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## ASSESSMENT OF GENETIC DIVERGENCE IN GROUNDNUT (*ARACHIS HYPOGAEA* L.) GERMPLASM BY MEANS OF CORRELATION, PRINCIPAL COMPONENT AND CLUSTER ANALYSIS



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### Abstract

Groundnut (*Arachis hypogaea* L.) is related to family Fabaceae and is a valuable crop worldwide. Genetic Divergence in groundnut germplasm is a useful genetic tool for breeding strategies. Pod Yield seems to be a complex quantitative trait which is mostly subject to the environment. The selection only for pod yield is not fruitful in enhancing groundnut production. Therefore, the selection competence may be increased by considering the yield contribution factors. Moreover, the presence of genetic divergence in existing germplasm is mandatory to create genetic variation and selection of parents in any breeding experiment. Keeping in view the above scenario, the current study was designed to analyze the interaction between pod yield and the traits related to it. This will help to exploit the variation present in groundnut germplasm and selection of suitable parents for future breeding strategies. Dry pod yield was directly associated with kernel weight, pod length, and No. of pods plant-1 and shelling %. That's why these parameters may be considered in the selection process when improving groundnut yield. Among studied germplasm, the strains 10AK005, 18AK002, 10CG002, 14CG009, 10AK003, 11AK0011, 14AK007, 17AK003, 17AK004, 14AK001 and BARI-2016 have maximum potential for yield contributing traits. Principal component and cluster analysis were utilized as selection tools to facilitate the breeder with an efficient and easy selection method. The findings of principal component analysis were in line with those of correlation studies. Cluster analysis demarked that the most superior cluster was cluster-3, having maximum values for yield and related parameters. The information gained from this study may be utilized for future breeding programmes with respect to the yield maximization of the groundnut crop.

**Keywords:** *Arachis hypogaea*, Cluster, Correlation, Dry pod yield, Genetic divergence, Principal components

## INTRODUCTION

Groundnut is well known cash commodity as it is oilseed, food and feed crop of kharif season and is usually grown on sandy loam soils of Pakistan. It belongs to genus *Arachis* and is known with various names in different parts of the world i. e. peanut, earthnut, monkeynut, ground bean and manilanut. *Arachis hypogaea* L. has distinctness in the genus that it is annual herb which develops fruit underground. Peanut is 13<sup>th</sup> important food crop, 4<sup>th</sup> with respect to edible oil and 3<sup>rd</sup> main source of vegetable proteins all over the world (1). It has potential for good quality edible oil (43-55%) with high amount of essential fatty acids viz., linoleic and linolenic acids and also digestible proteins (25- 28%) in its seeds (2, 3). In Punjab, groundnut was grown on 367.1 thousand acres during the year 2022-23 (4). In Punjab province, the districts of Pothowar, primarily Chakwal; Jhelum; Attock and Rawalpindi are key groundnut growing areas of Pakistan where unsure rainfalls, fluctuating environmental conditions and shortage of water are main yield restrictive factors. There exists a large gap between yield potential and average farmer yield of groundnut existing varieties. Therefore, it is need of the time to explore yield contributing factors such as 100-kernel weight,



pod length, No. of pods plant<sup>-1</sup> and shelling %. Correlation studies are one of the basic tools for identification of different factors contributing towards dry pod yield.

Every breeding technique is aimed for improvement in one or more characters with yield improvement being major objective (5, 6). Dry Pod yield is known as multifarious quantitative character, resultant from interaction of different yield related traits (7, 8). Yield is mainly affected by environmental conditions and usually it has less heritability (9). That's why, it will be less effective if breeder uses direct selection method for yield in improving groundnut production, yet this competence may be improved by exploring the association amongst dry pod yield and linked traits (7). Correlation analysis makes it possible to explicate the useful parameters which help in yield improvement (8, 10).

Screening of germplasm also plays important role for grouping existing genotypes with respect to desirable characters. For this purpose cluster analysis is ideal tool as it customizes existing variability into different clusters based upon their similarity in studied traits (11). For successful breeding plan, assortment of genetically divergent genotypes is vital, because it offers prospect for development of improved genotypes having desirable qualities (12, 13). The cluster as well as principal component analysis (PCA) being practical tools to determine genetic divergence in existing genotypes for crop improvement, as these tools group genetically analogous strains together and generate scatter plot of those strains with geometrical differences (14, 15). The study of genetic diversity facilitates breeder for selection, promotes crop improvement and also dictate methodical exploitation (16). Main concern of current investigation was to screen existing groundnut germplasm and explore the relationship among dry pod yield and related traits by using cluster, principal component and correlation analysis which will be helpful in groundnut productivity enhancement.

## MATERIALS AND METHODS

### RESEARCH MATERIAL, DESIGN AND SITE

Genetic material in current investigation consisted of forty genotypes (12 advanced lines from Groundnut Research Station, Attock, 09 germplasm accessions from Plant Genetic Resources Institute, Islamabad, 11 advanced breeding material along with one check from Barani Agricultural Research Institute, Chakwal and 07 germplasm strains from ICRISAT, Gene bank, India (Table I). The material was planted according to Alpha Lattice Design in two replications at the research area of Groundnut Research Station, Attock during kharif season 2023-24. Each entry was plotted in four rows having four meter length with 7.2 m<sup>2</sup> plot size. At Sowing time, the fertilizer used @ 30-80-50 kg ha<sup>-1</sup> NPK. At peg formation 500 kg ha<sup>-1</sup> Gypsum was also applied for betterment in seed development process. All recommended cultural practices i.e. weeding, hand hoeing and insect pest control were adopted.

**Table I.** Details of groundnut gemplasm studied

Genotype No.	Genotype Name	Source
1	10 AK002	Groundnut Research Station Attock, Pakistan
2	10 AK003	
3	11 AK0011	
4	14 AK001	
5	14 AK002	
6	14 AK007	
7	17 AK001	
8	17 AK002	
9	17 AK003	
10	17 AK004	
11	10 AK005	
12	18 AK002	
13	PG-963	Plant Genetic Resources Institute, Islamabad, Pakistan
14	PG-977	
15	PG-1026	
16	PG-1039	
17	PG-1090	
18	PG-1133	
19	PG-1160	



20	PG-1254	-do-
21	PG-1255	-do-
22	01CG007	Barani Agricultural Research Institute, Chakwal, Pakistan
23	08CG005	-do-
24	10CG002	-do-
25	14CG009	-do-
26	15CG003	-do-
27	16CG002	-do-
28	16CG005	-do-
29	17CG002	-do-
30	17CG004	-do-
31	17CG005	-do-
32	16CG001	-do-
33	ICGV86928	ICRISAT Gene bank, India
34	ICGV88316	-do-
35	ICGV88328	-do-
36	ICGV88338	-do-
37	ICGV88393	-do-
38	ICGV88429	-do-
39	ICGV88473	-do-
40	BARI-2016	Barani Agricultural Research Institute, Chakwal, Pakistan

## DATA RECORDING

For data collection, the crop was monitored regularly and after attaining physiological maturity, it was harvested. Data observations were taken from ten plants which were randomly selected in each plot. The studied characters include Biological Yield in Kgs (BYLD), 100-kernel weight in gms (KW), plant height in cms (PH), pods length in cms (PL), No. of pods plant<sup>-1</sup> (PDPP), shelling % (Shell) and dry pod yield in Kg ha<sup>-1</sup> (DPY). The data regarding biological yield was calculated by weighing all plants along with pods of each entry after harvesting while plant height was calculated by ruler, starting from base to top of main stem axis.

Pod number per plant was obtained at the time of harvest by counting fully mature pods on ten randomly selected plants and then taking average for each entry. Pod length was calculated from longest points of twenty randomly selected pods. For 100-kernel weight, hundred kernels were counted and weighed from each entry. For calculation of shelling %, a 100 gram pod sample was drawn randomly from each plot. After that sample was shelled, weighed and shelling% was obtained by using formula:

$$\text{Shelling \%} = \frac{\text{Kernel Weight}}{\text{Pod Weight}} \times 100$$

Dry Pod yield was taken by harvesting whole plot of each entry. The samples were then threshed manually, dried in sun and weighed. Yield per plot was then converted to dry pod yield in Kgs ha<sup>-1</sup>.

## STATISTICAL PROCEDURES ADOPTED

All collected data of required parameters was averaged and subjected to basic statistics, correlation, PCA and clusters analysis by using statistical Softwares Minitab version 17 and Statistix 8.1. Pearson correlation values, cluster analysis and PCA were carried out in keeping with previous standards (17).

## RESULTS & DISCUSSION

The results of basic statistics of different studied characters exhibited significant genetic variability in 40 groundnut strains.

## CORRELATION STUDIES

As reported earlier, correlation is very useful tool for investigation of association amongst various factors contributing towards yield (18). It is evident from correlation matrix (Table II) that biological yield has strong positive correlation with plant height while shelling percentage is negatively correlated with it. Kernel weight have very strong positive correlation with pod length, pod number per plant and dry pod yield while it also have some relationship with plant height and shelling percentage. Previously, same trend



of correlation among Pod number and dry pod yield was found (7). Pod length positively affects kernel weight, pod number per plant, shelling percentage and dry pod yield. Pod number per plant has direct positive relationship with kernel weight and dry pod yield. As dry pods yield and pod number plant<sup>-1</sup> has strong direct correlation so, it is possible that these parameters have some genes in common as reported by (19, 20). It was concluded from correlation analysis that major yield contributing factors in groundnut are kernel weight, Pod Length, No. of pods plant<sup>-1</sup> and shelling %. It was also evident from previous findings that these traits have positive association with dry pod yield (10, 21).

**Table II.** PC values of rotated component matrix for eight variables of chickpea

	BYLD	KW	PH	PL	PDPP	Shell
KW	0.0414					
PH	0.2541**	0.1800*				
PL	-0.1138	0.3927**	0.2458*			
PDPP	-0.0863	0.6241**	0.1634	0.3932**		
Shell	-0.2161*	0.2429*	0.2642*	0.7234**	0.2089	
DPY	-0.0072	0.7652**	0.2333	0.5097**	0.6780**	0.3980**

\*BYLD: Biological yield; KW: 100 kernel weight(g) PH: Plant Height (Cms); PL: Pod Length; PDPP: No. of Pods per Plant; Shell: Shelling%; DPY: Dry Pod Yield (Kg/ha)

## PRINCIPAL COMPONENT ANALYSIS

True exploitation of genetic resources may be made by partitioning total variance into various components. PCA also provide opportunity to utilize desirable germplasm in crop improvement (11). A variety of biometrical tools especially principal components analysis and cluster analysis were mentioned in past findings for grouping of genotypes among various clusters depending upon yield and related attribute (22). Investigating five principal components (PCs), just first three presented eigen values greater than 1 and were selected for interpretation. The three selected PCs contribute 80.9% towards the total variation in assessed strains in support of yield and related parameters (Table III) but left over components only contributed 19.1% in total variation. PC-I contribute utmost toward variability (45.3%) after that PC-II (18.5%) and PC-III (17.1%). Previously, similar findings were reported about first three PCs (16).

**Table III.** Principle component analysis for yield and related traits in groundnut

Variable	PC I	PC II	PC III
Eigen value	3.1710	1.2923	1.2001
% of total variance	0.453	0.185	0.171
Cumulative variance %	0.453	0.638	0.809
<b>Factor loadings by various traits</b>			
Variable	PC I	PC II	PC III
Plant Height (cm)	0.220	-0.446	-0.513
Biological Yield (kgs)	-0.065	-0.748	-0.215
100 Kernel weight (g)	0.446	-0.162	0.369
Pods per Plant	0.431	-0.106	0.380
Shelling %	0.361	0.366	-0.496
Pod Length	0.432	0.231	-0.350
Dry Pod Yield (kg /ha)	0.496	-0.131	0.204

The 1<sup>st</sup> two principal components played main role for presenting major diversity contributor when exploring different characters (23). In the first principal component, maximum contribution towards variation was depicted by pod yield, 20 pod length, 100 kernel weight and no. of pods per plant. While investigating second PC it was clear that maximum positive contribution was due to shelling percentage and maximum negative contribution in this component was due to biological yield. Plant height contributed maximum but negatively towards variation in PC-III. It is evident from loading plot and biplot (Fig. 1 & 2) that No. of Pods plant<sup>-1</sup>, 100 kernels weight and dry pods yield are strongly correlated with each other and the strains 10AK005, 18AK002, 10CG002, 14CG009, 10AK003, 11AK0011 and BARI-2016 have maximum potential for these traits. Shelling percentage and pod length are also correlated with each other and the strains 14AK007, 17AK003, 17AK004 and 14AK001 have maximum potential for these traits (Fig. 3). In previous findings, researchers emphasized on selection of genotypes having higher number of pods



per plant and also on larger pod size as these characters enhances market value of groundnut genotypes (16, 24). It is also clear from these results that major yield contributing characters in groundnut are No. of Pod per plant, 100 kernels weight, shelling% and pod length and the above mentioned genotypes having good potential for these traits can be utilized for yield enhancement of groundnut.

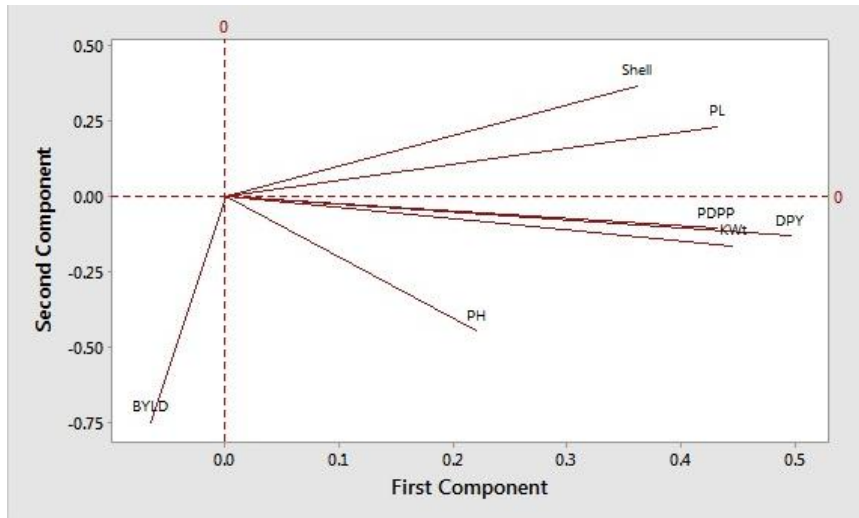


Fig. 1. Loading plot for yield and related traits of groundnut germplasm

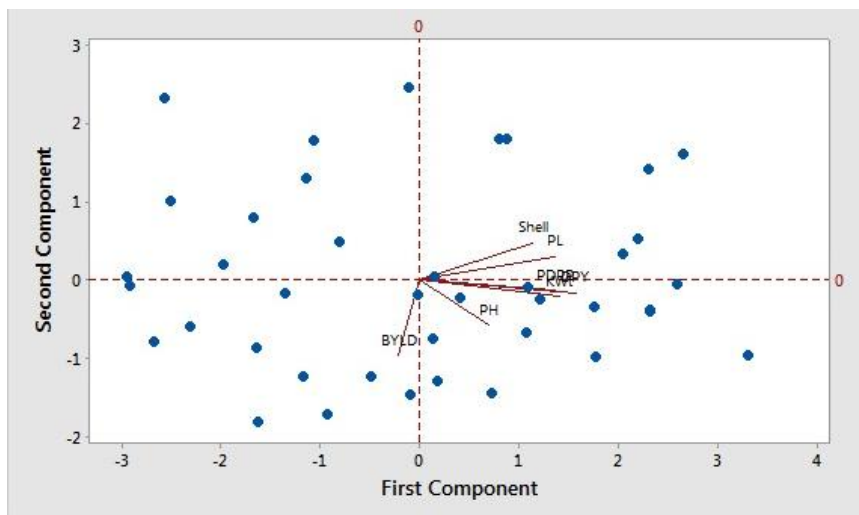


Fig. 2. Biplot for yield and related traits of groundnut germplasm

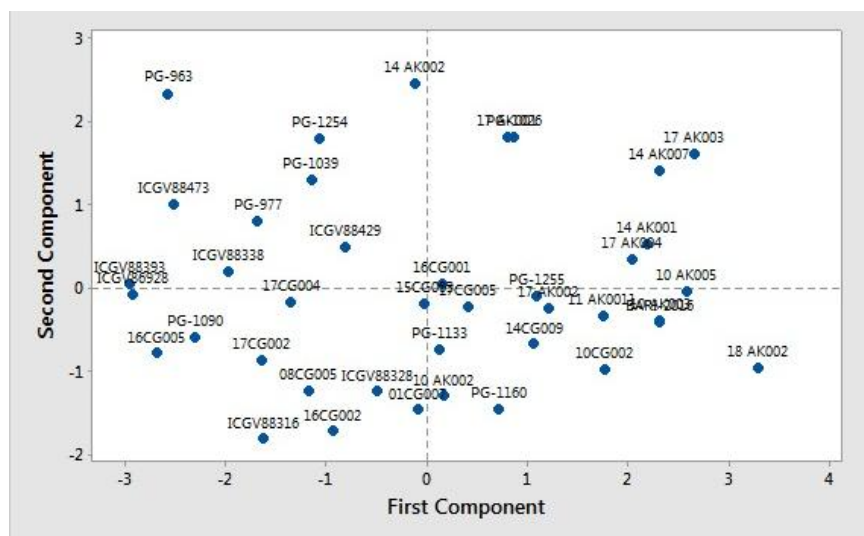


Fig. 3. Score plot for yield and related traits of groundnut germplasm

## CLUSTER ANALYSIS

The Clustering of genotypes depending upon their characters is very beneficial because it helps in selection and identification of top performers and genetically divergent strains (7). The level and nature of genetic divergence among genotypes is expressed by cluster analysis in dendrogram (16). In current study, the cluster analysis divided the studied germplasm into four clusters based on the similarity of explored characters. Largest clusters were Cluster-1 & 2 which comprised of 16 genotypes each followed by cluster-4 having six genotypes and clusters 2 having two genotypes (Table V & Fig. 4).

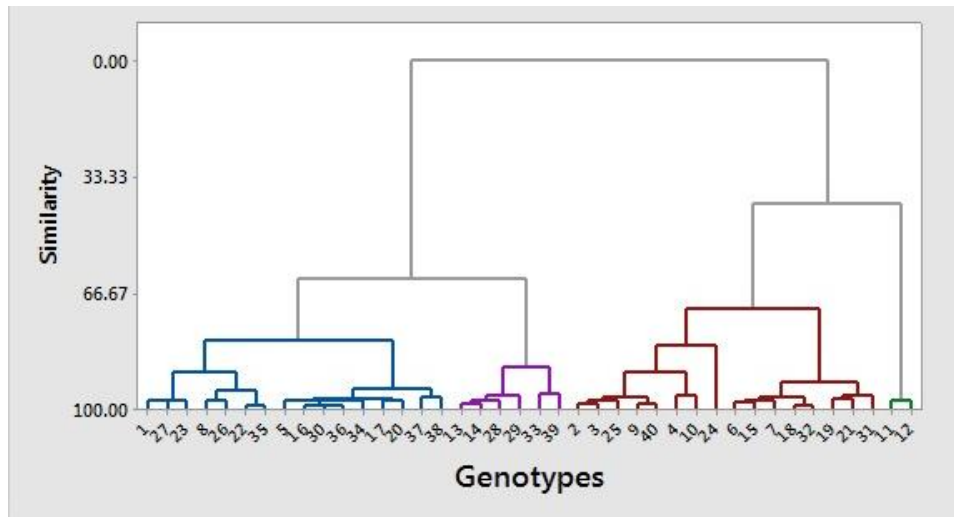


Fig. 4. Dendrogram, yield and related traits of groundnut germplasm, complete linkage, euclidean distance

Investigating clusters with respect to yield and related characters in table-4 revealed that the most superior cluster was cluster-3 having maximum values for dry pod yield and its contributing traits while inferior one in this regard was cluster 4. For creation of genetic variability, the genotypes from these two divergent clusters can be utilized as parents for crossing with each other in future breeding programmes. Findings of above study are related with preceding investigations who reported the existence of high genetic divergence in groundnut (7).

Table IV. Cluster analysis for yield and related traits of groundnut germplasm

Variable	Cluster-1	Cluster- 2	Cluster-3	Cluster-4
PH	35.00	35.48	35.50	29.33
BYLD	5.53	4.18	5.83	4.97
KW	61.21	71.31	73.33	55.00
PDPP	27.90	43.50	44.33	24.56
Shell	60.90	65.48	69.83	58.83
PL	60.46	64.77	67.00	57.61
DPY	1231.04	1464.58	1937.50	1022.50

Table V. Cluster membership of different genotypes

Cluster number	No. of genotypes	Genotype name
Cluster -1	16	10 AK002, 16CG002, 08CG005, 17 AK002, 01CG007, 15CG003, ICGV88328, 14 AK002, PG-1039, 17CG004, ICGV88338, ICGV88316, PG-1090, PG-1254, ICGV88393, ICGV88429,
Cluster -2	16	10 AK003, 11 AK0011, 14CG009, 17 AK003, BARI-2016, 14 AK001, 17AK004, 10CG002, 14 AK007, PG-1026, 17 AK001, PG-1133, 16CG001, PG-1160, PG-1255, 17CG005
Cluster -3	2	10 AK005, 18 AK002
Cluster -4	6	PG-963, PG-977, 16CG005, 17CG002, ICGV86928, ICGV88473

## CONCLUSION

The existence of genetic variability in the groundnut germplasm was confirmed in above mentioned findings. It was concluded from present research findings that major yield contributing factors in groundnut are kernel weight, pod length, number of pod per plant and shelling%. Among studied germplasm, the strains 10AK005, 18AK002, 10CG002, 14CG009, 10AK003, 11AK0011, 14AK007, 17AK003, 17AK004, 14AK001 and BARI-2016 have maximum potential for these traits. Cluster analysis demarked that the most superior cluster was cluster-3 having maximum values for yield and related parameters. Therefore, the genotypes in cluster-3 may be utilized further for yield enhancement of groundnut in future breeding strategies.

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### Conflict of interest:

The authors declare no conflict of interest.

### Authors' contribution:

S conducted experiment; MR wrote result and discussion; GN supervision; MSH review of literature; AAK managed references; MZ, WM Field data collection; MTAK proof read manuscript; AB, AF data analysis; YR helped in results and Discussion writeup; SH wrote introduction; JF editing; GA, MIK methodology. All authors read and approved the final manuscript.

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