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GERMPLASM CHARACTERIZATION OF CHICKPEA (*CICER ARIETINUM* L.) RELATED TO YIELD ENHANCING FACTORS USING PRINCIPAL COMPONENT ANALYSIS

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Abstract

In order to establish the selection criteria, seventy chickpea genotypes were assessed during the rabi season of 2023-24 across nine physiological traits. The selection of genotypes and traits relied on Principal Component Analysis. Results regarding PCA revealed that the first three PC's showed eigenvalues greater than 1; therefore, these were considered for the dissection of variation. The initial four principal components accounted for 76.8% of the overall variation. PC1 contributed to 38.9% of the total diversity, whereas PC2, PC3, and PC4 accounted for 16.0%, 11.9%, and 10.0% of the variability, respectively. The first principal component, PC1, exhibited strong positive loadings for Seed Yield (0.516), Pods per plant (0.483), and secondary branches (0.442), along with negative loadings for wilting disease (-0.501). The second principal component, PC2, displayed a high positive loading for 100 seed weight (0.349) but showed negative contributions for days to maturity (-0.534) and Seeds per Pod (-0.475). Principal component three (PC3) established high positive loadings for Days to flowering(0.720) and 100-seed weight(0.668). The traits, viz., secondary branches, seed yield, pods per plant, and disease tolerance (wilting percentage), exhibited a valuable positive correlation. The genotypes 22ACK13, 22ACK15, 14FCK10, 15FCK14, 17FCK05, 17FCK41, 17FCK60, 18FCK27, 19FCK11, 19FCK17, 19FCK18, and 20KCC101 have good potential for these characters. These results may assist chickpea breeders in future hybridisation programs for improving yield and related traits.

Keywords: *Chickpea, Cicer arietinum L., Eigen value, Genetic variability, Principal components*

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is considered as an important bean crop of Rabi season. Next to peanuts and soybeans, chickpea is highest protein legume which produces 52 kg protein per acre. It is the 3rd most important food legume which is grown in several countries of the world as food source (1). Selection of superior high yielding chickpea genotypes and their utilization in breeding strategies is key factor for yield improvement. Genetic divergence is elementary requirement for improvement in economically importance traits of crop species. Crop productivity may be improved by developing high yielding varieties, but it needs information relating to the extent of prevailing genetic variation, relationship amongst various economically important traits and range of genetic diversity in existing germplasm (1, 2). As yield is multifarious trait and is affected by different other traits and environment, therefore, a renowned technique was introduced which is known as principal component analysis (PCA) which is used to identify and prioritize the most effective traits for selection. Principal component analysis refers to a multivariate technique, which is being used to investigate the diversity present in specific population under study. PCA is considered as typical statistical method for multivariate data analysis as it is easy and non-parametric tool to extract desirable info from unclear data sets. It minimizes the number of dimensions in the data while preserving most of the variability within the dataset. PCA achieves this dimensionality

reduction by pinpointing directions known as principal components, where the data's variation is greatest. By utilizing only a limited number of components, each data sample can be expressed with fewer numerical values instead of using values from thousands of variables. Therefore, the main advantage of PCA stems from assessing the significance of each dimension in capturing the variability of a dataset. It involves a mathematical technique that converts a set of potentially correlated variables into a smaller set of uncorrelated variables, referred to as principal components (3). In the present research, the genetic divergence related to yield and factors affecting yield was visualized to identify diverse strains for exploitation in future hybridization programs aimed yield improvement.

MATERIALS AND METHODS

For investigation of existing chickpea germplasm, a study was conducted by means of Principal component analysis (PCA) during Rabi 2023-24 at Gram Breeding Research Sub-Station, Attock. The genetic material comprising seventy chickpea genotypes was sown in augmented design for evaluation of nine different traits (Table I). Each entry comprised of four rows having 4 meter length with row to row spacing 30 cms and plant to plant spacing 10 cm. Data related to eight traits under study was recorded from five guarded plants of each entry. The studied traits include; Plant height (PH), Days to flowering (DF), Days to maturity (DM), Secondary branches (SB), Pods per plant (PPP), Seeds per pod (SPP), 100 Seed weight (SW), Seed yield (SY) and wilting % (WLT). The mean values of all traits were used for computation of principal components using PCA with the help of statistical software packages of Minitab version 17. After analysis, the first two principal components were plotted to find out genetic divergence present amongst genotypes and studied traits.

Table I. Detail of genetic material studied

Genotype Code	Genotype Name	Category	Source
1	22ACK-06	Germplasm	Gram Breeding Research Station, Attock
2	22ACK-09	Germplasm	Gram Breeding Research Station, Attock
3	22ACK-10	Germplasm	Gram Breeding Research Station, Attock
4	22ACK-11	Germplasm	Gram Breeding Research Station, Attock
5	22ACK-12	Germplasm	Gram Breeding Research Station, Attock
6	22ACK-13	Germplasm	Gram Breeding Research Station, Attock
7	22ACK-14	Germplasm	Gram Breeding Research Station, Attock
8	22ACK-15	Germplasm	Gram Breeding Research Station, Attock
9	22ACK-19	Germplasm	Gram Breeding Research Station, Attock
10	22ACK-20	Germplasm	Gram Breeding Research Station, Attock
11	TAMMAN-13	Approved Variety	Barani Agricultural Research Institute, Chakwal
12	NOOR-9	Approved Variety	Pulses Research Institute, Faisalabad
13	14FCK05	Germplasm	Barani Agricultural Research Station, Fatehjang
14	14FCK09	Germplasm	Barani Agricultural Research Station, Fatehjang
15	14FCK10	Germplasm	Barani Agricultural Research Station, Fatehjang
16	14FCK12	Germplasm	Barani Agricultural Research Station, Fatehjang
17	15FCK08	Germplasm	Barani Agricultural Research Station, Fatehjang
18	15FCK14	Germplasm	Barani Agricultural Research Station, Fatehjang
19	15FCK21	Germplasm	Barani Agricultural Research Station, Fatehjang
20	15FCK32	Germplasm	Barani Agricultural Research Station, Fatehjang
21	17FCK05	Germplasm	Barani Agricultural Research Station, Fatehjang
22	17FCK07	Germplasm	Barani Agricultural Research Station, Fatehjang
23	17FCK16	Germplasm	Barani Agricultural Research Station, Fatehjang
24	17FCK38	Germplasm	Barani Agricultural Research Station, Fatehjang
25	17FCK39	Germplasm	Barani Agricultural Research Station, Fatehjang
26	17FCK40	Germplasm	Barani Agricultural Research Station, Fatehjang
27	17FCK41	Germplasm	Barani Agricultural Research Station, Fatehjang
28	17FCK54	Germplasm	Barani Agricultural Research Station, Fatehjang
29	17FCK60	Germplasm	Barani Agricultural Research Station, Fatehjang
30	17FCK64	Germplasm	Barani Agricultural Research Station, Fatehjang
31	18FCK13	Germplasm	Barani Agricultural Research Station, Fatehjang
32	18FCK15	Germplasm	Barani Agricultural Research Station, Fatehjang
33	18FCK17	Germplasm	Barani Agricultural Research Station, Fatehjang

34	18FCK27	Germplasm	Barani Agricultural Research Station, Fatehjang
35	18FCK28	Germplasm	Barani Agricultural Research Station, Fatehjang
36	18FCK39	Germplasm	Barani Agricultural Research Station, Fatehjang
37	18FCK40	Germplasm	Barani Agricultural Research Station, Fatehjang
38	18FCK41	Germplasm	Barani Agricultural Research Station, Fatehjang
39	18FCK43	Germplasm	Barani Agricultural Research Station, Fatehjang
40	18FCK44	Germplasm	Barani Agricultural Research Station, Fatehjang
41	18FCK46	Germplasm	Barani Agricultural Research Station, Fatehjang
42	18FCK47	Germplasm	Barani Agricultural Research Station, Fatehjang
43	18FCK48	Germplasm	Barani Agricultural Research Station, Fatehjang
44	18FCK49	Germplasm	Barani Agricultural Research Station, Fatehjang
45	18FCK52	Germplasm	Barani Agricultural Research Station, Fatehjang
46	18FCK55	Germplasm	Barani Agricultural Research Station, Fatehjang
47	18FCK56	Germplasm	Barani Agricultural Research Station, Fatehjang
48	18FCK57	Germplasm	Barani Agricultural Research Station, Fatehjang
49	18FCK58	Germplasm	Barani Agricultural Research Station, Fatehjang
50	18FCK60	Germplasm	Barani Agricultural Research Station, Fatehjang
51	18FCK61	Germplasm	Barani Agricultural Research Station, Fatehjang
52	19FCK11	Germplasm	Barani Agricultural Research Station, Fatehjang
53	19FCK12	Germplasm	Barani Agricultural Research Station, Fatehjang
54	19FCK14	Germplasm	Barani Agricultural Research Station, Fatehjang
55	19FCK15	Germplasm	Barani Agricultural Research Station, Fatehjang
56	19FCK17	Germplasm	Barani Agricultural Research Station, Fatehjang
57	19FCK18	Germplasm	Barani Agricultural Research Station, Fatehjang
58	20KCC-101	Germplasm	Barani Agricultural Research Institute, Chakwal
59	20KCC-102	Germplasm	Barani Agricultural Research Institute, Chakwal
60	20KCC-103	Germplasm	Barani Agricultural Research Institute, Chakwal
61	20KCC-104	Germplasm	Barani Agricultural Research Institute, Chakwal
62	20KCC-105	Germplasm	Barani Agricultural Research Institute, Chakwal
63	20KCC-106	Germplasm	Barani Agricultural Research Institute, Chakwal
64	20KCC-107	Germplasm	Barani Agricultural Research Institute, Chakwal
65	20KCC-108	Germplasm	Barani Agricultural Research Institute, Chakwal
66	20KCC-109	Germplasm	Barani Agricultural Research Institute, Chakwal
67	20KCC-110	Germplasm	Barani Agricultural Research Institute, Chakwal
68	20KCC-111	Germplasm	Barani Agricultural Research Institute, Chakwal
69	20KCC-112	Germplasm	Barani Agricultural Research Institute, Chakwal
70	NOOR-13	Approved Variety	Pulses Research Institute, Faisalabad

RESULTS & DISCUSSION

Principal component analysis refers to a multivariate technique, which is being used to investigate the diversity present in specific population under study. PCA is considered as typical statistical method for multivariate data analysis as it is easy and non-parametric tool to extract desirable information from unclear data sets. It minimizes the number of dimensions in the data while preserving most of the variability within the dataset. PCA achieves this dimensionality reduction by pinpointing directions known as principal components, where the data's variation is greatest. By utilizing only a limited number of components, each data sample can be expressed with fewer numerical values instead of using values from thousands of variables (4). Therefore, the main advantage of PCA stems from assessing the significance of each dimension in capturing the variability of a dataset (5). It involves a mathematical technique that converts a group of potentially related variables into relatively smaller group of uncorrelated attributes, referred to as principal components (6). Utilizing multivariate techniques like PCA can classify sets of strains having valuable traits, clarify the pattern of variation, and ultimately identify the association amongst genotypes under study (7). Principal component analysis (PCA) has the ability to transform different possibly associated variables into smaller group of variables called principal components (PCs) (8). In the current investigation, PCA was used for identification of yield and its attributing traits in chickpea.

In this research, only three out of eight PC's exhibited Eigen value more than 1.0 and showed 66.8% cumulative variability (Table II, Fig. 1). Therefore, these three PC's were selected for further exploitation. PC-1 is exhibits maximum amount of total variation in the data set of all studied variables while remaining components accounted for less variability respectively. The PC-1 elucidated 38.9% of total variance followed

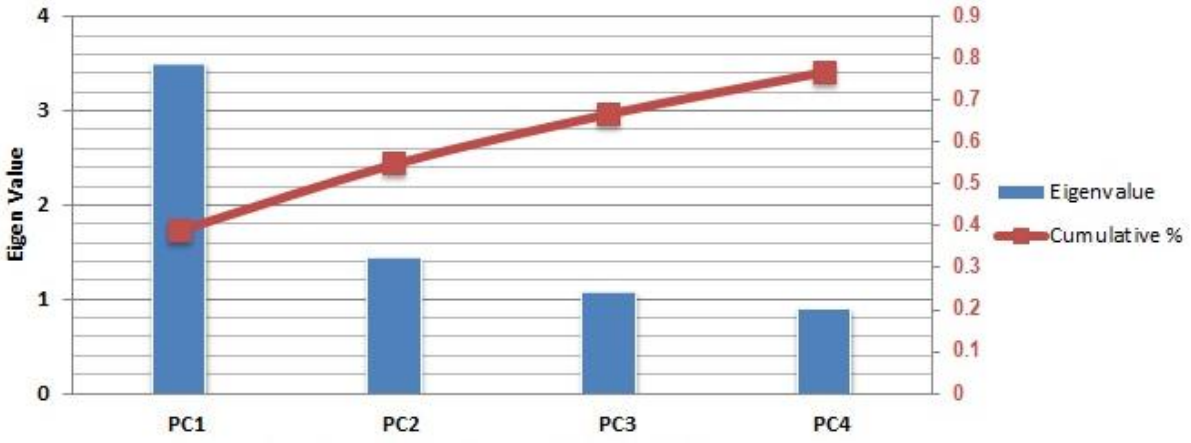

Fig. 1. Eigen value and commulative variability percentage

by PC-2 (16.0%) and PC-3 (11.9%) amongst the strains for traits under study as depicted in table-2 and figure-2. These findings are similar to the previous studies who mentioned cumulative variance of 84.1% in first three components (9). As depicted in Table II and Fig. 2 (a & b), the PC-1 showed maximum positive contribution for Seed yield (0.516), Pods plant^{-1} (0.483), secondary branches (0.442) while negative contribution for wilting disease (-0.501). While dissecting PC-2, extreme positive loadings was contributed by 100 seed weight (0.349) while negative contribution was exhibited for days to maturity (-0.534) and Seeds Pod^{-1} (-0.475). Third Principal factor enabled higher positive loadings in respect with Days to flowering (0.720) and 100 seed weight (0.668). PC-4 empowered maximum positive loading for days taken to maturity (0.475) and plant height (0.310), while negative loadings for seeds pod^{-1} (-0.789).

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

Traits	PC1	PC2	PC3	PC4
Eigenvalue	3.4978	1.4379	1.0746	0.9017
Variability %	0.389	0.160	0.119	0.100
Cumulative %	0.389	0.548	0.668	0.768
Traits				
Plant height (cm)	0.179	-0.441	-0.090	0.310
Days to flowering	0.017	-0.372	0.720	-0.090
Days to maturity	0.106	-0.534	0.035	0.475
Secondary Branches	0.442	0.144	-0.092	-0.204
Pods per plant	0.483	0.027	0.106	-0.032
Seeds per pod	-0.046	-0.475	-0.036	-0.789
100 Seed weight (g)	-0.095	0.349	0.668	0.053
Seed yield (Kg/ha)	0.516	0.038	0.056	-0.003
Wilting (%)	-0.501	-0.113	-0.045	0.056

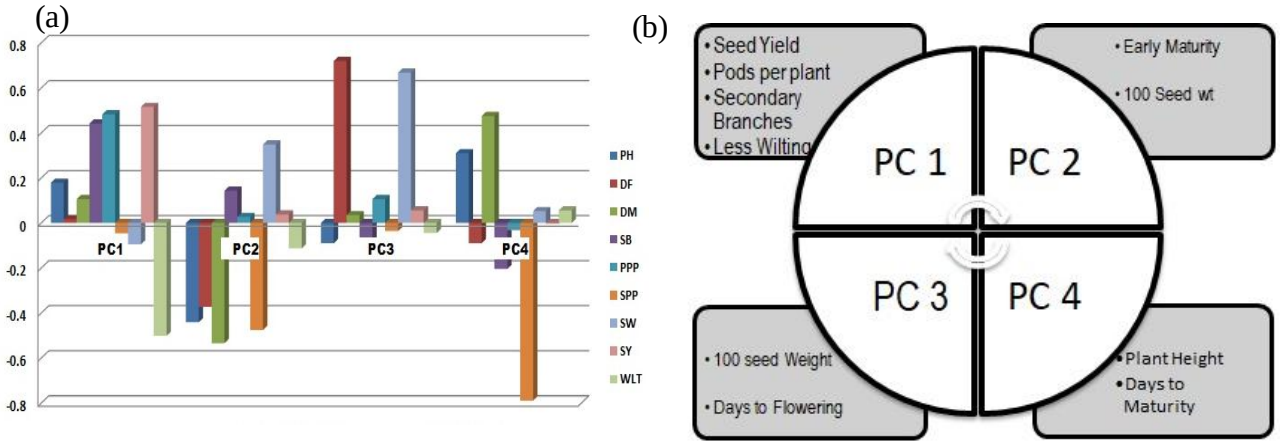

Fig. 2 (a). Rotated component matrix; **(b).** Major contributing traits in principal components

In score plot (Fig. 3), seventy genotypes of chickpea are scattered on the basis of their performance related to principal factors one and two. As depicted in score-plot, the characters secondary branches, seed yield, pods plant^{-1} and disease tolerance (wilting) have strong positive correlation with each other and the

genotypes 22ACK13, 22ACK15, 14FCK10, 15FCK14, 17FCK05, 17FCK41, 17FCK60, 18FCK27, 19FCK11, 19FCK17, 19FCK18, 20KCC101 have good potential for these characters. In earlier studies, similar findings were reported for these traits who mentioned strong positive correlation among them (10). While reviewing previous research, positive correlation was observed among seed yield and pods number per plant (11), while in contrast with present results, positive association was discovered between plant height and seed yield (12).

While discussing seeds per pod, the genotypes 22ACK09, 22ACK11, 14FCK12, 17FCK41, 18FCK15 and 18FCK55 have good potential. The genotypes 18FCK43, 18FCK44, 18FCK46, 18FCK47 and 20KCC110 exhibited good potential for seed weight. Earlier researchers reported that traits having high values of PC scores can be used for selection and for further exploitation in upcoming breeding programs (13). Above findings related to principal components are also in line with previous findings (14).

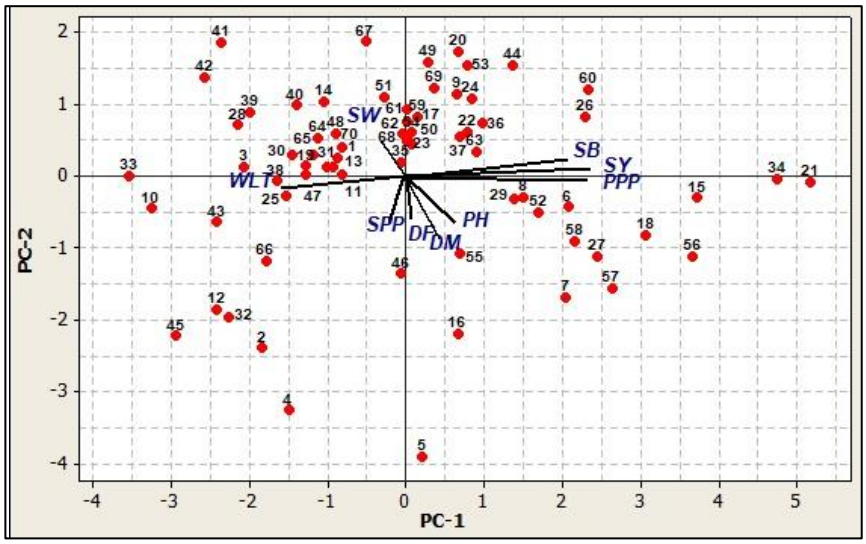

Fig. 3. Score plot of chickpea genotypes

CONCLUSION

While characterizing studied chickpea (*Cicer arietinum* L.) genotypes, it is discovered that better genetic divergence was present among the yield traits. Concluding the results of principal components and biplot analysis, the secondary branches, pods plant-1 and disease tolerance (wilting) seemed as main yield contributing traits for varietal improvement. The genotypes 22ACK13, 22ACK15, 14FCK10, 15FCK14, 17FCK05, 17FCK41, 17FCK60, 18FCK27, 19FCK11, 19FCK17, 19FCK18, 20KCC10120KCC101 have good potential for yield contributing traits and may be utilized for incorporation of these valuable traits in future breeding strategies. First three principal components added 66.8% of total diversity; therefore, these principal components may be utilized for instantaneous selection of yield related characteristics in chickpea.

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Conflict of interest:

The authors declare no conflict of interest.

Authors' contribution:

MR, MTAK wrote result and discussion; S conducted experiment; MZ, AA Field data collection; SH, GA wrote introduction; AB, MA data analysis; MSH review of literature; AAK AJ managed references; AA proof read manuscript; SAK removed plagiarism; MH methodology; AH supervision. All authors read and approved the final manuscript.

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