Genetic divergence and stability (AMMI) study in chickpea (*Cicer aeritinum* L.) under north western Himalayas of Jammu and Kashmir, India

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ABSTRACT

Genetic diversity of seventeen chickpea genotypes was studied through Mahalanobis D^2 Tocher's Method. The genotypes under study fall into five clusters. The cluster- IInd contained the highest number of genotypes (08) and Cluster IV and V contained the lowest (01). Cluster- II produced the highest mean value for days to maturity. The inter-cluster distances were much higher than the intra-cluster distances. Cluster-V exhibited the highest intra-cluster distance while the lowest distance was observed in cluster-IV and V. The highest inter-cluster distance was observed between cluster-III and V while the lowest was between cluster-I and IV. Considering all the characters, it is suggested that the genotypes 81-0-800, C-306, 96907, C-235 and SCS-3 could be used as parents for future breeding programmes to develop high yielding varieties of chickpea. As per AMMI model, two genotypes i.e. C-81 and 96911 were identified as having wider adaptability along with higher seed yield per plant.

Key words: Chickpea, D^2 statistics, Genetic divergence, Intra and inter-cluster distance.

INTRODUCTION

Chickpea is an important self-pollinated grain legume crop, grown mainly in West Asia, North Africa and the Indian subcontinent, where it is a basic component of the human diet. Vavilov (1926) was the first to identify areas with similar physiographic characteristics with maximum variability for the major cultivated species. Chickpea is a highly valued commodity and an important source of proteins for human consumption in several developing countries; it is classified among the high-protein seeds with a mean protein content of 22 %. Chickpea (*Cicer arietinum* L.) belongs to the family Fabaceae. On the basis of cultivated area, chickpea ranks 19th among the crops and is grown in 34 countries of the world. Area under pulses in India, Pakistan, Nepal and Bangladesh covers about 90% of the world acreage (Saxena, 2001). Chickpea is the second most important pulse crop in the world after dry bean. It is an important source of human and animal food. It also helps to improve soil fertility particularly in dry lands. Introduction of chickpea in a cereal based rotation, which is used particularly in developing countries, can break the disease and pest cycle and increase the productivity of the entire rotation (Jodha and Subba Rao, 1987). The total protein supply in our expanding population is decreasing day by day. A part of this problem can be solved by increasing the per hectare production and utilization of chickpea. The soil and climatic conditions of Poonch are suitable for growing chickpea in winter (rabi) season, as majority of the area remains uncultivated during rabi season due to extreme cold and snow falling between December to February. Hence, the study was undertaken to identify the more diverse parents for the development of varieties which shall be more suitable under such conditions and have wider adaptability.

MATERIALS AND METHODS

The experiment was conducted at the experimental field of Krishi Vigyan Kendra, Poonch of Sher-e Kashmir University of Agricultural Sciences & Technology Jammu, India during the *rabi* 2008-09 and 2009-10. The genetically pure and physically healthy seeds of seventeen genotypes were collected from Department of Crop Improvement of Choudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur. The experiment was laid out in a randomized block design with three replications. The seeds were sown in a row to row distance of 40 cm. Seeds were placed at 2-3 cm depth in each row keeping 15 cm distance between two hills. Two seeds were sown in each hill. The excess plants were thinned out keeping one plant in each hill at 15 days after sowing (DAS). The recommended agronomic practices were followed to get a good healthy crop. The data were recorded on 10 randomly selected plants for ten traits namely plant height, days to 50% flowering, days to maturity, number of pods/plant, number of seeds/pod, number of primary branches/plant, number of secondary branches/plant, seed yield/plant, 100 seed weight and pod length. Pooled data were subjected to statistical analysis. Number of days to flowering was recorded at the time when

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at least 50% plants showed the appearance of first flower. Days to maturity were calculated from the date of planting when 90% plants turned brown and ready for harvest. At maturity, ten plants were selected per plot at random to record data on plant height, primary branches per plant, secondary branches per plant, pods per plant, 100-seed weight and seed yield per plant.

Genetic diversity was estimated by D^2 analysis originally proposed and outlined by Mahalanobis (1928 and 1936) and extended by Rao (1952) and Tocher Method. Mean data of the characters were subjected to Multivariate analysis using Indostat 9.2 and Microsoft Excel 2000 software through four techniques *viz*. Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA). Mean and coefficient of variance (CV) were also estimated using Windo Stat 9.2.

RESULTS AND DISCUSSION

Significant differences were observed among seventeen genotypes of chickpea for all characters under study. Higher genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for number of pods per plant, 100 seed weight and seed yield/plant respectively, indicating that these traits could be used as selection indices for yield improvement (Table 1). Pod length, number of pods per plant and 100 seed weight exhibited high values of GCV and PCV. Maximum variation was found in number of pods/plant followed by number of secondary branches/plant, number of primary branches/plant and plant height. Other characters also showed considerable variability. Similar results were reported by Syed *et al.* (2012).

Based on the cluster analysis, seventeen genotypes of chickpea were grouped into five clusters (Table 2 and Fig. 1). Cluster IInd was the largest and consisted of eight genotypes followed by cluster-I which had four genotype.
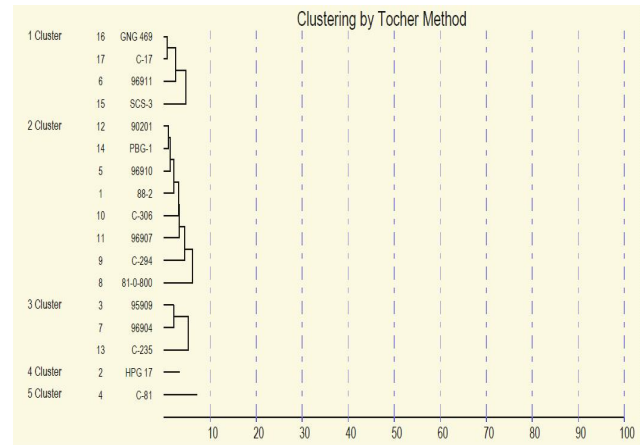

Fig 1: Variance dendogram of chickpea genotypes by clustering (Tocher Method)

The cluster-IV and cluster-V were unique having only one genotypes each. Cluster-III was having only three genotypes. It was observed from the distribution pattern that the geographic divergence did not follow the same trend as the varieties / genotypes within the same cluster as they originated from different countries. The clustering pattern of the genotypes under study did not necessarily follow their geographical distribution. However, those were distributed at random. The geographical distribution was in agreement with Devi *et al.* (2004) who reported that the pattern of clustering had no general association between ecological distribution of genotypes and genetic divergence. This might be due to differential adoption, selection criteria, selection pressure and environment. Murty and Arunanchalam (1996) reported that genetic drift and selection in different environments could cause greater diversity than the geographic distance.

Inter and Intra-cluster distances are presented in the Table 3, which revealed that the inter-cluster distances

Table 1: Estimates of traits for genetic variability

Components/Traits	PH	NPB	NSB	P/Pl	S/P	DFL	100SW	SY	DTM	PL
GCV	10.78	10.20	12.34	31.86	14.07	2.23	29.75	37.20	4.42	21.47
PCV	18.32	22.46	28.77	57.18	19.18	3.69	32.78	39.16	4.81	21.67
h²% (B S)	35.00	21.00	18.00	31.00	54.00	37.00	82.00	90.00	84.00	98.00
G A 5%	7.13	0.15	0.45	33.50	0.41	3.97	9.90	24.91	16.13	0.90
G A 1%	9.13	0.20	0.58	42.93	0.53	5.09	12.69	31.92	20.67	1.15
CV	14.81	20.00	25.99	47.48	13.03	2.94	13.75	12.20	1.89	2.91
General Mean	54.59	1.61	4.17	91.59	1.94	142.90	17.80	34.21	192.52	2.05
Exp Mean next Gen.	61.71	1.76	4.62	125.08	2.35	146.87	27.70	59.11	208.65	2.95

Table 2: Distribution of seventeen genotypes of chickpea in five clusters

Clusters	No of genotypes	Name of genotypes
Cluster-I	04	GNG469, C-17, 96911, SCS-3
Cluster-II	08	90201, PBG1, 96910, 88-2, C-306, 96907, C-294, 81-0-800
Cluster-III	03	95909, 96904, C-235
Cluster-IV	01	HPG-17
Cluster-V	01	C-81

in all cases were larger than intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups. The highest inter-cluster distance was observed between clusters III and V (55.46), followed by I and V (43.77), II and V (38.05) and IV and V (37.93) which indicated that the genotypes grouped in these clusters were highly divergent from each other. Similar findings were reported by Lal *et al*. (2001). Choosing parents belonging to the maximum divergent clusters are expected to manifest maximum heterosis in crossing and wide variability in genetic architecture (Chowdhury *et al*. 2002). The least genetic distance at inter-cluster level was observed between clusters I and IV (19.97) followed by I and III (24.09), II and III (30.23) and IV and V (37.94) which indicated that the genotypes of these clusters were genetically close, suggesting that the genotypes in these clusters may be used as parents in hybridization programme to obtain desirable recombinants. The inter-cluster distance criterion is used for selection of varieties as parents for hybridization using D^2 analysis. Intra-cluster distances were estimated using inter-genotypic distance, as quoted of Singh and Choudhary (1985). The maximum inter-cluster distance was observed between cluster III and V (55.47) followed by that between III and IV (47.20), II and IV (44.16) and I and V (43.77) indicating wide divergence among the clusters. This also suggests that genetic architecture of the varieties in one cluster differs entirely from those included in the other cluster.

The clustering pattern of D^2 analysis followed the similar trend of distribution of genotypes in PCA (Fig. 2). The D^2 and PCA were found to be alternative methods in yielding information regarding the clustering pattern. Moreover, the PCA provided information on contribution of the characters towards divergence.

Cluster means were found highest for different characters (Table 4) *viz*., Cluster-V showed highest mean performance for days to maturity (192.51) followed by days to 50% flowering (142.89) and number of pods per plant and same is the trend with other clusters.

It is evident from the Table 5 that the pod length (48.53%) contributed maximum for genetic diversity followed by seed yield/plant (30.15), days to 50% flowering (11.76) and seeds/pod (5.88). Therefore, these characters contributed maximum for getting the diversity.

AMMI 2 Biplot: The IPCA 1 versus IPCA 2 (i.e. AMMI 2 biplot) Figure 2 explains the magnitude of interaction of each genotype and environment. The genotypes and environments that are farthest from the origin being more responsive fit the worst. Genotypes and environments that fall into the same sector interact positively; negatively if they fall into the opposite sectors (Osiru *et al.* 2009). Genotype showing high positive interactions in an environment obviously has the ability to exploit the agro-ecological or agro-management conditions of the specific environment and are therefore best suited to the environment. AMMI analyses permits estimation of interaction effect of a genotype in each environment and
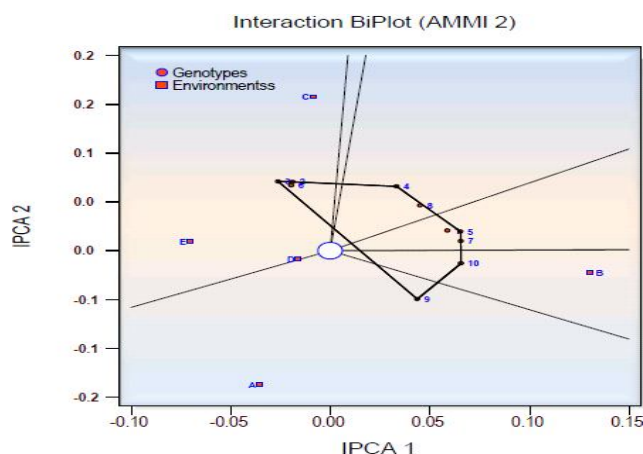

Fig 2: Biplot of the IPCA-1 axis versus the IPCA-2 for Chickpea genotypes

Table 3: Average Inter and Intra-cluster-distance (Tocher Method)

Clusters	Cluster-1	Cluster-II	Cluster-III	Cluster-IV	Cluster-V
Cluster-I	11.98	42.81	24.09	19.96	43.77
Cluster-II	-	12.31	30.22	44.15	38.05
Cluster-III	-	-	15.89	47.20	55.46
Cluster-IV	-	-	-	0.00	37.93
Cluster-V	-	-	-	-	0.00

Table 4: Cluster mean for 10 characters of seventeen genotypes of chickpea

Traits/Clusters	PH	NPB	NSB	P/PL	S/Pl	DFL	100SW	SY	DTM	PL
Cluster-I	55.17	1.58	4.05	96.29	1.80	142.08	13.88	26.36	188.49	1.64
Cluster-II	55.22	1.47	3.71	94.38	2.12	140.74	26.82	53.22	196.27	2.08
Cluster-III	52.71	1.94	4.70	75.69	2.31	149.22	18.10	54.43	185.75	1.62
Cluster-IV	49.52	1.58	4.41	85.49	2.01	144.59	16.62	24.94	189.72	2.36
Cluster-V	60.15	1.67	4.23	83.17	1.92	141.86	22.36	45.43	205.39	2.70
Mean	54.58	1.60	4.16	90.00	1.94	142.89	17.79	34.20	192.51	2.05

Table 5: Per cent contribution of different characters to genetic diversity

Source	Times Ranked 1st	Contribution
Plant height cm	0	0.00
NPB	0	0.00
NSB	0	0.00
P/Pl	0	0.00
S/Pod	8	5.88
DFL	16	11.76
100 Seed Weight	4	2.94
Seed Yield	41	30.15
Days To Maturity	1	0.74
Pod length cm	66	48.53

NPB- No. of primary branches/plant, NSB- No. of secondary branches/plant, P/Pl- No. of pods/plant, S/Pod- No. of seeds /pod and DFL- days to 50% flowering

Table 6: Latent vectors for 10 principal component characters of 17 genotypes of chickpea

	Vector 1	Vector 2	Vector 3
Eigene Value (Root)	3.15	2.07	1.37
% Var. Exp.	31.53	20.72	13.76
Cum. Var. Exp.	31.53	52.26	66.02
Plant height (cm)	0.05	0.53	0.22
Number of Primary branches	0.03	-0.10	-0.19
Number of secondary branches	-0.13	-0.34	-0.53
Pods /Plant	0.44	0.21	0.19
Seeds/Pod	-0.49	-0.09	0.30
Days to 50% flowering	-0.51	-0.13	0.21
100 Seed Weight	-0.27	0.48	-0.32
Seed Yield	-0.27	0.48	-0.07
Days To Maturity	0.25	0.09	-0.41
Pod length	-0.23	0.18	-0.41

it helps to identify genotypes best suited for specific environmental conditions. From figure 2, it is evident that the genotypes C-81, HPG-17 and 96911 are the most stable because they are closer to the origin as compared to 96910 and 96904 which fall farther away from origin. Contribution of the characters towards divergence is presented in Table 6. The Canonical variate analysis revealed that in the both vectors (Vector I and Vector II) plant height (0.05 and 0.54), pods per plant (0.44 and 0.21) and days to maturity (0.25 and 0.09) were positive. Such results indicated that these characters contributed maximum towards divergence of the genotypes. In vector II, 100 seed weight, seed yield and pod length played significant roles. The greater divergence in the present material due to those characters will offer a good scope for improvement of yield through rational selection of parents for producing heterotic genotypes. Similar results were reported by Fentie *et al.* (2013). From Table 6, it can

be concluded that these genotypes HPG 17, C-81, SCS-3 and 96911 having low vector 1 and vector 2 values have high seed yield per plant. Hence, these genotypes would be stable in performance with no effect of environment along with higher yield.

From the present study, it was concluded that the genotypes included in the diverse clusters namely, III and V and II and IV hold good promise as parents for obtaining potential hybrids and thereby creating greater variability of these characters to improve the yield. Considering all the characters, it was suggested that the genotypes 81-0-800, C-306, 96907, C-235 and SCS-3 could be used as parents for future breeding programs to develop high yielding varieties of chickpea. As per AMMI model, two genotypes i.e. HPG17, C-81 and 96911 were identified as having general adaptability along with good seed yield per plant.

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