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PATTERNS OF MORPHOLOGICAL DIVERSITY AND CHARACTER ASSOCIATION IN CHICKPEA GENOTYPES THROUGH MULTIVARIATE APPROACH

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ABSTRACT

Pattern of morphological diversity and character association in twenty chickpea genotypes was assessed through multivariate approach. Three principal components were deduced (eigen value > 1) which contributed to a total of 62.83% variability among the genotypes. PC-I contributed 34.78% to total variation. Factor loadings revealed that all the characters contributed positively to PC-I except days to flowering and plant height. Days to flowering exerted maximum negative load on the factor I while the highest positive contribution to the PC-I was endorsed by number of pods/plant, seeds/plant, biological yield, and grain yield/plant. Secondary branches, plant height, seeds/plant, 100-seed weight and biological yield had positive weight on PC-II where secondary branches followed by plant height showed the maximum contribution. Days to maturity, primary branches, plant height, seeds/pod and 100-seed weight exerted positive factor loadings on PC-III among which the highest weight was contributed by plant height followed by number of primary branches. Cluster I and II comprised of seven lines each. Long duration genotypes with high number of seeds/pod came under cluster I. However, the cluster II, classified genotypes with better grain yield and its components. However, the other six genotypes were long duration with maximum plant height and fell in cluster III. This study suggested enough scope for selection for grain yield and its components.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is the second most important legume crop in the world after dry bean (Yucel *et al*., 2006). In addition to improving soil fertility, it is also an important source of human food and animal feed. Its grains are the cheap source of high quality protein and are used as salads, ground into flour, cooked and ground into a paste called hummus locally called as 'basen', or roasted, spiced and eaten as a snack (Al-Rifaee *et al*., 2007). Generally chickpea is divided into two main types i.e., desi and kabuli which are cultivated in the important growing zones of the world (Kumar and Abbo, 2001; Siddique *et al*., 2002). Desi types are characterized as small, dark seeded with rough coat and an average seed weight of 170 to 250 mg per seed. However, morphologically the seeds of kabuli varieties have light colour and larger in size with a smooth coat. The average seed weight of kabuli types ranges between 270 and 550 mg per seed (Siddique *et al*., 2002). Chickpea is the second most significant Rabi season crop in Pakistan after wheat. Its ability to grow on marginal lands and low input demand especially in case of irrigation water makes it a good choice for the farming community of arid zones of the country (Vural and Karasu, 2007). It is also a very common member of crop rotations in cropping patterns of dry areas to enhance the nutrient status of the soil (Al-Rifaee *et al*., 2007).

Chickpea with especial reference to desi types has its centre of maximum diversity in the subcontinent which revealed that it might be originated in this region. Desi types are wide spread in this region due their high adaptability, preference of the local people, small life span, high nutritional value and utilization in various edible forms. The kabuli types are well adapted to temperate regions while the desi types are mostly grown in the semi-arid tropics (Malhotra *et al*., 1987). Yield of chickpea is determined by numerous aspects including genotype, growing season, geographical site, and agronomic practices (Tawaha *et al*., 2005). However, in a particular chickpea genotype grain yield is an amalgamation of various yield contributing traits and has been remained the constant objective of the plant breeders (Saleem *et al*., 2002).

Determination of correlation coefficients between different parameters is of utmost significance for the selection of desirable plant genotypes (Ali *et al*., 2008). Positive association of grain yield with its contributing characters is vital and must be identified and explored by the gram scientists. Though direct selection for different characters could be deceptive, indirect selection via associated parameters with high heritability might be more efficient than direct selection (Toker, 2004; Toker and Cigirgan, 2004). Conventionally, correlation, regression and path coefficient analysis have been utilized for the determination of character

interrelationships (Toker and Cagirgan, 2003). However, considering many traits simultaneously requires that the dimensionality of the data set be reduced.

Analysis of principal components (PC) commonly known as factor analysis, designed by Godschalk and Timothy (1988) is a proficient statistics for data reduction in much larger investigations. For example, principal components may be inputs to a multiple regression or cluster analysis (Vural and Karasu, 2007). Additionally, principal components are one 'factoring' of the covariance matrix for the factor analysis model (Johnson and Wicherin, 1992). Factor analysis is a multivariate statistical method to understand the patterns of variation in a set of variables based on morphological relationships among them (Awan *et al*., 2007). Factor analysis was commonly implicated in chickpea (Halila and Strange, 1997; Toker & Cagirgan, 2003; Toker and Cigirgan, 2004; Naghavi and Jahansouz, 2004; Vural and Karasu, 2007). Cluster analysis is an important exploratory technique to systematize the data which lead to divide the germplasm into various groupings. Grouping can provide comfortable means for the evaluation of dimensionality, identifying-outliers and signifying interesting hypotheses regarding associations (Johnson and Wicherin, 1992; Vural and Karasu, 2007).

In the light of this information present studies were initiated with the objective to investigate the genetic variability, pattern of variability and relationship among some polygenic traits using factor and cluster analysis in some elite chickpea genotypes.

MATERIALS AND METHODS

The plant material comprising of eighteen chickpea genotypes viz; BRC-27, CS-30, 102, 114, 209, 549, 576, 660, 777, 836, 930, 1011, 1012, 1084, 1117-1, 1129, 1230, 5002 along with two standards (Bittal-98 & Paidar-91) was sown in the research area of Plant Breeding and Genetics, University of Agriculture, Faisalabad Pakistan. The experiment was laid out in randomized complete block design (RCBD) with three replications. Each plot consisted of 4 lines of 4 m length. The plant-to-plant and row-to-row distance was maintained at 15 cm and 30 cm, respectively. The experimental field was fertilized with N-P-K at the rate of 30-75-25 Kg/ha. Irrigation both by canal and turbine water was applied to the experimental material. Three to four irrigations were applied during the total crop season. Weeding was done manually to keep the experiment in weed free condition. The data obtained were assessed for morphological diversity and character association using multivariate approach during 2009-10.

***Morphological traits studied*:** At maturity, ten equally competitive guarded plants were ear marked from each genotype for recording data on morphological traits. Number of days to 50% flowering (NDTFF) was determined from the sowing date to the date of 50 percent flowering. Number of days to maturity (NDTM) was calculated from the date of sowing to the harvesting date of the crop. Number of primary branches (NPB) was recorded as the branches sprouting from the main stem. Number of secondary branches (NSB) was counted as the branches originating from the main stem which are directly pod bearing branches. Plant height (PH) was determined in centimeters from soil surface to the top of the main branch. The data on number of pods per plant (NPP) was calculated as total number of pods recorded at maturity. After harvest, biological yield (BY) of each genotype was recorded in grams as total dry weight at maturity. Grain yield per plant (GYP) was recorded in grams after threshing. Number of seeds per plant (NSP) was counted and was divided by number of pods to get the data of number of seeds per pod (NSPD). 100-seed weight (100-SWt.) was measured on two 100-seed assessments and recorded in grams.

Statistical analysis: The collected data were analyzed by the analysis of variance technique to determine significant varietal differences among the 20 genotypes using M-STATC (MSTAT-C development Team, 1989). Genotypic and phenotypic correlations were computed following Kwon and Torrie (1964). Path coefficients were estimated according to Dewey and Lu (1959), where grain yield plant per plant was kept as resultant variable and other contributing characters as causal variables.

Basic statistics and phenotypic correlation coefficients among the traits were worked out using 'SPSS' 12.0 for Windows. Simple statistics and numerical taxonomic techniques were analyzed using the procedure of cluster and principal component analysis (Sneath and Sokal, 1973) with the help of computer software 'Statistica' and 'SPSS' 12.0 for Windows. Cluster analysis was conducted on the basis of average distance of k-means and the accessions in each cluster were then analyzed for basic statistics.

RESULTS AND DISCUSSION

Descriptive statistics for eleven morphological characters demonstrated means for all traits comprising of their minimum and maximum values, comparable along with the values of standard deviation (Table 1). The same procedure for comparison of means was also adopted by Ali *et al*., 2002 and Malik *et al*., 2009. Grain yield per plant exhibited maximum standard deviation (15.26) followed by number of pods per plant (8.99) showing maximum variation to the data recorded. These findings were in accordance to the findings of Malik *et al*. (2009). Maximum variations were recorded for grain yield per plant, number of pods per plant and number of

days to 50% flowering which indicated that the genotypes used were of diverse origin. Such observations were also noticed by Bukhsh *et al*. (2003). The variations present among the chickpea genotypes for grain yield per plant and number of pods per plant depicted the scope of variation for the improvement in yield and yield related traits. However, the variability for the number of days to 50% flowering indicated the early and late flowering genotypes. This variability of the germplasm entries can be utilized in further breeding programme for improvement in these particular traits. The data on 11 plant traits were subjected to analysis of variance (Steel *et al*., 1997). Highly significant genetic differences ($P<0.01$) were found among the genotypes for all the traits under study (Table 2).

Improvement in individual traits would be misleading due to involvement of environmental component. It is therefore, advisable to analyze the data for relative contribution of various components to yield. The simple correlation analysis is one of the effective tools of statistics used for this purpose to assess the interaction between the two traits. Simple correlation coefficients for various polygenic traits studied are given in table 3. Correlation coefficients of yield and its components estimated in this study indicated that most of the traits studied in the present investigation were positively and significantly correlated with yield. Grain yield per plant was significantly and positively correlated to number of primary branches and number of seeds per pod. However, the main yield contributing traits (number of pods per plant and biological yield) also had a significant and positive correlation with grain yield per plant which coincides with the findings of Malik *et al*. (2009).

A multivariate analysis can be used with a substantial number of correlated variables. The purpose of its use was to explore the total variation underlying in the correlation coefficients. The principal component analysis reduces the large set of variables to a single set thus representing the large set by exploring the total variation of the correlation coefficients as well as of error variance (Brown, 2001). Three components (factors) were extracted having eigen value > 1. The eigen values were calculated to decide the number of factors (Gorsuch, 1983). These factors contributed to a total of 62.83% variability amongst the genotypes studied (Table 4). PC-I, PC-II and PC-III explained 34.78%, 16.52% and 11.54% respectively of total variance as explained by the factor analysis. The first two principal components were plotted in a scatter plot diagram to observe relationship between the clusters (Fig. 1). Scatter plot diagram indicated that the three clusters displayed clear separation from each other. Cluster II was not clearly separated, which might be due to mixture of accessions with different traits, especially grain yield per plant and its components as all the accessions with higher grain yield per plant and its attributes were grouped in this cluster.

The communalities as shown in table 4, accounted for the total proportion of variance that the analysis accounted for in each of the traits. The communalities of the principal component-I/factor-I were mostly associated with number of pods per plant (0.78), number of seeds per plant (0.95), biological yield (0.95) and grain yield per plant (0.78) as the variability found for these traits was much higher than the total cumulative variability of 62.83%. Similarly, communalities showed that factor-II was more related to number of pods per plant (0.83), number of seeds per plant (0.96), number of seeds per pod (0.62), 100-seed weight (0.69), biological yield (0.96) and grain yield per plant (0.84) (Vural and Karasu, 2007). However, the third principal component/factor-III suggested a high degree of similarity among especially grain yield per plant (0.92) and the yield contributing traits like number of pods per plant (0.90), number of seeds per plant (0.97), biological yield (0.96) and grain yield per plant (0.92). All the three principal components exhibited high communalities for days to 50% flowering, number of pods per plant, number of seeds per plant, biological yield and grain yield per plant (Table 4). This advocated high level of genetic association among these morphological and agronomic traits (Vural and Karasu, 2007).

Factor loadings were computed by correlation of the respective principal components with the variables/traits under study. Table 4, revealed that all the characters contributed positively to PC-I except days to 50% flowering (-0.70) and plant height (-0.05). The negative value of factor loadings for number of days to 50% flowering is an indication towards the earliness (less days taken to 50% flowering) in flowering however, the positive values for the same trait exhibited late (more days to 50% flowering) flowering. Number of days to 50 % flowering exerted a maximum negative load on the PC-I while the highest positive contribution to the PC-I was endorsed by number of pods per plant, number of seeds per plant, biological yield, and grain yield per plant. This suggested that early flowering genotypes tended to increase the grain yield and its attributes like number of pods per plant, number of seeds per plant and biological yield. Halila and Strange (1997) working on screening of kabuli chickpea germplasm comprising of 1915 genotypes for resistance to Fusarium wilt showed that > 80% of the variation of the resistant lines was explained by 100-seed weight and days to maturity. Upadhyaya *et al*. (2003) working on ICARDA gene bank containing 16820 accessions showed that days to 50% flowering showed the highest pooled diversity index. Toker (2004) reported that in factor-I; seed yield, biological yield, number of pods per plant, flowering duration and 100-seed weight had positive effect; while plant height, first

pod height and days to flowering showed negative interrelationship.

Number of secondary branches (0.64), plant height (0.32), number of seeds per plant (0.11), 100-grain weight (0.59) and biological yield (0.10) had a positive weight on PC-II whereas, number of secondary branches (0.64) followed by 100-seed weight (0.59) showed the maximum contribution (Table 4). Conversely, number of days to 50% flowering (-0.10; earliness), days to maturity (-0.71), number of pods per plant (-0.22), number of seeds per pod (-0.70) and grain yield per plant (-0.26) contributed negatively to PC-II showing that the highest negative influence of days to maturity for this factor. Upadhyaya *et al*. (2006) suggested that early maturity is valuable in chickpea to avoid terminal water stress and make enough use of available soil moisture during development, as it is usually cultivated on conserved soil moisture, where soil moisture reduces towards maturity such as in rain fed areas.

Table 1. Descriptive statistics grain yield and its attributes in 20 chickpea lines

Characters	Mean	Minimum	Maximum	Std. Deviation
Number of days to 50 % flowering	114.9	78.33	120.33	8.810
Number of days to maturity	163.3	160.00	166.33	1.815
Number of primary branches	2.338	2.23	2.50	0.079
Number of secondary branches	6.145	5.66	6.63	0.280
Plant height	67.82	58.80	77.67	5.822
Number of pods/plant	65.83	51.27	80.30	8.995
Number of seeds/plant	22.70	18.77	31.82	3.626
Number of seeds/pod	1.596	1.44	1.72	0.083
100-seed weight	19.65	17.43	24.47	2.072
Biological yield	47.17	39.79	63.39	6.609
Grain yield/plant	117.9	95.67	141.70	15.259

Table 2. Analysis of variance for various quantitative traits in chickpea

SOV	DF	NDTFF	NDTM	NPB	NSB	PH	NPP	NSP	NSPD	100-Seed Wt.	BY	GYP
Reps	2	4.61**	0.42	0.12	1.45	0.23	0.47	0.25	1.45	0.32*	0.06	0.17
Genotypes	19	4.36**	2.71**	0.34**	5.05**	39.54**	28.37**	23.29**	5.03**	12.87**	135.37**	37.88**

* = Significant at P<0.05 level, ** = Highly significant at P<0.05 and P<0.01 levels

SOV= Source of variation, DF= Degree of freedom, NDTFF= Number of days to 50% flowering, NDTM= Number of days to maturity, NPB= Number of primary branches, NSB= Number of secondary branches, PH= Plant height, NPP= Number of pods/plant, NSP= Number of seeds/plant, NSPD= Number of seeds/pod, 100-Seed Wt.= 100-seed weight, BY= Biological yield, GYP= Grain yield plant

From the present results (Table 4) it was inferred that early maturity for the genotypes might result in more number of secondary branches and high plant heights. However, Naghavi *et al*. (2005) reported that the greatest weight on PC-II was due to number of seeds per plant and grain yield per plant, whereas PC-III was mainly related to number of pods per plant, number of seeds per pod and 100-seed weight and PC-IV was positively related to number of pods per plant and negatively to number of branches per plant.

Days to maturity (0.17), number of primary branches (0.56), plant height (0.80), number of seeds per pod (0.02) and 100-seed weight (0.22) exerted positive factor loadings on PC-III among which the highest weight was contributed by plant height (0.80) followed by number of primary branches (0.56) (Table 4). Other characters like number of days to 50% flowering (-0.28), number of pods per plant (-0.26), number of seeds per plant (-0.03), biological yield (-0.03) and grain yield per plant (-0.27) exerted negative effects on the factor-III with highest negative weight of the number of secondary branches (-0.56). This revealed that tall plants with spreading habit (more number of primary branches) may result in less number of secondary branches.

The means and standard deviation values for the three clusters based on quantitative traits were compared to their respective values of standard deviations as explained in table 5. In all the cases, a controlled level of variability was observed as in all of the cases the standard deviation values remained less than that of means. The values of cluster analysis showed that the advanced lines with the highest days to maturity (168.52) and number of seeds per pod (1.65) belonged to cluster I (Table 5). This cluster comprised of seven lines viz. CS 1011, 209,

Table 3. Simple correlation coefficients of polygenic traits studied in chickpea genotypes

	Values of Correlation Coefficient									
	NDTFF	**NDTM**	**NPB**	**NSB**	**PH**	**NPP**	**NSP**	**NSPD**	**100-Seed Wt.**	**BY**
NDTM	0.25									
NPB	- 0.49*	0.18								
NSB	0.04	-0.43	-0.10							
PH	-0.06	-0.07	0.35	-0.16						
NPP	-0.43	0.16	0.45*	0.20	-0.22					
NSP	-0.64*	0.01	0.57**	0.31	-0.01	0.85**				
NSPD	-0.38**	0.31	0.26	-0.28	-0.26	0.33	0.25			
100-Seed Wt.	-0.53*	-0.14	0.41	0.37	0.18	0.23	0.63**	-0.22		
BY	-0.62**	0.01	0.58**	0.31	-0.01	0.85**	0.99**	0.24	0.64**	
GYP	-0.43	0.19	0.45*	0.18	-0.25	0.99**	0.85**	0.36	0.22	0.84**

** = Significant at P<0.05 and P<0.01 levels

NDTFF= Number of days to 50% flowering, NDTM= Number of days to maturity, NPB= Number of primary branches, NSB= Number of secondary branches, PH= Plant height, NPP= Number of pods/plant, NSP= Number of seeds/plant, NSPD= Number of seeds/pod, 100-Seed Wt.= 100-seed weight, BY= Biological yield, GYP= Grain yield plant

Table 4: Principal components (PCs) for multi-genic traits in chickpea genotypes

Traits	**PC-I**	**PC-II**	**PC-III**			
Eigen value	4.87	2.31	1.62			
Cum. Eigen value	4.87	7.18	8.80			
Total variance (%)	34.78	16.52	11.54			
Cumulative variance %		62.83				
	Communalities			**Factor Loadings**		
	PC-I	**PC-II**	**PC-III**	**PC-I**	**PC-II**	**PC-III**
NDTFF	0.49	0.50	0.58	-0.70	-0.10	-0.28
NDTM	0.01	0.50	0.53	0.05	-0.71	0.17
PB	0.43	0.44	0.75	0.66	-0.08	0.56
SB	0.06	0.47	0.78	0.24	0.64	-0.56
PH	0.01	0.11	0.74	-0.05	0.32	0.80
NPP	0.78	0.83	0.90	0.88	-0.22	-0.26
NSP	0.95	0.96	0.97	0.98	0.11	-0.03
NSPD	0.12	0.62	0.62	0.35	-0.70	0.02
100-Seed Wt.	0.34	0.69	0.74	0.58	0.59	0.22
BY	0.95	0.96	0.96	0.97	0.10	-0.03
GYP	0.78	0.84	0.92	0.88	-0.26	-0.27

NDTFF= Number of days to 50% flowering, NDTM= Number of days to maturity, NPB= Number of primary branches, NSB= Number of secondary branches, PH= Plant height, NPP= Number of pods/plant, NSP= Number of seeds/plant, NSPD= Number of seeds/pod, 100-Seed Wt.= 100-seed weight, BY= Biological yield, GYP= Grain yield plant

Paidar 91, CS 777, 1230, 30 and CS 114 (Table 6). The maximum variability in cluster I was contributed by grain yield per plant as evident from the higher values of its variance (36.55) and standard deviation (6.05). This proposed that this cluster might be utilized in breeding programs especially aimed to produce the genotypes with high number of seeds per pods; and maximum selection for grain yield per plant might be advantageous from this group of elite lines. This also advocated that long duration chickpea lines were also related to this group and were closely associated to number of seeds per pod.

A view of cluster II (Table 6) also having seven genotypes namely CS 102, Bittal 98, CS 836, 5002, BRC 27, CS 1129 and CS 930 revealed that the genotypes with uppermost values of number of primary branches (2.38), number of secondary branches (8.55), number of pods per plant (75.32), number of seeds per plant (26.56), 100-seed weight (20.98), biological yield (54.26) and grain yield per plant (134.34) as evident from table 5. This was an indication that these characters were positively correlated for this set of genotypes. Days to 50% flowering was the main factor donating variation as evident from the variance (205.33) and standard deviation (14.33) values in this cluster which provided huge chances for selection for short duration genotypes. From this it is inferred that this is the main group of genotypes; contributing towards yield and these advanced lines must be the part of breeding programs organized with the objective of high grain production in chickpea. The identification of the agronomical superior diverse parents

with high 100-seed weight, early-maturity will prompt breeders to use them in crop improvement programs (Upadhyaya *et al*. 2006).

The genotypes CS 549, 1084, 660, 1117-1, 1012 and CS 576 belonged to long duration cluster III (Table 6) along with maximum plant height. The character contributing at maximum to genetic divergence was plant height (71.73) as shown in table 5, which recommended this cluster to the selection for plants with different statures. Naghavi *et al*. (2005) working on the assessment of variation in the agronomic and morphological traits of 362 Iranian chickpea accessions, grouped the germplasm into four clusters where each cluster had some specific characteristics of its own.

Table 5. Means, standard deviations and variances for clusters with number of genotypes based on quantitative traits in chickpea

Characters	Cluster I (7)			Cluster II (7)			Cluster III (6)		
	Mean ± SD		Variance	Mean ± SD		Variance	Mean ± SD		Variance
NDTFF	116.52	1.64	2.70	110.81	14.33	205.33	117.89	2.73	7.45
NDTM	168.52	1.46	2.14	163.52	2.53	6.40	160.89	1.39	1.94
NPB	2.33	0.08	0.01	2.38	0.09	0.01	2.10	0.04	0.02
NSB	5.80	0.12	0.01	8.55	6.65	44.25	6.06	0.34	0.12
PH	64.93	4.83	23.33	67.36	5.32	28.31	71.73	6.04	36.50
NPP	65.53	4.15	17.19	75.32	3.04	9.22	55.11	3.41	11.63
NSP	21.25	1.86	3.47	26.56	3.15	9.90	19.90	0.86	0.73
NSPD	1.65	0.08	0.01	1.61	0.07	0.01	1.55	0.09	0.01
100-Seed Wt.	18.03	0.84	0.71	20.98	2.57	6.58	19.98	1.13	1.29
BY	44.35	3.27	10.70	54.26	5.75	33.06	42.20	1.53	2.35
GYP	117.41	6.05	36.55	134.34	5.24	27.50	99.36	4.05	16.42

NDTFF= Number of days to 50% flowering, NDTM= Number of days to maturity, NPB= Number of primary branches, NSB= Number of secondary branches, PH= Plant height, NPP= Number of pods/plant, NSP= Number of seeds/plant, NSPD= Number of seeds/pod, 100-Seed Wt.= 100-seed weight, BY= Biological yield, GYP= Grain yield plant

There should be some logical basis while making the clusters that for which characters the genotypes are differing, if they are so closely related then divide it according to those traits which are significantly differed.

Table 6. Clusters based on quantitative traits of chickpea genotypes

Clusters	Traits	Chickpea lines in the clusters
Cluster I	NDTFF, NDTM & NSPD	CS 1011, 209, Paidar 91, CS 777, 1230, 30, 114
Cluster II	NPB, NSB, NPP,NSP, 100-Seed Wt., BY & GYP	CS 102, Bittal 98, CS 836, 5002, BRC 27, CS 1129, 930
Cluster III	PH	CS 549, 1084, 660, 1117-1, 1012, 576

NDTFF= Number of days to 50% flowering, NDTM= Number of days to maturity, NPB= Number of primary branches, NSB= Number of secondary branches, PH= Plant height, NPP= Number of pods/plant, NSP= Number of seeds/plant, NSPD= Number of seeds/pod, 100-Seed Wt.= 100-seed weight, BY= Biological yield, GYP= Grain yield plant

Please give some basics of clusters also in this table what does cluster-I indicate

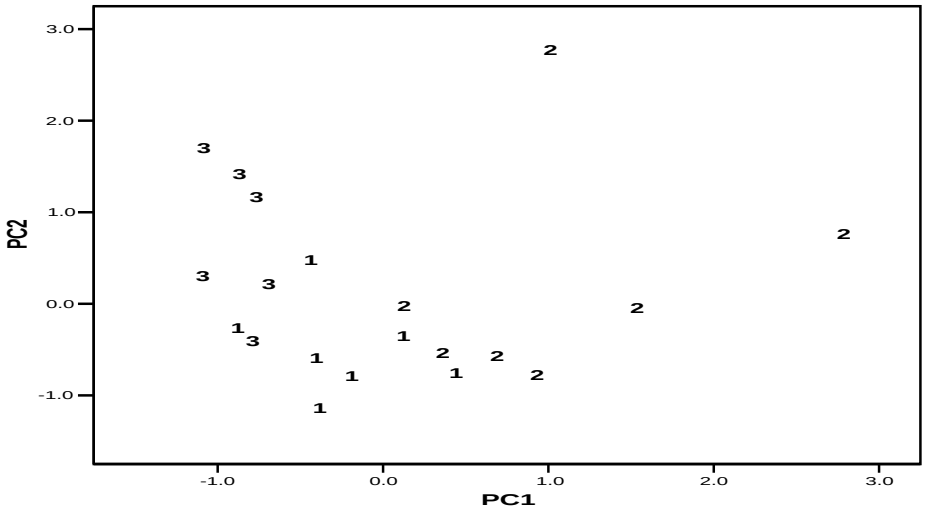

Fig. 1. Scatter plot of chickpea genotypes for first two PCs. The digits 1, 2 & 3 indicate cluster numbers.

Conclusions: From the approach used in this manuscript; it is easy to deduce all of the factors responsible for controlling a common quantitative trait of interest whose inheritance is of complex nature. PC-I contributed 34.78% to total variation. PC-I was endorsed by number of pods/plant, seeds/plant, biological yield, and grain yield/plant. Secondary branches, plant height, seeds/plant, 100-seed weight and biological yield had positive weight on PC-II where secondary branches followed by plant height showed the maximum contribution. Days to maturity, primary branches, plant height, seeds/pod and 100-seed weight exerted positive factor loadings on PC-III among which the highest weight was contributed by plant height followed by number of primary branches. Hence, a large set of genotypes were evaluated and were grouped into clusters on the basis of their variability differences. Long duration genotypes with high number of seeds/pod came under cluster I. However, the cluster II, comprised of genotypes with better grain yield and its related components. Thus, variability among the genotypes was compressed into clusters for which a an effective breeding programme can be devised for improvement. This approach to assess the variability can be equally utilized for the breeding programmes of both in the major as well in minor crops. Something should be there about findings also, how much contribution of each PC and what clusters say?

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