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Exploring genetic diversity and analyzing seed yield characters through principle component analysis in chickpea (*Cicer arietinum* L.)

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Abstract

A total of 40 lines, along with a check, were evaluated in Randomized Complete Block Design (RCBD). All the traits except number of primary branches per plant showed significant variation among the lines. Based on D² values, 41 genotypes were grouped into four clusters. The cluster II consists of maximum 21 genotypes followed by cluster IV, cluster III and cluster I, which had 10, 6 and 4 genotypes, respectively. Whereas, days to maturity (25.50) followed by days to 50% pod setting (19.58), days to 50% flowering (14.23) and harvest index (10.59) contributed maximum diversity. Based on cluster Euclidean distance matrix genotypes C-205 and CSJ-1100 had recorded maximum diversity (10.152). The PF Score creates a perfect base for the estimation of variability and for proper selection among complex characters. PCA-1 and PCA-2 join together come up with (51.61%) of variation among seed yield characters. Based on cluster means, cluster distances and *per se* performance C-205, CSJ-1100, ICC-21168, C-1028 and C-223 were identified for inclusion in hybridization programme in this region.

Keywords: Chickpea, genetic diversity and principle component analysis

Introduction

Chickpea is an important winter legume both in terms of nutrition and production in India. Its flour is used in traditional Indian snacks. It is cheap and good source of protein (21%) and consists of aspartic acid (10.9%) followed by leucine (8.6%) and lysine (7.1%) but deficient in sulphur containing methionine, cysteine and cystine. Chickpea is a kind of legumes. Fruit is known as pod, which is the edible portion. It is a strictly self-pollinated and out crossing in mutant material ranges from 0.0 to 1.25% (Toker *et al.*, 2009) [1]. Approximately 13.0 micro grams of beta carotene presents in 100gms of chickpea seeds. There are two cultivated types of chickpea, desi (*Cicer arietinum*) and kabuli (*Cicer kabulium*).

Understanding the genetic variation in and among species is crucial before conducting any hybridization, as a matter of fact, genetic diversity moreover aids in identifying diverse lines which can be encompass in crop improvement. To increase the yield of chickpea, it is necessary to enhance the ability of associated seed yield characters and exploit the diversity exists in the germplasm. Studying the genetic diversity in any gene pool helps to identify the superior parents for the hybridization, which also aids in developing improved varieties. Principle Component Analysis (PCA) is a devoid parametric method to decipher the complex data into simple data sets, the core understanding of PCA is clearly illustrated by (Agrawal *et al.*, 2018) [1]. In the present study we operated multivariate analysis *i.e.*, Principle Component Analysis (PCA) and Euclidian cluster analysis to analyze the degree intra gene pool divergence.

Materials and Methods

The experimental was carried out at the Field Experimentation Centre of the Department of Genetics and Plant Breeding. The site is located at 25.28 N latitude, 81.54 E longitude and 98 meter above the sea level. Prayagraj has sub-tropical and semi-arid climate. Lies 102m above sea level. The average annual rainfall is 1042 mm and comes under middle gangetic plains (Agro climatic zone IV). The experimental plot had sandy loam soil with fairly uniform topography and normal fertility status. The plot is well drained and assured irrigation facility. Total 40 chickpea genotypes along with a check were collected from the department of Genetics and Plant breeding were grown in randomized block design (RBD) with three

replications. Total twelve quantitative characters were taken into consideration for the estimation of genetic relationship among chickpea genotypes, the quantitative characters such as days to 50% flowering, days to 50% pod setting, plant height (cm), number of primary branches, number of secondary branches, days to maturity, number of pods per plant, number of seeds per plant, seed index (g), biological yield (g), harvest index (%) and seed yield per plant (g). The recorded data was subjected to Mahalanobis D² statistic by Mahalanobis (1936) and Rao (1952). The degree of divergence also plotted by using principle component analysis (PCA).

Results and Discussions

Genetic parameters of yield and yield components in chickpea lines the high genotypic coefficient of variation was found for seed yield per plant (24%) followed by Biological yield (20%) and Number of pods per plant (19%), while it was smaller in days to maturity (5%), days to 50% flowering (7.18%) and days to 50% pod setting (9%). High phenotypic coefficient of variation was also found in seed yield per plant (26%) followed by biological yield (23%) and number of pods per plant (22%), And similar results were reported by Joshi *et al.* (2018) and Swetha and Lavanya (2019) [5, 10].

Table 1: Correlation coefficient among 41 chickpea genotypes

Traits	DF50	DPS	PH	NPB	NSB	DM	NPP	NSP	HSW	BM	HI	GYPP
DF50	1											
DPS	0.43**	1										
PH	0.16	0.32*	1									
NPB	-0.02	0.03	0.15	1								
NSB	-0.13	0.24	0.29	0.49**	1							
DM	0.56**	0.66**	0.13	-0.17	0.09	1						
NPP	-0.34*	0.06	0.03	0.35*	0.43**	-0.18	1					
NSP	-0.31*	0.10	0.13	0.28	0.27	-0.07	0.73**	1				
HSW	-0.21	0.19	0.06	0.10	0.40**	-0.01	0.41**	0.40**	1			
BM	-0.18	0.11	-0.22	-0.07	-0.03	0.02	0.35*	0.32*	0.35*	1		
HI	0.34*	0.52**	0.22	0.29	0.45**	0.50**	0.14	0.06	0.36*	0.11	1	
GYPP	0.13	0.42**	0.15	0.21	0.26	0.16	0.31*	0.41**	0.35*	0.55**	0.50**	1

*5% level of significance, ** 1% level of significance

DF50: Days to 50% flowering, DPS: Days to 50% pod setting, PH-Plant height (cm), NPB-No. of primary branches, NSB: No. of secondary branches, DM: Days to maturity, NPP: No. of pods per plant, NSP: No. of seeds per plant, HSW: Hundred seed weight (g), BM: Biomass (g), HI: Harvest index (%), GYPP: Grain yield per plant (g)

Whereas, the lowest was recorded for days to maturity (5%) and days to 50% flowering (7%). Shengu *et al.* (2018) [9] reported phenotypic coefficients of variation (PCV) were found to be higher than genotypic coefficients of variation (GCV) for all the traits. In the present investigation, plant height (96.80) followed by days to 50 per cent flowering (96.20), days to maturity (91.70), seed index (91.00) and all other characters showed high estimates of heritability (broad sense). Analogous findings were reported by Mallu *et al.* (2014) and Khan *et al.* (2011) [6].

The correlation results also clearly showed the seed yield per plant showed positive and significant correlation with biological yield followed by harvest index, days to pod setting, number of seeds per plant and number of pods per plant, whereas seed yield per plant exhibited positive non significant correlation with number of secondary branches

followed by number of primary branches, plant height and days to 50% flowering. Biological yield exhibited significant positive relation with seed index, number of pods per plant and number of seeds per plant and showed negative non significant correlation with plant height followed by days to 50% flowering, number of primary branches per plant and number of secondary branches per plant. Harvest index showed significant positive correlation with days to pod setting followed by days to maturity, number of secondary branches, seed index and days to 50% flowering. Number of seeds per plant showed positive significant correlation, number of pods per plant showed non-significant positive relation with number of primary branches followed by number of secondary branches, plant height, days to pod setting,

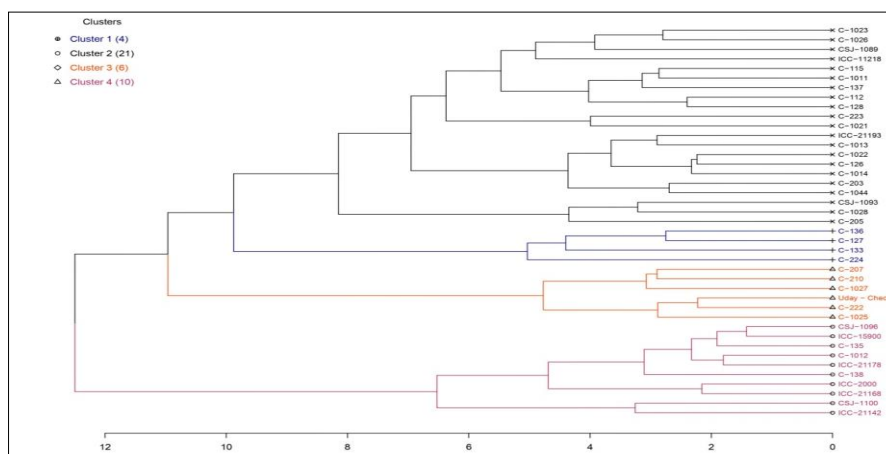


Fig 1: Euclidean cluster based on 12 characters observed in chickpea genotypes

Table 2: Grouping of chickpea germplasm into 4 different clusters

Clusters	Germplasm
I	C-127, C-136, C-133, C-224
II	C-1021, C-223, C-1044, C-1011, C-128, C-1026, C-1023, C-205, C-115, C-126, C-137, C-1022, C-1014, C-203, C-112, C-1013, CSJ-1089, C-1028, ICC-11218, ICC-21193, CSJ-1093
III	C-222, C-210, C-1025, C-1027, C-207, Uday-Check
IV	ICC-21142, CSJ-1100, ICC-21168, C-138, ICC-2000, ICC-21178, ICC-15900, CSJ-1096, C-1012, C-135

Showed negative significant and non-significant with days to 50% flowering and days to maturity. Number of pods per plant The estimates of D² values ranged from 1.41 to 10.15. This clearly indicates the presence of adequate diversity between genotypes studied Jida and Alemu (2019), Tamvar *et al.* (2019), Jakhar *et al.* (2016), Yadav *et al.* (2010)^[4, 3, 12]. Reported wide genetic diversity in chickpea germplasm.

The highest D2 value was between a pair of the genotype *viz.*, C-205 and CSJ-1100 (10.152). While lowest was between ICC - 15900 and CSJ - 1096. The aim of cluster formation and measuring intra and inter cluster divergence is to provide the basis for selecting parents for greater the divergence between the two clusters, wider is the genetic diversity in the genotypes.

Table 3: Cluster means of 4 clusters formed from chickpea germplasm following Euclidean method for different agronomic traits

Traits	Cluster 1	Cluster 2	Cluster 3	Cluster 4
DF50	80.17	78.25	69.00	79.63
DPS	107.17	112.98	99.50	102.73
PH	64.60	53.56	52.57	49.03
NPB	2.88	2.76	2.74	2.37
NSB	5.18	4.67	4.59	3.59
DM	137.67	143.46	128.28	140.70
NPP	24.73	26.96	33.70	23.04
NSP	28.03	32.59	36.65	29.12
HSW	16.42	17.73	19.22	15.27
BM	7.35	16.44	16.57	14.24
HI	62.17	63.82	51.16	51.41
GYPP	8.32	13.10	11.32	9.18

Table 4: Top ten maximum and minimum diverse lines in relation to all the 41 germplasm of chickpea

S. No.	Pairs of Germplasm showing maximum diversity	Diversity	Pairs of Germplasm showing minimum diversity	Diversity		
1	C-205	CSJ-1100	10.152	ICC-15900	CSJ-1096	1.419
2	C-205	ICC-21168	9.270	ICC-21178	CSJ-1096	1.573
3	C-1028	CSJ-1100	8.703	ICC-15900	C-135	1.716
4	C-223	CSJ-1100	8.607	CSJ-1096	C-1012	1.768
5	C-205	ICC-2000	8.268	ICC-21178	C-1012	1.800
6	C-1021	CSJ-1100	8.267	CSJ-1096	C-135	1.873
7	C-1028	ICC-21168	8.217	ICC-15900	C-1012	1.997
8	C-205	ICC-21142	8.053	ICC-21178	C-135	2.036
9	C-128	CSJ-1100	7.998	C-1012	C-135	2.128
10	C-210	ICC-21168	7.929	ICC-2000	ICC-15900	2.131

The crosses involving the parents with extreme divergence have also been reported to exhibit decrease in heterosis. (Khan *et al.*, 1990)^[6]. In the present investigation forty one genotypes were grouped into four clusters. Cluster II had highest number of genotypes (21), cluster IV with 10 genotypes, cluster III with 6 genotypes and cluster I with 4 genotypes. Kumar *et al.* (2021) reported 11 genotypes in a

single cluster.

The cluster mean revealed that clusters II and IV varied considerably for most of the characters from those of other clusters. This indicates that the genotypes included in these clusters might have entirely different genetic architecture from the genotypes included in the other clusters.

Table 5: PCA Analysis of 12 traits of chickpea germplasm

Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
DF50	0.01	-0.50	0.01	-0.14	0.31	-0.06	0.52	-0.02	0.53
DPS	0.30	-0.38	0.09	0.22	0.00	-0.17	-0.20	-0.63	-0.20
PH	0.17	-0.17	-0.39	0.64	0.14	0.47	-0.04	0.11	0.15
NPB	0.24	0.11	-0.47	-0.48	0.37	-0.02	0.06	-0.37	-0.14
NSB	0.35	0.04	-0.40	-0.14	-0.33	-0.05	-0.42	0.03	0.36
DM	0.15	-0.48	0.16	0.08	-0.13	-0.44	-0.17	0.17	-0.05
NPP	0.34	0.34	-0.03	0.10	0.12	-0.40	0.06	0.17	0.39
NSP	0.34	0.29	0.05	0.34	0.27	-0.35	0.23	0.14	-0.30
HSW	0.34	0.15	0.12	0.04	-0.60	0.20	0.56	-0.28	0.01
BM	0.23	0.16	0.58	-0.11	0.12	0.21	-0.30	-0.11	0.38

HI	0.36	-0.29	-0.05	-0.33	-0.19	0.10	0.07	0.52	-0.27
GYPP	0.39	-0.05	0.27	-0.11	0.34	0.41	-0.06	0.12	-0.21
Eigen value	3.51	2.68	1.58	0.90	0.84	0.69	0.46	0.35	0.32
Variance percent	29.29	22.33	13.13	7.48	6.99	5.76	3.87	2.88	2.71
Cumulative variance.	29.29	51.61	64.74	72.22	79.21	84.97	88.84	91.72	94.42

The cluster mean revealed high variability among the clusters for the traits, plant height, days to maturity, days to 50 per cent flowering, biological yield, seed yield per plant, number of pods per plant. Among few of these traits, plant height showed highest percent. Bohre *et al.* (2020) observed that characters like seed index and days to 50% flowering are contributed maximum to the diversity. Nimbalkar and Harer (2001) [7] reported maximum genetic divergence due to plant

height and 100 seed weight. In these studies Principle Component Analysis (PCA) has been used to analyze the effective impact of different traits on seed yield. It is clearly observed from the results, among the top 3 PCA's having eigen value about 64.75, out of which PCA-1 accounted for the high proportion of variance (29.29%) and remaining two PCA's showed (22.33%) and (13.13%) apparently. The present studies analyzed by both cluster analysis and PCA.

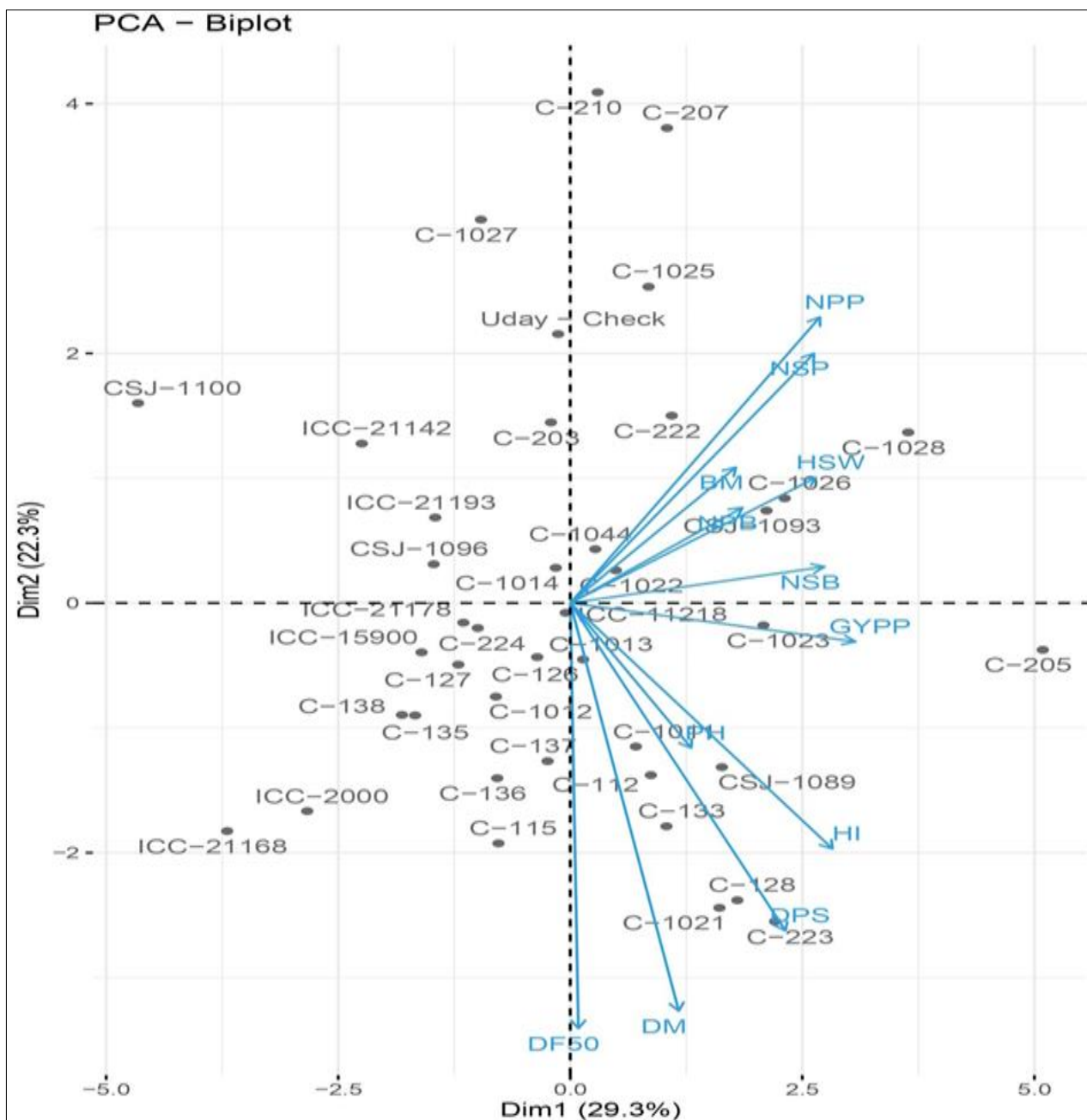


Fig 2: Principle component analysis plot combine

This PF Score creates a perfect base for the estimation of variability and for proper selection among complex characters. PCA-1 and PCA-2 join together come up with (51.61%) of variation among seed yield characters. The

positive side of the PC-1 include characters such as seed yield per plant, days to maturity, plant height, days to pod setting and days to 50% flowering, genotypes which fall in this side are C-1022, C-1044, CSJ-1093, C-1026, C-1028 and C-222,

while positive side of PC-2 includes number of primary branches and number of secondary branches combined for them, genotypes which included are C-1014, CSJ-1096, ICC-21193, C-203, ICC-21142 and CSJ-1100. The characters biological yield, seed index and harvest index, the genotypes include C-1025, C-207 and C-210.

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