Genetic Variability Studies in Marker Assisted Backcross Lines of Chickpea (*C. arietinum*)

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A B S T R A C T

The present investigation was carried out for estimation of genetic variability in 242 BC_3F_4 chickpea (*Cicer arietinum* L.) lines derived from the cross Annigeri-1 × WR-315 through marker assisted backcrossing (MABC) studied under rainfed condition. The yield and yield attributing traits were studied in BC_3F_4 MABC lines to understand the existence of genetic variability parameters. The MABC lines exhibited significant amounts of variability for all the characters studied. The wide range of variation provides scope to select superior and suitable genotypes. It was found that low GCV and PCV with narrow differences were recorded for days to 50 per cent flowering (3.79 and 4.78%) and days to maturity (1.33 and 1.86%) indicating that there was less influence of environmental factors. In general high heritability accompanied by high genetic advance as expressed in percentage of mean (GAM) was recorded for seed yield per plant, number of pods per plant followed by 100 seed weight respectively. This research paper reports that high heritability is due to the additive gene effects and promoted use high estimates of heritability coupled with high genetic advance for genetic improvement of these traits through selection in BC_3F_4 MABC lines of chickpea for future breeding programme.

Introduction

Chickpea (*Cicer arietinum* L.) is known as third most important pulse crop in the world (Padmavathi *et al.,* 2013). The genus *Cicer* belongs to the family Leguminosae and to the sub-family Papilionoideae. It is considered to have originated in South-Eastern Turkey and the adjoining Northern region of Syria (Singh, 1987) and that evolved from its wild progenitor *Cicer reticulatum* by selection (Van der Maesen, 1987). Most of the *Cicer*

species are diploids with $2n = 2x = 16$ chromosomes and a genome size of about 738 Mb (Jain *et al.,* 2013 and Varshney *et al.,* 2013). It provides good source of protein, energy, fiber, vitamin and minerals and considered healthy food in many developed countries (Nair and Mehta, 2014). It is also good source of amino acids like tryptophan and lysine (Awasthi *et al.,* 1991). Apart from providing dietary benefits to human beings

chick pea is very useful in management of soil fertility due to nitrogen fixation ability (Gul *et al.,* 2011). Chickpea is a highly nutritious grain containing 20–30 % protein, 40 % carbohydrate and 3–6 % oil (Gil *et al.,* 1996). It provides a high-quality protein source for people in both developed and developing countries. The stover of chickpea is also fed to some animals as a nutrient-rich supplement to their major cereal fodder in lean seasons (Deb and Khaleque 2009).

Chickpea reached a record of high global area of 13.5 m ha and production of 13.1 m t (FAOSTAT, 2015). India is the largest chickpea producing country cultivated over an area of 8.35 m ha with 7.17 m t production and productivity of 859 kg/ha (Anonymous, 2016). The other major chickpea producing countries include Australia, Pakistan, Turkey, Myanmar, Iran, Ethiopia, Canada and USA. Kalaburagi is very important potential district in the country for extensive cultivation of chickpea and pigeonpea and hence known as 'Pulse bowl' of Karnataka. It is also grown in Bidar, Bijapur, Dharwad, Gadag, Raichur, Bellary and Belgaum districts of Northern Karnataka. In Karnataka, chickpea occupies an area of 1.37 m ha, with production and productivity of 0.90 m t and 654 kg/ha respectively (Anonymous, 2016).

The science of crop improvement plays a vital role in creation of variability which provides greater opportunity for the selection of trait of interest. Hence, it is essential to study and utilize the existing variability in BC_3F_4 MABC lines of chickpea.

Johanson (1903) gave the basic idea of variability, while developing concept of pureline. Vavilov (1951) ascertained that greater the variability more the chances of obtaining desirable genotypes and prove it to be the basic fundamental for improvement of crop plant through selection.

Accessibility of sufficient genetic variability is pre requisite for commencing systematic crop improvement programme to be fruitful. The first and foremost requirement in any crop improvement programme is to increase the yield potential of the crop. Seed yield is the most important economic character and very complex in nature because it is governed by polygenes and greatly influenced by environmental factors (Singh *et al.,* 2014). Therefore, it is essential for a plant breeder to measure the variability with the help of parameters like phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance. Lush (1940) suggested the method of estimation of phenotypic, genotypic and environmental variances, which further permits estimation of phenotypic coefficients of variation (PCV), genotypic coefficients of variation (GCV) and environmental (ECV) (Burton, 1952). Therefore, study of genetic variability of seed yield and its component characters among different BC_3F_4 MABC lines provides a strong basis for selection of desirable genotypes for increasing yield and other agronomic characters.

Thus, the present research paper aims at thorough understanding of the genetic variation for different traits, their heritability and relationship with yield and yield attributing traits are important for any crop improvement programme. The information achieved will be employed in planning the breeding scheme in chickpea development programme.

Materials and Methods

Research was carried out at the All India Coordinated Research Project on Chickpea (AICRP on Chickpea) at Agricultural Research Station, Kalaburagi, UAS, Raichur, during post rainy season (October to February) of 2015-16, which is situated in

North Eastern Dry Zone (Zone-2) of Karnataka between 16° 2' N latitude and 76° 42' E longitude and 443 meters above mean sea level.

Two hundred and forty two chickpea BC_3F_4 MABC lines were evaluated in normal condition during *Rabi* season 2015-16 by following augmented design. The seeds were sown in single row length of 4 m with spacing of 30 cm x 10 cm and the recommended packages of practices were adopted for the better growth and development of healthy crop.

The data recorded on the mean values of five randomly selected plants in each genotype. Data regarding seven traits *viz.,* days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of pods per plant, seed yield per plant (g) and 100-seed weight (g) were recorded for all the chickpea genotypes.

The characters were subjected to statistical analysis as per Federer (1977) was recorded in order to assess the variability among the genotypes. The data was analysed using Windostat ver. 9.1 software which is one of the advanced biometric programmes which gives accurate and reliable results with less amount of time. Both genotypic and phenotypic coefficients of variability for all the characters were computed as per the method given by Burton and De vane (1953).

The broad sense heritability (h^2 bs) for all the characters were estimated as a percentage of the ratio of genotypic variance to phenotypic variance as per Allard's formula (1960). Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. Genetic advance (GA) and genetic advance as per cent mean (GAM) was computed by using the formula elucidated by Johnson *et al.,* (1955).

Results and Discussion

The MABC lines exhibited significantly wide range of variation for all the characters studied. The wide range of variation provides scope to select superior and suitable genotypes. The results of the present investigation are in a line with the observations of Kumar *et al.,* (2014) for Days to flowering, Days to maturity, Plant height at maturity (cm), Primary branches, Number of pods per plant, Seed yield per plant (g), and 100-Seed weight (g).

The variation in 242 BC_3F_4 MABC lines for all the seven quantitative characters is evident from the analysis of variance (Table 1). Different parameters like range, phenotypic and genotypic variance, phenotypic and genotypic coefficients of variance, heritability estimates and predicted genetic advance over mean for all the characters are presented in Table 2, Fig. 1 and Fig. 2. The description of individual character is presented below.

The variability is assessed through a simple approach of examining the range of variation in MABC population. The extent of variability as measured by genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) also give information regarding the relative amount of variation in different characters.

In the present study the MABC lines have shown low GCV (3.79, 1.33%) and PCV (4.78, 1.86%) for days to 50 per cent flowering and days to maturity respectively and these findings are in accordance with the earlier findings of Meena *et al.,* (2014)**;** Bala *et al.,* (2015)**;** Jeena *et al.,* (2005) and Akanksha *et al.,* (2016). For these traits, narrow difference between phenotypic and genotypic variance was observed, indicating that there was less influence of environmental factors.

Table.1 Analysis of variance for seven quantitative characters of BC_3F_4 MABC lines of chickpea

| Source of variations	df	D.F	D.M	P.H	P.B	N.P.P	SY/ P (g)	100 SW (g)
Block (eliminating Check + Var)	10	8.273**	7.187**	1.884	0.188	56.085**	3.418*	0.321
Entries (ignoring Blocks)	244	5.676**	3.459*	19.529**	0.411	210.296**	10.086**	11.740**
Checks	2	3.303	15.848**	20.818**	1.091*	372.758**	42.939**	185.818**
Varieties	241	4.345**	3.255*	17.668**	0.399	209.812**	9.743**	9.753**
Checks vs. Varieties	1	331.256**	27.774**	465.601**	1.968**	2.117	26.997**	118.088**
ERROR	20	1.536	1.515	1.285	0.224	14.057	1.373	0.585

** = Significant at P = 0.01 * = Significant at P = 0.05, df: Degrees of freedom; DF: Days to 50% flowering; DM: Days to maturity; PH: Plant height; PB: Primary branches; NPP: Number of pods per plant; SY/P: Seed yield per plant; SW: Seed weight

Table.2 Estimation of range, mean and different genetic parameters for yield and yield attributing traits of BC_3F_4 MABC lines of chickpea

Sl. No	Traits	Range		Mean	Variation		Co-efficient of variation (%)		h^2bs (%)	GA (%)	GAM (%)
		Min	Max		Genotypic	Phenotypic	Genotypic	Phenotypic			
1	Days to 50 Flowering	39.00	49.00	42.00	2.56	4.10	3.79	4.78	62.53	2.61	6.15
2	Days to Maturity	90.00	100.00	95.00	1.59	3.10	1.33	1.86	51.18	1.86	1.96
3	Plant height	11.00	44.00	35.00	14.96	16.24	10.91	11.37	92.09	7.64	21.56
4	Primary branches	2.00	5.00	3.00	0.16	0.38	11.53	17.88	41.61	0.53	15.32
5	Number of pods per plant	16.00	127.00	52.00	178.70	192.76	25.63	26.62	92.71	26.56	50.84
6	Seed yield per plant (g)	3.00	26.00	10.00	7.64	9.01	28.08	30.50	84.77	5.24	53.27
7	100 seed weight (g)	13.00	19.00	16.00	8.37	8.95	18.65	19.29	90.55	5.76	37.14

h^2bs: Broad sense heritability; GA: Genetic advance; GAM: Genetic advance as % mean

Fig.1 Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for 7 characters in chickpea
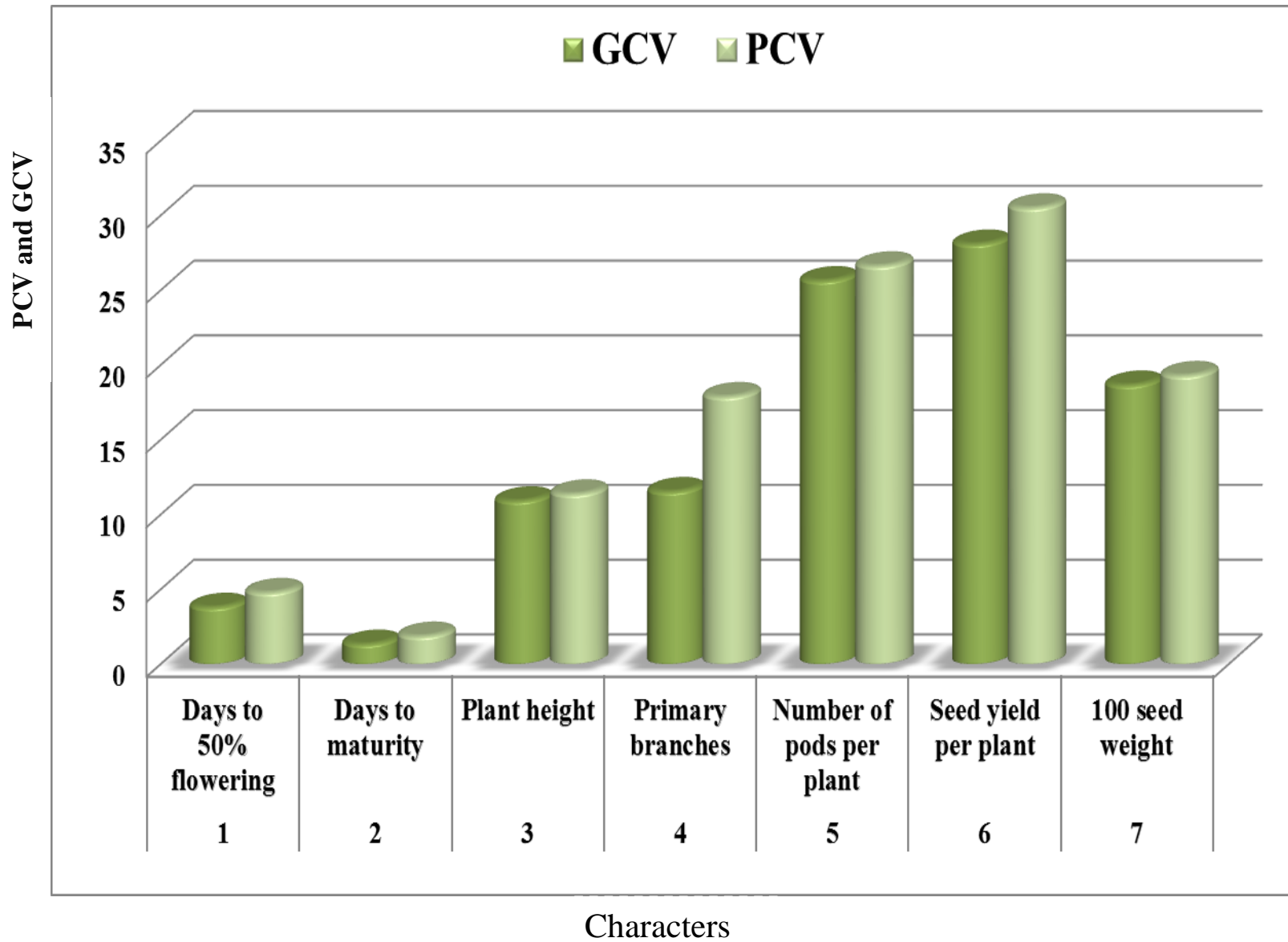
Fig.2 Heritability (h^2) and genetic Advance as per cent mean (GAM) for 7 characters in Chickpea
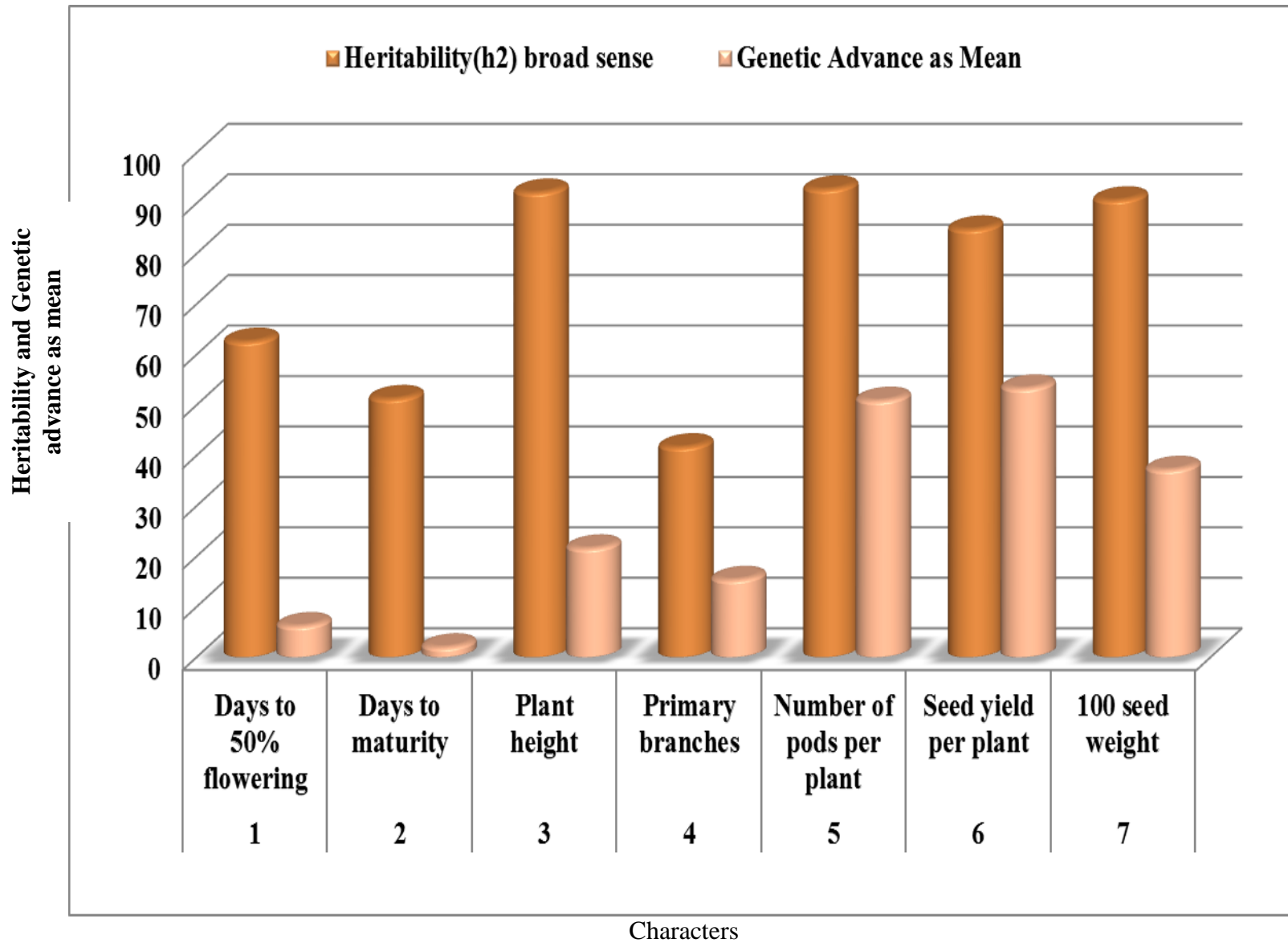
High heritability (62.53 %) coupled with low genetic advance as a per cent mean (6.15 %) for days to flowering indicated that the trait was under the influence of non-additive gene action and thus selection for this trait would result in less genetic gain. These results are in agreement with Meena *et al.,* (2014), Jeena *et al.,* (2005) and Arshad *et al.,* (2004). The high heritability may be due to favourable influence of environment rather than genotype and selection for such traits may be non-rewarding. Further, revealed that moderate heritability (51.18%) coupled with low genetic advance (1.86%) for days to maturity, was in accordance with earlier findings of Babbar *et al.,* (2015).

Plant height and primary branches per plant revealed moderate GCV (10.91, 11.53%) and PCV (11.37, 17.88%) respectively. These findings are in accordance with the earlier workers *viz.*, Bala *et al.,* (2015), Meena *et al.,* (2014) and Nizama *et al.,* (2013). For these traits, narrow difference between phenotypic and genotypic variance was observed, indicating that there was less influence of environmental factors. Similarly, Moderate GCV (18.65%) and PCV (19.29%) were recorded for 100 seed weight. This finding was in accordance with the earlier findings of Babbar *et al.,* (2015), Singh *et al.,* (2009) and Gul *et al.,* (2013). Further, selection based on such traits results in desired direction.

High heritability (92.09%) (Singh and Singh, 2009) coupled with high genetic advance as a per cent mean (21.56%) for plant height suggesting a possibility of isolation of superior lines for this character in MABC lines. In case of primary branches per plant exhibited low heritability (41.61%) coupled with low genetic advance observed for this trait and these results were in accordance with Malik *et al.,* (2010), Babbar *et al.,* (2015), Singh *et al.,* (2009) and Gul *et al.,* (2013). This character is highly influenced by

environmental effect and selection would be ineffective. Further, seed yield per plant and 100 seed weight showed high heritability (84.77, 90.55%) coupled with moderate genetic advance (5.24, 5.76%) findings were in accordance with Meena *et al.,* (2014), Kumar *et al.,* (2014), Waseem *et al.,* (2014), Sachin *et al.,* (2014) and Mohamed *et al.,* (2015), it is indicative of non-additive gene action. The high heritability is being exhibited due to favourable influence of environment rather than genotype and selection for such traits may not be rewarding. These findings are in accordance with the earlier findings of Malik *et al.,* (2010) Babbar *et al.,* (2015) and Jadhav *et al.,* (2014).

High GCV (25.63, 28.08%) and PCV (26.62, 30.05%) were recorded for number of pods per plant and seed yield per plant respectively. High value of PCV and GCV for these traits have also been reported by Vaghela *et al.,* (2009), Qurban *et al.,* (2011), Ali *et al.,* (2011), Gaikwad *et al.,* (2011), Shweta *et al.,* (2013), Peerzada *et al.,* (2014) and Alka Dev *et al.,* (2017). This indicates that these traits are main yield contributing characters given by Kumar *et al.,* (2016).

In general high heritability accompanied by high genetic advance as expressed in percentage of mean (GAM) was recorded for seed yield per plant (84.77, 53.27%), number of pods per plant (92.71, 50.84%) followed by 100 seed weight (90.55, 37.14%) respectively. The same results were also reported by Vaghela *et al.,* (2009), Shweta *et al.,* (2013), Waseem *et al.,* (2014), Kumar *et al.,* (2014) and Kumar *et al.,* (2016). The traits having high heritability coupled with high genetic advance generally indicates that heritability is more due to the additive gene effect and advocated the use of high estimates of heritability along with high magnitude of genetic advance for genetic improvement in any trait through selection.

The study indicated that seed yield per plant and number of pods per plant exhibited high amount of high heritability values and greater genotypic and phenotypic coefficient of variations coupled with genetic advance expressed as percentage of mean. The phenotypic selection for these traits would be most effective for future chickpea breeding programme.

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