

MULTIVARIATE ANALYSES IN CHICKPEA (*CICER ARIETINUM* L.)

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Abstract

Thirty genotypes of chickpea were evaluated for 10 quantitative traits using multivariate techniques. The first three PCs with eigen values >1 contributed 83.38% of the variability amongst genotypes. Populations with high PC₁ values were high yielding and characterized by high yield potential, 100-seed weight and harvest index. The populations with high PC₂ values were early in flowering and maturity, high in biological yield and pods but low in seed weight and harvest index. Seven characters were positive to PC₁ and five contributed maximum, thus this principal component is a weighted average of the characters. The scattered diagram on the basis of first 3 factors gave separation of two groups. One group in the left half consisted six accessions and of these five originated from the District Khushab, whereas other group in the right half of the graph consisted accessions from the Districts of Bhakkar and Layyah alongwith two checks. Cluster analysis also confirmed the findings of principal component analysis. The promising accessions may be chosen from particular groups or cluster for hybridization programs. Clusters with superior agronomic types identified, may be exploited for genetic potential to transfer the desirable genes to improve yield potential of the crop.

Introduction

Chickpea is an important grain legume in the Indian Subcontinent, West Asia, North Africa, South Europe, North and Central America. It is one of the most important legume crops throughout the world and is cultivated under a wide range of agro-ecological conditions mainly of rainfed nature (Singh, 1997). It is economical under rainfed conditions and gives good grain yield with excellent source of protein. Its great popularity as a human food is due to its mild, acceptable flavour and to the unique ability of its principal proteins to form a good combination with cereals. Although it is adapted to dry areas but several biotic and abiotic stresses are serious threats to this crop. Among these, diseases and water deficit have adverse effects on its productivity (Singh *et al.*, 1997a). Among the diseases, *Ascochyta* blight is the most devastating worldwide, causing up to 100% yield losses in the severely affected fields. *Ascochyta* blight resistance sources have been identified and many resistant cultivars have been developed (Singh *et al.*, 1997b).

The green revolution has drawn attention of the scientists on cereals, therefore, legumes remained relatively neglected. Sound breeding programme in any field crop depends mainly upon the availability of genetic variability either existing and/or created (Ghafoor *et al.*, 2001). Variance of relatively highly heritable quantitative traits provides an estimate of genetic diversity. Various numerical taxonomic techniques have been successfully used to classify and measure the pattern of genetic diversity in bean germplasm,

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as in chickpea (Filippetti & Margano 1983, Singh *et al.*, 1989, Singh *et al.*, 1990), blackgram (Shanmugam & Shreerangaswamy, 1982; Dasgupta & Das, 1984 & 1985), mungbean (Singh, 1988), pea (Amurrio *et al.*, 1995); soybean (Perry & McIntosh, 1991); alfalfa (Smith *et al.*, 1995), and lentil (Ahmad, *et al.*, 1997). Unlike cereals, pulses have been grown for centuries under marginal conditions of moisture and soil fertility. Keeping in view the importance of the crop, chickpea germplasm collected from (Layyah, Bhakkar and Khushab) districts of the Punjab province was evaluated under field conditions for various quantitative traits for further utilization by the breeders. These districts contribute more than 70% to the total production. The objective of this study was to determine the genetic diversity of chickpea landraces being cultivated in these districts and their utilization in the ongoing breeding programmes.

Materials and Methods

Thirty genotypes of chickpea including two checks (C 44 and Paidar 91) were evaluated for agronomic traits under field conditions at the National Agricultural Research Centre (NARC), Islamabad, Pakistan (33.40° N and 73.07° E). The experiment was conducted during winter season (1999) in a randomised complete block design (RCBD) with four replications. Two rows of 4 meter length for each genotype were planted in each replication with 10 cm intra-row spacing, whereas inter-row distance was kept at 50 cm. Pesticides and fungicides were sprayed to save the crop from infestation of pests and *Ascochyta rabiei*. For evaluation, data were recorded following chickpea descriptors (Anon., 1985). The data for days to flowering and maturity were recorded on line basis at 50% of flowering and 90% pod maturity and each genotype was represented by a single value. Other quantitative data i.e., plant height, primary and secondary branches, pods, grain yield (g) and biological yield (g) were recorded on 10 plants sampled randomly. Seed weight was recorded after counting 100 seeds in grams from bulk samples and harvest index was determined as economic yield expressed in percentage over total biomass.

The data recorded were analyzed for mean, standard deviation, variance, broad sense heritability and genetic advance. Broad sense heritability was estimated as a ratio between genotypic and phenotypic variance (Singh & Chaudhry, 1985). The averaged data were analyzed by numerical taxonomic techniques using the procedure of cluster and principal component analyses (Sneath & Sokal 1973) with the help of computer software "Statistica" and "SPSS" for Windows.

Results

Genotypes included in the study differed significantly for all the traits under study (Table 1). Medium to high genetic variance was observed for days to flowering, maturity, secondary branches and 100-seed weight, whereas for other characters, low to medium heritability (broad sense) alongwith low to medium genetic advance was observed. Improvement of these traits through simple selection might be limited from germplasm used in the present study.

Table 1. Analysis of variance and basic statistics for 30 genotypes of chickpea.

	Mean squares				σ^2_g	σ^2_p	h^2	GA
	Genotypes	Replicates	Error	SE				
Days to flowering	15.30**	15.44**	1.67	0.64	3.41	5.08	0.67	2.62
Days to maturity	27.63**	1.47	2.56	0.80	6.27	8.83	0.71	3.65
Plant height (cm)	242.45**	125.00	63.66	3.98	44.70	108.36	0.41	7.43
Primary branches	0.69**	1.23*	0.31	0.28	0.10	0.41	0.23	0.26
Secondary branches	7.07**	18.83**	1.17	0.89	1.48	2.65	0.56	1.57
Pods per plant	149.47*	899.01**	71.18	5.03	19.57	90.75	0.22	3.55
100-seed weight (g)	9.14**	0.01**	0.20	0.00	2.24	2.44	0.92	2.48
Biological yield (g)	186.98**	298.68**	61.46	5.27	31.38	92.84	0.34	5.63
Grain yield (g)	41.52**	69.27**	10.26	2.25	7.82	18.08	0.43	3.18
Harvest index (%)	47.77**	67.14**	11.19	2.79	9.15	20.34	0.45	3.51

SE- standard error, σ^2_g - genotypic variance, σ^2_p - phenotypic variance, h^2 - heritability (broad sense),

GA- genetic advance at 10% selection differential.

Principal component analyses

The first three components, with eigen values >1 contributed 83.38% of the variability amongst genotypes evaluated for 10 quantitative traits (Table 2). Other PCs (4 to 10) had eigen values less than 1. The first PC was more related to days to maturity, plant height, primary branches, 100-seed weight, grain yield and harvest index, whereas the second PC contrasts variables that relate solely to phenology (flowering, maturity) with those that are associated with reproductive development i.e., plant height, pods and biological yield. The variation for plant height and biological yield was distributed among all the components. Seven characters contributed positively to PC₁: thus this component is a weighted average of the characters. The characters with the greatest weight on this component suggested that this component reflects the yield potential of each accession. The characters with the greatest positive weight on PC₂ were plant height, pods and biological yield, whereas days to flowering and maturity had a substantial negative weight. These findings suggest that this component reflects the tendency of each accession to emphasize vegetative, as opposed to reproductive growth. Although PC₃ exhibited positive effects for all the characters but the magnitude was low except primary and secondary branches, pods and biological yield. This suggests that the genotypes that emphasize vegetative growth tend to have low yield, whereas those that emphasize reproductive growth tend to have many small ones. The first three principal components contributed more than 80% of the variability, hence these were plotted to observe relationships between the clusters (Fig. 1). In both the figures, PC₁ that contributed 54.97% of the variation was kept as in the X-axis, whereas PC₂ and PC₃ were plotted simultaneously against Y-axis. Both of these figures gave similar results, although PC₁ vs PC₃ gave clear separation of two groups. All the five accessions collected from District Khushab were grouped in the left half and one accession from Bhakkar was mixed with them. Group B in cluster analysis was separated which clearly occupied the right half of the graph. This cluster consisted of accessions collected from the Districts of Bhakkar and Layyah alongwith two checks included in the material.

Table 2. Principal Components (PCs) for 10 quantitative characters in 30 genotypes of chickpea.

		PC ₁	PC ₂	PC ₃
Eigen value		5.49	1.58	1.27
Proportion of σ^2		54.97	15.75	12.66
Cummulative σ^2		54.97	70.72	83.38
	Communality	Eigen vectors		
Days to flowering	0.915	-0.938	-0.065	0.178
Days to maturity	0.818	0.647	-0.584	0.243
Plant height (cm)	0.779	0.688	0.542	0.105
Primary branches	0.737	0.667	-0.446	0.305
Secondary branches	0.817	-0.291	-0.389	0.762
Pods/plant	0.608	-0.577	0.392	0.348
100-seed weight (g)	0.924	0.959	-0.029	-0.059
Biological yield/plant (g)	0.830	0.429	0.596	0.539
Grain yield/plant (g)	0.958	0.927	0.253	0.185
Harvest index (%)	0.952	0.948	-0.114	-0.201

Table 3. Mean, standard error (SE) and standard deviation (σ) for 3 clusters based on 10 quantitative characters in 30 accessions of chickpea.

	Cluster 1		Cluster 2		Cluster 3	
	Mean \pm SE	σ	Mean \pm SE	σ	Mean \pm SE	σ
Days to flowering	140 \pm 0.89	2.17	124 \pm 0.38	1.07	122 \pm 0.55	2.22
Days to maturity	170 \pm 1.28	3.15	177 \pm 0.55	1.55	173 \pm 0.55	2.21
Plant height (cm)	49.2 \pm 1.66	4.07	63.3 \pm 1.17	3.32	62.6 \pm 2.34	9.36
Primary branches per plant	2.4 \pm 0.12	0.30	3.5 \pm 0.10	0.29	3.0 \pm 0.09	0.34
Secondary branches per plant	10.3 \pm 0.07	0.16	10.6 \pm 0.30	0.86	8.7 \pm 0.17	0.68
Pods per plant	56.0 \pm 11.41	27.94	36.1 \pm 1.53	4.34	33.0 \pm 1.45	5.80
100-seed weight (g)	12.30 \pm 0.07	0.17	22.45 \pm 0.40	1.14	21.57 \pm 0.41	1.62
Biological yield per plant (g)	24.54 \pm 0.25	0.60	30.46 \pm 1.46	4.14	26.83 \pm 1.58	6.31
Grain yield per plant (g)	5.43 \pm 0.11	0.28	16.78 \pm 0.78	2.22	14.36 \pm 0.69	2.78
Harvest index (%)	20.33 \pm 0.57	1.41	55.18 \pm 0.70	1.99	55.00 \pm 0.74	2.97

Cluster analysis

Euclidean dissimilarity coefficients of 30 genotypes ranged between 1.83 and 11.50. At the 25% linkage distance three clusters were observed, whereas clusters II and III unite to form one group (B) and cluster I constituted group A (Fig. 2). Six accessions were grouped together in the group A (cluster I) and out of these 5 accessions were collected from the areas in District Khushab, whereas one accession (52935) was collected from District Bhakkar (Fig. 2). The group B consisted 24 accessions including two checks. These accessions were collected from the Districts of Layyah and Bhakkar. Cluster II consisted of seven and cluster III fifteen accessions, whereas one check (C 44) was in cluster II and other (Paidar 91) was in cluster III.

Mean values alongwith standard deviation for each cluster presented in Table 3 revealed that accessions collected from the District Khushab (cluster I) were late in flowering but early in maturity, short statured, low in harvest index and low yielder. The average performance of the accessions falling in cluster II and III (group B) were similar, as both of these were late in maturity and high yielding along with high seed weight and harvest index.

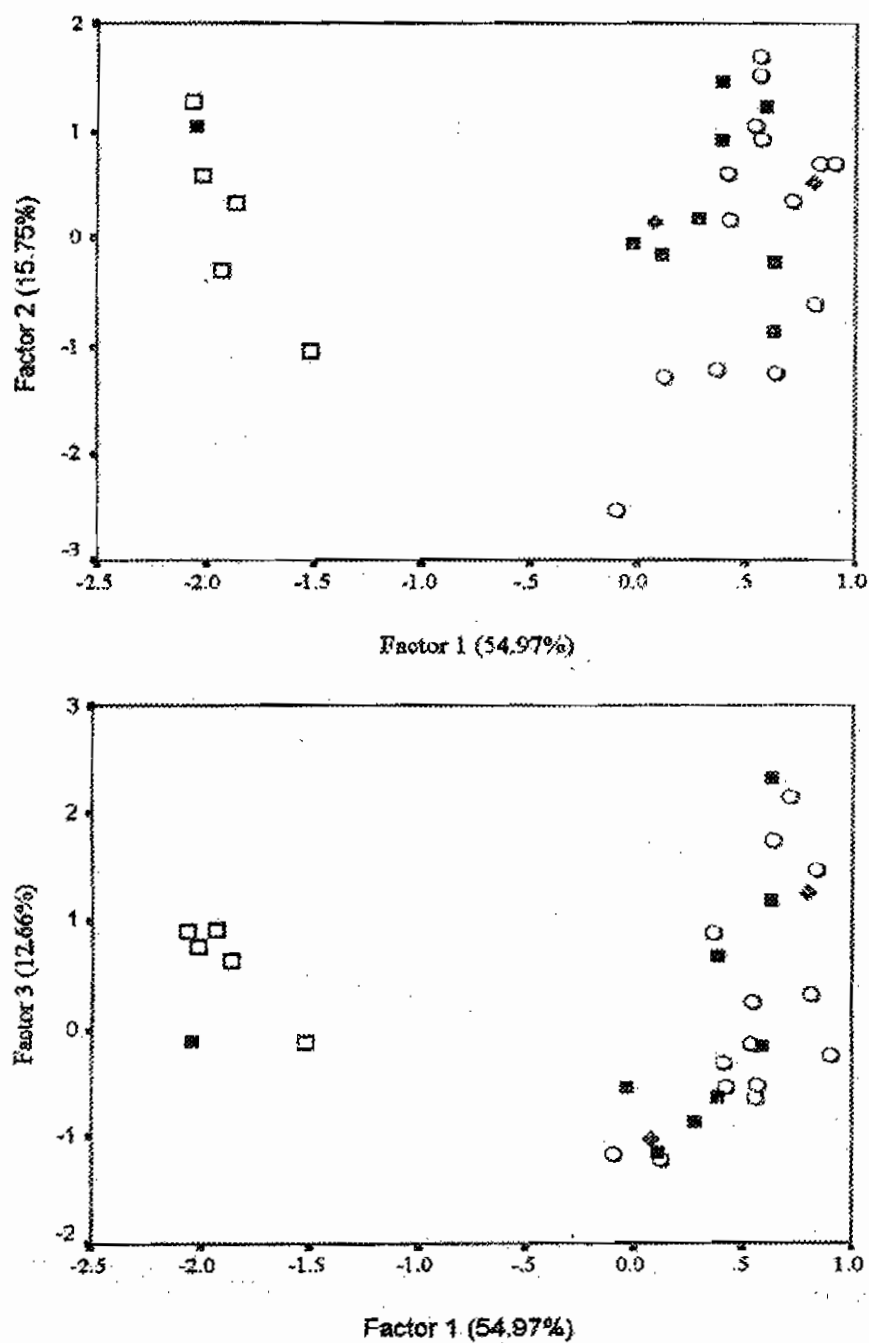


Fig. 1. Scattered diagram based on quantitative traits for first 3 factors in chickpea. The marks represent as ○- District Layyah, ■- District Bhakkar, □- District Khushab, and ◆- approved varieties.



Fig. 2. Cluster diagram of 30 chickpea genotypes selected on the basis of better performance from a broad based germplasm. The symbol K represents Khushab, B for Bhakkar, L for Layyah and V represents varieties.

Discussion

High heritability coupled with high genetic advance for days to flowering, days to maturity, secondary branches and 100-seed weight revealed additive type of gene effects, hence simple selection could be practised for exploitation of genetic variation to improve this crop. Partitioning of variance into its components assists genetic resources conservation and their utilization. It enables planning for use of appropriate gene pools in crop improvement for specific plant attributes (Pecetti *et al.*, 1996, Ghafoor *et al.*, 2001). Medium to high variance was observed for days to flowering, maturity, secondary branches and 100-seed weight, whereas for other characters, low to medium variance indicated the limited scope of improvement through the exploitation of present material. Genes for yield and yield components should be explored from other sources through more collections from the areas of maximum diversity or acquisition of germplasm from other sources. In chickpea, due to breeding work and epidemics of *Ascochyta* blight, important landraces might have extinct and hence acquisition of exotic germplasm seems to be more useful for developing broad based gene-pool. Lghetti *et al.*, (1998) advocated that maximum genetic conservation would be achieved by sampling populations from as many environments as possible. Superior accessions from distinct clusters are suggested to be utilized in breeding programme

as such genotypes give better hybrids (Ghafoor *et al.*, 2000). Elite accessions could also be utilized directly because such cultivars gave better performance under wide range of environments (Ghafoor *et al.*, 1992). Cluster analysis grouped together accessions with greater genetic similarity and the clusters include accessions from same origin in one group. The group A consisted all the accessions collected from the District Khushab except one accession and group B consisted all the accessions originated from the Districts of Layyah and Bhakkar. These two districts are adjoining and, traditionally, have similar geographic and soil feature. Hence, the grouping pattern could be related with geographic distribution of the crop and both the statistics confirmed the results indicating the validity of these two statistics for germplasm classification.

First PC was more related to days to maturity, plant height, primary branches, 100-seed weight, biological yield, grain yield and harvest index, whereas the second PC contrasts variables that relate to vegetative growth. First PC was a weighted average of the characters as seven characters were positive to this PC and out of these five contributed maximum. The findings suggest that this component reflects the tendency of each accession to emphasize vegetative and reproductive growth. Although PC₃ exhibited positive effects for all the characters but the magnitude was low except secondary branches, pods and biological yield. This suggests that the genotypes that emphasize vegetative growth tend to have low yield, whereas those that emphasise reproductive growth tend to have lower vegetative growth. Results reported by Falcinelli *et al.*, (1988 and Ghafoor *et al.*, (2001) showed multivariate analyses to be a valid system to deal with germplasm collections. The promising accessions may be chosen from particular groups for hybridization programme. Clusters with superior agronomic types have been identified which might be exploited for genetic potential to transfer the desirable genes to improve yield potential of the crop (Singh, 1988; Clements & Cowling, 1994).

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