



ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2021; 10(5): 1704-1706
© 2021 TPI

www.thepharmajournal.com

Received: 05-03-2021

Accepted: 08-04-2021

Neha

PhD Scholar, Department of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh, India

Shiva Nath

Associate Professor, Department of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh, India

Study of genetic variability, heritability and genetic advance in chickpea

Neha and Shiva Nath

Abstract

Pulses are dried edible seeds harvested from the pods of a variety of leguminace plant species. They are important for providing a balanced protein component in people's diets, as well as crop rotation, diversification, and productivity, as they increase soil fertility. Chickpea genetic improvement can be achieved through a comprehensive breeding program that presupposes precise information on the nature and magnitude of genetic variability present in the material. The investigation was undertaken with nineteen chickpea genotypes type (Four testers and fifteen lines) with two standard checks, which were initially screened for desired characters at student farms, ANDUAT, Narendra Nagar (Kumarganj), Ayodhya, U.P. The results indicated that the mean sum of squares (MSS) due to genotypes was found to be highly significant for all the characters under both E1 and E2 conditions. These results suggested the preponderance of sufficient genetic variability in the experimental material. In the present investigation both GCV and PCV estimates were found to be moderate for Plant height (cm), No. of primary branches per plant, No. of secondary branches per plant, and Harvest index in both environmental conditions. The little difference between PCV and GCV values in most of the traits indicated that the apparent variation was due to varieties but with insignificant influence of environment. High heritability and high genetic advance for the traits plant height (cm), No. of pods per pod, biological yield (g) and seed yield per plant (g) indicated the presence of additive genes in the trait and suggested reliable chickpea improvement through selection of the traits.

Keywords: Chickpea, genetic variability, heritability, genetic advance

Introduction

Pulses are dried edible seeds harvested from the pods of a variety of leguminosae plant species. They are important for providing a balanced protein component in people's diets, as well as crop rotation, diversification, and productivity, as they increase soil fertility. Pulses are a significant source of protein for India's vegetarian population, as well as for household food security and income production as a cash crop. The United Nations General Assembly designated 2016 as "The International Year of Pulses" (IYP 2016) in 2013, recognizing the relevance and potential of pulses for global agricultural systems, nutrition, and food security. India is the largest producer of pulses in the world covering 29.16 million hectares area with production 22.08 million tons and 757 kg/ha productivity (Directorate of Economics and Statistics, 2020). Chickpea genetic improvement can be achieved through a comprehensive breeding program that presupposes precise information on the nature and magnitude of genetic variability present in the material, which will aid in the understanding of evolutionary mechanisms involved in intra-specific divergence and the selection of desirable parents for the development of superior hybrids with high yield.

It is important to divide the present variability into its heritable and non-heritable components with the help of suitable genetic parameters such as phenotypic and genotypic coefficient of variations, heritability estimates, and genetic advance under selection (Singh *et al.*, 2015) [13]. Genotypic coefficient of variability gives the magnitude of genetic variance present in the population. Heritability denotes the proportion of phenotypic variance that is due to genotype, i.e., heritable and is act as a tool to predict the gain from selection in a population i.e., genetic advance. Genetic advance is also important as it indicates the magnitude of the expected genetic gain from one cycle of selection (Hamdi, 1992) [7]. However, heritability estimates together with genetic advance are more important to predict the resulting effect of selecting the best individuals (Johnson *et al.*, 1955) [9]. Genetic advance depends upon the heritability of the character under selection, genetic variability of the genotypes and intensity of selection. The information on the nature and the magnitude of variability present in the genetic

Corresponding Author:

Neha

PhD Scholar, Department of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh, India

material is of prime importance for a breeder to initiate any effective selection program.

Therefore, present investigation was conducted to evaluate the degree of genetic variability, heritability and genetic advance in different chickpea genotypes and to identify superior chickpea cross combinations for better crop yield production.

Material methods

The investigation was undertaken with nineteen chickpea genotypes type (Four testers and fifteen line) with two standard checks, which were initially screened for desired characters. The parents namely ICCV 10, JG 11, JG 14, JG 16, JG 315, NDG 5-21, NDG 11-12, Phule G 5, BG 362, HC 3, Rajash, Vaibhav, RSG 888, PDG 84-16, JAKI 9218 used as diverse lines of chickpea and which was crossed with four testers namely Pant G 186, BG 372, GCP 105 and Udai. These genotypes were crossed in Line \times Tester pattern fashion to produce 60 F_{1s} during *Rabi* season 2019-20 and were evaluated in the following year during *Rabi* season 2020-21. The final experiment comprising of 60 F_{1s} , 4 testers and 15 lines was grown in RBD with 3 replications in two different dates of sowing i.e. timely sown (E1) and late sown (E2) conditions. These diverse elite strains were selected from the collection of genetic stock available in Pulse Section of the Department of Genetics and Plant Breeding, N. D. University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya, Uttar Pradesh. The observations were recorded for 11 morphological traits like days to 50% flowering, Days to maturity, Plant height (cm), Primary branches per plant, Secondary branches per plant, Pods per plant, Seeds per pod, 100 seed weight (g), Biological yield per plant (g), Harvest index (%), and Seed yield per plant (g) in both the environments on five randomly selected plants except for the traits namely Days to 50% flowering, and days to maturity which was recorded on plot basis. To test the significance of differences between treatments, analysis of variance was done as suggested Panse and Shukhatme, (1967). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated according to Singh and Chaudhary (1985).

Result and Discussion

Analysis of variance

The Analysis of Variance (ANOVA) was carried out using three replications in Randomized Block Design (RBD) for seventy-nine genotypes of chickpea for 11 different morphological traits. The experimental material was grown in two different conditions i.e. timely sown (E1) and late sown (E2) conditions. The results indicated that the Mean Sum of Squares (MSS) due to genotypes was found to be highly significant for all the characters under both E1 and E2 conditions. These results suggested the preponderance of sufficient genetic variability in the experimental material. The presence of genetic variability in experimental material is very important as sufficient variability indicates that there are chances of crop improvement by selection.

Genetic variability

Effectiveness of any selection program depends upon the existence of genetic variability present within the population. The variability at phenotypic level arises due to genotypic and environmental influences that contribute towards the development of phenotype. The results on phenotypic (PCV) and genotypic (GCV) coefficients of variability are presented

in Table 1.

Deshmukh *et al.*, (1986) [3] categorized GCV and PCV as low (<10%), moderate (10-20%) and high (>20%). In the present investigation both GCV and PCV estimates were found to be moderate for Plant height (cm), No. of primary branches per plant, No. of secondary branches per plant and Harvest index in both environmental conditions. Low genotypic and phenotypic coefficient of variations was observed for Days to maturity in both environmental conditions while for the trait days to 50% flowering it is observed in early showing condition. It is clear from result that, in general, PCV estimates were higher than the corresponding GCV estimates in both E1 and E2 environments, which indicated that these characters were influence by environment. The variability at phenotypic level arises due to genotypic and environment influences, which contribute towards the development of phenotype. The little difference between PCV and GCV values in most of the traits indicated that the apparent variation was due to varieties but with insignificant influence of environment. The results for most of the traits showed much difference between PCV and GCV in comparison to other traits indicating higher influence of environment. Borate *et al.*, (2010) [2] and Dev *et al.*, (2017) [4] also reported similar results for phenological and different agronomic traits.

In case of E1 as well as E2 environment the high estimates of PCV as well as GCV (>20 %) were recorded for traits number of seeds per pod, biological yield and seed yield per plant. The presence of high estimates of PCV and GCV for these characters in different environmental condition indicated that the desirable improvement could be achieved by practicing selection in these characters. The presence of large amount of variability indicates that there is ample scope of improvement for these characters through hybridization. The results were in consonance with the findings of Jeena *et al.*, (2005) [10], Khan *et al.*, (2011) [11] and Kumar *et al.* (2016) [12].

Heritability and genetic advance as percent of mean

The ratio of genotypic variance to phenotypic variance or total variance is known as heritability in broad sense. It is generally expressed in percentage. The heritability is the heritable portion of phenotypic variance. It is a good index of transmission of characters from parents to their offspring. The estimates of heritability help the plant breeder in selecting superior genotypes from diverse genetic populations. The high estimates of heritability (>60 %) were obtained for all the traits under both the environments. Johnson *et al.*, (1955) [9] suggested that heritability estimates coupled with genetic advance as per-cent of mean together provide a better judgment rather than heritability alone in predicating the resultant effect of selection. The estimates of genetic advance as per-cent of mean were high (>20 %) for all the studied traits except the trait days to 50 per-cent flowering in late showing environment (E2) and days to maturity in both the environments.

High heritability and high genetic advance for the traits Plant height (cm), No. of pods per pod, Biological yield (g) and Seed yield per plant (g) indicated the presence of additive genes in the trait and suggested reliable chickpea improvement through selection of the traits.

Thus, 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.

Table 1: Mean, range, coefficient of variation, heritability and genetic advance for 11 characters in chickpea E1 & E2

Characters		Coefficient of variation (%)		Heritability in broad sense	Genetic advance	Genetic advance as percent of mean
		Genotypic	Phenotypic			
Days to 50% flowering	E1	7.77	7.89	0.97	12.33	15.77
	E2	18.84	19.00	0.98	2.34	38.49
Days to maturity	E1	4.32	4.41	0.96	12.16	8.74
	E2	5.05	5.15	0.96	12.16	10.21
Plant height (cm)	E1	14.31	14.39	0.99	20.35	29.34
	E2	15.00	15.08	0.99	20.31	30.75
No. of primary branches per plant	E1	13.39	16.20	0.68	0.50	22.79
	E2	14.91	17.27	0.75	0.53	26.52
No. of secondary branches per plant	E1	17.50	17.64	0.98	2.34	35.74
	E2	18.84	19.00	0.98	2.34	38.49
No. of pods per pod	E1	25.55	25.59	1.00	41.81	52.55
	E2	29.27	29.34	1.00	36.27	60.14
No. of seeds per pod	E1	17.59	18.55	0.90	0.76	34.38
	E2	17.10	18.20	0.88	0.68	33.10
100 Seed weight (g)	E1	18.46	18.46	1.00	8.20	38.02
	E2	19.15	19.15	1.00	8.20	39.44
Biological yield (g)	E1	38.24	38.48	0.99	74.16	78.27
	E2	39.69	40.02	0.98	55.91	81.07
Harvest index (%)	E1	9.81	9.95	0.97	8.02	19.92
	E2	12.34	12.62	0.96	9.26	24.86
Seed yield per plant (g)	E1	41.82	42.14	0.99	33.22	85.51
	E2	43.89	44.35	0.98	23.53	89.45

Conclusion

The present study can be concluded that genetic variability exists among the studied genotypes for all the traits. There was closeness between GCV, and PCV values for the traits namely; Days to 50% flowering, Days to maturity, Plant height (cm), Primary branches per plant, Secondary branches per plant, Pods per plant, Seeds per pod, 100 seed weight (g), Biological yield per plant (g), Harvest index (%), and Seed yield per plant (g) which indicate that these traits were less influenced by both environment condition. The estimates of genetic advance as per-cent of mean were high (>20%) for all the studied traits except the trait days to 50 per-cent flowering in late showing environment (E2) and days to maturity in both the environments. Thus, 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.

References

- Allard RW. Principles of Plant Breeding. John Wiley and Sons, Inc. New York 1960, 138-142.
- Borate VV, Dalvi VV, Jadhav BB. Estimates of genetic variability and heritability in chickpea. J Maharashtra Agric. Univ 201035(1):47-49.
- Deshmukh SN, Basu MS, Reddy PS. Genetic variability, character association and path coefficient analysis of quantitative traits in Virginia bunch varieties of groundnut. Indian Journal of Agricultural Science 1986;56(1):816-821.
- Dev A, Verma P, Kumhar BL. Genetic Character Variability Studies in Desi Chickpea (*Cicer arietinum* L.) Genotypes. Int. J Curr. Microbiol. App. Sci 2017;6(4):20-25.
- Directorate of Economics and Statistics 2020. Annual report on chickpea 2020.
- Falconer DS, Trudy FCM. Introduction to Quantitative Genetics 4th ed. Longman Group Limited. Malaysia 1996, 450.
- Hamdi A. Heritability and combining ability of root

- characters in lentil (*Lens culinaris* Medik). Egyptian Journal of Agricultural Research 1992;70(1):247-255.
- Hayman BI. The theory and analysis of diallel crosses. II. Genetics 1958;43:63-65.
- Johnson HW, Robinson HF, Comstock RE. Estimation of genetic and environmental variability in soybeans. Agronomy Journal 1955;47(7):314-318.
- Jeena AS, Arora PP, Ojha OP. Variability and correlation studies for yield and its components in chickpea. Legume Research 200528(2):146-148.
- Khan R, Farhatullah, Khan H. Dissection of genetic variability and heritability estimates of chickpea germplasm for various morphological markers and quantitative traits. Sarhad J Agric 2011;27(1):67-72.
- Kumar M, Kushwaha S, Dwivedi VK, Dhaka SS. Genetic variability and correlation analysis of various traits in chickpea genotypes (*Cicer arietinum* L.) under rainfed condition in western Uttar Pradesh 2016.
- Singh M, Mishra DK, Shukla RS, Samaiya RK. Variation and heritability for some quality characteristics and grain yield in bread wheat (*Triticum aestivum* L.). Trends in Biosciences 2015;8(1):68-70.