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Research Article

Genetic divergence, variability and character association analysis in chickpea (*Cicer arietinum* L.) genotypes under normal and late sown conditions

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Abstract
Forty five chickpea genotypes were evaluated under normal and late sown conditions during *Rabi,*2017-18 in the experimental field of the Department of Genetics and Plant Breeding, C.C.S. University, Meerut Uttar Pradesh. The genotypes were sown in Randomized Block Design with three replications and observations were recorded for each genotype in each replication for all studied characters. Analysis of variance showed significant variation among all the genotypes for all the characters in both the conditions (normal and late sowing). The highest values of GCV and PCV were recorded for the number of pods per plant, the number of seeds per plant, 100 seed weight, biological yield per plant, the number of seeds per pod and seed yield per plant. Heritability coupled with genetic advance as per cent of mean was recorded as high for the number of pods per plant, the number of seeds per plant, the number of seeds per pod, 100 seed weight, biological yield and seed yield per plant in both conditions. Seed yield was significant and positively correlated with the number of pods per plant, the number of seeds per plant, the number of branches per plant and biological yield per plant in both conditions. Furthermore, the biological yield per plant, harvest index, the number of seeds per plant and 100 seed weight showed a positive and direct effects toward the seed yield per plant under the both situations. Forty five genotypes were grouped into five clusters (Environment I) and four clusters (Environment II) in normal and late sowing, respectively. The maximum inter cluster distance was observed between clusters I and II for normal sowing and between clusters II and IV for late sowing conditions.

Keywords: Chickpea, Correlation, Genetic Divergence, Heritability, Normal and late sowing

INTRODUCTION

Chickpea (*Cicer arientinum* L.) commonly known as gram or Bengal gram, or Indian pea, belongs to the genus *Cicer*, species *arietinum* and family *Fabaceae.* It originated in southeastern Turkey around 7,000 BC. Chickpea is a self-pollinating legume with a diploid (2n=16) genome of approximately 740 MB. It is grown in the semi-arid tropical and Mediterranean region, which later spread to India and Middle Eastern countries such as, Pakistan, Turkey, Iran, Myanmar and Ethiopia. There are two types of cultivated chickpeas namely Desi and Kabuli. Global production of chickpeas consists of about 75% Desi and 25% Kabuli species. In 2019, the world production of chickpeas was 14 million tons, led by India with 70% of the world total, followed by Turkey in second place (FAO STAT, 2021). From a nutritional point of view, in addition to being a good source of protein chickpea is also a good source

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of carbohydrates and together account for about 80% of total seed dry matter. The carbohydrate content of chickpeas has been reported to be around 61-62%, with a caloric value of 396 kcal/100g. The crude protein content of chickpeas varies between 18 and 22%, while it also contains 4.5% fat.

Despite their nutritional value and economic importance, chickpea production in the country is relatively low. This is mainly due to the poor genetic makeup of the available varieties. Genetic variability is very important for crop improvement and is a prerequisite in any breeding program that allows a plant breeder to select high-yielding genotypes. The higher the variability in the population, the greater the chance of producing the desired plant species. Heritability and genetic advance estimates in a population give information about the expected gains in the subsequent generations. The estimation of heritability helps to select a specific genotype from different genetic populations. Genetic advance gives an idea of a possible improvement of the new population through selection compared to the original population.

Yield is a complex and polygenic trait that depends on the nature and magnitude of the heritable portion of the total variation. In order to study it properly, it is required that the yield contributing factor must be considered and evaluated in terms of yield. Approaches to significantly improve chickpea production require information about the nature and extent of genetic variation in quantitative traits and their interrelationship in a population with different genotypes, which are important prerequisites for a systematic breeding program. The association of one or more characters can be statistically estimated by correlation coefficients coupled with path coefficient analysis. For purposeful hybridization, the precise information about the genetic divergence helps the plant breeder to select diverse parents among the population (Samsuddin, 1985). The genetic divergence analysis is based on the D^2 statistic of Mahalanobis proposed by Mahalanobis (1936). The present study was therefore aimed to evaluate the genetic variations, heritability, expected genetic advance, character association and genetic divergence for yield and yield attributing traits in chickpea under normal and late sowing conditions.

MATERIALS AND METHODS

The experimental material consisted of 45 diverse genotypes of chickpea and used for the present study and they were evaluated in a Randomized Block Design (RBD) with three replications during *rabi,* 2017-2018 with two sowing dates (Normal and Late) at the research farm of C.C.S. University, Meerut (U.P.) India. In the experiment, row to row and plant to plant distances were kept at 30 cm and 10 cm, respectively. To avoid the border effects, the experimental plot was surrounded on all sides by non-experimental rows. All recommended agronomic practices were used in each experiment to grow a good crop. Observations were recorded on five randomly selected plants from each genotype in each replication for twelve quantitative characters *viz,* days to 50% flowering, days to maturity, plant height (cm), the number of pods per plant, the number of seeds per pod, the number of seeds per plant, the number of branches per plant, 100 seed weight (g), biological yield (g), harvest index (%), protein content (%) and seed yield (g). The mean value of recorded data from each replication in both environments was subjected to statistical analysis. Total nitrogen and protein content of chickpea seeds of different treatments were evaluated through Kel plus nitrogen analyzer. Total protein content was estimated by the Bradford method (1976). Analysis of variance was calculated based on the method suggested by Panse and Sukhatme*,* (1967). Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) were calculated based on the formula proposed by Burton and De Vane (1953). Heritability and genetic advance were calculated through methods developed by Johnson *et al.* (1955). Character association was done as per the formula suggested by Johnson *et al.* (1955). Genetic divergence analysis was performed as per Mahalanobis D^2 method (1936).

RESULTS AND DISCUSSION

In the present investigation, forty five diverse genotypes of chickpea were evaluated to assess the above given statistical analysis under two different environments (normal sowing and late sowing). The results of analysis of variance for all studied characters under both environments are presented in **Table 1**. The mean sum of squares due to genotypes showed significant differences for all characters in both the environments indicating the presence of an adequate amount of variability among all the forty five chickpea genotypes for all characters included in the present study. Similar results were also earlier reported by Thapa *et al.* (2019), Hailu (2020) and Alemayo *et al*. (2021).

The availability of genetic variability among existing germplasm is a prerequisite for plant breeders to develop desirable genotypes with high yield potential and is the basic requirement for a successful breeding program. Therefore, to achieve self sufficiency and sustainability in food production, varieties with a diverse genetic base need to be developed. The variability among the populations can be estimated by variability parameters such as phenotypic coefficients of variation (PCV) and the genotypic coefficients of variation (GCV). For both the environments, estimates of PCV and GCV for twelve characters of chickpea are presented in **Table 2**. We found that the PCV was relatively higher than GCV for all the twelve corresponding characters *viz.,* 100- seed weight, the number of pods per plant, the number of seeds per plant, biological yield per plant and seed yield per plant. Similar results were also reported by previous investigators Teja *et al*. (2020), Thapa *et al.* (2020), Kumar *et al.* (2021) and Raju *et al*. (2021).

Table 1. Analysis of variance (ANOVA) for twelve characters in forty five genotypes of chickpea (*Cicer aerinitum* L.) in timely and late sowing (Environment I& II)

		Mean Squares											
Source of Variation	**d.f.**	**Days to 50% flowering**	**Days to maturity**	**Plant height**	**Number of pods per plant**	**Number of seeds per pod**	**Number of seeds per plant**	**Number of branches per plant**	**100 seed weight**	**Biological yield**	**Harvest index**	**Protein content**	**Seed yield**
Environment I													
Replication	2	7.94	5.96	5.78	1.25	0.01	1.27	0.05	0.01	0.03	0.89	2.20	1.19
Treatment	44	15.35**	5.68**	16.46**	96.95	0.15**	168.69**	1.17**	51.53**	210.47**	66.79**	13.36**	47.24**
Error	88	1.84	1.47	1.66	0.69	0.004	1.20	0.03	0.25	3.03	3.74	0.62	0.63
Environment II													
Replication	2	1.15	7.76	1.87	0.14	0.001	0.01	0.010	0.25	1.35	4.59	4.38	1.09
Treatment	44	16.75**	8.25**	15.78**	7.07**	0.120**	17.16**	0.2503**	36.80**	125.0**	98.38**	13.47**	49.57**
Error	88	3.50	1.41	0.73	0.08	0.003	0.18	0.0116	0.35	1.25	4.07	1.21	0.33

**= Significant at P=0.01 level.

Table 2. Value of mean, range, genotypic and phenotypic coefficient of variation (GCV and PCV), heritability (bs), genetic advance, genetic advance as percent of mean, for twelve characters of chickpea in timely sowing and late sowing (Environment I & II)

S.N.	**Characters**	**Mean**		**Range**		**Heritability (%)**		**Genetic advance**		**Genetic advance as % of mean**		**GCV (%)**		**PCV (%)**	
		E1	**E2**	**E1**	**E2**	**E1**	**E2**	**E1**	**E2**	**E1**	**E2**	**E1**	**E2**	**E1**	**E2**
1	Days to 50% flowering	132.54	113.21	127.33-138.33	105.00-117.00	70.97	55.78	3.68	3.23	2.78	2.86	1.60	1.86	1.90	2.49
2	Days to maturity	163.56	140.76	161.00-166.67	138.33-144.33	48.83	61.69	1.71	2.44	1.04	1.73	0.72	1.07	1.04	1.37
3	Plant height (cm)	31.68	22.73	26.27-38.00	16.73-27.27	74.76	87.34	3.96	4.31	12.48	18.97	7.01	9.86	8.11	10.55
4	Number of pods per plant	20.50	7.53	9.07-34.60	4.53-11.80	97.89	96.65	11.54	3.09	56.30	41.04	27.63	20.26	27.92	20.61
5	Number of seeds per pod	1.49	1.42	1.03-1.97	1.00-1.87	92.68	92.78	0.43	0.39	28.99	27.70	14.62	13.96	15.18	14.49
6	Number of seeds per plant	27.53	10.57	11.27-42.13	5.61-16.90	97.90	96.90	15.23	4.82	55.32	45.66	27.14	22.52	27.43	22.88
7	Number of branches per plant	3.96	2.68	2.40-5.33	2.00-3.53	93.71	87.31	1.23	0.54	31.09	20.27	15.59	10.53	16.10	11.27
8	100 seed weight (g)	13.90	12.92	9.12-30.60	8.93-25.93	98.54	97.24	8.48	7.08	61.00	54.82	29.83	26.99	30.05	27.37
9	Biological yield (g)	42.79	26.45	20.67-60.67	12.33-43.67	95.80	97.05	16.77	13.03	39.19	49.27	19.43	24.28	19.86	24.65
10	Harvest index (%)	51.57	50.72	41.14-61.13	38.90-60.09	84.88	88.54	8.70	10.87	16.87	21.43	8.89	11.06	9.65	11.75
11	Protein content (%)	22.87	26.72	18.34-26.75	21.22-29.22	87.26	77.15	3.96	3.66	17.34	13.69	9.01	7.57	9.64	8.62
12	Seed yield (g)	21.89	13.50	11.37-31.98	6.24-25.47	96.09	98.03	7.96	8.26	36.37	61.23	18.01	30.02	18.37	30.32

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The estimates of broad sense heritability were higher in both the environments for characters such as, 100 seed weight, the number of seeds per plant, the number of pods per plant, seed yield per plant, biological yield per plant and the number of seeds per pod while moderate heritability was observed for characters, days to 50% flowering, days to maturity and plant height (**Table 2**). The results are in agreement with the previous work of Kuldeep *et al.* (2014), Makarand *et al.* (2019), and Gautam *et al*. (2021). The selection of superior genotypes only on the basis of heritability may not be substantiation for genetic improvement. Therefore, heritability estimates along with genetic advance, would be more effective in the selection of superior genotypes for crop improvement. In the present investigation, high values of genetic advance estimates as per cent of mean were recorded for six characters *viz.,* 100 seed weight, the number of pods per plant, the number of seed per plant, biological yield per plant, seed yield per plant and the number of seeds per pods in both environments. Similar finding were earlier reported by Kusuma and Lal (2021) and Singh *et al.* (2021).

The inter-relationship between important yield components is best estimated by correlation coupled with path coefficient analysis. Correlation is one of the most important techniques used by many researchers to make an effective indirect selection of desirable characters based on the correlated and uncorrelated responses. Analysis of the phenotypic correlation coefficient revealed that, seed yield had a significant and positive correlation with the number of pods per plant, the number of seeds per plant, the number of branches per plant and biological yield per plant in both the environment (**Table 3**). However, seed yield per plant showed a significant and positive correlation with plant height, 100 seed weight and harvest index in late sown conditions.

Among the *inter se* associations, the magnitude of correlation coefficient for the number of seeds per plant showed significant and positive relationship with characters; the number of pods per plant, the number of seeds per pods, the number of branches per plant, biological yield per plant in both environments while with harvest index in late sown condition. However, number of seeds per plant also showed a significant and negative association with 100 seed weight in normal sowing. In both environments, the number of pods per plant showed significant and positive association with the number of seeds per plant, the number of branches per plant and biological yield per plant, while in normal sowing, it showed a significant and negative association with 100 seed weight. The number of branches per plant showed a significant and positive correlation with the number of pods per plant, the number of seeds per plant and the biological yield per plant in both environments. Biological yield per

Table 3. Phenotypic correlation coefficient in environment I (above diagonal) and phenotypic correlation coefficient in environment II (below diagonal) among the twelve characters in chickpea

S.No.	Characters	DTF	DTM	PH	NPP	NSP	SPP	BPP	100 SW	BY	HI	PC	SY
1	Days to 50% flowering	-	0.372**	-0.095	-0.169	-0.045	-0.078	0.215	0.005	0.105	-0.441**	0.111	-0.115
2	Days to maturity	0.240	-	0.263	0.042	-0.175	-0.003	0.213	0.178	0.366*	-0.402**	-0.065	0.202
3	Plant height	0.045	0.176	-	-0.101	-0.007	-0.187	0.185	0.410**	0.304*	-0.172	0.052	0.267
4	Number of pods per plant	0.049	0.133	0.247	-	0.120	0.751**	0.401**	-0.411**	0.553**	0.021	-0.026	0.645**
5	Number of seeds per pod	0.107	-0.108	-0.071	-0.133	-	0.379**	0.065	-0.567**	-0.066	0.261	-0.130	0.037
6	Number of seeds per plant	0.072	0.023	0.193	0.745**	0.491**	-	0.374**	-0.597**	0.568**	-0.047	-0.217	0.635**
7	Number of branches per plant	-0.108	-0.089	0.219	0.358*	0.105	0.397**	-	-0.085	0.612**	-0.327*	0.119	0.517**
8	100 seed weight	-0.147	0.253	0.379**	0.158	-0.487**	-0.161	0.031	-	0.086	-0.088	0.199	0.046
9	Biological yield	-0.011	0.161	0.446**	0.705**	-0.024	0.575**	0.354*	0.554**	-	-0.456**	0.004	0.873**
10	Harvest index	-0.052	0.282	0.169	0.309*	0.047	0.301*	0.115	0.413**	0.190	-	-0.040	-0.028
11	Protein content	-0.084	0.014	0.035	0.132	-0.224	-0.031	-0.168	0.132	0.037	-0.006	-	-0.031
12	Seed yield	-0.039	0.254	0.448**	0.695**	-0.008	0.596**	0.330*	0.650**	0.907**	0.548**	0.007	-

*, **= Significant at P = 0.05 and P = 0.01 levels, respectively

DTF= Days to 50% flowering, DTM= Days to maturity, PH= Plant height , NPP= Number of pods per plant, NSP= Number of seeds per pod, SPP= Number of seeds per plant, BPP= Number of branches per plant, 100SW= 100 seed weight , BY= Biological yield, HI= Harvest index , PC= Protein content , SY= Seed yield .

plant showed a significant positive association with plant height, the number of pods per plant, the number of seeds per plant and the number of branches per plant in both the environments, whereas in environment I it showed a significantly and negative association with harvest index. Similar findings were also earlier reported by Dawane *et al.* (2020), Jan *et al.* (2021) and Xalxo *et al.* (2021).

Path coefficient analysis is an important tool for partitioning or dividing the correlation coefficient into direct and indirect effects of the independent components on the dependent component. The direct and indirect effects of investigated characters on seed yield at the phenotypic level are presented in **Tables 4 and 5**. Path coefficient analysis showed that biological yield per plant, harvest index, number of seeds per plant and 100 seed weight exhibited a maximum positive direct effect on seed yield in both environments. The earlier studies for direct effect on grain yield for biological yield and harvest index were reported by Pattanayak *et al.* (2021) and Yadav *et al.* (2020).

Genetic diversity is one of the major criteria of parent selection in hybridization programme, quantified through a biometrical tool such as Mahalanobis's D^2-statistics has been used to select genetically divergent parents for purposeful hybridization programmes. The divergence analysis showed that all the forty five genotypes were grouped into five clusters, cluster I contain the maximum (fifteen) number of genotypes followed by cluster III contain thirteen genotypes, cluster V contain nine genotypes, cluster IV with five genotypes and cluster II with three genotypes in normal sowing **(Table 6).** In late sown condition, cluster II contains maximum (Eighteen) number of genotypes followed by cluster I contain fourteen genotypes, cluster III contains seven genotypes and cluster IV contains six genotypes. The maximum inter-cluster distance was observed between clusters I and II in normal sowing and clusters II and IV in late sown conditions (**Table 7 and 8**). The maximum intra-cluster distance was observed for cluster IV (normal sowing) and clusters I (late sowing). The genotypes of these clusters which have maximum inter-cluster distance may be recommended for hybridization to isolate transgressive segregants for the development of high yielding chickpea cultivars. Similar results were also reported by; Shedge *et al.* (2019) and Bohare *et al.* (2020).

In the present study, the analysis of variance revealed significant genetic variations among the chickpea genotypes for all twelve quantitative characters studied under both the environmental conditions, suggesting the presence of an adequate amount of variability among genotypes to be used in further selection and breeding

Table 4. Direct effect (bold values) and indirect effect of different characters towards the seed yield at phenotypic level in timely sowing (Environment I)

S.No.	Characters	DTF	DTM	PH	NPP	NSP	SPP	BPP	100 SW	BY	HI	PC	Correlation with grain yield
1	Days to 50% flowering	**0.0001**	-0.0002	-0.0065	-0.0055	0.0021	-0.0153	0.0045	0.0004	0.0941	-0.1881	-0.0004	-0.115
2	Days to maturity	0.0000	**-0.0005**	0.0181	0.0014	0.0081	-0.0006	0.0044	0.0151	0.3271	-0.1716	0.0002	0.202
3	Plant height	0.0000	-0.0001	**0.0690**	-0.0033	0.0003	-0.0366	0.0038	0.0349	0.2723	-0.0735	-0.0002	0.267
4	Number of pods per plant	0.0000	0.0000	-0.0070	**0.0327**	-0.0055	0.1468	0.0084	-0.0349	0.4950	0.0091	0.0001	0.645**
5	Number of seeds per pod	0.0000	0.0001	-0.0005	0.0039	**-0.0462**	0.0741	0.0014	-0.0482	-0.0595	0.1111	0.0004	0.037
6	Number of seeds per plant	0.0000	0.0000	-0.0129	0.0245	-0.0175	**0.1955**	0.0078	-0.0507	0.5083	-0.0202	0.0007	0.635**
7	Number of branches per plant	0.0000	-0.0001	0.0127	0.0131	-0.0030	0.0731	**0.0208**	-0.0072	0.5473	-0.1396	-0.0004	0.517**
8	100 seed weight	0.0000	-0.0001	0.0283	-0.0134	0.0262	-0.1167	-0.0018	**0.0849**	0.0766	-0.0376	-0.0007	0.046
9	Biological yield	0.0000	-0.0002	0.0210	0.0181	0.0031	0.1110	0.0127	0.0073	**0.8949**	-0.1946	0.0000	0.873**
10	Harvest index	0.0000	0.0002	-0.0119	0.0007	-0.0120	-0.0092	-0.0068	-0.0075	-0.4084	**0.4265**	0.0001	-0.028
11	Protein content	0.0000	0.0000	0.0036	-0.0009	0.0060	-0.0424	0.0025	0.0169	0.0036	-0.0169	**-0.0034**	-0.031

Residual effect = 0.0541

****= Significant at P = 0.01 level.**

DTF= Days to 50% flowering, DTM= Days to maturity, PH= Plant height , NPP= Number of pods per plant, NSP= Number of seeds per pod, SPP= Number of seeds per plant, BPP= Number of branches per plant, 100SW= 100 seed weight , BY= Biological yield, HI= Harvest index , PC= Protein content , SY= Seed yield .

Table 5. Direct effect (bold values) and indirect effect of different characters towards the seed yield at phenotypic level in late sowing (Environment II)

S.No.	Characters	DTF	DTM	PH	NPP	NSP	SPP	BPP	100 SW	BY	HI	PC	Correlation with grain yield
1	Days to 50% flowering	**-0.0082**	0.0041	0.0002	0.0003	0.0008	0.0138	0.0013	-0.0337	-0.0065	-0.0142	0.0034	-0.039
2	Days to maturity	-0.0020	**0.0170**	0.0007	0.0009	-0.0008	0.0044	0.0011	0.0580	0.0988	0.0765	-0.0006	0.254
3	Plant height	-0.0004	0.0030	**0.0042**	0.0016	-0.0005	0.0371	-0.0027	0.0868	0.2742	0.0457	-0.0014	0.448**
4	Number of pods per plant	-0.0004	0.0023	0.0010	**0.0066**	-0.0010	0.1437	-0.0044	0.0362	0.4330	0.0837	-0.0054	0.695**
5	Number of seeds per pod	-0.0009	-0.0018	-0.0003	-0.0009	**0.0072**	0.0947	-0.0013	-0.1116	-0.0149	0.0129	0.0091	-0.008
6	Number of seeds per plant	-0.0006	0.0004	0.0008	0.0049	0.0035	**0.1928**	-0.0048	-0.0369	0.3533	0.0815	0.0012	0.596**
7	Number of branches per plant	0.0009	-0.0015	0.0009	0.0024	0.0008	0.0765	**-0.0121**	0.0071	0.2172	0.0313	0.0068	0.330*
8	100 seed weight	0.0012	0.0043	0.0016	0.0010	-0.0035	-0.0310	-0.0004	**0.2293**	0.3404	0.1120	-0.0054	0.650**
9	Biological yield	0.0001	0.0027	0.0019	0.0046	-0.0002	0.1109	-0.0043	0.1270	**0.6144**	0.0516	-0.0015	0.907**
10	Harvest index	0.0004	0.0048	0.0007	0.0020	0.0003	0.0580	-0.0014	0.0947	0.1169	**0.2712**	0.0003	0.548**
11	Protein content	0.0007	0.0002	0.0001	0.0009	-0.0016	-0.0059	0.0020	0.0302	0.0227	-0.0017	**-0.0406**	0.007

Residual effect = 0.0233
*, **= Significant at P = 0.05 and P = 0.01 levels, respectively

DTF= Days to 50% flowering, DTM= Days to maturity, PH= Plant height , NPP= Number of pods per plant, NSP= Number of seeds per pod, SPP= Number of seeds per plant, BPP= Number of branches per plant, 100SW= 100 seed weight, BY= Biological yield , HI= Harvest index , PC= Protein content (%), SY= Seed yield

Table 6. Distribution of forty five genotypes of chickpea in different cluster in timely sowing and late sowing (Environment I & II)

Clusters	Number of genotypes	Name of genotypes
Environment - I		
I	15	ICC-10489, ICC-15911, PDG-05, ICC-17007, PDG-84-10, ICC-14775, BKG-21204, ICC-15896, ICC-4648, BGG-21168, ICC-6874, P- 6225, GL-29061, 78126, PBG-85-4
II	3	ICC-15119, 74040, VISHAL
III	13	GL-769, IPC-5-74, PDE-2-E, GPF-02, ICC-71, IPC-02-2, ICC-14268, P- 1059, B- 714, P- 740, BGM-572, KPG- 39, P- 79086
IV	5	ICC-11218, ICC-1608, BG-5028, P- 602, K-850
V	9	IPC-95-01, ICC-15680, RADHE , P- 145, BG-547, K- 1052, KDG-1288, P- 85, 8011
Environment - II		
I	14	PDE-2-E, ICC-15911, PDG-05, GPF-02, ICC-11218, BKG-21204, ICC-14268, B- 714, 74040, K-1052, KDG-1288, P- 85, P- 6225, GL-29061
II	18	IPC-5-74, IPC-95-01, ICC-10489, ICC-17007, PDG-84-10, ICC-14775, ICC-71, ICC-15896, ICC-4648, ICC-6874, IPC-02-2, P- 79086, P- 145, PBG-85-4, GL-769, P- 1059, P- 740, 78126
III	7	ICC-15119, ICC-15680, ICC-1608, BG-5028, RADHE , BG-547, 8011
IV	6	BGG-21168, P- 602, K-850, BGM-572, VISHAL, KPG- 39

Table 7. Average inter and intra-cluster (bold values) distances involving forty five genotypes of chickpea in timely sowing (Environment I)

Clusters	I	II	III	IV	V
I	**2.309**				
II	6.434	**2.818**			
III	2.548	4.805	**2.434**		
IV	4.771	6.250	4.526	**3.029**	
V	3.173	4.203	2.844	4.897	**2.249**

Table 8. Average inter and intra-cluster (bold values) distances involving forty five genotypes of chickpea in late sowing (Environment II)

Clusters	I	II	III	IV	V
I	**2.828**				
II	3.113	**2.464**			
III	3.475	3.323	**2.807**		
IV	3.376	5.396	4.006	**2.379**	

programmes that leads to transgressive segregants and genetic improvement of chickpea. The value of phenotypic coefficient of variation (PCV) was relatively higher than the corresponding genotypic coefficient of variation (GCV) for all the studied characters, indicating the vital role of environmental interaction in the expression of the characters. High heritability coupled with high genetic advance as per cent of mean for major characters in both the environments showed that these characters are determined by additive genetic action and could be improved through selection. A high heritability of a particular character indicated that these characters were less influenced by environmental effects. The selection of the characters that showed positive and significant correlation with seed yield may be utilized for chickpea crop improvement Path coefficient analysis based on seed yield showed that biological yield and harvest index had the highest direct effects on seed yield and showed a positive correlationwith seed yield. Therefore, both those traits are helpful for indirect selection to improve yield in chickpeas.

High inter cluster distance was observed between clusters, suggesting that there is a wide diversity between them and the genotypes in these clusters could be used as parents in a hybridization programme to develop high yielding chickpea genotypes under both environments nevertheless genotypes with maximum genetic diversity are useful for developing a large number of variable segregants through crossbreeding programme that may be further utilized in the breeding program of chickpea.

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