



Exploration of Genetic Divergence and Performance of Morpho-Agronomic Traits of Chickpea

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Abstract: Genetic diversity for morpho-agronomic traits among various strains of desi chickpea (*Cicer arietinum* L.) under moisture stress conditions was assessed at Gram Breeding Research Station, Kallurkot, Pakistan. D² statistics, principal component analysis (PCA) and cluster analysis were employed for the purpose. Mean performance of attributes showed wide dispersion of data for range, coefficient of variation and standard deviation indicating presence of sufficient amount of genetic variation. Principal component analysis revealed six PCs, out of which, first two PCs expressed more than one Eigen value and explained 77.67% of total genetic variability. PCA revealed that maximum variation was contributed by 100 seed weight (28%), followed by grain yield (25%) and plant height (17%). Cluster analysis distinguished the strains in five clusters on the basis of similarity. Dendrogram was constructed, using Euclidean distance. Maximum Euclidean distance was observed in cluster-V in performance of morpho-agronomic traits. Relatively higher values for plant height, 100 seed weight and grain yield were observed in members of cluster-V, followed by cluster-I, indicating that the members of clusters-V and cluster-I possess the best constitution of morpho-agronomic traits exhibiting major contribution in genetic diversity. The study suggested that the members of these clusters have sufficient genetic diversity and they may be included in future chickpea breeding program.

Key words: Genetic divergence, Cluster analysis, Principal component analysis, Chickpea.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is the most important food legume crop widely grown in almost all the continents of world and helps in provision of nutritious food for expanding global population (Millan *et al.*, 2015; Muehlbauer and Sarkar, 2017; Rachwa-Rosiak *et al.*, 2015). Pakistan ranks 2nd among world's leading chickpea growing countries in terms of area under crop and 3rd in production (FAOSTAT, 2015). In Pakistan, chickpea is grown on 1.094 million hectares, for which Punjab contributes 80% and leads in acreage and production of crop (GOP, 2016). In Punjab, it is mostly grown on marginal land and sand dunes of Thal in rain fed conditions. Thal region consists of districts Bhakkar, Layyah, Chakwal, Khushab, Mian Wali, Faisalabad, and Jhang (Fig. 1) and solely contributes 90% of overall Punjab production (Khan *et al.*, 2017). In Pakistan, most of the area under crop is arid or semi-

arid, therefore, evolution and release of chickpea varieties with limited moisture requirements and capable of better performance under moisture stress conditions will serve as driving force for uplifting the production of this region.

Exploration of genetic diversity in parental material is important for a successful breeding program (Annicchiarico *et al.*, 2018; Boukar *et al.*, 2018; Upadhyaya *et al.*, 2007). The study of genetic diversity provides appropriate basis for classification of genetic material and information on genetic diversity in parental material assists the breeders to identify and select the most suitable types from a mixed population (Ghafoor *et al.*, 2003; Sharifi *et al.*, 2018; Agrawal *et al.*, 2018). Genetic diversity serves as the most basic source for production of new and valuable combinations and measurement of extent of such variability and its sources is thus of prime importance in breeding programs (Mahmood *et al.*, 2016).

Principal component analysis and cluster analysis have been found most appropriate series methods to study the genetic diversity of a large scale data of genotypes by grouping and identifying the pattern and extent of diversity (Sharifi *et al.*, 2018). Principal component analysis and cluster analysis have already been used for assessment of genetic variability of

agronomic traits by many researchers (Patil *et al.*, 2003; Bisht *et al.*, 2005; Farshadfar and Farshadfar, 2008; Johnson *et al.*, 2015). D^2 statistics, proposed by Mahalanobis (1928 and 1936), has been utilized extensively by researchers and for measurement of genetic diversity.

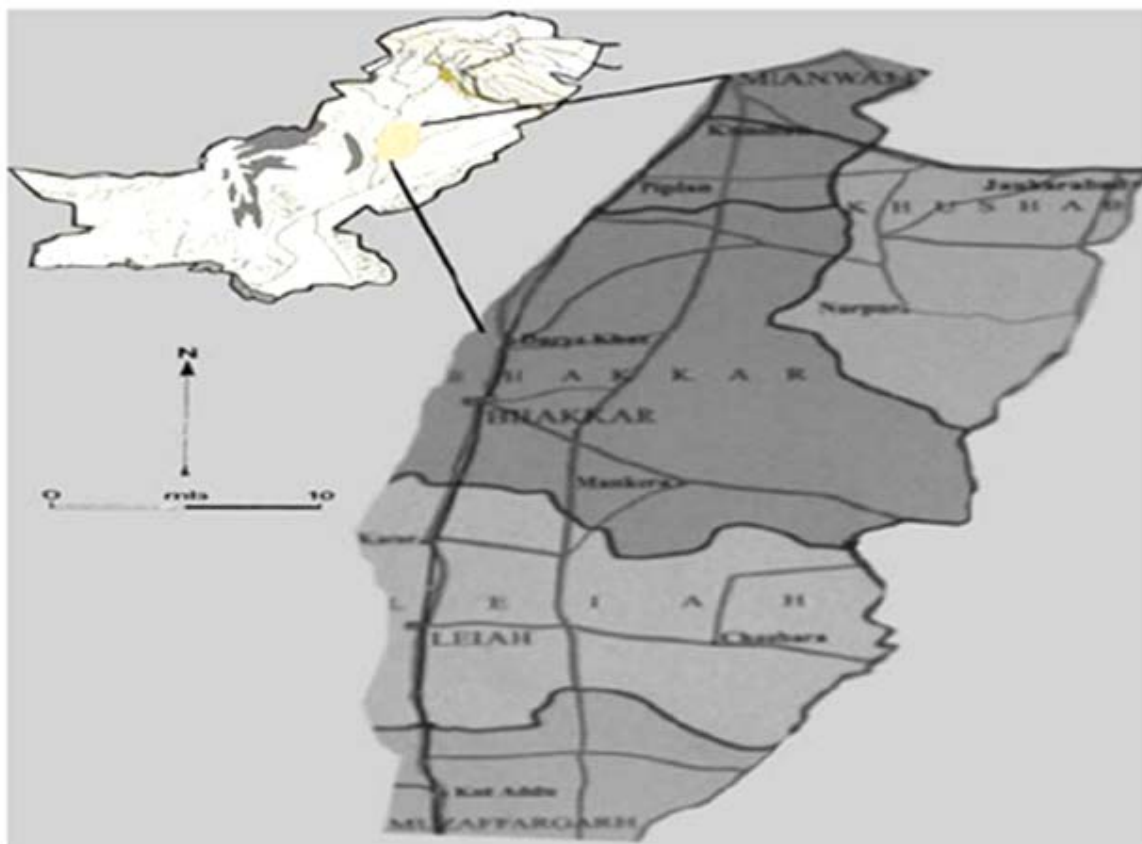


Fig. 1: Thal desert, Punjab, Pakistan.

Main purpose of the present study was to explore genetic variation and performance of morpho-agronomic traits for identification of most suitable parental genotypes capable of higher yield potential under moisture stress conditions, so that, most divergent types can be utilized further in breeding material.

MATERIALS AND METHODS

The experiment, consisting of 150 desi chickpea strains, was carried out at the Gram Breeding Research Station, Kallurkot, at longitude and latitude 71.280°E and 32.157°N, respectively, during 2017-18. The layout used was randomized complete block design with two replications. The experimental strains were sown in mid of October 2017 by dibbler keeping 10cm plant-to-plant distance in a single row of 4 meter length. Initially, two seeds were sown in each hole and after germination, thinning of plants was done and one plant was retained in each hole to keep recommended plant to plant distance. Only one

irrigation was applied to provide moisture for germination of seed and no supplementary irrigations were applied throughout the crop period. Total rainfall recorded during the crop period was 23 mm in three spells. Manual hoeing was done twice to keep the crop weed free. Insecticide, Emamectin benzoate @ 600 ml ha⁻¹ was sprayed against pod borer attack at the pod formation stage.

Data on six morpho-agronomic traits viz., plant height (cm), primary branches plant⁻¹, secondary branches plant⁻¹, pods plant⁻¹, 100 seed weight (g) and grain yield (kg ha⁻¹) were recorded. The data were subjected to D^2 Statistics as outlined by Mahalanobis (1928; 1936). Principal component analysis and cluster analysis were performed through Statistical Tool for Agriculture Research (STAR) version 2.0.1.

RESULTS AND DISCUSSION

Through D^2 Statistics range, mean, standard deviation and coefficient of variation were measured (Table1). From the data, it is evident that traits

showed wide dispersion for range, standard deviation and coefficient of variation. Higher values of standard deviation and coefficient of variation indicated presence of sufficient amount of variation among the

genotypes for included morpho-agronomic traits. These results are in line with the previous findings of Dwevedi and Lal (2009); Malik *et al.* (2014) and Syed *et al.* (2012).

Table 1: Mean performance of chickpea attributes.

Attributes	Range	Mean(μ)	Standard deviation (σ)	C.V %
Plant height	22-70	39.20	11.30	28.82
Primary branches plant ⁻¹	1-10	3.02	0.64	21.00
Secondary branches plant ⁻¹	1-12	4.64	1.10	23.70
Pods plant ⁻¹	8-100	26.59	5.38	20.23
100 seed weight	18-31	22.97	3.64	15.84
Grain yield	41-1091	275.97	98.24	35.64

Principal component analysis extracted six PCs, out of which, first two PCs showed more than 1 Eigen values (Table2). Scree plot indicating Eigen values was also constructed to show better illustration of results (Fig.2). Results revealed that PC-1 reflected the highest contribution in genetic variation (60.42%), followed by PC-2 (17.25%). Similar findings were reported by Talebi and Rokhzadi (2013); Malik *et al.* (2014) and Agrawal *et al.* (2018). The cumulative percent of variance of PC-1 and PC-2 was 77.67. Biplot among PC-1 and PC-2 was constructed to illustrate the contribution of various morpho-agronomic traits in variation. From Fig. 3, it is clear

that the traits are superimposed on plots as vectors. The traits, contributing in formation of PC-1 and PC-2, have been shown in Table 3. Maximum cumulative percent of variance was contributed by the 100 seed weight (28%), followed by yield (25%), plant height (17%), pods plant⁻¹ (12%), secondary branches plant⁻¹ (12%) and primary branches plant⁻¹ (6%). The results are in line with Syed *et al.* (2012), Zubair *et al.* (2017) and Sharifi *et al.*, 2018. From PCA results, it is clear that 100 seed weight, yield and plant height are playing a prime role in contribution towards genetic diversity.

Table 2: Principal component analysis of chickpea strains.

Principal component	Eigen value	Percentage of variance	Cumulative percentage of variance
PC 1	3.625	60.42	60.42
PC 2	1.035	17.25	77.67
PC 3	0.461	7.68	85.36
PC 4	0.360	5.99	91.35
PC 5	0.260	4.35	95.71
PC 6	0.257	4.29	100

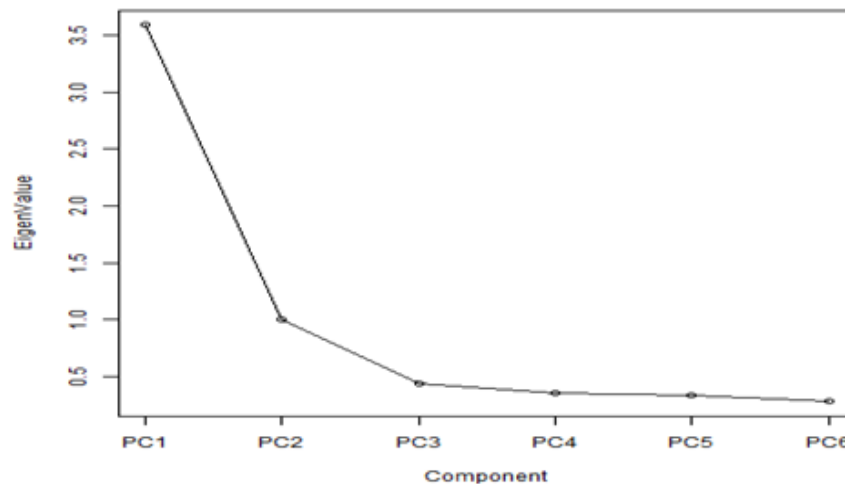


Fig.2: Scree plot showing Eigen values of principal components.

Table 3: Extraction method of variable in principal component 1 and 2.

Trait	Component1	Component2	Percentage of contribution in variation
Plant height	0.834	-0.009	17
Primary branches plant ⁻¹	0.765	-0.441	6
Secondary branches plant ⁻¹	0.831	-0.248	12
Pods plant ⁻¹	0.857	-0.260	12
100 seed weight	0.619	0.705	28
Grain yield	0.732	0.462	25

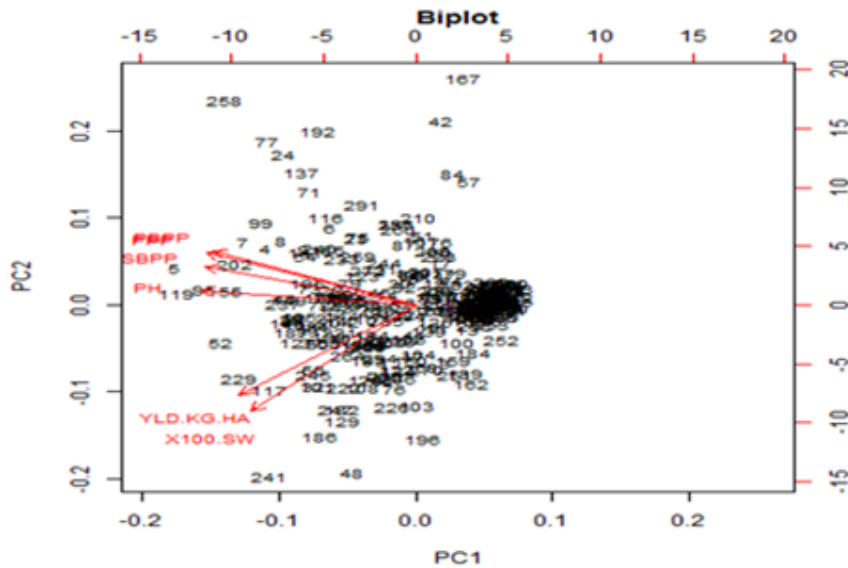


Fig. 3: Biplot between PC-1 and PC-2.

Cluster analysis distributed the strains in five clusters on the basis of similarity (Table 4). Maximum numbers of strains were grouped in cluster I (64), followed by cluster II (41), cluster III (22), cluster IV (19) and cluster V (4). Cluster membership of strains is shown in Table 5. Mean values of morpho-agronomic traits revealed that strains with higher values of plant height were grouped in cluster V, while minimum were found in cluster II. Maximum

primary branches plant⁻¹ were shown in cluster I and minimum in cluster II. Similarly, more secondary branches plant⁻¹ were found in cluster I and less were found in cluster II. Strains with maximum number of pods plant⁻¹, 100 seed weight and yield were grouped in cluster V, while the minimum were grouped in cluster II. Similar results have already been found in studies of Lal *et al.* (2001); Upadhyaya *et al.* (2007); Gupta *et al.* (2011) and Dwevedi and Lal (2009).

Table 4: Mean values of different attributes in cluster analysis.

Trait	Cluster				
	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Plant height	48.23	33.69	47.19	40.00	50.17
Primary branches plant ⁻¹	4.61	2.34	3.72	4.50	4.17
Secondary branches plant ⁻¹	8.28	3.41	5.94	7.00	6.24
Podsplant ⁻¹	38.67	20.56	31.40	31.50	42.06
Seed weight	26.54	20.84	25.91	26.48	27.00
Grain yield	653.91	180.03	275.60	439.23	985.02

Table 5: Cluster membership of 150 strains of chickpea.

Clusters	Members
Cluster 1	09AG009, CH10/08, CH39/08, CH-1036/09, CH-19/10, CH-32/10, D-00173, D-01014, D-01017, D-01067, D-01072, D-01079, D-02001, D-02004, D-02005, D-02006, D-02013, D-02017, D-02002, D-02023, D-02040, D-08025, D-02070, D-03001, D-03005, D-03007, D-04024, D-05014, D-05020, D-05028, D-05029, D-05030, D-06001, D-06002, D-06003, D-06004, D-06005, D-06006, D-06007, D-07008, D-07009, D-07020, D-08006, D-08030, D-09013, D-09024, D-09027, D-10039, D-11030, D-11033, D-11035, D-12011, DCD, NIFA-1, NIFA-2, NIFA-3, PAIDAR-91, PB-98, TG-1218, TGx228, THAL, D-02050, D-02052, D-08010.
Cluster 2	AZC, Bhakkar-2011, Bittle-16, BRC-424, CH-19/07, CH-25/10, CH-28/07, CH-40/09, CH-49/09, CM-584/09, CM-98, D-00170, D-00172, D-01008, D-02043, D-02044, D-020068, D-03008, D-03009, D-03010, D-04004, D-06040, D-08016, D-08041, D-09029, D-10008, D-12005, D-12036, D-13011, D-13012, D-13036, D-14005, Pb-2000, Pb-2008, TG-1221, WANHAR, D-05009, D-06024, D-08026, D-13029, D-13030.
Cluster 3	Balkasar, Bittle-98, C-44, CH-17/08, CM-1026/09, D-00152, D-00155, D-00156, D-00174, D-00184, D-01032, D-01055, D-02009, D-02042, D-03006, D-03022, D-04010, D-05015, D-07007, D-07041, D-08017, TG-1306.
Cluster 4	BRC-457, D-02060, D-02075, D-02080, D-02093, D-03019, D-03026, D-04025, D-04043, D-05002, D-05007, D-06052, D-07012, D-14014, D-12025, D-13031, LS-05-64, TG x 220, D-14008.
Cluster 5	D-02055, D-07045, D-1004, D-03024.

Dendrogram was also constructed, using Euclidean distance (Fig.4). Maximum Euclidean distance was noted in cluster V in performance of morpho-agronomic traits. Cluster analysis indicated that grouping of strains into distinct clusters provided valuable basis to chickpea breeders for selection of appropriate types. Through cluster analysis, it is also evident that higher values for plant height, 100 seed weight and grain yield were observed in members of

cluster V, followed by cluster I, indicating that the members of clusters V are genetically superior and selection of parents for breeding program from this group may be emphasized. However, the members of cluster I may also be utilized for inclusion into breeding material. These findings are in agreement with the previous results of Patil *et al.* (2003); Bisht *et al.* (2005) and Sharifi *et al.* (2018).

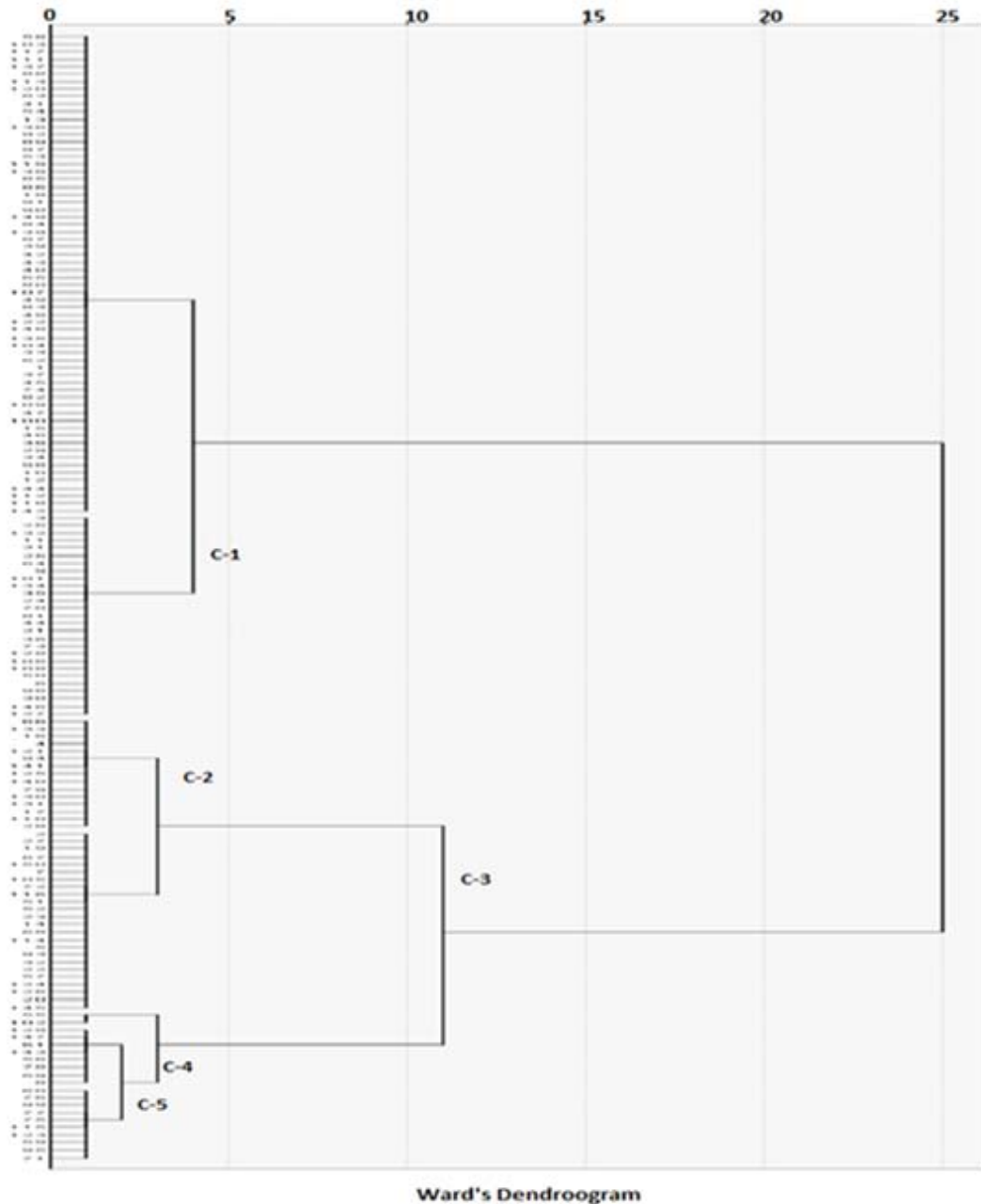


Fig. 4: Ward's Dendrogram, using Euclidean distance.

CONCLUSION

From the current study, it may be concluded that sufficient genetic variation exists in included strains for various yield related traits. PCA identified 100 seed weight, grain yield and plant height as major traits reflecting the maximum amount of genetic variation. Cluster analysis also verified that members of cluster V expressed higher values for 100 seed weight, yield and plant height followed by cluster I indicating that members of these groups may be given preference accordingly and can be exploited further for future chickpea breeding program.

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