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Scrutinizing principal component analysis of agromorpho-genetic traits in advance breeding lines of *Desi* chickpea (*Cicer arietinum* L.)

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Abstract

To ascertain the selection criteria, the advance breeding lines of *desi* chickpea were assessed during the *rabi* cropping season 2019-2020 and 2020-21 for fourteen traits including phenological and quantitative traits. Selection of yield and yield contributing traits along with genotypes were established elicited from Principal component analysis. Out of fourteen PCS identified, 5 PCs manifested more than 1.0 Eigen value and revealed about 79.80% variability. The PC1 elucidated 26.21% variability among traits, while, PC2, PC3, PC4 and PC5 exhibited 22.14%, 12.55%, 10.19% and 8.71% variability respectively. PC1 revealed high positive loading for days to pod initiation, plant height, number of primary branches per plant and seed yield per plant. Principal factor two PC2 explained high positive loading for days to flower initiation, days to 50% flowering and days to maturity, while, PC3 was mostly related with trait total number of pods per plant. Principal factor four PC4 were correlated with biological yield per plant and seed yield per plant, whereas, PC5 was dominated by 100 seed weight. Therefore, these five principal components can be allowed for simultaneous selection of yield and yield attributing traits in *desi* chickpea. On the basis of high PC scores genotypes *viz.*, BG 3091, GL 14015, DC16-116, GNG 2367, JG 36 and IPC 2010-14 found in PC1, JG 36, GL 14015, BRC 302, JG 11 × JG 14, ICCV 15118, DC16-116 and RKG 13-205 in PC2, JG 2016-1614, BG 3091 and GL 14015 in PC3, JG63 × ICC4958, JG2017-49 and JG24 in PC4 and JG 11 × JG 14, ICCV 15118, RKG17-04, GL 14015, PG 187, GJG 1503 and JG 2016-1614 were identified in PC5. These genotypes may be utilized in precise crop improvement programme of chickpea for enhancing seed yield and its attributing traits.

Keywords: Principal component analysis, Eigen value, *desi* chickpea, yield attributing traits

Introduction

Chickpea (*Cicer arietinum* L.) is a cool season food legume crop mostly use as poor man's vegetable protein source. India is the largest producer contributing to 65% of world's chickpea production. However to meet the demand of ever increasing population, it is quite indispensable to enhance the production and area under cultivation. Due to biotic and abiotic stresses along with dearth of high yielding varieties, the area under chickpea cultivation decreased (Hameed *et al.*, 2009) ^[1]. To meet this enigma, with selection of promising genotypes that directly correlated with seed yield and its attributing traits boost the grain yield of chickpea. As yield is a complex trait affected by several unpredictable factors *i.e.* environment, hence, principal component analysis provides a roadmap to reduce the dimensionality of the complex data set into lower dimension obtaining relevant information with minimum efforts and minimize the number of traits for effective selection. It involves a mathematical procedure that transforms a number of (possibly) correlated variables into a (smaller) number of uncorrelated variables called principal components (Muniraja *et al.*, 2011) ^[2]. Thus the foremost advantage of PCA arises from quantifying the significance of each dimension for describing the variability of a data set.

Materials and Methods

The present study pertaining to assess the promising genotypes by using Principal component analysis was conducted during *Rabi* cropping season of timely sown during both 2019-20 and 2020-21 at Seed Breeding Research cum Farm at JNKVV, Jabalpur, Madhya Pradesh. The experiment was laid in randomized complete block design with three replications along with incorporation of recommended packages and practices essential for a healthy crop. The experimental material comprised of 30 advance lines of *desi* chickpea including 3 checks (JG14, JG24 and JG36) evaluated for fourteen quantitative traits, received from AICRP on

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chickpea Department of Plant breeding and Genetics, JNKVV, Jabalpur, Madhya Pradesh and ICRISAT, Patancheru, Hyderabad. The rows/ plot were 2 and the row length was 4.0m with maintained spacing between rows was 30 cm. According to the (Massay, 1965) [3] and (Jolliffe, 1986) [4] PCA is a well-known method of dimension reduction that can be used to reduce a large set of variables to a small set which still contains most of the information in the large set. Therefore, the purpose of the present investigation was to identify promising genotypes and rank important yield contributing traits and genotypes on the basis of principal component analysis of pooled data of *rabi* 2019-20 and 2020-21 for evolving better hybrid in chickpea which may be utilized in precise breeding programme.

Results and Discussion

Principal component analysis is well known non-parametric method for obtaining relevant information from confusing data sets which provides a roadmap for how to reduce a complex data set to a lower dimension to sometimes hidden, simplified structures that often underlines it with minimum efforts. PCA is a statistical procedure that uses the orthogonal transformation to convert a set of observations of potentially correlated variables into a set of values of linear unrelated variables known as the principal components whose number of original components is less than or equal to the number of original variables. This transformation is defined in such a way that the first principal component has the highest possible variation and in turn each subsequent component has as many variations as possible under the limit that the orthogonal components are preceding components. The resulting vectors are an unrelated orthogonal base set. The principal components are orthogonal because they are the Eigen vector of the co- variance matrix, which is symmetrical. In the current research, principal component analysis was performed for seed yield and its contributing traits of advance breeding lines of *desi* chickpea.

Principal component analysis was performed for fourteen quantitative traits of chickpea. According to (Brejda *et al.*, 2000) [5] data were considered in each components with Eigen value >1 which determined at least 10% of the variation. Out

of 14, only 5 PC’s exhibited more than 1.0 Eigen value and showed 79.80% cumulative variability among the traits under study. Therefore these five PCs were given due important for the further explanation. The PC1 explained maximum contribution to the total variation (26.21%) followed by PC2 (22.14%), PC3 (12.55%), PC4 (10.19%) and PC5 (8.71%) were presented in table1. From the above results, it can be concluded that seed yield and its attributing traits were having the highest variation in PC 1 followed by PC2, PC3, PC4 and PC5 (Table 1 and Fig 1).

Table 1: Total Variance Depicted by Different Principal Components in Chickpea Genotypes in Pooled Analysis

Traits	Principal components	Eigen value	Variance percent explained (%)	Cumulative variance percent explained (%)
DTFI	PC1	3.669	26.21	26.20
DT50%F	PC2	3.100	22.14	48.30
DTPI	PC3	1.758	12.55	60.90
DTM	PC4	1.427	10.19	71.10
PH	PC5	1.219	8.71	79.80
PB	PC6	0.879	6.28	86.10
SB	PC7	0.627	4.48	90.60
TNPPP	PC8	0.459	3.28	93.80
NEPP	PC9	0.336	2.4	96.20
NSPP	PC10	0.194	1.39	97.60
100 SW	PC11	0.126	0.9	98.50
BY	PC12	0.094	0.67	99.20
HI (%)	PC13	0.08	0.57	99.80
SYPP	PC14	0.031	0.22	100.00

Where,

DTF: Days to flower initiation, DT50%F: Days to 50% flowering, DTPI: Days to pod initiation, DTM: Days to maturity, PH: Plant high, PB: Number of primary branches per plant, SB: Number of secondary branches per plant, TNPPP: Total Number of pods per plant, NEPPP: Number of effective pods per plant, NSPP: Number of seeds per pod, 100SW: 100 seed weight, BY: Biological yield per plant, HI%: Harvest index, SYPP: Seed yield per plant

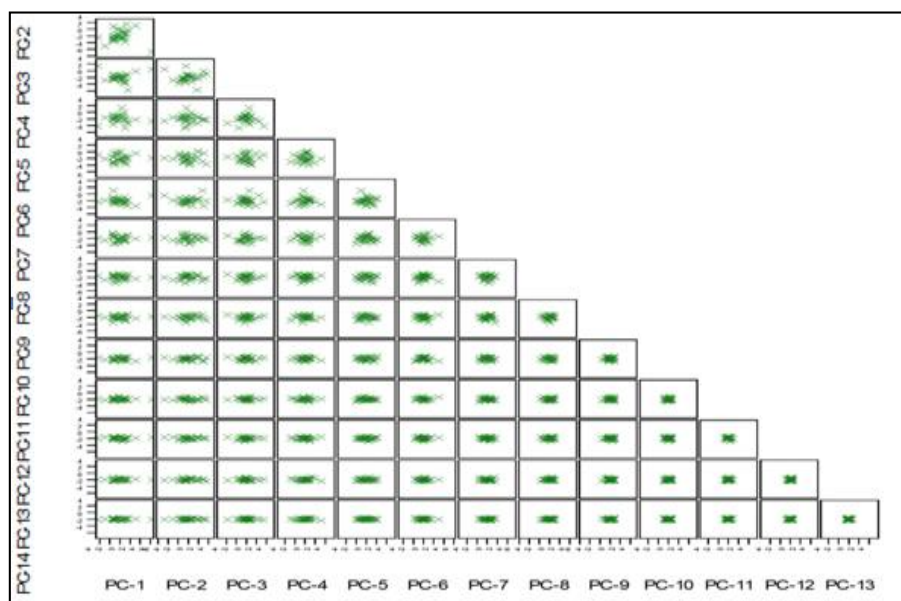


Fig 1: Principal Components of Different Traits in Pooled Analysis

Semi curve line *i.e.* Scree plot between principal components and Eigen values which explained percentage of variance associated with each principal component. Therefore, maximum variation was noticed in PC1 in comparison to other 4PCs, hence selection of genotypes for traits under PC1 may be advantageous (Fig.2).

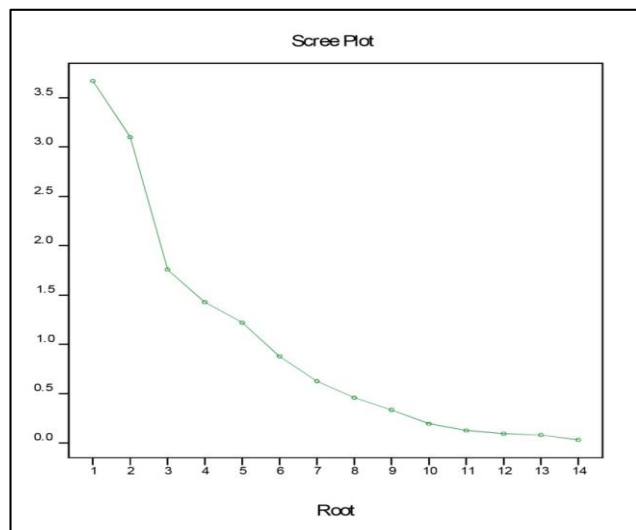


Fig 2: Scree Plot between Principal Components and Eigen Value in Pooled Analysis

Rotated component matrix (Table 2, 3 and Fig 3) revealed that PC1 depicted highest variability which mostly related with yield attributing traits like days to pod initiation, plant

height, number of primary branches per plant and seed yield per plant. These results are getting support from the findings of (Rekha *et al.*, 2013) [6]. PC2 was dominated by phenological traits *viz.*, days to flower initiation, days to 50% flowering and days to maturity. PC3 was mostly related with total number of pods per plant. Traits like biological yield per plant and seed yield per plant were coupled with PC4, whereas, traits namely 100 seed weight was associated with PC5. As PC1, PC3, PC4 and PC5 were mostly constituted by yield and yield attributing traits (yield factor), hence simultaneous selection procedure can be designed to bring about further improvement and development of chickpea.

Table 2: PC Values of Rotation Component Matrix for Fourteen Quantitative Traits in *Desi* Chickpea in Pooled Analysis

Traits	Principal components				
	PC1	PC2	PC3	PC4	PC5
DTFI	0.29252	0.52556	0.00584	-0.207	0.03961
DT50%F	0.29923	0.52467	-0.05295	-0.15073	0.05542
DTPI	0.51337	0.32722	0.03449	-0.2753	0.1532
DTM	-0.25284	0.52022	0.03699	0.06803	-0.01137
PH	0.5039	-0.23739	0.22749	0.0097	0.18611
PB	0.53325	-0.29509	0.27141	-0.08976	-0.00371
SB	-0.25874	0.3003	-0.27453	0.21706	0.04785
TNPPP	-0.25402	0.14132	0.53342	0.02326	0.2876
NEPP	-0.22782	0.23359	0.39526	-0.05	0.06353
NSPP	-0.28707	0.00341	0.08986	-0.05858	-0.57265
100 SW	0.01422	-0.0227	-0.40279	0.51094	0.50058
BY	0.2529	0.16695	0.17993	0.5218	-0.3551
HI (%)	-0.17673	-0.05525	0.34611	0.21714	0.37039
SYPP	0.51334	0.1237	0.17486	0.54374	-0.16094

Table 3: Rotated Matrix Results of Yield and Yield Contributing Traits (>0.500) in Pooled Analysis

	PC1	PC2	PC3	PC4	PC5
Traits	Days to pod initiation	Days to flower initiation	Total no. of pods per plant	Biological yield per plant	100 seed weight
	Plant height	Days to 50% flowering		Seed yield per plant	
	No. of primary branches per plant	Days to maturity			
	Seed yield per plant				

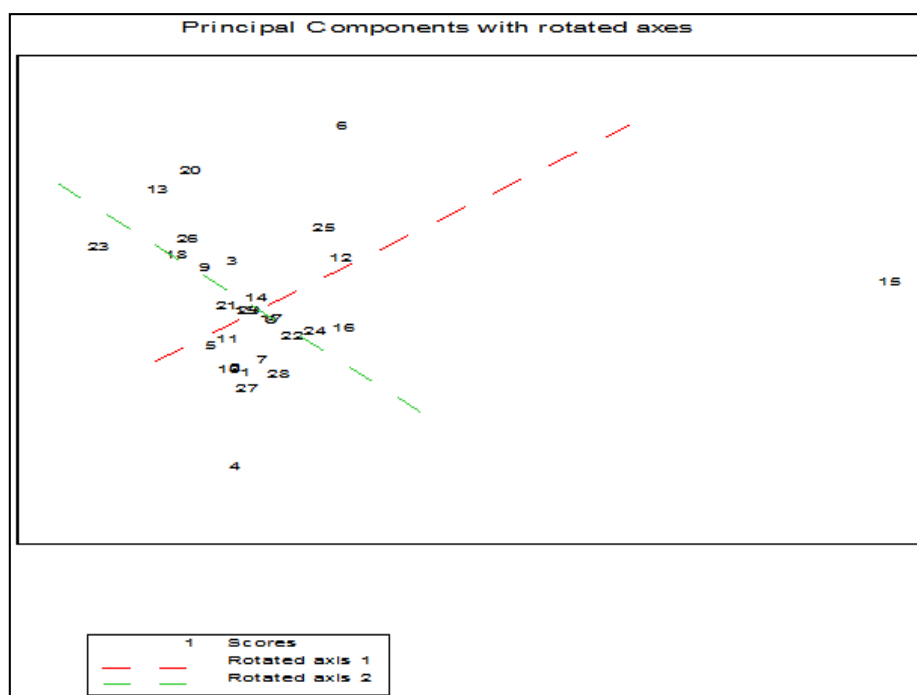


Fig 3: Principal Components with Rotated Axes in Pooled Analysis

PC1, had high positive loading value ranged from 0.1978 (26th genotype) to 6.3846 (15th genotype), while negative loading value ranged from -4.4351 (1st genotype) to -0.2332 (14th genotype). PC2 had high positive loading value of the component ranged from 0.0244 (29th genotype) to 3.5147 (20th genotype) and negative loading value ranged from -4.7302 (15th genotype) to -0.3757 (7th genotype). In PC3, positive loading value ranged from 0.2491 (19th genotype) to 3.4074 (1st genotype) and negative loading value from -3.698 (13th genotype) to -0.0106 (14th genotype). PC4 showed the positive loading value ranged from 0.0152 (2nd genotype) to

3.2173 (7th genotype), while negative loading value ranged from -2.7917 (12th genotype) to -0.1313 (3rd genotype) In PC5, the positive loading value ranged from 0.0006 (3 number genotype) to 2.0411 (26th genotype), while, loading value ranged from -1.9758 (5th genotype) to -0.0914 (30th genotype). Hence, from these PCA scores under study, a precise selection indices can be proposed whose intensity can be decided by variability explained by each of principal component. High loading value for a particular genotype suggests high values for the variables in that particular genotype (Table 4 and Fig 4).

Table 4: Scoring of Genotypes in Different PC's in Pooled Analysis

S. no.	Genotypes	PC1	PC2	PC3	PC4	PC5
1	JG 2016-1614	-4.4351	-0.4672	3.4074	-2.2099	1.0154
2	JSC 55	-1.0818	-1.0907	-0.6355	0.0152	-1.2253
3	BRC 305	0.8856	0.661	-1.2878	-0.1313	0.0006
4	NOG 15-5	-2.9403	-2.9899	-0.8198	0.3554	-0.1624
5	Phule G 1018-9-6	-1.0903	0.1648	0.9013	0.712	-1.9758
6	GL 14015	3.1526	3.0597	1.8214	-0.1869	1.46
7	JG63 × ICC4958	0.398	-0.3757	0.5169	3.2173	-0.1577
8	PG 187	-0.8214	-0.602	-0.1229	-0.7002	1.2332
9	RKG 13-205	0.6403	1.2975	-0.2335	0.9768	-0.4533
10	JG 14	-1.2869	-0.9168	-0.4209	0.2382	-0.8892
11	JG74 × ICCV4958	-1.4166	-0.4838	-0.2952	-0.4274	0.4402
12	IPC 2010-14	1.0473	-0.7018	-1.4696	-2.7917	-1.0081
13	DC16-116	1.6212	1.7722	-3.698	-1.2703	0.4311
14	JG12 × JG 16-1	-0.2332	0.1662	-0.0106	-0.4911	-0.4602
15	BG 3091	6.3846	-4.7302	2.5155	-0.7485	0.0546
16	JG12 × JG 16-3	0.8979	-1.8051	-1.8168	-0.2189	0.7631
17	RVSSG-60	0.4555	-0.5821	-1.0671	0.2681	-0.752
18	ICCV 15118	-0.6009	1.8676	0.3797	0.3664	2.0335
19	JG2017-49	0.7403	0.5217	0.2491	1.906	-1.414
20	JG 36	1.2512	3.5147	0.9979	-0.4392	-1.7934
21	GJG 1503	-0.3647	0.4346	-0.0144	0.8232	1.1335
22	ICC 96029 × JG315	-0.2463	-0.3942	0.9088	0.8706	-0.3512
23	BRC 302	-1.2015	2.7994	0.5626	-0.2592	-0.9952
24	BG 3092	0.4877	-0.9147	-0.2702	0.9003	0.4036
25	GNG 2367	1.3206	0.8299	0.3937	-1.1084	0.0238
26	JG 11 × JG 14	0.1978	1.8748	-0.2633	0.5172	2.0411
27	JG24	-1.3337	-1.2454	-0.0823	1.2426	0.4369
28	RKG17-04	-1.1627	-1.6891	-0.7343	0.2068	1.4919
29	RG 2011-04	-1.2652	0.0244	0.5877	-1.6334	-1.3244
30	PG 205	0.5123	0.0558	0.9700	0.2537	-0.0914

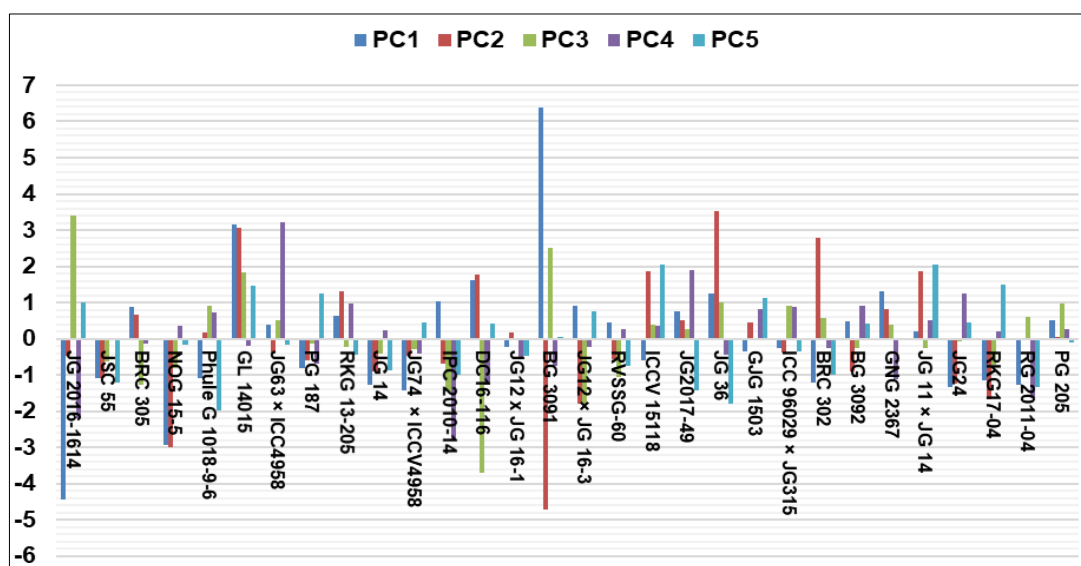


Fig 4: PCA Scores of Different Genotypes in Pooled Analysis

Promising genotypes were screened on the basis of top PC scores presented in table no 5. Genotypes namely; BG 3091, GL 14015, DC16-116, GNG 2367, JG 36 and IPC 2010-14 were associated with PC1 mostly related with the traits *viz.*, days to pod initiation, plant height, number of primary branches per plant and seed yield per plant. PC2 was correlated by the traits like days to flower initiation, days to 50% flowering and days to maturity which contributed by genotypes namely; JG 36 GL 14015, BRC 302, JG 11 × JG 14, ICCV 15118, DC16-116 and RKG 13-205. PC3 was associated with genotypes *viz.*, JG 2016-1614, BG 3091 and GL 14015 mostly related with total no. of pods per plant. PC4 was comprised with highest value for traits *viz.*, biological yield per plant and seed yield per plant which were coupled with the genotypes namely; JG63 × ICC4958, JG2017- 49 and JG24, while, genotypes JG 11 × JG 14, ICCV 15118, RKG17-04, GL 14015, PG 187, GJG 1503 and JG 2016-1614 were accompanied with 100 seed weight which was contributed by

PC5.

An efficient simultaneous selection procedure can be designed from these genotypes obtained from different PCs for improving seed yield which may be considered as an ideotype breeding material for selection of traits *viz.*, total number of pods per plant, biological yield per plant and 100 seed weight for future chickpea breeding programme. Those genotypes which are common in more than 1 PCs like GL 14015 in PC1, PC2, PC3 and PC5, BG 3091 in PC1 and PC3, JG 36 in PC1 and PC2, JG 11 × JG 14 and ICCV 15118 in PC2 and PC5, and JG 2016-1614 in PC3 and PC5 suggested that selection of genotypes from these PCs is more rewarding in further crop improvement programme of chickpea. These findings are in close harmony with (Ghafoor *et al.*, 2001 Toker and Cagirgan 2004, Miladinovic *et al.*, 2006; Akande, 2007; Iqbal *et al.*, 2008; Ojo *et al.*, 2012; Amrita *et al.*, 2014; Shivwanshi and Babbar, 2017; Kumar *et al.*, 2019 and Kumar *et al.*, 2021) [7, 8, 9, 10, 11, 12, 13, 14, 16, 15].

Table 5: Screening of Promising Genotypes on the basis of PCA Scores in Pooled Analysis

	PC1	PC2	PC3	PC4	PC5
Genotypes	BG 3091	JG 36	JG 2016-1614	JG63 × ICC4958	JG 11 × JG 14
	GL 14015	GL 14015	BG 3091	JG2017-49	ICCV 15118
	DC16-116	BRC 302	GL 14015	JG24	RKG17-04
	GNG 2367	JG 11 × JG 14			GL 14015
	JG 36	ICCV 15118			PG 187
	IPC 2010-14	DC16-116			GJG 1503
		RKG 13-205			JG 2016-1614

Conclusion

Principal component analysis suggested that enormous amount of variability present the experimental material *i.e.* in the chickpea genotypes and traits *viz.*, days to pod initiation, plant height, number of primary branches per plant, seed yield per plant, total numbers of pods per plant and 100 seed weight were principal discriminatory characteristics contributed greatly to the total variation in yield which was in associated with first five principal components explaining 79.80% of the total variations. Therefore, PC1, PC2, PC3, PC4 and PC5 can be allowed for simultaneous selection for enhancing seed yield characteristics in *desi* chickpeas. Hence, the important traits and genotypes collectively in various PCs may be kept into consideration in further utilization in chickpea precise breeding programme.

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