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Variability assessment for yield component and protein content in chickpea (*Cicer arietinum* L.) genotype

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Abstract

Genetic variability analysis for seed yield and its component along with protein content, were estimated in 42 genotypes. Analysis of variance on fourteen characters showed significant value in mean sum of square (MSS) for all traits. Occurrence of significant level of variation in the observed traits implies the presence of variability. GP 10, GP 94, GP 2 and GP 15 were the four genotypes which reported high values for protein content ranging from 25.33 to 26.85%. Number of secondary branches, pods per plant, hundred seed weight, biological yield, harvest index, plot yield, and seed yield per plant showed high PCV coupled with high GCV. Plant height, height of first pod, number of seeds per pod and protein % showed moderate values of PCV along with moderate values of GCV. Traits exhibiting high values of PCV, GCV, heritability and GAM were number of secondary branches, pods per plant, hundred seed weight, biological yield, harvest index, plot yield, seed yield per plant and protein %.

Keywords: Chickpea, variability, protein content, heritability, genetic advance

Introduction

Chickpea (*Cicer arietinum* L.) is a winter annual crop belonging to the family Leguminosae/Fabaceae. It is the third most important legume in the world after dry beans and dry peas. Chickpea has played a major role in realization of 'Pulse Revolution' in India making the country near self-sufficient in Pulses. The world's area, production and productivity are 13.7 MHa, 14.24 MT, and 1038.4 Kg^{ha}⁻¹, respectively (FAO-STAT, 2019) [5]. India mostly produces desi chickpeas, as compared to Kabuli chickpeas. Chickpeas' area, yield, and productivity in India are 10.73 million hectares, 10.90 million tons, and 1016 kg/ha, respectively (FAO-STAT, 2019) [5]. Production per unit area has been consistently increasing at around 6 kg/ha each year (Merga *et. al.*, 2019) [10].

Genetic variability is crucial for crop improvement as well as survival of species in nature. It is also acts as row matter for crop evolution through artificial and natural selection. For a plant breeder genetic diversity is prerequisite for development of new and improved cultivar, which have desirable characteristics. Genetic variability is expressed in term of genotypic coefficient of variation. ANOVA identifies the variation present between groups and among groups. The variation within groups is solely due to environment and is categorized into environmental variance. The genetic characteristic of a population can be determined by the relative magnitude of GCV and PCV. For the examined variables, the high heritability and low level of differences between PCV and GCV indicated that cultivar has a greater influence on expression. High heritability combined with high genetic advance shows that heredity is more owing to the additive gene impact, and high estimates of heritability combined with a large magnitude of genetic advance it is recommended to improve any trait through selection.

Materials and Methods

The experimental material comprising 42 genotypes of chickpea was grown in Randomized Complete Block Design with two replications at Research cum Instructional farm Department of Genetics and Plant Breeding, College of agriculture, Indira Gandhi Agricultural University, Raipur, Chhattisgarh, during the Rabi season of 2021-22. Data was recorded on five randomly tagged plant in each replication for days to flowering, Days to maturity, Plant height (cm), Height of first pod (cm), number of primary branches, number of secondary branches, Pods per plant, Seeds per pod, Hundred seed weight, Biological yield (g), Harvest index (%), Plot yield (g), protein content (%) and Seed yield per plant (g). Pooled data were subjected to statistical analysis by using O.P. STAT software.

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Results and Discussion

Genetic variability present in population estimated by different statistical tool like range, genotypic and phenotypic coefficients of variations (PCV and GCV), and the probability of their transfer to next generation estimated through heritability analysis (h²bs) and genetic advance as percent mean (GA %).

Analysis of variance on fourteen characters showed significant value in mean sum of square (MSS) for all traits. Occurrence of significant level of variation in the observed traits implies the presence of adequate variability in experimental material (table 1). This variability can be exploited and utilised to improve genotype development.

Table 1: Analysis of variance for 14 yield and contributing traits in 42 chickpea germplasm along with check varieties

SV	DF	MSS						
		DTF	DM	PH	HOFP	NPB	NSB	PPP
Replication	1	5.76	4.31	4.53	11.69	0.04	0.04	76.55
Genotypes	41	49.61**	36.17**	55.23**	35.62**	0.58*	18.49**	138.70**
Error	41	4.32	4.64	5.30	3.40	0.29	1.62	36.02

SV	DF	MSS						
		SPP	HSW	BY	HI	PLYG	Protein	SYP
Replication	1	0.03	0.29	0.27	232.93*	2389.33	12.96	0.58*
Genotypes	41	0.11**	40.49**	12.75**	190.50**	46827.09**	15.58**	1.99**
Error	41	0.03	1.10	1.07	40.14	1632.04	2.46	0.10

*and ** significant at 0.05 and 0.01 probability level.

DTF = Days to flowering; DM = Days to maturity; PH = Plant height (cm); HOFP = Height of first pod (cm); PB = Primary branches; SB = Secondary branches; PPP = Pods per plant; SPP = Seeds per pod; HSW = Hundred seed weight (g); BY = Biological yield (g); HI = Harvest index (%); PLYG = Plot yield (g); Protein = protein content (%); SYP = Seed yield per plant (g).

The range of days to 50% flowering varied from the minimum being 46 days and the maximum being 70.5 days with a mean value of 60.81 days. Out of 42 genotypes studied, one genotype JG-24 had flowered at 46 days while GP-181 and GP-160 had flowered at 70.5 days (Table 2). The classification of genotypes based on their time taken for flowering has been listed below:

Table 2: Classification of genotypes based on days to 50% flowering#

Classification	Genotypes	DTF	Classification	Genotypes	DTF
Early (40-60 Days)	JG24	46.00	Medium (60-80) Days	GP2	60.50
	CG CHANA2	53.50		GP161	60.50
	GP13	55.50		GP17	61.00
	GP60	55.50		GP81	61.00
	GP80	55.50		GP96	61.00
	GP91	55.50		GP152	61.50
	GP156	55.50		GP11	62.00
	GP5	56.00		GP51	62.00
	GP29	56.00		GP164	62.00
	GP12	57.00		GP19	62.50
	JG315	57.00		GP58	63.00
	GP79	58.00		GP10	63.50
	GP82	58.50		GP94	63.50
	GP127	59.00		GP87	64.50
	GP8	59.50		GP159	65.00
	GP16	59.50		GP154	65.50
	GP54	59.50		GP6	66.00
	T39-1 (Blue)	59.50		GP97	66.00
	T39-1 (Pink)	60.00		GP165	67.00
				GP52	68.50
		GP15	70.00		
		GP160	70.50		
		GP181	70.50		

As per DUS descriptor PPV&FRA 2007

Days to maturity ranged from 97 (JG-315) days to 114 (GP-152) days with an average of 107.46 days. Of the total genotypes, JG 315 (97 days) and JG 24 (99 days) showed

medium duration maturity (90-100 days) and rest of the entries fell into late duration (>100 days) (Table 3).

Table 3: Classification of genotypes based on days to maturity

Classification	Genotypes	DM	Classification	Genotypes	DM
Medium (90-100 days)	JG315	97.00	Medium (90-100 days)	JG24	99.00
Late (>100 days)	GP96	101.50	Late (>100 days)	GP6	108.50
	T39-1 (P)	101.50		GP15	108.50
	T39-1 (B)	101.50		GP19	108.50
	GP2	101.98		GP94	108.50
	GP10	102.00		GP159	108.50
	GP13	102.50		GP165	108.50
	GP97	103.50		GP156	109.00
	CG CHANA2	104.00		GP127	110.00
	GP8	105.50		GP58	110.50
	GP17	105.50		GP51	111.00
	GP5	106.00		GP60	111.50
	GP54	106.00		GP154	111.50
	GP87	106.00		GP52	112.00
	GP11	106.50		GP161	112.50
	GP160	106.50		GP181	112.50
	GP12	107.00		GP79	113.00
	GP16	107.50		GP81	113.00
	GP91	107.50		GP80	113.50
	GP29	108.00		GP82	113.50
	GP164	108.00		GP152	114.50

In the experimental material, the tallest genotype recorded is 42.92 cm (JG-24) while the shortest genotype recorded a height of 31.50 cm (GP-16) with mean height of 36.98 cm. The lowest and highest height noted for 1st pod height was 16.33 cm (GP-6) and 33.92 cm (GP-19), respectively with the mean being 22.32 cm. The lowest value recorded for number of primary branches was 1.15 (GP-2) and while the highest being 3.75 (GP-181) with an average of 2.21. The lowest and highest values for secondary branches were 3.4 (GP-80) and 16.92 (GP-16) with a mean value of 7.87.

Lowest numbers of pods observed was for GP-181 with 6.50 pods per plant while the highest number was observed for GP-54 with 53 pods per plant with a mean value of 19.82 pods per plant. The mean numbers of seeds per pod are 1.33 while the range lies between 1.05 to 2.1 seeds per pod. GP-91 recorded the highest value for number of seeds per pod while GP-154 has lowest. The hundred seed weight ranged from 8.88 g to 35.78 g with an average of 14.22 g. T39-1(Blue flower) had the least weight i.e. 8.88 g; while GP-54 recorded the highest hundred seed weight i.e. 35.78 g. The least biological yield observed is 4.17 g for GP-181 while, the highest observed is 14.75 g for T39-1(B). Mean value for biological yield is 8.25 g.

Harvest index ranged from a minimum of 13.28% for to a highest of 59.54% for GJG 1913 with averaging at 48.16%. The plot yield ranged from 139.50 g to highest of 652.50 g while averaging at 398.83 g. Lowest plot yield (g) was recorded for GP-181(139.50 g) while the highest was recorded by GP-54 (652.50 g) as shown in table 4.

Table 4: Top ten genotypes based on high Plot yield (g).

Genotypes	Plot yield (g)	Genotypes	Plot yield (g)
GP 51	553.00	GP 81	589.00
GP 2	565.00	GP 16	594.00
GP 10	571.00	GP 11	617.00
GP 12	584.00	GP 5	634.00
GP 13	588.00	GP 54	652.00

Lowest seed yield per plant was recorded for genotype GP-154 (1.30 g) while highest was recorded for genotype GP-54 (6.85 g) with an average of 2.56 g.

The study of variation is based on the division of variation into components attributed to various sources (genetic and environmental). The relative amounts of these elements can have an impact on a population's genetic makeup. Statistics has provided a number of analytical approaches for evaluating genetic variability. GCV and PCV are two of the most common methods for determining the amount of heritable and non-heritable variation in the material under investigation. Magnitudes of PCV were greater than GCV magnitudes; this demonstrated the influence of the environment on the genotypic effect, which in turn influenced the phenotypic effect. The results are presented in table 5.

Seven characters, number of secondary branches, pods per plant, hundred seed weight, biological yield, harvest index, plot yield, and seed yield per plant showed high PCV coupled with high GCV.

The highest and least values for both PCV and GCV are recorded for pods/ plant (PCV = 4.2% and GCV = 3.7%) and days to maturity (PCV = 47.16% and GCV = 36.15%), respectively. Similar result was concluded by Kishor *et al.*, (2018) [6].

High PCV values and low GCV values for number of primary branches and number of seeds per pod indicates that the variability present in these characters is due to the effects of environment. Similar conclusion for respective characters concluded by, Sharma *et al.*, (2010) [7], Mishra *et al.* (2014) [11], Babbar *et al.*, (2015) [1], Bhanu *et al.* (2017) [3], Thakur *et al.*, (2018) [8], Deepika *et al.*, (2021) [4]. Heritability is good index for the transmission of character from parents to their offspring. The ratio of total genetic variance to phenotypic variance is used to calculate broad sense heritability.

The term "genetic advance" refers to an increase in the mean genotypic value of selected plants compared to the parental population. High heritability along with high genetic advance indicates that the heritability is due to additive gene effect and selection will be effective. The characters which show high

heritability and genetic advance are, days to flowering, days to maturity, plant height, height of first pod, number of secondary branches, seed yield per plant, biological yield, hundred seed weight, plot yield and protein %.

The maximum value of heritability expressed by hundred seed weight (94.71%) while, minimum heritability by number of primary branches (33.30%). In case of GA as % of mean, seed yield per plant (74.98%) had maximum value while pods per plant (6.69%) expressed minimum.

Traits exhibiting high values of PCV, GCV, heritability and GAM were number of secondary branches, pods per plant, hundred seed weight, biological yield, harvest index, plot yield, seed yield per plant and protein %. This indicates the additive gene effects of the trait and the effect of the environment on heritability. Estimates for heritability and genetic advance as percentage mean with different scale is given in the table 6.

Table 5: Variability parameters for yield attributing traits and protein content in chickpea genotypes

Parameters	DTF	DM	PH	HOFP	PB	SB	PPP	SPP	HSW	BY	HI	PLYG	Protein	SYP
Grand Mean	60.81	107.46	36.98	22.32	2.21	7.87	19.82	1.33	14.22	8.25	32.42	398.83	22.41	2.56
S.E.	0.77	0.66	0.81	0.65	0.08	0.47	1.28	0.04	0.69	0.39	1.51	23.61	0.43	0.15
CV (%)	8.19	3.96	14.21	18.91	24.36	38.62	42.02	17.35	31.64	30.59	30.10	38.37	12.45	38.94
Min.	46.00	97.00	31.50	16.34	1.15	3.40	6.50	1.05	8.88	4.18	13.28	139.50	13.87	1.30
Max.	70.50	114.50	53.50	33.92	3.75	16.92	53.00	2.10	35.79	14.75	53.40	652.50	26.86	6.85
PCV (%)	8.54	4.20	14.88	19.79	29.84	40.27	47.16	19.28	32.07	31.85	33.12	39.03	13.40	39.86
GCV (%)	7.83	3.70	13.51	17.99	17.22	36.90	36.15	15.17	31.21	29.28	26.74	37.69	11.43	38.00
h^2 (bs) (%)	83.97	77.26	82.48	82.58	33.30	83.94	58.77	61.94	94.71	84.55	65.19	93.26	72.74	90.88
GA as % of mean	14.77	6.69	25.28	33.67	20.47	69.64	57.10	24.60	62.57	55.47	44.48	74.98	20.08	74.62

DTF = Days to flowering; DM = Days to maturity; PH = Plant height (cm); HOFP = Height of first pod (cm); PB = Primary branches; SB = Secondary branches; PPP = Pods per plant; SPP = Seeds per pod; HSW = Hundred seed weight (g);

BY = Biological yield (g); HI = Harvest index (%); PLYG = Plot yield (g); Protein = protein content (%); SYP = Seed yield per plant (g).

Table 6: Classification of the high values of heritability and genetic advance

Scale	h^2 (bs) (%)	Traits	Scale	GA as % of mean	Traits
Low	33.30	PB	Low	6.69	PPP
Medium	58.77	PPP	Medium	14.77	PB
	61.94	SPP		20.08	PLYG
High	65.19	HI	High	20.47	Protein
	72.74	Protein		24.60	HOFP
	77.26	DM		25.28	SPP
	82.48	PH		33.67	HI
	82.58	HOFP		44.48	BY
	83.94	SB		55.47	DTF
	83.97	DTF		57.10	PH
	84.55	BY		62.57	SB
	90.88	SYP		69.64	DM
	93.26	PLYG		74.62	HSW
94.71	HSW	74.98	SYP		

DTF = Days to flowering; DM = Days to maturity; PH = Plant height; HOFP = Height of first pod; PB = Primary branches; SB = Secondary branches; PPP = Pods per plant; SPP = Seeds per pod; HSW = Hundred seed weight; BY = Biological yield; HI = Harvest index; PLYG = Plot yield; Protein = protein content; SYP = Seed yield per plant.

Conclusion

Analysis of variance on fourteen characters showed significant value in mean sum of square (MSS) for all traits. Occurrence of significant level of variation in the observed traits implies the presence of variability. GP 10, GP 94, GP 2 and GP 15 were the four genotypes which reported high values for protein content ranging from 25.33 to 26.85%.

Seven characters, number of secondary branches, pods per plant, hundred seed weight, biological yield, harvest index, plot yield, and seed yield per plant" showed high PCV coupled with high GCV. Four characters, namely, plant height, height of first pod, number of seeds per pod and protein % showed moderate values of PCV along with

moderate values of GCV.

High heritability along with high genetic advance indicates that the heritability is due to additive gene effect and selection will be effective. The characters which shows high heritability and genetic advance are, days to flowering, days to maturity, plant height, height of first pod, number of secondary branches, seed yield per plant, biological yield, hundred seed weight, plot yield and protein %. Traits exhibiting high values of PCV, GCV, heritability and GAM were number of secondary branches, pods per plant, hundred seed weight, biological yield, harvest index, plot yield, seed yield per plant and protein%. This indicates the additive gene effects of the trait and the effect of the environment on heritability.

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