

Assessment of Genetic Variability, Heritability and Genetic Advance among Groundnut (*Arachis hypogaea* L.) Genotypes

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ABSTRACT

Fourteen genotypes of groundnut were obtained from International Crop Research Institute for the Semi Arid Tropics (ICRISAT), Patancheru, Hyderabad, Andhra Pradesh, India were evaluated during Kharif season of 2013 for quantitative parameters. The crop was grown at the field experimental centre, Department of Genetics and Plant Breeding, Sam Higginbottom Institute of Agriculture Technology and Sciences, (Formerly Allahabad Agricultural Institute) Deemed-to-be-University, Allahabad, Uttar Pradesh. The present experiment was carried out in Randomized Block Design with three replications for variability, heritability and genetic advance. Observations were recorded on twelve quantitative characters. Analysis of variance revealed the presence of significant amount of variability among the groundnut genotypes. Maximum genotypic coefficient of variation and phenotypic coefficient of variation was recorded for kernel yield (18.45q/ha.). All the characters showed maximum heritability was recorded for plant height (31.97 cm) and high genetic advance as percentage of mean was recorded for field emergence (235.5%). These characters may serve as an effective selection parameter during breeding programme for crop improvement in future.

Keywords Genetic variability, Genotypes, Groundnut, Quantitative parameters, RBD.

INTRODUCTION

Groundnut (*Arachis hypogaea* L.), belongs to family Leguminosae a vital crop among oilseeds, is a self pollinated having chromosome number (2n=40) grow in tropical and sub-tropical parts of the world. Groundnut is believed to be the native of Brazil. It was introduced in India during the first half of the sixteenth century from one of the conciliatory

islands of China, where it was introduced prior from either Central America or South America. India having second position in groundnut production after China. In India the total cultivated area under groundnut is (4.94 million hectare), production is (9.34 million tonnes) with productivity of (1.89 million tonnes/hectare) (United State Department of Agriculture, 2019).

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Groundnut is the largest oilseed producer crop in India in terms of production. Groundnut is one of the most important cash crops of our country and it has been other synonymous is peanut, earthnut, monkeynut, goober, panda and manila nut. Groundnut is the also known as “The king of oilseeds” and it contains on the average 12 to 15% carbohydrates, 25 to 30% protein and 45-50% oil. The nuts may be chewed uncooked, but are usually eaten boiled or roasted. The nuts can also be boiled, fried, ground into groundnut butter or crushed for oil. Groundnut butter is extensively used in the preparation of soup and as bread spread by Singh *et al.* (2013) and Shukla and Rai (2014).

Groundnut accounts around 25% of the total oilseed production of the country. Annual production of Indian Peanuts and Indian peanuts oil are around 5-8 million tonnes and 1.5 million tonnes respectively. Peanuts Production is highly vulnerable to rainfall deviations and display huge fluctuation between years. Lack of genetic variability even between the botanical groups of groundnut as evidenced by molecular analysis limits the improvement of the crop. Hence, in this study 14 accessions of groundnut were evaluated to assess the nature and magnitude of genetic variability among the genotypes for further utilization in the breeding programmes (Directorate of Groundnut Research, 2015).

MATERIALS AND METHODS

Fourteen groundnut genotypes namely- ICG 525, ICG 5236, ICG 5475, ICG 5494, ICG 5609, ICG 5662, ICG 5663, ICG 5745, ICG 5779, ICG 5827, ICG 5891, ICG 6022, ICG 6057 and ICG 6201 were obtained from International Crop Research Institute for the Semi Arid Tropics (ICRISAT), Patancheru, Hyderabad, Andhra Pradesh, India were evaluated at field experimentation center, Department of Genetics and Plant Breeding, Higginbottom University of Agriculture, Technology and Sciences (SHUAST), Allahabad during Kharif season of 2013. On the basis of meteorological condition Sam Higginbottom University of Agriculture,

Technology and Sciences (SHUAST) was situated at 25°40” N Latitude and 81°85” E Longitude. The experiment was carried out in Randomized Block Design (RBD) having three replications with 35 cm inter and 10 cm intra row spacing. Standard agronomic practices and plant protection measures were taken randomly. Observations were recorded on five randomly selected plants from each replication for various characters *viz.* Field emergence percentage, days to 50% flowering, plant height(cm), primary branches/plant, days to maturity, pod yield/plant(g), pod yield(q/ha), 100-kernel weight(g), sound matured kernels(%), kernel uniformity(%), shelling(%) and kernel yield(q/ha). Analysis of variance to test the significance difference among accessions for each character was carried out as per methodology suggested by Panse and Sukhatme (1967). Phenotypic coefficient of variation and genotypic coefficient of variation were calculated by the formula given by (Burton, 1952). Heritability in broad sense (h^2) was worked out by using formula suggested by Burton and Devane (1953) and genetic advance *i.e.* the expected genetic advance were calculated by using the procedure given by Johnson *et al.*, (1955).

RESULTS AND DISCUSSION

The analysis of variance for dissimilar characters is presented in Table 1. The mean sum of squares due to genotypes showed significant difference for all 12 quantitative characters *viz.* Field emergence percentage, days to 50% flowering, plant height(cm), primary branches/plant, days to maturity, pod yield/plant(g), pod yield(q/ha), 100-kernel weight(g), sound matured kernels(%), kernel uniformity(%), shelling(%) and kernel yield(q/ha) were studied. The mean sums of squares were signifying that the selected genotypes were genetically variable and significant amount of variability existed among them. Similar results were also reported by Savaliya *et al.*, (2009) in groundnut crop.

Table 1: Analysis of Variance for 12 Quantitative Characters in 14 Groundnut Genotypes During 2013

S. No.	Characters	Mean sum of squares		
		Replications (d. f. =02)	Treatment (d. f. =14)	Error =28
1.	Field emergence	308.88	235.55*	111.27
2.	Days to 50% flowering	9.11	12.67*	3.51
3.	Plant height(cm)	0.46	31.97*	0.38
4.	Number of primary branches/plant	0.46	0.40*	0.18
5.	Days to maturity	3.75	10.51*	1.22
6.	Pod yield/plant(g)	5.62	26.38*	1.83
7.	Pod yield(q/ha)	15.59	42.00*	4.92
8.	100-kernels weight(g)	73.49	104.20*	25.86
9.	Shelling percentage	1.56	35.59*	3.94
10.	Kernel yield/plant(g)	6.82	18.45*	4.46
11.	Sound matured kernels	2.06	36.25*	1.76
12.	Kernel uniformity	2.98	17.24*	2.10

* Significant at 5% level of significance

The genotypic coefficient of variation provides a measure to compare of genetic variability present in 12 quantitative parameters. High estimates of genotypic coefficient of variation was recorded for kernel yield (21.30), pod yield (20.54), moderate for pod yield/plant (14.83), seed index (12.25), field emergence (11.40) and low genotypic coefficient of variation value was observed for plant height (6.62), shelling % (5.43), sound matured kernels (4.95), days to 50% flowering (4.62), number of primary branches/plant (4.44), kernel uniformity (3.07) and days to maturity (1.48) (Table 2). Similar finding were reported by (Kadam et al., (2001) in Soya bean. Phenotypic coefficient of variation which measures total relative variation was high for kernel yield (25.36), pod yield (24.29), field emergence (21.89), moderate for pod yield per plant (16.41), seed index (17.28) and low estimate of phenotypic coefficient of variation value was observed in days to 50% flowering (8.55), number of primary branches/plant (8.74), plant height (6.74), sound matured kernels (5.80), shelling % (5.84), kernel uniformity (4.29) and days to maturity (1.74) (Table 2) Similar finding were observed for days to maturity by Kumar et al. (2008) in groundnut crop.

Heritability is a measure to extent of phenotypic caused by the action of gene. For making effective improvement in the character for which selection is practiced, heritability

has been adopted by genetic variability, which is transmitted from parent to its offspring is reflected heritability. The estimates of heritability in broad sense for 12 quantitative traits ranged from number of primary branches/plant (25.80%) to plant height (96.46%). High estimates of heritability were observed for characters like plant height (96.46), shelling (%) (86.69), pod yield per plant (81.67%), sound matured kernels (72.78%), days to maturity (71.68%), pod yield (71.52%) and kernel yield (70.60%). Moderate estimates of heritability were observed for characters like kernel uniformity (51.08%), seed index (50.24). The low estimate of heritability was observed for character like number of primary branches per plant (25.80%), field emergence (27.13%) and days to 50% flowering (29.20%) (Table 2). Accordingly, the characters like plant height, shelling percentage and pod yield per plant had very high heritability. This indicates that selection will be the best measure for selecting groundnut genotypes having these traits with very high heritability. This is because there would be a close correspondence between the accessions and the phenotype due to the relative small contribution of the environment to the total variability. The results are in according with the findings of Narayanan & Murugan (2013); and Singh & Singh (1999) in days to maturity and plant height in groundnut crop.

Table 2: Genetic Parameters of 12 Quantitative characters in 14 Groundnut Genotypes

S. No.	Characters	VG	VP	GCV (%)	PCV (%)	h ² (%)	GA	GG=GA as % of mean
1.	Field emergence	41.43	152.70	11.40	21.89	27.13	24.18	42.84
2.	Days to 50% flowering	0.07	0.26	4.62	8.55	29.20	0.99	16.72
3.	Plant height(cm)	10.53	10.92	6.62	6.74	96.46	6.47	13.18
4.	Number of primary branches/plant	0.07	0.27	4.44	8.74	25.80	1.01	17.10
5.	Days to maturity	3.10	4.32	1.48	1.74	71.68	4.07	3.41
6.	Pods yield/plant(g)	8.18	10.02	14.83	16.41	81.67	6.19	32.11
7.	Pod yield(q/ha)	12.36	17.28	20.54	24.29	71.52	8.14	47.53
8.	Seed index	26.11	51.98	12.25	17.28	50.24	14.11	33.82
9.	Sound matured kernel	10.55	14.49	4.95	5.80	72.78	7.45	11.36
10.	Kernel uniformity	4.66	9.13	3.07	4.29	51.08	5.91	8.40
11.	Shelling percentage	11.50	13.26	5.43	5.84	86.69	7.13	11.42
12.	Kernel yield/plant(g)	5.05	7.15	21.30	25.36	70.60	5.23	49.62

Where, VG = Genotypic variance, VP = Phenotypic variance, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, h² = Heritability, GA = Genetic advance.

A perusal of genetic advance for different traits revealed that it varied from 1.01 (number of primary branches per plant) to 24.18 (field emergence -10 days). The field emergence -10 days (24.18) exhibited highest estimates of genetic advance followed by seed index (14.11), pod yield (q/ha) (7.20). The low estimate of genetic advance was observed for character like number of primary branches/plant (1.01) (Table 4.3). Moderate heritability coupled with low genetic advance was noticed for kernel uniformity indicating that they are highly influenced by the environment and selection may not be effective (Parameshwarappa et al. 2005). The findings of heritability and genetic advance are in conformity with Singh (2005) in Chickpea.

A perusal of genetic advance as percent of mean for different traits revealed that it varied from 3.41 (days to maturity) to 49.62 (kernel yield (q/ha)). Genetic advance as percent of mean for various characters are presented in table and noticed that high genetic advance as percent of mean was recorded for kernel yield (q/ha) (49.62) followed by pod yield q/ha (47.53), field emergence 10 days (42.84). The low estimate of genetic advance as percent of mean was observed for character like days to maturity (3.42) (Table 4.3). Similar finding were reported by Narasimhulu et al. (2012) in groundnut crop. The present study showed that high heritability coupled with high genetic advance as percent of mean for kernel yield(q/ha), pod yield(q/ha), pod

yield/plant(g). These characters were controlled by additive gene effects and phenotypic selection for these characters would likely to be effective than other characters measured (Narayanan & Murugan 2013). The results from the present study were outcome of one year evaluation. It is generally believed that evaluation carried out across year (at least two year) derived reliable conclusions on the range of the quality traits measured from each entry. Our results provide some useful information for genetic improvement of the cultivated groundnut.

CONCLUSION

On the basis of above finding concluded that the genotype ICG 6057 identified as best genotype for pod yield (47.53q/ha), kernel yield (49.62q/ha) and pod yield/plant (14.83g). High Genotypic Coefficient of Variation and Phenotypic Coefficient of Variation values were recorded for character like kernel yield(q/ha) while highest heritability were observed for plant height(cm). The maximum genetic advance was recorded for field emergence and maximum value of genetic advance as percent of mean was recorded for the characters like- kernel yield(q/ha) followed by pod yield(q/ha), field emergence, seed index(100 kernel weight) and pod yield/plant(g). Hence, these genotypes can be utilized as parents in the future hybridization programme.

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REFERENCES

- Burton, G. W., & Devane, E.W. (1953). Estimating heritability, GCV and PCV in tall Fescue from replicated clonal material. *Journal of Agronomy*, 45, 171-181.
- Directorate of Groundnut Research. (2015). Genetic Improvement of Groundnut. Annual Report, 2015-16. *Directorate of Groundnut Research, Junagadh, Gujarat*, India, pp. 152.
- Johnson, R. E., Robison, H. W., & Comstock, H. F. (1955). Estimates of Genetic and environmental variability in rice. *Journal of Agronomy*, 47, 314-318.
- Kadam, P.S., Desai, D.T., Jagdish, U., Chauhan, D.A., & Shelke, B.L. (2007). Variability, heritability and genetic advance in groundnut. *Journal of Maharashtra Agricultural University*, 32, 71-78.
- Kumar, R., Hariprasanna, A.L., Lalwani, K., and Singh, H.B. (2008). Genetic improvement in Spanish type groundnut (*Arachis hypogea* L.) varieties in India over the years. *Journal of Oilseeds Research*, 27(1), 1-7.
- Narasimhulu, R., Kenchanagoudar, P.V., & Gowda, M.V.C. (2012). Study of genetic variability and correlations in selected Groundnut Genotypes. *International Journal of Applied Biology and Pharmaceutical Technology*, 3, 355-358.
- Narayanan, R., & Murugan, S. (2013). Studies on variability and heritability in sesame (*Sesamum indicum* L.). *International Journal of Current Agricultural Research*, 2(11), 052-055.
- Panase, V.G., & Sukhatme, P.V. (1967). Statistical methods for agricultural workers (2ndEd.). *Indian Council of Agricultural Research*, New Delhi, pp. 259.
- Parameshwarappa, K.G., Kenchanagoudar, P.V., Bentur, M.G., & Patil, R.K. (2005). Genetic variability and correlation in adopted genotypes of Spanish bunch groundnut. National Symposium: Enhancing Productivity of Groundnut for Sustaining Food and National Security, NRCG, Junagadh, pp. 74-75.
- Savaliya, J.J., Pansuriya, A.G., Sodavadiya, P.R., & Leva, R.L. (2009). Evaluation of inter and intraspecific hybrid derivatives of Groundnut (*Arachis hypogea* L.) for yield and its components. *Legume Research*, 32(2), 129-132.
- Shukla, A. K., & Rai, P. K. (2014). Evaluation of Groundnut Genotypes for Yield and Quality Traits. *Annals of Plant and Soil Research*, 16(1), 41-44.
- Singh, S., Kumar, A., Tiwari, V, Maurya M. K., Chaurasia, A. K., & Rai, P. K. (2013). Study on the performance of ground nut (*Arachis hypogaea* L.) accessions for seed yield and quality parameters for north east plain zone of Uttar Pradesh. *Progressive Research*, 8(2), 237-240.
- Singh, S.B. (2005). Genetic variability and character association in groundnut. *Annal of Agricultural Research*, 26, 1-4.
- Singh, S.B., & Singh, J.P. (1999). Estimates of variability parameters for some quantitative characters in groundnut (*Arachis hypogaea* L.). *Indian Journal of Agricultural Science*, 69, 800-801.
- United State Department of Agriculture (2019). World Agricultural Production. *Circular Series WAP*, 10-18 October 2019, pp. 39-45.