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Genetic Diversity Analysis of Morpho-Genetic Traits in *Desi* Chickpea (*Cicer arietinum*)

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Abstract

Genetic diversity of 113 *desi* chickpea genotypes was studied through descriptive, principal component and cluster analysis. High variances were observed for days to flowering, maturity, plant height, pods plant^{-1}, biological yield and harvest index. These traits also showed positive significant correlation with yield which was confirmed through principal component analysis. Principal component analysis (PCA) revealed that the first 4 principal components accounted for 71.99% of the total variation. Seed yield, biological yield, pods plant^{-1}, secondary branches and plant height in chickpea showed positive relation with the first component (PC1). Days to flowering, days to maturity, 100-seed weight showed positive correlation with the second component (PC2). The genotypes were grouped into four clusters using cluster analysis. Genotypes with early flowering and maturity were gathered in cluster I while cluster II showed dominant contribution for grain yield plant^{-1}, harvest index and number of pods plant^{-1}. The grouping of genotypes would be of practical value to chickpea breeders in identifying the genotype with desired trait for utilization in breeding program for genetic improvement. © 2014 Friends Science Publishers

Keywords: Chickpea; Diversity; Correlation; Cluster analysis; Principal component analysis

Introduction

Chickpea is an important food legume crop of Pakistan. It is an important source of protein and also plays vital role in the improvement of soil fertility. Chickpea is grown on more than 1 million ha in Pakistan and its productivity is 0.6 t/ha, which is low in comparison with the productivity of 0.8 t/ha worldwide (Upadhyaya *et al*., 2001). There are two types of chickpea '*Desi*' and '*Kabuli*'. The *Desi* type is most important in Pakistan as it is cultivated on >90% of total chickpea area. Major constraint in achieving high yield potential is the low genetic diversity for yield, yield components and resistance against major diseases. In plants genetic diversity determines the potential for improved efficiency and hence their use for breeding, which eventually may result in enhanced food production. The knowledge of genetic diversity helps in the tagging of germplasm, identification of gene stock and establishment of core collections Upadhyaya *et al.* (2007). If the parents selected for hybridization have diverse background the more are the chances of improving the characters under consideration (Chowdhury *et al.*, 2002).

Criteria for estimation of the genetic diversity can be different, including morphological traits (Upadhaya *et al.*, 2007) or molecular markers (Rao *et al.*, 2007). Quantitative traits provide an estimate of genetic diversity and numerical taxonomic techniques including principal component and cluster analyses have been successfully used to classify and measure the pattern of genetic diversity in germplasm (Ghafoor *et al.*, 2001). Principal component and cluster analysis procedures were found to be efficient to assess genetic diversity for agro-morphological traits in chickpea and were reported by many research workers (Parameshwarappa *et al*., 2011; Gupta *et al*., 2011; Nihal and Adak, 2012).

The objectives of the present studies were to assess the amount of genetic diversity in a collection of chickpea genotypes using multivariate techniques based on morpho-genetic parameters and to identify the potential genotypes for future utilization in chickpea breeding programs.

Materials and Methods

One hundred and thirteen *Desi* chickpea genotypes were evaluated in the Experimental Field of Pulses Research Program, National Agricultural Research Center, Islamabad (33^{o} 43' N and 73^{o} 06' E) for the year 2008-09. Experiment was conducted in augmented design with a single 4 meter row of each genotype, keeping row to row and plant to plant distances at 30 cm and 10 cm respectively.

Pesticides were sprayed to protect the crop from pests especially pod borer. Recommended agronomic practices were followed to raise a good crop stand. The data were recorded on days to 50% flowering, days to maturity, plant

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height, primary branches plant^{-1}, secondary branches plant^{-1}, pods plant^{-1}, seeds pod^{-1}, 100 seed weight, seed yield plant^{-1}, biological yield plant^{-1} and harvest index. Days to flowering and maturity were recorded at 50% of flowering and 90% maturity, respectively. Plant height (cm), primary branches plant^{-1}, secondary branches plant^{-1}, pods plant^{-1}, seed yield plant^{-1} (g), and biological yield plant^{-1} (g) were recorded on 10 plants sampled randomly. Seeds/pod was recorded on 10 pods sampled at random within each genotype. 100 seed weight (g) was recorded for each genotype and harvest index was calculated as economic yield articulated as percentage of total biological yield.

The data recorded for all parameter were averaged. Means of the genotypes were used in analysis for descriptive statistics and range, mean, variance and standard deviation were computed. Correlation coefficients were estimated to determine the level of interrelationship between all pairs of traits using the method given by Singh and Chaudhary (1979). The numerical taxonomic techniques viz., cluster and principal component analyses (Sneath and Sokal, 1973) were also used to analyze morpho-genetic characters. Prior to cluster and principal component analyses, data were standardized to avoid effects due to scaling differences. Cluster analysis was performed using the euclidean distances to study similarities among the genotypes using statistics software, Statistica, Version 6.0. The first two principal components (PCs) were utilized to view a graphical illustration called scatter plots that show the pattern of variation among the genotypes.

Results

Results regarding descriptive statistics for eleven quantitative traits revealed considerable diversity for these traits in the present material. Wide range and high variances values were observed for days to 50% flowering; days to maturity, plant height, pods plant^{-1}, biological yield plant^{-1} and harvest index (Table 1). Little variability was observed for primary branches, secondary branches and seed pod^{-1}. Coefficients of correlation between the means of eleven quantitative characters were also estimated for 113 genotypes of *Desi* chickpea and are given in the Table 2. Seed yield is a complicated character which is the outcome of interaction among various plant traits and the traits are influenced by the genetic makeup and environment. Seed yield plant^{-1} (SYP^{-1}) showed positive and significant association with primary branches plant^{-1} (PBP^{-1}), secondary branches plant^{-1} (SBP^{-1}), pods plant (PP^{-1}), seed pod^{-1} (SP^{-1}), biological yield plant^{-1} (BYP^{-1}) and harvest index (HI). Days to flowering (DF) had strong positive association with days to maturity (DM) and SBP^{-1} showed positive correlation with (PP^{-1}).

Principal component analysis (PCA) was conducted to sum up the significant information from the data. PCA also lowers the number of traits responsible for the maximum percentage of overall variation of the experimental data. The

Table 1: Descriptive statistics of 11 quantitative traits in 113 chickpea genotypes

Traits	Range	Mean±SE	σ^2	σ
Days to 50% flowering	98.0-140.0	117.2±0.7	49.7	7.1
Days to maturity	144.0-180.0	171.1±0.6	46.9	6.8
Plant height (cm)	26.8-67.6	45.6±0.7	49.9	7.1
Primary branches	1.3-5.1	3.0±0.1	0.5	0.7
Secondary branches	4.8-12.8	7.1±0.1	2.2	1.5
Pods per plant	11.1-55.1	29.6±1.0	104.2	10.2
Seed per pod	1.0-2.2	1.3±0.0	0.1	0.2
100 Seed weight (g)	16.8-39.4	27.4±0.3	13.7	3.7
Biological yield per plant(g)	12.3-57.7	30.3±0.9	101.9	10.1
Seed yield per plant (g)	3.2-30.2	12.3±0.5	34.0	5.8
Harvest index	21.4-64.6	39.7±0.9	83.3	9.1

σ^2 =Variance; σ = Standard deviation; SE= Standard error

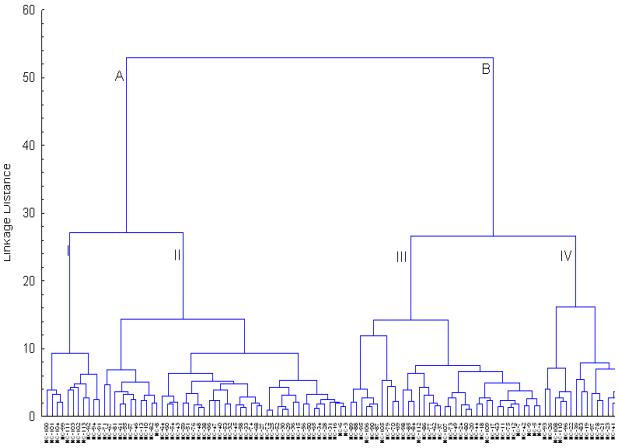

Fig. 1: Dendrogram depicting genetic relationships of 113 *Desi* chickpea *Cicer arietinum* L. genotypes based on 11 quantitative traits

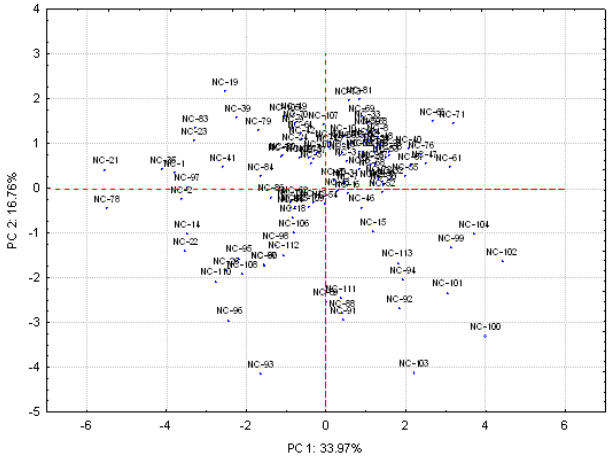

Fig. 2: Scatter plot of first two principal components contributing 50.73% of the total variation for 11 quantitative traits in 113 *Desi* chickpea genotypes

first 4 PCs eigen values >1 explained 71.99% variation among the 113 genotypes (Table 3). The PC1 explained

Table 2: Correlation coefficients among 11 quantitative traits of 113 *Desi* chickpea genotypes

Variables	DM	PH	PB	SB	PP	SP	100SW	BY	SY	HI
DF	0.68**	0.09	0.02	0.20*	0.02	0.27**	-0.09	0.01	0.11	0.21*
DM		0.35**	0.08	0.06	0.12	0.19*	-0.05	-0.04	0.13	0.34**
PH			0.34**	-0.03	0.14	-0.10	-0.06	0.06	0.14	0.14
PB				0.28**	0.16	0.18	0.06	0.19*	0.22*	0.16
SB					0.51**	0.24*	-0.17	0.43**	0.48**	0.36**
PP						0.11	-0.23*	0.80**	0.82**	0.52**
SP							-0.12	0.20*	0.24*	0.20*
100SW								-0.09	-0.11	-0.14
BY									0.88**	0.35**
SY										0.72**

* Significant at 5% probability level
** Significant at 1% probability level

DF	Days to 50% flowering	PB	Primary branches	SP	Seed/pod	GY	Seed yield/plant
DM	Days to maturity	SB	Secondary branches	100SW	100 Seed weight	HI	Harvest index
PH	Plant height	PP	Pods/plant	BY	Biological yield/plant		

33.97% of total variation and ten traits had positive contribution except 100-seed weight (100-SW) that showed negative value. Major contributors in variation were SYP^{-1}, PP^{-1}, BYP^{-1}, SBP^{-1} and HI. PC2 added 16.76% of the total variation and the traits with major contribution in this component were DF, DM, PH, PP^{-1}, SYP^{-1} and BYP^{-1}. The third PC was mainly related to PH, PBP^{-1} and DF. The fourth PC was positively related to PBP^{-1}, SBP^{-1}, SP^{-1} and 100-SW.

Cluster analysis further helps to group the genotypes on the basis of morpho-genetic traits. Cluster analysis grouped 113 genotypes into 2 main groups (A and B) and four clusters (Fig. 1). Range, means and standard deviation for two groups and four clusters are given in Table 4. Group A was comprised of 58 genotypes and further divided into two clusters (I and II). Cluster I contained 11 genotypes which were characterized by early in DF, DM, medium in SBP^{-1}, BYP^{-1} and high 100-SW. Cluster II comprised of 47 genotypes classified by late DF and DM, medium number of PBP^{-1}, SBP^{-1} and PP^{-1}. BYP^{-1} and SYP^{-1} of the genotypes in this cluster were lower. 55 genotypes in group B was further sub-divided into 2 clusters (Cluster III and Cluster IV). Cluster III comprised of 37 genotypes which were late in DF, DM and had medium to high average for PBP^{-1} and SBP^{-1}, PP^{-1}, BYP^{-1}, SYP^{-1} and HI. Cluster IV contained 18 genotypes characterized by late DF and DM and high mean values for number of PBP^{-1}, SBP^{-1}, PP^{-1}, BYP^{-1} and SYP^{-1}.

Discussion

Wide range and high variances values were observed for DF 50%, DM, PH, PP^{-1}, BYP^{-1} and HI. Higher values of variances for PH, BYP^{-1}, DF in different chickpea collections were also reported by Ghafoor *et al.* (2003), Malik *et al.* (2010) and Khan *et al.* (2011) indicating the importance of these traits in yield improvement. The quantitative traits showed significant variability and had high variance could be exploited either by direct selection for traits or through inclusion of selected genotypes as parents with desired traits in crossing program for genetic enhancement in this set of chickpea genotypes (Talebi *et al*., 2008). In present study little variability was observed for PBP^{-1}, SBP^{-1} and SP^{-1} hence, there is a limited possibility of selection for these traits in the current genotypes hence germplasm from other sources could be used to find more variability of these traits. If genotypes showed variability for economically important traits then it is essential to evaluate their association with seed yield. The utility of correlation for qualifying the degree of relationship between characters in a genetically diverse population at genotypic level (Bello *et al*., 2006) would serve as an effective tool for making meaningful progress in this crop improvement. Hence the analysis of yield components and their relative contribution towards yield would give better chance for selection for high yielding genotypes. In the present study, SYP^{-1} showed positive and significant association with PBP^{-1}, SBP^{-1}, PP^{-1}, BYP^{-1} and HI. These finding are in agreement with Saleem *et al.* (2002), Arshad and Bakhsh (2004), Malik *et al.* (2010) and Biabani *et al.* (2011). Significant and positive association of HI and SYP^{-1}also indicated the chances of yield improvement through indirect selection based on HI (Kumar *et al*., 2003). The findings of present study suggest that characters viz., pods per plant, secondary branches per plant, biological yield and harvest index showing positive correlation and could be exploit as selection criteria for developing chickpea genotypes with high yield potential.

Principal component analysis is useful technique as it gave information about the groups where certain traits are more important allowing the breeders to conduct specific breeding programs Salimi *et al.* (2012). In our study, first four PCs explained 71.99% of variation among 113 genotypes and these results were supported by the finding of Ghafoor *et al.* (2003), Upadhyaya *et al.* (2007), Hamayoon *et al.* (2011), and Shiv *et al.* (2012) and who studied chickpea genotypes of ICARDA, Pakistan and India. PCA biplot (Fig. 2) based on first two factors showed genetically different genotypes by the pattern on scattering. The dispersion of genotypes in all four sections of biplot indicated the presence of fair amount of genetic diversity. The genotypes closer to each other had little or no

Table 3: Eigen values, proportion of variability and quantitative traits that contributed to the four principal components in 113 Desi chickpea genotypes

Statistical parameters	PC1	PC2	PC3	PC4
Eigenvalue	3.74	1.84	1.28	1.06
Cumulative Eigenvalue	3.74	5.58	6.86	7.92
Variance (%)	33.97	16.76	11.62	9.63
Cumulative Variance	33.97	50.73	62.35	71.99
Traits				
Days to 50% flowering	0.282	0.783	0.291	0.009
Days to maturity	0.315	0.847	-0.025	-0.158
Plant height (cm)	0.221	0.372	0.757	-0.210
Primary branches	0.348	-0.102	0.556	0.590
Secondary branches	0.653	0.088	0.176	0.260
Pods per plant	0.855	0.279	-0.037	-0.207
Seed per pod	0.358	-0.244	0.436	0.552
100 Seed weight (g)	-0.242	0.054	-0.296	0.444
Biological yield per plant(g)	0.806	0.390	-0.017	-0.010
Seed yield per plant (g)	0.929	0.210	-0.027	-0.079
Harvest Index	0.728	-0.137	0.018	-0.154

Table 4: Descriptive statistics of morpho-genetic traits for 113 *Desi* chickpea genotypes grouped under four clusters

Traits	Cluster-I (11 genotypes)		Cluster-II (47 genotypes)		Cluster-III (37 genotypes)		Cluster-IV (18 genotypes)	
	Mean	SD	Mean	SD	Mean	SD	Mean	SD
Days to 50% flowering	107.3	4.6	118.0	4.5	118.2	6.2	118.6	9.6
Days to maturity	157.7	7.4	172.6	3.2	173.2	4.7	171.1	8.4
Plant height (cm)	37.3	7.3	47.3	5.6	44.0	5.9	49.8	8.0
Primary branches	2.1	0.7	3.1	0.6	2.8	0.5	3.6	0.8
Secondary branches	6.8	1.3	6.3	0.8	7.2	1.3	8.8	1.5
Pods per plant	21.8	8.3	23.0	4.8	33.5	7.0	42.7	10.5
Seed per pod	1.1	0.1	1.2	0.2	1.4	0.3	1.3	0.2
100 Seed weight (g)	28.1	6.2	27.9	4.1	27.3	2.4	26.3	2.0
Biological yield per plant(g)	26.4	10.1	23.6	4.3	32.8	7.5	44.3	9.3
Seed yield Per plant (g)	7.7	3.5	8.5	2.4	13.9	3.2	21.4	5.7
Harvest index	28.9	5.9	36.0	7.4	42.9	6.1	48.4	9.7

differences with respect to traits under study. Genotypes far from the origin exhibited more variability for quantitative traits and could be utilized as diverse parents in broadening the genetic base of chickpea through hybridization.

Cluster analysis of the *Desi* chickpea genotypes showed that genotypes in each cluster had some specific characteristics. This grouping is of practical value to chickpea breeders. In the current investigations the genotypes, having different traits were grouped into various clusters. Selection of genotypes with desired traits could be made from these for utilization in cross breeding program to attain high hybrid vigour and improved segregants. Similar conclusions were drawn by, Ghafoor *et al.* (2003) in chickpea. Representative genotypes may be chosen from different groups and core collection can be assembled for extensive studies and further exploitation of genetic diversity in breeding programs.

The characterization of present *Desi* chickpea genotypes gave rise to some promising lines for specific traits. It was also concluded that *Desi* chickpea genotypes showed considerable genetic diversity for majority of the traits studied. The emphasis should be given on number of SBP^{-1}, number of PP^{-1} and BYP^{-1} to improve the overall yield. These traits also showed positive significant correlation with yield and it was also confirmed through principal component analysis. The clustering of genotypes could help the chickpea breeders to identify and select desired genotypes. These genotypes with economically important traits could be used to combine desired traits in one line with broad genetic base.

References

Arshad, M. and A. Bakhsh, 2004. Path coefficient analysis in chickpea (*Cicer arietinum* L.) under rainfed conditions. *Pak. J. Bot.*, 36: 75–81

Bello, D., A.A. Sajo, D. Chubado and J.J. Jellason, 2006. Variability and correlation studies in okra (*Abel moschusesculentus* (L.) Moench). *J. Sustain. Develop Agric. Environ.*, 2: 120–126

Biabani, A., M. Katozi, M.M.A.G. Bahlake and A.H.G. Khani, 2011. Correlation and relationships between seed yield and other characteristics in chickpea (*Cicer arietinum* L.) cultivars under deterioration. *Afr. J. Agric. Res*., 6: 1359–1362

Chowdhury, M.A., B. Vandenberg and T. Warkentin, 2002. Cultivar identification and genetic relationship among selected breeding lines and cultivars in chickpea (*Cicer arietinum* L.). *Euphytica*, 127: 317–325

Ghafoor, A., A. Sharif, Z. Ahmad, M.A. Zahid and M.A. Rabbani, 2001. Genetic diversity in Blackgram (*Vigna mungo* (L.) Hepper). *Field Crops Res.*, 69: 183–190

Ghafoor, A., F.N. Gulbaaz, M. Afzal, M. Ashraf and M. Arshad, 2003. Inter–relationship between SDS–PAGE markers and agronomic traits in chickpea (*Cicer arietinum* L.). *Pak. J. Bot.*, 35: 613–624

Gupta, D., H.C. Sharma, P. Pathania, S. Pande, L. Clements and I. Bala, 2011. Evaluation of cultivated chickpea (*Cicer arietinum* L.) for agro–morphological traits and resistance to rust in North western Indian Himalaya. *Plant Dis. Res*., 26: p. 171

Hamayoon, R., H. Khan, S. Shah, L. Naz, I. Munir, M. Arif, I.A. Khalil and A.Z. Khan, 2011. Performance of chickpea genotypes under two different environmental conditions. *Afr. J. Biotech*., 10: 1534–1544

Khan, R., F. Ullah and H. Khan, 2011. Dissection of Genetic Variability and Heritability Estimates of Chickpea Germplasm for Various Morphological Markers And Quantitative Traits. *Sarhad J. Agric*., 27: 67–72

Kumar, S., P.P. Arora and A.S. Jeena, 2003. Correlation studies for yield and its component in chickpea. *Agri. Sci. Digest*, 23: 229–230

Malik, S.R., Bakhsh, A., M.A. Asif, U. Iqbal and S.M. Iqbal, 2010. Assessment of genetic variability and interrelationship among some agronomic traits in chickpea. *Int. J. Agric. Biol*., 12: 81–85

Nihal, K. and M.S. Adak, 2012. Associations of Some Characters with Grain Yield in Chickpea (*Cicer arietinum* L.). *Pak. J. Bot*., 44: 267–272

Parameshwarappa, S.G., P.M. Salimath, H.D. Upadhyaya, S.S. Patil and S.T. Kajjidoni, 2011. Genetic Divergence under three environments in a minicore collection of Chickpea (*Cicer arietinum* L.). *Ind. J. Plant Gene. Res.*, 24: 177–185

Rao L.S., P. Usha Rani, P.S. Deshmukh, P.A. Kumar and S.K. Panguluri, 2007. RAPD and ISSR fingerprinting in cultivated chickpea (*Cicer arietinum* L.) and its wild progenitor *Cicer reticulatum* Ladizinsky. *Genet. Resour. Crop Evol.*, 54: 1235–1244

Saleem, M., K. Shahzad, M. Javed and S.A. Rauf, 2002. Heritability estimates for grain yield and quality characters in chickpea (*Cicer arietinum* L.). *Int. J. Agric. Biol*., 4: 275–276

Salimi, S., H.S. Lahiji, G.M. Abadi, S. Salimi and S. Moradi, 2012. Genetic diversity in soybean genotypes under drought stress condition using factor analysis and cluster analysis. *World Appl. Sci. J*., 16: 474–478

Singh, R.K. and B.D. Chaudhary, 1979. *Biometrical methods in quantitative genetic analysis.* Pp: 303. Kelyani publisher, New Delhi, India

Shiv, S., M.A. Iquebal, N. P. Singh, R.K. Solanki and Sarika, 2012. Genetic diversity studies in chickpea (*Cicer arietinum* L.) germplasm. *J. Food Legumes*, 25: 31–36

Sneath, P.H.A. and R.R. Sokal, 1973. *Numerical Taxonomy: the Principles and Practice of Numerical Classification*, p: 573. W.F. Freeman & Co., San Francisco, California, USA

Talebi, R., F. Fayaz, M. Mardi, S.M. Pirsyedi and A.M. Naji, 2008. Genetic relationships among chickpea (*Cicer arietinum*) elite lines based on RAPD and agronomic markers. *Int. J. Agric. Biol*., 10: 301–305

Upadhyaya, H.D., P. J. Bramel, S. Singh. 2001. Development of a chickpea core subset using geographic distribution and quantitative traits. *Crop Sci.*, 41: 206–210

Upadhyaya, H.D., S.L. Dwivedi, C.L.L. Gowda and S. Singh. 2007. Identification of diverse germplasm lines for agronomic traits in a chickpea (*Cicer arietinum* L.) core collection for use in crop improvement. *Field Crops Res.*, 100: 320–326

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