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Determination of Genetic Variability, Heritability and Genetic advance Estimates for Phonological and Yield Traits in Chickpea (Cicer arietinum L.) Genotypes under Late Sown Conditions.

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Abstract

A study was conducted to evaluate the magnitude of genetic variability, heritability in broad sense and genetic advance among sixteen chick pea genotypes for growth and grain yield characters. The study was conducted at the field experimentation center of Genetics and Plant Breeding during Rabi season 2010-2011. Randomized Complete Block Design with three replications was used for these locations. The result showed that number of primary branches, pods per plant, seeds per plant and harvest index had high genotypic and phenotypic coefficients of variation for all characters, phenotypic coefficient of variation was higher than genotypic coefficient of variation indicating that there was environmental influence on these traits. The combined results for heritability showed that the high estimates of heritability and genetic advance were scored for seeds per plant and seed yield indicating that these characters were under the control of additive genetic effects. High genetic advance expected as percent of mean coupled with high heritability was observed for pods per plant, Harvest Index, number of seeds per plant, Seed Yield per Hectare, Days to fifty percent flowering ,biological yield for combined analysis. The present findings could be useful for establishing selection criteria for high seed yield in the chick pea breeding

Key words : Genetic Variability; Chickpea; Heritability, Genetic advance

Introduction

Chickpea (*Cicer arietinum L.*) is an important Rabi season legume having extensive geographical distribution. Chickpea is known by different names in various countries such as Gram, Chana, Bengal gram etc. Chickpea is a diploid species with a chromosome number 2n = 16. It is a self-pollinated crop and it belongs to sub family Papilionaceae of the family Leguminaceae. India is the largest producer of, importer and consumer of pulse in the world, accounting for 25% of the global production, 15% trade, and 27% consumption, as sizable population the country still depends on vegetarian diets to meet its protein requirement.

Chickpea reached a record high global area of 13.3 million ha and production of 11.75 million tons during 2011. In 2013 the area of chickpea cultivation increased to 13.5 m ha but production remained at 13.1 MT (FAOSTAT 2015). Chickpea is currently the second most important food legume in the world after common bean. Chickpea is mostly consumed in the form of processed whole seed (boiled, yeasted, parched, fried, steamed, sprouted etc) or Dal and flour (besan). Gram is a good source of protein (18-22%), carbohydrate (52-70%) and fat (4-10%). (IIPR Publication, 2002) despite its nutritional values and economic importance, chickpea production is relatively low in the country. This is primarily due to poor genetic makeup of cultivars available. Genetic variability is a prerequisite for any breeding programme, which provides opportunity to a plant breeder for selecting high yielding genotypes.

Materials and Methods

The experiment was carried out during *Rabi* 2010-11 comprising 15 genotypes along with one check (15+1) of chickpea with thee replication Design of experiment Randomized Block Design (RBD) at field experimentation centre of Department of Genetics and Plant Breeding, Sam Higginbottom Institute of Agriculture, Technology and Sciences, Deemed to be University, Allahabad. Adopting following spacing Row to row 30 cm, Plant to plant: 10 cm. Materials used in the present experiment consist of 16 chickpea genotypes obtained from (IIPR) Kanpur, Uttar Pradesh India, which were evaluated for variability studies.

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The technique of random sampling was adopted for recording the observation of various quantitative characters of chickpea. By using to these method five plants of each treatment and each replication were selected randomly at the time of recording the data of various characteristics. Reading from five plants averaged replication-wise and mean data was used for statistical analysis. The recommended package and practices were used for raising a healthy crop. Days to 50% flowering, Plant height (cm),Days to maturity, Number of branches per plant, Number of pods per plant, Biological yield per plant (g), Seed Index (g), Harvest index (%): (Donald & Hamblin,1796),Seed yield per plant (g), Seed yield (q/ha),

Results and Discussion

The analyses of variance for different 10 characters are present in table 2. The result showed significant difference for mean sum of square at 5% level for all the characters under study among 16 genotypes. These characters are days to 50% flowering, plant height, days to maturity, number of primary branches per plant, number of pods per plant, biological yield per plant, seed yield per plant, 100 seed weight, seed yield (q/hac), harvest index,

This suggested that the genotype selected for research were quite variable and constant levels of variability are present among them. Thus indicating ample scope for selection of different qualitative characters in chickpea improvement. Burli *et.al.* (2004) also reported high genetic variability for different characters in chickpea.

Table 1. : Analysis of variance of 10 quantitative characters for 16 chickpea genotype.

S.No.	Quantitative characters	Mean sum of square		
		Replications (df=2)	Treatments (df=19)	Error (df=38)
1.	Days to 50% flowering	13.65	1258.66*	67.98
2.	Plant height	17.03	845.63*	24.90
3.	Days to maturity	32.05	89.28*	93.84
4.	No. of primary branches/plant	0.30	5.10*	3.45
5.	No. of pods/plant	11.05	8983.66*	73.58
6.	Biological yield/plant	0.69	1365.72*	114.71
7.	Seed index	3.77	680.68*	83.25
8.	Harvest index	0.17	1977.68*	3.54
9.	Seed yield/plant	2.13	172.03*	6.22
10.	Seed yield q/hac	0.46	204.79*	5.96

*** Indicate significance at 5% level**

Estimation of phenotypic variance (Vp) and genotypic variance (Vg) were obtained from different characters and are presented in table 2. A wide range of phenotypic variance was observed for characters like number of pod per plant, harvest index and seed yield per plant. Seed yield per plant, number of pods per plant; harvest index exhibited moderated range of phenotypic variance, whereas lower range of phenotypic variance was observed for characters number of primary branch per plant, days to maturity, protein content, 100 seed weight, and plant height, seed yield per hectare, days to 50 % flowering and biological yield per plant. Estimates of phenotypic variance revealed that pods per plant exhibited highest phenotypic variance followed by harvest index. It was also observed that genotypic variance for all the yield and yield contributing characters. This indicates the influence of environmental factor of these traits.

Magnitude of variability may be measured by estimating variance, but this magnitude of variability is not comparable hence, converting it in to coefficient of variation makes it more useful. Environment plays an important role in expression of phenotypic observation hence, the observed variability can be conveniently divided into heritable and non-heritable variation. Information about these parameters can be obtained through biometric measure like genotypic coefficient of variation (GCV), heritability (bs) and genetic gain (GG) these would be a great help to the breeder in developing a selection programme for genetic improvement of plant.

In the present investigation, highest value of phenotypic coefficient of variation was recorded for number of pods per plant (25.17) and moderate values were recorded for harvest index (23.67) and seed yield per plant. On the other hand, comparatively low estimates of phenotypic coefficient of variation were recorded for characters like days to maturity

(1.76), days to 50% flowering (7.25), plant height (8.51), no of primary branches/plant (13.99), biological yield/plant (14.70), Burli *et al.* (2004), Muhammad et al. (2002), Ajinder *et al.* (2004), reported the highest value for 100 seed weight and seed yield per plant. Parshuram (2003) observed high PCV for days to maturity and number of pods per plant that support the result. In the present study low values of PCV was observed for days to maturity.

Genotypic coefficient of variation (GCV) ranged from 0.85 for days to maturity to 25.01 for number of pods per plant. Higher magnitude of genotypic coefficient of variation was recorded for number pods per plant (25.01), harvest index (23.64) and seed yield q/h (19.71) on other hand comparatively low estimates of genotypic coefficient of variation were recorded for characters like, days to maturity (0.85), days to 50% flowering (6.96), plant height. (8.33), no of primary branches/plant (8.79), biological yield (13.82), seed yield/plant (18.15) and seed index (18.39). Sable *et al. (*2000) and Jeena and Arora (2000) observed high genotypic coefficient of variation for 100 seed weight. In the present study maximum highest value of GCV was observed in no. of pods/plant.

In general, estimates of phenotypic coefficient of variation (PCV) were higher than their corresponding genotypic coefficient of variation (GCV) however, good correspondence was observed between GCV and PCV for all the characters (Table 2).

The higher magnitude of genotypic coefficient of variation and phenotypic coefficient of variation were recorded for number of pods per plant, seed yield per plant, harvest index suggesting sufficient variability and thus other better scope for genetic improvement through selection of these traits.

A perusal of table 2. In broad sense of heritability for all characters studied. The estimates ranged from 99.73 for harvest index to 23.13 for days to maturity High heritability was observed for harvest index (99.73), no of pods/plant (98.78), seed yield q/h (95.75), seed yield/plant (94.75), plant height (95.70), days of 50% flowering (92.31), biological yield/plant (88.37), 100 seed weight (83.65), Remaining two characters should low estimates of heritability, viz., days to maturity (23.13) and no of primary branches/plant (39.43).

Table 2. : Genetic parameters for 12 quantitative characters

S.No.	Quantitative Characters	$\sigma^2 g$	$\sigma^2 p$	GCV %	PCV%	h^2 (bs)%	GA
1.	Days to 50% flowering	27.21	29.48	6.96	7.25	92.31	10.30
2	Plant height	18.51	19.34	8.33	8.51	95.70	8.65
3.	Days to maturity	0.94	4.06	0.85	1.76	23.13	0.95
4.	No. of primary branches/ plant	0.07	0.19	8.79	13.99	39.43	0.34
5.	No. of pods per plant	198.81	201.27	25.01	25.17	98.78	28.85
6.	Biological yield per plant	29.07	32.89	13.82	14.70	88.37	10.43
7.	Seed index	14.20	16.97	18.39	20.11	83.65	7.08
8.	Harvest index	43.90	44.02	23.64	23.67	99.73	13.62
9.	Seed yield per plant	3.75	3.96	18.15	18.65	94.75	3.86
10.	Seed yield per hectare (q)	4.48	4.68	19.71	20.14	95.75	4.26

ó²g = Genotypic variance, ó²p = Phenotypic variance, GCV = Genotypic coefficient of variance,

PCV = Phenotypic coefficient of variation, h2 (bs) % = Heritability (broad sense),

GA = Genetic advance, GA % (ì) = Genetic advance as percent of mean.

Knowledge of heritability of character is important as it indicate the possibility and extent to which improvement is possible through selection. It is a measure of genetic relationship between plant and progeny and has been widely used to assess the degree to which a character may be transmitted from parent to offspring. It also indicates that relative important of heritability and environment in the expression of characters. High heritability alone is not enough to make sufficient improvement through selection in advance generation unless accompanied by substantial amount of genetic advance. The heritability in combination with intensity of selection and amount of variability present in the population influence the gain to be obtained from selection. Burli *et al.* (2004) reported highest heritability recorded estimates for day's maturity, days to 50% flowering. Sable *et al.* (2002) recorded high heritability estimates for seed yield per plant and 100 seed weight. Heritability estimates of various traits help researches to

determine a suitable strategy for crop improvement selection.

Genetic advance is the improvement in the mean of selected family over the base population (Lush, 1949 and Johnson et al. 1955). It is also expressed as the shift in gene frequency towards the superior side on exercising selection pressure. Johnson *et al*. (1955) suggested that heritability and genetic advance when calculated together would prove more useful in predicting the resultant effect of selection on phenotypic expression.

The highest genetic advance were recorded for number of pods per plant (28.85) while moderate genetic advance recorded for harvest index (13.62), biological yield per plant (10.43), days to 50% flowering (10.30) and plant height (8.65 cm). On the other hands, comparatively low estimates of genetic advance for seed index (7.08 g), seed yield q/h (4.26), seed yield/plant (3.86 g), days to maturity (0.95) and number of primary branches per plant (0.34) was obtained.

Conclusion

Genotype C-406 was identified as best performer for the seed yield and its contributing traits. The characters like No. of pods per plant and Harvest index, showed maximum genotypic coefficient of variation, Phenotypic coefficient of variation, Heritability (bs) and genetic advance. Hence these characters should be given top priority during selection in Allahabad agro climate condition.

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