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Research Article

Variability Analysis and Multivariate Analysis in Chickpea (*Cicer arietinum* L.)

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Abstract

A field trial was conducted to assess the magnitude of genetic variability, heritability and genetic advance and genetic diversity using 105 diverse genotypes of chickpea (*Cicer arietinum* L.). The analysis of variance indicated the prevalence of sufficient genetic variation among the genotypes for all the eleven traits. High heritability coupled with high genotypic coefficient of variation (GCV) and high genetic advance as per cent of mean (GA %) were observed for seed yield per plant, biological yield per plant, harvest index, number of pods per plant and 100-seed weight which indicated that response to selection would be very high for these yield components. Mahalanobis' D^2 analysis resulted 13 diverse clusters. Cluster I topped with maximum (46) genotypes followed by cluster II (18), cluster III (16) and cluster IV(12). While cluster VII to XIII were solitary clusters. Maximum genetic distance (D) was found between cluster V and XI followed by between cluster V and X. Four clusters namely V, IX, X and XI were important with respect to construct plant ideotypeincluding seed yield per plant which could be utilized for further crop improvement programme. Three traits *viz,*,seed yield per plant, 100-seed weight and number of pods per plant contributed more than 63% of towards total genetic divergence.

Key words: Chickpea, variability, heritability, genetic divergence.

Introduction:

Chickpea (*Cicer arietinum* L., *2n=2x=16*, *Fabaceae*) is one of the first grain legumes to be domesticated by humans in old world (Van der Maesen, 1972). It is originated in Western Asia from where it spread in to India and other parts of the world. India is a leading chickpea growing country accounting for about 65 % of the world production. Madhya Pradesh, Uttar Pradesh, Maharashtra, Rajasthan, Gujarat, Andhra Pradesh, Karnataka and Bihar are the major chickpea growing states in the country.

Chickpea seeds contain 17.7 % protein, 0.49 % lysine, 0.11 % methionine (Katiyar, 1982), 56.6 % carbohydrates, considerable amount of calcium, phosphorus, iron and vitamin B (Thakur, 1980). Chickpea is used as dal in split form and whole fried or boiled seeds are also eaten. Green immature chickpea is also used as vegetable and its dry flour is a major ingredient in snacks and sweets in India and Pakistan. Husk and bits of dal are used as nutritious feed for animals. Chickpea plant as such can also be used as green fodder, while straw is an excellent dry fodder for animals.

The morphological characterization of germplasm is used to understand the genetic variation since a wide range of genetic variation among parents is essential for hybridization programmes. Nature and magnitude of genetic variability and heritability in a population as genetic and non-genetic factors is pre-requisites in any successful hybridization programme to get desirable segregants. Arunachalam (1981) stated that multivariate analysis using Mahalanobis' D^2 statistic is a powerful tool to know the clustering pattern to establish the relationship between genetic and geographical divergence and to determine the role of different quantitative characters towards total genetic divergence. Hence, the present experiment was planned on variability analysis along with genetic divergence using 105 genotypes of chickpea.

Material and methods

The experimental material comprised of 105 diverse genotypes of chickpea collected from various parts of India (Table 1). The material was evaluated in randomised block design with three replications at Pulses Research Station, Junagadh Agricultural University, Junagadh during *Rabi* 2009-10. Each plot consisted of single row plot of 4.0m length with inter and intra row spacing of 45 and 10cm, respectively. All the recommended agronomical package of practices and plant protection measures were followed timely to raise a good crop.

The observations were recorded on five randomly selected competitive plants for eleven traits *viz.*, days to 50% flowering, days to maturity, reproductive phase duration, plant height, number of branches per plant, number of pods per plant, biological yield per plant, 100-seed weight, seed yield per plant, harvest index and protein content. The genotypic and phenotypic coefficient of variation was estimated as per Burton (1952), while heritability in broad sense and expected genetic advance were estimated as Allard (1960). Genetic diversity was calculated using Mahalanobis (1936) D^2 statistic and genotypes were grouped into clusters by Tocher's method as described by Rao (1952).

Results and discussion

Analysis of variance revealed highly significant differences among the genotypes for all the eleven characters indicating the existence of sufficient variability in the material studied. The experimental material showed wide range of phenotypic variation for seed yield per plant, number of pods per plant, biological yield per plant, harvest index, 100-seed weight and number of branches per plant as revealed by high values of coefficient of range.

Variability Analysis:The values of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV), in most of the cases, indicating more influence of environmental factors (Table 2). However, low differences were also observed between PCV and GCV for days to 50% flowering, days to maturity, 100-seed weight and protein content which revealed that these four traits were comparatively less influenced by the environments. The values of GCV and PCV were highest for seed yield per plant followed by number of pods per plant, harvest index, biological yield per plant and 100-seed weight indicating the presence of wide variation for these traits to allow selection for individual traits. These results are in agreement with the findings of Tripathi (1998), Patel (2005),Vaghela *et al.* (2009). Moderate estimates of GCV and PCV were observed for number of branches per plant, plant height, days to 50% flowering and reproductive phase duration, while low estimates of GCV and PCV was observed for days to maturity and protein content indicated narrow genetic variability for both these characters.

The coefficient of variation indicated only the extent of variability present for different characters and did not indicate the heritable portion. To obtain the heritable portion of variability, it was essential to know the heritability estimates for different traits (Burton, 1952). Johnson *et al.* (1955) suggested that the heritability estimate along with genetic advance is more useful than the heritability alone in predicting the resultant effect of selection. In the present study, the estimates of high heritability coupled with high genetic advance as per cent of mean was observed for seed yield per plant, number of pods per plant, 100-seed weight, biological yield per plant and harvest index indicated preponderance of additive gene action and selection pressure could profitably be applied on these characters for improving the seed yield (Panse, 1957). On the other hand, high to moderate heritability along with low GCV and low genetic gain were observed for days to 50% flowering, days to maturity and plant height, which indicated that these three traits were regulated by non-additive gene action and presence of high genotypic x environment interaction. For the remaining traits like reproductive phase duration, plant height, number of branches per plant and protein content, major variation was environmental, leading to low heritability and low expected genetic advance and hence, little gain is expected through straight selection.

Multivariate Analysis: Multivariate analysis using Wilk's 'Л' criterion was carried out to test the differences among 105 genotypes for aggregate of 11 characters. The value of V-statistic (8223.938) which follows χ^2 distribution for 1144 degrees of freedom showed highly significant differences among the genotypes for aggregate of 11 characters. Thus, one can proceed for further diversity analysis. The D^2-values computed for 5460 pairs ranged from 0.85 (between GCP 9603 and JCP 145) to 80.66 (between ICCV 96029 and JCP-56) indicated the presence of high genetic diversity among the genotypes for all the traits.

On the basis of D^2-values, the genotypes were grouped into 13 clusters so that genotypes within a cluster had smaller D^2 values among themselves than those belonging of different clusters (Table 3). The cluster I was largest having 46 genotypes from different geographical regions, comprising 33 genotypes from Junagadh (Gujarat); two from Dharwad (Karnataka) and one each from Rahuri (Maharashtra), Akola (Mah.), Faridkot (Punjab), Bhatinda (Punjab), Diggi (Raj.), IARI (New Delhi), Jabalpur (MP), ICRISAT (Hyderabad), Banglore, Durgapur (Raj.). Likewise, cluster II, III and IV comprised of 18, 16 and 12 genotypes, respectively from different locations of India. While cluster V and VI both possessed three genotypes each. The clusters from VII to XIII had only single genotype in each cluster. The clustering pattern of genotypes showed that genetic origin was totally independent of their geographical origin. Murty and Arunachalam (1966) also stated that genetic drift and selection in varied environments could cause greater diversity than geographic distance. Further, free exchange of seed materials among the different regions consequently causes characters constellations because of the human interference and material may lose its individuality. Dubey and Shrivastava (2007), Singh *et al.*(2007) and Dwevedi and Lal (2009) also reported that there was no parallelism between geographic distribution and genetic diversity in chickpea.

In general, intra cluster distances were lower than the inter cluster distances (Table 4). Thus, the genotypes included within a cluster tended to diverse less from one another. The intra cluster distance was ranged from (4.70 in cluster I) to (6.76 in cluster VI). The maximum inter-cluster distance (D) was observed between cluster V and XI (D=14.81) followed by that between cluster V and X (D=14.01), while the closest proximity was noticed between cluster VIII and IX (D=4.18). The genotypes belonging to the clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates. In this context, genotypes from cluster V (JCP 56, GJG 0109 and BG 1101) and cluster X (JCP 139) and cluster XI (GJG 0415) could be selected as parents in hybridization programme.

The clustering pattern could be utilized in selection of parents for crossing and deciding the best cross combinations which may generate the highest possible variability for various traits. In the present study, the cluster IX differed from other clusters (Table 5) in respect of seed yield per plantand reproductive phase duration,while cluster V was the bestfor biological yield per plant. The cluster XI had desirable rating for days to 50% flowering, days to maturity, and plant height. Cluster II was good for number of branches per plant, while cluster X was the bestfor number of pods per plant and protein content.The cluster III, V and XIII was the best for 100-seed weight, biological yield per plant and harvest index,respectively.

An assessment of contribution of different characters towards total genetic divergence (Table 5) revealed that seed yield per plant (23.41 %) had contributed maximum towards total divergence.Three traits contributed more than 63% of diversity *viz.* seed yield per plant (23.41%), 100-seed weight (21.26%) and number of pods per plant (18.66%). Hence, selection of divergent parents based on these three traits would be useful for hybridization programme followed by isolation of desirable transgressive segregantsin chickpea. Similar findings were also reported by Nimbalkar and Harer (2001) and Dwevedi and Lal (2009).

Overall, it can be concluded that high heritability along with high GCV and high genetic gain were observed for seed yield per plant, biological yield per plant, harvest index, number of pods per plant and 100-seed weight which might be attributed to additive gene actionin their inheritance and phenotypic selection could be effective. Maximum contribution of seed yield per plant, followed by 100-seed weight and number of pods per plant were observed on total genetic divergence. Hence due consideration should be given to these traits while imposing selection for amenability in seed yield per plant in chickpea.

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Table1. List of genotypes, their pedigree and state of origin used in chickpea

Sr. No.	Name of genotypes	Pedigree	Place of origin
1	JCP 13	JG 71 X P380	J.A.U. Gujarat
2	JCP 16	JG 71 X P380	J.A.U. Gujarat
3	JCP 22	JG 71 X P380	J.A.U. Gujarat
4	JCP 27	JG 71 X P380	J.A.U. Gujarat
5	JCP 43	JG 71 X WR 315	J.A.U. Gujarat
6	JCP 52	PUSA 212 X WR 315	J.A.U. Gujarat
7	JCP 56	PUSA 212 X D.Yellow	J.A.U. Gujarat
8	JCP 60	Sel. From HK 106	J.A.U. Gujarat
9	JCP 93	Sel. From IC 800044	J.A.U. Gujarat
10	JCP 96	Sel. From IC 800006	J.A.U. Gujarat
11	JCP 104	IV 820044-2	J.A.U. Gujarat
12	JCP 125	WR 315 X ICCC 32	J.A.U. Gujarat
13	JCP 128	WR 315 X ICCC 32	J.A.U. Gujarat
14	JCP 139	WR 315 X ICCC 32	J.A.U. Gujarat
15	JCP 141	K 850 X D. Yellow	J.A.U. Gujarat
16	JCP 145	K 850 X D. Yellow	J.A.U. Gujarat
17	JCP 184	ICCC 4 X WR 315	J.A.U. Gujarat
18	JCP 189	ICCC 4 X WR 315	J.A.U. Gujarat
19	JCP 202	Chaff X Gaurav	J.A.U. Gujarat
20	JCP 208	Chaff X Gaurav	J.A.U. Gujarat
21	JCP 222	WR 315 X D. Yellow	J.A.U. Gujarat
22	JCP 224	WR 315 X D. Yellow	J.A.U. Gujarat
23	JCP 228	K 850 X D. Yellow	J.A.U. Gujarat
24	JCP 245	ICCC 4 X WR 315	J.A.U. Gujarat
25	ICCV 10	P 1231 X P 1265	ICRISAT (AP)
26	ICC 6926	NEC 1186	ICRISAT (AP)
27	PG 92004	(KPG 36 X P 326) X ICCL 82108	Rahuri (Mah.)
28	HR 406	-	-
29	GWG 231	-	-
30	DGM 810	Local Selection	Durgapur (Raj.)
31	JG 315	Sel.From Line P 315	Jabalpur (MP)
32	BG 256	(JG 62 X 850 - 3/27) X (2550 X H 208)	IARI, New Delhi
33	BGD 103	(JG 62 X ICC 1223) X JG 62	Dharwad (Karnataka)
34	Chaffa	Local Sel. From niphad	J.A.U. Gujarat
35	KGDB 1181	BG 256 X K 977	CSAU, Haryana
36	KGDB 1178	AVA X K850	CSAU, Haryana
37	BGD 109	ICCV 42 X K 850	Dharwad (Karnataka)
38	BGD 116	-	Dharwad (Karnataka)
39	BCP 17	BDNG 35 X JG 62	Badnapur (Bihar)
40	CSJD 901	RSG 44 X PDG 84-10	Diggi (Raj.)
41	IPC 96-57	BG 256 X ICC 12483	IIPR (Kanpur)
42	JAKI 9218	(ICC 37 X GW 5--7 X ICC 37	Akola (Mah.)
43	PBG 68	GL 87069 X GL 7079	Bathinda (Punjab)
44	FG 694	-	Faridkot, Punjab
45	ICCV 97017	ICCV 2 X BG 276	ICRISAT (AP)
46	ICCV 97024	ICCL 82108 X Annigeri	ICRISAT (AP)
47	ICCV 96029	Annigeri x ICC 12237	ICRISAT (AP)
48	FG 712	GP 8936 X C 235	Faridkot, Punjab
49	CSG 8962	Sel. From GPF 7035	-
50	RSG 143-1	-	Durgapur (Raj.)
51	ICCV 96030	-	ICRISAT (AP)
52	BG 1101	(Pusa 365 x C. raticulatum) x pusa 362	IARI, New Delhi
53	Annegeri	-	Bangalore
54	Phule G 9425-5	-	MPKV,Rahuri
55	GCP 101(GG 1)	GCP 2 X ICCV2	J.A.U. Gujarat

Contd..

Table 1 :Contd….

Sr. No.	Name of genotypes	Pedigree	Place of origin
56	GCP 104	GCP 2 X PANT G 114	J.A.U. Gujarat
57	GCP 106	ICCC 4 X WR 315	J.A.U. Gujarat
58	GCP 9405	PG 5 X ICCC 32	J.A.U. Gujarat
59	GCP 9412	F1 (ICCV 10 X ICCL 86103) X K 850	J.A.U. Gujarat
60	GCP 9504	K 850 X H 355	J.A.U. Gujarat
61	GCP 9509	Sele From ICCV 93004	J.A.U. Gujarat
62	GCP 9511	Sele From ICCV 91115	J.A.U. Gujarat
63	GCP 9514	F1 (ICCC 22 X JG 74) X K 850	J.A.U. Gujarat
64	GCP 9516	ICCL 84224 X Annigeri	J.A.U. Gujarat
65	GCP 9520	Sele From RSG 555	J.A.U. Gujarat
66	GCP 9523	ICCC 4 X ICC 32	J.A.U. Gujarat
67	GCP 9527	Sele From ICC 90026	J.A.U. Gujarat
68	GCP 9601	(H 77-51 X JG 315)X(JG 62 X ICC 506 EB)	J.A.U. Gujarat
69	GCP 9603	(ICCC 37 X K 850) X (ICCL 8322 X A 1)	J.A.U. Gujarat
70	GCP 9606	Phule G 12 X ICCC 23	J.A.U. Gujarat
71	GCP 9612	(JG 62 X ICC 12237) X JG 62	J.A.U. Gujarat
72	GCP 9626	COG 2 X ICC 12237	J.A.U. Gujarat
73	GCP 9629	ICCV 2 X K 315	J.A.U. Gujarat
74	GCP 9707	(KPG 59 X ICCV 10) X ICCV 89344	J.A.U. Gujarat
75	GCP 9710	(KPG 59 X ICCV 10) X ICCV 89344	J.A.U. Gujarat
76	CCP 9803	ICC X 790166-17P-1P-1P X ICCL 85150	J.A.U. Gujarat
77	GCP 9805	ICCV 89851 X H 86-143	J.A.U. Gujarat
78	GJG 9807	(BG 256 X ICCV 88109) X ICCV 89230	J.A.U. Gujarat
79	GCP 9809	(ICCV 10 X ICC 10448) X K 850	J.A.U. Gujarat
80	GCP 9812	JG 62 X ICC 12230 X JG 62	J.A.U. Gujarat
81	GJG 9905	(H-86-142 X ICCV-10) X ICCV 89344	J.A.U. Gujarat
82	GJG 2001	Kankaria X JCP-29	J.A.U. Gujarat
83	GJG 2004	Kankaria X JCP-29	J.A.U. Gujarat
84	GJG 2012	PG 81-1-1 X ICCV-10	J.A.U. Gujarat
85	GJG 2018	{(BDNG-776 X ICC-122527) X} AKA-46	J.A.U. Gujarat
86	GJG 0104	ICCV-92014 X ICCV-10	J.A.U. Gujarat
87	GJG 0107	ICCV-93001 X ICCV-10	J.A.U. Gujarat
88	GJG 0109	ICCV-93001 X ICCV-10	J.A.U. Gujarat
89	HC 3	-	Kanpur (UP)
90	K 850	-	Kanpur (UP)
91	Pant G 186	-	Kanpur (UP)
92	Radhe	-	Kanpur (UP)
93	GJG 0201	ICCV 89224 x ICCV 10	J.A.U. Gujarat
94	GJG 0207	ICCV 93001 x ICCV 10	J.A.U. Gujarat
95	GJG 0305	ICCV 10 x GCP 101	J.A.U. Gujarat
96	GJG 0315	ICCV-10 x K 850) x (ICCV 89230 x JG 74)	J.A.U. Gujarat
97	GJG 0415	(IPC 92-1 x KGD 1168) x DCP 92-3	J.A.U. Gujarat
98	Vishal	-	Kanpur (UP)
99	WCG-2000-7	-	J.A.U. Gujarat
100	GJG-0307	PG-81-1-1 x DAHOD YELLOW	J.A.U. Gujarat
101	GAG-0419	ICCV 92065 x ICCV 8820	J.A.U. Gujarat
102	GJG-0514	ICCV 820065 x ICCV 10	J.A.U. Gujarat
103	GJG-0603	GCV-107 x GCV-9504	J.A.U. Gujarat
104	GJG-0610	PG-92014 x GCV-107	J.A.U. Gujarat
105	GJG-0612	PG-92014 x GCV-107	J.A.U. Gujarat

Table 2. Phenotypic range, coefficient of range, phenotypic and genotypic coefficient of variation, heritability, genetic advance and genetic advance expressed as per cent of mean for various characters in chickpea

Characters	Range	CV (%)	Mean ± S.Em	PCV (%)	GCV (%)	h^2 (bs) (%)	GA	GAM
Seed yield per plant (g)	0.95-16.84	89.32	7.17 ± 0.996	55.95	50.50	81.50	6.73	93.99
Days to 50% flowering	38.67-64.67	25.16	53.95 ± 1.939	10.12	7.98	62.20	7.00	10.95
Days to maturity	86.00-103.00	8.99	95.57 ± 1.923	5.73	4.55	63.00	7.10	7.43
Reproductive phase duration (days)	32.00-47.67	19.67	41.62 ± 2.385	11.75	6.29	28.70	2.89	6.94
Plant height (cm)	31.33-52.60	25.34	37.93 ± 1.856	12.49	9.17	53.90	5.26	13.87
No. of branches per plant	1.80-4.20	40.00	2.69 ± 0.261	20.46	11.66	32.50	0.37	13.75
No. of pods per plant	11.87-94.00	77.58	41.25 ± 5.618	49.64	43.68	77.40	32.66	79.18
100 Seed weight (g)	8.70-26.33	50.33	16.74 ± 1.141	26.30	23.50	79.90	7.25	43.31
Biological yield per plant (g)	6.24-39.59	72.76	22.41 ± 2.622	35.96	29.71	68.20	11.33	50.58
Harvest index (%)	10.52-62.84	71.32	31.77 ± 3.854	42.71	37.18	75.80	21.19	66.70
Protein content (%)	22.31-23.78	3.19	23.59 ± 0.117	1.18	0.81	47.40	0.27	1.15

Table 3.Grouping of 105 genotypes of chickpea on the basis of D^2 statistic in various clusters

Cluster	No. of genotypes	Name of genotypes	Place of origin
I	46	JCP 145, GCP 9603, GCP 9606, JCP 16, GCP 9629, GCP 9514, GJG-0514, JCP 224, JCP 43, JCP 222, GJG 0415, JCP 125, JCP 22, JCP 27, WCG-2000-7, GCP 9511, JCP 141, GJG 0315, JCP 96, GCP 9601, GCP 9707, GJG 2018, GJG 2001, JCP 13, GCP 104, GCP 106, GCP 9523, CCP 9803, GJG 0104, GJG 0201, JCP 208, JCP 184, JCP 93	Junagadh (Gujarat)
		Phule G 9425-5	Rahuri (Mah)
		JAKI 9218	Akola (Mah)
		FG 712	Faridkot (Punjab)
		PBG 68	Bhatinda (Punjab)
		CSJD 901	Diggi (Raj.)
		BGD 103, BGD 116	Dharwad(Karnataka)
		BG 256	IARI (New Delhi)
		JG 315	Jabalpur(MP)
		ICCV 10	ICRISAT (Hydrabad)
		Annegeri	Banglore
		RSG 143-1	Durgapur (Raj.)
		GWG 231	Unknown
II	18	JCP 128, JCP 189, JCP 228, JCP 245, Chaffa, GCP 9405, GCP 9504, GCP 9516, GCP 9520, GCP 9805, GJG 9807, GCP 9809, GCP 9710, GJG 9905, GAG-0419	Junagadh (Gujarat)
		Pant G 186	Kanpur (U.P)
		ICCV 97017	ICRISAT (Hyderabad)
		HR 406	Unknown
III	16	JCP 52, GCP 9412, GCP 9527, GCP 9626, GJG 2012, GJG 0107, GJG-0603, GJG-0610, GJG-0612	Junagadh (Gujarat)
		HC 3, K 850, Vishal	Kanpur (U.P)
		PG 92004	Rahuri (Mah)
		BCP 17	Badnapur (Mah)
		BGD 109	Dharwad(Karnataka)
		KGDB 1178	CSAU (Haryana)

Contd..

Table 3. contd..

Cluster	No. of genotypes	Name of genotypes	Place of origin
IV	12	JCP 104, JCP 202, GCP 9612, GCP 9812, GJG 0315, GJG-0307	Junagadh (Gujarat)
		DGM 810	Durgapur (Raj.)
		KGDB 1181	CSAU (Haryana)
		IPC 96-57	IIPR (Kanpur)
		FG 694	Faridkot (Punjab)
		ICCV 96030	ICRISAT (Hydrabad)
		Radhe	Kanpur (U.P)
V	3	JCP 56, GJG 0109	Junagadh (Gujarat)
		BG 1101	IARI (New Delhi)
VI	3	ICCV 97024	ICRISAT (Hydrabad)
		GCP 101(GG 1)	Junagadh (Gujarat)
		CSG 8962	Unknown
VII	1	ICC 6926	ICRISAT (Hyderabad)
VIII	1	GCP 9509	Junagadh (Gujarat)
IX	1	GJG 2004	Junagadh (Gujarat)
X	1	JCP 139	Junagadh (Gujarat)
XI	1	GJG 0415	Junagadh (Gujarat)
XII	1	GJG 0207	Junagadh (Gujarat)
XIII	1	JCP 60	Junagadh (Gujarat)

Table 4.Average inter and intra- cluster distance (D) values in chickpea

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	**4.70**	6.38	7.17	6.32	9.27	7.82	5.61	7.31	8.02	8.21	7.90	9.34	8.22
II		**6.26**	8.86	8.49	10.75	8.93	5.18	7.06	6.99	7.00	9.25	9.39	8.11
III			**5.22**	8.05	7.45	10.21	7.69	7.27	9.62	11.67	11.83	7.65	10.22
IV				**6.66**	9.90	8.81	8.01	9.57	10.35	10.03	8.49	11.16	10.52
V					**5.14**	11.82	10.59	9.97	12.52	14.01	14.81	10.82	12.06
VI						**6.76**	8.55	10.29	10.27	10.34	10.01	12.08	10.40
VII							**0.00**	5.76	6.39	5.99	8.23	6.89	5.71
VIII								**0.00**	4.18	8.60	11.63	6.16	9.99
IX									**0.00**	6.75	10.82	8.68	11.09
X										**0.00**	7.83	11.74	9.97
XI											**0.00**	12.64	10.69
XII												**0.00**	9.85
XIII													**0.00**

Table 5.Cluster means for different characters in chickpea

Clusters	Seed yield/ plant (g)	Days to 50% flowering	Days to maturity	Reproductive phase duration (days)	Plant height (cm)	No. of branches /plant	No. of pods per plant	100 Seed weight (g)	Biological yield/plant (g)	Harvest index (%)	Protein content (%)
I	6.13	54.14	95.87	41.86	36.41	2.77	37.28	15.28	20.99	29.53	23.61
II	10.92	53.94	96.52	42.57	38.92	5.68	64.64	14.86	26.47	43.32	23.63
III	7.44	53.48	94.77	41.29	39.01	2.53	31.20	23.42	22.28	33.26	23.60
IV	2.96	54.50	95.11	40.61	39.70	2.67	25.24	16.16	16.48	18.29	23.61
V	6.79	57.67	100.44	42.78	49.38	3.11	31.84	22.34	36.13	18.47	23.70
VI	6.66	57.44	97.89	40.44	38.38	3.09	40.31	13.31	24.13	24.40	22.48
VII	11.13	51.67	88.33	36.67	37.40	2.40	61.73	16.06	23.26	49.07	23.60
VIII	14.22	57.00	97.00	40.00	33.67	1.93	64.33	20.03	34.43	41.64	23.72
IX	16.84	54.00	99.67	45.67	32.73	2.60	87.80	18.71	36.00	46.82	23.64
X	12.25	50.33	90.33	40.00	36.00	2.27	94.00	14.55	32.08	39.74	23.74
XI	2.45	42.00	86.00	44.00	31.00	2.33	32.00	9.80	10.89	22.30	23.69
XII	14.62	44.67	87.33	42.67	37.87	1.80	49.40	21.71	26.57	55.06	23.61
XIII	7.81	54.67	86.67	32.00	34.27	2.67	40.33	11.52	12.52	62.84	23.52
Mean	7.17	53.95	95.57	41.62	37.93	2.69	41.25	16.74	22.41	31.77	23.59
SEm	0.996	1.939	1.923	2.385	1.856	0.261	5.618	1.141	2.622	3.854	0.117
% Contribution towards total genetic divergence	23.41%	7.53%	5.60%	0.00%	3.97%	2.14%	18.66%	21.26%	5.71%	7.07%	4.63%
No. of times ranked 1st	1278	411	306	0	217	117	1019	1161	312	386	253