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Variability, heritability and genetic advance for quantitative traits in chickpea (*Cicer arietinum* L. var. *microsperma*)

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Abstract

Study was carried out for genetic variability, heritability and genetic advance of twelve characters in 60 genotypes. The ANOVA revealed highly significant differences among the genotypes for all the characters indicating a presence of considerable amount of genetic variability. The phenotypic variance (σ_p^2) and phenotypic coefficient of variation (PCV) was slightly higher than the genotypic variance (σ_g^2) and genotypic coefficient of variation (GCV) for all the traits. NG-24 (62.66 days) was the earliest genotype to flower and genotypes, NGD-1663 (21.86g) recorded the highest seed yield/plant. High heritability coupled with high genetic advance was recorded for number of secondary branches/plant, height at first pod, seed yield/plant and 100-seed weight indicating that these characters are controlled by additive gene effect and phenotypic selection of these characters would be effective for further breeding purpose.

Keywords: Genetic variability, heritability, genetic advance, chickpea

1. Introduction

Chickpea (*Cicer arietinum* L. var. *microsperma*) is cool season food legume crop grown on more than 10 million ha in 45 countries. It is a self-fertilizing annual grain legume of the family Fabaceae, subfamily Faboideae. It is also known as Gram, Bengal gram, Garbanzo bean, and Egyptian pea. Chickpea is a highly nutritious pulse crop and places second most important food legume in the world after beans in terms of area (14.5 million hectares) and production (14.7 million tonnes) with the productivity of 1013 kg/ha. India is the leading country in terms of area (9.53 million hectares), production (9.07 million tonnes) and productivity of 951.4 kg/ha followed by Australia, Myanmar and Ethiopia. FAOSTAT, (2017)^[1]. Chickpea seeds contain on an average 23% protein, 64% total carbohydrates (47% starch, 6% soluble sugar), 5% fat, 6% crude fiber and 2% ash. It is also reported to contain high mineral content: phosphorus (340 mg/100 g), calcium (190 mg/100 g), magnesium (140 mg/100 g), iron (7 mg/100 g), zinc (3 mg/100 g) Jukanti *et al.* (2012)^[11]. It also plays important role in low input and rainfed agriculture by fixing atmospheric nitrogen. It has a status of an important winter seed legume crop grown in Indian sub-continent.

In order to make availability of the pulses as per WHO standard and to encounter the nutrition wants of diversified population there is a great need and indeed to have high yielding chickpea varieties resistant to biotic and abiotic stresses along with the wider adaptability and stability to overcome the malnutrition problem. Success of any crop improvement programme depends upon the amount of innate variability, selection of parents for hybridization and selection procedure adopted. The seed yield of Gram is a complex and multiplicative character, which is vastly prejudiced by environmental variations. Information on nature and magnitude of variability present in a population due to genetic and non-genetic causes is an important prerequisite for systematic breeding programme. Therefore, an attempt was made here to evaluate the variability, heritability and genetic advance of some quantitative characters in a set of genotypes.

Materials and Methods

Description of the study area

The field experiment was conducted at Pulses and Castor Research Station, Navsari Agricultural University, Navsari during *rabi* season of the year 2018. The place is located 12 km away in the east from the great historical place "Dandi" on the Arabian seashore. Geographically, it is situated at 20°-57'N latitude and 72°-54'E longitude with an elevation of 10.0 meter above mean sea level on the western coastal belt of India. For this study, sixty genotypes of chickpea obtained from Pulses and Castor Research Station, NAU, Navsari (Table-1) were used. The experiment was laid out in Randomized Block Design (RBD) with three replications. A spacing of 45 cm between rows and 10 cm between plants within the row was maintained. For each genotype five randomly taken plants in each replication were used to record data on number of primary branches per plant, number of secondary branches per plant, pods per plant, plant height (cm), height at first pod (cm), seed yield per plant (g), 100-seed weight (g), seed volume per weight (ml/g), harvest index (%), protein content (%). Days to flowering and days to maturity were recorded on plot basis.

Data analysis

Phenotypic and genotypic variance, phenotypic and genotypic coefficient of variation, range and mean of five randomly selected plants were used to estimate the variability in the population. Thus, phenotypic and genotypic coefficients of variation were estimated according to the method suggested by Burton and Devane (1953) [4]. Broad sense heritability expressed as the percentage of the ratio of the genotypic variance (σ^2_g) to the phenotypic variance (σ^2_p) and was estimated on genotype mean basis as described by Allard (1960) [2]. According to Johnson *et al.* (1955) [10], genetic advance expected under selection and genetic advance in percent of the mean were calculated at 5% selection intensity

Results and Discussion

The magnitude of heritable variability is the most important component in any breeding material. Therefore, the occurrence of genetic variability is pre-requisite for any crop improvement programme as it provides a wider scope for selection. Accordingly, chickpea genotypes were evaluated for their genetic potential in a response of yield and yield attributes.

Assessment of range and mean

The sixty genotypes of chickpea evaluated showed broader range of variability for most of the character studied (Table 2). Eclectic ranges were noted for seed yield/plant, number of secondary branches/plant, pods/plant, height at first pod, protein content, 100 seed weight, harvest index, seed volume/weight whereas, the lowest ranges were recorded for number of primary branches/plant, days to maturity and days to flowering. Genotype NG-24 (62.66 days) was the earliest to flower. Among all the genotypes, NGD-1663 (21.86 g) recorded the highest seed yield per plant and lowest was from genotype NGDE-1677 (7.21g). The analysis of variance revealed highly significant differences among the genotypes for all the characters indicating a considerable amount of genetic variability among the genotypes evaluated and for most of the traits studied. Such wide variations indicated the scope for improving for these traits. Wide variability has also been reported by Kumar *et al.* (2016) [13], Chopdar *et al.* (2017) [5] and Thakur *et al.* (2018) [15].

Assessment of phenotypic and genotypic variance

The analysis of variance revealed highly significant differences among the genotypes for all the characters indicating a considerable amount of genetic variability among the genotypes evaluated. Wide variability has also been reported by Jivani *et al.* (2013) [9], Yadav *et al.* (2015) [16], Kumar *et al.* (2016) [13], Chopdar *et al.* (2017) [5] and Thakur *et al.* (2018) [15].

The phenotypic variance (σ^2_p) and phenotypic coefficient of variation (PCV) was slightly higher than the genotypic variance (σ^2_g) and genotypic coefficient of variation (GCV) for all the traits but in some cases the two values differed only slightly suggesting the presence of environmental influence to some extent in the expression of these traits. According to Deshmukh *et al.* (1992) [7], PCV and GCV values greater than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10 and 20% to be medium. With this scale, high GCV value was recorded for seed yield per plant (27.99 %), number of secondary branches per plant (27.06 %), 100-seed weight (23.14 %) and height at first pod (21.85 %). This offers a wide scope of opportunity to make selection for these traits. The result of the present study was in agreement with the finding of Ramanappa *et al.* (2013) [14] and Kuldeep *et al.* (2014) [12].

The highest value of PCV was observed for seed yield per plant (31.33 %), number of secondary branches per plant (30.45 %), pods per plant (28.41 %), 100-seed weight (25.43 %) and height at first pod (25.11 %). The phenotypic variation present in these traits also create chance for selection to improve these traits. The result of the present study was in agreement with finding of Ramanappa *et al.* (2013) [7], Kuldeep *et al.* (2014) [12] and Bhanu *et al.* (2017) [3].

Assessment of broad sense heritability

The estimated heritability ranges from 12.8% for harvest index to 89.1% for protein content (Table 2). Dabholker, (1992) [6] classified heritability estimates as low (5 to 10%), medium (10 to 30%) and high (30 to 60%). Considering this standard, heritability was high for protein content (89.1 %), followed by 100-seed weight (81.88 %), seed yield per plant (79.82 %), number of secondary branches per plant (78.96 %), height at first pod (75.77 %) and days to 50 % flowering (60.00 %). The parallel result was observed for by Yadav *et al.* (2015) [16], Kumar *et al.* (2016) [13] and Bhanu *et al.* (2017) [3].

Similarly, low estimation of heritability value was recorded for days to maturity (19.80 %) and harvest index (12.8 %) whereas the remaining traits showed moderate heritability values which indicated that total variability was due to genetic causes as well as due to environment. Hence, improvement for these traits through selection has limited possibility. The equivalent result was observed by Kumar *et al.* (2016) [13] and Bhanu *et al.* (2017) [3].

Assessment of expected genetic advance

The genetic advance as percent of mean at 5% selection intensity for 12 traits are presented in Table 2. Estimate of GA for seed yield per plant was 5.95g indicating that whenever it is selected the best 5% high yielding genotypes as parents, mean yields of progenies could be improved by 5.95g for the first cycle, that is mean genotypic value of the new population for seed yield per plant will be improved from 11.55 to 17.5g and the same holds true for all traits considered under this study.

In the present study, estimates of genetic advance as percent of mean at 5% selection intensity ranged from 3.44% for days to maturity to 51.52% for seed yield per plant. Relatively high GAM values were observed for seed yield per plant followed by number of secondary branches per plant, 100-seed weight, height at first pod and pods per plant. Parallel result was observed by Yadav *et al.* (2015) [16] and Hussain *et al.* (2016) [8] for seed yield per plant and 100-seed weight; Kuldeep *et al.* (2014) [12] for number of secondary branches per plant; Bhanu *et al.* (2017) [3] for pods per plant.

High heritability with high genetic advance as per cent of mean was recorded for number of secondary branches per plant, height at first pod, seed yield per plant and 100-seed weight. Similar results were recorded by Hussain *et al.* (2016) [8] for seed yield per plant and for 100-seed weight. It indicates the predominance of additive gene action. Therefore, improvement in these traits would be more effectively be done through selection in the present material.

Protein content showed high heritability with moderate genetic advance which indicates that, the genotypes under

study have moderate potential of genetic improvement under selection. Similar results were recorded by Kumar *et al.* (2016) [13].

Moderate heritability with moderate genetic advance as per cent of mean was observed for plant height. The result of the present study was in agreement with the finding of Bhanu *et al.* (2017) [3] for plant height. This indicates the genotypes under study have moderate genetic potential.

Low values for heritability and genetic advance as per cent of mean for days to maturity and harvest index thereby indicating these traits were greatly influenced by the environment and low potential of genetic improvement through selection. Similar results were recorded by Yadav *et al.* (2015) [16] for days to maturity.

The heritability estimate provides the information on the magnitude of inheritance of quantitative characters but does not indicate the magnitude of genetic gain obtained by selection of best individual from the best population. So, heritability along with genetic advance is more useful than the heritability alone.

Table 1: List of Chickpea genotypes

1	NGD-1651	11	NGDE-1665	21	NGDE-1677	31	GG-6	41	NG-66	51	NG-230
2	NGD-1652	12	NGDE-1666	22	NGDE-1678	32	Dahod Yellow	42	NG-71	52	NG-305
3	NGD-1654	13	NGDE-1667	23	NGDE-1680	33	NG-139	43	NG-72	53	NG-323
4	NGD-1655	14	NGDE-1668	24	NGDE-1681	34	NG-367	44	NG-73	54	NG-365
5	NGD-1656	15	NGDE-1669	25	NGDE-1682	35	NG-461	45	NG-74	55	NG-366
6	NGD-1657	16	NGDE-1670	26	NGDE-1684	36	NG-9	46	NG-113	56	NG-493
7	NGD-1658	17	NGDE-1673	27	GG-1	37	NG-22	47	NG-165	57	NG-495
8	NGD-1661	18	NGDE-1674	28	GG-2 (C)	38	NG-24	48	NG-191	58	NG-496
9	NGD-1663	19	NGDE-1675	29	GG-3	39	NG-52	49	NG-206	59	NG-94
10	NGD-1664	20	NGDE-1676	30	GG-5 (C)	40	NG-55	50	NG-223	60	NG-96

Table 2: Range of variation, mean, phenotypic and genotypic coefficients of variation, heritability (b.s.), Genetic advance and genetic advance expressed as per cent of mean for twelve characters in chickpea.

Characters	Range of variation	Mean	σ_g^2	σ_p^2	GCV (%)	PCV (%)	h^2_{bs} (%)	GA (%)	GA % of mean
Days to 50 % flowering	62.66-83.66	78.81	17.75	29.61	5.34	6.905	60.00	6.72	8.53
Days to maturity	100.00-116.33	106.13	15.81	80.00	3.76	8.471	19.80	3.64	3.44
No. of primary branches/plant	1.33-2.66	2.21	0.03	0.10	8.39	14.57	33.12	0.22	9.94
No. of secondary branches/plant	4.46-15.46	9.70	6.89	8.73	27.06	30.45	78.96	4.80	49.53
Pods per plant	17.41-46.13	28.49	28.57	65.55	18.76	28.41	43.60	7.27	25.52
Plant height (cm)	24.08-50.17	41.05	20.54	46.17	11.04	16.55	44.49	6.22	15.17
Height at first pod (cm)	10.49-26.86	17.57	14.75	19.47	21.85	25.11	75.77	6.88	39.19
Seed yield per plant (g)	7.21-21.86	11.55	10.45	13.10	27.99	31.33	79.82	5.95	51.52
100-seed weight (g)	15.36-37.46	26.01	36.24	43.78	23.14	25.43	82.80	11.28	43.37
Seed volume per weight (ml/g)	60.56-92.26	80.51	22.52	37.68	5.89	7.62	59.77	7.55	9.38
Harvest index (%)	38.82-50.93	45.28	5.961	46.55	5.39	15.06	12.8	1.80	3.97
Protein content (%)	14.20-22.08	18.57	2.040	2.29	7.68	8.14	89.1	2.77	14.94

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