

## Principal Component Analysis of Promising Advance Chickpea Lines (*Cicer arietinum* L.)

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### ABSTRACT

An experiment was conducted to evaluate 30 promising chickpea genotypes grown in Randomized Completely Block Design with three replications during *rabi* 2018-19. Observations were recorded on 15 traits viz., days to flower initiation, days to 50% flowering, days pod initiation, days to maturity, plant height (cm), stem height at first fruiting node (cm), number of primary branches per plant, number of secondary branches per plant, total number of pods per plant, number of effective pods per plant, number of seeds per pod, 100 seed weight (g), biological yield per plant (g), harvest index (%) and seed yield per plant (g) and showed that out of 15, only 6 principal components (PCs) displayed more than 1

Eigen values and demonstrated approximately 86.7% variation in the attributes under investigation. The genotypes from PC1 will be given due importance because it accounted for 28.6 % of total variability. The genotypes viz; JG 63 × JG 4958, ( JG 74 × JG 315 ) – 14, ICC 96029 × ICC 11551, JG 24, JG 11 × JG 14 , ICCV 15119 , ICC 552241 × JG 11, JG 11 × RVSSG-1 highest positive PC values for yield related traits. Thus, these genotypes can be utilized in chickpea improvement program.

**Keywords** Chickpea, Gram, Principal component analysis.

### INTRODUCTION

The chickpea (*Cicer arietinum* L. 2n=2x=16), commonly referred to as the garbanzo bean, Indian pea, or bengal gramme, is a self-fertile, annual, diploid grain legume in the family Fabaceae and subfamily Papilionaceae with a genomic size of approximately 738 Mbp. It is originated in South-eastern Turkey.

Principal component analysis (PCA), a potent dimension-reduction technique, can be used to condense a huge collection of variables into a smaller set while keeping the majority of their information. This method lowers the dimensionality of enormous data sets, which are frequently challenging to interpret. A large number of linked variables are condensed into a smaller number of uncorrelated variables or principal components by the use of principal component analysis (PCA).

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## MATERIALS AND METHODS

The experiment was conducted at the Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, Jabalpur (MP) during *rabi* 2018-19. The experimental material comprised of 30 promising chickpea advance lines grown in Randomized Completely Block Design with three replications. Observations were recorded on phenological traits viz., days to flower initiation, days to 50% flowering, days to pod initiation and days to maturity, eleven quantitative traits viz., plant height (cm), stem height at first fruiting node (cm), number of primary branches per plant, number of secondary branches per plant, total number of pods per plant, number of effective pods per plant, number of seeds per pod, 100 seed weight (g), biological yield per plant (g), harvest index (%) and seed yield per plant (g). A popular method of dimension reduction is PCA (Massy 1965, Jolliffe 1986), which looks for linear combinations of the columns of X with maximal variance, or alternatively, high information. Therefore, the objective of this research was to assess the chickpea germplasm with the aim to identify and rank significant genotypes and features with the help of principal component analysis for initiating a hybridization program in order to create improved chickpea cultivars.

## RESULTS AND DISCUSSION

A multivariate statistical method for exploration and simplifying complex data sets is principal component analysis. PCA was used in the current work to analyze chickpea quantitative traits.

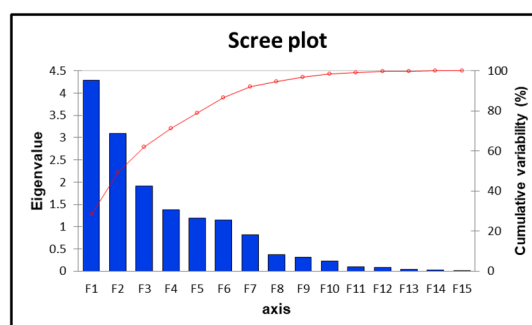
Out of 15, only 6 principal components (PCs) displayed more than 1 eigen values and demonstrated approximately 86.7% variation in the attributes under investigation. Out of which only 6 principal components were prioritized appropriately for further explanation. The PC1 had the highest variability (28.6%), followed by PC2 (20.6%), PC3 (12.8%), PC4 (9.2%), PC5 (7.9%) and PC6 (7.6%) for traits under study (Table 1). Scree plot explained the percentage of variance associated between eigen values and principal components with each PC obtained by drawing a graph (Fig. 1).

According to the results of the rotation of the

**Table 1.** Principal components of chickpea genotypes for different traits.

Traits	Principal component (PC)	Eigen value	Variability (%)	Cumulative (%)
Days to flower initiation	PC1	4.3	28.6	28.6
Days to 50% flowering	PC2	3.1	20.6	49.2
Days to pod initiation	PC3	1.9	12.8	62.0
Days to maturity	PC4	1.4	9.2	71.2
Plant height	PC5	1.2	7.9	79.1
Stem height at 1 <sup>st</sup> fruiting node	PC6	1.1	7.6	86.7
No. of primary branches per plant	PC7	0.8	5.5	92.2
No. of secondary branches per plant	PC8	0.4	2.5	94.7
Total no. of pods per plant	PC9	0.3	2.1	96.8
No. of effective pods per plant	PC10	0.2	1.6	98.3
No. of seeds per pod	PC11	0.1	0.7	99.0
100 seed weight	PC12	0.1	0.5	99.6
Biological yield per plant	PC13	0.0	0.2	99.8
Harvest index %	PC14	0.0	0.1	100.0
Seed yield per plant	PC15	0.0	0.0	100.0

component matrix, which showed that the first 6 PCs represent the largest variability (86.7%); therefore the traits falling within these 6 PCs may be given significant consideration in chickpea breeding program. It revealed that the first principal component (PC1) which accounted for the highest variation (20.6%)



**Fig. 1.** Scree plot between eigen value and principal components.

**Table 2.** Principal component values of rotation component matrix of chickpea genotypes.

Traits	Principal components					
	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6
DTF	<b>0.75</b>	-0.44	-0.30	0.01	-0.08	-0.17
DT50%F	<b>0.69</b>	-0.55	-0.24	0.07	-0.27	0.04
DTP	<b>0.57</b>	-0.63	-0.27	-0.11	-0.37	-0.03
DTM	<b>0.21</b>	-0.43	-0.40	-0.29	0.06	-0.11
PH	0.35	<b>0.59</b>	-0.17	0.57	0.01	0.02
SH at 1 <sup>st</sup> F	0.24	-0.01	-0.28	<b>0.74</b>	0.08	-0.41
PB	0.29	-0.26	0.48	0.08	-0.21	<b>0.59</b>
SB	<b>0.59</b>	-0.35	0.07	0.17	0.38	0.43
TNPP	<b>0.67</b>	0.04	0.62	-0.16	0.04	-0.34
NEPPP	0.62	0.05	<b>0.64</b>	-0.07	0.06	-0.40
NSPP	0.00	-0.52	-0.12	0.11	<b>0.76</b>	0.12
100SW	0.31	<b>0.69</b>	-0.48	-0.12	-0.22	0.19
BY	<b>0.77</b>	0.58	-0.09	-0.12	0.13	0.13
HI%	-0.36	-0.39	0.37	<b>0.55</b>	-0.37	0.12
SYPP	<b>0.78</b>	0.49	0.12	0.07	0.03	0.21

was mostly related with phenological traits such as days to flower initiation, days to 50% flowering, days to pod initiation, days to maturity number of secondary branches per plant, total number of pods per plant, biological yield per plant and seed yield per plant. The second principal component (PC2) was dominated as plant height and 100 seed weight. The PC3 was dominated for number of effective pods per plant, while PC4 was dominated for stem height at first fruiting node and harvest index. PC5 was

dominated by number of seeds per pod, while PC6 was dominated for number of primary branches per plant. (Tables 2-3).

Where, DTF: Days to flower initiation, DT50%F: Days to 50% flowering, DTP: Days to pod initiation, DTM: Days to maturity, PH: Plant height, SH at 1<sup>st</sup> F: Stem height at first fruiting node, PB: Number of primary branches per plant, SB: number of secondary branches per plant, TNPP: 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.

### PC scores of genotypes

The PC scores of the each component (PC1, PC2, PC3, PC4 PC5 and PC6) had positive and negative values (Tables 4-5). These scores can be utilized to propose precise selection indices whose intensity can be decided by variability explained by each of principal component. A high PC score for a specific genotype in a specific component indicates high values for the variables in that specific genotype.

Maximum positive PC score was recorded in JG 24, JG 11 × JG 14, ICCV 15119, ICC 552241 × JG 11, JG 63 × JG 4958, ICC 96029 × ICC 11551, JG 12 × JG 16-3, ( JG 74 × JG 315 ) – 14, JG 63 × ICC 1205, JG 14 × JG 226, JG 2016 – 1614, JG 26 × ICC 251741, JG 23 × ICC 251741, JG 36, JG 315 × ICCV 96029, JG 63 × ICC 14407, JG 14-16 × JG

**Table 3.** Rotated matrix results of different traits (>0.500).

	PC1	PC2	PC3	PC4	PC5	PC6
	Days to flower initiation	Plant height	No. of effective pods per plant	Stem height at first fruiting node	No. of seeds per pod	No. of primary branches per plant
	Days to 50% flowering	Hundred seed weight		Harvest index		
Traits	Days to pod initiation					
	Days to maturity					
	No. of secondary branches per plant					
	Total no. pods per plant					
	Seed yield per plant(g)					

**Table 4.** List of different PCA scores of the chickpea genotypes.

Genotype	PC1	PC 2	PC3	PC4	PC5	PC6
JG 24	<b>4.68</b>	-0.08	-3.57	<b>1.06</b>	-0.59	-0.61
JG 12 × JG 16-3	0.56	<b>1.49</b>	1.21	-0.37	-0.30	<b>2.10</b>
JG 63 × ICC 1205	-1.47	-0.67	-0.04	<b>2.32</b>	-0.51	-0.79
JG 9605 × JG 1307	0.62	-1.43	-0.07	-0.16	0.16	-0.32
JG 63 × JG 4958	0.38	<b>1.21</b>	<b>1.72</b>	-0.52	-0.30	-0.12
JG 12 × JG 14	0.54	-0.49	0.86	0.06	-0.38	-1.00
(JG 74 × JG 315) – 14	-1.82	-1.24	<b>1.21</b>	<b>2.58</b>	-1.61	<b>2.22</b>
JG 315 × ICCV 96029	-2.87	1.00	-0.48	<b>1.37</b>	-0.71	-0.90
JG 11 × JG 14	<b>3.89</b>	-4.35	<b>2.43</b>	-0.73	-0.04	0.68
JG 36	-1.24	-0.40	<b>1.59</b>	0.83	0.87	1.00
PA058 (1033(8))	0.20	-0.47	0.06	-0.32	-0.33	0.73
ICCV 15119	<b>1.27</b>	<b>2.23</b>	-0.73	-1.19	0.11	0.32
ICC 96029 × ICC 11551	0.17	-0.74	<b>1.18</b>	0.84	<b>1.37</b>	-1.04
JG 14 × JG 226	-1.63	-0.24	-0.98	0.50	<b>1.76</b>	0.78
JG 2016-1411	-1.37	0.65	-1.23	-0.07	0.61	-1.01
JG 2016 – 1614	-0.56	0.79	<b>2.89</b>	-1.67	<b>1.21</b>	-2.28
PA030 1063 (152)	-2.42	-1.17	-0.05	-1.99	-1.89	0.81
JG 23 × ICC 251741	-1.11	<b>1.72</b>	-0.14	<b>1.65</b>	-0.13	-0.48
JG 26 × ICC 251741	0.75	-0.40	-0.27	-0.80	0.00	<b>1.85</b>
JG 14-16 × JG 11	-1.38	<b>2.52</b>	-0.34	-1.10	0.11	-0.07
ICC 552241 × JG 11	<b>6.81</b>	<b>3.13</b>	0.31	1.12	-0.72	-0.23
JG 11 × RVSSG-1	1.00	<b>2.25</b>	<b>1.26</b>	-0.86	0.90	0.31
JG 74 × JG 11551	-1.10	-2.40	-0.97	-1.38	-1.19	-1.87
JG 63 × ICC 14407	0.72	-4.04	-2.27	-0.11	<b>3.00</b>	0.49
JG 1307 × ICC 7441	0.58	-0.95	0.80	0.70	-0.39	-1.55
JG 74 × ICC 4958	-1.15	0.74	-2.13	-0.13	-0.60	0.04
ICC 15118	0.22	0.25	-1.82	-2.14	-0.61	0.83
JG 74 × JG 14	-1.72	-0.28	-0.28	-0.86	-1.72	-0.44
JG 12	-0.43	-1.28	0.31	<b>1.12</b>	-0.25	-0.23
JG 12 × JG 16-1	-2.21	<b>2.64</b>	-0.44	0.25	<b>2.16</b>	0.78

11, JG 23 × ICC 251741, JG 11 × RVSSG-1, JG12 and JG 12 × JG 16-1.

**Table 5.** Promising genotypes on the basis of scores of principal components.

PC 1	PC 2	PC 3	PC 4	PC 5	PC 6
JG 24	JG 12 × JG 16-3	JG 63 × JG 4958	JG 24	ICC 96029 × ICC 11551	JG 12 × JG 16-3
JG 11 × JG 14	JG 63 × JG 4958	(JG 74 × JG 315) – 14	JG 63 × ICC 1205	JG 14 × JG 226	(JG 74 × JG 315) – 14
ICCV 15119	ICCV 15119	JG 11 × JG 14	(JG 74 × JG 315) – 14	JG 2016 – 1614	JG 26 × ICC 251741
ICC 552241 × JG 11	JG 23 × ICC 251741	JG 36	JG 315 × ICCV 96029	JG 63 × ICC 14407	
	ICC 552241 × JG 11	ICC 96029 × ICC 11551	JG 23 × ICC 251741	JG 12 × JG 16-1	
	JG 14-16 × JG 11	JG 11 × RVSSG-1	ICC 552241 × JG 11		
	JG 11 × RVSSG-1	JG 2016 – 1614	JG 12		
	JG 12 × JG 16-1				

Using the top PC scores, promising genotypes were identified and categorized in the Table 5. Genotypes JG 24 common in PC1 and PC4. Genotypes JG 11 x JG 14 was common in PC1 and PC3 and genotypes ICCV 15119, ICC 552241 x JG 11 and JG 11 x RVSSG-1 was common in PC1 and PC2. Genotypes JG 63 × JG 4958 was common in PC2 and PC3, while JG 23 x ICC 251741 was common in PC2 and PC3. Genotypes (JG 74 × JG 315) – 14 were common in PC3, PC4 and PC5, while genotypes ICC 96029 x ICC 11551 were common in PC3 and PC5.

These findings confirm in earlier studies of Nawab *et al.* (2013), Waseem *et al.* (2014), Malik *et al.* (2014) and Shivwanshi and Babbar (2017).

## CONCLUSION

The genotypes from PC1 will be given due importance because it accounted for 28.6 % of total vari-

ability. The genotypes viz; JG 63 × JG 4958, ( JG 74 × JG 315 ) – 14, ICC 96029 × ICC 11551, JG 24, JG 11 × JG 14 , ICCV 15119 , ICC 552241 × JG 11, JG 11 × RVSSG-1 highest positive PC values for yield related traits. As a result, these genotypes can be carefully chosen in order to create suitable genotypes and to transfer desirable features.

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