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Short Communication

Diversity analysis of advanced chickpea (*Cicer arietinum* L.) derivatives

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Abstract

Genetic diversity analysis of 130 advanced interspecific chickpea derivatives derived from four wide crosses (Cross I: PUSA 372 X ILWC 229, Cross II: PBG 5 X ILWC 229, Cross III: PBG 5 X ILWC 246 and Cross IV: BGD 72 X ILWC 246) was estimated at CSK HPKV, Research Sub-Station, Berthin, Bilaspur during *rabi* 2019-20. On the basis of Mahalanobis D^2-statistics these interspecific derivatives along with 4 checks were grouped into 8 main clusters. Cluster I was the largest cluster among all having forty six derivatives. Maximum inter-cluster distance was observed between cluster IV and cluster VI and maximum intra cluster distance was showed by cluster IV. Therefore, a hybridization programme involving lines from cluster IV and cluster VI can be devised to yield desirable transgressive segregants. The principal component analysis, revealed that 75.27 per cent of total variation has been contributed by the first three principal components i.e., PC1 explained 45.15 per cent, PC2 explained 17.57 per cent and PC3 explained 12.55 per cent of total variation. The positive correlation between days to 50 per cent flowering, days to 75 per cent maturity, inter-node length and branches per plant as revealed by two-dimensional ordination bi-plot can be utilized effectively for the indirect selection of lines with early maturity and high yield.

Key words: Chickpea, Divergence, Principal component analysis, Variability.

Chickpea is a self-pollinated pulse crop belongs to the family Fabaceae. It is an important source of dietary protein in the developing world. Being a leguminous crop chickpea plays an important role in the improvement of soil fertility as roots of chickpea bear nodules in which symbiotic bacteria convert atmospheric nitrogen to plant-available forms, which subsequently increases crop yields. Genetic diversity among the parents or genotypes in hybridization programme is a pre requisite to obtain maximum number of segregants from which a breeder can select the desirable ones (Dwivedi and Gaibriyal, 2009). The distinct cluster formation and placement of high yielding and low yielding genotypes into various clusters suggested that genetic diversity played significant role in the genetic expression of individual genotypes and traits (Verma *et al*., 2008). So, studies on genetic diversity help in selecting diverse parents for hybridization programme. Principal component analysis was invented by Karl Pearson in 1901. It is also known as discrete Karhunen-Love transform (KLT) or proper orthogonal decomposition (POD). It is a true eigenvector-based multivariate analysis. PCA transforms a number of possibly correlated variables into smaller number of uncorrelated variables called principle components. Components whose eigen values are greater than 1 are considered as major principal components, because these components provide high magnitude of variance in population whereas, the components whose eigen values are less than 1, referred as minor components only shows very small or negligible variance.

Grouping of advanced interspecific chickpea derivatives can make the opportunity to the breeder to select appropriate lines for further crossing programme in cultivated chickpea. Cluster analysis

and principal component analysis are used together to understand the behavior of data. Principal component and cluster analysis procedures together are used to assess genetic diversity in the population and the variability within. This information can be utilized not only to predict the advancement that can be achieved through selection but also to decide the parents for a hybridization programme if the existing variability is not sufficient. PCA and cluster analysis are different from each other. PCA groups variables whereas cluster analysis groups observations rather than variables. PCA reduces large data series into smaller number of components be focusing on groups having very strong inter-correlation in a set of variables. Keeping this in mind the present study was conducted to study the genetic divergence and variability through D^2 and principal component analysis, respectively in 130 chickpea interspecific derivatives.

The present investigation was carried out at CSK HPKV, Research Sub Station, Berthin, Bilaspur, Himachal Pradesh during *rabi* 2019-20. The experimental site was located at an elevation of about 625 m above mean sea level, representing the sub-mountain, low hill, sub-tropical zone of the State. The F_6 derivatives of *Cicer arietinum* with *Cicer reticulatum* (ILWC 229) and *Cicer echinospermum* (ILWC 246) were evaluated along with 4 checks i.e., Him Palam Chana 1 (DKG 986), Himachal Chana 1 (HC 1), GPF 2 and Himachal Chana 2 (HC 2). A set of 130 lines of four crosses i.e. Cross I (PUSA 372 X ILWC 229 = R-1 to R-50), Cross II (PB 5 X ILWC 229 = R-1 to R-46), Cross III (PB 5 X ILWC 246 = R-1 to R-08) and Cross IV (BGD 72 X ILWC 246 = R-1 to R-26) were evaluated in augmented block design (Federer, 1955). In each block 10 lines with 4 checks were sown in a line of 3 m with spacing of 30 cm x 10 cm from row to row and plant to plant, respectively. Standard agronomic management practices for the area were followed throughout the experiment. Phenotypic data on different traits *viz*., days to 50 per cent flowering, days to 75 per cent maturity, plant height (cm), branches per plant, inter-node length (cm), biological yield per plant (g), number of pods per plant, number of seeds per pod, 100-seed weight (g), harvest index (%) and seed yield per plant (g) were collected during the growth period and at maturity. All the chickpea derivatives were clustered into different groups following Tocher's method (Rao, 1952), the intra and inter cluster distance were also computed (R Softwares and Python).

Study of genetic diversity is the process by which variation among individuals or groups of individuals or populations is analyzed. Data often involves numerical measurements and, in many cases, combinations of different types of variables. Phylogenetic relationships based on morphophysiological data provide a way of making a relatively rapid assessment of the diversity. Principal component analysis reflects the importance of the largest contributor to the total variation of the each axis of differentiation (Sharma *et al*., 1998).

Cluster analysis: In the present investigation for cluster analysis, the genetic divergence between populations was estimated using Mahalanobis's D^2-Statistic (1936). Mahalanobis D^2-Statistics grouped 130 chickpea interspecific derivatives and four checks into eight main clusters (Table 1 & Fig. 1), Cluster I was the largest comprising of forty six derivatives followed by cluster III and IV (17 derivatives), cluster II (16 derivatives), cluster VI (13 derivatives) and cluster V (11 derivatives).

The average cluster mean values for different traits showed (Table 2) that among eight clusters, cluster IV showed the maximum cluster mean values for maximum number of traits, i.e. pods per plant, seeds per pod, 100-seed weight, seed yield per plant and biological yield per plant, thus lines falling in cluster IV would be selected directly on the basis of these traits and could be used in hybridization programme.

Maximum inter cluster distance (Table 3) was observed between cluster VI and IV (55.15) followed by cluster VII and VI (50.97) and cluster VII and III (50.70). Minimum cluster distance was observed between cluster VI and V (30.32) and cluster II and I (30.92). Intra cluster distance ranged from 18.17 to 30.87. Maximum intra cluster distance was observed for cluster IV (30.87) followed by cluster VI (24.25), cluster VII (22.16), cluster III (21.95) and cluster I (21.17). It has been well established that more the genetically diverse parents used in hybridization programme, greater will be the chances of obtaining high heterotic hybrids and transgressive segregants. Similar types of cluster pattern were also observed by

Kashyap and Rastogi (2003), Syed *et al*. (2012), Singh *et al*. (2012) and Nimbalkar *et al*. (2017).

Principal component analysis

The number of principal components was eleven (Table 4). The first three principle components showed eigen values more than 1 and exhibited 75.27 per cent of the total variation therefore, only these components were considered for further study (Table 5). The PC1 explained 45.15 per cent of total variation and had positive contribution with days to 50 per cent flowering, days to 75 per cent maturity and inter-node length. The PC 2 explained 17.57 per cent of total variance and ten traits had positive contribution except biological yield per plant. Major contributors in variation were days to 50 per cent flowering, days to 75 per cent maturity and branches per plant. The PC 3 explained 12.55 per cent of total variance and had positive contribution with plant height and branches per plant. Similar type of findings were also reported by different workers such as Toker and Cagirgan (2004), Farshadfar and Farshadfar (2008), Ghorbani *et al*. (2013), Malik *et al*. (2014) and Sharifi *et al*. (2018) while studied PCA in chickpea genotypes and concluded that first three principal components were most important. Alipoor Yamchi *et al*. (2013) and Talebi and Rokhzadi (2013) reported that first four principal components contributed 81.65 per cent and

Table 1. Grouping of 130 chickpea interspecific derivatives along with four checks based on Mahalanobis D^2 statistic

Cluster number	Number of lines in cluster	Lines
Cluster I	46	**Cross 1-** R -17, 12, 49, 16, 4, 26, 11, 19, 38, 22, 3, 29, 40, 41, 18, 13, 14, 5, 15, 24, 8, 27, 2, 42, 50, 28
		Cross 2 – R- 1, 3, 9, 2, 11, 27, 28, 34, 49, 53
		Cross 3 – R- 2, 7, 1, 4, 5
		Cross 4 – R- 4, 3, 2, 13, 5
Cluster II	16	**Cross 1** - R- 47, 30, 45, 32, 48, 44, 35, 34, 33, 21, 39, 37
		Cross 2 - R- 44, 46, 48
		Cross 3 – R- 6
Cluster III	17	**Cross 1 –** R- 9, 1, 10
		Cross 2 – R- 42, 37, 45, 20, 21, 15, 10, 8
		Cross 4 – R- 8, 16 DKG 986, HC 2, GPF 2, HC 1
Cluster IV	17	**Cross 1 –** R- 23, 7, 6, 46, 36
		Cross 2 – R- 6, 7, 16, 19, 29, 31, 32, 35, 43
		Cross 4 – R- 7, 9, 17
Cluster V	11	**Cross 2 –** R-14, 17, 18
		Cross 4 – R- 22, 19, 21, 14, 12, 25, 20, 18
Cluster VI	13	**Cross 1 –** R- 43, 25, 31
		Cross 2 – R- 33, 36, 38, 13, 51, 52
		Cross 3 – R- 8
		Cross 4 – R- 1, 15, 6
Cluster VII	4	**Cross 2 –** R- 4
		Cross 4 – R – 11, 23, 24
Cluster VIII	10	**Cross 1 –** R- 20
		Cross 2 – R- 22, 23, 12, 39, 30, 5
		Cross 3 – R-3
		Cross 4 – R- 26, 10

Table 2. Cluster mean values for different traits of chickpea derivatives

Cluster	Days to 50 per cent flowering	Days to 75 per cent maturity	Plant height (cm)	Branches per plant	Inter-node length (cm)	Pods per plant	Seeds per pod	100-seed weight (g)	Seed yield per plant (g)	Biological yield per plant (g)	Harvest index (%)
Cluster I	99.56*	154.27*	35.45*	2.90*	3.60	32.63	1.65	18.92	14.19	36.66	38.51
Cluster II	101.71	155.74	44.06	2.97	3.76	28.84	1.53*	15.58*	11.37*	32.48	34.72*
Cluster III	100.91	155.12	61.82**	3.12	3.52	31.05	1.59	15.87	11.53	32.74	35.57
Cluster IV	103.44	157.49	59.16	3.17	3.42*	46.73**	1.98**	26.92**	21.28**	48.62**	42.79
Cluster V	108.85	160.44	45.35	2.97	3.81	37.59	1.75	19.50	14.74	36.74	40.04
Cluster VI	114.59**	166.55**	40.04	2.93	3.88**	28.54*	1.54	15.47	11.42	32.20*	35.33
Cluster VII	99.98	154.65	41.17	2.91	3.83	44.89	1.98	25.06	20.05	46.28	43.16**
Cluster VIII	112.72	164.79	56.58	3.22**	3.87	33.36	1.64	17.39	12.59	34.18	36.69

Table 3. Average intra (diagonal) and inter cluster distance among chickpea 130 advanced derivatives

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	21.17	30.92	43.20	50.50	32.59	34.47	42.38	42.64
Cluster II		18.17	35.61	49.83	31.39	38.67	47.23	35.86
Cluster III			21.95	46.82	38.80	47.78	50.70	32.94
Cluster IV				30.87	43.54	55.15	36.16	47.69
Cluster V					22.08	30.32	39.19	32.36
Cluster VI						24.25	50.97	35.87
Cluster VII							22.16	49.10
Cluster VIII								20.48

Table 4. Eigen values, variance (%) and cumulative variance (%) of Principal Components

Principle Component	Eigen Values	Per cent of Variance	Cumulative Variance Per cent
PC 1	4.966	45.15	45.15
PC 2	1.932	17.57	62.72
PC 3	1.380	12.55	75.27
PC 4	0.917	8.34	83.61
PC 5	0.699	6.35	89.97
PC 6	0.619	5.62	95.60
PC 7	0.246	2.24	97.84
PC 8	0.148	1.34	99.19
PC 9	0.060	0.54	99.74
PC 10	0.024	0.22	99.96
PC 11	0.003	0.03	100.00

Table 5. Loading values of first three principal components for different traits

Parameters	PC 1	PC 2	PC 3
Days to 50 per cent flowering	0.045	0.631	-0.253
Days to 75 per cent maturity	0.100	0.625	-0.230
Plant height	-0.020	0.250	0.636
Branches per plant	-0.008	0.359	0.470
Inter-node length	0.045	0.036	-0.496
Pods per plant	**-0.413**	0.079	-0.011
Seeds per pod	**-0.305**	0.088	0.000
100-seed weight	**-0.435**	0.028	-0.032
Seed yield per plant	**-0.441**	0.001	-0.032
Biological yield per plant	**-0.430**	-0.020	-0.002
Harvest index	**-0.393**	0.053	-0.099

Fig. 1: Mahalanobis D^2-cluster dendogram

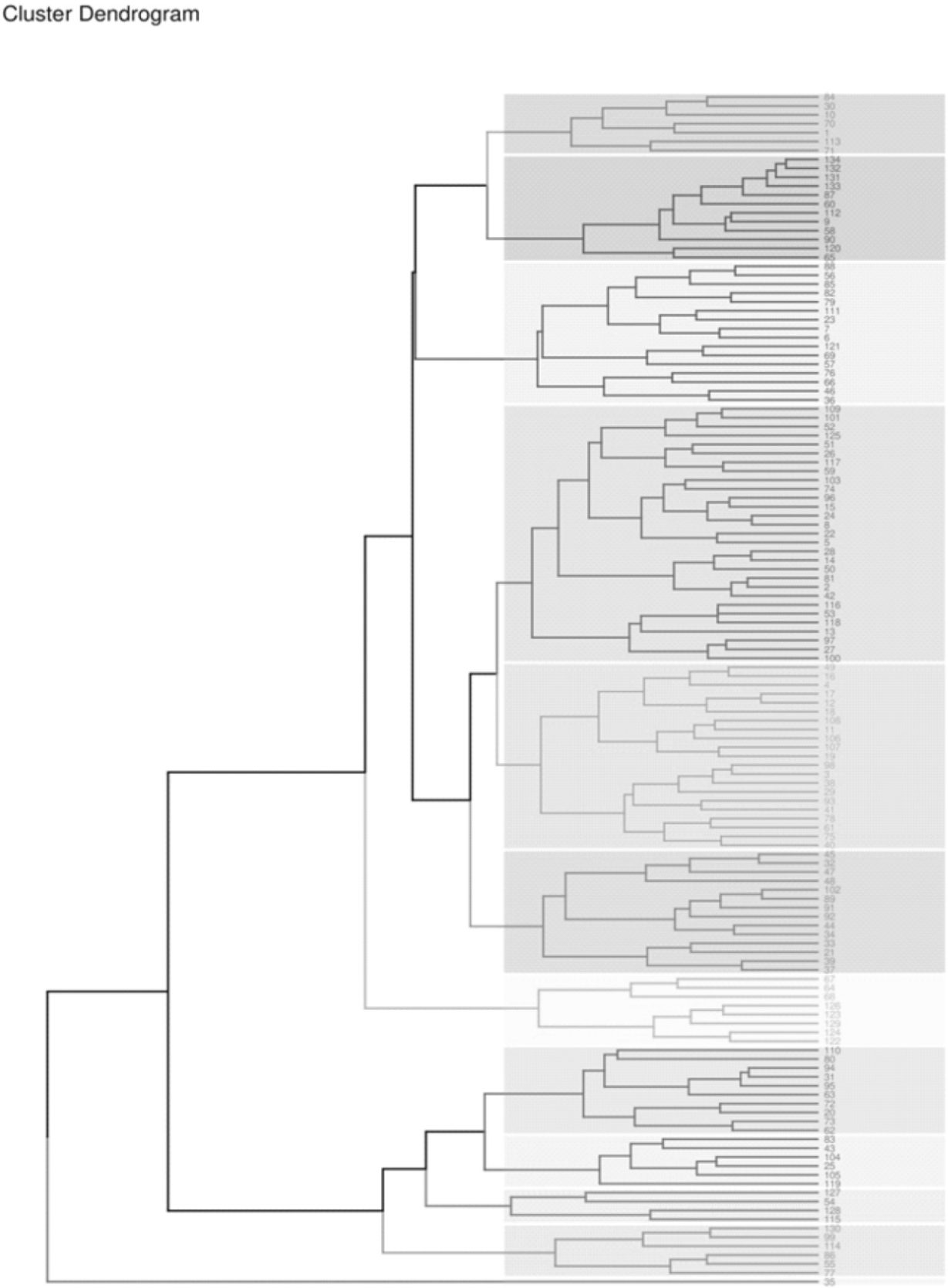
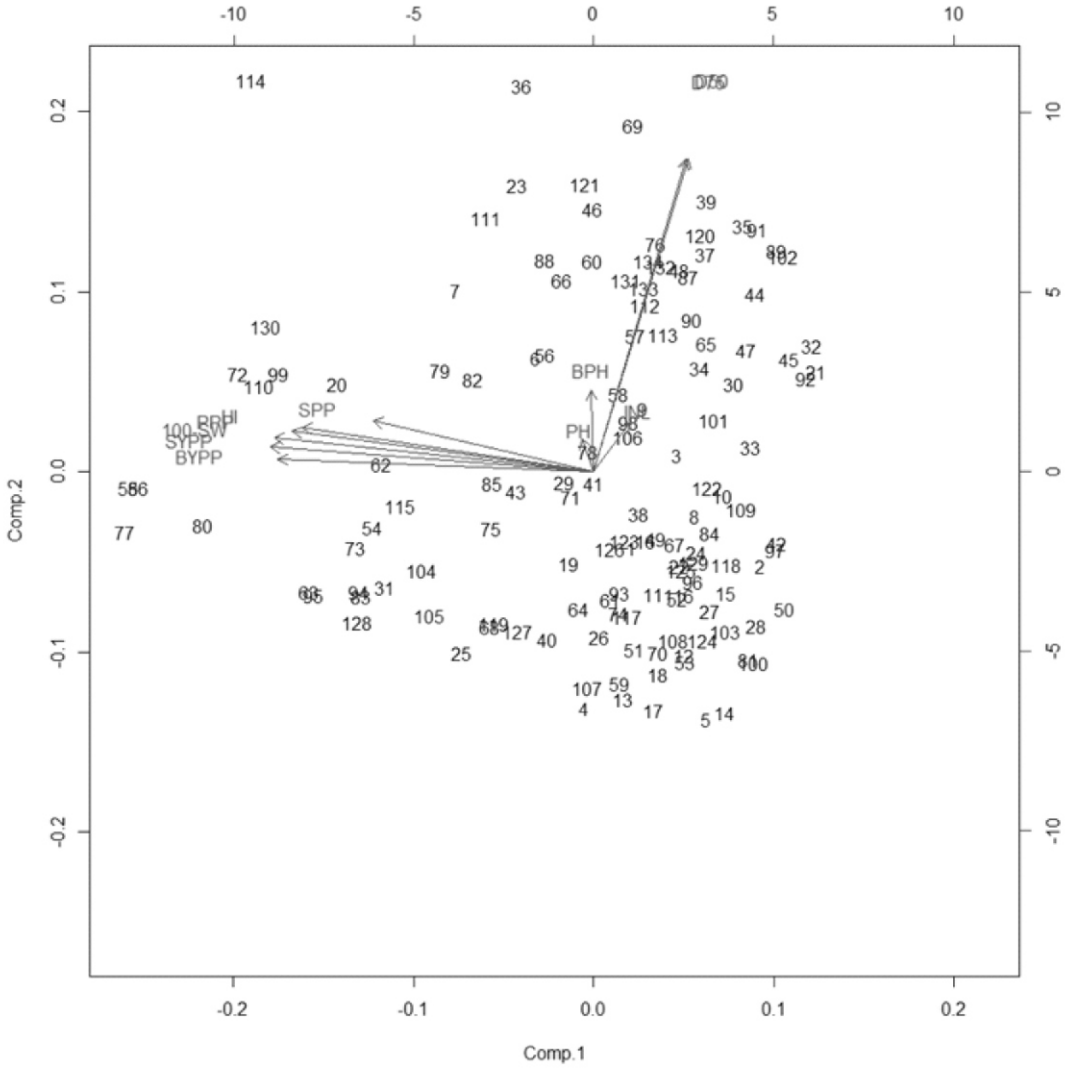


Fig. 2. Bi-plot of different variables and genotypes on PC1 and PC2



79 per cent of total variance, respectively while studied PCA in chickpea genotypes.

PCA bi-plot (Fig. 2) based on first two principal components showed genetic differences among chickpea lines by the pattern of scattering. The dispersion of lines in all sections of bi-plot revealed that there is a presence of fair amount of genetic diversity. The lines which are closer to each other had little or no differences with respect to traits under study. Genotypes which were far from the origin had more variability for quantitative traits and could be used as diverse parents in widening the genetic base of chickpea through hybridization. Two-dimensional ordination bi-plot revealed positive correlation between days to 50 per cent flowering, days to 75 per cent maturity, inter-node length and branches per plant. Sharifi *et al*. (2018) revealed that in bi-plot, if the angle between vectors is < 90° than the two traits are positively correlated, if the angle is > 90° means two traits are negatively correlated and if angle is equal to 90° means they are independent.

Promising lines for specific traits were identified from 130 advanced chickpea interspecific derivatives. It was also concluded that chickpea derivatives showed considerable genetic diversity for majority of the traits under study. The clustering of lines could help the chickpea breeders to identify and select desired diverse genotypes. The diverse chickpea genotypes with economically important traits will be evaluated at multi location trials and other desired

lines could be used in future hybridization programme.

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