



Assessment of Groundnut (*Arachis hypogaea* L.) Cultivars on Yield and Yield Contributing Traits using Principal Component Analysis

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ABSTRACT

Background: The breeder's ability to identify and exploit genetic diversity at the genotypic level is essential for the success of any breeding effort. It requires evaluating various treatments for a variety of traits in order to choose parents with the greatest genetic diversity. The purpose of this research is to characterize the genetic variation among 48 groundnut accessions with 6 checks.

Methods: Experiment was conducted to study groundnut genotypes for 15 varied traits such as phenological, yield attributing and biochemical ones. Data analysis for principal component analysis (PCA) is done using R software.

Result: Principal component analysis (PCA) was carried out to investigate the principal components of variance using traits of study. Total variance among characters are classified into 15 principal components. Out of which first five components have eigen value >1 contributing to 65.9% total variance. PC 1 alone accounted for highest variance of 16.3%, followed by PC 2 with 12.6%. PC1 explained a large amount of variation in important traits as number of mature kernels per plant, total number of kernels per plant, pod yield per plant and kernel yield per plant. PC 2 have positive influence on days to 50% flowering, days to maturity, number of branches per plant, biological yield per plant, number of mature kernels per plant, total number of kernels per plant, sound mature kernel percentage, oil content and harvest index.

Key words: *Arachis hypogaea*, Biplot, Groundnut, PC, PCA, Principal components, Scree plot, Variability, Variance.

INTRODUCTION

Groundnut is an annual plant well known as an oilseed crop, belonging to genus *Arachis* and species *hypogaea*. It comes under the family Leguminosae, the Aeschynomeneae tribe and the Stylosanthinae subtribe. It is self-pollinated and a tropical legume (Diallo *et al.*, 2008). It is an allotetraploid with chromosome number $2n = 4X = 40$. Its genome is represented as AABB (Mallikarjuna *et al.*, 2014). Groundnut is grown in tropical and temperate regions of world. It is marked for its nutrition value, with good fatty acid composition so it is well known for its oil quality (Ahuja, 1993).

As per 2019-2020 census, land under groundnut cultivation was 31.57 mha (million hectares) with production of 53.64 mt (million tonnes) worldwide. Among all the countries, India was in position 1 in area. India's land under cultivation was 15.30% in acreage then China with 14.57% and Nigeria having 12.89% of land (Prajapati *et al.*, 2022). According to USDA (United States Department of Agriculture), In 2022, China ranked highest in groundnut production followed by India, Nigeria, United States, Sudan, Senegal, Burma, Guinea, Argentina and Tanzania. China contributes 37% of total world production that is, 18,300 million tonnes (MT) whereas India with 13% - 6300 million tons (MT) of share in it. In India, Gujarat stands in 1st position with 33% of production then with Rajasthan (21%), Tamil Nadu (14%) andhra Pradesh (7%) and Madhya Pradesh (6%) - No change as edited before (Peanut Explorer, 2022).

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Production of groundnut in India during 2022 is 10.14 million metric tons and is expected to be as 10.6 million metric tons in 2023 year (Statista, 2023).

It is challenging for every breeder to produce superior hybrids having high yield and good oil content in groundnut crop. The presence of genetic variability is a fundamental requirement for the enhancement of crops, as it offers a broader range of options for selection. The efficacy of selection is contingent upon the scope and range of genetic diversity that exists within the material (Gowda *et al.*, 2012). Therefore, the current study aimed to evaluate specific groundnut cultivars in order to analyse the diversity of significant characteristics through PCA. Principal component analysis (PCA) is a multivariate technique that

involves the transformation of a set of potentially correlated variables into a reduced set of variables known as principal components. It relies upon eigen vectors and eigen values to signify data (Datta *et al.*, 2017).

MATERIALS AND METHODS

The experiment was performed under Agricultural Research farm, Department of Genetics and Plant Breeding, Lovely Professional University, Phagwara (Punjab). Investigation site is located at latitude 31.241890°N, longitude of 75.6971100°E and at an altitude of range 232 metres above MSL (Mean Sea Level). The experimental material comprised of 48 test genotypes from National Research Centre for Groundnut, Junagadh and with 6 checks in Augmented design. Each block has 12 treatments and 6 checks (Table 1). Checks are repeated each time in each block. These genotypes are sown in 10-meter length row plots with a spacing of 45 (row) X 10 (plant) cm during 2022-2023. All package of practices were followed as per standard recommendations under irrigated conditions.

Research on diversity is done with 54 accessions on 15 traits. These include days to 50% flowering (DFF), days to maturity (DTM), plant height (PH), number of branches per plant (NBP), biological yield per plant (BYP), number of mature kernels per plant (NMK), total number of kernels per plant (TKP), sound mature kernel percentage (SMK), shelling percentage (SP), test weight (TW), harvest index (HI), oil content (OC), protein content (PC), kernel yield per plant (KYP) and pod yield per plant (PYP). Principal Component Analysis (PCA) aims to detailed study of contribution of genotypes and traits to total variance (Ingebriston and Lyon, 1985). Data analysis is done using R software version 4.2.2 and metan R package with “ggplot2”, “gridExtra”, ggbiplot, “corrplot” and factoextra data packages. (Luci and Olivoto, 2020); (Mendiburu, 2021).

RESULTS AND DISCUSSION

Analysis of variance (ANOVA)

Table 2 shows the results of an ANOVA for the 15 attributes that were taken into consideration in the research to identify

Table 1: List of genotypes.

S.No	Genotype name	Accession number	S.No	Genotype name	Accession number
I. Test genotypes:					
01.	T1	NRCG-1156	25.	T25	NRCG-12333
02.	T2	NRCG-14887	26.	T26	NRCG-10708
03.	T3	NRCG-11119	27.	T27	NRCG-14392
04.	T4	NRCG-10402	28.	T28	NRCG-4409
05.	T5	NRCG-9285	29.	T29	NRCG-16092
06.	T6	NRCG-10545	30.	T30	NRCG-14028
07.	T7	NRCG-1325	31.	T31	NRCG-13920
08.	T8	NRCG-14038	32.	T32	NRCG-15010
09.	T9	NRCG -14070	33.	T33	NRCG-10392
10.	T10	NRCG-229	34.	T34	NRCG-15082
11.	T11	NRCG-5568	35.	T35	NRCG-10732
12.	T12	NRCG -10501	36.	T36	NRCG-15071
13.	T13	NRCG-13955	37.	T37	NRCG-14670
14.	T14	NRCG-15068	38.	T38	NRCG-14435
15.	T15	NRCG-17049	39.	T39	NRCG-11020
16.	T16	NRCG-16891	40.	T40	NRCG-10907
17.	T17	NRCG-10390	41.	T41	NRCG-14344
18.	T18	NRCG-7109	42.	T42	NRCG-4140
19.	T19	NRCG-236	43.	T43	NRCG-11668
20.	T20	NRCG-203	44.	T44	NRCG-10887
21.	T21	NRCG-12202	45.	T45	NRCG-12460
22.	T22	NRCG -13964	46.	T46	NRCG-12459
23.	T23	NRCG-16905	47.	T47	NRCG-10978
24.	T24	NRCG -208	48.	T48	NRCG-1028
II. Checks:					
01.	C1	Tag-24	04.	C4	Kadiri-218
02.	C2	Kadiri Case	05.	C5	G-2
03.	C3	Javari	06.	C6	KadiriLepaksh

NRCG - National Research Centre for Groundnut.

significant differences at the block and treatment levels. At the treatment level, there were significant variations in traits like DTM, PH, BYP, NMK, TKP, SMK, TW, HI, OC, PC, KYP and PYP. Block differences reported non-significant for all traits including DFF, DTM, PH, NBP, BYP, NMK, TKP, SMK, SP, TW, HI, OC, PC, KYP and PYP. Similar results were reported by Bhargavi *et al.* (2017) for the traits biological yield per plant, test weight and oil content.

Principal component analysis

PCA in the study takes into account 2 biochemical traits and 13 quantitative traits. 15 Principal Components (PCs) are used to break down the whole set of data. In Table 3, the first five PCs have eigenvalues >1, which accounts for 66% of the overall variability. With an eigenvalue of 3.9437, PC1 alone contributed 26.3% of the total variance. With regard to PC1 in Table 3, NMK (0.436) has the highest positive correlation, followed by TKP (0.425), KYP (0.409), PYP (0.373), SP (0.262), BYP (0.171) and OC (0.164), while NBP (0.065) and HI (0.006) have the lowest positive correlation. PC1 has a strong negative connection on DTM (-0.337), DFF (-0.146) and a weak negative effect on PC (-0.062), TW (-0.097) and PH (-0.011).

PC2 has an eigenvalue of 1.8927 and a 12.6% total variability (Table 4). PC2 is highly positive correlated with HI (0.348), continued by BYP (0.296), OC (0.286), NMK (0.266), TKP (0.25), DTM (0.174), NBP (0.157), SMK (0.144) and DFF (0.093). It has a strong negative correlation with qualities such as TW (-0.369), KYP (-0.351), SP (-0.344), PYP (-0.278) and PC (-0.17) as well as a weak negative correlation with PH (-0.086) (Table 4).

The third principal component (PC3) had an eigenvalue of 1.5818 and it contributed 10.5% to overall variability (Table 3). Traits like PH (0.511), BYP (0.472), PYP (0.231), DTM (0.203), TW (0.148), DFF (0.114), HI (0.105), SMK (0.083), KYP (0.082), NMK (0.062), TKP (0.029), SMK (0.083) and KYP (0.082) are positively influenced with PC3, while negative correlation with NBP (-0.311), SP (-0.261), OC (-0.43) and PC (-0.09) (Table 4).

Variance data based on (Table 3 and Table 4) proved that 4th Principal Component (PC4) have significant positive correlation with SMK (0.479) followed by PC (0.452), DFF (0.327), TW (0.234), DTM (0.189), NMK (0.188), HI (0.133) and least significant positive influence on PYP (0.061), TKP (0.059) and KYP (0.018). while same PC4 is negatively correlated with traits PH (-0.473), OC (-0.206), NBP (-0.144), BYP (-0.131) and negligible negative relation with SP (-0.066).

The final PC to contribute more than 1 eigen value is PC5 with total variance of 7.2% and an eigenvalue of 1.0839 with reference to (Table 3) DFF (0.517), preceded by NBP (0.489), SMK (0.308), SP (0.184), BYP (0.138), are significantly positively related while least positive correlation with TW (0.054), DTM (0.042), KYP (0.038) and PH (0.008). Negatively correlated traits are PC (0.414), HI (-0.364), TKP (-0.143), OC (0.105), PYP (-0.044) and are NMK (-0.042) (Table 4).

Table 2: Analysis of variance of all traits in germplasm of groundnut (*Arachis hypogaea* L.).

Source	Df	DFF	DTM	PH	NBP	BYP	NMK	TKP	SMK	SP	TW	HI	OC	PC	KYP	PYP
Treatment (ignoring blocks)	53	2.07	35.23*	18.69*	0.38	27.02**	48.79**	51.46**	113.2**	38	44.85**	64.01**	66.92**	10.68**	3.91**	4.15**
Treatment: Check	5	5.54*	79.47**	41.52**	1.9	38.77**	12.54**	6.74**	62.13**	96.51*	138.24**	10.27**	22.51**	11.14*	15.74**	14.03**
Treatment: Test vs. Check	1	2.01	321.01**	78.06**	5.44*	12.78*	874.66**	611**	1579.25**	159.25*	0.07	65.47**	1077.37**	17.27*	20.32**	13.57**
Treatment: Test	47	1.7	24.45	15**	0.11	26.07**	35.07**	44.31**	87.44**	29.19	35.87**	70.67**	50.15**	10.49**	2.3*	2.9**
Block (eliminating treatments)	3	1.93	9.89	0.45	1.94	1.7	2.06	0.99	8.27	28.01	2.76	2.69	0.15	1.74	0.77	0.22
Residuals	15	1.5	14.96	1.43	0.69	2.54	0.75	1.05	2.52	28.62	3.16	1.71	3.63	3	0.87	0.68
CV(%)		4.22	3.45	6.78	16.45	6.89	4.62	4.51	1.94	7.06	4.62	1.97	4.27	7.35	10.31	6.94

DFF- Days to 50% flowering; DTM- Days to maturity; PH- Plant height; NBP- Number of branches per plant; BYP- Biological yield per plant; NMK- Number of mature kernels per plant; TKP- Total no. of kernels per plant; SMK- Sound mature kernel percentage; SP- Shelling percentage; TW- Test weight; HI- Harvest index; OC- Oil content; PC- Protein content; KYP- Kernel yield per plant; PYP- Pod yield per plant.

Chaudhari *et al.* (2021) reported contribution of 6PCs with cumulative percentage of variance 82.54% with kernel yield that have significant positive correlation in PC1. Similar outcomes were utilized by Al Mamun *et al.* (2022) to categorize all of the data into PCs. It was discovered that PC1 variant has a negative correlation (-0.18) with days to 50% flowering. While PC2 has a total variance of 15.13 percent and significant positive effect on NBP and BYP. Alanyoet *et al.* (2022) conducted experiments that classified highest variance in 1st 3 PCs with 21.8, 14, 11.6% total variation and 8.95, 3.28, 1.12 eigenvalue.

Table 3: Eigen analysis of correlation matrix.

PCs	Eigenvalue	Proportion of variance (%)	Cumulative variance percent
PC1	3.9437	26.3	26.3
PC2	1.8927	12.6	38.9
PC3	1.5818	10.5	49.5
PC4	1.3989	9.3	58.8
PC5	1.0839	7.2	66
PC6	0.9943	6.6	72.6
PC7	0.9047	6	78.7
PC8	0.8333	5.6	84.2
PC9	0.6467	4.3	88.5
PC10	0.5655	3.8	92.3
PC11	0.4556	3	95.3
PC12	0.4251	2.8	98.2
PC13	0.2694	1.8	100
PC14	0.0028	0	100
PC15	0.0017	0	100

PC- Principal component.

Dama (2022) has similar investigations of PCA with 29.77% variance in PC1 and a 5.04 eigenvalue with significantly related various characteristics for kernel yield, dry pod yield and harvest index. The overall variance percentage for PC2 was 14.71% and the eigenvalue was 2.50. Nigatu (2022) identified PC1 as having 4.37 eigenvalue and 31.24% overall variation. He provided an explanation for the positive effects of PC1 on kernel yield (0.45), pod yield (0.44) and plant height (-0.34) using a negative covariance matrix.

Abteu *et al.* (2023) explored that the first four PCs were responsible for a total variance of 76.7%. PC1 explained 49.04% of the variation in plant height, days to maturity and pod weight, which is substantial and greatest. After that trend went declined. Days to 50% blooming and shelling percentage are related to PC2, with a total variance of 12.39%. Esan *et al.* (2023) validated the results with decreasing order of variation from PC1 to PC8 in which PC1 has highest variance. Total variance attributing traits of PC1 is mature pod number per plant, harvest index and yield per plant. PC2 shown total variance with plant height and biomass per plant.

Scree plot

The scree plot is a graphical representation of the overall variance contribution of each PC. The largest variance contribution is shown in increasing order in the bar graph. According to this, PC1 is more closely related to variance and from PC2 to PC10, this relationship begins to decline. Principal Component Analysis (PCA) findings from PC1 to PC5 are discussed above since they contain a lot of variance whereas remaining PCs showed minimal variation.

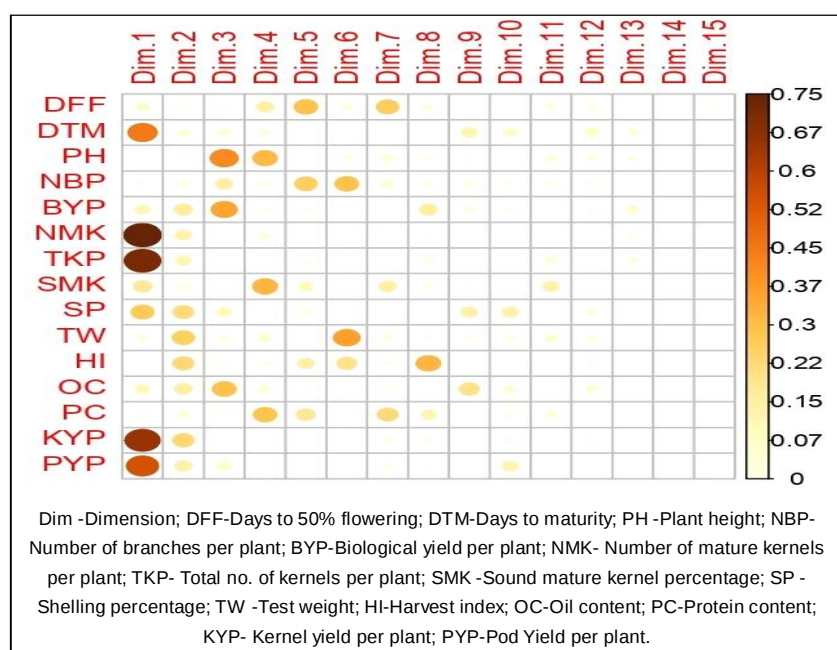


Fig 1: Contribution of traits to 1 and 2 dimensions.

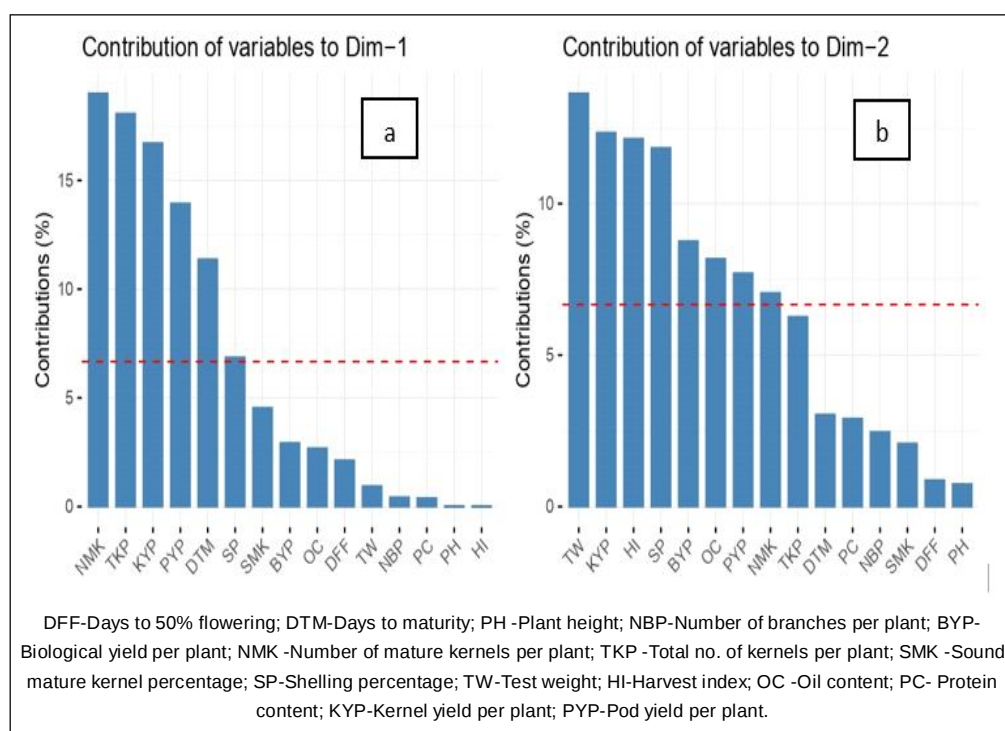


Fig 2: a) Bar graph of contribution of individual traits in variance to Dim 1.

b) Bar graph of contribution of individual traits in variance to Dim 2.

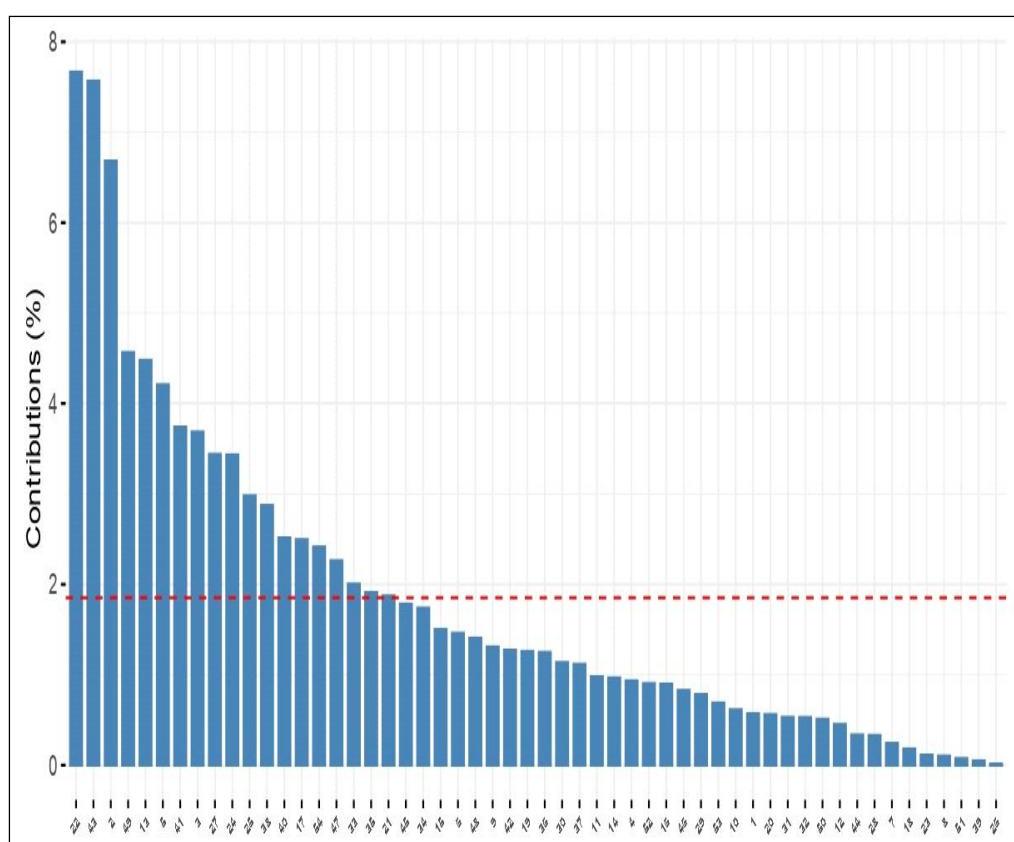


Fig 3: Bar graph contribution to total percentage of variation of 54 genotypes.

Table 4: Correlation matrix and its contribution of traits to principal components.

Variable	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	PC13	PC14	PC15
DFF	-0.146	0.093	0.114	0.327	0.517	-0.221	0.539	-0.229	0.022	0.099	0.304	0.285	0.082	0.001	0
DTM	-0.337	0.174	0.203	0.189	0.042	-0.11	0.053	0.084	-0.44	-0.397	0.034	-0.461	-0.435	-0.021	0.001
PH	-0.011	-0.086	0.511	-0.473	0.008	0.18	0.25	-0.147	-0.139	0.141	-0.326	0.315	-0.384	0.003	0.009
NBP	0.065	0.157	-0.311	-0.144	0.489	0.54	0.266	0.186	0.262	-0.174	-0.225	-0.248	-0.079	0.004	-0.008
BYP	0.171	0.296	0.472	-0.131	0.138	0.052	0.01	0.44	-0.259	0.186	0.066	-0.19	0.534	0.019	-0.001
NMK	0.436	0.266	0.062	0.188	-0.042	0.024	-0.051	0.118	0.07	0.046	0.124	0.121	-0.312	-0.722	-0.159
TKP	0.425	0.25	0.029	0.059	-0.143	0.001	0.066	0.192	0.126	0.01	0.335	0.083	-0.386	0.623	0.136
SMK	0.213	0.144	0.083	0.479	0.308	0.026	-0.405	-0.191	-0.165	0.078	-0.552	0.131	-0.021	0.207	0.055
SP	0.262	-0.344	-0.261	-0.066	0.184	0.053	0.03	-0.129	-0.463	0.494	0.176	-0.306	-0.155	0.053	-0.276
TW	-0.097	-0.369	0.148	0.234	0.054	0.609	-0.215	0.137	-0.198	-0.231	0.366	0.332	0.037	0.002	0.002
HI	0.006	0.348	0.105	0.133	-0.364	0.453	0.139	-0.618	0.003	0.094	0.106	-0.247	0.17	0.01	-0.001
OC	0.164	0.286	-0.43	-0.206	-0.105	-0.033	0.167	-0.05	-0.568	-0.339	-0.065	0.386	0.176	-0.001	-0.002
PC	-0.062	-0.17	-0.09	0.452	-0.414	0.107	0.499	0.384	-0.079	0.219	-0.347	0.036	0.016	0.009	0.006
KYP	0.409	-0.351	0.082	0.018	0.036	-0.072	0.164	-0.144	-0.063	-0.206	-0.012	-0.21	0.085	-0.163	0.724
PYP	0.373	-0.278	0.231	0.061	-0.044	-0.118	0.181	-0.12	0.127	-0.477	-0.108	-0.106	0.162	0.132	-0.594

DFF- Days to 50% flowering; DTM- Days to maturity; PH- Plant height; NBP- Number of branches per plant; BYP- Biological yield per plant; NMK- Number of mature kernels per plant; TKP- Total no. of kernels per plant; SMK- Sound mature kernel percentage; SP- Shelling percentage; TW- Test weight; HI- Harvest index; OC- Oil content; PC- Protein content; KYP- Kernel yield per plant; PYP- Pod yield per plant.

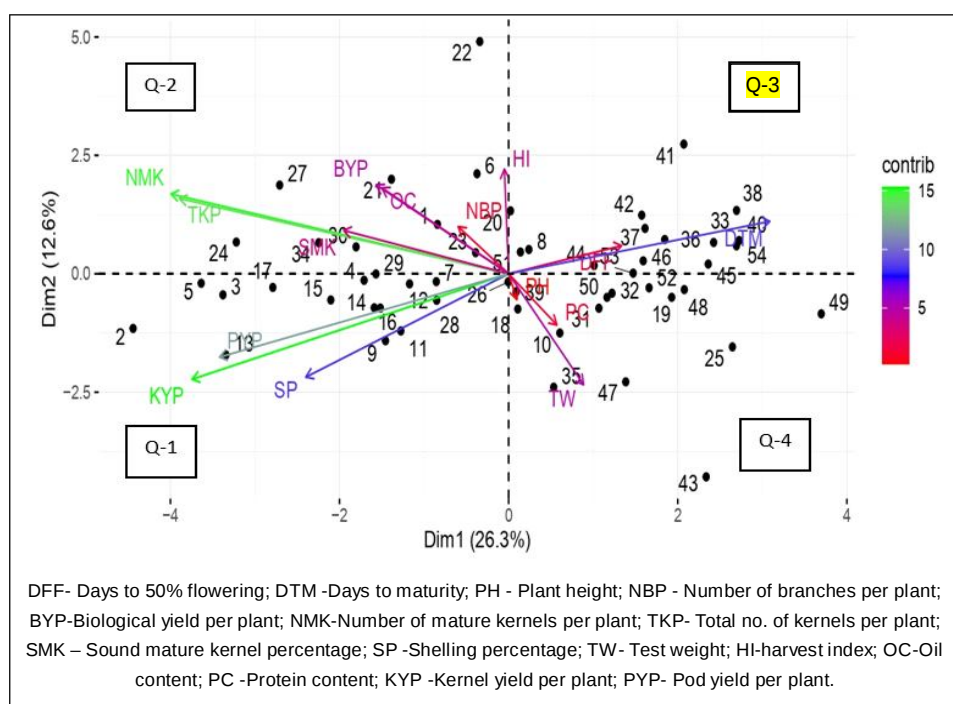


Fig 4: Biplot analysis of PC1 and PC2 in contribution of variance to traits and genotypes of study.

The picture (Fig 1) depicts the contribution of traits to PCs. Dim (Dimensions) are Principal Components ranging from 1 to 15. Darker the colour of each PC in trait, more is the variation. Colour is clearly visible in Dim.1 in NMK, TKP, KYP, PYP and DTM. Later, the intensity started to decrease and it completely faded in Dim 14 and 15.

Fig 2 A shows that NMK contributed greater variation to Dim.1 than other contributors. The horizontal line in a bar graph displays the average variance of all features. The overall variance for TKP, KYP, PYP and DTM stands above average after NMK. In proximity to the average variance line, SP is situated. The average variance level is not satisfied by any other attributes, including SMK, BYP, OC, DFF, TW, NBP and PC. PH and HI are not significant to take into consideration variance. In the instance of Dim. 2 (Fig 2b), TW is followed by KYP, HI, SP, BYP, OC, PYP and NMK which all have larger variation than average across all features. In contrast, TKP, DTM, PC, NBP, SMK, DFF and PH height have variance below average. The selection of genotypes for those qualities in Dim.1 and Dim.2 is not very significant, according to both graphs for traits that are below the average line. Significant results can be seen if traits show much variance from each other in other words that are above average line.

To find out how genotypes react to overall variability, studies are conducted (Fig 3). When all genotypes were compared, it was found that genotype 22 had the highest level of variation in Dims. 1 and 2. Following it are genotypes 43, 2, 49 and 5. Close to average variation has been reported in 54th, 47th and 21st genotype. The 51st, 39th and 26th genotypes are the least varied.

Biplot analysis

Biplot's PCA in (Fig 4) is split into four quadrants by considering Dim 1 in X-axis and 2 in Y-axis that accounted for maximum variance. As biplot spots variance between traits and genotypes, colour is used as an intensity of variance. Green colour denotes high variance whereas blue and red colour indicates moderate and low variance respectively. Quadrant 1 (Q-1) is the one that is directly above the centroid and has a positive effect on both Dim. 1 and Dim. 2. Genotypes viz, 41, 42, 8, 44, 42, 20, 37, 53, 46, 36, 33, 8, 40, 54, 45, 46, 36, 33, 38, 40, 40, 54 and 45 (Table 1) are grouped in Q-1 with traits DTM and DFF. 41 genotype is observed as highest contributing accession and DTM have strong and high variance as they lie away from the graph line.

Accessions such as 22, 27, 6, 21, 1, 24, 34, 30, 23 and 29 (Table 1) falls under quadrant 2 (Q-2) that lies left above to the centre which has a positive effect on Dim.2 and negative effect on Dim.1. that contribute variance in traits like NMK, TKP, SMK, BYP, OC, NBP and HI. Genotype 22 and traits NMK and TKP are said to highly diverse attributes and best for selection.

The third quadrant (Q-3) lies to the left of the centre and has negative influence on both Dim.1 and Dim.2. Genotypes like 5, 3, 17, 15, 4, 7, 5, 15, 14, 12, 26, 16, 28, 9, 11, 2 and 13 (Table 1) are highly associated with KYP followed by PYP and SP. Contribution of variance is high with variables KYP and genotype 2.

Right below the centroid, in quadrant 4 (Q-4), are the positive effect on Dim.1 and negative effect on Dim.2, respectively. Variables such as TW, PC and PH are

correlated with genotypes 39, 50, 32, 52, 31, 19, 48, 25, 49, 47 and 43. Contribution of variance is high with 43rd genotype and TW in Q-4.

Biplot (Fig 4) shown that variation in traits like NMK, TKP and KYP were highly significant while PC, PH and NBP traits all had minimal variance contribution. Genotypes viz., 22 in Q-2 accounted for greater variability then by 43 from Q-4, 41 in Q-1 and 2 in Q-3. Biplot concluded that there is a strong correlation between NMK and TKP. The genotype NRCG - 13955 (13) is well suited for PYP and NRCG -15082 (34) for NMK and TKP (Table 1).

Al Mamun *et al.* (2022) discussed the same in biplot by characterizing variation in 7 genotypes with trait such as number of stems in the negative region of biplot. According to Akkareddy *et al.* (2023) biplot study, there is a high rate of association between kernel weight and hundred kernel weight, as well as plant height contributing to total proportionate variance. Mekonen (2022) have similar findings by construction of biplot using 40 groundnut accessions in which hundred seed or test weight took positive side of graph. Biplot Kohar *et al.* (2023) studied noteworthy findings on plant height with the greatest varying 3 genotypes. High significant variation was found in the pod yield, shelling % and protein content according to Iler *et al.* (2023) biplot analysis.

CONCLUSION

Using PCA, researchers learn how much variation each genotype and study characteristic contribute. Every breeder should use highly variable genotypes for their breeding programs. From proportional variance data, PCA has the potential to choose such a variety of parental accessions. However, biplot links genotypes to traits to ensure that there is a connection between them in variability. Biplot analysis detected the variation in traits like kernel yield per plant, number of mature kernels per plant and total number of kernels per plant. These are crucial and in contributing to total yield. PCA look into this and provide information regarding selection of variable traits that increase productivity of crop.

Conflict of interest

All authors declare that they have no conflicts of interest.

REFERENCES

- Abteu, W.G., Mekonen, G.S., Oselebe, H.O., Tesfaye, A.A., Uba, C.U. (2023). Exploring phenotypic variation of diverse bambara groundnut (*Vigna subterranea* L) origin and development of mini core collection for future breeding. Food and Energy Security. 12(4): 460. doi: 10.1002/fes3.460.
- Ahuja, K.L., Bansal, U.K., Satija, D.R. (1993). Oil composition of diverse groundnut (*Arachis hypogaea* L) genotypes in relation to different environments. Journal of the Science of Food and Agriculture. 63(1): 17-19.
- Akkareddy, S., Kumar, A.R.N., Madhuri, K.V.N., Reddy, C.B.R., Reddy, C.K.K., Sukrutha, B., Vemireddy, L.N. (2023). Principal component analysis and path coefficient analysis for groundnut yield and seed quality attributes (*Arachis hypogaea* L.). Legume Research-An International Journal. doi: 10.18805/LR-5075.
- Al Mamun, M., Jusoh, M., Khaliqi, A., Khan, M. M. H., Oladosu, Y., Rafii, M.Y., Ramlee, S.I. (2022). Unveiling genetic diversity, characterization and selection of bambara groundnut [*Vigna subterranea* (L.) Verdc] genotypes reflecting yield and yield components in tropical malaysia. BioMed Research International. 1-23.
- Al Mamun, M., Jusoh, M., Khan, M.M.H., Rafii, M.Y., Ramlee, S. I. (2022). Hereditary analysis and genotype x environment interaction effects on growth and yield components of Bambara groundnut [*Vigna subterranea* (L.) Verdc.] over multi-environments. Scientific Reports. 12(1).
- Alanyo, M., Alenoma, G., Ddamulira, G., Ifeyinwa, M.O., Karwani, G., Kiyowa, M., Umeugochukwu, O.P. (2022). Morphological characterization and diversity of bambara groundnuts in uganda. Journal of Agricultural Science. 14(9): 86-94.
- Bhargavi, G., Rao, Satyanarayana, V., Babu, Ratna, D., Rao Narasimha, L.K. (2017). Genetic variability studies in virginia bunch groundnut (*Arachis hypogaea* L.). Agricultural Science Digest. 37(4): 310-313. doi: 10.18805/ag-D-4524.
- Bhargavi, G., Rao, Satyanarayana, V., Babu, Ratna, D. (2017). Studies on variability, heritability and genetic advance as per cent of mean in Spanish bunch groundnut genotypes (*Arachis hypogaea* L.). Legume Research. 40(4): 773-777. doi: 10.18805/lr.v0i0.7848.
- Chaudhari, S., Manohar, S.S., Mashilo, J., Pasupuleti, J., Seltene, A., Shimelis, H. (2021). 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. 61(3): 1926-1943.
- Dama, D.B. (2022). Genetic variability and association among agro morphological and quality traits in groundnut (*Arachis hypogaea* L.) genotypes in Eastern Ethiopia (Doctoral dissertation, Haramaya University).
- Datta, S., Laishram, M., Mishra, S.P., Panda, S., Saikhom, R., Sarkar, U., Swain, D., Taraphder, S. (2017). Multivariate statistical data analysis-principal component analysis (PCA). International Journal of Livestock Research. 7(5): 60-78.
- De Mendibru, F. (2021). Agricolae: Statistical Procedures for Agricultural Research. R package version 1: 3-5.
- Diallo, A.T., Ndjeunga, J., Waliyar, F. (2008). Groundnut seed production manual. Patancheru 502 324 andhra Pradesh, India: International Crops Research Institute for the Semi-Arid Tropics (ICRISAT). 20.
- Esan, V.I., Ogunbode, T.O., Oke, G.O. (2023). Genetic variation and characterization of Bambara groundnut [*Vigna subterranea* (L.) verdc.] accessions under multi-environments considering yield and yield components performance. Scientific Reports. 13: 1498. https://doi.org/10.1038/s41598-023-28794-8.

- Gowda, M.V.C., Kenchanagoudar, P.V., Narasimhulu, R. (2012). Study of genetic variability and correlations in selected groundnut genotypes. *International Journal of Applied Biology and Pharmaceutical Technology*. 3(1): 355-358.
- Ingebriston, S.E. and Lyon, R.J.P. (1985). Principal components analysis of multi-temporal image pairs: *Journal of the Indian Society of Remote Sensing*. 6: 687-696.
- Işler, N., Şahin, C.B., Yildiz, R., Yilmaz, M. (2023). Comparison of quality and yield components of peanut market types Using PCA. *KSU. J. Agric Nat*. 26(3): 610-618.
- Kohar, G.R. and Yadav, D.R. (2023). Evaluation of groundnut genotypes for yield and yield attributing traits through genotype by trait biplot analysis. *International Journal of Recent Advances in Multidisciplinary Topics*. 4(1): 33-37.
- Le C.N., Thai T.H., Tran D.H., Nguyen T.L., La T.T.H., Nguyen X.V. (2018). Genetic diversity of groundnut rhizosphere antagonistic bacteria and biological control of groundnut wilted diseases in central Vietnam. *Legume Research*. 42(3): 405-410. doi: 10.18805/LR-427.
- Lucio, A.D. and Olivoto, T. (2020). Metan: An R package for multi environment trial analysis. *Methods in Ecology and Evolution*. 11(6): 83-789.
- Mallikarjuna, N., Shilpa, K., Pandey, M., Janila, P., Varshney, R.K. (2014). Groundnut broadening the genetic base of grain. *legumes International Crops Research Institute for Semi-Arid Tropics (ICRISAT)*. 161-173.
- Mekonen, G.S. (2022). Phenotypic and genotypic variability of bambara groundnut (*Vigna subterranean* L.) accessions at Tepi South west, Ethiopia (Doctoral dissertation, Jimma University).
- Nigatu, D. (2022). Genetic variability and association of traits in groundnut (*Arachis hypogaea* L.) genotypes at Pawe North Western Ethiopia.
- Peanut Explorer. (2022). Foreign Agricultural Service, United States Department of Agriculture.
- Prajapati, M.R. and Ramoliya, R.K. (2022). A study on level of Input and economics of production of groundnut in gujarat, current. *Journal of Applied Science and Technology*. 41(37): 30-41
- Statista. (2023). India: Groundnut Production Volume 2023.