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Genotypic and phenotypic association among yield and yield contributing components in chickpea (*Cicer arietinum* L.)

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Abstract

Globally, chickpea holds third position in pulses after common beans and sweet peas. Due to cultivation on marginal lands its low yield is major problem. In Pakistan its yield is 472 kg/hectare which is less than rest of world. In present study focus is to screen chickpea germplasm based on yield limiting and yield enhancing traits to cope low yield situation in Pakistan. For this purpose, 20 chickpea genotypes were screened. The experiment was laid out following randomized complete block design (RCBD) having three replications. The genotypes were evaluated for nine morphological parameters. The data were precisely collected and analyzed for determining the association of these parameters with yield using correlation analysis. Genotypic and phenotypic correlation of seed yield per plant with plant height, and number of primary branches was positive and highly significant. Genotypic correlation of seeds yield per plant with seeds per pod was negative.

Keywords: Chickpea, Genotypic association, Phenotypic association

Introduction:

Chickpea (Cicer arietinum L.) is most important rabi legume crop of Pakistan. It is divided into two main categories based on seed size and coat color i.e. micro-sperma; commonly known as desi type and macro-sperma, commonly known as kabuli type. Desi type is mostly small seeded having dark brown coat color, while kabuli type is large seeded having cream or beige coat color (Jukantiet al., 2012). Being a legume crop it fix nitrogen from environment and increase soil fertility, the process called biological nitrogen fixation. It is mostly grown in arid and semi-arid zones around the globe.

Chickpea play important role in provision of balanced diet. It is a rich source of nutrition having about 18-20% protein contents, 4-10% lipids, 52-71% carbohydrates, and 10-23% fibers. It also contains traces of calcium, iron, carotene, riboflavin and ascorbic acid (Jukantiet al., 2012). Moreover, it is a good source of vitamin K, vitamin A, vitamin B, and vitamin C which are crucial for many metabolic activities (Zhu et al., 2007).

The usage of chickpea seeds is multipurpose i.e. when fresh, it is consumed as vegetable and when dried it can be used as food supplement because in this form it has a longer shelf life. Moreover, roasted, dried and snack forms are also delicious and have consumer acceptance making it the cheap source of dietary protein in those areas of the world where animal protein is expensive. That is the reason it is called as poor man's meat. It also contains essential amino acids i.e. lysine and tryptophan which are not present in sufficient amount in cereals. So, when chickpea is used with the combination of cereals it forms a well-balanced diet (Mushtaqet al., 2013).

In Pakistan it is cultivated on an area of approximately 960 thousand hectares, of which most of area is under desi type cultivars. Its annual production in Pakistan is about 480 thousand tons (Govt. of Pakistan, 2014-15). Due to increasing demand of kabuli type Pakistan imports it from Iran, Australia and Turkey. So, it is need of time to increase the production of kabuli type cultivars. In Punjab 90% of chickpea production arrives from rain fed areas like Bhakkar, Jhang, Layyah and Mianwali. The average production of chickpea is relatively lower in Pakistan, However, an increase in production of chickpea had been observed during the year of 2014-15. In this year production was increased about 22% when compared to last year production. The per hectare production is 472 kg which is far less when compared to world average production per hectare. It can be explained on the basis of these limitations i.e. lack of stress tolerant varieties, less response of cultivated germplasm to fertilizers and agronomic practices, very low fertile land under cultivation and most importantly unavailability of high yielding cultivars (Anonymous 2011-2012).Keeping the above problematic context under consideration, it becomes the need of the day to characterize the major limiting factors which contribute towards higher growth and ultimately to

the yield of chickpea (Ali et al., 2009). As we know that grain yield is a very complex trait which depends upon both genetic as well as environmental interactions. That is why when we breed a crop for grain yield, the direct selection can be deceptive. So, a more precise selection can be achieved by collecting information on genetic variability and by associating morpho-agronomic traits with grain yield.

Materials and Methods:

A trail was conducted in research area of the Department of Plant Breeding and Genetics. University of Agriculture, Faisalabad, Pakistan, during the Rabi, 2016. The experimental material comprised of 20 lines of chickpea. The experimental design followed was a triplicated randomized complete block design. Standard agronomic practices were performed during growing season. Data were collected for 9 parameters i.e. Plant height, Days to flowering, Primary branches/plant, Secondary branches/plant, Pods/plant, Seeds per pod, Seeds/plant, 100-Seed weight and Seed yield/plant.

Statistical Analysis

The data recorded for traits was analyzed by standard analysis of variance technique as given by Steel et al. (1997).

Correlation analysis

Genotypic and phenotypic correlation coefficients among the characters under study were estimated according to the statistical techniques outlined by Kwon and Torrie (1964).

Results and Discussion:

Analysis of variance (ANOVA) and genotypic and phenotypic correlations were probed out to ascertain the possible effects of genotype and environment on various plant characters. Analysis of variance (Table-2) for plant height revealed significant differences among genotypes. Plant height ranged from 58.07 to 80.83 cm. Variety TG-1205 showed maximum plant height followed by CM-1036, D-11035 and K01241 respectively. Genotype CH-49 showed minimum plant height followed by PB-2008 and CH-28 respectively. The estimation of genotypic, phenotypic and environmental variances was 35.55, 75.57 and 39.9, respectively (Table 3). The genotypic, phenotypic and environmental coefficients of variance were 71.71%, 104.52% and 51.30% respectively. High estimation of broad sense heritability (0.8948) was observed for this trait and coefficient of variability was 9.30. Similar results were represented by Jadav et al. (2014) and Mushtaq et al. (2013).

The results presented in (Table-2) revealed that the differences among the genotypes were significant regarding secondary branches. Secondary branches ranged from 4.57 to 8.23. GenotypeTG-1205 showed maximum secondary branches per plant followed by CH-72 and K01241respectively. Genotype AUG-424 showed minimum secondary branches while D-12005, TG-1210 and CM-2008 stands intermediate. Medium level of coefficient of variance was indicated (13.15%) for secondary branches. Genotypic, phenotypic and environmental variances were estimated as 0.80, 1.42 and 0.61 respectively. Coefficients of variance for genotypic, phenotypic and environmental were 36.39%, 41.33% and 31.80% respectively. Estimation of broad sense heritability was 0.6582 observed for this trait. Results were supported by the findings of Noor et al. (2003) and Ali et al. (2011). They reported moderate broad sense heritability for this trait.

The results presented in (Table-2) revealed that the differences among genotypes were highly significant regarding days to flowering. Days to flowering ranged from 116.00 to 123.17 days. Genotypes BRC-390 had maximum days to flowering followed by TG-1210, D-11033, AUG-424 and TG-1205 respectively. Genotype D-11030 took minimum days to flowering followed by D-12005, PB-2008 and CH-72 respectively. Medium level of coefficient of variance was indicated (15.67%) for days to flowering. Genotypic, phenotypic and environmental variances were estimated as 10.13, 14.75 and 4.20 respectively. Coefficients of variance for genotypic, phenotypic and environmental were 25.56%, 27.98% and 10.98% respectively. Estimation of broad sense heritability (49%) was observed for this trait with a genetic advance 0.9219. Results were in support with the findings of Noor et al. (2003), Atta et al. (2008).

The results given in (Table-2) revealed that the differences among genotypes were highly significant when considering the trait number of seeded pods per plant. On an average number of fertile pods ranged from 12-34. Genotype BRC-403 had the maximum average for this trait i.e. 29 while the genotype AUG-424 had minimum of 16. Coefficient of variance was (9.30%). The estimation of genotypic, phenotypic and environmental variances was 8.39, 17.65 and 9.25 respectively. The genotypic, phenotypic and environmental coefficient of variance was 58.50%, 84.84% and 61.44% respectively. Results were in support with the findings of Noor et al. (2003), Atta et al. (2008).

Based on grain yield per plant results of analysis of variance (Table-2) revealed that the differences among genotypes were significant. The value ranged from 17.16 to 29.0 for grain yield per plant.

Genotypes TG-1210 showed maximum grain yield per plant followed by genotype D-11035.Genotype D-11030 showed minimum grain yield per plant 17.16. High value (11.12%) of coefficient of variability was indicated for grain yield per plant. The estimation of genotypic, phenotypic and environmental variances was 8.39, 17.65 and 9.25 respectively. The genotypic, phenotypic and environmental coefficient of variance was 58.50%, 84.84% and 61.44% respectively. High estimation of broad sense heritability (0.47) was observed for this trait with a genetic advance of 0.0465. The coefficient of variance was 1.37%. Genotypic and phenotypic variances were 28.92 and 88.28 respectively. While genotypic and phenotypic coefficient of variance were 2.04 and 3.60. Greater phenotypic coefficient of variability indicated favorable environment into genotype interaction. Findings of this study corroborate with finding of Ali et al. (2008) and Ali et al. (2011).

Analysis of variance (Table-2) for pods per plant revealed that the differences among genotypes were significant. Number of pods per plant ranged from 16.37 to 27.47. Genotype TG-1205 showed maximum number of pods per plant followed by K01241 and D-12036 respectively. Genotype AUG-424 showed minimum number of pods per plant. The estimation of genotypic, phenotypic and environmental variances was 4.57, 10.76 and 6.18 respectively. The genotypic, phenotypic and environmental coefficient of variance was 43.84%, 67.23% and 50.97% respectively. High estimation of broad sense heritability (0.9711) was observed for this trait. They reported high heritability of this trait. Similar results were represented by Jadav et al. (2014) and Mushtaq et al. (2013).

The results presented in (Table-2) revealed that the differences among genotypes were highly significant regarding 100-grain weight. 100-grain weight ranged from 17.86 to 26.13 grams. Genotype K01241 showed maximum 100-grain weight. Genotype Bhakr-2011 showed minimum 100-grain weight. Coefficient of variance was indicated (3.2%) for 100-grainweight. Genotypic, phenotypic and environmental variances were estimated as 3.29, 0.63 and 0.0.83 respectively. Coefficient of variance for genotypic, phenotypic and environmental was 37.11%, 40.55% and 16.33% respectively. Estimation of broad sense heritability was 0.83observed for this trait with a genetic advance 2.9413. Results were supported by the findings of Saleem et al. (2002), Ali et al. (2011).

Results of analysis of variance (Table-2) revealed that the differences among genotypes were highly significant. The value ranged from 2.83 to 3.87 for primary branches. Genotypes CH-49 showed maximum primary branches followed by genotypes K-01241 and D-12046. High value (12.00%) of coefficient of variability was indicated for primary branches per plant. The estimation of genotypic, phenotypic and environmental variances was 0.30, 1.42 and 0.11 respectively. The genotypic, phenotypic and environmental coefficient of variance was 30.45%, 35.61% and 18.47% respectively. High estimation of broad sense heritability (0.9445) was observed for this trait. Results of analysis of variance Table-14 revealed that the differences among genotypes were highly significant. The value ranged from 19.73 to 37.78 for seeds per plant. Genotypes AUG-424 showed maximum seeds per plant followed by genotypes TG-1205 and K01241. Low value (11.17%) of coefficient of variance was indicated for seeds per plant. The estimation of genotypic, phenotypic and environmental variances was 10.46, 21.36 and 10.89 respectively. The genotypic, phenotypic and environmental coefficient of variance was 61.20%, 87.43% and 62.44% respectively. High estimation of broad sense heritability (0.4850) was estimated. Findings of this study corroborate with finding of Singh (2007) and Hassan et al. (2005).

Correlation

Correlation is the measure of the extent of relationship between two or more independent variables and it indicates the degree to which various traits of plant are associated with economic productivity. Correlation analysis reveals the relative importance of different plant traits, which can be of the value in crop breeding program. The estimates of genotypic correlation refer to the relationship between two plant traits due to the genetic composition of the plant, while phenotypic correlation means the correlation between the phenotypic appearance of the plant for certain pair of plant trait. Correlation analysis between yield and other various yield related traits to overall seed yield. Genotypic and phenotypic correlation coefficients worked out among all possible combinations of 09 different traits and presented in Table 4.

Days to flowering was associated positively and significantly at genotypic and phenotypic levels with secondary branches per plant, while negative and non-significant with seeds per plant, seeds per pod, 100-grain weight and seed yield per plant. Positive and significant correlation was observed between days to flowering with plant height at genotypic level, while positive and non-significant at phenotypic level. Negative and significant correlation was observed between days to flowering with pods per plant at genotypic level, while positive and non-significant at phenotypic level. Days to flowering had negative and non-significant association with primary

branches per plant at genotypic level but positive and non-significant at phenotypic level. Similar results have been reported by Ali et al. (2008) and Mushtaq et al. (2013).

Plant height had positive and signification correlation with days to flowering, pod per plant and seed yield per plant. A negative and significant association was observed between plant height and seeds per pod. Plant height had positive and non-significant relationship with 100-seed weight at both genotypic and phenotypic level. A positive and non-significant correlation was observed between plant height and secondary branches per plant at genotypic, while positive and significant at phenotypic level. Similar results have been reported by Singh (2007) and Kumar et al. (1999).

Primary branches per plant exhibited positive and significant correlation with 100-grain weight and yield per plant, while negative and significant with pod per plant, secondary branches per plant, plant height and days to flowering at both genotypic and phenotypic levels. Plant height showed positive and non-significant association at both genotypic and phenotypic levels with seeds per pod. A negative significant association was observed between primary branches per plant with seeds per plant at genotypic level, while negative and non-significant at phenotypic level. Similar results have been reported by Jadhav et al. (2014).

Positive and significant correlation was observed between secondary branches per plant with days to flowering, pods per plant and seeds per pod at both genotypic and phenotypic levels. Secondary branches per plant showed positive and non - significant correlation with yield per plant. Secondary branches per plant had positive significant association with 100-seed weight at genotypic level, while positive and significant at phenotypic level. A negative and significant association was observed between secondary branches per plant with primary branches per plant at both genotypic and phenotypic levels. Secondary branches per plant showed positive and non - significant association with plant height at genotypic level, while positive and significant at phenotypic level. A negative and significant association was observed between secondary branches per plant with seeds per pod at genotypic level, while negative and significant at phenotypic level. Similar results have been reported by Saleem et al. (2002).

Pods per plant had positive and significant correlation with plant height, secondary branches per plant, seeds per pod and yield per plant while a negative and significant association was observed of pods per plant with days to flowering, primary branches per plant and seeds per pod at both genotypic and phenotypic level. These results were supported and similar to the findings of Arora et al. (2003) and Ali et al. (2011).

Seeds per plant had positive and significant association with plant height, secondary branches per plant and pods per plant, while negative and significant association with days to flowering and seeds per pod at both genotypic and phenotypic levels. Seeds per pod showed positive and significant correlation with 100-seed weight and seed yield per plant at genotypic level, while positive and non-significant at phenotypic level. A negative and significant correlation was observed between seeds per pod with primary branches per plant at genotypic level, while negative and non-significant at phenotypic level. Similar results were obtained by Ali et al. (2011).

Seeds per pod had negative and significant association with days to flowering, plant height, pods per plant, seeds per plant and 100-seed weight at both genotypic and phenotypic level. A positive and significant association was observed between seed per pod and primary branches per plant at genotypic level, while negative and non-significant at phenotypic level. Seeds per plant showed positive and significant association with secondary branches per plant at genotypic level but negative and significant at phenotypic level. A negative significant correlation was observed between seeds per plant with seed yield per plant at genotypic level, while negative and non-significant at phenotypic level. Similar results have been reported Arshad et al. (2003).

100-seed weight was positively and significantly correlated with primary branches per plant, while negatively and significantly with seeds per pod at both genotypic and phenotypic levels. A positive and non-significant association was observed among 100-seed weight, plant height and pod per plant at both genotypic and phenotypic level. 100 seed weight had positive and non-significant correlation with days to flowering and seed yield per plant at genotypic level, while negative and non-significant at phenotypic level. A positive and significant association was observed among 100-seed weight and secondary branches per plant and seeds per plant at genotypic level, while negative and significant phenotypic level at phenotypic level. Similar results have been reported Arshad et al. (2003).

Seed yield per plant had positive and significant association with plant height, while positive and non-significant with primary branches per plant secondary branches per plant at both genotypic and phenotypic levels. A positive significant association was observed among seed yield per plant, days to flowering, pods per plant and seeds per plant at

genotypic level, but positive and non-significant at phenotypic level. Seed yield per plant had negative and significant correlation with seed per plant at genotypic level while negative and non-significant at phenotypic level. Similar results have been reported Arshad et al. (2003).

Conclusion:

Seed yield per plant had positive and significant association with plant height, while positive and non-significant with primary branches per plant, secondary branches per plant at both genotypic and phenotypic levels. A positive significant association was observed among seed yield per plant, days to flowering, pods per plant and seeds per plant at genotypic level but positive and non-significant at phenotypic level. Seed yield per plant had negative and significant correlation with seed per plant at genotypic level while negative and non-significant at phenotypic level. A positive and non-significant association was observed between seed yield per plant at genotypic level, while negative and non-significant at phenotypic level.

Seeds per pod, seed yield /plant, pod/plant and secondary branches/ plant showed high broad sense heritability so, these are important selection indices for future.

Abbreviations:

rg= genotypic correlation, rp= phenotypic correlation, DF=days to flowering, PH=plant height, PB=primary branches/plant, SB=secondary branches/plant, PP=pods/plant, SPP= Seeds per pod, SP=seeds/plant, HW=100-Seed weight and SYP=Seed yield/plant.

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Table 1. Genotypes

Serial Number	Genotypes	Serial Number	Genotypes
1	TG-1210	11	CM-584
2	BRC-390	12	Bhakkar-2011
3	TG-1205	13	D-12005
4	PB-2008	14	D-11035
5	BRC-403	15	D-11030
6	D-12046	16	D-11033
7	CH-28	17	CM-1036
8	CH-49	18	K-01241
9	CH-72	19	CM-2008
10	D-12036	20	AUG-424

Table 2. Analysis of Variance:

SOV	PH	DF	SPP	SP	SYP	PP	HW	PB	SB
S.S	4327.76	546.779	2.27806	1008.59	2.27806	642.856	223.467	10.9498	86.3493
M.S	225.25	20.33	0.166	47.007	0.166	47.94	12.035	0.433	7.7
F(c)	3.39**	0.04*	2.69**	4.39**	2.69**	3.39**	16.5**	1.78*	4.39**
F(t)	0.0007	0.02	0.0046	0.0001	0.0046	0.0007	0.0000	0.063	0.0001

Table 3. Genotypic, phenotypic and environmental variances:

	PH	**DF**	**SPP**	**SP**	**SYP**	**PP**	**HW**	**PB**	**SB**
CV	9.1	15.7	9.3	9.7	12.4	10.4	3.3	11.1	11.8
Genotypic variance	35.6	10.1	8.4	0.013	8.4	4.6	3.3	0.3	10.5
Phenotypic variance	75.5715	14.75	17.65	0.03719	17.652	10.7672	3.9375	0.41206	21.368
Environmental variance	39.999	4.2	9.25	0.02368	9.25896	6.18857	0.63883	0.11085	10.8982
Genotypic coefficient of variation	71.712	25.56	0.36	0.46323	0.47547	0.42524	0.83776	30.4514	0.48998
Phenotypic coefficient of variation	104.524	27.98	58.5	9.2347	58.5057	43.842	37.1196	35.614	61.2035
Environmental coefficient of variation	76.043	10.98	84.84	15.3217	84.8468	67.2324	40.5554	18.4731	87.436
Broad sense heritability	0.26026	0.49	61.44	12.226	61.4497	50.9711	16.3351	0.73098	62.4431

Table 4. Phenotypic and Genotypic correlation

Traits		DF	PH	PB	SB	PP	SPP	SP	HW	SYP
DF	rg	1.00	0.23*	-0.14	0.32*	-0.13*	-0.20	-0.17	-0.12	-0.28
	rp	1.00	0.18	0.071	0.31*	-0.10	-0.12	-0.18	-0.11	-0.26
PH	rg		0.87**	-0.60**	1.00	0.79**	0.50**	-0.36**	0.14	0.42**
	rp		0.89**	0.034**	0.75**	0.81*	0.59*	-0.38**	0.054	0.27*
PB	rg			0.59**	-0.66**	-0.62**	-0.35**	0.02	0.47*	0.55**
	rp			0.84*	-0.36**	-0.30*	-0.20	0.015	0.35**	0.46**
SB	rg				0.76**	0.89**	0.61**	-0.41**	0.30*	0.17
	rp				0.79**	0.66**	0.49*	-0.025	0.20	0.15
PP	rg					0.67**	0.84**	-0.61**	0.17	0.43**
	rp					0.77**	0.77**	-0.57**	-0.11	0.22
SPP	rg						0.91**	-0.68**	0.26*	0.28*
	rp						0.82**	-0.25*	0.18	0.19
SP	rg							0.88**	-0.44**	-0.49**
	rp							0.92*	-0.27*	-0.19
HW	rg								0.89**	0.06
	rp								0.59**	-0.035
SYP	rg									1.00**
	rp									1.00**

*= significant at 1%, ** = significant at 5%,rg= genotypic correlation, rp= phenotypic correlation,DF=days to flowering, PH=plant height, PB=primary branches/plant, SB=secondary branches/plant, PP=pods/plant,SPP= Seeds per pod,SP=seeds/plant, HW=100-Seed weight and SYP=Seed yield/plant