-46.30	40.74	34.04	69.84	12.55	58.61
DS_75	5	2-6	19.57	17.77	82.51	1.52	33.26
DS_90	6	4-8	12.93	11.16	74.41	1.21	19.82
DS_102	8	6-9	9.12	8.71	91.23	1.42	17.15
PYD (g)	11.61	4.06-37.70	49.12	46.53	89.73	10.54	90.80

DFF - Days to 50 per cent flowering DM - Days to maturity
 MPD - Mature pods per plant IPD - Immature pods per plant TPD - Total pods per plant
 MSD - Mature seeds per plant ISD - Immature seeds per plant HSW - Hundred seed weight
 SH - Shelling per cent HUW - Haulm weight per plant PYD - Pod yield per plant
 DS_75 - LLS disease score at 75 days after sowing
 DS_90 - LLS disease score at 90 days after sowing
 DS_102 - LLS disease score at 102 days after sowing
 PCV - Phenotypic coefficient of variation (%) GCV - Genotypic coefficient of variation (%) GA - Genetic advance GAM - Genetic advance as per cent of mean

Conclusion:

The high genetic variability in the form of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was observed for number of mature pods per plant, total pods per plant, immature pods per plant, immature seeds per plant, mature seeds per plants, haulm weight per plant and LLS disease score at 75 DAS and pod yield per plant of all F₂ Populations. High heritability of these traits indicates that whatever variation occurred is mainly genetic and less influenced by the environment (Rudra Naik *et al.* 2009). Therefore, priority should be given for these traits during selection.

References:

- 1] Azad MAK, Hamid MA. Genetic variability, character association and path analysis in groundnut (*Arachis hypogaea* L.). Thailand Journal of Agricultural Science. 33 (3-4): 153-157, 2000.
- [2]Dolma T, Reddi Sekhar M and Raja Reddy P. Genetic variability, correlation and path analysis for yield, its components and late leaf spot resistance in groundnut (*Arachis hypogaea* L.). Journal of Oilseeds Research. 27 (2): 154-157, 2010.
- [3]FAO. 2012. Statistical data on crops, groundnut, area, production and productivity of India & World, 2012. <http://faostat.fao.org/site/567/default.aspx.#ancor>.
- [4]Falconer DS 1989. Introduction to Quantitative Genetics, Ed. 3. Longmans Green/John Wiley & Sons, Harlow, Essex, UK/New York.
- [5]Hanson CH, Robinson HF and Comstock RE. Biometrical studies on yield in segregating population of Korean lespeadesa. Agron. Journal. 48: 268-272, 1956.
- [6]John K, Vasanthi RP and Venkateswarlu O. Estimates of genetic parameters and character association in F₂ segregating populations of Spanish x Virginia crosses of groundnut (*Arachis hypogaea* L.). Legume Research. 31(4): 235-242, 2008.
- [7]Johnson HW, Robinson H F and Comstock RE. Estimates of genetic and environmental variability in soybeans. Agronomy Journal. 47: 314-318, 1955.
- [8]Kavani RH, Golakia PR, Makne VG and Mandaria R.B. Genetic variation and trait association in Valencia groundnut (*Arachis hypogaea* L.) National symposium: "Enhancing productivity of Groundnut for Sustaining Food and Nutritional security", October 11-13: 27-28, 2004.
- [9]Khedikar Y P. 2008. Molecular tagging and Mapping of resistance to late leaf spot and rust in groundnut (*Arachis hypogaea* L.). Ph.D. Thesis. University of Agricultural Science, Dharwad, India.
- [10]Khote AC, Bendale VW, Bhavé SG and Patil P. P. Genetic variability, heritability and genetic advance in some exotic genotypes of groundnut (*Arachis hypogaea* L.). Crop Research. 37 (1, 2 & 3): 186-191, 2009..
- [11]Rudra Naik V, Bentur M G, Salimath PM and Parameshwarappa KG. Introgression of non spiny and high oil content in adapted generations of safflower (*Carthamus tinctorius* L.). Karnataka J. Agric. Sci, 22 (1): 39-43, 2009.
- [12]Sarvamangala S Ch. 2009. Construction of genetic linkage map and QTL analysis for foliar disease resistance, nutritional quality and productivity traits in groundnut (*Arachis hypogaea* L.). Ph.D. Thesis. University of agricultural sciences, Dharwad.
- [13]Savaliya JJ, Pansuriya AG, Sodavadiya PR and Leva RL. Evaluation of inter and intraspecific hybrid derivatives of groundnut (*Arachis hypogaea* L.) for yield and its components. Legume Research. 32 (2): 129-132, 2009.
- [14]Sawargaonkar SL, Giri RR and Hudge BV. 2010. Character association and path analysis of yield component traits and late leaf spot disease traits in groundnut (*Arachis hypogaea* L.). Agricultural Science Digest. 30(2): 115 – 119
- [15]Shoba D, Manivannan N and Vindhiyavarman P. Studies on variability, heritability and genetic advance in groundnut (*Arachis hypogaea* L.). Electronic Journal of Plant Breeding. 1: 74-77, 2009.
- [16]Singh AK, Mehan V K and Nigam SN. Sources of resistance to groundnut fungal and bacterial diseases: An update and appraisal. Information Bulletin No. 50. International Crops Research Institute for the Semi Arid Tropics, Patancheru, Andhra Pradesh, India, p. 48, 1997.
- [17]Subrahmanyam P, Moss J P, McDonald D, Rao PVS and Rao VR. Resistance to leaf spot caused by *Cercosporidium personatum* in wild *Arachis* species. Plant Disease. 69: 951-954, 1985.