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Impact of Genetic Divergence on the Expression of Individual Trait in Chickpea (*Cicer Arietinum* L.)

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ABSTRACT

Chickpea (*Cicer arietinum* L). contributes in both area and production approximately 30 and 35% respectively among all the pulse crops in India. Fortunately, India alone contribute about 60% in area and productions at global level. However, its productivity at national and international levels is stagnating around 800 kg/ha. The present investigations were carried out to understand various reasons particularly genetic potential and diversity of diverse groups of chickpea genotypes. For this purpose 108 genotypes were divided into four different groups of cultivars on the basis of seed size viz. (i) *desi*-medium seeded (ii) *desi*-bold seeded (iii) *kabuli*-bold seeded and (iv) *kabuli*-extra-bold seeded. The plantings of there cultivars were carried out in three diverse and contrasting environments viz. normal, medium and plantings. Thus major objectives for these investigations were (i) to assess the amount of genetic divergence among the genotypes (ii) to know the differential behavior of genotypes under different environments (iii) to study the influence of environment on the expression of individual traits (iv) identification of high yielding and low yielding clusters. All the diverse genotypes were planted in a Randomized Block Design with three replications in a four row plot maintaining distance of 20x40 cm apart with row length of 4 m. Single plant observations were recorded for quantitative traits viz. plant height (cm), number of branches per plant, number of pods per plant, days to flowering, days to maturity, seed size/100-seed weight (g), biological yield per plant (g), seed yield per plant (g), harvest index and grain yield per plant. Statistical analysis was carried out for superior performance of different traits, which revealed highly significant differences for all the above mentioned traits under different planting environments. Results on various quantitative traits indicated that group-I of *desi*-medium seeded types had poor performance in seed yield and group III of *kabuli*-bold seeded types showed best performance. Thus excellent genetic variability existed between various groups of cultivars. Results on various cluster formation showed clear cut distinction between high yielding and low yielding clusters. Interestingly, clear demarcation existed in the placement of high yielding and low yielding genotypes within a cluster and between the clusters. Thus on the basis of these observations it was concluded that excellent genetic variability existed among various groups of chickpea cultivars. The existing variability is impacting greatly the expression of individual quantitative trait. The distinct cluster formation and placement of high yielding and low yielding genotypes into various clusters suggested that genetic variability played significant role in the genetic expression of individual genotypes and traits.

Key words: Chickpea, genetic variability, quantitative traits, groups of genotypes.

Introduction

Chickpea (*Cicer arietinum* L). is most important grain legume, occupying first position both in area and production among the Indian pulse food crops. Fortunately, due to its wide adaptation it is cultivated in all

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the continents in more than 50 countries. This crop was domesticated in West Asia some 10,000 years ago and was subjected to a series of bottle necks which narrowed genetic base and placed important limitations where the crop can be grown (Abbo *et al.,* 2003). Interestingly, chickpea became very popular among the various strata of the Indian society in pre- historic times more than 10,000 years and is well documented in Puranas, Upanishad's and Veda's of Hindu scriptures.

Chickpea cultivation is speared all over India on more than 7 million hectares and its production is about 6 million tones. During past three decades, it has got set back in area on account of competition with high yielding and input responsive crops like wheat in irrigated and mustard in rainfed areas. It failed in competition on account of it s low yield potential. In order to make this crop competitive with those grown during winter season breeding of high yielding and input responsive varieties is the only solution. For achieving this goal, the development of new varieties largely depends on the amount of genetic variability in the base material and the extent of variability for the desired trait. The nature and magnitude of genetic divergence plays an important role in the formation of successful breading programmes. The genetically diverse genotypes are likely to produce heterotic effect and superior sergegants when incorporated in hybridization in crop improvement programmes. The importance of existing genetics diversity has been emphasized by several workers (Joshi and Dhawan, 1966; Murty and Arunachalam, 1966; Kumar and Arora, 1992) The multivariate analysis by means of D^2 statistic (Mahalanobis, 1936) is a powerful tool in quantifying the degree of divergence at genotypic level in respect of several traits considered together.

Any genetic investigation carried out on the quantitative traits becomes complicated when more than one environment considered because of the change in the gene expression that may occur with change in the environments. Therefore, the present investigation was carried out to understand the genetic divergence of 108 diverse genotypes of chickpea under normal, medium and late planting environments. The major objectives are; (i) to assess the amount of genetic divergence among the genotypes (ii) to know the differential behavior of genotypes under different environments (iii) to study the influence of environment on the expression of individual traits (iv) identification of high yielding and low yielding clusters.

Materials and Methods

The present investigations were carried out with 108 diverse chickpea genotypes of both *desi* and *kabuli* types. These genotypes were selected and collected from national and international organizations, like Indian Agricultural Research Institute (IARI), New Delhi, India; International Center for Agricultural Research in Dry Areas (ICARDA), Aleppo, Syria; International Center for Research in Semi-Arid Tropics (ICRISAT), Patancheru, A.P., India, etc. Four major phenotypic groups were formulated on the basis of seed size/seed weight *viz*. Group I: *desi*-medium seeded which included 37 genotypes having 100-seed weight less than 20 g; Group II: *desi*-bold seeded having 38 genotypes with 100-seed weight more than 20 g; Group III: *kabuli* -bold seeded having 16 genotypes with 100-seed weight between 20-30 g and Group IV: *kabuli*-extra bold seeded constituting 17 genotypes with 100-seed weight more than 30 g. The experimental material was planted at two different locations *viz.* (i) Division of Genetics, Indian Agricultural Research Institute, New Delhi, India and (ii) J.V. College, Baraut, Baghpat, U.P., India. To represent the wide growing conditions three planting environments *viz.* (i) Normal planting environment (25th October), (ii) Medium planting environment (15th November) and (iii) Late planting environment (5th December) were selected. The experiments were conducted at both the locations adopting uniform agronomic practices during 2004-05 and 2005-06.

The experimental material was planted in Randomized Block Design with three replicates. Each genotype was space-planted maintaining 20x40 cm distance apart in a four row plots of 1.60 m wide and 4.00 m long, maintaining a uniform plant density in each plot. Seeds were pre-treated with Bavistine to minimize the probability of soil born diseases such as *Fusarium* wilt (*F. oxysporum* Schlechtend) and root rot (*Rhizoctonia bataticola* Taubenhaus), and thereafter, inoculated with Group N rhizobia immediately prior to plantings. The pre-sowing irrigation was applied at both the locations during both the years. Di-Ammonium Phosphate (DAP) fertilizer and Gypsum were applied at the rate of 100 and 200 kg/ha respectively. Pod borer (*Helicoverpa armigera* Hiibner) was controlled from flowering stage onwards with the application of insecticide (Endosulfan) at the rate of 2.0 l/ha.

The experimental observations on a wide range of quantitative traits like plant height (cm), number of branches per plant, days to flowering, days to maturity, number of pods per plant, number of seeds per pod, 100-seed weight (g), biological yield per plant (g) and seed yield per plant (g) were recorded on five randomly selected plants in two central rows to avoid border effect in each plot. Harvest index was calculated on the basis of seed yield and biological yield in percentage. The data were subjected to multivariate analysis using Mahalanobis' generalized distance D^2 statistics (Mahalanobis, 1936). The genotypes were grouped in to clusters according to Tocher's method (Rao, 1952).

Results and Discussion

Statistical analyses for experimental observations were carried out by pooling all the data from both the locations of both the years. The ANOVA was prepared from analyzed data as per RBD analysis (Table. 1), which revealed highly significant differences among genotypes for all the traits studied over the environments. This indicated that the genotypes under investigation possess vast genetic variations and divergence for various quantitative traits.

The treatment means of various quantitative traits for different groups of both *desi* and *kabuli* cultivars under varying planting environments during both the years have presented in table 2. Interestingly, the minimum plant height (53.66 cm) was recorded in group-I of *desi*-medium seeded types and maximum (59.33 cm) in group-IV of *kabuli* extra bold seeded types. Thus, significantly lower plant height among all the group of cultivars was observed in group-I and significantly higher height was observed in group-IV. Whereas plant height in genotypes of group-II and III showed no differences. Therefore, wide plant height variations were observed among all the groups of cultivars. In case of number of branches per plant minimum branches 37.79 per plant were observed in group-IV and maximum 46.36 in group-II. However, no significant differences were observed between group-I, II and III, on the other hand group-IV was significantly inferior in producing number of branches per plant.

In case of days to 50% flowering both groups of *desi* types showed similar duration of flowering (75 days). On the other hand group-III of *kabuli* bold seeded types showed significantly short flowering duration (65 days) in comparison to all the other groups of cultivars, while group-IV of *kabuli*-extra bold seeded types showed significantly longer flowering duration (79 days) in comparison to rest of the groups of cultivars. Thus, these observations indicated clear variations for this trait among different groups of cultivars. Interestingly, the same pattern like days to flowering was also observed for days to maturity among all the groups of cultivars, which indicated that excellent variations existed for this trait.

In case of number of pods per plant the minimum pods (63.4) per plant were observed in group-IV of *kabuli*-extra bold seeded types and maximum (77.5) in group-II of *desi*-bold seeded types. Thus it is pertinent to mention that significantly higher number of pods was observed in group-II in comparison to other group of cultivars. However, between group-I and group-III non-significant differences were observed for this trait. Therefore, high variations existed for number of pods per plant among various group of cultivars.

It is pertinent to mention that significant differences existed for both number of seeds per pod and 100-seed weight among various groups of cultivars. However, maximum number of seeds per pod (1.6) was recorded in group-I of *desi*-medium seeded types and minimum (1.24) in *kabuli*-extra bold seeded types which indicates negative correlation between seed size and seeds per pod. In group-II and III the number of seeds per pod was recorded at par. Interestingly, the same pattern like number of seeds per pod was also observed for 100-seed weight among all the groups of cultivars and minimum (16.32 g) and maximum (33.66 g) 100-seed weight was observed in group I and group IV respectively, while in group II and Group III it was at par. These observations for these two traits indicated that number of seeds per pod is directly and proportionately related with 100-seed weight, it means that more number of seeds per pod is responsible for small seed size and vice-versa. Thus the group of cultivars which is having maximum 100-seed weight will contain minimum number of seeds per pod. It suggested existence of excellent genetic variations or variability among various group of cultivars for this trait.

It is important to mention that significantly lowest (64.87 g) biological yield per plant was recorded in group-I of d*esi*-medium seeded types and maximum (81.10 g) in group-IV of *kabuli*-extra bold seeded types. Interestingly, in group-II and III no differences were observed and both groups yielded 76.70 and 76.67 g respectively.

It is well established that seed yield is the final product and many traits contribute to its performance. Therefore, its outcome directly or indirectly is dependent on the performance of other related traits. Fortunately, under present investigations significant variations existed between group of small seeded types and large seeded types. Thus, the minimum seed yield 18.72g was recorded in the *desi*-medium seeded group of cultivars and maximum 25.86 g in the group of *kabuli*-bold seeded types. Likewise, same pattern was also observed in case of grain yield q/ha. Significant differences were also observed for harvest index among various groups of cultivars. The minimum (29.02%) and maximum (33.42%) harvest index was recorded in group-I and III, respectively.

The above mentioned observations for various quantitative traits indicated highly significant and excellent genetic variations among different groups of cultivars, which indicated that these genetic variations are responsible for the expression of individual quantitative traits. Thus these variations are creating great impacts on the overall expressivity of different traits. Therefore, the existing genetic divergence in the experimental material can be a useful source for genetic improvement in chickpea.

Table 1: Analysis of variance (ANOVA) for eleven quantitative traits of 108 chickpea genotypes over the environments during 2004-06

Source of variance	d.f.	Mean square										
		Plant height (cm)	Number of branches/plant	Days to flowering	Days to maturity	Number of pods/plant	Number of seeds/pod	100-seed weight (g)	Biological yield/plant (g)	Seed yield /plant (g)	Harvest index (%)	Grain yield (q/ha)
Environment (E)	2	87079.00**	34035.37**	7327.75**	3337.00**	77309.75**	3.62**	773.90**	88905.75**	7130.78**	1281.50**	6457.26**
Replication (R)	2	93.37**	189.69**	18.50**	19.00	386.50**	0.27**	8.40**	623.00**	85.98**	5.34*	77.78**
E x R	4	11.00**	24.53**	5.75	24.50	22.88**	0.012**	0.34*	30.87**	3.42*	0.73	5.50**
Treatment (T)	107	181.78**	665.75**	1566.90**	798.16**	2286.28**	0.65**	446.16**	1547.60**	280.4**0	153.66**	90.64**
E x T	214	44.92**	310.59**	120.45**	77.94*	627.09**	0.10**	4.48**	355.84**	64.52**	45.50	14.89**
Error	642	1.65	2.98	2.57	23.82	5.40	0.01	0.10	3.61	0.47	0.45	0.46

* significant at 5% and ** significant at 1% level, respectively

Table 2: Mean Performance of quantitative traits of different groups of chickpea cultivars under varying planting environments during 2004-06.

Group	Plant height (cm)	Number of branches/plant	Days to flowering	Days to maturity	Number of pods/plant	Number of seeds/pod	100-seed weight (g)	Biological yield/plant (g)	Seed yield /plant (g)	Harvest index (%)	Grain yield (q/ha)
Group-I *desi*-medium seeded	53.66	45.00	75.06	150.40	75.77	1.60	16.32	64.87	18.72	29.02	15.26
Group-II *desi*-bold seeded	56.34	46.36	75.43	148.89	77.50	1.40	25.14	76.70	25.28	33.22	19.04
Group-III *kabuli*-bold seeded	57.08	44.27	68.59	144.15	76.81	1.39	25.64	76.67	25.86	33.42	18.48
Group-IV *kabuli*-extra bold seeded	59.33	37.79	79.03	153.48	63.40	1.24	33.66	81.10	25.22	31.41	18.19
Over all mean	56.60	43.35	74.52	149.23	73.37	1.41	25.19	74.83	23.77	31.77	17.74
SEm±	0.60	0.81	0.75	2.30	1.09	0.020	0.15	0.89	0.32	0.31	0.32
CD at 5%	1.20	1.62	1.50	4.60	2.18	0.04	0.30	1.78	0.64	0.62	0.64

Cluster Formation

On the basis of Z_1 and Z_2 values all the 108 diverse genotypes were classified in various clusters. Interestingly, major eight clusters were formed from these genotypes under normal planting environment (Table 3).

Distance between intra and inter cluster centroids

Understanding of genetic divergence within the cluster (intra-cluster) and between the various clusters (inter-cluster) indicates the divergence among the genotypes falling within particular cluster and genotypes of different clusters. The intra and inter cluster distances are presented in table 3.

The comparison of intra and inter cluster distances showed that minimum distance was among various genotypes falling in cluster-VIII, while maximum genetic distance was among genotypes falling in cluster-VI. On the other hand, low to moderate genetic distance ranging from 1.65 to 2.31 in cluster-I, II, III, IV, V and VII. Interestingly, the minimum (1.98) genetic distance was observed between cluster-VI and VIII and maximum inter cluster distance (11.66) between cluster-III and VIII. On the other hand the inter cluster distance between rest of the clusters ranged from 2.56 to 4.59.

Table 3: Distances between cluster centroids in 108 chickpea genotypes under normal planting environments during 2004-06.

Cluster	I	II	III	IV	V	VI	VII	VIII
I	2.267							
II	3.654	2.307						
III	14.164	13.262	2.230					
IV	5.164	2.905	11.298	2.003				
V	2.566	2.654	13.368	3.238	1.654			
VI	4.564	4.169	13.204	0.075	2.830	2.552		
VII	3.867	4.132	11.237	3.448	2.901	3.602	1.917	
VIII	4.596	4.108	11.658	2.696	2.560	1.985	2.593	0.000

Placement of genotypes into various clusters

On the basis of Z1 and Z2 values all the 108 diverse genotypes were placed into various clusters environment wise. The detailed categorization and placement of genotypes as per the planting environments and cluster formation are presented in table 4. It is interesting to mention that 8 clusters under normal planting and 9 clusters were formed in each medium and late planting environments. Interestingly, on the basis of seed yield performance under normal planting, four high yielding clusters were observed. Cluster-III contained only one solitary high yielding genotype (BGD-70), cluster-VI contained 9 high yielding genotypes out of 10 genotypes, cluster-VII contained 7 high yielding genotypes out of 9 and cluster-VIII contained 12 high yielding genotypes out of 18 genotypes. Thus, cluster-III, VI, VII and VIII possesses maximum high yielding genotypes. On the other hand, cluster I and II contained maximum low yielding genotypes, thus these 2 clusters were identified as low yielding clusters and cluster V contained maximum medium yielding genotypes which was identified as medium yielding cluster. Interestingly, cluster-IV contained 4 genotypes each of high, medium and low yielding genotypes under normal planting environment.

It is evident from the results in table 4 that placement of genotypes into various clusters was drastically changed from environment to environment. Interestingly, cluster VI had 9 genotypes of high yielding category in each normal and medium planting, and 7 under late planting. Thus these genotypes showed similar types of pattern under all the planting environments. This indicated that these high yielding genotypes are highly

flexible having adjustable phenology to different environments. This also indicated that they belong to medium duration maturity group which help in adoption to various environments leading to high yields due to early or medium-early maturity. In cluster-I and II, the high yielding genotypes are performing well either in normal or in late planting only indicating the specific adaptation of these genotypes for a specific environment. This can be happened due to early or late phenology of these genotypes. In cluster VIII there are maximum numbers of high yielding genotypes (12 and 14) in normal and late planting, respectively, whereas there were only 3 high yielding genotypes under medium planting. This clearly indicates that these genotypes have specific adaptation for different environments.

These results also indicated that the placement of various genotypes into different clusters was highly influenced by growing environments. The placement of high, medium and low yielding genotypes into separate clusters indicated that a group of genotypes which is having more or less similar nature constituted same clusters on the basis of their performance.

Thus, these observations suggested that individual quantitative trait in diverse group of genotypes is influenced by environmental factors greatly and affected their expressivity significantly due to changed climatic conditions. It also suggested that existing genetic variations in various groups of cultivars were developed during their developmental stages due to different gene pools. These gene pools are greatly influencing the expression of individual traits.

Discussion

Significant achievements in plant type and seed yield improvement of wheat, rice and maize are reported from different part of the world. However, such genetic enhancement in case of chickpea is still a myth. Though, intensive breeding efforts are being made by many national and international organizations, but real plant type improvement and increased seed yield still lag behind. The reasons for low productivity are poor adaptation, complexity of biotic and abiotic stresses, poor genetic variations and poor genetic enhancement in this crop. Therefore, it is essential to understand genetic variability at genotypic level as well as trait- specific variations available in this crop.Interestingly, highly significant differences were observed for all the quantitative traits under investigation. Thus, excellent genetic divergence is available in the experimental material which can be utilized for further population improvement.

It is interesting to mention that large genetic differences existed for various quantitative traits like plant height, number of branches, days to flowering duration, number of pods, seed size, biomass production and seed yield among all the various groups of cultivars. The significant variations existed in different traits like vegetative, reproductive, biomass, and seed traits etc among different groups of genotypes indicated the impact of genetic variability and gene pool on the expressivity of individual trait. Thus, these observations also indicated that various groups of cultivars belongs to different groups of plant type containing different gene pools.

In depth investigation of individual plant group also suggested existence of excellent divergence for individual vegetative traits, reproductive traits, seed traits and seed yield between these groups of cultivars. However, the lowest production of seed yield and biomass, the smallest seed size and poorest harvest index in group-I of *desi*-medium seeded types indicated poor expressivity and poor gene pool of this group. On the other hand, high seed yield, high harvest index, more number of pods and early in maturity in group-III of *kabuli*-bold seeded types indicated excellent adaptation and presence of desirable high yielding gene pool. It is important to mention that group-IV of *kabuli*-extra bold seeded types possess maximum plant height, days to maturity, seed size and biomass production and minimum production of number of branches per plant, number of pods per plant and number of seeds per pod , which indicated that this group of cultivars belong to different group of plant type. Thus these observations suggested that this plant group is quite different from other plant groups and contained a separate gene pool.

The above observations indicated that various plant groups under investigation belong to different plant types or category and individual traits expression or expressivity differ greatly due to presence of genetic variations among different plant groups. Thus, it is concluded that these plant groups contained divergent gene pools which are responsible for superior or inferior performance of individual quantitative trait. It is also concluded that genetic divergence between different plant groups is governed by separate gene pool.

The observations on various cluster formations under different environments; inter- and intra-cluster distances among experimental genotypes have also suggested that large array of genetic divergence existed between various clusters and genotypes. Formation of major clusters was more or less similar under different planting environment, however, placement of genotypes among clusters was differing due to genotypic variations (Fig. 1). Thus, these significant differences existed between clusters indicated existence of excellent genetic divergence among the genotypes and plant groups for various quantitative traits. This corroborate the

above hypothesis that various plant groups belong to separate plant type and containing different gene pools. It is evident from the placement of various genotypes within a cluster into high, medium and low yielding types that the genetic differences for various quantitative traits within a cluster and between the clusters existed greatly. The placement of various genotypes presented in table 4 into different categories is a clear cut indication of genetic variations or genetic divergence existed between various genotypes and clusters. Interestingly, there were clear cut demarcation between high yielding and poor yielding number of genotypes within a cluster and between the clusters. Such demarcations of high yielding and poor yielding clusters are an indication of divergent gene pools as well as clusters and such gene pool is responsible for the expression of individual trait.

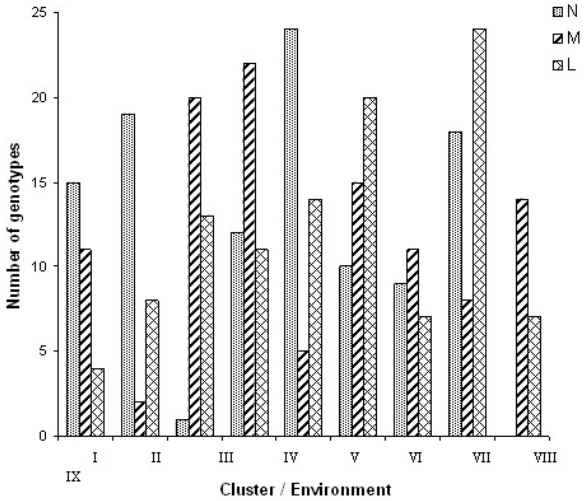

Fig.1: Formation of clusters and placement of Genotypes under different planting environments.

Table 4: Placement of high, medium and low yielding genotypes into various clusters under different planting environments during 2004-06.

Cluster	Number of Genotypes											
	Normal Planting				Medium Planting				Late Planting			
	Total	HY	MY	LY	Total	HY	MY	LY	Total	HY	MY	LY
I	15	2	3	10	11	5	3	3	4	Nil	1	3
II	19	Nil	10	9	2	2	Nil	Nil	8	6	2	Nil
III	1	1	Nil	Nil	20	5	4	11	13	2	6	5
IV	12	4	4	4	22	6	9	7	11	1	9	1
V	24	9	13	2	5	Nil	4	1	14	Nil	6	8
VI	10	9	1	Nil	15	9	4	2	20	7	12	1
VII	9	7	2	Nil	11	3	3	5	7	1	3	3
VIII	18	12	6	Nil	8	3	5	Nil	24	14	10	Nil
IX	--	--	--	--	14	5	5	4	7	2	2	3

HY = High Yielding; MY = Medium Yielding; LY = Low Yielding genotypes.

Conclusion

The observations on various quantitative traits between different plant groups showed highly significant genetic differences. On the basis of these observations it was concluded that excellent genetic variations / divergence existed between various plant groups. Thus it was suggested that due to these variations separate plant groups were developed during developmental stages which contained separate gene pools and these gene pools are responsible for the expressivity of quantity traits. It was further concluded that the formation of distinct clusters and placement of high yield and poor yielding genotypes within a cluster and between the clusters is directly a resultant of genetic variations existed in the experimental genotypes. Thus, it is suggested that the available genetic distance between various clusters of plant groups for individual traits can be utilizes for further population improvement in chickpea to achieve significant genetic gains.

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