Genetic Variability and Correlation Studies among Advanced Lines of Groundnut under Agro-Climatic Conditions of North East Hill (NEH) Region

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The introduction of groundnut germplasm in North East Hill (NEH) region of India is essential to enrich genetic resources for crop improvement. The soil under NEH region is characterized by with pH less than 5.5 (acidic) and Ca, P, Mg and K deficiencies. In view of this, a field experiment was conducted during *Kharif*, 2007 at foothills of Experimental and Extension Centre, Andro, Imphal East, Manipur to assess the genetic parameter, character association and path analysis for nine different morphological traits among eighteen advanced genotypes in groundnut. The genotypes demonstrated highly significant difference ($P<0.01$) for all the traits studied. High estimates of GCV and heritability coupled with genetic advance as per cent of mean were registered for number of mature pods, number of primary branches and pod yield. The correlation and path coefficients analysis also showed that number of mature pods and number of primary branches had significant and positive correlation with pod yield as well as maximum positive direct effect on pod yield. Hence, results clearly showed that genetic improvement of pod yield can be initiated by putting positive selection pressure on number of mature pods and number of primary branches in groundnut. The hierarchical analysis by complete linkage method using Euclidean distance classified the eighteen advanced genotypes in two genetically diverse clusters with 5 (I) and 13 (II) genotypes. The second cluster further divided in to two clusters (II A and II B) with 7 and 6 genotypes, respectively. The genotypes from diverse clusters may be utilized in crossing programme to produce desirable segregants for developing high yielding acidic tolerant genetic stock/varieties.

Key Words: *Arachis hypogaea*, Correlation coefficients, Genetic variability, Hierarchical clustering Path analysis,

Introduction

Groundnut (*Arachis hypogaea* L.) is the World's fourth most important source of edible oil and third most important source of vegetable protein. Groundnut seeds contain high quantity of edible oil (50%), easily digestible protein (20%) and carbohydrates (25%). In India, about 80% (6 million ha) of total groundnut area is confined to Gujarat, Andhra Pradesh, Tamil Nadu, Karnataka, and Maharashtra with 84% (6 million tonnes) of total production (Anonymous, 2008). With the demand of ever increasing population as well as malnutrition problem, the expansion of groundnut cultivation in the non-traditional area of north east is the only alternative where the yield potential of 3 to 4 t/ha of pods are easily achieved in 100-120 days (Singh *et al*., 2006). In order to exploit north eastern areas of the country, the evaluation of superior genotypes is important for utilization in breeding programme or for using them as such as varieties after conducting preliminary yield trials. Identification of superior genotypes, therefore, becomes imperative for promoting its introduction, productivity and quality of produce. However, for their efficient use in breeding programme the introduced genotypes need to be classified into different groups based on variability available for the best exploitation of heterosis as well as for ease in selection. The selection of superior genotypes based on yield per se is very complicated in groundnut compared to other crops due to the fact that economic part (pods) is formed under the soil which necessitates to establish the magnitude and direction of association of pod yield with its direct and indirect components. Hence, basic information on genetic parameters and nature of association is required in formulating appropriate breeding programme for targeted environments. In view of the above perspectives, the present study was taken up to assess genetic parameters and nature of association among yield and its contributing characters in advance breeding lines of groundnut for rainfed situation under foot hills of Manipur.

Materials and Methods

The eighteen semi spreading advanced lines including 10 from International Crop Research Institute for Semi Arid Tropics (ICRISAT), Hyderabad; 6 from Bhabha Atomic Research Centre (BARC), Mumbai and 2 released varieties were evaluated at Experiment and Extension Centre, Andro, Imphal East District, Manipur (latitude 24°45'N, longitude 94°03'N, altitude 810 m above msl and average annual rainfall 1,400 mm) during *Kharif*,

2007. The soil of experimental field is sandy clayey loam having pH 5 to 5.3, EC 0.25 to 0.29 dsm^{-1} and 0.06 to 0.72% organic carbon. The availability of N, P and K in the soil is 283, 18.6 and 124 kg/ha, respectively. The experiment was laid out in Randomized Complete Block Design with three replications. Each genotype was sown in raised bed of 5×1.5 m^2 size accommodating 5 rows each of 5 m length with spacing of 30×10 cm. The recommended package of practices was followed to raise the good crop. The lime application at recommended dose of 300 kg/ha was also applied as side placement at the time of pegging (35-40 days after sowing) due to acidic nature of soil. At flowering and maturity stages, the observations were recorded on days to 50% flowering, days to maturity, plant height (cm), primary branches/plant, mature pods/plant, 100-kernel weight (g), shelling out turn (%), oil content (%) and pod yield/plant (g) from ten randomly selected plants in each plot in each replication. The plot mean values were subjected to analysis of variance. The genotypic and phenotypic coefficients of variation (GCV and PCV) were estimated according to the method outlined by Burton (1952). Heritability (broad sense) and expected genetic advance (as per cent of mean) was estimated as per Johnson *et al*. (1955). Correlation coefficients and path analysis were calculated as explained by Singh and Chaudhary (1985). The advance lines were also clustered by complete linkage method using Euclidean distances. In complete linkage method, the distance between clusters are determined by the greatest distance between any two genotypes in the different clusters. Estimation of Euclidean distance and cluster analysis was performed by Statistica (1996).

Results and Discussion

Variability Analysis

The analysis of variance revealed highly significant differences for all the traits under study indicating adequate scope for selection of superior and diverse genotypes (Table 1). The extent of variability measured in terms of range, grand mean, phenotypic coefficients of variation (PCV), genotypic coefficients of variation (GCV), heritability (broad sense) and genetic advance of nine characters are presented in Table 2. The narrow differences between phenotypic and genotypic coefficients of variation were observed for all the characters indicating the less influence of environment on expression of characters studied. The high estimates of PCV and GCV were obtained for pod yield, number of mature pods and number of primary branches and revealed that genotypes have a broad genetic background as well as good potential that will respond positively to selection for improving these characters. The higher magnitude of GCV and PCV was also reported by Kadam *et al.* (2007) for pod yield, number of mature pods and primary branches; and by John *et al*. (2005) for number of mature pods and pod yield. The moderate PCV and GCV values were also observed for 100-kernel weight, plant height

Table 1. Analysis of variance showing mean of squares for nine characters in advanced groundnut genotypes

Source of variation	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ plant	Mature pods/ plant	100-kernel weight (g)	Shelling (%)	Oil content (%)	Pod yield/ plant (g)
Replications	0.68	4.09	14.45	0.68	4.80	15.07	13.51	2.98	1.06
Genotypes	52.88**	241.84**	46.55**	14.79**	50.33**	261.66**	20.81**	35.07**	30.03**
Error	1.39	2.43	3.27	0.86	1.02	3.26	2.64	2.40	0.34

** Significant at P<0.01

Table 2. Estimates of genetic parameters for nine characters in advanced groundnut genotypes

Characters	Mean±SE	Range	Coefficient of variation (%)		Heritability (%) (broad sense)	Genetic advance	Genetic advance as % of mean
			GCV	PCV			
Days to 50% flowering	32.9±0.68	26.3-44.3	12.58	13.08	92.5	8.20	24.92
Days to maturity	110.96±0.90	98.3-125.6	8.05	8.17	97.04	18.12	16.33
Plant height (cm)	26.38±1.04	20.9-32.9	14.39	15.95	81.49	7.07	26.80
Primary branches/plant	8.33±0.53	5.4-13.4	25.85	28.4	84.42	4.08	48.94
Mature pods/plant	12.15±0.58	7.2-22.4	33.36	34.39	94.12	8.10	66.69
100-kernel weight (g)	52.47±1.04	39.9-68.8	17.68	18.02	96.35	18.77	35.76
Shelling (%)	64.39±0.93	59.4-68.8	3.82	4.58	69.52	4.23	6.57
Oil content (%)	42.87±0.89	37.0-49.7	7.69	8.50	81.91	6.15	14.35
Pod yield/plant (g)	8.06±0.33	4.4-14.6	39.10	39.65	96.71	6.37	79.06

and days to 50% flowering indicating substantial amount of genetic variability. The characters, *viz.*, shelling per cent and oil content had the lower estimates of GCV and PCV indicating a limited opportunity to further improve these characters.

The coefficient of variation indicated only the extent of variability present in different characters and did not indicate its heritable portion. Heritable portion can be ascertained with greater degree of accuracy when it is associated with genetic advance. In present study, high heritability was accompanied with high genetic advance as per cent of mean for pod yield, number of mature pods, 100-kernel weight and primary branches indicating the presence of additive genetic effects. Similar observations were also reported by John *et al.* (2005) for both number of mature pods and pod yield; and by Kadam *et al.* (2007) for pod yield. The high heritability along with moderate to low genetic advance as per cent of mean were observed for days to 50% flowering, plant height, days to maturity, oil content and shelling per cent. This suggested that these characters might be controlled by both additive and non-additive gene action and selection based on such characters may be effective to some extent.

High estimate of genotypic coefficients of variation and heritability coupled with genetic advance as per cent of mean was registered for number of primary branches, number of mature pods and pod yield indicating predominance of additive gene effects and simple directional selection may be effective to improve these characters.

Correlation and Path Coefficients Analysis

The genotypic and phenotypic correlation studies are essential in evaluating the possibility of simultaneous improvement for many characters and also the impact of selection for one trait on the other related ones under particular environment. The genotypic correlations were generally higher than their corresponding phenotypic correlations (Table 3). The lower values of phenotypic correlations may be attributed to lower modifying effect of environment on the association of characters at the gene level (Mamun-Hossain and Joarder, 1987). The results pertaining to correlation revealed that number of primary branches and number of mature pods were highly significant and positively correlated with one another as well as pod yield at both genotypic and phenotypic levels which indicated that these two characters are important components for improvement of pod yield in groundnut and also the possibility of simultaneous improvement of these trait by selection. Such positive association of pod yield with number of primary branches and mature pods was also reported by Lakshmaiah *et al.* (1983). The pod yield exhibited non-significant but positive association with days to 50% flowering (r_g=0.374, r_p=0.370), days to maturity (r_g=0.427, r_p=0.414) and plant height (r_g=0.454, r_p=0.393), whereas, it showed non-significant and negative association with 100-kernel weight (r_g=0.249, r_p=-0.242) and shelling per cent (r_g=-0.324, r_p=-0.265). The oil per cent had relatively weak positive association with pod yield (r_g= 0.085, r_p= 0.102). Similar results were in agreement with findings of Uddin *et al.* (1995) for 100-kernel weight and of Mane

Table 3. Genotypic (G) and phenotypic (P) correlation coefficients among nine characters in advanced groundnut genotypes

Characters		Days to maturity (cm)	Plant height plant	Primary branches/ plant	Mature pods/ (g)	100-kernel weight (g)	Shelling (%)	Oil content (g)	Pod yield/ plant
Days to 50% flowering	G	0.816 **	0.301	0.491*	0.171	-0.063	-0.477*	0.301	0.374
	P	0.783 **	0.255	0.469*	0.173	-0.047	-0.350	0.285	0.370
Days to maturity	G		0.404	0.561*	0.356	-0.194	-0.503*	0.442	0.427
	P		0.362	0.509*	0.343	-0.190	-0.435	0.385	0.414
Plant height (cm)	G			0.218	0.460	-0.186	-0.263	0.269	0.454
	P			0.184	0.435	-0.185	-0.218	0.274	0.393
Primary branches/plant	G				0.729**	-0.425	-0.349	0.414	0.744**
	P				0.638**	-0.404	-0.318	0.338	0.670**
Mature pods/plant	G					-0.248	-0.345	0.332	0.790**
	P					-0.234	-0.274	0.286	0.752**
100-kernel weight (g)	G						0.483*	0.098	-0.249
	P						0.429	0.087	-0.242
Shelling (%)	G							-0.063	-0.324
	P							0.019	-0.265
Oil content (%)	G								0.085
	P								0.102

,*= Significant at P<0.05 and P<0.01 levels, respectively *et al*. (2008) for days to maturity and oil per cent. In the present study, the 100-kernel weight displayed positive and significantly genotypic correlation with shelling per cent. Days to 50% flowering and days to maturity exhibited positive and significant genotypic and phenotypic correlations with each other and with primary branches which indicated that higher number of primary branches might be expected with prolonged days to maturity.

Path coefficient analysis (Table 4) based on pod yield revealed that all the traits except shelling per cent and oil content exhibited positive direct effects on pod yield. Number of primary branches made maximum and positive direct contribution (0.691) and also exerted appreciable magnitude of indirect influence (0.504) towards pod yield via number of mature pods. Pod yield was highly influenced by number of primary branches and mature pods both directly and indirectly. The direct effect of number of mature pods on pod yield was also observed by Uddin *et al*. (1995) and Mane *et al*. (2008). The genotypic correlation coefficients of these two characters were also positive and highly significant. Hence, emphasis on these two traits for groundnut improvement may be rewarding. The plant height showed moderate direct effect on pod yield in spite of non-significant but considerable estimate of correlation coefficients with pod yield. This indicated that plant height could be included in selection criteria list. On the other hand, oil per cent exerted the highest negative direct effect (-0.428) on pod yield following by shelling per cent (-0.016). Similar observations were also recorded by Francies and Ramalingam (1997) in F_2 population of groundnut. It was observed that correlation of 100-kernel weight with pod yield was negative but its direct effect was moderate and positive, so that a restricted simultaneous model is to be followed, *i.e.*, restrictions are to be imposed to nullify the undesirable indirect effects in order to make use of the direct effects (Singh and Kakar, 1977). Further, the residual factor was low which suggests that the variables chosen in the present study were sufficient to explain pod yield**.** These findings are in agreement with Azad and Hamid (2000).

The results of correlation and path coefficients analysis revealed that number of primary branches and mature pods had highly significant and positive correlation as well as maximum direct effect on pod yield. Thus, selection for these two traits could be of greater importance for selecting better genotypes for pod yield in groundnut.

Hierarchical Cluster Analysis

Hierarchical cluster analysis has been carried out to choose the parents for hybridization. This approach helps in reducing the large amount of data about the parents to manageable proportions (Peter and Martinalli, 1989). Multivariate hierarchical clustering was performed for nine different morphological characters (Fig.1). The eighteen advanced lines were mainly grouped into two genetically diverse clusters with 5 (I) and 13 (II) genotypes at 36.5 linkage distance units. The cluster II was again divided into two sub clusters, *i.e.*, II A and II B at 31.8 linkage distance units with 7 and 6 genotypes, respectively. Based on inter cluster distance and *per se* performance, the genotypes, namely, ICGV 4122 and ICGV 4148 (cluster I), and ICGV 3157 and ICGV 3063 (cluster IIA) for pod yield along with primary branches and mature pods; ICGV 3206 (cluster IIA) for earliness and TDG 56 (cluster IIB) for large seed size (as confectionary purpose) due to high 100-kernel weight (>60 g) may be utilized in groundnut breeding programme. Further, the clustering pattern from dendrogram clearly depicted that the lines from same location were grouped in to single cluster. Thus, again choice of parents for hybridization should be decided on the basis of genetic diversity rather than geographical diversity.

Table 4. Genotypic path analysis of different quantitative characters on pod yield in advanced groundnut genotypes

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ plant	Mature pods/ plant	100-kernel weight (g)	Shelling (%)	Oil content (%)	r_g with pod yield/ plant (g)
Days to 50% flowering	**0.006**	0.018	0.088	0.340	0.057	–0.015	0.008	–0.129	0.374
Days to maturity	0.005	**0.022**	0.118	0.388	0.120	–0.046	0.008	–0.189	0.427
Plant height (cm)	0.002	0.009	**0.291**	0.150	0.155	–0.044	0.004	–0.115	0.454
Primary branches/plant	0.003	0.012	0.063	**0.691**	0.246	–0.101	0.005	–0.177	0.744**
Mature pods/plant	0.001	0.007	0.135	0.504	**0.338**	–0.059	0.005	–0.142	0.790**
100–kernel weight (g)	–0.000	–0.004	–0.054	–0.294	–0.084	**0.238**	–0.008	–0.042	–0.248
Shelling (%)	–0.003	–0.011	–0.076	–0.241	–0.116	0.115	**–0.016**	0.027	–0.323
Oil content (%)	0.002	0.009	0.078	0.286	0.112	0.023	0.001	**–0.428**	0.084

Residual = 0.404; Direct effects = diagonal; Indirect effects = above and below diagonal

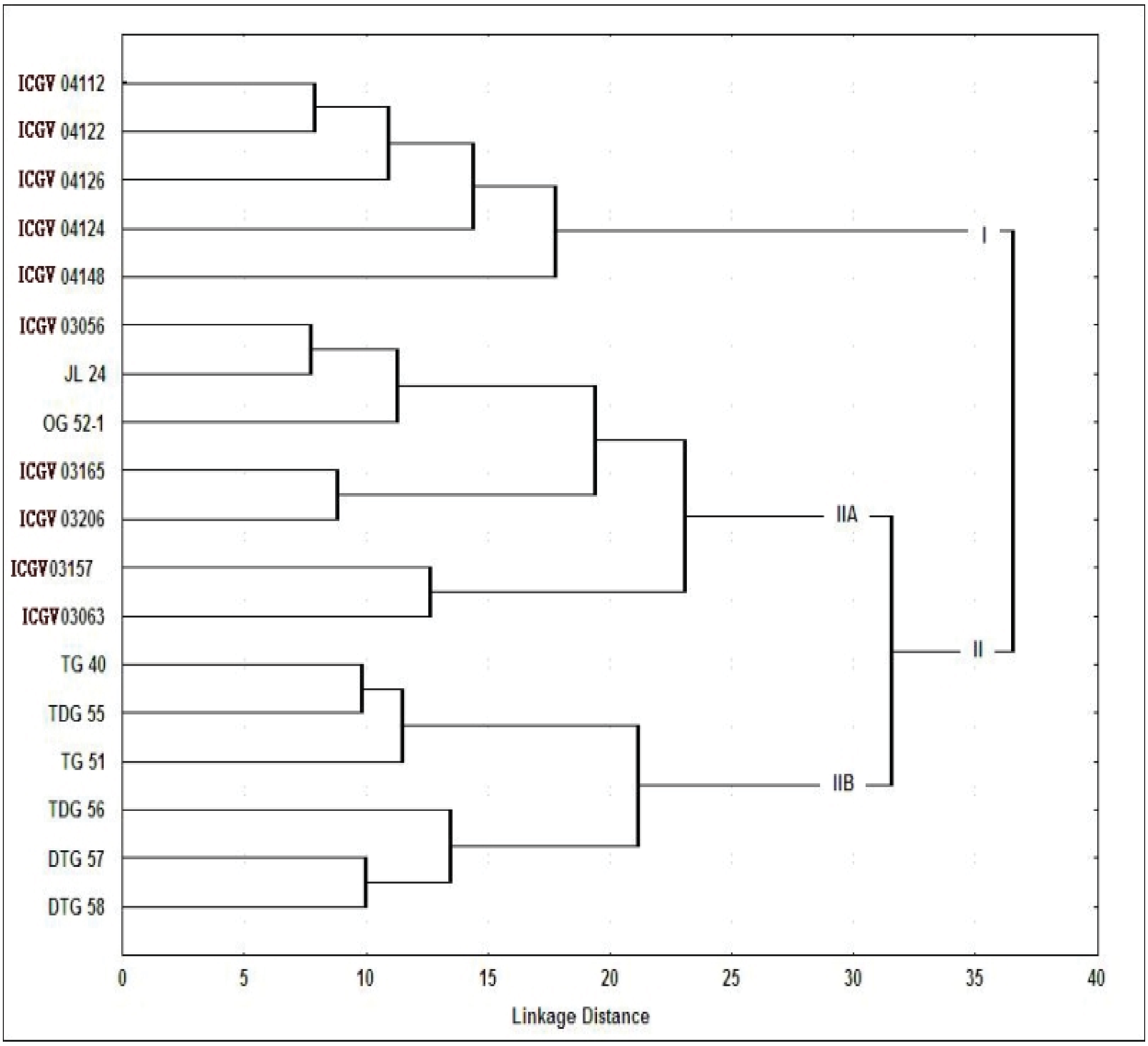

Fig. 1: Dendrogram depicting the genetic diversity among groundnut breeding lines

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