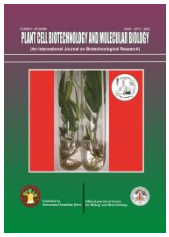

Plant Cell Biotechnology and Molecular Biology

Volume 25, Issue 7-8, Page 61-70, 2024; Article no.PCBMB.12196
ISSN: 0972-2025

Assessment of the Genetic Diversity in Groundnut (*Arachis hypogaea* L.) Genotypes for Yield and its Attributing Traits Using D^2 Statistics

Sunil Kumar [a++*], Vaidurya Pratap Sahi [a#], Shivani Choudhary [a++] and Anoj Kumar Singh [a++]

[a] Department of Genetics and Plant Breeding, Naini Agricultural Institute, SHUATS, Prayagraj, Uttar Pradesh, India.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: https://doi.org/10.56557/pcbmb/2024/v25i7-88740

Open Peer Review History:
This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: https://prh.ikprress.org/review-history/12196

Original Research Article

Received: 17/04/2024
Accepted: 20/06/2024
Published: 21/06/2024

ABSTRACT

The forty-five genotypes of groundnut were evaluated at Field Experimentation Centre of the Department of Genetics and Plant Breeding, Naini Agricultural Institute, SHUATS, Prayagraj (U.P.) during *kharif,* seasons of 2021-22 and 2022-23 in four environments condition of Randomized Block Design with three replications. Observations were recorded on 17 yield and its attributing characters. Analysis of variance revealed the presence of significant amount of variability among the groundnut genotypes. The findings of the ANOVA observed a highly significant variation ($p \leq 0.01$) for all the traits evaluated. Maximum genotypic coefficient of variation (23.12) and phenotypic coefficient of variation (25.92) was recorded for number of branches per plant. The topmost

---

[++] *Ph.D. Scholar;*
[#] *Associate Professor & Head;*
**Corresponding author: E-mail: sunilmahalapc@gmail.com;*

Cite as: Kumar , S., Sahi , V. P., Choudhary , S., & Singh , A. K. (2024). Assessment of the Genetic Diversity in Groundnut (Arachis hypogaea L.) Genotypes for Yield and its Attributing Traits Using D2 Statistics. PLANT CELL BIOTECHNOLOGY AND MOLECULAR BIOLOGY, 25(7-8), 61–70. https://doi.org/10.56557/pcbmb/2024/v25i7-88740

heritability was recorded for hundred pod weight (98.70%) followed by days to maturity (98.60%) with genetic advance hundred pod weight (41.47%) and days to maturity (24.34%). The traits with least influenced by the environment as well as governed by the additive genes and direct selection for improvement of such traits can be beneficial. Analysis of genetic diversity using Mahalanobis' D^2 statistic was carried out in 45 genotypes. These genotypes were grouped into seven clusters. Cluster IV had the maximum number of genotypes. The analysis further indicated that the genotypes of common geographic origin or same location were grouped into different clusters which suggested a lack of relationship between genetic and geographic diversity. Plant height showed relative contribution was the highest 16.67%, then followed by hundred pod weight (14.95%) and pod yield per plant (8.59%).

Keywords: Variation; percent of contribution; selection; cluster distance; grouped.

1. INTRODUCTION

"Peanut or groundnut (*Arachis hypogaea* L.) is one of the important oil crops of the *kharif* season. It is widely grown in tropical and subtropical regions of the world" [1]. "It belongs to the genus *Arachis* and the family Fabaceae. The genus *Arachis* comprises about 80 species which include diploids and tetraploids. The cultivated type of peanut is a self-pollinated plant having genome size of about 2891 Mbp, which is concentrated on 40 chromosomes exhibiting its tetraploid nature. This genus is divided into nine taxonomic sections based on geographical distribution, cross compatibility and plant morphology" [2].

Groundnut is an important oilseed crop in India which occupies first position in terms of area and second position in terms of production after soybean. In India about 70% of the area and 75% of the production are concentrated in the seven states Gujarat, Andhra Pradesh, Tamil Nadu, Karnataka, Maharashtra, Madhya Pradesh and Uttar Pradesh. The total word production of 48.80 million tonnes and along with India area of 5.0 million hectares with a production 6.73 million tonnes and a productivity of 1992 kg/ha.

"Groundnut crop exhibits sufficient morphological, biochemical, and physiological variability. It has a narrow genetic base because of its monophyletic origin, lack of gene flow due to the ploidy barrier, and self-pollination" [3]. "The evaluation of genetic variability is a basic step in a crop enhancement programme. Yield is a complex character influenced by several yield-contributing characters governed by polygenes and also affected by the environment. Heritability estimates are used for assessing the amount of variation present in the population as a whole. Heritability combined with genetic advance will bring out the genetic gain predicted by selection" [4-7]. Hence, it becomes, necessary to partition the variation that is observed in heritable and non-heritable components measured as genotypic and phenotypic coefficients of variations, heritability and genetic advance to account for created variability to be used in efficient breeding programme.

"Genetic diversity is the prerequisite for a hybridization programme for getting desirable genotypes. Genetic diversity is extremely important to meet the various objectives in plant breeding such as producing genotypes with increased yield wider adoption, desirable quality and diseases resistance" [8]. Quantification of the degree of differences in a given experimental material is of immense value in the proper choice of parents for hybridization realizing higher heterosis and obtaining valuable recombinants.

2. MATERIALS AND METHODS

An investigation was conducted at the Field Experimentation Centre of the Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj (U.P). The groundnut comprised 45 genotypes, including one check obtained from Rajasthan Agricultural Research Institute, Durgapura, Rajasthan. The list of groundnut genotypes along with their pedigree and origin is presented in Table 1. The investigation field was laid out in Randomized Block Design with three replications during *kharif* (2021-22 and 2022-23). Each entry was accommodated in a single row of 1.5 m length with a spacing of 30 cm between rows and 10 cm between plants within the row. At regular intervals, weeding was carried out and the earthing-up operation was undertaken after applying gypsum. Necessary plant protection measures were adopted except for the spray of fungicides during the crop growth period in all environments. All the recommended package of

practices was followed for raising healthy crop. Data were recorded on randomly selected five plants per replication from each genotype of groundnut and average value was used for the statistical analysis for 17 traits *viz.,* days to 50 per cent flowering, days to maturity, plant height (cm), number of branches per plant, number of pegs per plant, number of mature pods per plant, pod yield per plant (g), hundred pod weight (g), kernel yield per plant (g), hundred kernel weight (g), shelling (%), biological yield per plant (g), harvest index (%), SPAD chlorophyll meter reading (SCMR) at 60 DAS, SPAD chlorophyll meter reading (SCMR) at 80 DAS, protein content (%) and oil content (%). Except days to 50 per cent flowering and days to maturity data were recorded on the basis of plot. The data subjected to different statistical analysis *viz.,* analysis of variance (ANOVA), magnitude of genetic variability were performed following the standard procedures, phenotypic and genotypic coefficient of variation as suggested by Burton and Devane [9] heritability (broad sense) (Hanson et al*.* 1956) and genetic advance as followed by Johnson et al*.* 1955. Mahalanobis [10] D^2 analysis was used for assessing the genetic divergence among the test genotypes involving yield and its attributing characters.

Table 1. List of groundnut genotypes together with their pedigree and origin

S. N.	Genotypes	Pedigree / Selection	Origin
1	SC-28	Pureline selection from Samarala local	PAU, Punjab
2	TMV-10	Selection/ Natural mutant of 'Argentina'	TNAU
3	GG-16	JSP-14 × JSSP-4 (S-94-15-B-10-1-B-B)	JAU, Junagarh
4	AH-114	G.221 × Go386	CSAUAT, Mainpuri
5	TG-37A	TG-25 × TG-26	BARC, Mumbai
6	TMV-3	Pureline selection from Bassi × Saloum (W.Africa)	TNAU
7	GG-7	S-206 × FESR-8 (1-1-9-B-B)	JAU, Junagarh
8	RG-562	ICG-5013 × RG-141-3	RARI, Durgapura
9	GG-21	Somnath × NCAc 2232	JAU, Junagarh
10	T-28	G.221 × ICG-1697	CSAUAT, Mainpuri
11	PG-1	Selection from Samarala local	PAU, Punjab
12	GG-14	GG-11 × R-33-1	JAU, Junagarh
13	RG-578	ICG-5013 × RG-141	RARI, Durgapura
14	GJG-19	JSSP-12 × LGN-2 (K-99-13-B-1-2-B-B)	JAU, Junagarh
15	GNL	RG-319 × RG-341	RARI, Durgapura
16	RS-1	ICG-5013 × RG-143-2	RARI, Durgapura
17	GJG-18	JSSP-12 × LGN-2 (K-99-13-B-1-1-B-B)	JAU, Junagarh
18	ICGV-00350	ICGV-87290 × ICGV-87846	RARS, Tirupati
19	GJG-17	JSSP-11 × GG-6 (K-99-2-B-1-B-B)	JAU, Junagarh
20	MH-1	AS-414 × AI-703	HAU, Haryana
21	RG-574	ICG 5013-3 × RG-141	RARI, Durgapura
22	AH-334	G.221 × Go343	CSAUAT, Mainpuri
23	RG-382	ICG-5013 × RG-143	RARI, Durgapura
24	RG-575	ICG 5013-2 × RG-141	RARI, Durgapura
25	AK-159	JL-24 × CGC-4018	PDKV, Akola
26	GG-20	27-4-1 × JL-24 (30-2-2-B-B)	JAU, Junagarh
27	S-230	37nc × Arc-1 (301) (Pureline)	UAS, Raichur
28	GG-11	GG-11 × R-33-2	JAU, Junagarh
29	TMV-1	Introduction selection from Ah.288	TNAU
30	RG-561	ICG-5013 × RG-141-2	RARI, Durgapura
31	GG-5	27-5-1 × JL-24	JAU, Junagarh
32	TG-22	TGS-1 × TGE-2	BARC, Mumbai
33	TMV-12	Pureline selection from Uganda	TNAU
34	JL-776	[(ICGV92069 × ICGV93184) SIL4 × ICGV98300]	MPKV, Jalgaon
35	TMV-2	Mass selection from 'Gudiatham' bunch AH.32	TNAU
36	GG-6	27-5-1 × JL-24 (30-3-1-B-B)	JAU, Junagarh
37	TMV-4	Pureline from N.Carolina variety	TNAU
38	LGN-1	Selection from LGN-2	MAU, Latur
39	GG-8	27-5-1 × JL-24 (30-3-2-B-B)	JAU, Junagarh

S. N.	Genotypes	Pedigree / Selection	Origin
40	RG-141	Kadiri-3 × NCAc 2821	RARI, Durgapura
41	JL-501	Selection from TAG-24	MPKV, Jalgaon
42	RG-510	RG-318 × RG-340	RARI, Durgapura
43	RG-559-3	[(TKG-19A × Kadiri-3) × TKG-19A]	RARI, Durgapura
44	CSMG-2003-19	Amber × ICG-1697	CSAUAT, Mainpuri
45	CSMG-9510	Unnat × ICG-1697	CSAUAT, Mainpuri

3. RESULTS AND DISCUSSION

The results obtained from the present investigation as well as relevant discussion have been summarized under following heads:

3.1 Analysis of Variance

The ANOVA was analysis for 45 genotypes across four environment-wise and pooled over all environments. All 45 genotypes of groundnut showed significant variations for all the traits studied showing the presence of inherent genetic variability in the material used in the current investigation. Selection for characters showing high heritability with high genetic advance, positive and high significant correlation and showing high direct effects will helpful in the improvement of yield in the groundnut. Similar results were obtained by Satish, [11] and Haj Hussein et al. (2018).

3.2 Genetic Parameters

To understand the extent to which the observed variation is due to genetic factors the phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense and genetic advance as per cent of mean were computed for the 17 traits in 45 genotypes in groundnut. Phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV) which indicates somewhat role of environmental factors on the expression of various characters. Similar finding reported by Shankar et al. [12] and Abadya et al. [13].

PCV, GCV, heritability, and genetic advance over mean studies are helpful in figuring out how to utilize selection to enhance a given population for a given trait. A trait's high heritability and high genetic advancement indicate the presence of an additive genetic effect and the possibility that selection is driving the trait's improvement. Since broad sense heritability include both additive and non-additive gene action, analyzing broad sense heritability alone is not a suitable criterion for determining which gene action is present. As shown in Table 2, the highest estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for number of branches per plant (24.11 & 25.80) and hundred pod weight (20.17 & 20.30). Vaishali et al. [14] and Sab et al. [15] recorded high GCV and PCV for primary branches per plant. Higher heritability and Genetic Advance as a percent of mean were observed for all traits. Gupta et al. [16] reported high GCV and PCV for harvest index and kernel yield per plant. For these traits, selection would be effective to improve yield in groundnut genotypes.

Moderate GCV and PCV were found for traits like days to maturity (10.65 & 10.73), plant height (11.17 & 11.67), number of pegs per plant (11,14 & 11.38), number of mature pods per plant (15.09 & 15.89) and hundred kernel weight (10.92 & 11.56). Similar results were also obtained for days to maturity by Dolma et al. [17] and Gupta et al. [16].

Low GCV and PCV were found for remaining traits like days to 50 per cent flowering, pod yield per plan, kernel yield per plant, shelling, biological yield per plant, harvest Index, SPAD chlorophyll meter reading (SCMR) at 60 DAS, SPAD chlorophyll meter reading (SCMR) at 80 DAS, protein content and oil content. Similar results were also obtained for days to 50 per cent flowering, protein content and oil content [16] SPAD chlorophyll reading [12] and shelling [18].

Burtan (1952) suggested that “heritability estimates conjugated with GCV would provide an accurate picture about the extent of genetic advance to be expected through selection. It is considered a good estimate of genetic gain to be expected from the selection on a phenotypic basis”. The high estimates of heritability (broad sense) were recorded for all the characters studied. These findings are in agreement with the results of Satish [11]. Genetic advance as per cent of mean was high for characters number of branches per plant (46.42%), hundred pod weight (29.54%), days to maturity (21.79%), plant height (22.03%), number of pegs per plant

(22.45%), number of mature pods per plant (29.54%) and hundred kernel weight (21.23%). High genetic advance along with high heritability was found for the same above characters which imply that selection can be done in genotypes under study for the improvement of these traits.

However, moderately genetic advance as percent of mean along with high heritability was observed for pod yield per plant (10.38%). This was supported by the findings of Khote et al. [19] and Nath et al. [20]. These traits having moderately genetic advance with high heritability shows the presence of non-additive gene action therefore, simple selection procedures will not be effective for screening of desired traits.

3.3 Genetic Divergence

In order to provide greater variation and a strong heterotic effect in the segregating population, varied parents in a cross are essential for choosing parents in a hybridization program. The results of the analysis of variance indicated that there was sufficient genetic variability for each of the variables under investigation, with the mean sum of squares owing to groundnut genotypes for all the traits examined being extremely significant. Nevertheless, analysis of variance is unable to account for the level of genetic variety. As a way to quantify genetic variation between any two genotypes or group of genotypes, Mahalanobis, D^2 statistics described by Rao [21] was used so that genotypes could be grouped into various clusters on the basis of Ward's minimum variance method.

3.4 Grouping of Genotypes into Various Clusters

The Table 3 reveals the distribution pattern of 45 groundnut genotypes in different clusters. A total of seven clusters were formed. Cluster pattern revealed that cluster IV had maximum number of genotypes which is 13, second largest cluster formed was cluster II which had 11 genotypes. Further two clusters I and III had a sevengenotypes in each cluster followed by cluster VII with five genotypes. Cluster V and VI was the smallest having remaining one genotypes each cluster.

Table 2. Estimates of genetic variability parameters for yield and yield attributing traits of groundnut in pooled over four environments

Sr. No.	Source of Variation	Mean	GCV	PCV	h^2 (Broad Sense)	Genetic Advance	Gen. Adv. as % of Mean 5%
1	DFF	27.06	8.26	8.69	90.40	4.38	16.19
2	DM	111.69	10.65	10.73	98.60	24.34	21.79
3	PH	44.40	11.17	11.67	91.70	9.78	22.03
4	NBP	8.66	24.11	25.80	87.30	4.02	46.42
5	NPP	59.50	11.14	11.38	95.80	13.36	22.45
6	PPP	30.63	15.09	15.89	90.30	9.05	29.54
7	PYP	33.17	6.33	7.96	63.30	3.44	10.38
8	HWT	100.45	20.17	20.30	98.70	41.47	41.28
9	KYP	22.78	6.62	8.94	54.80	2.30	10.10
10	HKW	43.48	10.92	11.56	89.20	9.23	21.23
11	SH	68.66	2.31	3.53	42.80	2.14	3.11
12	BYP	68.35	6.90	7.54	83.70	8.89	13.00
13	HI	48.56	2.61	4.37	35.60	1.56	3.21
14	SPAD SIXTY	54.03	2.83	4.78	35.10	1.87	3.46
15	SPAD EIGHTY	43.39	2.78	5.36	26.80	1.29	2.96
16	PC	24.13	1.52	3.07	24.60	0.38	1.56
17	OC	45.40	1.93	3.59	28.80	0.97	2.13

DFF-days to 50 per cent flowering, DM-days to maturity, PH-plant height, NBP-number of branches per plant, NPP-number of pegs per plant, PPP-number of mature pods per plant, PYP-pod yield per plant, HWT-hundred pod weight, KYP-kernel yield per plant, HKW-hundred kernel weight, SH-shelling, BYP-biological yield per plant, HI-harvest Index, SPAD SIXTY-SPAD chlorophyll meter reading (SCMR) at 60 DAS, SPAD EIGHTY-SPAD chlorophyll meter reading (SCMR) at 80 DAS, PC-protein content and OC-oil content.

Table 3. Distribution of 45 groundnut genotypes into different clusters based on D^2 statistics

Clusters	Number of genotypes	Name of genotypes
I	7	SC-28, TG-37A, ICGV-00350, TG-22, JL-776, GG-6, GG-8
II	11	PG-1, RG-578, GJG-19, AH-334, GG-20, S-230, TMV-1, RG-510, RG-559-3, CSMG-2003-19, CSMG-9510
III	7	TMV-10, AH-114, GG-7, GG-21, GG-5, TMV-2, RG-141
IV	13	GG-16, TMV-3, RG-562, T-28, GG-14, RS-1, GJG-18, GJG-17, RG-574, RG-382, GG-11, RG-561, TMV-4
V	1	RG-575
VI	1	LGN-1
VII	5	GNL, MH-1, AK-159, TMV-12, JL-501

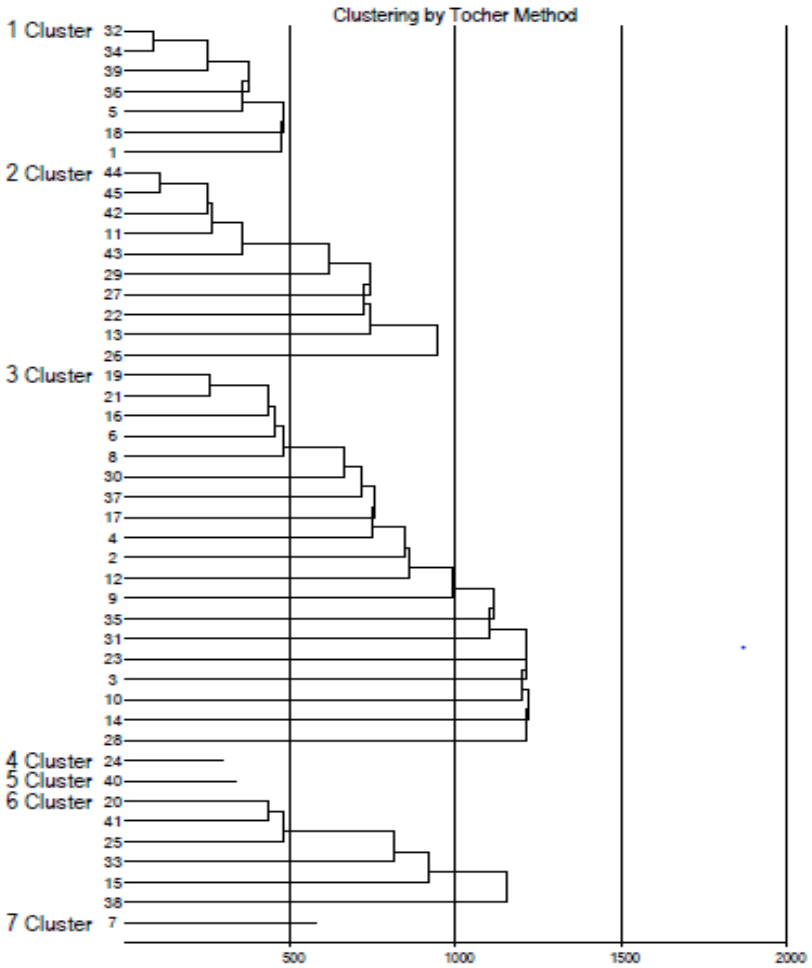

Fig. 1. Clustering representation of 45 groundnut genotypes by Tocher's method

3.5 Intra and Inter-Cluster Average D^2 Values

The intra and inter cluster average D^2 values among 45 groundnut genotypes are given in Table 4. The highest intra-cluster D^2 value was observed for cluster VII (17.41) and inter-cluster distance was observed between cluster I and cluster V (80.81). In contrast to this, minimum inter-cluster distance was seen between cluster VI and cluster VII (22.21), followed by cluster II and cluster III (22.12) and cluster V and cluster VI (19.27) depicting less diverse groundnut genotypes belonging to these clusters.

Table 4. Average intra and inter-cluster distance of 45 groundnut genotypes

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	8.52	74.61	22.12	47.93	80.81	39.42	31.38
Cluster II		14.31	49.33	39.27	20.30	24.94	45.12
Cluster III			14.19	28.51	54.40	34.22	35.48
Cluster IV				16.91	50.45	43.17	58.04
Cluster V					0.00	19.27	46.78
Cluster VI						0.00	22.21
Cluster VII							17.41

Table 5. Cluster mean values for different yield and yield attributing characters in 45 groundnut genotypes

Sr. No.	Clusters	I	II	III	IV	V	VI	VII	Mean
1	DFF	24.44	28.28	25.67	29.21	28.50	24.67	24.63	26.49
2	DM	94.80	120.86	107.08	121.46	116.75	107.58	96.05	109.23
3	PH	47.09	42.09	45.30	45.25	48.83	47.72	40.67	45.28
4	NBP	7.67	9.71	7.23	9.86	7.09	6.98	7.26	7.97
5	NPP	60.67	61.27	62.41	56.91	50.40	56.44	59.06	58.17
6	PPP	33.46	30.68	25.52	31.05	22.06	36.67	33.15	30.37
7	PYP	34.57	33.89	31.06	33.19	31.00	29.48	33.68	32.41
8	HWT	82.46	125.87	85.74	87.94	132.50	123.00	111.92	107.06
9	KYP	23.73	23.17	21.33	22.95	21.08	20.43	23.01	22.24
10	HKW	40.14	44.57	42.92	43.27	40.42	36.42	49.10	42.41
11	SH	68.67	68.30	68.62	69.09	67.93	69.23	68.44	68.61
12	BYP	72.80	69.32	63.29	68.63	62.40	61.07	69.01	66.65
13	HI	47.51	48.89	49.09	48.41	49.67	48.25	48.78	48.66
14	SPAD SIXTY	53.86	55.42	53.32	53.17	53.31	51.80	55.02	53.70
15	SPAD EIGHTY	43.44	44.31	43.05	42.77	42.89	43.40	43.46	43.33
16	PC	24.19	24.25	23.91	24.11	23.62	24.57	24.13	24.11
17	OC	44.95	45.50	45.45	45.53	44.42	45.31	45.59	45.25

DFF-days to 50 per cent flowering, DM-days to maturity, PH-plant height, NBP-number of branches per plant, NPP-number of pegs per plant, PPP-number of mature pods per plant, PYP-pod yield per plant, HWT-hundred pod weight, KYP-kernel yield per plant, HKW-hundred kernel weight, SH-shelling, BYP-biological yield per plant, HI-harvest Index, SPAD SIXTY-SPAD chlorophyll meter reading (SCMR) at 60 DAS, SPAD EIGHTY-SPAD chlorophyll meter reading (SCMR) at 80 DAS, PC-protein content and OC-oil content.

3.6 Mean Values of Different Clusters for 17 Characters

As shown in Table 5, the data depicted considerable differences among all the clusters for most of the characters under study. It was evident that days to 50% flowering mean value was the lowest in cluster I (24.44) while it was the highest in cluster IV (29.21). Cluster II had the lowest days to maturity mean value (94.80) while it was the highest in cluster IV (121.46). The mean value of plant height its highest value in cluster II (42.09) while its lowest value was found in cluster V (48.83). Number of branches per plant mean value had its highest value in cluster IV (9.86) while its lowest value was found in cluster VI (6.98). The mean value of number of pegs per plant its highest value in cluster III (62.41) while its lowest value was found in cluster V (50.40). Number of mature pods per plant mean value had its highest value in cluster VI (36.67) while its lowest value was found in cluster V (22.06). Pod yield per plant mean value had its highest value in cluster I (34.57) while its lowest value was found in cluster VI (29.48). Kernel yield per plant mean value had its highest value in cluster I (23.73) while its lowest value was found in cluster VI (20.41). Hundred pod weight mean value had its highest value in cluster II (125.87) while its lowest value was found in cluster I (82.46). The success and usefulness of Mahalanobis, D^2 analysis in quantifying genetic divergence has been studied by Hampannavar and Khan [22] Waghmode et al. [23] and Ashutosh et al. [24].

Table 6. Relative contribution of 17 traits towards divergence in 45 groundnut genotypes

Sr. No.	Source traits	Relative Contribution %	Times ranked 1st
1	DFF	5.86%	58
2	DM	6.57%	65
3	PH	16.67%	165
4	NBP	5.66%	56
5	NPP	6.26%	62
6	PPP	6.26%	62
7	PYP	8.59%	85
8	HWT	14.95%	148
9	KYP	2.22%	22
10	HKW	5.96%	59
11	SH	2.32%	23
12	BYP	2.83%	28
13	HI	0.40%	4
14	SPAD SIXTY	7.98%	79
15	SPAD EIGHTY	1.92%	19
16	PC	4.65%	46
17	OC	0.91%	9

DFF-days to 50 per cent flowering, DM-days to maturity, PH-plant height, NBP-number of branches per plant, NPP-number of pegs per plant, PPP-number of mature pods per plant, PYP-pod yield per plant, HWT-hundred pod weight, KYP-kernel yield per plant, HKW-hundred kernel weight, SH-shelling, BYP-biological yield per plant, HI-harvest Index, SPAD SIXTY-SPAD chlorophyll meter reading (SCMR) at 60 DAS, SPAD EIGHTY-SPAD chlorophyll meter reading (SCMR) at 80 DAS, PC-protein content and OC-oil content.

3.7 Relative Contribution of Characters Towards Diversity

As shown in Table 6, the data depicted considerable differences among the relative contribution for all the characters under study. It was evident that plant height relative contribution was the highest 16.67%, then followed by hundred pod weight (14.95%), pod yield per plant (8.59%), SPAD chlorophyll meter reading (SCMR) at 60 DAS (7.98%), days to maturity (6.57%), number of peg per plant (6.26%), number of mature pods per plant (6.26%), hundred kernel weight (5.96%), days to 50 per cent flowering (5.86%), number of branches per plant (5.66%), protein content (4.65%), biological yield per plant (2.83%), shelling (2.32%), kernel yield per plant (2.22%), SPAD chlorophyll meter reading (SCMR) at 80 DAS (1.92%), oil content (0.91%) and harvest index relative contribution was the lowest (0.40%).

4. CONCLUSIONS

The study found that the genotypes of groundnuts that were evaluated varied significantly genetically for the qualities that were measured, a finding that might be used to the advantage of groundnut breeding. The perfect correlation between the morphological characteristics and the field yield was also strongly resolved by the current study. The yield-related traits like number of branches per plant and hundred pod weight recorded high GCV and PCV values were ≥20% with high genetic advance also a low relative difference. It is evident from this present study that the enhancement of yield and other yield-related traits can be attained through effective selection based on estimates of heritability and genetic advance. This kind of study can help future breeding and population improvement programs.

The implementation of a hybridization program requires diversity. Different backgrounds and clusters of genotypes performed better for various essential and desirable qualities for groundnut crop population growth and yield increase. Choosing parents only on the basis of phenotype rarely produces the desired outcomes. Rather, choosing parents according to the cluster mean and intra- and inter-cluster distances aids in the creation of superior recombinants or transgressive segregants.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Abbas M, El-Shabrawi H, Hamza M, Wahba H, Shahba M. Association between productivity, fatty acid profiles, oil bodies' ultrastructure and molecular markers in peanut (*Arachis hypogaea* L.) cultivars. Agronomy. 2020;10(9):1401.
2. Valls JF, Simpson CE. New species of Arachis (*Leguminosae*) from Brazil, Paraguay and Bolivia. Bonplandia. 2005; 14(1-2):35-63.
3. Mondal S, Badigannavar AM, Kale DM, Murty GSS. Induction of genetic variability in a disease resistant groundnut breeding line. Bhabha Atomic Research Centre: BARC Newsletter. 2007;285:237-246.
4. Rao VT. Genetic variability, correlation and path coefficient analysis under drought condition in groundnut (*Arachis hypogaea* L.). Legume Research an International Journal. 2016.39(2):319-322.
5. Mohammed KE, Afutu E, Odong TL, Okello DK, Nuwamanya E, Grigon O, Rubaihayo PR, Okori P. Assessment of Groundnut (*Arachis hypogaea* L.) Genotypes for Yield and Resistance to Late Leaf Spot and Rosette Diseases. J. Exp. Agric. Int. 2018; 21(5):1-13.
   [Accesson: 2024 Jun. 12];
   Available:https://journaljeai.com/index.php/JEAI/article/view/122
6. Chandran AS, Rai PK, Lal GM, Kumar R, Yadav B. Evaluation of Groundnut Genotypes for Agronomic and Seed Quality Traits. Int. J. Plant Soil Sci. 2016; 13(2):1-7.
   [Accesson: 2024 Jun. 12];
   Available:https://journalijpss.com/index.php/IJPSS/article/view/372
7. Kebede B A, Getahun A. Adaptability and stability analysis of groundnut genotypes using AMMI model and GGE-biplot. Journal of crop science and biotechnology. 2017;20:343-9.
8. Joshi AH, Dhawan NL. Genetic improvement of yield with special reference to self-fertilizing crop. Indian Journal of Genetics and Plant Breeding. 1966;26(A):101-113.
9. Burton GW. Quantitative inheritance in grasses. Proceeding on 6th International Grassland Congress Journal. 1952;1:277-283.
10. Mahalanobis PC. On the generalized distance in statistics. Proceedings of the National Institute of Science of India. 1936; 2:49-55.
11. Satish Y. Genetic variability and characters association studies in Groundnut (*Arachis hypogaea* L). International Journal of Plant, Animal and Environmental Sciences. 2014; 4(4):298-300.
12. Shankar M, Babu BH, Gobu R. Studies on genetic variability, heritability and genetic advance in groundnut (*Arachis hypogaea* L.) genotypes under normal and moister stress condition in vegetative stage. Journal of Pharmacognosy and Phytochemistry. 2019;8(3):4271-4277.
13. Abadya S, Shimelis H, Pasupuleti J, Mashilo J, Chaudhari S, Manohar SS. Assessment of the genetic diversity of groundnut (*Arachis hypogaea* L.) genotypes for kernel yield, oil and fodder quantity and quality under drought conditions. Crop Science. 2021;61(3): 1926-1943.
14. Vaishali G, Saravanan S, Arumugam Pillai M, Sheela J, Kavitha Pushpam A, JR J. Genetic variability and heritability studies in groundnut (*Arachis hypogaea* L.) germplasm. The Pharma Innovation Journal. 2023;12(9):970-973.
15. Sab S, Shanthala J, Savithramma D, Bhavya M. Study of genetic variability and character association for water use efficiency (WUE) and yield related traits advance breeding lines of groundnut (*Arachis hypogaea* L.). International Journal of Current Microbiology and Applied Sciences. 2018; 7(6):3149-3157.
16. Gupta RP, Vachhani JH, Kachhadia VH, Vaddoria MA, Reddy P. Genetic variability and heritability studies in Virginia groundnut (*Arachis hypogaea* L.). Electronic Journal of Plant Breeding. 2015; 6(1):253-256.
17. Dolma L, Sekhar MR, Reddy KR. Genetic divergence studies in groundnut (*Arachis hypogaea* L.). Journal of Oilseeds Research. 2010;27(2):158-160.
18. Khan MMH, Rafii MY, Ramlee SI, Jusoh M, Mamun A. Genetic variability, heritability and clustering pattern exploration of Bambara groundnut [*Vigna subterranea* (L.) Verdc] accessions for the perfection of yield and yield-related

traits. BioMed research international. 2020;1-31.
19. Khote AC, Bendale VW, Bhave SG, Patil, PP. Genetic variability, heritability and genetic advance in some exotic genotypes of groundnut (*Arachis hypogaea* L.). Crop Research. 2009;37(1-3):186-191.
20. Nath UK, Alam MS. Genetic variability, heritability and genetic advance of yield and related traits of groundnut (*Arachis hypogaea* L.). OnLine Journal of Biological Sciences. 2002;2:762-764.
21. Rao CR. Advanced Statistical Methods in Biometric Research. John Wiley Sons, New York. 1952;390.
22. Hampannavar MH, Khan H. Analysis of genetic diversity of groundnut (*Arachis hypogaea* L.) genotypes collected from various parts of India. Journal of Pharmacognosy and Phytochemistry. 2018;7(2):1100-1103.
23. Waghmode BD, Navhale VC, Sonone NG. Bhave SG. Assessment of genetic diversity in groundnut (*Arachis hypogaea* L.) genotypes under Konkan condition in Maharashtra. Advanced Agricultural Research and Technology Journal. 2017; 1(1):84-87.
24. Ashutosh K, Soma G, Sheetal RS, Pradhan K, Kuldeep K. Study on genetic diversity in groundnut (*Arachis hypogaea* L.) using morphological markers. The Bioscan. 2016;11(4):3105-3109.

Peer-review history:
The peer review history for this paper can be accessed here:
https://prh.ikprress.org/review-history/12196