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Interrelationships among yield and yield contributing traits in chickpea (*Cicer arietinum* L.)

Sajid Fiaz^{1,3*}, Muhammad Aslam¹, Fahad Masood Wattoo⁴, Aamir Riaz^{2,3}, Ikram Bashir¹

¹Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan

²Department of Agronomy, University of Agriculture, Faisalabad, Pakistan

³State Key Laboratory of Rice Biology, China National Rice Research Institute, Hangzhou, China

⁴Department of Plant Breeding and Genetics, PMAS-Arid Agriculture University, Pakistan

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Abstract

Chickpea (*Cicer arietinum* L.), being considered as vital protein source throughout the world, is grown widely in Pakistan as a major protein contributor. For better improvement of crop performance, essential knowledge about the genetically controlled yield and yield contributing traits is vital. Therefore, present study was conducted with objective to compare the performance of yield components and further their interrelationships for twenty chickpea genotypes including four varieties. That were evaluated for the existence of genetic variability and to know the interrelationship among yield traits under study during 2013-2014, at University of Agriculture, Faisalabad. The experiment was laid out in a randomized complete block (RCB) design with three replications. Data were recorded on number of days taken to flowering, number of primary branches plant⁻¹, number of secondary branches plant⁻¹, plant height, number of days taken to maturity, number of pods plant⁻¹, numbers of seed pods⁻¹, total plant weight, Number of grains plant⁻¹, 100- seed weight and grain yield plant⁻¹. The obtained data were analyzed for genetic variability parameters, correlation and path coefficient analysis. Higher values of broad sense heritability estimates were obtained for 100-seed weight (0.977), plant height (0.971), total plant weight (0.971) and number of primary branches plant⁻¹. Genetic advance was higher for plant height (9.054), total plant weight (9.054), number of pods plant⁻¹ (6.414) and 100-seed weight (2.941). The phenotypic coefficient of variation (PCV) was invariably slightly higher than their corresponding genetic coefficient of variation (GCV) due to influence of environment on character expression. Heritability estimates were higher for all characters except number of days taken to maturity and number of grains per plant, which exhibited moderate heritability. Hundred seed weight, plant height, total plant weight and primary branches per plant would be the suitable selection criteria to accomplish better grain yield in chickpea.

* Corresponding Author: Sajid Fiaz ✉ fiazsajid05@yahoo.com

Introduction

Chickpea (*Cicer arietinum* L.) commonly known as gram belongs to the family leguminosae is a major pulse crop that contributes about 12 % of the world pulse production (Khan *et al.*, 2011). It has the ability to fix the atmospheric nitrogen and improve soil fertility that ultimately lowers the cost of production (Ali *et al.*, 2008). It is the third most important pulse crop after dry bean and peas with a wide distribution across the tropics, sub tropics and temperate regions (Singh, 1997). It is an important source of dietary protein of the pre dominant population of Indian sub-continent (Viveros *et al.*, 2001). The Asian region contributes 70% to the total world's chickpea production (Malik *et al.*, 2010). In Pakistan, it is cultivated on 0.98 million hectares with total annual production of 0.67 million tons (Anonymous, 2012-13). Which is much lower than its production potential as well as the average yield harvested by other chickpea growing countries, and almost only one third of the potential yield is harvested in country.

For any breeding program the genetic variability plays an important role as it provides opportunity to plant breeder for selection of high yielding genotypes. Meanwhile, the information of yield and its association with yield contributing parameters provide the basis for the effective selection of improved varieties (Saleem *et al.*, 2005). Information of the genetic variation with the help of suitable parameters such as genetic advance, heritability estimate and genetic coefficient of variation are the prime requirements of an effective breeding program. The concept of heritability determines the difference observed among the characters is due to environmental influence or a result of genetic makeup. Genetic advance gives an idea of possible improvement of new population through selection, when compared to the parent population. The genetic advance depends upon the amount of genetic variability and magnitude of the epistasis effect of the environment (Gul *et al.*, 2013).

Some of the attributes/traits are significantly

associated among themselves and with grain yield by a simple or complex paths and identification of ideal path for the improvement of yield potential is the breeder's responsibility. The analysis of relationships among these characters and their associations with grain yield is essential to establish selection criteria (Atta *et al.*, 2008). Because yield contributing traits (plant population, height, number of leaves and pods) are the primary precursors of better plant growth and improved grain yields (Noor *et al.*, 2016). Progress in any breeding program depends upon the nature and magnitude of variability present in the parent population. Assessment of the extent of genetic variability within chickpea is fundamental task for chickpea breeding (Qureshi *et al.*, 2004).

During chickpea breeding, heritability must be given significant consideration along with genetic advance as alone heritability is not a good indicator of the amount of desirable genetic variability (Noor *et al.*, 2003). The information regarding genetic variability, heritability and association of various characters provide a foundation to plant breeders in breeding the chickpea genotypes possessing higher yield potentials. Selection based on grain yield, a polygenic character, is usually not much efficient, but selection based on its component characters could be more efficient for improved yields.

Grain yield is the main consideration and the most complex trait for breeder point of view as it depends on the interaction of genetic makeup of plant and environment. Apart from direct selections for grain yield, the objective of enhanced yield may, in most situations, be more effectively fulfilled on the basis of performance of yield and its components. These components may contribute directly or indirectly to the overall yield (Zeeshan *et al.*, 2013). Path coefficient analysis is one of the reliable statistical techniques to quantify the interrelationships of different yield contributing components, keeping yield as dependent variable (Mushtaq and Saleem, 2013).

The present study was initiated with the prime objective of estimating mutual relationships among different quantitative traits and the type and extent of their contribution to ultimate grain yields of chickpea.

Materials and methods

Plant material and site description

Twenty chickpea genotypes including four varieties obtained from different national institutions were selected for evaluation of agronomic traits and planted in the randomized complete block design (RCBD) with three replications, in the experimental field of Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, during growing season of 2013-14. The experimental material comprised of 20 elite breeding lines including four commercial varieties of chickpea namely Noor2009, 290, 1276, 6001, 1017, PB2000, 210, 1286, 1288, 3019, 6060, CH7, 6009, 220, 214, 114, 1031, 1159, 7020, PB2008. Each genotype was planted in a separate plot which was consisted of three rows of four meter length, with a plant-to-plant and row-to-row distance of 15 and 30 cm, respectively. The plots were separated by a distance of 60 cm.

Agronomic measurements

Ten randomly selected plants from each entry were tagged for data recording for the phenology and yield attributes of selected chickpea genotypes. Number of days to flowering, at the time when at least 50% flowering, was recorded for yield and similarly days to maturity were also recorded when 90% plants were observed as mature (brown color plots). Likewise, various yield contributing traits were recorded according to standard procedures, including number of primary and secondary branches per plant, plant height, number of days taken to maturity, number of pods plant⁻¹, number of grains per pod, plant dry weight, number of grains per plant, 100- grain weight and grain yield per plant and mean values were computed.

Statistical Analysis

The data were subjected to statistical analysis by a statistical software SAS (Statistical Analysis System) version 9. The mean values of the genotypes of each parameter were further compared by using Duncan's New Multiple Range Test.

Analysis of variance and covariance

The statistical analysis was done according to Steel *et al.* (1997) by using the data collected for the traits to ascertain the differences among various genotypes for variability and co-variability. Genotypic, phenotypic variances and coefficient of variation were estimated according to Singh and Chaudhary (1985). Total variance was partitioned into genotypic and phenotypic components.

Genotypic variance: ($\delta^2 G$) = (VMS-EMS) / r

Environmental variance: ($\delta^2 E$) = EMS

Phenotypic variance: ($\delta^2 P$) = $\delta^2 E$ + $\delta^2 G$

Where, VMS = Mean squares of genotypes; EMS = Mean squares for error; r = Number of replications

Covariance between i^{th} and j^{th} traits was calculated as under:

$Cov_g = VMP - EMP / r$

Coefficient of variability

Calculation for mean and coefficient of variability were made according to standard statistical techniques given by Steel *et al.* (1997) as under:

$$GCV = [(\sqrt{\delta^2}) / \bar{X}] \times 100$$

Phenotypic coefficient of variability is given by the formula

$$PCV = [(\sqrt{\delta^2_p}) / \bar{X}] \times 100$$

Where δ^2_g = Genetic variance; δ^2_p = Phenotypic variance; $\bar{X} = \sum X / N$

Correlation Analysis

Genotypic and phenotypic correlation coefficients among the characters under study were estimated according to the statistical techniques given by Kwon and Torrie (1964), which is as follows:

$$rg = \frac{Cov_{gij}}{\sqrt{(\delta^2_{gi})(\delta^2_{gj})}}$$

Where rg = genotypic correlation coefficient; Cov_{gij} = genotypic covariance of i^{th} and j^{th} traits; δ^2_{gi} , δ^2_{gj} = genotypic variance of trait i and j.

$$r_p = M_{ij} / \sqrt{(M_{ii})(M_{jj})}$$

Where r_p = phenotypic correlation coefficient; M_{ij} = mean product of accessions for i_{th} and j_{th} traits; M_{ii} and M_{jj} = genotypic mean square for i_{th} and j_{th} traits respectively.

$$r_e = EMP_{ij} / \sqrt{(EMS_{ii})(EMS_{jj})}$$

Where r_e = Environmental correlation coefficient; EMP_{ij} = Error mean product of accession of i_{th} and j_{th} traits; EMS_{ii} and EMS_{jj} = Error mean square for i_{th} and j_{th} traits respectively.

Significance test for genotypic correlation

$$SE(r_g) = 1 - r_g^2 / \sqrt{2} \sqrt{(SEh_i^2 / h_i^2)(SEh_j^2 / h_j^2)}$$

Where $SE(r_g)$ = Standard error for genotypic correlation; r_g = Genetic correlation

h_i^2 and h_j^2 = Heritability coefficients of traits i and j respectively; SEh_i^2 and SEh_j^2 = Standard error for heritability associated with i_{th} and j_{th} traits respectively.

A genetic correlation was considered significant statistically if its absolute value exceeds the twice of the respective standard error.

Significance test for phenotypic correlation

Statistical significance of phenotypic correlation was determined by using t-test as described by Steel *et al.* (1997).

$$t = r_p / \sqrt{(1 - r_p^2) / (n - 2)}$$

Where r_p = phenotypic correlation coefficient; n = number of observations.

Phenotypic correlation was considered significant if t-calculated was greater than t-tabulated.

Path Analysis

Path coefficient analysis was performed according to the method given by Dewey and Lu (1959) in yield related traits keeping grain yield as resultant variable and yield related traits such as days to flowering, days to maturity, primary branches per plant, secondary branches per plant, plant height, number of pods per plant, number of grains per pod, pod length, 100-grain weight, grain yield per plant and biomass per plant as causal variable.

Results and discussion

Genotypes differed for all the characters recorded, indicating a considerable range of genetic variability (Table 1).

Table 1. Results of analysis of variance parameters for 20 genotypes of chickpea (*Cicer arietinum* L.).

Genotypes	DF	DM	PH	PB	SB	WP	PP	SP	GP	100GW	GY
Noor-2009	121.76	166.01	81.74	3.833	6.16	58.63	68.60	1.550	104.3	16.87	21.32
290	121.40	164.50	66.67	3.065	5.43	67.23	59.63	1.650	115.1	19.60	20.92
1276	120.16	164.34	72.03	2.631	5.80	62.90	57.10	1.727	123.1	18.30	18.26
6001	120.00	164.23	58.63	3.701	5.76	81.73	61.90	1.713	122.1	18.87	22.04
1017	119.16	164.00	67.24	2.963	6.10	68.67	69.60	1.653	115.4	18.13	21.96
PB-2000	118.83	163.80	67.47	2.765	5.83	72.03	61.53	1.633	114.3	21.00	21.95
210	118.73	163.83	65.23	3.232	5.80	65.83	56.07	1.623	112.3	20.50	19.83
1286	117.83	163.60	66.83	2.334	6.06	67.47	66.10	1.537	99.50	21.56	24.43
1288	117.66	163.50	78.50	3.232	6.40	76.57	65.93	1.607	109.0	19.97	23.47
3019	117.50	163.50	68.66	3.834	6.30	75.53	50.50	1.653	115.9	18.60	17.20
6060	117.43	163.33	69.01	2.400	5.53	65.23	64.23	1.690	120.6	17.60	19.34
CH-7	116.40	163.21	67.13	2.299	6.10	69.00	67.73	1.553	105.5	20.87	23.03
6009	116.26	162.71	80.74	2.400	5.61	60.87	57.30	1.550	99.97	18.83	19.96
220	116.00	162.30	60.87	3.466	5.56	78.87	61.70	1.710	91.90	17.00	21.40
214	115.83	162.15	65.72	2.503	6.13	66.83	61.30	1.650	121.4	18.27	21.32
114	115.83	161.60	76.59	2.431	5.60	80.74	54.47	1.713	115.0	17.80	17.27
1031	115.40	161.50	78.85	3.202	6.40	65.73	63.73	1.527	122.6	23.83	24.71
1159	115.33	161.30	65.85	2.931	6.23	67.13	53.80	1.640	97.23	20.63	19.48
7020	115.26	161.19	75.53	2.400	5.66	66.67	63.70	1.537	114.4	20.46	21.29
PB-2008	113.33	160.72	62.90	2.365	5.83	78.50	62.93	1.710	121.2	25.13	26.72
MS (V)	13.4**	5.36**	133.1**	0.83**	0.16**	133.0**	81.29**	0.014**	264.1**	13.9**	18.0**
MS (R)	8.149	0.1175	0.097	0.0065	0.0605	0.097	16.117	0.008	24.745	0.165	0.892
MS (E)	9.71	2.7485	3.841	0.0445	0.0535	3.841	9.740	0.007	36.482	0.3128	2.697

* = significance at 0.05 ** = significant at 0.01 percent probability level, respectively. DF= Days to Flowering; DM= Days to Maturity; PH= Plant Height; PB=Primary Branches; SB= Secondary Branches; WP= Weight of Plant; PP= Pods Plant⁻¹; SP= Seed Plant⁻¹; GP= Grains Plant⁻¹; 100GW= 100 Grain Weight; GY= Grain Yield Plant⁻¹

The maximum grain yield was recorded in the variety PB-2008, while the lowest yield was obtained from the genotype 3019. The phenotypic coefficient of variation (PCV) was invariably slightly higher than their corresponding genetic coefficients of variations (GCV) due to influence of environment on character expression (Table 2). Phenotypic variances were larger as compared to genotypic

variances for all the traits indicating the influence of environmental effect. Uddin *et al.* (1990), Noor *et al.* (2003), Arshad *et al.* (2004a), Ozcelik and Bozoglu (2004) and Idrees *et al.* (2006) have reported similar results in chickpea. Estimates of broad sense heritability varied from 0.945 in number of primary branches plant⁻¹ to 0.977 for 100 seed weight.

Table 2. Genetic parameters for various quantitative characters in 20 chickpea genotypes.

Character	Mean $\pm$ SE	Range	CV (%)	h (%)	G.A.*
Number of days taken to flowering	111.62 $\pm$ 9.71	113.3-124.7	1.53	76.12	2.2319
Number of primary branches plant ⁻¹	2.8935 $\pm$ 0.045	3.384-2.299	7.35	94.45	0.6941
Number of secondary branches plant ⁻¹	5.915 $\pm$ 0.0535	5.43-640	3.90	65.82	0.2107
Plant height (cm)	70.185 $\pm$ 3.84	58.63-81.74	2.82	97.12	9.050
Number of days taken to maturity	154.891 $\pm$ 2.75	160.72-166.01	1.04	49.0	0.9219
Number of pods plant ⁻¹	5.9145 $\pm$ 9.740	50.50-69.60	5.10	88.02	6.4142
Number of seed pods ⁻¹	1.6313 $\pm$ 0.007	1.527-1.727	5.21	48.50	0.0465
Total plant weight (g)	69.808 $\pm$ 3.841	39.14-57.70	2.81	97.11	9.0542
Number of grain plant ⁻¹	112.04 $\pm$ 36.5	91.90-123.1	5.39	86.19	0.0465
100-grain weight (g)	19.691 $\pm$ 0.313	16.87-25.13	2.83	97.74	2.9412
Grain yield plant ⁻¹ (g)	21.295 $\pm$ 2.70	17.20-26.72	7.71	84.96	2.9080

Mean $\pm$ SE= Mean $\pm$ Standard Error; CV (%) = coefficient of variability; h (%) = heritability in Broad sense; G.A.*= Genetic Advance (5% selection intensity).

The genetic advance (5% selection intensity) was the highest for total plant weight (9.054), plant height (9.054), number of pods plant⁻¹ (6.414), 100 grain weight (2.941) and grain yield plant⁻¹ (2.908), while it was the lowest for number of grains plant⁻¹ (0.046) and number of secondary branches plant⁻¹ (0.211). Jeena & Arora (2000) also reported high heritability estimates for secondary branches, pods per plant, 100 seed weight and seed yield per plant, which support the present findings. It indicated that improvement could be achieved through simple selection from total plant weight, plant height and number of pods plant⁻¹. Heritability alone is not useful in identifying the genetic progress for selection of best individual but this statistic along with genetic advance is valuable (Yadav *et al.*, 2003). For number of primary branches plant⁻¹, number of grains pods⁻¹ and number of secondary branches plant⁻¹, high heritability was associated with low genetic advance,

indicating the influence of dominant and epistatic genes for these characters. Similar findings have been reported by Vivek *et al.*, (1999) and Mishra & Yadav (1994). High genetic advance of total plant weight and plant height coupled with high heritability, indicated that additive genes effect were important in determining these characters.

The genotypic and phenotypic correlation coefficients revealed that the genotypic correlations were greater than phenotypic for most of the characters (Table 3). Grain yield plant⁻¹ was positive and significantly correlated with total plant weight, number of pods plant⁻¹, number of grains plant⁻¹ and 100 grain weight but it was negatively correlated with number of grains plant⁻¹. The days taken to maturity show negative and highly significant correlation with grain yield plant⁻¹. Similarly, significant positive correlation of primary and secondary branches,

number of pods per plant and 100 seed weight with grain yield, had been observed by Singh *et al.*, (1999) and also this positive relation was reported for days to maturity by Singh *et al.*, (1990) in chickpea. Positive

correlation was also seen for primary branches and number of pods per plant in chickpea with that of grain yield for different locations (Bakhsh *et al.*, 2006).

Table 3. Estimates of Genotypic (r_g) and Phenotypic (r_p) correlation coefficients of various character combinations.

Character	NPB	NSB	PH	NDM	NPP	NSP	TPW	NGP	HGW	GYP	
NDF	G	0.4868*	0.3283*	-0.3730	0.0995*	0.1731*	0.1344*	-0.3021	0.2020	-0.6019	-0.2720
	P	0.3277*	0.2902*	-0.2282	0.0812	0.1436	0.1052	-0.2714*	0.0228	-	-0.2658*
NPB	G	-0.1674		0.4605	-0.0333	-0.0751	-0.1047	0.3265*	0.3136	0.1056	0.1024
	P	-0.1175		0.3440**	-0.0258	-0.0829	-0.0963	0.2981*	0.2364	0.0928	0.1012
NSB	G			-0.1672	0.3246*	0.0233	0.1104	0.5086*	-0.0834	0.4591*	0.3438
	P			-0.1082	0.2912*	0.0485	0.1016	0.3573**	-0.1044	0.3750**	0.2886*
PH	G				0.6960*	0.1141*	0.1185*	-0.3300	-0.1750	-0.1571	-0.1448
	P				0.4551**	0.0925	0.0930	-0.3181*	-0.1275	-0.1579	-0.1315
NDM	G					-0.0131	-0.1836	-0.8430	-1.0995	-	-0.6188
	P					0.0125	-0.0601	-0.5451**		-0.4515**	-
NPP	G						0.9999*	0.1680*	-0.1792	0.1059*	0.7068*
	P						0.9762**	0.1929	-0.0774	0.1043	0.6859
NSP	G							0.2788*	-0.1117	0.1613*	0.7344*
	P							0.3073*	-0.0193	0.1541	0.7223**
TPW	G								0.8335*	0.5298*	0.55705*
	P								0.5179**	0.4939**	0.5640**
NGP	G									0.1371	-0.0318
	P									0.0712	0.0068
HGW	G										0.8075*
	P	-									0.7342**
*	= Significant		(0.05				** = Highly significant		(0.01		

* = Significant

(0.05

** = Highly significant (0.01

NDF= Number of Days to Flowering

NPB= Number of Primary Branches

NSB= Number of Secondary Branches

PH= Plant Height (cm)

NDM= Number of days to maturity

NPP= Number of Pods plant⁻¹

NSP= Number of Seed pod⁻¹

TPW= Total Plant Weight (g)

NGP= Number of Grains plant⁻¹

HGW=100- Grain Weight

GYP= Grain Yield plant⁻¹(g).

The estimation of contribution by the individual character in the grain yield, which showed that number of grains per pods had maximum positive direct effect on grain yield per plant followed by 100 grain weight, number of grains per plant,

number of secondary branches, number of days taken to maturity, number of primary branches, number of days taken to flowering while characters like plant height and total plant weight had negative direct effects on grain yield,

which was in line with the findings of Singh *et al.* (1990) and Khan & Sharma (1999). Arshad *et al.*, (2004b) also narrated a negative and non-significant correlation for days to flowering with pods per plant and positive non-significant correlation with days to maturity. Primary branches were also reported to exhibit significant, positive genotypic and phenotypic correlation with

secondary branches (Khan & Qureshi, 2001). Improvement in grains per pod, primary branches, pods per plant and 100 seed weight may help to compensate the negative effect of plant height and total plant weight, which was negligible. Therefore, direct selection for the grains per pod, 100 grain weight, number of grains per plant and days to maturity will be quite effective for breeding progress.

Table 4. Direct and indirect effect of yield components in 20 chickpea genotypes.

Character	DF	DM	PH	PB	SB	WP	PP	SP	GP	100GW	GY
DF	(-0.0195)	0.0095	0.0794	0.0064	-0.0079	0.0059	0.0034	0.0039	0.0027	-0.0117	-0.2916
DM	0.0369	(-0.0759)	0.0528	-0.0127	-0.0127	-0.064	-0.0009	-0.0834	-0.0139	-0.0479	-0.6947
PH	-0.0204	-0.1428	(-0.2051)	0.0069	-0.0666	-0.068	-0.2341	0.0358	-0.0243	0.3223	0.0784
PB	0.01583	-0.008	-0.0016	(-0.0483)	0.0222	0.0158	-0.0036	0.0152	-0.005	0.005	0.0542
SB	-0.0318	-0.0142	0.0276	0.0392	(-0.0852)	0.0433	0.019	-0.0071	0.0094	0.039	0.2587
WP	0.02993	0.0836	0.0327	-0.0324	-0.0504	(-0.099)	-0.0167	-0.8257	-0.2762	-0.0525	0.6814
PP	0.07081	-0.0054	0.0467	-0.0308	0.0092	0.0687	(-0.0409)	-0.0732	0.409	0.0434	0.1042
SP	0.01784	-0.0971	-0.0155	0.0277	-0.0074	0.0737	-0.0159	(-0.8832)	-0.0099	0.0121	0.0519
GP	0.03686	-0.0503	0.0325	-0.0287	0.0303	0.0765	0.2743	-0.0606	(-0.2743)	0.0443	0.2256
100GW	-0.4476	-0.4698	-0.1169	0.0785	0.3414	0.3934	0.7878	0.0102	0.1199	(-0.7436)	0.744

DF= Days to Flowering; DM= Days to Maturity; PH= Plant Height; PB=Primary Branches; SB= Secondary Branches; WP= Weight of Plant; PP= Pods Plant⁻¹; SP= Seed Plant⁻¹; GP= Grains Plant⁻¹; 100GW= 100 Grain Weight; GY= Grain Yield Plant⁻¹

An overall appraisal of the correlation matrix and path coefficient analysis reveals that number of grains per plant and number of pods per plant exerted great influence both directly and indirectly on grain yield. Our findings are almost consistent with that observed by Khattak *et al.*, (1999) in the mungbean crop.

Correlation between numbers of grains per plant and grain yield was greatly reduced owing to the indirect negative influence of number of pods per plant. If maximum grain yield is to be obtained, a compromise is made during selection for these two traits and other traits have to give consideration.

In past studies, it is well reported that 1000 seed weight and pods per plant proved the best selection indices for developing high yielding genotypes for mash (Ghafoor *et al.*, 1990) and mungbean (Khattak *et al.*, 1995, 1997, 1999). Suitable recombination might be obtained through biparental mating, mutation breeding or diallal selective mating to break undesirable linkage (Ghafoor *et al.*, 1990).

Conclusion

The results obtained from the present study suggested that plant height, total plant weight, primary branches per plant and 100 grain weight gave more yield when selection was based on these characters. Genetic potential of genotypes revealed highly significant differences for all the studied traits. Genotype 4009 and 1288 had maximum total plant weight. Genotype 1017 and variety Noor-2009 had maximum pods per plant. Genotype 1115, 210 and Variety PB-2008 had maximum 100-grains weight. These genotypes can safely be used in future chickpea breeding programs for further exploitation of their genetic variability.

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