Journal of Advances in Biology & Biotechnology

Volume 27, Issue 10, Page 834-846, 2024; Article no.JABB.124439
ISSN: 2394-1081

Genetic Variability and Character Association in F_3 Generation of Chickpea (*Cicer arietinum* L.) under Rainfed and Irrigated Conditions

Banwari Lal Kumhar [a*], Varsha Kumari [a], Dinesh Kumar Gothwal [a], Ram Kunwar [a], Manoj Kumar Meena [a] and Ashok Singh Kharbas [a]

[a] Department of Genetics and Plant Breeding, SKN College of Agriculture, Sri Karan Narendra Agriculture University, Jobner-303329, Rajasthan, India.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: https://doi.org/10.9734/jabb/2024/v27i101506

Open Peer Review History:
This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: https://www.sdiarticle5.com/review-history/124439

Original Research Article

Received: 01/08/2024
Accepted: 02/10/2024
Published: 07/10/2024

ABSTRACT

The goal of the current study was to analyze the genetic variability and character association in F_3 generations of chickpea under rainfed and irrigated conditions to finalize appropriate selection criteria for improvement of seed yield in chickpea under irrigated and rainfed conditions. Five F_3 generations of chickpea crosses were evaluated in compact family block design with three replications at Research Farm, ARSS, Hanumangarh, Rajasthan, India. In analysis of variance, mean sum of squares indicated significant differences among the generations for all the characters

**Corresponding author: E-mail: kumharbl71@gmail.com, blkumhar.pbg@sknau.ac.in;*

Cite as: *Kumhar, Banwari Lal, Varsha Kumari, Dinesh Kumar Gothwal, Ram Kunwar, Manoj Kumar Meena, and Ashok Singh Kharbas. 2024. "Genetic Variability and Character Association in F3 Generation of Chickpea (Cicer Arietinum L.) under Rainfed and Irrigated Conditions". Journal of Advances in Biology & Biotechnology 27 (10):834-46. https://doi.org/10.9734/jabb/2024/v27i101506.*

under both conditions. The highest range of variation was observed for seed yield per plant followed by fruiting branches per plant, pods per plant, 100 seed weight and seeds per pod in irrigated condition, whereas in rainfed condition the highest range of variation was registered by seed yield per plant followed by biological yield per plant, 100 seed weight and pods per plant. The RSG-895 x RSG-888 showed high GCV and PCV for fruiting branches per plant, pods per plant, biological yield per plant, and seed yield per plant in both conditions, as well as for seeds per pod under irrigated condition. Under irrigated condition high value of GCV and PCV were noted in IPC-94-94 x RSG-888 for harvest and in CSJD-901 x RSG-931 for pods per plant, seeds per pod and seed yield per plant. Under rainfed high GCV and PCV were observed in cross RSG-888 x ICC-4958 for seeds per pod. This indicates the existence of wide variability for these traits in the progenies of particular crosses and scope of improvement through simple selection. High heritability coupled with high genetic advance as percentage of mean (GAM) was noted in RSG-888 x ICC-4958 for pod per plant under both conditions. Under irrigated condition, the cross CSJD-901 x RSG-931 for pods per plant, RSG-895 x RSG-888 for seed yield per plant, RSG-888 x ICC-4958 for harvest index, RSG-888 x ICC-4958 and CSJD-901 x RSG-931 for 100-seed weight showed high heritability along with high GAM. Whereas under rainfed, the crosses RSG-895 x RSG-888 and IPC-94-94 x RSG-888 for pods per plant, BG-362 x RSG-931 for seed yield per plant, and IPC-94-94 x RSG-888 for harvest index, demonstrated high heritability along with high GAM. This result indicates the importance of additive gene action in inheritance of these characters, hence simple selection can be used to improve seed yield. Seed yield per plant exhibited positive and significant correlation with fruiting branches per plant, pods per plant, biological yield per plant, harvest index and 100-seed weight under both irrigated and rainfed conditions. In irrigated condition seed yield per plant had significant and positive correlation with days to 50% flowering, days to maturity and plant height, whereas in rainfed condition it had significant and positive association with protein content. Further, *inter se* these characters were also significantly positively correlated. So, selection based on these characters is expected to bring improvement in the seed yield.

Keywords: Chickpea; genetic variability; rainfed condition; F_3 generation.

1. INTRODUCTION

Chickpea (*Cicer arietinum* L.) is one of the most important cultivated legumes, also known as Gram or Bengal gram, grown all over the world ranking third in production among the pulses after dry bean and dry pea. India is the largest producer of chickpea in the world with a 75.0% share in global production followed by Australia (5.9%), Pakistan (4.6%), Myanmar (3.8%), Turkey (3.8%), Ethiopia (3.3%) and Iran (2.3%). The global production of chickpea in 2022 was 18.09 million tons from an area of 14.81 million hectares with productivity of 1221 kg/ha. In India, chickpea cultivation was done on 10.74 million hectares with production of 13.54 million tons and productivity of 1261 kg/ha in the year 2022 [1].

Chickpea has special significance in the diet of the vegetarian population, as it contains more protein (23%), which is complementary with cereals in amino acids profile. Production and productivity of chickpea have been stagnant for the past three decades; one of the main reasons of this is its sensitivity to moisture stress at critical stages since more than 80% area under chickpea is rainfed. Significant variation among genotypes for yield and yield contributing characters under moisture stress condition in chickpea has been observed by Meena et al. [2], Krishnamurthy et al. [3] and Mishra and Babbar [4].

The success of any breeding programme would depend on the magnitude of variability and heritability in early generation populations for important economic traits [5]. Heritability estimates show how much of the phenotypic variability has a genetic origin and how much due to influence of environment [6]. Genetic advance is another parameter on which effectiveness of selection depends. For the selection to be effective and for making improvement in the crop, moderate or high heritability should be accompanied by sufficient amount of genetic advance [7]. Further, variability parameters were studied by many workers using fix or stable genetic material. Very few reports are available which include segregating material.

Therefore, the present study was conducted to estimate genetic variability, heritability, genetic advance and character association for yield and

yield components in F_3 generations of chickpea under irrigated and rainfed conditions. This will help us to finalize appropriate selection criteria for improvement of seed yield in chickpea under irrigated and rainfed conditions.

2. MATERIALS AND METHODS

2.1 Experimental Materials

Five F_3 generations of chickpea crosses namely, RSG-895 (Medium bold) x RSG-888 (Medium bold), RSG-888 (Medium bold) x ICC-4958 (Bold), IPC-94-94 (Bold) x RSG-888 (Medium bold), CSJD-901(Medium bold) x RSG-931(Medium bold) and BG-362 (Bold) x RSG-931(Medium bold) were evaluated in compact family block design with three replications under irrigated (two supplemental irrigations) and rainfed (on receding soil moisture) conditions at Research Farm, Agricultural Research Sub Station, Hanumangarh, Rajasthan, India. Seeds were sown in 3 meter long rows where parents were sown in two rows, F_1s in one row and F_3s in four rows. Row to row and plant to plant distance was kept 30 cm and 10 cm, respectively. Recommended agronomic practices were followed to raise a good crop. The observations on characters namely, plant height (cm), fruiting branches per plant, pods per plant, seeds per pod, biological yield per plant (g), seed yield per plant (g), harvest index (%), 100-seed weight (g) and protein content (%) were recorded on 10 randomly selected plants in the parents and F_1s, and on 20 randomly selected plants in the F_3 generations in each replication. The observations for days to 50% flowering and days to maturity were recorded on plot basis.

2.2 Statistical Analysis

The analysis of variance was done as per compact family block design for comparison of crosses as well as generations. Data recorded on individual plant basis were subjected to calculate the means, variances, standard error of mean and coefficient of variation by standard procedures given by Snedecor and Cochran [8]. Goulden [9] stated that the variation occurring in any segregating generation is phenotypic variance and the variation occurring in any uniform or non-segregating population is due to environment. Hence, phenotypic variance (Vp), genotypic variance (Vg) and environmental variance (Ve) computed as:

Phenotypic variance (Vp)= V_{F3}

Genotypic variance (Vg) = Vp – Ve

Environmental variance (Ve) = $(V_{P1}+V_{P2}+2V_{F1}) / 4$

Where, V_{P1} = Variance of individuals of the P_1 family

V_{P2} = Variance of individuals of the P_2 family

V_{F1} = Variance of individuals of the F_1 family

V_{F3} = Variance of individuals of the F_3 family

The genotypic and phenotypic coefficients of variation were estimated using the formula suggested by Burton [10].

Genotypic coefficient of variation (GCV) = $\frac{\sigma_g}{\bar{X}} \times 100 = \frac{\text{Genotypic standard deviation}}{\text{Grand mean}} \times 100$

Phenotypic coefficient of variation (PCV) = $\frac{\sigma_p}{\bar{X}} \times 100 = \frac{\text{Phenotypic standard deviation}}{\text{Grand mean}} \times 100$

The estimates of PCV and GCV can be divided into three classes as low (<10 %), medium (10-20%) and high (>20%) as suggested by Burton and Devane [11].

The heritability in broad sense was computed as the ratio of genotypic variance to phenotypic variance as suggested by Allard [12] and denoted by h^2

Heritability (h^2) = $\frac{\sigma_g^2}{\sigma_p^2} \times 100 = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$

According to Robinson [13] heritability values are categorized as low (<30%), moderate (30-60%) and high (>60%).

The expected genetic advance was estimated by using the following method suggested by Johnson et al. [7].

Genetic advance (GA) = $K.\sigma_p.h^2$

Where, K = Selection differential constant, the value equal to 2.06 at 5% selection intensity

σ_p = Phenotypic standard deviation

h^2 = Heritability in broad sense

Genetic advance (as percentage of mean) = $\frac{GA}{\bar{X}} \times 100$

Where, $\bar{X}$ = Mean value of F_3 generation in a cross for a respective character

The genetic advance as percentage of mean is categorized as low (<10 %), moderate (10-20%) and high (>20%) as suggested by Johnson et al. [7]. Character association was estimated as per the method suggested by Panse and Sukhatme [14].

3. RESULTS AND DISCUSSION

The analysis of variance (mean sum of squares) revealed the significant differences among the crosses for all the characters under both the conditions (Table 1), suggesting ample scope of exploiting such variability through selection. The estimates of mean, variance, genotypic coefficient variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense, genetic advance and genetic advance as percentage of mean of F_3 generations of five chickpea crosses under both irrigated and rainfed conditions are presented in Table 2.

Phenotypic variance was higher than the corresponding genotypic variance for all the studied characters under both the conditions (Fig. 1). This finding agrees with Shivakumar et al. [15], Raju et al. [16] and Rathod et al. [17]. Higher difference between genotypic variance and phenotypic variance was recorded for pods per plant, biological yield per plant, harvest index, plant height, fruiting branches per plant and seed yield per plant (Table 2), indicating more contribution of environment in the phenotypic appearance of these traits than their genetic makeup. Low difference was registered for the traits like seeds per pod, protein content, days to 50% flowering and days to maturity under both the conditions.

The magnitudes of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters in all the crosses under both the conditions (Table 2); this implies that there was the influence of environment on the expression of these characters under both the conditions. The highest range of variation was observed for seed yield per plant followed by fruiting branches per plant, pods per plant, 100 seed weight and seeds per pod in irrigated condition, whereas in rainfed condition the highest range of variation was registered by seed yield per plant followed by biological yield per plant, 100 seed weight and pods per plant. Selection should therefore be based on traits with a broad range of variation in the relevant environmental conditions. High GCV and PCV displayed by the cross RSG-895 x RSG-888 for fruiting branches per plant, pods per plant, biological yield per plant and seed yield per plant under both the conditions and for seeds per pod under irrigated condition. Similarly, high GCV and PCV for harvest index in IPC-94-94 x RSG-888, for pods per plant, seeds per pod and seed yield per plant in CSJD-901 x RSG-931 were noted in irrigated condition. Whereas under rainfed condition high GCV and PCV were observed in cross RSG-888 x ICC-4958 for seeds per pod. This indicates that there is wide variability for these traits in the progenies of these crosses and have scope of improvement through simple selection. Low values of GCV and PCV were recorded for days to 50% flowering, days to maturity and protein content in all the crosses under both the conditions and for plant height in rainfed condition in most of the crosses, indicating the presence of low variability for these traits.

These findings agree with the earlier reports of Vekariya et al. [18] in F_2 generation of chickpea, Meena et al. [19] in chickpea genotypes, Bala et al. [20] in chickpea genotypes, Akanksha et al. [21] in genotypes of chickpea, Talekar et al. [22] in F_2 generation of chickpea, Raval et al. [23] in F_2 generation of chickpea and Rathod et al. [17] F_2 generation of chickpea.

Heritability, which indicates the proportion of phenotypic variance due to genotypic variance and transmissible from parent to offspring, is actually a character selection index. High heritability in broad sense estimates were obtained for days to 50 % flowering in RSG-895 x RSG-888, pods per plant in RSG-888 x ICC-4958 and for harvest index in RSG-888 x ICC-4958 under both the conditions. Under irrigated condition high heritability was observed for days 50 % flowering in RSG-888 x ICC-4958, for pods per plant in CSJD-901 x RSG-931, seed yield per plant in RSG-895 x RSG-888, for harvest index in IPC-94-94 x RSG-888, for 100-seed weight in RSG-888 x ICC-4958 and CSJD-901 x RSG-931. High heritability for days to 50 % flowering in the crosses CSJD-901 x RSG-931 and BG-362 x RSG-931, for pods per plant in RSG-895 x RSG-888 and IPC-94-94 x RSG-888, for seed yield per plant in BG-362 x RSG-931 was observed under rainfed condition. This result indicates that these traits were highly heritable and hence were less affected by the environment. Such types of results were also reported by Sidramappa et al. [24] in inbred lines of chickpea, Joshi et al. [25] in recombinant inbred lines in chickpea, Babbar and Tiwari [26] in chickpea, Parmar and Monpara [27] in F_3 generation of chickpea.

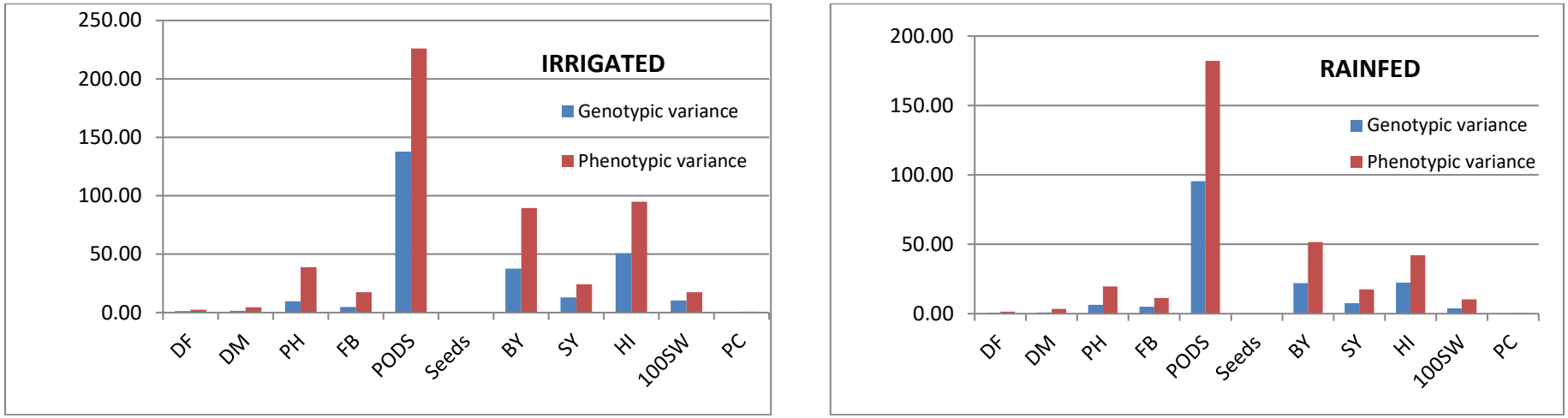

Fig. 1. Genotypic and phenotypic variance for different characters in chickpea under irrigated and rainfed conditions

Table 1. Analysis of variance (mean sum of squares) for different characters in F_3 generation of chickpea under irrigated (IRG) and rainfed (RF) conditions

Characters	IRG			RF		
	Rep. (2 df)	Crosses (4 df)	Error (8 df)	Rep. (2 df)	Crosses (4 df)	Error (8 df)
Days to 50% flowering	0.112	602.955**	0.278	0.553	174.414**	0.252
Days to maturity	0.314	89.403**	1.025	0.112	136.549**	0.077
Plant height (cm)	0.014	55.537**	0.548	0.143	19.718**	0.726
Fruiting branches per plant	0.421	2.048*	0.370	0.184	7.169**	0.096
Pods per plant	0.658	38.302**	2.396	0.364	79.690**	0.500
Seeds per pod	0.001	0.047**	0.000	0.000	0.019**	0.001
Biological yield per plant (g)	0.500	16.172**	0.529	0.461	28.708**	0.337
Seed yield per plant (g)	0.234	6.618**	0.284	0.180	19.331**	0.252
Harvest index (%)	0.316	9.239**	0.627	0.254	51.073**	0.294
100-seed weight (g)	0.314	33.069**	0.150	0.092	27.194**	0.237
Protein content (%)	0.014	0.608**	0.029	0.009	0.760**	0.011

**, ** Significant at 5% and 1% level, respectively*

Table 2. Mean, variances, coefficient of variations, heritability, genetic advance (GA) and genetic advance as percentage of mean (GAM) in F_3 generations of chickpea crosses under irrigated (IRG) and rainfed (RF) conditions

Cross/Character	Env.	Mean	Variance		Coefficient of variation (%)		Heritability (%)	Genetic advance (GA)	GAM (%)
			Genotypic	Phenotypic	Genotypic	Phenotypic			
Days to 50% flowering									
RSG-895 x RSG-888	IRG	89.90	4.15	6.48	2.27	2.83	64.00	3.36	3.74
	RF	84.33	0.61	0.77	0.92	1.04	79.00	1.43	1.70
RSG-888 x ICC-4958	IRG	92.33	1.31	2.12	1.24	1.58	62.00	1.86	2.01
	RF	89.33	0.32	1.45	0.63	1.35	22.00	0.55	0.62
IPC-94-94 x RSG-888	IRG	88.33	0.13	1.44	0.42	1.36	9.00	0.22	0.25
	RF	67.00	1.69	3.25	1.94	2.69	52.00	1.93	2.88
CSJD-901 x RSG-931	IRG	90.67	0.27	0.77	0.57	0.97	35.00	0.63	0.69
	RF	84.00	0.53	0.77	0.87	1.04	69.00	1.25	1.49
BG-362 x RSG-931	IRG	93.67	0.66	1.44	0.87	1.28	46.00	1.14	1.22
	RF	92.67	0.64	0.77	0.86	0.94	83.00	1.50	1.62
Days to maturity									
RSG-895 x RSG-888	IRG	135.67	0.30	3.08	0.40	1.29	10.00	0.36	0.27
	RF	128.00	1.00	3.44	0.78	1.45	29.00	1.11	0.87
RSG-888 x ICC-4958	IRG	136.33	0.17	3.18	0.30	1.31	5.00	0.18	0.13
	RF	132.00	0.65	3.09	0.61	1.33	21.00	0.76	0.58
IPC-94-94 x RSG-888	IRG	127.67	3.97	8.50	1.56	2.28	47.00	2.82	2.21
	RF	112.00	1.18	4.88	0.97	1.97	24.00	1.09	0.97
CSJD-901 x RSG-931	IRG	133.00	0.50	3.17	0.53	1.34	16.00	0.59	0.44
	RF	127.33	0.17	3.07	0.33	1.38	6.00	0.22	0.17
BG-362 x RSG-931	IRG	135.67	1.89	4.88	1.01	1.63	39.00	1.78	1.31
	RF	133.33	1.00	3.07	0.75	1.31	33.00	1.19	0.89
Plant height (cm)									
RSG-895 x RSG-888	IRG	54.80	26.39	57.28	9.37	13.81	46.00	7.17	13.08
	RF	48.92	5.16	18.11	4.64	8.70	29.00	2.54	5.19
RSG-888 x ICC-4958	IRG	61.17	1.77	43.28	2.17	10.75	4.00	0.54	0.88
	RF	55.15	4.61	20.60	3.89	8.23	22.00	2.06	3.74
IPC-94-94 x RSG-888	IRG	51.90	1.44	29.53	2.31	10.47	5.00	0.56	1.08
	RF	43.60	3.83	13.92	4.49	8.56	28.00	2.15	4.93
CSJD-901 x RSG-931	IRG	51.23	11.45	29.67	6.61	10.63	39.00	4.38	8.55
	RF	52.17	6.53	17.51	4.90	8.02	37.00	3.19	6.11
BG-362 x RSG-931	IRG	62.93	7.91	34.06	4.47	9.27	23.00	2.77	4.40
	RF	51.20	12.10	27.72	6.79	10.28	44.00	4.77	9.32

Cross/Character	Env.	Mean	Variance		Coefficient of variation (%)		Heritability (%)	Genetic advance (GA)	GAM (%)
			Genotypic	Phenotypic	Genotypic	Phenotypic			
Fruiting branches per plant									
RSG-895 x RSG-888	IRG	14.77	9.14	19.61	20.46	29.98	47.00	4.29	29.05
	RF	12.98	7.14	13.00	20.58	27.77	55.00	4.09	31.50
RSG-888 x ICC-4958	IRG	18.58	7.75	20.79	14.98	24.54	37.00	3.48	18.73
	RF	16.02	3.01	8.42	10.84	18.12	36.00	2.15	13.42
IPC-94-94 x RSG-888	IRG	12.37	2.20	12.74	12.00	28.86	17.00	1.25	10.11
	RF	15.65	5.80	11.96	15.39	22.10	48.00	3.42	21.85
CSJD-901 x RSG-931	IRG	13.20	3.08	18.97	13.29	32.99	16.00	1.44	10.91
	RF	12.80	1.97	9.89	10.97	24.57	20.00	1.30	10.16
BG-362 x RSG-931	IRG	19.33	2.11	15.28	7.51	20.22	14.00	1.13	5.85
	RF	17.32	7.39	13.19	15.69	20.97	56.00	4.19	24.19
Pods per plant									
RSG-895 x RSG-888	IRG	44.70	237.52	396.65	34.48	44.56	60.00	24.62	55.08
	RF	45.05	170.58	224.66	28.99	33.27	76.00	23.47	52.10
RSG-888 x ICC-4958	IRG	69.68	148.27	211.98	17.48	20.89	70.00	20.99	30.12
	RF	62.65	140.30	222.37	18.91	23.80	63.00	19.35	30.89
IPC-94-94 x RSG-888	IRG	65.53	62.63	126.86	12.08	17.19	49.00	11.37	17.35
	RF	55.20	81.60	134.81	16.36	21.03	61.00	14.59	26.43
CSJD-901 x RSG-931	IRG	51.23	136.91	217.18	22.84	28.77	63.00	19.13	37.34
	RF	46.77	56.22	147.67	16.03	25.98	38.00	9.51	20.33
BG-362 x RSG-931	IRG	67.65	103.79	176.64	15.06	19.65	59.00	16.15	23.87
	RF	60.02	29.05	181.03	8.98	22.42	16.00	4.43	7.38
Seeds per pod									
RSG-895 x RSG-888	IRG	1.45	0.09	0.29	20.44	37.00	31.00	0.34	23.45
	RF	1.55	0.06	0.19	15.25	27.81	30.00	0.27	17.42
RSG-888 x ICC-4958	IRG	1.28	0.05	0.25	18.15	39.37	21.00	0.22	17.19
	RF	1.36	0.08	0.17	20.26	29.95	46.00	0.39	28.68
IPC-94-94 x RSG-888	IRG	1.88	0.13	0.37	19.50	32.55	36.00	0.45	23.94
	RF	1.78	0.11	0.24	18.95	27.74	47.00	0.48	26.97
CSJD-901 x RSG-931	IRG	1.59	0.14	0.30	23.93	34.72	48.00	0.55	34.59
	RF	1.54	0.05	0.19	14.98	28.54	28.00	0.25	16.23
BG-362 x RSG-931	IRG	1.55	0.04	0.13	13.58	23.62	33.00	0.25	16.11
	RF	1.49	0.06	0.22	16.49	31.50	27.00	0.26	17.45
Biological yield per plant (g)									
RSG-895 x RSG-888	IRG	34.52	52.16	100.81	20.92	29.09	52.00	10.76	31.17
	RF	30.41	44.79	90.11	22.01	31.22	50.00	9.78	32.16

Cross/Character	Env.	Mean	Variance		Coefficient of variation (%)		Heritability (%)	Genetic advance (GA)	GAM (%)
			Genotypic	Phenotypic	Genotypic	Phenotypic			
RSG-888 x ICC-4958	IRG	40.72	58.18	134.30	18.73	28.46	43.00	10.27	25.22
	RF	42.52	18.70	59.91	10.17	18.20	31.00	4.94	11.62
IPC-94-94 x RSG-888	IRG	36.46	19.54	61.35	12.12	21.48	32.00	5.16	14.15
	RF	37.94	9.42	30.29	8.09	14.51	31.00	3.51	9.25
CSJD-901 x RSG-931	IRG	41.35	16.09	56.34	9.70	18.15	29.00	4.48	10.83
	RF	28.43	14.43	34.40	13.36	20.63	42.00	5.07	17.83
BG-362 x RSG-931	IRG	47.61	41.69	94.16	13.56	20.38	44.00	8.80	18.48
	RF	42.91	22.44	43.03	11.04	15.29	52.00	7.03	16.38
Seed yield per plant (g)									
RSG-895 x RSG-888	IRG	20.43	20.93	30.68	22.39	27.11	68.00	7.76	37.98
	RF	10.98	11.00	19.93	30.20	40.65	55.00	5.06	46.08
RSG-888 x ICC-4958	IRG	22.43	13.46	26.79	16.36	23.08	50.00	5.33	23.76
	RF	21.49	7.31	23.01	12.58	22.32	32.00	3.16	14.70
IPC-94-94 x RSG-888	IRG	15.98	6.61	17.72	16.09	26.34	37.00	3.21	20.09
	RF	18.91	2.88	12.61	8.98	18.78	23.00	1.68	8.88
CSJD-901 x RSG-931	IRG	13.95	10.25	21.44	22.95	33.19	48.00	4.58	32.83
	RF	11.26	2.25	10.98	13.33	29.43	21.00	1.43	12.70
BG-362 x RSG-931	IRG	21.91	14.11	25.06	17.15	22.85	56.00	5.78	26.38
	RF	20.50	14.65	20.61	18.67	22.15	71.00	6.64	32.39
Harvest index (%)									
RSG-895 x RSG-888	IRG	51.70	60.60	110.76	15.06	20.36	55.00	11.92	23.06
	RF	37.33	34.19	59.70	15.66	20.70	57.00	9.07	24.30
RSG-888 x ICC-4958	IRG	52.50	66.55	107.37	15.54	19.74	62.00	13.23	25.20
	RF	53.04	32.78	52.69	10.79	13.69	62.00	9.27	17.48
IPC-94-94 x RSG-888	IRG	41.15	74.28	103.98	20.94	24.78	71.00	14.91	36.23
	RF	52.62	25.24	51.18	9.55	13.60	49.00	7.22	13.72
CSJD-901 x RSG-931	IRG	40.61	24.29	69.48	12.14	20.53	35.00	6.01	14.80
	RF	42.60	4.27	20.85	4.85	10.72	20.00	1.88	4.41
BG-362 x RSG-931	IRG	48.04	28.32	82.33	11.08	18.89	34.00	6.36	13.24
	RF	51.37	15.14	26.20	7.58	9.97	58.00	6.12	11.91
100-seed weight (g)									
RSG-895 x RSG-888	IRG	18.20	8.50	15.56	16.02	21.68	55.00	4.47	24.56
	RF	17.80	6.21	11.54	13.99	19.08	54.00	3.78	21.24
RSG-888 x ICC-4958	IRG	26.48	17.14	25.26	15.63	18.98	68.00	7.04	26.59
	RF	24.86	2.21	7.79	5.98	11.23	28.00	1.61	6.48
IPC-94-94 x RSG-888	IRG	23.41	11.00	19.71	14.17	18.96	56.00	5.12	21.87

Cross/Character	Env.	Mean	Variance		Coefficient of variation (%)		Heritability (%)	Genetic advance (GA)	GAM (%)
			Genotypic	Phenotypic	Genotypic	Phenotypic			
	RF	21.63	0.06	7.23	1.11	12.43	1.00	0.06	0.28
CSJD-901 x RSG-931	IRG	17.80	11.04	14.49	18.67	21.39	76.00	5.96	33.48
	RF	17.43	6.17	14.93	14.25	22.17	41.00	3.26	18.70
BG-362 x RSG-931	IRG	24.47	3.77	12.72	7.93	14.58	30.00	2.20	8.99
	RF	22.86	4.19	9.79	8.96	13.69	43.00	2.77	12.12
Protein content (%)									
RSG-895 x RSG-888	IRG	16.99	0.56	1.13	4.40	6.26	50.00	1.09	6.42
	RF	17.60	0.15	0.56	2.19	4.25	27.00	0.42	2.39
RSG-888 x ICC-4958	IRG	18.43	0.16	0.55	2.18	4.03	29.00	0.44	2.39
	RF	18.70	0.18	0.56	2.27	4.00	32.00	0.49	2.62
IPC-94-94 x RSG-888	IRG	17.50	0.17	0.60	2.35	4.43	28.00	0.45	2.57
	RF	18.51	0.23	0.57	2.62	4.10	41.00	0.64	3.46
CSJD-901 x RSG-931	IRG	18.63	0.20	0.55	2.38	3.97	36.00	0.55	2.95
	RF	18.80	0.19	0.55	2.34	3.96	35.00	0.54	2.87
BG-362 x RSG-931	IRG	18.19	0.34	0.92	3.20	5.27	37.00	0.73	4.01
	RF	18.93	0.28	0.55	2.78	3.91	51.00	0.78	4.12

Table 3. Phenotypic correlation among different characters in F_3 generation of chickpea under irrigated (IRG) and rainfed (RF) conditions

Characters	Env.	Days to 50% flowering	Days to maturity	Plant height (cm)	Fruiting branches per plant	Pods per plant	Seeds per pod	Biological yield per plant (g)	Seed yield per plant (g)	Harvest index (%)	100-seed weight (g)	Protein content (%)
Days to 50%	IRG	1.000	0.765**	0.732**	0.616**	0.253*	-0.372**	0.407**	0.402**	0.359**	0.348**	0.581**
flowering	RF	1.000	0.996**	0.740**	0.101	0.125	-0.416**	0.171	0.075	-0.078	0.145	0.207*
Days to maturity	IRG		1.000	0.570**	0.511**	-0.065	-0.543**	0.180	0.451**	0.596**	0.051	0.211*
	RF		1.000	0.757**	0.058	0.096	-0.423**	0.128	0.030	-0.121	0.120	0.154
Plant height (cm)	IRG			1.000	0.556**	0.274**	-0.282**	0.224*	0.441**	0.460**	0.512**	0.221*
	RF			1.000	0.081	0.239*	-0.400**	0.152	0.127	0.031	0.160	0.291**
Fruiting branches	IRG				1.000	0.597**	-0.319**	0.721**	0.764**	0.393**	0.360**	0.227*
per plant	RF				1.000	0.825**	-0.135	0.833**	0.800**	0.488**	0.403**	0.325**
Pods per plant	IRG					1.000	0.038	0.655**	0.598**	0.107	0.487**	0.257*
	RF					1.000	-0.166	0.856**	0.836**	0.453**	0.362**	0.319**
Seeds per pod	IRG						1.000	-0.093	-0.294**	-0.380**	-0.141	-0.153
	RF						1.000	-0.167	-0.129	-0.004	-0.124	-0.091
Biological yield	IRG							1.000	0.676**	0.017	0.195	0.340**

Characters	Env.	Days to 50% flowering	Days to maturity	Plant height (cm)	Fruiting branches per plant	Pods per plant	Seeds per pod	Biological yield per plant (g)	Seed yield per plant (g)	Harvest index (%)	100-seed weight (g)	Protein content (%)
per plant(g)	RF							1.000	0.950**	0.501**	0.502**	0.368**
Seed yield per	IRG								1.000	0.584**	0.358**	-0.066
plant (g)	RF								1.000	0.708**	0.566**	0.457**
Harvest index (%)	IRG									1.000	0.297**	-0.160
	RF									1.000	0.534**	0.551**
100-seed weight	IRG										1.000	0.214*
(g)	RF										1.000	0.371**
Protein content	IRG											1.000
(%)	RF											1.000

**, ** Significant at 5 per cent and 1 per cent level, respectively*

Johnson et al. [7] and Lerner [28] suggested that heritability estimates when used in combination with genetic advance would provide better information than the heritability alone in predicting the resultant best individuals. In the present study, high heritability coupled with high genetic advance as percentage of mean (GAM) for pod per plant was observed in RSG-888 x ICC-4958 under both the conditions. It was displayed in CSJD-901 x RSG-931 for pods per plant, in RSG-895 x RSG-888 for seed yield per plant, in RSG-888 x ICC-4958 for harvest index, in RSG-888 x ICC-4958 and CSJD-901 x RSG-931 for 100-seed weight in irrigated condition. Whereas, under rainfed condition high heritability coupled with high genetic advance as percentage of mean observed for pods per plant in the crosses RSG-895 x RSG-888 and IPC-94-94 x RSG-888, for seed yield per plant in BG-362 x RSG-931 and for harvest index in IPC-94-94 x RSG-888. These results indicated the importance of additive gene action in the inheritance of these characters and these traits may be subjected to any selection scheme to develop stable genotypes in particular crosses. Similar results were also reported by Joshi et al. [25], Moucheshi et al. [29], Gautam et al. [30] and Singh et al. [31].

Low heritability coupled with low genetic advance observed for days to maturity, plant height and protein content in RSG-895 x RSG-888, RSG-888 x ICC-4958 and IPC-94-94 x RSG-888 under both conditions under both conditions, indicates that these characters were highly influenced by the environmental effects and selection for such traits would be ineffective in these crosses. In these traits; improvement can be made opting the two to three cycles of recurrent selection followed by either pedigree or single seed descent method of breeding.

The phenotypic correlation coefficients were also estimated under both irrigated and rainfed conditions and are presented in Table 3. A positive correlation between the desired traits is required by breeder for effective selection. In the present investigation, seed yield per plant exhibited positive and significant correlation with fruiting branches per plant, pods per plant, biological yield per plant, harvest index and 100-seed weight under both irrigated and rainfed condition. Seed yield per plant had significant and positive correlation with days to 50% flowering, days to maturity and plant height in irrigated condition, whereas under rainfed condition it had significant and positive association with protein content. Seed yield per plant exhibited negative correlation with seeds per pod under both the conditions. Further, *inter se* these characters were also significantly positively correlated. So selection based on these characters is expected to bring improvement in the seed yield. These results confirm the findings of earlier workers Moucheshi et al. [29], Shivakumar et al. [32], Rathod et al. [17], Telekar et al. [22], Manasa et al. [33] and Madhuri et al. [34].

4. CONCLUSION

The existence of variability among F_3 generations of five chickpea crosses indicates that the selection will be effective in enhancing the seed yield by progeny selection. The highest range of variation was observed for seed yield per plant followed by fruiting branches per plant, pods per plant, 100 seed weight and seeds per pod in irrigated condition, whereas in rainfed condition the highest range of variation was registered by seed yield per plant followed biological yield per plant, 100 seed weight and pods per plant. Hence, selection should be done for these characters under the respective environmental condition. High GCV and PCV for fruiting branches per plant, pods per plant, biological yield per plant and seed yield per plant under both the conditions and for seeds per pod under irrigated condition were displayed by the RSG-895 x RSG-888. Similarly, high GCV and PCV for harvest index in IPC-94-94 x RSG-888, for pods per plant, seeds per pod and seed yield per plant in CSJD-901 x RSG-931 were noted in irrigated condition. Whereas under rainfed condition high GCV and PCV were observed in cross RSG-888 x ICC-4958 for seeds per pod. This indicates that there is wide variability for these traits in the progenies of these crosses and have scope of improvement through simple selection. High heritability coupled with high genetic advance as percentage of mean for pod per plant was observed in RSG-888 x ICC-4958 under both the conditions. For pods per plant in CSJD-901 x RSG-931, for seed yield per plant in RSG-895 x RSG-888, for harvest index in RSG-888 x ICC-4958 and for 100-seed weight in RSG-888 x ICC-4958 and CSJD-901 x RSG-931 under irrigated condition. Under rainfed condition it was shown by the cross RSG-895 x RSG-888 and IPC-94-94 x RSG-888 for pods per plant, by BG-362 x RSG-931 for seed yield per plant, by IPC-94-94 x RSG-888 for harvest index. These results indicated the importance of additive gene action in inheritance of these characters, hence

simple selection can be used to improve seed yield. As per association analysis selection based on fruiting branches per plant, pods per plant, biological yield per plant, harvest index and 100 seed weight under both the conditions, on plant height in irrigated and on protein content in rainfed condition may bring improvement in seed yield of chickpea.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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Peer-review history:
The peer review history for this paper can be accessed here:
https://www.sdiarticle5.com/review-history/124439