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EVALUATION OF CHICKPEA (*CICER ARIETINUM* L.) GERMPLASM FOR GENETIC VARIABILITY

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ABSTRACT

An experiment comprising 64 chickpea germplasm was evaluated to assess the genetic variability present among the genotype. Genotype coefficient of variation was observed high for seed yield per plant, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, harvest index and days to 50% flowering. High estimates of heritability coupled with high genetic advance as per cent of mean was registered for seed yield per plant, seed index, days to maturity, number of pods per plant and days to 50% flowering indicating that the genetic variance for these traits are probably owing to their high additive gene effects and thus there is better scope for improvement of these traits through direct selection.

Key words : *Genetic variability, heritability, genetic advance, chickpea.*

Chickpea (*Cicer arietinum* L.) is the third most important pulse food legumes crop in the world after soybean and dry pea and widely cultivated in west and south Asia. In India, it is grown in about 8.25 mha area giving annual production of 7.05 million tons in 2008 (1). India contributes 67 per cent of the global chickpea production. It is valued for its nutritive seed with high protein content from 25.3-28.9 per cent after dehulling (2). The genetic reconstruction of a plant type is required for developing high yielding varieties by incorporating and improving the yield component characters. Therefore, evaluation of germplasm for genetic variability is essential for the present as well as future crop improvement programmes. Moreover, proper utilization of germplasm requires testing of genetic potential under local condition or the target environment for which the breeding programme is aimed in the view of the above perspectives, the present study was taken up to assess genetic variability in chickpea germplasm to identify genetically diverse and agronomically superior genotypes.

MATERIALS AND METHODS

The experimental material consisted of 64 genotypes of chickpea collected from different geographical regions of India and abroad grown in *Rabi,* 2010-11 for field experimentation at Pulses Research Centre, Mokama, Bihar Agricultural University, Sabour (Bhagalpur). The experiment was laid out in a randomized complete block design with three replications in plot size was 4.8 m^2, with 1 row of 4.0 m length. Inter row spacing distance was kept 30 cm and plant to plant spacing was 30 x 10 cm. The recommended packages of practices were followed to raise a healthy crop. Data were recorded on ten quantitative traits viz. 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, 100 seed weight (g), biological yield (g), harvest index and seed yield per plant. The days to 50% flowering and days to maturity were recorded on a plot basis and plant height, number of branches per plant, number of pods per plant, 100 seed weight (g), biological yield, harvest index and seed yield per plant were recorded from a random sample of five plants in each plot. The pooled mean values over seasons were subjected to analysis of variance for 10 traits carried out as per (3). Genotypic and Phenotypic coefficient of variation (GCV and PCV) were calculated by following the method given (4). Heritability and expected genetic advance were estimated by (5).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences for all 10 characters under study, indicating that significant amount of genetic variability present in the chickpea germplasm (Table-1). The variability among the genotypes, suggested that ample scope for improvement through selection. Knowledge of genetic system controlling yield and its components is useful in understanding the prepotency of the parents and thus help to select parents possessing inbuilt genetic potential. The genotypes like IPC2010-62, was

Table-1 : Analysis of variance for ten quantitative characters of Chickpea Germplasm.

Sl. No.	Characters	Mean Sum of Squares		
		Replication (d.f. = 02)	Treatment (d.f. = 63)	Error (d.f. = 126)
1.	Days to 50% flowering	2.08	38.28**	16.41
2.	Plant height (cm)	2.46	376.52**	98.09
3.	No. of Primary branches per plant	3.71	7.01**	2.28
4.	No. of Secondary branches per plant	7.84	28.59**	7.04
5.	No. of Pods per plant	205.12	792.24**	66.12
6.	Days to Maturity	8.362	938.48**	7.89
7.	100-seed weight(g)	7.88	45.52**	3.36
8.	Biological Yield per plant (g)	652.82	2975.84**	362.02
9.	Harvest index (%)	92.62	369.53**	38.64
10.	Seed yield per plant (g)	36.88	39.47**	4.25

*, ** = Significant at 5% and 1% levels of significance, respectively.

Table-2 : Potential genotypes identified for different attributes in chickpea germplasm.

Sl. No.	Characters	Potential genotypes identified
1.	Days to 50% flowering	AKG70, BGD1082, BG3046, BGD1075, RKG12.286, H09-96, NDG11-24, NDG14-24, GCP105, IPC2012-49
2.	Plant height	GL26069, IPC2010-62, JG14, CSJ515, GNG2127, IPC2012-98, NBeG507, BG3067
3.	No. of Primary branches per plant	CSJ515, Local MKA, Local NLA, PhuleG97030, GNG2299, IPC2010-62, KWR108, PG186, NDG14-24
4.	No. of Secondary branches per plant	H-12-62, JG14, IPC2010-62, KWR108, NDG14-24, GNG2264, BG3067, GNG2304, PhuleG13110
5.	No. of Pods per plant	IPC2010-62, JG14, CSJ515, GNG2299, CSJ887, GCP105
6.	Days to Maturity	AKG70,IPC2012-98, BG3067, CSJ887, IPC2010-62
7.	Seed Index	NBeG49, NBeG507, JG14, NDG14-24, IPC2010-62
8.	Biological Yield per plant	PhuleG13110, IPC2010-62, KWR108, BG372, PBC501, GNG469, BG3043
9.	Harvest index	IPC2010-62, JG14, KPG59, PG170, GL1203, GNG469,
10.	Seed yield per plant	CSJ515, IPC2010-62, PhuleG13110, JG14, GCP105, NBeG507, H12-55, GNG469, BG3043, AKG70, PG186, PhuleG97030, KWR108, GCP105, BG372, PBC501, NDG14-24

Table-3 : Estimates the genetic parameters for ten characters of 64 Chickpea germplasm.

Sl. No.	Characters	GCV	PCV	Heritability (h^2bs)	Genetic advance	GA as % of mean
1.	Days to 50% flowering	22.95	26.92	76.74	19.86	40.63
2.	Plant height	17.18	31.21	29.18	0.68	18.67
3.	No. of Primary branches per plant	29.93	38.89	56.39	7.47	44.47
4.	No. of Secondary branches per plant	26.69	36.68	53.51	2.72	39.16
5.	No. of Pods per plant	28.84	34.59	66.45	19.95	46.28
6.	Days to Maturity	16.85	20.72	67.34	3.84	26.79
7.	Seed Index	18.84	20.63	82.35	3.41	33.75
8.	Biological Yield per plant	9.04	13.44	46.15	10.02	12.66
9.	Harvest index	24.69	29.69	36.49	0.56	13.40
10.	Seed yield per plant	32.42	37.91	75.42	7.13	56.35

identified as a desirable for multiple characters like medium plant height, more number of primary and secondary branches per plant, more number of pods per plant, medium maturity, more 100 seed weight, biological yield per plant and seed yield per plant. AKG70 was identified for early flowering and maturity. JG14 was found maximum number of pods per plant and 100 seed weight. CSJ515 and IPC2010-62 was recorded high seed yield per plant (Table-2).

Higher magnitude of GCV were recorded for seed yield per plant (32.42%) followed by number of primary branches per plant (29.93%), numbers of pods per plant (28.84%), number of secondary branches per plant (26.69%), harvest index (24.69%) and days to 50% flowering (22.95%), while plant height (17.18%), seed index (18.84%) and days to maturity (16.85%) showed moderate GCV values, indicating substantial amount of genetic variability. However, some where it was recorded high genotypic coefficient of variation for plant height, number of branches per plant, number of pods per plant and seed yield per pant. A wide range of phenotypic coefficient of variation was observed and ranged from 13.44% for days to maturity to 38.89% for number of primary branches per plant. Seed yield per plant (37.91%), number of secondary branches per plant (36.68%), number of pods per plant (34.59%), Plant height (31.21%), Harvest index (29.69%) and days to 50% flowering (26.92%) registered higher magnitude of PCV values, suggested favourable effect of environment in the expression of these characters (Table-3). However, high magnitudinal differences between PCV and GCV were observed for number of primary branches per plant followed by numbers of pods per plant and plant height, indicated greater influence of environment, whereas relatively low magnitudinal differences were observed for seed index and days to maturity. Similar results were also observed by (6,7,8).

The perusal of the Table-3 revealed the estimates of heritability (%) in broad sense for 10 characters studied, which ranged from 29.18% for plant height to 82.35% for 100-seed weight. Days to 50% flowering (76.74%), seed yield per plant (75.42%), days to maturity (67.34%) and number of pods per plant (66.45%) exhibited high heritability. (4) Suggested that genetic variation along with the heritability estimates would give a better idea about the expected efficiency of selection. Thus, a character possessing high GCV along with the high heritability will be valuable in a selection programme. Seed yield per plant and number of pods per plant recorded high estimates of GCV coupled with high heritability.

Maximum genetic advance was recorded for number of pods per plant (19.95) followed by days to 50% flowering (19.86). However, high estimates of genetic advance as per cent of mean was registered for seed yield per plant (56.35%), number of pods per plant (46.28%), number of primary branches per plant (44.47%), days to 50% flowering (40.63%), number of secondary branches per plant (39.16%), seed index (33.75%) and days to maturity (26.79%), suggesting that these characters are governed by additive genes and selection will be rewarding for improvement of such traits. Low genetic advance as per cent of mean was recorded for biological yield per plant (12.66%) and harvest index (13.40%), indicating the involvement of non additive gene action in controlling this trait and heterosis breeding may be useful for further generation of variability for this character.

Heritability estimates along with genetic advance are more useful than heritability alone in predicting the effectiveness of selection. Further, the heritability estimates coupled with expected genetic advance as per cent of mean indicates the mode of gene action in choosing an appropriate breeding methodology. High genetic advance as per cent of mean coupled with high heritability recorded for days to 50% flowering, number of pods per plant, days to maturity, seed index and seed yield per plant. This situation indicates that the genetic variances for these traits are probably owing to their high additive gene effects reported by (5, 9 and 10) and thus there is better scope for improvement of these traits through direct selection.

High estimates of genotypic coefficient of variation and heritability and genetic advance as per cent of mean indicate the predominance of additive gene action in controlling these characters and simple directional selection may be effective to improve these characters.

CONCLUSION

The genotypes CSJ515, PhuleG13110, GCP105, NBeG507, H-12-55, GNG469, BG3043, AKG70, PhuleG97030, IPC2010-62, KWR108, PG186, BG372, PBC501, JG14 and NDG14-24 were identified as genetically diverse parents, which can be utilized for future crop improvement programme in Chickpea. The study of diversity index reflects that in present set of germplasm, ample genetic variation exists for seed yield per plant, therefore a direct selection based on seed yield can be done to develop high yielding varieties. However, after further evaluation, some genotype may be used as parents in the crossing programme to create the better genetic recombinants for improving yield *per se*. The above results indicate that the genotypes, viz. AKG70, IPC2010-62, CSJ515, NDG14-24, GNG469, PhuleG13110, BG3046, GCP105 and PG186 have maximum genetic diversity and useful for developing a large number of segregants through crossing programme by using maximum diverse genotypes.

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