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Assessment of genetic variability, heritability and genetic advance for physio-biochemical and root traits in groundnut (*Arachis hypogaea* L.) under irrigated conditions

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Abstract
Crop: Groundnut is one of the proteins and oil-producing legume crop of arid and semi-arid regions of the world.
The Objective of the study: To estimate the genotypic coefficient of variation, heritability and genetic advance for physio-biochemical and root related traits among groundnut germplasm under the irrigated condition and To put guideline to establish a breeding program for developing genotype (s) with higher yield using suitable selection criteria through genetic variability studies.
Research location and season: The College of Horticulture, Hiriyur during rabi 2016-17.
Experimental design: Randomized complete block design with two replications.
Methodology: forty groundnut genotypes including ICRISAT based advanced breeding lines and existed cultivars were evaluated under field condition. The crop was taken care of as per the standard recommended package of practices. Data was recorded on physio-biochemical and root related parameters at different stages of crop growth. The resulted mean data was subjected to statistical analysis using Genstat 14.1 software.
Results: Results revealed highly significant differences for all the traits under study indicating the presence of genetic variation among the genotypes**.** The characters like MSI (99.89 & 112.99%), leaf phenols (99.63 & 74.26%), seed phenols (99.06 & 73.05%) and root to shoot ratio (86.19 & 21.04%) exhibited high heritability coupled with high genetic advance over mean.
Conclusion: It can be concluded that the presence of additive gene action in governing these traits. Thus, there is ample scope for improving these characters based on the direct selection from the genetic stock studied which means if these characters are subjected to any selection scheme for exploiting fixable genetic variance; a widely adopted genotype can be developed.

Keywords: additive gene action, selection, protein, phenolic content

1. Introduction

Groundnut (*Arachis hypogaea* L.,), is a segmental allotetraploid, a member of family *Fabaceae*, and self-pollinated annual leguminous oilseed cash crop having genome AABB and somatic chromosome number 2n = 4x = 40. It is popularly known as the “King” of oilseeds or “Wonder nut” or “Poor man’s cashew nut”. It is grown throughout the tropical, sub-tropical and warm temperate regions of the world. Its seeds are valued both for its oil and protein contents. (Preeti Pachauri and RS Shikarvar 2019; Anamika *et al*. (2018) [1]; Manjubhargavi *et al*., 2018) [11].

Presence of genetic variability is pre-requisite to upgrade a crop as per requirement by providing sufficient scope for selection. Yield, being a quantitative trait, is having low heritability and more influenced by environmental effects. Therefore, direct selection based upon the phenotype can be misleading. Hence, proper understanding of heritable nature of variation is important before devising 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 (Anamika *et al*. (2018) [1]; Omima *et al*. 2018) [15].

With this background, the present study was undertaken to achieve the following objectives:

a) To estimate the genotypic coefficient of variation, heritability and genetic advance for physio-biochemical and root related traits among groundnut germplasm under irrigated condition.
b) To put guideline to establish a breeding program for developing genotype (s) with higher yield using suitable selection criteria through genetic variability studies.

2. Material and Methods

Forty groundnut genotypes comprised of advanced breeding lines and existing cultivars procured from different sources were evaluated at the College of Horticulture, Hiriyur (located in Central Dry Zone (Zone-IV) of Karnataka at 13º 57' North latitude, and 76º 40' East longitudes with an altitude of 630 meters above the mean sea level) during Rabi 2016-17 using randomized complete block design with two replications. The details of the genetic material employed in this study are furnished in table 1. Each entry was represented by two rows of 3 meter length following a spacing of 30 cm X 10 cm at a depth of 4cm approximately. The crop was taken care of the standard recommended package of practices. The data was recorded on randomly tagged five plants per genotype per replication for various physiological, biochemical and root related parameters (Mentioned in table 2). The resulted mean data was subjected to the analysis of variance using Genstat 14.1 software at ICRISAT, Hyderabad. The formulae utilized to estimate the genetic estimates *Viz*., genotypic coefficient of variation (GCV), heritability (h^2), and genetic advance as percent mean (GAM @ 5%) cited in table no 3 and also their categorization are presented in table no 4.

Table 1: List of genotypes employed in the present experimental study

Sl. No.	Genotype	Source of collection	Features (Branching type)
1	ICGV 15114, ICGV 15119, ICGV 15120, ICGV 15122, ICGV 15123 ICGV 15124, ICGV 15138, ICGV 15141, ICGV 15143, ICGV 15145, ICGV 15146, ICGV 15148, ICGV 15149, ICGV 15151, ICGV 15152, ICGV 15153, ICGV 15154, ICGV 15158, ICGV 15159, ICGV 15161	ICRISAT, Patancheru	Erect type
2	SB-1, SB-14, SB-15, SB-17, VB, VB-11, VB-14	NBPGR, New Delhi	Erect type
3	DH-86, DH-101, DH-234, GPBD-4, GPBD-5, TMV-2, G2-52	UAS, Dharwad	Erect type
4	K-9, K-6, KCG-6, KCG-2	UAS, Bangalore	Erect type
5	LOCAL-1	Local	Erect type
6	R-2001-3	UAS, Raichur	Erect type

Table 2: Physiological, biochemical and root related parameters, their abbreviations, units of measurement and reference for groundnut genotypes understudy

Sl. No.	Trait	Estimation	Unit	Reference
1	Relative Water Content (RWC)	$\mathrm{RWC} = \frac{\mathrm{FW} - \mathrm{DW}}{\mathrm{TW} - \mathrm{DW}} \times 100$	Percentage (%)	Bars and Weatherly (1962) Dhopte and Manuel (2002)
2	Membrane stability index (MSI)	$\mathrm{MSI} = \frac{\mathrm{EC_b} - \mathrm{EC_a}}{\mathrm{EC_c}} \times 100$	Percentage (%)	Blum and Ebercon (1981)
3	SCMR	SPAD meter (Soil Plant Analytical Development)	Unit-less	
4	Leaf and seeds protein content	Bradford's Assay of protein estimation	Percentage (%)	(Bradford, 1976)
6	Leaf and seed phenolic content	Malik and Singh's Assay of phenols estimation	(µg/g)	Malik and Singh (1980).
8	Oil content	Nuclear Magnetic Resonance spectrometer (NMR)	Percentage (%)	
9	Root to shoot ratio	$\text{Root to shoot ratio} = \frac{\text{Length of root (cm)}}{\text{Length of shoot (cm)}}$	unit-less	
10	Root length	from base of the shoot to the tip of root	Centimeter (Cm)	

Where, FW -Fresh weight; DW -Dry weight and TW -Turgid weight of leaf samples

Table 3: Genetic variability estimates

Sl.no	Name of the indices	Equation	Reference
1	Genotypic variance(σg^2)	$(\sigma g^2) = \frac{\text{MSS (treatment)} - \text{MSS (error)}}{\text{Number of replications}}$	Lush (1940) and, Chaudhary and Prasad (1968).
4	Genotypic Coefficient of Variation (GCV)	$(\mathrm{GCV}) = \left(\frac{\sigma g}{\bar{X}}\right) \mathrm{x}\, 100$	Burton and Devane (1953).
6	Heritability (h^2_{bs}) (expressed as percentage)	$(h^2_{bs}) = (\sigma g^2/ \sigma p^2) \times 100$	Hanson *et al.*, (1956)
7	Genetic advance (GA)	$GA = h^2bs \times K \times \sigma P$	Johnson *et al.*, (1955) [10].
8	Genetic Advance as per cent Mean (GAM)	$GAM (\%) = (GA/\bar{X} \times 100)$	

Where, h^2bs = Heritability in broad sense; K = Selection differential, a constant (z/p) the value of which is 2.06 at 5% selection intensities; σP = Phenotypic standard deviation; $\bar{X}$ = Grand mean of the character; σp = Phenotypic standard deviation; σ^2g = Genotypic variance; σ^2p = Phenotypic variance

Table 4: Categorization of genetic estimates

Estimates	Categories			Reference
	Low	Moderate	High	
GCV (%)	0-10	10.1-20	20.1 and Above	Subramanian and Menon (1973).
Heritability (h^2) (%)	0-30	30.1-60	60.1 and Above	Robinson *et al.*, (1949).
GAM (%)	0-10	10.1-20	20.1 and above	Johnson *et al.* (1955) [10].

3. Results

3.1 Analysis of variance

The results of analysis of variance for various physiological, biochemical and root related traits under irrigated condition are presented in table 5. ANOVA results revealed highly significant differences for all the traits under study indicating the presence of genetic variation among the genotypes which were differing for genes controlling traits studied. Mean ± S.

Em values showed that the variation around the mean value was very low for root to shoot ratio (0.47 ± 0.01) followed by leaf proteins (0.73 ± 0.05) whereas, it was high for seed phenols (643.89 ± 15.78) followed by leaf phenols (369.50 ± 10.24) indicating that root to shoot ratio and leaf proteins were most stable indices and was useful to selections across genotypes. Similar results published by Shankar *et al*. (2019b & 2019a) [12], Meghala (2019) [8], Manjubhargavi *et al*., (2018) [11], Anamika and Amaravati (2018) [1].

Table 5: Mean squares of physio-biochemical and root traits in groundnut

Characters	Mean Squares		
	Replications (df=1)	Genotypes (df=39)	Error (df=39)
RWC (%)	25.43	27.08**	0.93
MSI (%)	1.02	606.78**	0.39
SCMR	45.62	28.84**	6.44
Leaf proteins (%)	0.05	0.02**	0.01
Seed proteins (%)	0.21	11.44**	1.39
Leaf phenols (µg/g)	4.02	113702.79**	209.72
Seed phenols (µg/g)	1360.11	105756.16**	498.31
Oil content (%)	19.55	17.86**	0.19
Root to shoot ratio	0	0.01**	0
Root length (cm)	57.16	2.16**	1.04
** , * = Significant at 0.01 and 0.05 probability level respectively			

Table 6: Estimates of Genetic parameters for physiological, biochemical and root attributes under normal moisture condition

Characters	Mean	Range	GCV (%)	h^2 (%)	GAM (%)
RWC (%)	75.66±0.68	66.44-86.24	4.78	93.36	9.51
MSI (%)	31.72±0.44	6.31-71.49	54.88	99.89	112.99
SCMR	42.17±1.79	35.13-50.37	7.93	63.50	13.02
Leaf proteins (%)	0.73±0.05	0.40-0.88	11.73	58.90	18.55
Seed proteins (%)	24.44±0.83	20.67-28.66	9.16	78.30	16.71
Leaf phenols (µg/g)	369.50±10.24	217.44-1548.94	64.47	99.63	74.26
Seed phenols (µg/g)	643.89±15.78	346.43-1638.50	35.63	99.06	73.05
Oil content (%)	45.98±0.31	40.46-51.37	6.46	97.93	13.19
Root to shoot ratio	0.47±0.01	0.35-0.61	11.00	86.19	21.04
Root length (cm)	12.25±0.72	9.45-15.38	10.45	75.95	18.76

3.2 Genetic variability parameters
The estimates of various genetic parameters under normal moisture condition are given in tables 6.

3.2.1 Mean
The characters like root to shoot ratio (0.47) and seed phenolic content (643.89 µg/g) recorded minimum and maximum mean values under irrigated conditions respectively. The mean of different quantitative traits as performed by the available genotypes suggested that selection of desirable genotypes based on the traits from materials evaluated, can be effective.

3.2.2 Range
The widest and narrow ranges were recorded for seed phenols (346.43-1638.50 µg/g) and root to shoot ratio (0.35-0.61) under normal moisture respectively. These findings (widest range) indicated the presence of sufficient variability among the genetic stock under study which would help in selecting the best genotypes from existing collection. However, narrow range value indicating minimum variation and less scope for selection from the present collection.

3.2.3 Genotypic coefficient of variation (GCV)
The GCV was ranged between leaf phenolic content (64.47%) and relative water content (4.78%). High GCV values were recorded for membrane stability index (54.88%), and, leaf and seed phenolic contents (64.47 and 35.63%). Similar results were published by Shankar *et al*. (2019b). Moderate GCV values were exhibited by leaf proteins (11.73%), root to shoot ratio (11.00%) and root length (10.45%) respectively. Relative water content (4.78%), SCMR (7.93%), seed proteins (9.16%) and oil content (6.46%) recorded low GCV values under irrigated condition. The low estimates of GCV for oil content and protein content were in agreement with the reports of Shankar *et al*. (2019b), Meghala (2019) [8], Manjubhargavi *et al*., (2018) [11], Anamika and Amaravati (2018) [1], Sudhir *et al*. (2008) [20] and Shukla *et al*. (2014) [18]. The high magnitude of GCV further revealed that greater extent of variability presence in the characters, thereby suggesting good scope for improvement through selection of this crop. These findings of clearly indicated that selecting genotypes through the traits with moderate to high GCV will be effective for further crop improvement under irrigated condition. However, low GCV under normal conditions indicated the presence of low variability among the tested genotypes.
The estimation of genetic coefficient of variation indicates the amount of genetic variation present for different desirable traits while the heritability gives an insight into the proportion of variation which is inherent.

3.2.4 Heritability (h^2)
The heritability values were distributed between MSI (99.89%) and leaf proteins (58.90%). In this study, heritability in broad sense was found to be high for all the characters except for leaf proteins (58.90%) suggesting the important role of genetic constitution in the expression of the character and such traits are considered to be dependent from breeding point of view. Similar results published by Shankar *et al*. (2019b & 2019a) [12]

[12], Meghala (2019) [8], Manjubhargavi *et al*., (2018) [11], Anamika and Amaravati (2018) [1]. From the above heritability estimates, it is clear that all the traits under study in normal moisture environment are less influenced by the environmental factors and are controlled by additive gene effect and selection will be effective for these characters.

3.2.5 Genetic advance over the mean (GAM)

The GAM was varied between relative water content (9.51%) and membrane stability index (112.99%). In this study, except relative water content (9.51%), all the traits exhibited high genetic advance over mean. Similar results published by Shankar *et al*. (2019b & 2019a) [12]

The heritability estimate gives an idea about the proportion of observed variability, which is attributed to genetic difference. Heritability in broad sense may play greater role about information of relative value of selection, but Johnson *et al.* (1955) [10] had shown that heritability and genetic advance should be jointly considered for reliable conclusion. In crop improvement programme, selection is practiced directly or indirectly. Selection parameters include the study of heritability and genetic advance (direct selection parameters) and correlation between yield and component traits and path coefficient analysis (indirect selection parameters).

3.2.6 Heritability (h^2) and Genetic advance over the mean (GAM)

Out of 11 characters studied, in the present study, High heritability estimates were accompanied by lower genetic advance over the mean for relative water content (85.35 and 4.55%). Similar results were published by Meghala *et al*. (2019) [8] for RWC. This suggests that selection may not be useful for the improvement of this trait because of the narrow range of phenotypic variation among the genotypes in respect to this character. In other words, this trait is influenced by higher environmental effect and non-additive gene action.

High heritability coupled with moderate GAM was observed for SCMR (63.50 & 13.02%), seed proteins (78.30 & 16.71%), oil content (97.93 & 13.19%) and root length (75.95 & 18.76%) implied importance of additive gene action and lesser environmental influence. In other words, these traits indicated that their manifestation is governed by additive lesser environmental effect and therefore, selection should be practiced in later segregating generations i.e. by hybridization programme to exploit hybridity. The results are on par with the results of Shankar *et al*. (2019b & 2019a) [12], Anamika and Amaravati (2018) [1] for SCMR and Meghala *et al*. (2019) [8] for SCMR and oil content.

However, moderate heritability alongside with moderate GAM was noticed for leaf proteins (29.35, 6.00%) indicating this trait is governed by both additive and non-additive gene action with moderate influence of environment in its inheritance. The traits controlled by non-additive gene action can be improved by hybrids and inter-mating among selected ones in early generation followed by selection.

The characters like MSI (99.89 & 112.99%), leaf phenols (99.63 & 74.26%), seed phenols (99.06 & 73.05%) and root to shoot ratio (86.19 & 21.04%) exhibited high heritability coupled with high GAM indicating the predominance of additive gene components in governing these traits. Thus, there is ample scope for improving these characters based on direct selection from the genetic stock studied which means if these characters are subjected to any selection scheme for exploiting fixable genetic variance; a widely adopted genotype can be developed. Similar results were reported by Shankar *et al*. (2019b & 2019a) [12] for MSI and root to shoot ratio.

4. Conclusion

It can be concluded that the existence of significant genetic variability among the tested material for the traits studied suggesting the possibility of improving the traits through direct and indirect selection. Traits with high heritability and genetic advance are important traits which should be given attention in order to bring an effective response of yield improvement of the concerned varieties under saline sodic soil.

5. Future Line of Work

a. The traits with high heritability coupled with GAM under investigation could successfully be used selection for further crop improvement.

b. Genetic differences among genotypes give great opportunities to use these genotypes as a source of genetic material for the further crop improvement in groundnut.

6. References

1. Anamika Roy, Lal Ahmed M, Y Amaravathi, K Viswanath, J Dayal Prasad Babu and B Sreekanth. Genetic Variability, Heritability and Genetic Advance of yield and yield attributes in Groundnut (*Arachis hypogaea* L.). The Andhra Agric. J. 2018; 65(1):88-91.
2. Bars HD, Weatherly PE. A re-examination of the relative turgidity technique for estimating water deficits in leaves. Australian J. Biol. Sci. 1962; 15:413-428.
3. Blum A, Ebercon E. Cell membrane stability as a measure of drought and heat tolerance in wheat. Crop Sci. 1981; 21:43-47.
4. Bradford MM. A rapid and sensitive for the quantitation of microgram quantities of protein utilizing the principle of protein-dye binding. Analytical Biochemistry. 1976; 72:248-254.
5. Burton GN, Devane EM. Estimating heritability in tall fescue (*Festuca arundianacea* L.) from replicated clonal material. Agron. J. 1953; 45:478-481.
6. Chaudhary LB, Prasad B. Genetic variation and heritability of quantitative characters in Indian mustard (*Brassica juncea*). Indian J. Agric. Sci. 1968; 38:820-825.
7. Dhopte AM, Manuel LM. Principals and Techniques for Plant Scientists. 1st Edn. Updesh Purohit for Agrobios, Jodhpur, India. 2002; 81:373. ISBN: 7754-116.
8. G Meghala Devi, M Shanthi Priya, M Reddi Sekhar, P. Latha.Variability Studies for Yield, Yield Attributes, Water Use Efficiency and Quality Traits in Groundnut (*Arachis hypogaea* L.). Ind. J. Pure App. Biosci. 2019; 7(5):393-398.
9. Hanson CH, Robinson HR, Comstock RS. Biometrical studies of yield in segregating population of korean lespedeza. Agron. J. 1956; 48:268-272.
10. Johnson HW, Robinson, HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Agron. J. 1955; 47:413-418.
11. M Manjubhargavi, M Shanthi Priya, D Mohan Reddy, B Ravindra Reddy. Variability studies in groundnut (*Arachis hypogaea* l.) under organic management. Frontiers in Crop Improvement. 2018; 6(1):56-59.
12. M Shankar BN. Harish Babu, R Gobu and Sheshaiah. Studies on Genetic variability, Heritability and Genetic Advance in Groundnut (*Arachis hypogaea* L.) genotypes under normal and osmotic Stress in *In vitro* Condition. Int.J.Curr.Microbiol.App.Sci. 2019a; 8(5):473-483.

13. M Shankar, BN Harish Babu, R Gobu, Sheshaiah. Studies on genetic variability, heritability and genetic advance in groundnut (*Arachis hypogeae* L.) genotypes under normal and moister stress condition in vegetative stage. Journal of Pharmacognosy and Phytochemistry. 2019b; 8(3):4271-4277.
14. Malik CP, Singh MB. Plant Enzymology and Histoenzymology, Kalyani Publishers, New Delhi, 1980, 286.
15. Omima BHH, Ahmed HAA, Adel MF, Amin ASA. Variability Heritability and Genetic Advance of Some Groundnut Genotypes (*Arachis Hypogaea* L.) under Saline Sodic Soil. Ann Rev Resear. 2018; 1(1):0018-0022.
16. Preeti Pachauri, RS Shikarvar. Study on genetic variability, heritability and genetic advance in groundnut (*Arachis hypogaea* L.). International Journal of Chemical Studies. 2019; 7(4):1768-1770.
17. Robinson HF, Comstock RE, Harvey VH. Estimates of heritability and degree of dominance in corn. Agron. J. 1949; 41:353-359.
18. Shukla AS, Rai PK. Evaluation of groundnut genotypes for yield and quality traits. Annals of Plant and Soil Research. 2014; 16(1):41-44.
19. Subramanian SS, Menon M. Heterosis and inbreeding depression in rice. Madras Agric. J. 1973; 60:1139.
20. Sudhir KI, Venkataravana P, Gururaja Rao MR. Evaluation of new germplasm and advanced breeding lines of groundnut (*Arachis hypogaea L*.) Under late kharif situation. Legume Research. 2008; 31(4):254-258.