

# EVALUATION OF CHICKPEA GERMPLASM (DESI) (*CICER ARIETINUM* L.) FOR YIELD AND YIELD CONTRIBUTING TRAITS

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## ABSTRACT

Thirty six genotypes of chickpea were evaluated to study the magnitude of genetic variability, heritability and genetic advance in yield and yield contributing characters. The genotype RKG135 recorded highest mean performance (94.60) for number of pods/plant and biological yield / plant (g) (38.83) while genotype NBeG 13 recorded highest mean performance (56.67) for plant height. Highest mean performance for seed yield q/ha (19.61) was recorded in genotype RVSSG 1 while genotype H 04-75 recorded highest mean performance (126.33) for days to maturity. Genotype BG 3004 showed highest mean performance for 100 seed weight (28.85) and No. of branches / plant (5.00) and BGD 1053 recorded highest mean performance (19.93) for protein content. High genotypic (31.68) and phenotypic (31.82) co-efficients of variance were recorded for number of pods per plant. High heritability (99.8) coupled with high genetic advance (52.19) were recorded for seed yield q/ha and highest genetic gain (64.97) was recorded for No. of pods/plant. Hence these characters indicate the presence of a considerable proportion of total variability due to genetic causes and may serve as effective selection parameter during breeding program for crop improvement.

## INTRODUCTION

Pulses are the important food crop of the world because it provides good source of vegetable dietary protein, mostly in areas where economy does not support large scale production and utilization of animal protein. Pulse grain protein nutritionally complements the protein in cereal grains.

Chickpea (*Cicer arietinum* L.) is the 3<sup>rd</sup> most important pulse crop in the world, after dry beans and field peas (FAOSTAT, 2008). It is grown mainly in the arid and semi-arid regions of the world with a total annual production of 9.6 million ton from 11.5 million hectares and an average yield of 0.84 ton ha<sup>-1</sup> (FAOSTAT, 2009). Chickpea is an important source of human food and animal feed due to its high protein, vitamins, minerals and fibre content. The total seed yield production is quite low in most chickpea growing countries and a wide gap exists between the potential (5 ton ha<sup>-1</sup>) and actual (0.8 ton ha<sup>-1</sup>) yields (FAOSTAT, 2008). The low yields have been attributed to several factors among which include low genetic diversity of cultivated chickpea and several biotic and abiotic stresses (Gaur *et al.*, 2012).

Chickpea plays an important role to improve soil fertility by fixing up atmospheric nitrogen with the help of root nodules (Singh *et al.*, 2005). A healthy crop of chickpea can fix up to 141 kg nitrogen per hectare (Rupela, 1987) Presently India produces around 8567.8 thousand tonnes of total pulse from an area of nearly 23 million hectare of land (FAO, 2012-13).

During the year 2009-10, the country produced 14.66 million tones of pulses from 23 million ha area, with an average yield of 637 kg/ha (Ali and Gupta, 2012). The future requirement of pulses is expected to rise further mainly due to ever-increasing population and preference for pulses as the cheapest source of dietary protein.

Further genotypic variance is a prerequisite for an effective breeding programme. The value of germplasm relies not only on the number of accessions it possesses, but also upon the genetic variability present in those accessions for agronomic and yield components (Reddy *et al.*, 2012). In addition to genetic variation, heritability of economically important characters is essential for effective breeding programme and selection of specific traits. High broad sense heritability has been reported in chickpea for 100 seed weight and seed yield per plant (Sachin *et al.*, 2014) and days to flowering and plant height (Khan *et al.*, 2011).

Genetic variability is an essential component for any breeding programme designed to improve the characteristics of crop plant. Limited or lack of genetic variability is important factor for the limited progress achieved in increasing the productivity of grain legumes including chickpea (Ramanujam, 1975). The progress due to selection in nature, in quantitative traits depends on the nature and magnitude of variability present in the population to be improved. Genetic variability can be observed for various characters on plant of heterogeneous

populations in the form of genotypic difference. The present studies were undertaken to study the extent of genetic variability, heritability and genetic advance present in chickpea germplasm for quantitative characters and protein content.

## MATERIALS AND METHODS

The research experiment was conducted in Rabi season at the field experimentation centre of Department of Genetics and Plant Breeding and Seed Science and Technology, Sam Higginbottom Institute of Agriculture, Technology and Sciences, Deemed to be University, Allahabad. The experimental material for the present study consisted of 36 genotypes of chickpea (desi), which were evaluated in a Randomized Block Design in three replications. The material was obtained from IIPR Kanpur, Uttar Pradesh, India. The chickpea samples were analyzed for 11 key characters viz. Days to 50% flowering, plant height (cm), days to maturity, No. of branches per plant, No. of pods per plant, biological yield per plant (g), 100-seeds weight(g), harvest index (%), protein content (%), seed yield per plant (g), and seed yield per hectare (q).

Number of days was counted from the day of sowing of seeds in field to the days to 50% flower emergence for calculation of days to 50% flowering. Number of days from date of sowing to pod maturity in each treatment were recorded and counted for counting days to maturity. While the other characters like plant height, No. of branches/plant, No. of pods/plant, Biological yield/plant, 100-seeds weight, harvest index, seed yield/plant and seed yield (q/ha) were evaluated by selecting randomly five plants from each plot and averaged. The test of significance was carried out as per the methodology of Panse and Sukhatme (1967). The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were estimated according to the methods suggested by Burton (1952). Heritability ( $h^2$ ) and genetic advance were estimated by employing the methods suggested by Burton and Devane (1953) and Johnson *et al.* (1955). respectively Protein content was determined by the Lowry *et al.* (1951) method.

### Layout Description

The layout description which is used in the experiment is as follows.

Design of experiment : Randomized Block Design (RBD)

Number of genotypes	:	36
Number of replications	:	3
Net area	:	432 m <sup>2</sup>
Gross area	:	611 m <sup>2</sup>
Spacing	:	
Row to row	:	30 cm
Plant to plant	:	10 cm

## RESULTS AND DISCUSSION

The results estimated from the data a present investigation, which was point out to assess genetic variability, genetic parameters and identification of best germplasm are presented and discussed under

The performance results of 11 different characters are shown in Table 1. On the basis of mean performance for quality parameter genotype RVSSG 1 was identified as best performer for the seed yield q/ha and the genotype BG 3004 was best in number of branches/plant and 100 seeds weight. On the other hand, the genotype RKG 135 was found best in number of pods per plant and biological yield per plant. The character protein content and seed yield/plant showed highest heritability and highest genetic advance was shown by No. of pods/plant respectively. The results are in confirmation with the findings of Pratap *et al.* (2004), Jeena *et al.* (2005), Tadele *et al.* (2005) and Tomar *et al.* (2009).

The understanding of genetic variability provides many avenues for genetic amelioration of the crop however; very limited information is available on the extent of genetic variation in newly bred genotypes developed through recombinant breeding in chickpea. The analysis of variance showed significant difference for mean sum of square at 5% level for all the characters under study among 36 genotypes. 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. Muhammad *et al.* (2002) and Ali and Ahsan (2012) also reported high genetic variability for different characters in chickpea. High genetic variability was also reported by Nagy *et al.* (2012) in pigeonpea.

According to Deshmukh *et al.* (1986) PCV and GCV values greater than 20 are regarded as high, whereas values less than

**Table List of genotypes**

S.No.	Genotypes	S.No.	Genotypes	S.No.	Genotypes
1.	GJG 0703	13.	GNG 1958	25	RKG 135
2.	BG 3003	14	KGD 1209	26	RVSSG-2
3.	H 04-08	15	IPC 2004-17	27	RKG 141
4.	Phule G 00110	16	BAUG 7	28	JG 14-11
5.	JG 9-3	17	GNG 1936	29	NBeG 13
6.	HIR-70	18	GCP 105 (Ch)	30	Phule G 97030
7.	H 04-75	19	KGD 1249	31	KWR 108 (Ch)
8.	CSJ 515	20	RBSSG-1	32	PBC 161
9	NDG 9-21	21	BAUG 12	33	GL 26083
10	Tungbhadra	22	GJG 0714	34	BGD 1053
11	IPC 2004-1	23	BG 3004	35	BGM 569
12	RSG 811	24	GL 26054	36	BDNG 2001-2-1

**Table 1: Mean performance of 11 characters for 36 chickpea genotypes**

Genotypes	Days to 50% flowering	Plant height (cm)	Days to maturity	No. of branches / plant	No. of Pods/ plant	Biological yield/ plant (g)	100 seed weight (g)	Seed Yield/ plant (g)	Seed yield/ ha (q)	Harvest Index (%)	Protein content (%)
GJG 0703	101.00	43.47	130.33	4.33	62.40	32.83	21.81	21.48	9.63	65.42	17.81
BG 3003	100.00	38.43	129.33	3.67	39.40	26.67	23.88	18.25	6.05	65.75	18.88
H 04-08	96.00	49.07	129.00	3.33	30.80	22.00	15.12	17.22	9.72	78.27	14.12
Phule G 00110	100.33	38.90	129.67	3.67	28.73	25.00	23.80	16.12	12.05	64.48	18.79
JG 9-3	98.33	44.30	132.33	4.00	37.53	30.67	27.67	18.92	10.60	61.68	19.67
HIR-70	96.67	39.40	133.67	3.00	33.27	29.17	23.27	17.67	5.27	60.57	18.27
H 04-75	91.33	55.87	126.33	3.33	40.67	24.50	15.09	18.40	9.49	75.10	14.08
CSJ 515	83.00	48.73	128.33	4.00	70.13	20.33	14.03	19.98	17.27	98.27	13.03
NDG9-21	94.67	40.00	131.33	4.33	64.13	22.33	26.32	21.44	14.38	96.01	19.23
Tungbhadra	95.33	41.47	132.00	3.00	53.00	21.17	23.26	19.48	12.60	92.01	18.26
IPC 2004-1	97.00	45.63	130.33	4.00	54.33	18.00	22.09	18.79	15.60	93.95	18.08
BG 3004	102.00	35.67	135.33	5.00	47.93	26.33	28.85	18.44	8.72	70.03	19.84
GL 26054	95.67	42.00	130.33	4.00	55.13	29.50	20.12	19.66	17.55	66.64	18.12
RKG 135	92.67	50.33	128.33	4.67	94.60	38.83	16.09	23.76	17.05	82.41	13.08
RVSSG-2	94.00	49.97	132.33	3.00	87.60	30.67	25.23	22.55	17.55	73.52	18.23
RKG 141	96.00	44.00	129.33	3.67	83.00	24.17	18.94	22.17	16.49	91.72	18.18
JG 14-11	95.00	44.00	127.33	4.00	68.93	30.67	17.48	21.79	17.83	71.04	18.75
NBeG 13	100.33	56.67	134.67	2.67	45.73	22.33	19.85	18.24	6.49	81.68	19.18
Phule G 97030	100.33	40.83	130.33	2.33	61.60	17.00	25.75	21.62	12.55	98.27	13.86
KWR 108 (Ch)	99.33	40.17	131.67	3.00	43.27	22.17	20.76	18.27	8.38	82.40	13.05
PBC 161	92.33	37.17	127.33	4.67	79.73	27.83	17.87	21.55	15.11	77.43	13.32
GL 26083	92.00	40.67	131.00	3.67	68.00	21.50	14.05	21.37	12.83	97.86	12.68
BGD 1053	94.00	40.83	127.67	4.00	72.13	23.50	14.32	22.08	15.55	93.95	19.93
BGM 569	95.00	36.17	127.00	3.67	69.53	20.50	12.68	21.06	14.05	79.57	18.95
BDNG 2001-2-1	97.33	49.67	134.00	4.00	42.87	30.17	27.93	18.68	7.33	61.91	13.48
Grand Mean	95.24	43.16	130.39	3.87	59.54	25.77	20.65	20.26	12.96	77.74	16.74
Range Min.	83.00	34.67	126.33	2.33	28.73	21.17	12.68	16.12	5.27	59.05	12.06
Max	102.00	56.67	135.33	5.00	94.60	38.83	28.85	23.76	19.61	98.27	19.93
Coefficient of Variance (CV)	4.62	12.34	1.75	16.63	31.73	19.11	22.91	1.87	1.28	1.17	3.02
F- test	S	S	S	S	S	S	S	S	S	S	S
S. Ed. (±)	0.59	0.53	0.43	0.15	1.47	0.68	0.64	0.61	0.81	1.49	0.73

10% are considered to be low and values between 10% and 20% to be medium. In the study, estimates of phenotypic coefficients of variation (PCV) were comparable with respective genotypic coefficients of variation (GCV) for all the characters. However the estimates of PCV were, in general, higher than the corresponding estimates of GCV for all the characters. This may result due to the involvement of environment and genotype x environment effect in the expression of characters (Kavita and Reddy, 2002). GCV (genotypic coefficient of variance) ranged from 1.73 to 40.50, where as PCV (Phenotypic coefficient of variance) ranged from 1.78 to 40.53 these findings suggest that selection can be effective based on phenotypic along with equal probability of genotypic values. With the help of GCV alone, it is not possible to determine the extent of variation that is heritable. Hence, the knowledge of heritability helps the plant breeders in prediction. The genetic advance for quantitative characters aids in exercising necessary selection procedure. In the present study high heritability was found in the traits like seed yield q/ha (99.8), No. of pods/plant (99.1) t and seed yield/plant (g) (97.7), while lowest heritability was observed in No. of branches/plant (92.2) followed by days to maturity (94.8) (Table 2). Sachin *et al.* (2014) recorded highest heritability in 100 seed weight and seed yield/plant while Burly *et al.* (2004) recorded lowest heritability estimates for days to maturity and days to 50%

flowering.

The highest genetic advance was recorded for protein content (74.17) followed by seed yield q/ha (52.19), number of pods/plant (38.68), harvest index (22.44) and plant height (10.86). Similar findings have been reported by Samal and Jagdev (1989), Jahangirdar *et al.* (1994), Deshmukh and Patil (1995) While comparatively low estimates of genetic advance for number of branches/plant (1.26), days to maturity (4.53) and seed yield/plant (5.84) were obtained.

On the other hand, traits like seed yield q/ha (62.27), seed yield/plant (51.26), harvest index (49.73), protein content (48.73) and 100 seed weight (46.34) had shown high estimates of genetic gain. It indicates that most likely the heritability is due to additive gene effects and selection for these traits may be rewarding. Similar findings have been reported by Sachin *et al.* (2014) and Meshram *et al.* (2014) in blackgram. Rest of the characters had low genetic gain value, viz days to maturity (3.47), days to 50% flowering (9.35), plant height (25.17) and number of branches per plant (32.45). (Table 2). 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 overall results show that the genotype RVSSG 1 was identified as best performer for the seed yield q/ha and the

**Table 2: Genetic parameters of 11 quantitative characters for 36 chickpea genotype**

S.No.	Characters	VE	VG	VP	ECV	GCV %	PCV%	h <sup>2</sup> (bs)%	GA	GA as % of mean
1.	Days of 50% flowering	0.53	19.21	19.74	0.76	4.60	4.66	97.3	8.91	9.35
2	Plant height (cm)	0.42	28.23	28.65	1.51	12.31	12.40	98.5	10.86	25.17
3.	Days to maturity	0.28	5.10	5.38	0.41	1.73	1.78	94.8	4.53	3.47
4	No. of branches /plant	0.03	0.40	0.44	4.76	16.40	17.08	92.2	1.26	32.45
5.	No. of pods/plant	3.25	355.8	359.0	3.03	31.68	31.82	99.1	38.68	64.97
6.	Biological yield/ plant (g)	0.70	24.01	24.71	3.24	19.01	19.29	97.2	9.95	38.61
7.	100-seed weight (g)	0.62	22.18	22.80	3.81	22.80	23.12	97.3	9.57	46.34
8.	Seed yield/plant(g)	0.20	8.24	8.44	3.90	25.18	25.48	97.7	5.84	51.26
9.	Seed yield/ha (q)	0.027	15.49	15.52	1.69	40.50	40.53	99.8	52.19	62.27
10.	Harvest index (%)	5.40	123.8	129.2	5.15	24.66	25.19	95.8	22.44	49.73
11.	Protein content (%)	0.25	6.92	7.18	3.97	20.84	21.21	96.4	74.17	48.73

$\sigma^2_g$  = Genotypic variance,  $\sigma^2_p$  = Phenotypic variance, GCV = Genotypic coefficient of variance, PCV = Phenotypic coefficient of variation, h<sup>2</sup>(bs) Heritability (broad sense), GA = Genetic advance, GA % (I) = Genetic advance as percent of mean.

genotype BG 3004 were best in number of branches and 100 seeds weight. On the other hand, the genotype RKG 135 was found best in number of pods per plant and biological yield per plant. The character protein content and seed yield/ plant showed highest heritability and highest genetic advance was shown by No. of pods/plant respectively.

The highest value of VG, VP, GCV, PCV and GA as percent of mean was estimated in character No. of pods/plant while highest heritability was depicted in seed yield/ha.

On the basis of heritability and expected genetic advance as percent of mean for different characters studied in the present investigation, selection criteria based on seed yield per plant, seed yield q/ha, No. of pods per plant, biological yield/plant and 100 seed weight may be useful for further development of high yielding genotypes. Hence these characters should be given top priority for further improvement of yield and yield components. As the results are based on one year data, it can prove helpful in further experimentation.

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