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Principal Component Analysis of Morphological Characters in Groundnut Germplasm (*Arachis hypogaea* L.) under Dry Land Ecosystem of India

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***Abstract*:** To determine the principal component (PC) for ten quantitative attributes, the present experiment used 45 genotypes of groundnut during *kharif* season 2019 at S.K.N College of Agriculture, Jobner. To eliminate the diversity between the groundnut genotypes, ten characteristics was used in PCs. Out of ten, only six principal components (PC1 to PC6) exhibited more than 0.5 eigen value and showed 99.44% total variability among the characters. These six PCs were given due importance for further explanation. The best genotypes were those that were found on the extreme positive side of both axes, namely genotypes RG 578 (2.74), RG 575-1 (2.38), RG 642-1 (1.70), RG 623 (1.29) along PCA I axis and genotypes RG 639 (2.79), RG 633-1 (2.69), RG 632 (1.75), and RG 625 (1.68) along PCA II axis. These genotypes will may be used for advance hybridization programme.

***Keywords*:** Diversity, Dry land, Eigen values, Groundnut, Principal component analysis

Groundnut (*Arachis hypogaea* L.) is one of the most significant oilseed crop in India and is a Brazil native. It is grown in nearly 100 countries of the world. Major groundnut producer countries in the world are China, India, Nigeria, USA, Indonesia and Sudan (Zaman et al 2010). In India, it is cultivated over an area of 57.50 lakh hectares and producing a total of 101.10 lakh metric tonnes (Anonymous, 2022). Pod yield is a complex trait and is reportedly associated with a number of component traits. These traits are themselves inter-related. Selection for pod yield can only be effective if the desired genetic variability is present in a genetic stock. However, the development of improved plant cultivars is restricted mainly due to narrow genetic pool, which results into limited possibility to restructure the groundnut crop. Therefore, a technique is required for systematic reduction and summarization of data sets (Tanwar and Bisen 2017). Principal component analysis analyzes the data in which observations are described by several inter- correlated quantitative dependent variables, (Abdi and Williams 2010). PCA is a well-known method to identify the minimum number of components, which can explain maximum variability out of the total variability and also to rank germplasm on the basis of PC scores. The present designed with an objective to identify the minimum number of components, which can explain maximum variability out of the total variability and also to rank 45 groundnut germplasm on the basis of PC scores.

MATERIAL AND METHODS

Forty-five genotypes of groundnut were procured from the Rajasthan Agricultural Research Institute Jaipur, Rajasthan. During the *kharif* season of 2019, the genotypes of groundnut were assessed using randomized block design with three replications. Each genotype was planted in a 4.0 × 0.80 m plot with two rows that were 40 cm apart from one another. Plants were kept 15 cm apart from one another. Five plants were chosen at random from each genotype and replication to record observations on ten characteristics such as pods per plant, dry pod yield per plant, shelling percentage, solid mature kernel, biological yield per plant, harvest index and kernel yield per plant. However, observations on days to 50% flowering, days to maturity and 100-kernel weight were recorded on a plot-by-plot basis. Principal component analysis (PCA) is a standard tool in modern data analysis because it is a simple, non-parametric method for extracting relevant information from confusing data sets (Massay,1965, Jolilffle 1986) and transforms a number of possibly correlated variables into a smaller number of uncorrelated variables called principal components. The STAR (IRRI 2014) and XLSTAT (Addinsoft 2020) programmes were used to analyzed the PCA, scree plot, PCA plot, and scatter plot.

RESULTS AND DISCUSSION

Principal Component Scores (PCs) were used to dividing 45 groundnut genotypes into subgroups because most of the information from the original variables was stored in a few numbers of PCs. (Syafii et al 2015 and Dudhe et al 2018).

The first three PCs (PC1, PC2 and PC3) were responsible for 76.95% of the total variation. The first PC has the highest eigen value (3.975), explaining 39.75 percent of the variation. The remaining two PCs (PC2 & PC3) explained 22.13% and 15.07% of individual variance and 61.88% and 76.95% of cumulative variation (Table 1, Fig. 1). PCs with eigen values less than one were declared non-significant and so discarded since they are unlikely to have any practical significance (Mustafa et al 2015, Hlanga et al 2022).The majority of the variability in the set of all PCs was provided by PC1, while the remaining PCs tended to exhibit less variance. Like outcome was obtained by Mubai et al (2020) and Talekar et al (2022).

Factor loading of various characters: The factor loadings of various variables computed via PCA. In the first PC, days to 50% flowering, days to maturity, solid mature kernel had contributed greatest of the variation with positive significant coefficients of 0.1386, 0.1375 and 0.0556 respectively. Biological yield per plant also found positive coefficient (0.0204) which had contributed to the principal axis one and all remaining traits has negatively contributed to the principal axis one. High positive coefficients were for the days to 50% flowering (0.5304), days to maturity (0.5272) and 100-kernel weight (0.2689) in the second principal axis. Shelling (-0.3637), solid mature kernel (-0.3283) and biological yield per plant (-0.2857) exhibited a negative impact on the second principal axis. In the third principal axis, 100-kernel weight (0.3462) and biological yield per plant (0.1155) had the highest co-efficient values, whereas all other remaining traits were shown highly negative contribution (Table 2, Fig. 2).

PC score of germplasm: Three axes like X, Y, and Z were taken into consideration while analyzing the principal component analysis (PCA) scores for 45 groundnut genotypes in the initial three PCs were obtained, as well as the squared distance of each genotype from these axes

Table 1. Eigen values and percent variation contributed for the 10 PCs of 45 groundnut genotypes

Statistics	Eigen values	Expression of proportion of variance	Expression of cumulative proportion
PC 1	3.975	39.75	39.75
PC 2	2.213	22.13	61.88
PC 3	1.507	15.07	76.95
PC 4	0.918	9.18	86.13
PC 5	0.750	7.50	93.63
PC 6	0.581	5.81	99.44
PC 7	0.037	0.37	99.81
PC 8	0.014	0.14	99.95
PC 9	0.004	0.04	99.99
PC 10	0.001	0.01	100.00

Table 2. Factor loading of ten traits with respect to the significant of 45 groundnut genotypes

Statistics	PC1	PC2	PC3
Days to 50% flowering	0.1386	0.5304	-0.427
Days to maturity	0.1375	0.5272	-0.4133
Pods per plant	-0.4917	0.0725	-0.0928
Dry pod yield per plant (g)	-0.4923	0.0683	-0.1022
Shelling (%)	-0.1178	-0.3637	-0.2886
Solid mature kernel (%)	0.0556	-0.3283	-0.2144
100- kernel weight (g)	-0.0139	0.2689	0.3462
Biological yield per plant (g)	-0.466	0.192	0.1155
Biological yield per plant (g)	0.0204	-0.2857	-0.5881
Kernel yield per plant (g)	-0.4931	0.0045	-0.1393

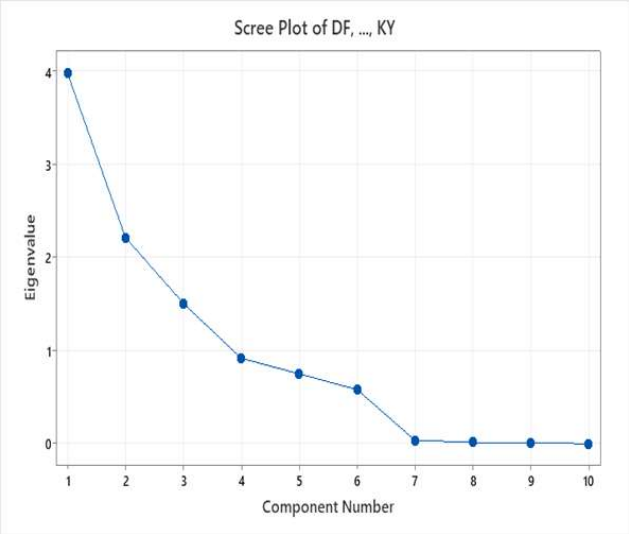

Fig. 1. Scree plot of 45 groundnut genotypes

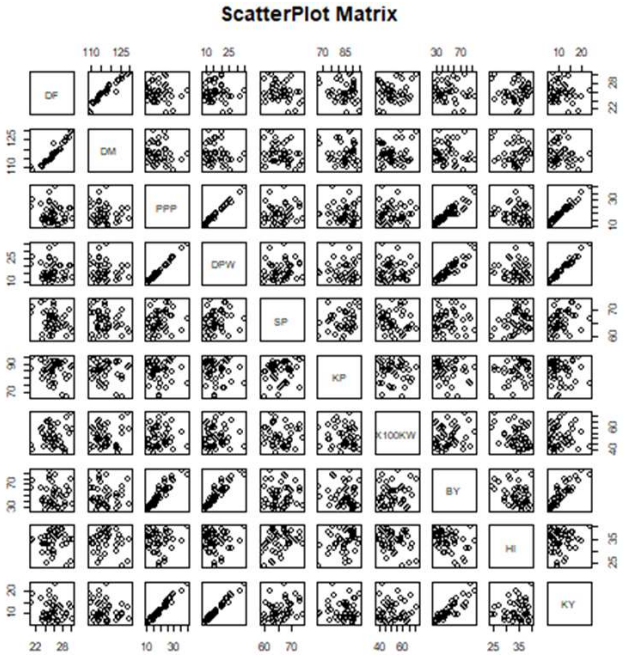

Fig. 2. Scatter plot with correlation value for ten traits of 45 groundnut genotypes

(Table 3). The best genotypes were those that were observed on the extreme positive side of both axes, such as RG 578 (2.74), RG 575-1 (2.38), RG 642-1 (1.70), RG 623 (1.29) along PCA I axis and genotypes RG 639 (2.79), RG 633-1 (2.69), RG 632 (1.75), RG 625 (1.68) along PCA II axis. These genotypes could be used in further hybridization development. The first two PCs are displayed in a biplot with trait loadings and the 45 groundnut genotypes dispersed throughout (Fig. 3). PCA clearly distinguished most of the

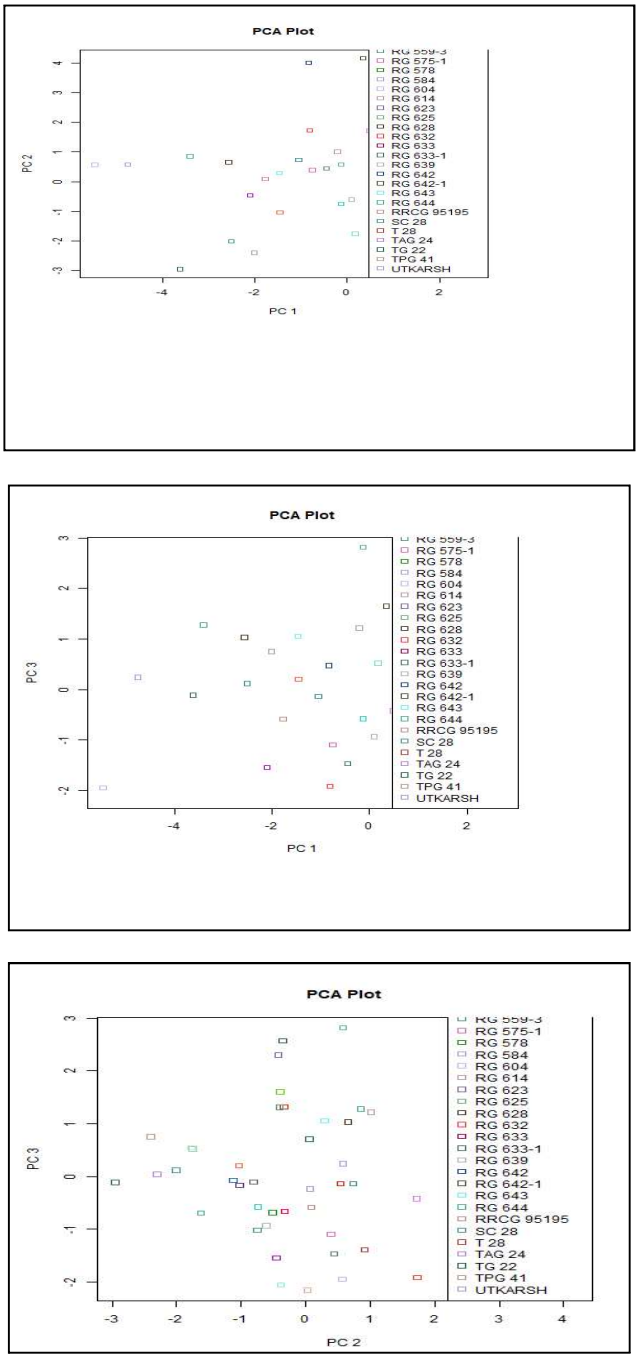

Fig. 3. Biplot of 45groundnut genotypesof PC I, PC II and PCIII

Table 3. PCA scores of 45 groundnut genotypes

Genotype	PC1 (X Vector)	PC2 (Y Vector)	PC3 (Z Vector)
CSMG 2003-19	-0.919	-0.228	-1.073
DGR 7	-0.491	-0.753	0.062
GG20	-0.244	1.156	0.347
GG21	-0.938	-0.269	-1.068
GIRNAR 2	-0.812	-0.348	0.559
HNG 10	-0.414	-1.095	0.569
HNG 69	-0.494	-0.267	-1.306
HNG 123	-1.252	0.039	-0.575
ICG 115-1	0.225	0.298	1.198
ICG 350	-1.368	0.042	0.196
ICG 3746	-0.807	-0.542	0.09
ICGV 6052	-1.242	-1.194	-0.443
ICGV 6119	-0.088	-1.179	-0.425
ICGV 86590	-1.302	-0.258	1.677
MH 1	0.066	-0.499	0.471
NRCG 12312	1.262	-1.353	-0.095
PUNJAB 1	-0.853	0.61	1.137
RG 382	-0.694	-0.24	-2.099
RG 420-1	1.01	-1.612	-0.613
RG 425	-0.472	-1.548	-0.034
RG 510	0.528	0.494	0.113
RG 559-3	0.381	0.265	0.893
RG 575-1	2.386	0.385	-0.198
RG 578	2.743	0.382	1.59
RG 584	0.109	0.679	-0.994
RG 604	-0.451	-0.284	-1.875
RG 614	0.069	0.391	-2.299
RG 623	1.29	0.442	-0.842
RG 625	0.41	1.162	1.562
RG 628	-1.176	1.686	1.116
RG 632	-0.31	1.754	0.177
RG 633	-0.047	-0.409	0.763
RG 633-1	0.422	2.69	-0.385
RG 639	-0.17	2.799	-1.343
RG 642	0.738	0.198	-0.86
RG 642-1	1.708	0.575	-1.043
RG 643	1.054	-0.307	1.26
RG 644	-0.269	-0.69	0.135
RRCG 95195	0.89	0.058	0.478
SC 28	0.73	-0.698	-0.169
T 28	1.82	-1.985	0.094
TAG 24	-0.522	-0.221	0.544
TG 22	-0.303	0.36	0.114
TPG 41	-1.168	-0.507	0.832
UTKARSH	-1.035	0.022	1.762

groundnut genotypes from each other. Similar results were observed by Sunday and Omolayo (2010).

CONCLUSION

The genotypes RG 578, RG 575-1, RG 642-1, RG 623, RG 639, RG 633-1, RG 632 and RG 625 had highest PC values for most important characters. Thus, these genotypes will may be used for advance hybridization programme.

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REFERENCES

Abdi H and Williams LJ 2010. Principal component analysis. *Wiley Interdisciplinary Reviews: Computational Statistics* **2**: 433-459.

Addinsoft 2020. *XLSTAT Statistical and Data Analysis Solution* New York, USA https//www.xlstat.com.

Anonymous 2022. *Agricultural Statistics at a Glance 2019*, Directorate of Economics and Statistics, Department of Agriculture, Cooperation & Farmers Welfare, Ministry of Agriculture & Farmers Welfare, Govt. of India, pp. 50.

Dudhe MY, Sujatha M, Rajguru AB, Bhoite KD, Kadam SM, Ranganatha AR and Reddy AV 2018. Characterization, evaluation and multivariate analysis of sunflower germplasm under semi-arid environments of three locations in two sunflower growing States in India. *Journal of Environmental Biology* **39**: 990-996.

Hlanga N, Modi A and Mathew I 2022. Agro-morphological diversity of Bambara groundnut lines evaluated under field conditions. *South African Journal of Plant and Soil* **39**(2): 142-152.

IRRI 2014. *Statistical Tool for Agricultural Research* (STAR) v2.01.

Jolliffie IT 1986. *Principal Component Analysis*. Springer, New York.

Massay WF 1965. Principal components regression in exploratory statistical research. *Journal of American Statistic Association* **60**: 234-246.

Mubai N, Sibiya J, Mwololo J, Musvosvi C, Charlie, H, Munthali W and Okori P 2020. Phenotypic correlation, path coefficient and multivariate analysis for yield and yield-associated traits in groundnut accessions. *Cogent Food and Agriculture* **6**(1): 182-190.

Mustafa HSB, Farooq J, Bibi T and Mahmood T 2015. Cluster and principal component analyses of maize accessions under normal and water stress conditions. *Journal of Agricultural Sciences, Belgrade* **60**(1): 33-48.

Sunday COM and Omolayo JA 2010. Multivariate analysis of genetic divergence in twenty two genotypes of groundnut (*Arachis hypogaea* L.). *Journal of Plant Breeding and Crop Science* **2**(7): 192-204.

Syafii MI, Cartika and Ruswandi D 2015. Multivariate analysis of genetic diversity among some maize genotypes under maize-albizia cropping systems in Indonesia. *Asian Journal of Crop Science* **7**: 244-255.

Talekar SC, Praveena, MV and Satish RG 2022. Genetic diversity using principal component analysis and hierarchical cluster analysis in rice. *International Journal of Plant Sciences* **17**(2): 191-196.

Tanwar A and Bisen R 2017. Principal components analysis for yield and yield attributing traits in sesame. *Indian Journal of Ecology* **44**(1): 99-102.

Zaman MA, Tuhina-Khatun M, Moniruzzaman M and Yousuf MN 2010. Genetic divergence in groundnut (*Arachis hypogaea* L). *Bangladesh Journal of Plant Breeding and Genetics* **23**(1): 45-49.

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