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Assessment of Genetic Variability Parameters for Yield and its Components in Chickpea (*Cicer arietinum* L.)

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ABSTRACT: An investigation consisted of 225 chickpea genotypes along with 5 checks *viz.*, PG-5, PG-3, H208, DCP-92-3 and GL10006 was conducted during the *rabi* season of year 2017-18 at N.E.B., C.R.C., GBPUA & T, Pantnagar, Uttarakhand. The objective of present study was to estimate magnitude of different parameters of genetic variability for yield and its attributes. The observations were recorded for thirteen different yield and its contributing characters and the obtained results indicated that in general the phenotypic coefficient of variance was found to be higher as compared to genotypic coefficient of variance for all studied traits. High heritability along with high genetic advance (% mean) was obtained for characters *viz.*, number of primary branches/plant (PB), number of secondary branches/plant (SB), first pod height (FPH), number of pods per plant (PPP), number of seed per pod (SPP), 100 seed weight (SW), biological yield (BY) and seed yield (Yield).Thus, the high heritability coupled with high genetic advance revealed the presence of additive gene effect for these characters and hence can be improved upon by selection.

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

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is a major food crop, especially in tropical and subtropical climates (Fikre and Bekele 2019), and is classified as one of the world's ancient and most often cultivated legumes in the *Fabaceae* (*Leguminosae*) family (Ullah *et al.*, 2020). It is a cool-season pulse crop (Zwart *et al.*, 2019), and also known as Gram, Bengal gram or Chana in Hindi (as well as other names). Despite the fact that it is a diploid (2n=2x =16) and primarily self-pollinated crop, cross-pollination by insects does occur on occasion (Ahmad *et al.*, 2005). It has spread across more than 50 countries, with Asia accounting for 89.7 percent of the total, Africa accounting for 4.3 percent, America accounting for 2.9 percent, Oceania accounting for 2.6 percent, and Europe accounting for 0.4 percent (Dixit *et al.*, 2019). In India, It is grown mainly as a rainfed crop. India accounts for a substantial share of the world's chickpea area (70 per cent) and production (67 per cent), and continues to be a major producer along with other countries *viz.*, Myanmar, Ethiopia, Turkey, and Pakistan (FAOSTAT, 2019). Madhya Pradesh (M.P), Maharashtra, Rajasthan, Uttar Pradesh (U.P), Andhra Pradesh (A.P), Karnataka, Chhattisgarh, Bihar, and Jharkhand are the states that produce the majority of the chickpeas, responsible for > 95 % of the total production. However, chickpea area, production, and productivity have risen significantly in recent years (Dixit *et al.*, 2019). The main concern for India is the decreasing area from 9.27 mha in 1961 to 8.39 mha in 2016. From 1961 to 2019, there has been a significant increase in production by 1.56 million tonnes (Merga and Alemu 2019). There is urgent need for development of selection criteria and action towards improving yield levels of chickpea.

Genetic variability is important indices for plant breeders because it provides a source of variation as well as raw material for yield enhancement (Gaur *et al.*, 2020; Verma *et al.*, 2018). The selection of yield contributing characters is important for crop improvement and the selection of such characters depends mainly on heritable variation as well as the heritability of the trait concerned. It is necessary to have a highly accurate and appropriate method for estimating genetic variability that is not affected by environmental factors in order to promote a valid estimation of parameters. Specifically, the magnitude of genetic variability present in breeding material has a significant impact on the amount of progress that has been made in crop improvement as a result of selection. Its expression is also influenced by the prevailing environment conditions. Hence, to fulfil growing demand for varietal improvement and increased productivity, it is essential to collect, analyse, and record all available genetic variability in genotypes. Knowledge and experience of variability is a prerequisite for breeder in any crop improvement programme. Both variability as well as heritability are important parameters that can aid breeders at various phases of crop improvement.

The effectiveness of the breeding programme would depend on the magnitude of variability and heritability in early-generation populations for important economic traits (Pal *et al*., 2018). The heritability estimate in combination with the genetic advance, is required to predict the specific impact from the selection of the most appropriate individuals for a given situation (Johnson *et al.*, 1955). Therefore, the current study conducted and analysed using potential genotypes to estimate variability, heritability, and genetic advance for yield and yield contributing traits in chickpea.

MATERIALS AND METHODS

Experimental Material and Field Trial. The experimental material for this study included 225 chickpea genotypes and five checks, namely PG-5, PG-3, H208, DCP-92-3, and GL10006. Considering each genotype as one treatment, the experiment was laid out in augmented design (Federer, 1955, 1961, and Federre & Raghavrao, 1975) with five blocks during *rabi* season of year 2017-18 at N.E.B., C.R.C., GBPUA&T, Pantnagar, Uttarakhand. Each block consisted of 50 elite genotypes including five checks. Each accession was planted in a single 4 meter long row with a row to row distance of 30 cm and plant to plant distance of 10-15 cm. The standard package of practices for chickpea cultivation was followed.

Observed traits and sampling measurements: The observations were recorded on 5 plants randomly selected from a single row of each chickpea genotypes for yield and its attributes (Table 1). The observation was recorded on whole row basis for DF and DM, whereas on the composite sample basis SW and HI were also calculated (Table 1). The observations were recorded as per protection of plant varieties and farmers right authority (PPV & FRA) DUS guidelines (2007) for chickpea. The mean values from each observation for each block were used for statistical analysis.

Table 1: Observations recorded for yield and yield contributing traits.

Sr.No.	Characters
1.	Days to50% flowering (DF)
2.	Days to maturity (DM)
3.	Plant height (cm) (PH)
4.	First pod height (cm) (FPH)
5.	Number of primary branches per plant (PB)
6.	Number of secondary branches per plant (SB)
7.	Pod size (mm) (PS)
8.	Number of pods per plant (PPP)
9.	Number of seeds per pod (SPP)
10.	100 seed weight (g) (SW)
11.	Biological yield (g) (BY)
12.	Harvest index (%) (HI)
13.	Seed yield (g) (Yield)

Statistical analysis: The phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) were computed according to the method suggested by Burton (1952). These values were categorized as high (>20 %), moderate (10-20 %) and low (<10%) as indicated by Sivasubramanian and Menon (1973). Heritability (h^2_{bs}) was estimated for each character as suggested by Hanson *et al*., (1956). The heritability was categorized as high (> 60 %), moderate (30-60 %) and low (<30 %) as given by Robinson *et al.*, (1949). For each character, genetic advance (GA) was estimated by method given by Johnson *et al*., (1955). Genetic advance as % of mean (GA % mean) was classified as high (>20%), moderate (10-20%) and low (<10%) as given by Johnson *et al*., (1955).

RESULTS AND DISCUSSION

Estimation of genetic variability parameters: A critical examination of Table 2 indicated that the used genotypes exhibited sufficient phenotypic variation. The high estimates (> 20 %) of PCV were reported for characters *viz.*, Yield (42.25 %) followed by PPP (38.63%), BY (37.69%), SB (23.68%), SPP (24.21%) and PB (20.27) (Fig 1).

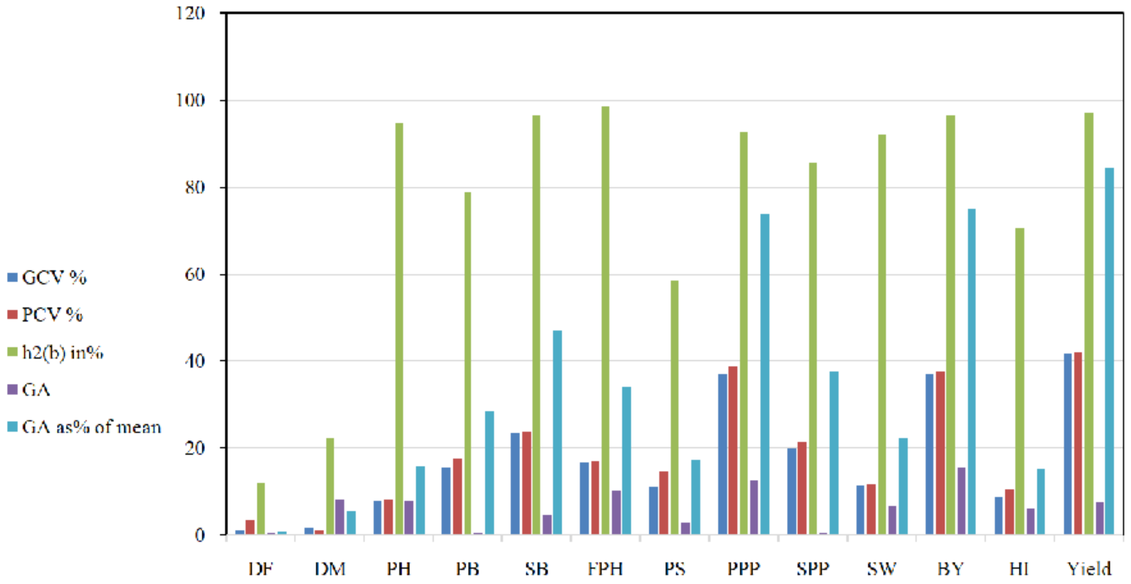

Fig. 1. Genetic variability parameters (GCV, PCV, heritability (bs), GA and GA as % of mean) for 13 morphological characters *viz.*, Days to 50 % flowering (DF), Days to maturity (DM), Plant height (PH), First pod height (FPH), Number of primary branches per plant (PB), Number of secondary branches per plant (SB), Pod size (PS), Number of pods per plant (PPP), Number of seed per pod (SPP), 100 Seed weight (SW), Biological yield (BY), Harvesting index (HI) and Seed yield (Yield).

For these studied characters presence of high PCV indicated the influence of prevailing environmental conditions. The moderate PCV (10-20 %) was observed for FPH (16.81%), PS (14.84 %), SW (11.66 %) and HI (10.48), while the low PCV (< 10 %) estimates were observed for PH (8.1 %), DF (4.57 %) and DM (2.40 %). The earlier findings of Kumar and Abbo (2001), Upadhyaya *et al.*, (2002); Dubey and Srivastava (2007) also supported the present results. In case of GCV the high estimates (>20 %) was observed for Yield (41.66%), PPP (37.22%), BY (37.07%), SB (23.28%) and SPP (22.80) while moderate GCV (10-20 %) was observed for FPH (16.71%), PB (18.64%), SW (11.2%), PS (11.15%). The low GCV (< 10 %) was noticed for HI (8.8 %), PH (7.93 %), DM (1.82 %) and DF (1.15 %). The results obtained by Wanjari *et al.*, (1996); Jeena *et al.*, (2005) corroborated with the above study. These obtained results indicated that in general the PCV was higher than that of GCV for all studied traits. The high PCV as compared to GCV indicated the effect of environment on trait expression. The character *viz.*, Yield, PPP, BY and SB exhibited high PCV along with high GCV.

Heritability measures the transmissibility of traits from generation to generation. The high heritability (> 60 %) estimates was observed for characters *viz.*, FPH (98.87 %), Yield (97.22 %), BY (96.75 %), SB (96.64 %), PH(95 %), PPP (92.83 %), SW (92.27 %), SPP (88.69 %), PB (84.58 %) and HI (70.51 %). Moderate heritability (30-60 %) was observed for PS (58.5 %) and DF (53.7) and low heritability (<30 %) was observed for DM (16.33 %). Similar observations were noted by, Kumar and Abbo (2001); Upadhyaya *et al.* (2002); Dubey and Srivastava (2007) ; Monpara and Gaikwad (2014). According to Johnson *et al.*, (1955) both heritability and genetic advance together provide better estimate as compared to heritability alone to predict effect of selection. The GA (% mean) were high (>20 %) for Yield (84.61 %) followed by BY (75.12 %), PPP (73.88 %), SB (47.16 %), SPP (37.64 %), PB (35.32 %), FPH (34.24 %), SW (22.16 %). Moderate GA (% mean) (10-20%) was observed for the traits like PS (17.27 %), PH (16 %), HI (15.22 %) and low GA (% mean) (<10 %) was observed for the traits *viz.*, DF (5.62 %) and DM (0.80 %). The high GA (% mean) was observed for Yield and PPP as reported by Raval (2001). Whereas, moderate to low GA (% mean) was recorded for BY, HI, PB, SW, SPP, DF, PH and DM. The study done by Raval (2001) and Arshad *et al.* (2004) showed the similar results. Thus the high heritability coupled with high GA (% mean) was observed for characters *viz.*, PB, SB, FPH, PPP, SPP, SW, BY and Yield (Table 2 and Fig 1). The high heritability coupled with high genetic advance for these traits was also reported earlier by Singh *et al.*, (2021). These obtained results from present study revealed that selection will be effective for these traits.

Table 2: Coefficient of variance, heritability, genetic advance and genetic advance as per cent of mean for different characters in chickpea genotypes.

Sr. No.	Name of characters	GCV %	PCV %	$h^2_{(b)}$ in%	GA	GA as% of mean
1.	Days to 50% flowering (DF)	1.15	4.57	53.71	4.13	5.06
2.	Days to maturity (DM)	1.82	2.40	16.33	1.16	0.80
3.	Plant height (cm) (PH)	7.93	8.10	95.0	7.95	16.0
4.	First pod height (cm) (FPH)	16.71	16.81	98.87	10.25	34.24
5.	Number of primary branches per plant (PB)	18.64	20.27	84.58	0.83	35.32
6.	Number of secondary branches per plant (SB)	23.28	23.68	96.64	4.54	47.16
7.	Pod size (mm) (PS)	11.15	14.84	58.50	2.71	17.27
8.	Number of pods per plant (PPP)	37.22	38.63	92.83	12.71	73.88
9.	Number of seeds per pod (SPP)	22.80	24.21	88.69	2.55	37.64
10.	100 seed weight (g) (SW)	11.20	11.66	92.27	6.61	22.16
11.	Biological yield (g) (BY)	37.07	37.69	96.75	15.44	75.12
12.	Harvest index (%) (HI)	8.80	10.48	70.51	6.31	15.22
13.	Seed yield (g) (Yield)	41.66	42.251	97.22	7.51	84.61

CONCLUSION

The presence of genetic variability is considered important criteria for crop improvement. Based on the findings of this study, it is concluded that a high variability estimates was observed for all studied traits. For all studied characters, the PCV was larger than GCV, showing that the environment had an impact on expression of these characters. High heritability coupled with high GA (% mean) was observed for PB, SB, FPH, PPP, SPP, SW, BY and Yield. The high heritability coupled with high genetic advance indicated that these characters can be improved upon by selection since they were under control of additive gene effect. Therefore, it is important to interpret expected genetic advance in relation to both genetic variability and heritability for deciding the possibilities of improvement through selection.

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Author contributions. RKP came up with the concept and designed the experiments. The manuscript was written by AG. AG and RKP analysed the data and carried out the experiments. The data and manuscript were finalized by AG, RKP, SKV, AA, AKG, and CP. The final manuscript has been read and approved by all authors.

Conflicts of Interest. The authors declare no conflict of interest.

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