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Assessment of Genetic Variability in Chickpea (*Cicer arietinum* L.)

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A B S T R A C T

The present investigation has been carried out to study the variability in Chickpea (*Cicer arietinum* L.). The magnitude of genotypic variance was highest for number of pods per plant followed by days to maturity, Harvest index and days to 50% flowering. The pods per plant recorded highest phenotypic variance followed by days to maturity and harvest index. Genotypic coefficient of variation (GCV) was highest for harvest index followed by number of pods per plant, seed yield per plant and number of secondary branches per plant. Phenotypic coefficient of variation (PCV) was highest for harvest index followed by number of pods per plant, seed yield per plant and number of secondary branches per plant. Maximum heritability was observed for 100 seed weight (95.00%) and that of the estimates of genetic advance was ranged from 0.33 to 22.53% at 5% level of significance and 0.42- 28.87% at 1% level of significance with the highest estimate in case of number of pods per plant (22.53%) and (28.87%).

Introduction

Among the pulse, the chickpea is a first important *Rabi* pulse crop of the region. Among all pulses chickpea contributes 36% area and 46% production in year 2017-18. During 2017-18 estimated area and production of chickpea in Maharashtra is 18.92 lakh ha and 17.61 lakh ton respectively. The productivity is also highest during 2016-17 (1006kg/ha). In India percentage of area is increased upto 10.81% during year 2017-18 as compared to previous year while percentage of area decreased by 4.38% in Maharashtra. Maharashtra is having 14.69% contribution in the area with 13.74% production share in the nation (average of last ten years). Madhya Pradesh is having highest area of 35.90 lakh

ha, production 45.95 lakh tons and productivity 1280 kg/ha during the year 2017-18. During 2017-18, the area in Maharashtra was 20 lakh ha with production of 17.61 lakh tons and productivity is 881 kg/ha. (Anonymous, 2017).

Genetic improvement of any crop mainly depends upon the genetic variability present in the population and the germplasm serves as a valuable source of base population and provides source for wide variability (Ramya and Senthilkumar, 2009). The wide genetic diversity that exists in the available genotypes provides ample scope for further improvement. Keeping this in view, the investigation was carried out with following objective to estimate the extent of genetic variability present among the germplasm lines under investigation.

Materials and Methods

The experimental materials used for study consisted of forty three genotypes of chickpea, out of which 25 genotypes were obtained from International Crop Research Institute for Semi-Arid Tropics, Hyderabad, 15 genotypes from the A.R.S. Badnapur and three standard checks. Forty genotypes of chickpea along with three standard checks *viz.* Akash (BDNG-797), Digvijay, JAKI 9218 were evaluated in a randomized block design with two replications during *Rabi* season of 2017-18. Each genotype was sown in two rows of 4 m length with spacing of 45 cm between rows and 10 cm within rows.

The data were recorded on five randomly selected plants of each replication for all characters such as days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, harvest index and seed yield.

Estimation of coefficient of variation

The genotypic and phenotypic coefficients of variation were calculated by using following formulae given by Burton (1952).

Genotypic coefficient of variation (GCV)

$$GCV\ (\%) = \frac{\sigma^2_g}{\overline{X}} \times 100$$

Where,

σ^2_g = Genotypic variance and,
X = Mean of character

Phenotypic coefficient of variation (PCV)

$$PCV\ (\%) = \frac{\sigma^2_p}{\overline{X}} \times 100$$

Where,

σ^2_p = Phenotypic variance and,
$\overline{X}$ = Mean of character

GCV and PCV estimates were classified as
Low : < 10 per cent,
Medium: 10 to 20per cent
High: > 20 per cent.

Estimation of heritability (b.s.)

Heritability in broad sense was estimated for various characters as suggested by Hanson *et al.,* (1956).

$$h^2 = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

h^2 = Heritability

σ^2_g = Genotypic variance
σ^2_p = Phenotypic variance

The high, medium and low heritability estimates were classified on the basis of values given by Robinson (1966).

Low heritability = < 10 %
Moderate heritability = 10-30 %
High heritability = > 30 %

Genetic advance (G.A.)

Genetic advance (at 5 % selection intensity) was calculated using the formula given by Allard (1961)

Genetic advance (G.A.)

$$G.A. = k \times \frac{\sigma^2_g}{\sigma^2_p} \times \sqrt{\sigma^2_p}$$

Where,

σ^2_g = Genotypic variance
σ^2_p = Phenotypic variance
k = Selection differential (at 5 % selection = 2.06)

G.A. as percentage of means (GAM)

$$GAM = \frac{GA}{\overline{X}} \times 100$$

Where,

G.A. = Genetic advance
$\overline{X}$ = Character mean

GA (As percentage of mean) was classified as

Low: 10 per cent
Medium: 10 to 20 per cent
High: > 20 per cent

Results and Discussion

Heritability and genetic advance

The variation among genotypes were highly significant for days to 50 % flowering, days to maturity, plant height, number of secondary branches per plant, number of pods per plant, 100 seed weight, harvest index and seed yield per plant (Table 1). In the present investigation the range of broad sense heritability was from 59.80% in seed yield per plant to 95.00 % in 100 seed weight. The highest broad sense heritability recorded by 100 seed weight (95.00 %), days to maturity (94.00 %), harvest index (93.70 %), days to 50 % flowering (91.50 %), Pods per plant (82.90 %) and number of secondary branches per plant (80.30 %). The broad sense heritability is referred to the genetic portion of the phenotypic variability. The character having maximum broad sense heritability, there is a scope for selection for that character.

The highest genetic advance was noticed for the character number of pods per plant followed by days to maturity, harvest index, days to 50 % flowering and 100 seed weight indicating that these traits are under control of additive gene action and potential possibilities exist for the improvement of these characters through simple selection where finding supported by similar noting of Kumar *et al.,* (2002) for number of pods per plant. Borate *et al.*,(2010) for days to flowering and days to 50% maturity, Akhtar *et al.,* (2011) for number of pods per plant and 100 seed weight, Jadhav *et al.,* (2012) for 100 seed weight, Gul *et al.,* (2013) for number of pods per plant.

In the present investigation, heritability for number of seeds per pod, number of primary and secondary branches per plant, yield per plant and plant height was not associated with high genetic advance, indicating that these characters are controlled by non-additive gene

action i.e. dominance deviation or epistasis, hence there is limited scope for further improvement through selection for these characters (Fig. 1).

Fig.1 Diagram showing the contribution towards divergence

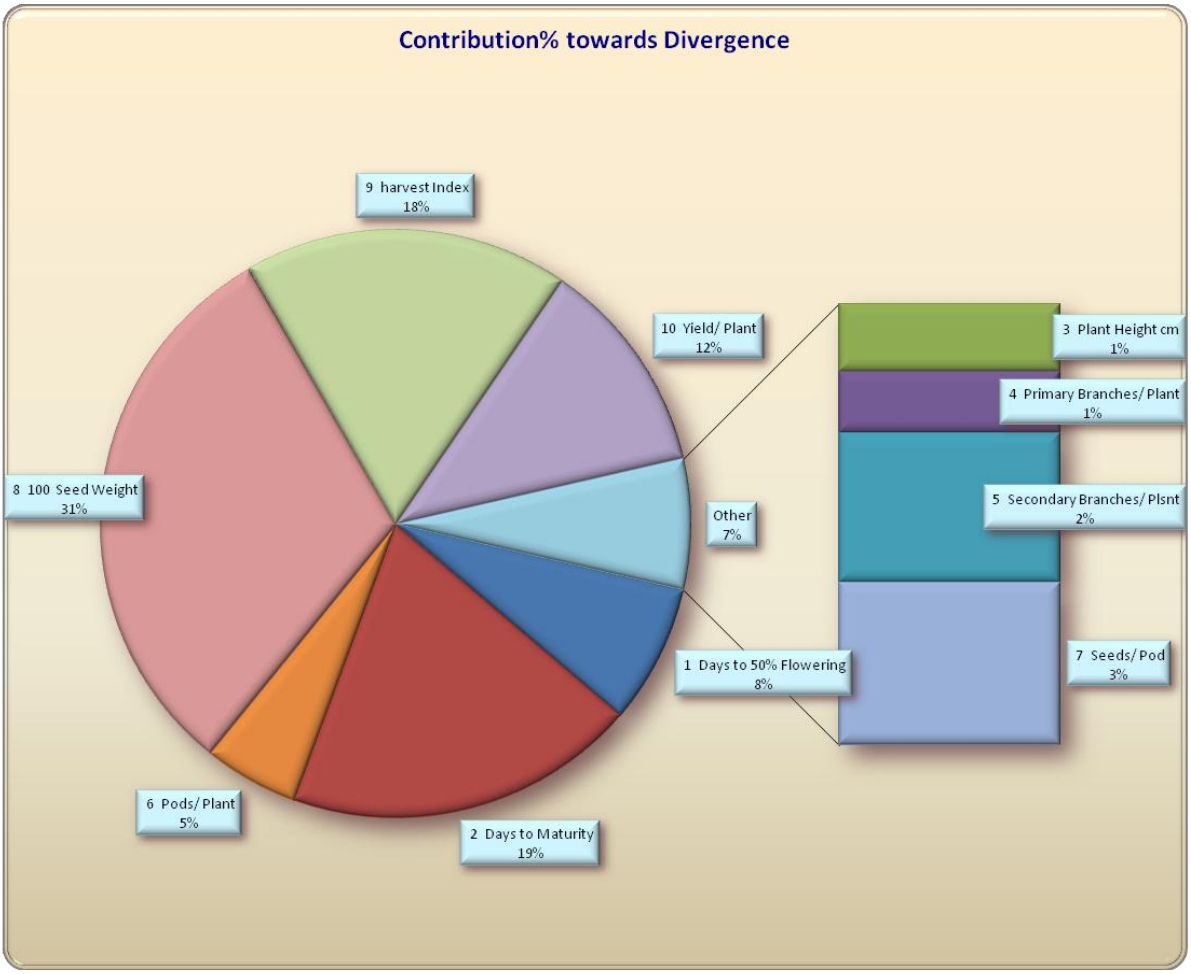

Table.1 Analysis of variance for ten quantitative characters in chickpea

Sr. No.	Name of the characters	Mean sum of square		
		Replications (df=1)	Genotypes (df=42)	Error (df=42)
1.	Days to 50 % flowering	6.69	93.02**	4.12
2.	Days to maturity	3.36	107.19**	3.31
3.	Plant height	0.32	26.57**	5.59
4.	Number of primary branches per plant	0.00	26.57**	0.10
5.	Number of secondary branches per plant	0.31	11.94**	1.30
6.	Number of pods per plant	66.80	318.13**	29.65
7.	Number of seeds per pod	0.02	0.09	0.01
8.	100 seed weight	0.32	25.55**	0.65
9.	Harvest index	4.74	25.55**	3.40
10	Seed yield per plant	5.64	17.19**	4.32

* -Significant at 5 % level of significance
**- Significant at 1 % level of significance

Table.2 Estimates of variability parameters for ten quantitative characters in chickpea

Sr. No.	Name of the characters	σ^2g	σ^2p	GCV (%)	PCV (%)	h^2 (b.s.) (%)	G.A. % (5%)	G.A. as % of mean (5%)
1.	Days to 50 % flowering	44.44	48.57	14.71	15.38	91.50	13.13	28.99
2.	Days to maturity	51.93	55.25	7.69	7.93	94.00	14.39	15.36
3.	Plant height	10.49	16.08	7.34	9.09	65.20	5.38	12.22
4.	Number of primary branches per plant	0.23	0.34	15.53	18.76	68.60	0.83	26.49
5.	Number of secondary branches per plant	5.31	6.62	19.90	22.22	80.30	4.25	36.74
6.	Number of pods per plant	144.24	173.89	25.19	27.66	82.90	22.53	47.26
7.	Number of seeds per pod	0.03	0.05	16.89	20.53	67.70	0.33	28.64
8.	100 seed weight	12.44	13.10	15.60	16.00	95.00	7.08	31.31
9.	Harvest index	50.73	54.14	34.23	35.36	93.70	14.20	68.27
10	Seed yield per plant	6.43	10.76	21.18	27.40	59.80	4.03	33.74

GCV and PCV analysis

Genotypic coefficient of variation (GCV) was highest for harvest index (34.23 %) followed by number of pods per plant (25.19%), seed yield per plant (21.18%) and number of secondary branches per plant (19.90%). Phenotypic coefficient of variation (PCV) was highest for harvest index (35.36) followed by number of pods per plant (27.66), seed yield per plant (27.40) and number of secondary branches per plant (22.22) (Table 2). In general, the magnitude of phenotypic coefficient of variation was higher than the genotypic coefficient of variation. The characters *viz.* number of pods per plant and harvest index showed high GCV and PCV, high heritability and high genetic advance as percent of mean. While number of secondary branches per plant and seed yield per plant showed high GCV and PCV, high heritability but medium genetic advance as percent of mean. Thus considering the estimates of genetic parameters like genotypic coefficient of variation, heritability and genetic advance as per cent of mean, it can be pointed out that, the characters like seed yield per plant, 100 seed weight, number of pods per plant, number of secondary branches per plant, number of primary branches per plant and number of seeds per pod are the most important characters in chickpea improvement.

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