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ASSESSMENT OF YIELD AND YIELD RELATED TRAITS IN RECOMBINANT INBRED LINES OF GROUNDNUT (*ARACHIS HYPOGAEA* L.) USING PRINCIPAL COMPONENT AND CLUSTER ANALYSIS

M. S. DARVHANKAR[1]*, J. H. KAMDAR[2], S. V. KASUNDRA[2], M. D. JASANI[2], G.U. KULKARNI[1] AND S. K. BERA[2]
[1]Department of Genetics and Plant Breeding, Junagadh Agricultural University, Junagadh - 362 001, INDIA
[2]ICAR- Directorate of Groundnut Research, P.B-5, Ivnagar Road, Junagadh - 362 001, Gujarat, INDIA
e-mail: mayurdarwankar@gmail.com

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***Corresponding author**

ABSTRACT
In the current set of an experiment sixty-nine Recombinant Inbred Lines (F_8 generation) obtained from a cross between genotypes ICG 4747 and TMV2NLM along with two parents and five elite cultivars were evaluated over three seasons by using principal component and cluster analysis. Analysis of variance revealed significant differences among genotypes for all the traits under study. The highest GCV and PCV were observed for pod yield per plant (PY) and harvest index (HI). Significant positive correlation was observed between pod yield per plant (PY) with biological yield per plant (BY), harvest index (HI), kernel yield per plant (KY), 100-kernel mass (HKM), sound mature kernel (SMK) and specific leaf area (SLA). Principal component analysis indicated that four important components accounted for about 73.2% of the total variation among traits in groundnut cultivars. The traits like pod yield per plant (PY), harvest index (HI), kernel yield per plant (KY), 100-kernel mass (HKM), and sound mature kernel (SMK) showed considerable positive loadings on PC1. On the other hand PC2 was corresponding diversity due to shelling out tern (SOT), root diameter (RD), 100-kernel mass (HKM) and kernel yield per plant (KY) with their considerable positive loadings.

INTRODUCTION

Cultivated groundnut (*Arachis hypogaea* L.) is an important oilseed crop of the world, which ranks thirteenth in its importance among the world food crops. 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. The seeds contain ~50 percent oil, ~25 percent protein and ~18 percent carbohydrates and are rich source of B-complex vitamins, especially thiamine and nicotinic acid. Thus, the crop is equally important as food crop too.

The knowledge on genetic variability is the basic requirement in any crop improvement programme (Kumar, 2015). The crosses between parents with maximum genetic divergence are generally the most responsive for genetic improvement (Arunachalam, 1981). Further, the variability should be highly heritable as improvement by selection depends on heritability, selection intensity and genetic advance of the character. Heritability and genetic advance estimates help the breeder to apply appropriate breeding methodology in the crop improvement programme. (Johnson *et al.,* 1955 and Darvhankar *et al.,* 2013). Thrust of any crop improvement programme is to enhance economic yield which is a complex dependent character, mostly inherited quantitatively and is determined by a number of yield components, greatly affected by environmental factors. The component traits which have high heritability and positive correlation with yield can be used in the indirect selection for improvement of yield. In determining the potential of genetically different lines and cultivars, breeders have to observe various traits that influence yield. Accurate evaluation of these characters is made more difficult by the genotype by environment interaction (Tadesse and Bekele, 2001). The objectives of the present study therefore, are to evaluate and determine the variation pattern in recombinant inbred lines of groundnut, identify characters that differentiate the genotypes into different groups, suggest the potential genotypes that could be used in improvement programme and appraise the suitability of the various multivariate techniques for classification of variation in groundnut.

MATERIALS AND METHODS

Plant materials

The material for the present investigation comprised of 69 Recombinant Inbred Lines (F_8 generation) of groundnut obtained by crossing between two parents ICG 4747 and TMV2 NLM, and five elite cultivars as a check (Somnath, Kaushal, GG-20, Girnar-2 and ICGS-76). ICG 4747 is an elite Valencia germplasm line having high specific leaf area (Basu and Nautiyal, 2004). TMV2NLM is an induced narrow leaf mutant (medium SLA and low HI) of an Indian Spanish cultivar, TMV 2 (Nigam *et al.,* 2001). These 74 genotypes were grown in three different seasons *viz*. *kharif*- 2013, *rabi*-2014 and *kharif*-2014 at ICAR- Directorate of Groundnut Research (ICAR-DGR) (formerly National Research Centre for Groundnut),

Junagadh, India (21º31′N, 70º36′E; alt.61m). The soil was a Vertisol Ustochropt (pH7.5) (C. Lal *et al.,* 2009). Experiments were sown in randomized block design with three replications. Each genotype was sown in single line of five meter bed with a spacing of 45 cm between lines and 10 cm between plants. Recommended crop management practices were followed for raising a healthy crop. Before sowing, fertilizer (25 N: 50 P: 0 K) was applied in furrows as basal dose. Life saving irrigation was applied as on when required.

Data collection

The biometrical observations were recorded for ten traits *viz.,* biological yield (BY) (g), pod yield (PY) (g), harvest index % (HI), Kernel yield (KY) (g), Shelling out turn (SOT), Hundred kernel mass (g) (HKM), Sound mature kernel (SMK %), Root diameter (RD), SPAD Chlorophyll Meter Reading (SCMR) and Specific Leaf Area (SLA) for five randomly selected plants per genotype per replication and expressed in per plant basis. SCMR was recorded at 60 DAS. Leaf area of these leaves was measured with a LI3100 leaf area meter (LI-COR Inc., Lincoln, NE, USA). Leaves were then oven dried at 60ºC for 72 h and weighed. SLA (cm^2/g) was calculated as the ratio of leaf area to leaf dry weight. The second or third, fully opened leaf from the apex of the main stem of the 5 randomly selected plants in each replication was sampled in morning (08:00-09:30 hours) for measuring SLA and SCMR.

Statistical analysis

All analysis was done based on pooled data over three seasons.

Variance analysis

The analysis of variance was performed following the standard procedures given by Panse and Sukhatme (1985).

Coefficient of variability

The phenotypic and genotypic coefficient of variation (PCV and GCV) was computed as per method described by Burton and DeVane (1953). PCV and GCV values were categorized as low (0-10%), moderate (10-20%) and high (>20) values as indicated by Sivasubranian and Menon (1973).

Heritability

Heritability (broad sense; hereafter denoted only heritability) estimate was computed by dividing the genotypic variance with phenotypic variance and then multiplying by 100 as suggested by Warner (1952). Heritability was classified as suggested by Robinson *et al*. (1949) into low (0-30%), moderate (30.1-60%) and high (>60%).

Genetic advance

Genetic advance was calculated by the formula as suggested by Lush (1949). Genetic advance was categorized into low (0-10%), moderate (10.1-20%) and high (>20%) as suggested by Johnson *et al*. (1955).

Correlation coefficient

Correlation coefficient at both genotypic and phenotypic level was computed according to Al-Jibouri *et al*. (1958).

Principal component

Principal component analysis was performed as proposed by Jeffers (1967) using SPSS software 16.0. A bi-plot display of the first two components was used for grouping genotypes illustrating the relationship between the genotypes and indices.

Cluster analysis

Cluster analysis was performed as proposed by Tryon and Robert C. (1939) and a dendogram was constructed using Ward linkage based on all morphological traits under study.

RESULTS AND DISCUSSION

Analysis of variance

The analysis of variance indicated the existence of significant differences among the genotypes studied (data not sown) and selection would be effective for improvement of desired traits (Kumar *et al*., 2015). Wide range of variations was observed for BY, SOT, HKM, HI, SMK and SLA indicating further scope of improvement in these traits. Maximum range was observed for SLA followed by SOT and HKM, while lowest was in RD (Table 2). Venkata ravana *et al*. (2000), Suneetha *et al*. (2004) and Golakia *et al*. (2005) reported similar wide range of variation for BY, SOT, HKM, HI, SMK and SLA. None of the traits recorded high GCV and PCV except KY which recorded only high PCV. However, Moderate PCV was observed for BY, PY, HI, SOT, HKM and SKM and moderate GCV was observed for BY, PY and HI. High heritability was observed for BY, PY, SCMR and SLA. On the other hand moderate heritability was observed for HI, HKM, SMK and RD. High GA was observed for BY and PY where as moderate GA was observed for HI, HKM and SMK. High heritability

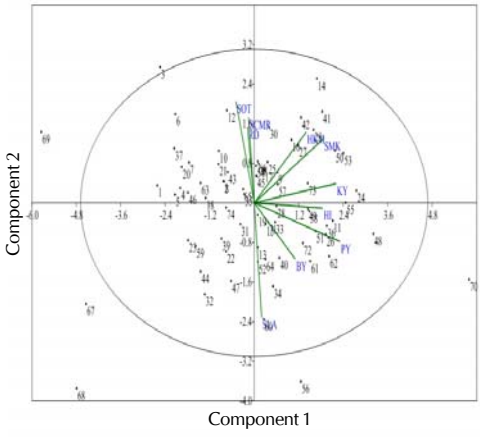

Figure 1: Bioplot between PCI and PC2 showing contribution of various traits in variability of ground nut on pooled basis

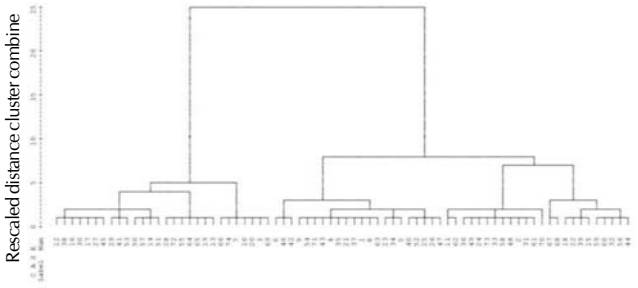

Figure 2: Dendogram using Ward method showing classification of groundnut genotypes based on 10 traits

Table 1: List of 67 Recombinant Inbred Lines along with two parents and five elite varieties of groundnut

Sr. No.	Name of genotypes	Sr. No.	Name of genotypes	Sr. No.	Name of genotypes
1	1-1	26	3-2	51	5-11
2	1-2	27	3-3	52	5-12
3	1-3	28	3-4	53	5-13
4	1-4	29	3-5	54	5-14
5	1-5	30	3-6	55	5-15
6	1-6	31	3-7	56	5-16
7	1-7	32	3-8	57	6-1
8	1-8	33	3-9	58	6-2
9	1-9	34	4-1	59	6-3
10	1-10	35	4-2	60	6-4
11	2-1	36	4-3	61	6-5
12	2-2	37	4-4	62	6-6
13	2-3	38	4-5	63	6-7
14	2-4	39	4-6	64	6-8
15	2-5	40	4-7	65	6-9
16	2-6	41	5-1	66	6-10
17	2-7	42	5-2	67	6-11
18	2-8	43	5-3	68	ICG4747 (P-1)
19	2-9	44	5-4	69	TMV2NLM (P-2)
20	2-10	45	5-5	70	Somnath (Ch-1)
21	2-11	46	5-6	71	Kaushal (Ch-2)
22	2-12	47	5-7	72	GG-20 (Ch-3)
23	2-13	48	5-8	73	Girnar-2 (Ch-4)
24	2-14	49	5-9	74	ICGS-76 (Ch-5)
25	3-1	50	5-10		

Table 2 : Variability parameters for pod yield and yield attributes in 74 genotypes of groundnut

CH	Mean	Range	PCV %	GCV%	H2	GA
BY	26.1	16.5-30.0	13.3	12.1	82.0	22.6
PY	9.3	4.5-13.7	17.8	14.6	67.6	24.8
HI	34.2	19.6-53.8	19.1	12.4	42.4	16.7
KY	6.0	2.6-7.8	21.9	6.7	9.5	4.3
SOT	66.6	50.9-79.7	10.9	5.4	24.5	5.5
HKM	50.1	36.3-58.6	12.3	7.9	41.6	10.5
SMK	60.2	40.1-51.1	12.3	6.2	40.1	11.6
RD	5.8	5.3-6.3	5.1	3.5	47.7	5.0
SCMR	36.8	32.2-43.7	5.8	4.6	62.1	7.5
SLA	167.5	147.9-184.5	5.5	4.5	68.1	7.7

Table 3 : Phenotypic (P) and genotypic (G) correlation coefficients among ten characters in 74 genotypes of groundnut

CH		PY	BY	HI	KY	SOT	HKM	SMK	RD	SCMR	SLA
PY	G	1.00	0.54**	0.96**	0.84**	-0.99**	0.52**	0.45**	0.04	-0.37**	0.40**
	P	1.00	0.27**	0.72**	0.40**	-0.25**	0.32**	0.43**	-0.19*	-0.06	0.14*
BY	G		1.00	-0.06	-0.10	-0.25**	-0.25**	0.64**	-0.40**	-0.94**	0.13*
	P		1.00	-0.17*	0.46**	-0.14*	0.23**	0.21**	0.03	-0.06	0.14*
HI	G			1.00	0.68**	-0.98**	0.69**	0.59**	-0.41**	-0.04	-0.09
	P			1.00	0.61**	-0.18*	0.18*	0.35**	0.02	-0.01	0.09
KY	G				1.00	-0.84**	0.90**	0.41**	-0.77**	-0.72**	0.38**
	P				1.00	0.29**	0.37**	0.57**	0.09	-0.06	0.16*
SOT	G					1.00	-0.03	-0.51**	0.26**	-0.58**	0.21**
	P					1.00	0.09	0.23**	0.05	0.08	0.01
HKM	G						1.00	0.36**	-0.23**	0.28**	0.23**
	P						1.00	0.25**	0.11*	0.04	0.08
SMK	G							1.00	-0.35**	0.12*	0.43**
	P							1.00	0.01	0.06	0.06
RD	G								1.00	0.91**	-0.51**
	P								1.00	-0.06	0.02
SCMR	G									1.00	-0.53**
	P									1.00	-0.21**
SLA	G										1.00
	P										1.00

*, ** significantly different at p = 0.05 and p = 0.01 levels respectively

Table 4 : Principal component analysis of different physiological traits of groundnut

Component	Eigen value	% variance	Cumulative %
1	3.460	34.601	34.601
2	1.522	15.215	49.816
3	1.332	13.317	63.133
4	1.010	10.097	73.231
5	0.911	9.108	82.338
6	0.829	8.292	90.630
7	0.568	5.682	96.313
8	0.351	3.514	99.826
9	0.011	0.115	99.941
10	0.006	0.059	100.0

Table 5 : Factor loading by various traits of groundnut

Variables	PC1	PC2	PC3	PC4
PY	0.231	-0.187	-0.076	0.061
BY	-0.016	-0.039	0.005	0.779
HI	0.278	-0.190	-0.091	-0.485
KY	0.284	0.160	-0.156	0.026
SOT	0.064	0.629	-0.164	-0.089
HKM	0.214	0.179	0.136	0.023
SMK	0.243	0.081	0.222	0.109
RD	0.043	0.335	0.054	0.023
SCMR	-0.011	-0.160	0.690	0.103
SLA	-0.055	-0.173	-0.411	0.069

coupled with high GA was observed for BY and PY. The higher phenotypic coefficient of variation over genotypic coefficient of variation was observed for all the traits indicating the expression of traits is more influenced with environment rather its genetic component. However, the difference between phenotypic and genotypic coefficient of variation were marginal which indicates that these traits are not likely to change extremely with the variation of environment (Majumdar *et al*., 1969). Thus marginal higher values of PCV over GCV also suggest that genetic component is equally responsible for the expression of these traits and warranted further improvement through selection. The moderate GCV and PCV were observed in BY. Similar results were also reported by Khan *et al*. (2001), Dashora and Nagda (2002), Suneetha *et al*. (2004), Golakia *et al*. (2005), and Korat *et al*. (2010). The moderate heritability was observed for RD. The results are in accordance with Katiyar *et al*. (1974) and Nath and Alam, (2002). However, only heritability value provides no indication about the amount of genetic progress that would result from selection of best individuals (Johnson *et al*., 1955). Thus heritability estimates along with genetic advance would be more useful in achieving genetic gain under phenotypic selection than heritability estimate alone. In the present study high heritability along with high genetic advance was observed for BY and PY.

Correlation coefficient

The selection based on variability studies does not always lead to expected genetic gain because of the presence of G x E interaction and the association of different characters with yield. Unfavorable association among the yield attributes under selection may results in genetic slippage and limits the genetic advance. Hence, knowledge of the correlations among such characters is essential while aiming a rational improvement in yield through selection. Correlation study is primarily aimed at to know the association between two traits for simultaneous selection because selection for one trait results in correlated response for several associated other traits (Dewey and Lu, 1959). Significant positive correlation between two traits helps in improvement of dependent traits by direct selection of independent traits while significant negative correlation between two traits helps in improvement of dependent traits by indirect selection of independent traits (Singh *et al*., 2013). Correlation coefficient analysis reveals that PY has significant positive correlation with BY, HI, KY, HKM, SMK and SLA while significant negative correlation with SOT and SCMR. BY recorded significant positive correlation with SMK and SLA while negative with SOT. HI recorded significant positive correlation with KY, HKM and SMK while significant negative with SOT. KY has significant positive correlation with HKM and SMK. HKM has significant positive correlation with SMK and SCMR has significant negative correlation with SLA. Khan *et al*. (2001) concluded that the PY had significant positive correlation with SOT, HKM, pods per kernel. Dashora and Nagda (2002) noticed significant and positive association between PY with SOT and KY. Suneetha *et al*. (2004) reported significant and positive correlation of PY and HI. Korat *et al*. (2010) reported that BY, HKM and HI had positive and significant association with PY at phenotypic level.

PCA and cluster analysis

Principal component analysis (PCA) reflects the importance of the largest contributor to the total variation at each axis of differentiation (Sharma 1998). In this study, Eigen value >1 was observed in four principal components (PCs) out of l0 extracted. These four PCs contributed 73.2% and the remaining components contributed 26.8% of the total variability amongst the genotypes assessed (Table 4). The PC1 contributed maximum towards the variability (34.0%) followed by PC2 (15.2%), PC3 (13.3%) and PC4 (10.0%). The traits like PY, HI, KY, HKM, and SMK showed considerable positive loadings on PC1. The PC2 was related to diversity due to SOT, RD, HKM and KY with their considerable positive and

HI, PY, SLA and SCMR with negative loadings. The PC3 explained variation among genotypes due to SCMR, SMK and HKM with their positive loadings while negative loadings exhibited by SLA, SOT and KY. The PC4 was elucidated by diversity among the genotypes for BY and SMK with a considerable positive loadings while HI with a negative loadings (Table 5).

Principal component analysis bi-plot of 10 yield related traits revealed the coefficient correlation among them. In the bi-plot diagram the angle between HKM, SMK and KY characters is acute angle, therefore they have positive correlation which conformed by correlation analysis. The PC 1 and PC2 axes which justify 49.81% of total variation mainly distinguish the indices of different groups. SOT, SCMR RD refers to group 1(G1). The PC's axes separated indices HKM, SMK, KY in group 2 (G2). HI, BY, PY were separated as a group 3-1 (G3-1) and SLA was separated as group 3-2 (G3-2) (Fig. 1). The most prominent relations revels a strong negative association between SOT, SCMR and RD with SLA as indicated by the large obtuse angles between their vectors. Further a near zero correlation among SOT, SCMR and RD with HI, BY and PY as well as HKM, SMK and KY with SLA. A strong positive correlation would be expected between SOT, SCMR and RD; between HKM and SMK as well as between KY, HI and BY as these indices formed acute angles between themselves. Thus bi-plot graph supported the relationship between traits revealed in correlation analysis. Bi-plot display based on the first two components genotypes were placed in four main groups depicted earlier. G1 with higher values for component-1 and component-2 includes genotypes 16, 27 29, 50, 53, 41 42 30, 14, 24. G2 with a higher value for component 2 and lower value for component-1 includes genotypes 12, 10, 21, 43, 6 and 37. On the other hand G3-1 and G3-2 had lower values for both components. G3-1 includes genotypes 51, 26, 72, 33, 19 and 15 while G3-2 includes genotypes 13, 52, 64, 34 and 40. Genotypes grouped under G1 and G3-1 could be high yielding genotypes since the related indices were directly related to PY in groundnut. Unlike genotypes grouped under G2 and G3-2 could be suitable under drought conditions as the related indices were directly related to water use efficiency in groundnut.

In order to determine the variation among different genotypes and determination of the genotypes far or nearness, cluster analysis was applied to place the similar genotypes in one group (Sajad-Bakaei *et al.,* 2008). Seventy four groundnut genotypes were subjected to cluster analysis using all ten characters under the study and genotypes were grouped into two major clusters based on various morphological traits (Fig. 2). Cluster-1 and cluster-II comprises of 28 and 46 genotypes, respectively. Cluster-II is further subdivided into two sub clusters. Sub cluster-I consists of 24 genotypes and sub cluster-II consists of 24 genotypes. In the present studies genotypes grouped together based on cluster analysis further supported the grouping of genotypes based on PCA described earlier.

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