The Journal of Animal & Plant Sciences, 26(5): 2016, Page: 1334-1338
ISSN: 1018-7081

ASSESSMENT OF GENETIC VARIATION AND MODE OF INHERITANCE OF SOME QUANTITATIVE TRAITS IN CHICKPEA (*CICER ARIETINUM* L.)

N. Hussain, A. Ghaffar, M. Aslam, K. Hussain and Naeem-ud-Din

Arid Zone Research Institute, P.O. Box No.15, Bhakkar, Punjab, Pakistan.
Corresponding Author Email: niazfm@gmail.com

ABSTRACT

The present study was conducted to explore the magnitude of genetic variation and mode of inheritance for some quantitative traits among the sixteen genotypes of chickpea at Arid Zone Research Institute, Bhakkar, during the Rabi crop season 2012-13. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The data regarding eight important quantitative traits was recorded. Four traits viz., number of pods per plant, 100-grain weight, biological yield per plant and grain yield per plant exhibited maximum genetic variation. Genotypic and phenotypic coefficient of variation (GCV and PCV %) was highest for grain yield per plant (19.73 and 20.10) followed by number of pods per plant (18.90 and 19.58), biological yield per plant (13.56 and 14.81) and 100-grain weight (11.60 and 12.25), respectively. High heritability value associated with high genetic advance expressed as percentage of mean was obtained for number of pods per plant (93.19 and 37.59), 100-grain weight (89.67 and 22.62), biological yield per plant (83.83 and 25.58) and grain yield per plant (96.40 and 39.91), respectively. Therefore, these traits can be considered as the most favourable attribute for their improvement due to the contribution of additive gene action and consequently high expected genetic gain from selection.

Key words: Chickpea, genetic variability, heritability, genetic advance.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is the third leading food legume after peas and beans in the world and first in South Asia. It is grown all over the five continents in about 50 countries, with 90% of its cultivated area in developing countries (Faostat 2014). Its range of cultivation extends from the Mediterranean basin to the Indian Sub-continent and South of Ethiopia and the East African highlands. Two types of chickpea, one namely Kabuli is grown in temperate regions while desi type of chickpea is grown in the semi-arid tropics (Muehlbauer and Singh, 1987). Chickpea is the major Rabi pulse crop and is an important source of calories in Pakistan which is predominantly grown in the huge rainfed areas of the country. Pakistan ranks second to India in terms of acreage under chickpea which is cultivated on an area of 960 thousand hectares and contributed the production of 484 thousand tonnes (Anonymous, 2014-15). In Punjab, about 90% chickpea is cultivated in rainfed areas; the major chickpea production belt is Thal including the Districts of Bhakhar, Mianwali, Layyah, Khushab and some parts of Jhang. Therefore, it is very much essential to improve its yield.

Chickpea is rich and readily available source of protein both for human and animals. It is the cheapest source of protein (19.5%), fats (1.4%), carbohydrates (57 to 60%) and high percentage of other mineral nutrients and unsaturated linoleic and oleic acid (Kerem *et al*., 2007). It also maintains the soil fertility by fixing of atmospheric nitrogen through symbiosis together with deep root system.

Existence of genetic variation for different traits in available germplasm is the basis for selection and ultimately for crop improvement. Assessment of genetic variability with the help of suitable parameters such as genotypic coefficient of variation, heritability and genetic advance are important to start an efficient breeding program (Mishra *et al.*, 1988).

Genetic diversity assessment is very helpful in gene-bank management and breeding experiments like tagging of germplasm, identification and elimination of duplicates in the gene stock and establishment of core collections. It is also an integral part of crop improvement. Genetic diversity among the parents is a prerequisite to improve the chances of selecting better segregants for various characters. The more diverse the parents within reasonable limits, the more are the chances of improving the characters under consideration. Varieties from distinct geographic regions are usually selected for a hybridization programme presuming the presence of considerable genetic diversity among them.

The natural variability for yield and its component traits is very narrow in highly self pollinated crops like chickpea and further selection for crop improvement becomes impracticable. However, proper evaluation of the extent of genetic variation available for yield components, their heritability values and genetic advance could be of great helpful to the breeders.

The present studies were undertaken to assess the genetic diversity in respect of various desirable traits

among the sixteen genotypes of chickpea. Therefore, it will help in isolating the promising genotypes and to identify divergent parents for future hybridization program for crop improvement.

MATERIALS AND METHODS

The present study was conducted in the experimental area of Arid Zone Research Institute, Bhakkar during Rabi crop season 2012-2013. The experimental material consisted of fifteen kabuli chickpea advance strains with one approved check (Table-1). The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Each treatment comprised of 4 lines, 5 meters in length, row-to-row and plant-to-plant distances were 30 and 10cm, respectively. The experiment was sown with single row hand drill. After germination, thinning was carried out to maintain the proper plant to plant distance.

Table 1. Genotypes name and their origins.

Sr. No.	Genotypes name	Origins
1	TG12K01	ICARDA
2	TG12K02	Pakistan
3	TG12K03	ICARDA
4	TG12K04	ICARDA
5	TG12K05	ICARDA
6	TG12K06	Pakistan
7	TG12K07	ICARDA
8	TG12K08	ICARDA
9	TG12K09	ICARDA
10	TG12K10	Pakistan
11	TG12K11	ICARDA
12	TG12K12	ICARDA
13	TG12K13	Pakistan
14	TG12K14	ICARDA
15	TG12K15	ICARDA
16	Nor-2009 (Check)	Pakistan

Recommended agronomic practices like irrigation and hoeing etc were equally provided to all the treatments to raise a good crop. Data from five randomly selected plants per row (20-plants per genotype) were recorded for eight quantitative traits regarding days to 50% flowering, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, 100-grain weight (g), biological yield per plant(g) and grain yield per plant (g).The data were subjected to analysis of variance (Steel *et al*., 1997) to determine the level of significance between treatments. Genotypic variance ($\sigma^2 g$), Phenotypic variance ($\sigma^2 p$) and environmental variance ($\sigma^2 e$) were determined by formulae proposed by Brewbaker (1964). Genotypic and phenotypic coefficients of variance based on mean ($\bar{X}$) and variance were computed by the formula suggested by Burton (1952).

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sqrt{\sigma^2 g}}{\bar{X}} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sqrt{\sigma^2 p}}{\bar{X}} \times 100$$

Broad sense heritability $[h^2(bs)]$ was estimated using the formula given by Singh and Choudhary (1979).

$$\text{Heritability } [h^2(bs)] (\%) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

The genetic advance (GA) was calculated according to Allard (1960) as under:

GA (Δ G) = K × σ_P × h^2(bs)

Where, K = Selection differential at 5% level of selection (2.06), σ_P = Standard deviation of the phenotypic variance and h^2(bs) = Heritability in broad sense

Genetic advance expressed as percentage of mean (GA %) was measured by the following formula.

$$\text{GA (\%)} = \frac{GA}{\bar{X}} \times 100$$

RESULTS AND DISCUSSION

The analysis of variance revealed that the genotypes differed considerably for all the traits under study (Table 2). Grand mean, standard error and range of the all traits under study are presented in Table 3. Wide range of variation was observed in all the characters. However, the range in mean values does not reflect the total variance in the material studied. Therefore, actual variance has to be estimated for the traits to know the extent of existing genetic variability.

The estimate of genotypic variance ($\sigma^2 g$), genotypic coefficient of variation (GCV), phenotypic variance ($\sigma^2 p$), phenotypic coefficient of variation (PCV), environmental variance ($\sigma^2 e$), heritability (h^2) and genetic advance as per cent mean (GAM) for eight different characters are depicted in Table 4. Relatively higher value of genotypic variances were found for number of pods per plant (94.93), biological yield per plant (75.30), grain yield per plant (34.27), plant height (30.71) and 100-grain weight (16.79), while the lower genotypic variances were found for days to 50% flowering (5.15), number of secondary branches per plant (0.69) and number of primary branches per plant (0.16). Upadhyaya *et al*., (2002) reported high genotypic variations for number of pods per plant and 100-grain weight. Kumar *et al*., (2001) reported high genotypic variations for number of pods per plant and seed yield per plant. The highest phenotypic variances were found for number of pods per plant (101.86), biological yield per plant (89.82), plant

height (38.96), grain yield per plant (35.55) and 100-grain weight (18.73), while the lower phenotypic variances were found for days to 50% flowering (8.73), number of secondary branches per plant (1.32) and number of primary branches per plant (0.27). Similarly, Khorgade *et al.,* (1985) revealed that pod number had great phenotypic variance. The highest environment variance was found for biological yield per plant (14.52) while the lowest for number of primary branches per plant (0.10).

Higher values of PCV and GCV indicate wider variability and vice a versa. In the same context, narrow differences between the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) implies lesser influence of environment on these traits. The phenotypic variance and phenotypic coefficient of variation (PCV) were more than their respective genotypic variance and genotypic coefficient of variation for all the traits indicating the influence of environment on the expression of these traits.

Genotypic coefficient of variations were comparatively greater in grain yield per plant (19.73), number of pods per plant (18.90 %), biological yield per plant (13.56%), number of primary branches per plant (12.75%) and 100-grain weight (11.60%), while it was smaller in days to 50% flowering (2.10%). Kumar *et al*., (2001) and Upadhyaya *et al*., (2002) observed higher genotypic coefficient of variations for number of pods per plant. Furthermore, Vijayalaxmi *et al*., (2000) studied genetic variation and heritable components of variation in desi, kabuli and intermediate chickpea indicated that selection might be emphasized on the basis of number of pods per plant and 100-grain weight. Shaukatali *et al.*, (2002) and Upadhyaya *et al*., (2002) also reported high genotypic variation for 100-grain weight.

Highest phenotypic coefficients of variations were recorded in grain yield per plant (20.10%), number of pods per plant (19.58%), biological yield per plant (14.81%), number of primary branches per plant (16.26%) and 100-grain weight (12.25%), while it was smaller in days to 50% flowering (2.74%). Days to 50% flowering recorded lower values of PCV and GCV. This indicate narrow genetic base for this character. Improvement in this character can be brought about through hybridization or induced mutation for widening genetic base followed by pedigree selection in advanced generations.

Overall, Grain yield per plant and number of pods per plant manifested high estimates of PCV and GCV suggesting that emphasis should be given on these characters during selection of improved genotypes because these characters have high range of genetic variation, hence, a better scope of improvement through selection. Dwevedi and Gaibriyal (2009) recorded highest phenotypic and genotypic coefficient of variation (PCV and GCV) for number of pods per plant followed by biological yield per plant and 100-grain weight.

Heritability and genetic advance: It is not possible to find out the quantity of variation that is heritable with the help of GCV alone. The GCV in concert with heritability estimates would give committed indication of the expected magnitude of improvement through selection (Johnson *et al*., 1955). Broad sense heritability gives an idea about portion of observed variability attributable to genetic differences. The difference between PCV and GCV estimates indicates the relative influence of environment on the character, which in turn decides the extent of their heritability. If the difference is low for a character then the influence of environment is less coupled with high heritability. Wide differences indicate considerable influence of the environment, thus resulting in low heritability estimates.

Broad sense heritability in the eight quantitative characters ranged from 52.38% to 96.40%. The traits in order of high heritability were grain yield per plant (96.40%), number of pods per plant (93.19%), 100-grain weight (89.67%), biological yield (83.83%) and plant height (78.83). Dubey and Srivastava (2007) reported high heritability (broad sense) for plant height, number of pods per plant, 100-grain weight and grain yield per plant. Burli *et al.,* (2004), and Dwevedi and Gaibriyal (2009) also observed high values of heritability (broad sense) for number of pods per plant and 100-grain weight in chickpea. The traits having relatively low heritability were number of secondary branches per plant (52.38%) and days to 50% flowering (58.99%). Arora and Jeena (2000) recorded low value of heritability for days to 50% flowering; Singh and Rao (1991) for number of primary branches per plant and Rao *et al.,* (1994) for number of secondary branches per plant respectively.

Heritability estimates alone provides no evidence for genetic improvement that would result from selecting the superior individuals. Johnson *et al.,* (1955) concluded that heritability estimates along with genetic gain would be more useful in predicting the effectiveness of selecting the best individual. Therefore, it is crucial to consider the predicted genetic advance along with heritability estimate as a tool in selection programme for better efficiency.

Genetic advance expressed as percentage of mean, revealed difference among the characters under study. In the current study, high heritability coupled with high genetic advance as percent of mean were recorded for grain yield per plant (39.91), number of pods per plant (37.59), biological yield per plant (25.58) and 100-grain weight (22.62). This indicates that there was low environmental influence on the expression of these characters. Similar findings were reported by Jahagirdar *et al.,* (1994), and Dubey and Srivastava (2007). Therefore, crop improvement could be achievable by

simple selection because high heritability in concert with high genotypic variation revealed the existence of an additive gene action (Noor *et al.*, 2003).

Similarly, low or moderate to high heritability associated with low genetic advance were observed for days to 50% flowering (3.33), plant height (15.41), number of secondary branches per plant (12.53) and number of primary branches per plant (20.58) revealed that expression of these characters were governed by non-additive gene action (dominance and epistasis). In this context, Arshad *et al.,* (2002) reported that number of primary branches was greatly influenced by the environment. Therefore, the appropriate usage of pure line selection may be valuable for improving these characters with moderate or high heritability and with low genetic advance.

The present studies revealed high heritability associated with high genetic advance as percent of mean for the characters viz., number of pods per plant, 100-grain weight, biological yield per plant and grain yield per plant indicating the presence of considerable variation and additive gene effects. Hence, improvement of these characters could be useful through phenotypic selection.

Table 2. Analysis of variance for yield and yield related traits in sixteen chickpea genotypes.

Sources of Variation	D.F.	DTF	PBP	SBP	PH	PPP	100G	BYP	GYP
Replications	2	11.31	0.37	0.16	176.60	21.32	0.65	16.01	6.31
Genotypes	15	26.18**	0.80*	3.95**	116.88**	305.58**	56.19**	269.45**	106.64**
Error	30	10.73	0.31	1.88	24.74	20.80	5.81	43.56	3.84

Where
DTF Days taken to 50% flowering, **PBP** Primary branches per plant, **SBP** Secondary branches per plant, **PH** Plant height (cm), **PPP** Pods per plant, **100G** 100-grain weight (g), **BYP** Biological yield per plant (g), **GYP** grain yield per plant (g)
****** Highly significant
***** Significant

Table 3. Mean, standard error, range and variance for 8 traits in 16 chickpea genotypes

Traits	Mean	Standard error	Range
Days to 50% flowering	107.81	1.89	97-115
Primary branches per plant	3.17	0.32	02-06
Secondary branches per plant	9.87	0.79	6.80-12.80
Plant height (cm)	65.78	2.87	49.60-81.80
Pods per plant	51.55	2.63	30-70.60
100-grain weight (g)	35.34	1.39	27.66-45
Biological yield per plant (g)	63.99	3.81	39.46-90
Grain yield per plant (g)	29.67	1.13	19.73-50

Table 4. Genetic parameters for various quantitative traits in chickpea genotypes

Traits	$\sigma^2 g$	GCV (%)	$\sigma^2 p$	PCV (%)	$\sigma^2 e$	$[h^2(bs)]$ (%)	GA	GA as percent of mean	CV%
Days to 50% flowering	5.15	2.10	8.73	2.74	3.58	58.99	3.59	3.33	3.04
Primary branches per plant	0.16	12.75	0.27	16.26	0.10	61.46	0.65	20.58	17.48
Secondary branches per plant	0.69	8.41	1.32	11.61	0.63	52.38	1.24	12.53	13.88
Plant height (cm)	30.71	8.43	38.96	9.49	8.25	78.83	10.14	15.41	7.56
Pods per plant	94.93	18.90	101.86	19.58	6.93	93.19	19.38	37.59	8.85
100-grain weight (g)	16.79	11.60	18.73	12.25	1.94	89.67	7.99	22.62	6.82
Biological yield per plant (g)	75.30	13.56	89.82	14.81	14.52	83.83	16.37	25.58	10.31
Grain yield per plant (g)	34.27	19.73	35.55	20.10	1.28	96.40	11.84	39.91	6.61

REFERENCES

Allard, R.W. (1960). Principles of Plant Breeding. John Wiley and Sons, Inc., N.Y.

Anonymous (2014-15). Economic Survey of Pakistan. Economic Advisor's Wing, Finance Division, Government of Pakistan, Islamabad.

Arora, P.P. and A.S. Jeena (2000). Variability in relation to response to selection in chickpea. Agric. Sci. Dig., 20: 267-298.

Arshad, M., A. Bakhsh, M. Bashir and A.M. Haqqani. (2002). Determining the heritability and relationship between yield and yield components in chickpea (*Cicer arietinum* L.). Pakistan J. Bot., 34: 237-245.

Brewbaker, J.L. (1964). Agricultural genetics. Printice Holl N.Y., Cap. IV.

Burli, A.V., S. M. More, B.N. Gare and S.S. Dodake (2004). Studies on genetic variability and heritability in chickpea under residual soil moisture condition. J. Maharashtra Agr. Uni., 29(3):353-354.

Burton, G.W. (1952). Quantitative inheritance in grasses. Proc. 6th Int. Grassld. Cong. 1 (pp. 277-283).

Dubey, K.K. and S.B.L. Srivastava (2007). Study of direct selection in chickpea (*Cicer arietinum* L.). Plant Archives., 7 (1): 211-212.

Dwevedi, K.K. and M.L. Gaibriyal (2009). Assessment of genetic diversity of cultivated chickpea (*Cicer arietinum* L.). Asian J. Agri. Sci., 1(1): 7-8.

Faostat. (2014). http://faostat.fao.org/. Accessed Oct 2014.

Gupta, S.P., R.C. Luthra, A.S. Gill and P.S. Phul (1969). Variability and correlation on yield and its components in gram. J. Res. Punjab Agric. Univ. 9(3): 405-409.

Jahagirdar, J.E., R.A. Patil and P.R. Khare (1994). Genetic variability and its relevance in chickpea improvement. Indian J. Pulses Res., 7 (2): 179-180.

Johnson, H.W., H.E. Robinson and R.E. Comstock (1955). Estimation of genetic and environmental variability in soybean, Agron. J., 47: 314-318.

Kerem, Z., S. Lev-Yadun, A. Gopher, P. Weinberg and S. Abbo (2007). Chickpea domestication in the neolithic levant through the nutritional perspective. J. Archaeol. Sci. 34: 1289-1293.

Khorgade, P.W., M.N. Narkhede and S.K. Raut (1985). Genetic variability studies in chickpea (*Cicer arietinum* L.). International Chickpea Newsletter, June, 12: 12-13.

Kumar, S., P.P. Arora and A.S. Jeena (2001). Genetic variability studied for quantitative traits in chickpea. Agriculture Sci. Digest, 21: 263 -265.

Mishra, R., S.K. Rao and L.K. Koutu (1988). Genetic variability, correlation studies and their implications in selection of high yielding genotypes in chickpea. Indian J. Agri. Res. 22: 51 – 57.

Muehlbauer, F.J. and K.B. Singh (1987). Genetics of chickpea (*Cicer arietinum* L.). In: M. C. Sexana and K. B. Singh (eds:), The chickpea CAB International, Wallingford, Oxon, OX10 8DE UK, p. 99-126.

Noor, F., M. Ashaf and A. Ghafoor (2003). Path analysis and relationship among quantitative traits in chickpea (*Cicer arietinum* L.). Pakistan J. Biol. Sci., 6: 551-555.

Rao, S.S., R. Singh and G.K. Das (1994). Genetic variability, heritability, expected genetic advance and correlation studies in chickpea. Indian J. Pulse Res., 7 (1): 25-27.

Shaukatali, Maher, A.B., M. Anwar and A. M. Haqqani (2002). Exploitation of genetic variability for grain yield improvement in chickpea. Int.J. Agric. Biol., 4: 148 – 149.

Singh, R.K. and B.D. Choudhary (1979). Biometrical methods in quantitative genetic analysis. P. 3204.

Singh, R.K. and S.K. Rao (1991). Heritability and genetic advance in segregating populations of chickpea. Res. Dev. Rep., 8: 21-26.

Steel, R.G.D., J.H. Torrie and D.A. Dickey (1997). Principles and Procedures of Statistics: A Biometrical Approach. 3rd Edi. McGraw Hill Book Co., New York, USA.

Upadhaya, H. D., R. Ortiz, P. J. Bramel and S. Singh. (2002). Phenotypic diversity for morphological characteristics in chickpea core collection. Euphytica, 12: 333-342.

Vijayalaxmi, N.V.S., K. Kumar and R.T. Nageshwar. (2000). Variability and correlation studies in desi, kabuli and intermediate chickpea. Legume Res., 23(4): 232-236.