Genetic Variability, Heritability and Genetic Advance for Yield and its Contributing Traits in Chickpea (*Cicer arietinum* L.) under Irrigated and Drought Stress Conditions

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ABSTRACT: Genetic variability was studied in BC$_2$F$_4$ backcross derived lines in chickpea during *Rabi* 2021-2022 under irrigated and non-irrigated environments. The study revealed highly significant differences for all the yield and its contributing traits, indicating the presence of high genetic variability. The phenotypic coefficient of variation was found high in drought stress trial for seed yield per plant and yield per plot. Biomass per plant, number of pods per plant and proline recorded moderate genotypic and phenotypic coefficients of variation under both stressed and non-stressed condition. This indicates substantial scope for improvement in these characters after hybridization and subsequent selection. High heritability coupled with high genetic advance was found for the traits *viz.*, biomass per plant, number of pods per plant, seed yield per plant in both environments, and also for yield per plot and proline in drought stress trial indicating that the traits are governed by additive gene action and reliability of these characters for selection.

Keywords: Genetic variability, PCV, GCV, Heritability, Genetic advance.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) crop is self-pollinated and diploid (2n =2x = 16) species. It belongs to genus *Cicer,* tribe Cicereae, family Fabaceae, and subfamily Papilionaceae. Chickpea is grown on 14.84 million hectares, with global production and productivity of 15.08 million tonnes and 1016 kg/ha, respectively (FAOSTAT, 2020). The top chickpea-growing countries are India, Pakistan, Turkey, Iran, Mexico, Myanmar, Ethiopia, Australia, and Canada (FAOSTAT, 2020). It is grown on 98.86 lakh hectares in India, with a yield of 107.37 lakh tonnes and a productivity of roughly 1086 kg/ha (Annual report, DPD, Ministry of Agri. & FW, Govt. of India, 2021-22).

Chickpea is generally considered to be the most drought tolerant cool-season food legume crop because it has a long taproot that can extract water from the lower depths of the soil profile. Chickpea requires only 6-10 inches of rainfall and/or irrigation water during the growing season and thus is well suited to dryland or limited-irrigation production. However, exposure of chickpea plants to terminal drought is one of the major constraints to increasing productivity. Therefore, development of early maturing cultivars with early growth vigor may help chickpea varieties utilize the available soil moisture more efficiently and produce higher yields. In the last decade, the main breeding strategy used to cope with terminal drought in chickpea was selecting for drought escape by reducing crop duration and securing seed yield before soil water was depleted. This strategy was successful in increasing yield stability and resulted in the release of early maturing varieties (Kashiwagi *et al.*, 2007; Sabaghpour *et al.*, 2006).

The development of high yielding chickpea cultivars is the main objective of any breeding programs in the world. The prerequisite to achieve this goal is to find sufficient amount of variability. Identification of superior genotypes with desirable traits and their subsequent use in breeding program and establishment of suitable selection criterion can further help for successful varietal development programme. Knowledge of the relative magnitude of various genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance for seed yield and yield components is essential for an efficient breeding programme. Genetic variation among traits is important for breeding and selecting desirable types. The estimates of heritability are more advantageous when expressed in terms of genetic advance. Johnson *et al.* (1955) suggested that without genetic advance the estimate of heritability will not be of practical value and emphasized the concurrent use of genetic advance along with heritability. Hanson (1963) stated that heritability and genetic advance are two complementary concepts. Thus, the present study was designed to evaluate genetic variability and heritability parameters

of yield and its component traits in the BC_2F_4 lines of the cross Digvijay × ICC4958.

MATERIAL AND METHODS

The present investigation was conducted during *Rabi* 2021-22 at Post Graduate Institute research farm, Mahatma Phule Krishi Vidyapeeth, Rahuri. The material of present experiment comprised of 31 lines of BC_2F_4 population of the cross Digvijay × ICC4958. Digvijay is a popular variety of chickpea, while ICC 4958 is having profuse root system and drought tolerant genotype. The advanced backcross segregating lines were evaluated in randomized block design (RBD) in three replications. In each replication row to row and plant to plant spacing was 30 cm and 10 cm, respectively. Observations were recorded on randomly selected five plants. Observations were recorded on days to first flowering, 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, biomass per plant (g), 100 seed weight, seed yield per plant (g), yield per plot (g), chlorophyll content index, proline (µmole g^{-1} fresh weight) and protein (%). The mean values of randomly selected observational plants for different characters were used for statistical analysis. Genetic parameters and the statistical methods adopted were as follows.

Statistical analysis. The analysis of variance for RBD was carried out separately for each character as per Panse and Sukhatme (1995).

Estimation of genetic parameters

(a) Genotypic variance ($\sigma^2 g$). Genotypic ($\sigma^2 g$), phenotypic variances ($\sigma^2 p$) and coefficients of variation from ANOVA Table were estimated as per Burton (1952) as follows:

Genotypic variance ($\sigma^2 g$) = [$\sigma^2 t - \sigma^2 e$]/r

Where,

$\sigma^2 t$ = mean square of treatment

$\sigma^2 e$ = error mean square

r = number of replications

(b) Environmental Variance ($\sigma^2 e$)

$\sigma^2 e$ = Error mean square

(c) Phenotypic variance ($\sigma^2 p$)

$\sigma^2 p = \sigma^2 g + \sigma^2 e$

Where,

$\sigma^2 p$ = phenotypic variance

$\sigma^2 g$ = genotypic variance

$\sigma^2 e$ = error mean square

(d) Phenotypic coefficients of variation (PCV)

$$PCV = \frac{\sqrt{\sigma^2 p}}{X} \times 100$$

Where, $\sigma^2 p$ = phenotypic variance

X = mean of the character

(e) Genotypic coefficient of variation (GCV)

$$GCV = \frac{\sqrt{\sigma^2 g}}{X} \times 100$$

Where,

$\sigma^2 g$ = genotypic variance

X = mean of the character

The estimates of GCV and PCV were classified as low, moderate and high according to Sivasubramanian and Madhavamenon (1973).

< 10 percent = low

10-20 percent = moderate

> 20 percent = high

(f) Heritability (h^2): Heritability in broad sense for all characters was computed using the formula given by Falconer (1989).

Heritability (h^2) = $\sigma^2 g / \sigma^2 p$ × 100

Where,

h^2 = heritability in broad sense

$\sigma^2 p$ = phenotypic variance

$\sigma^2 g$ = genotypic variance

The range of heritability was categorized as low, moderate and high according to Johnson *et al.* (1955).

Low = Less than 30%

Moderate = 30-60 %

High = More than 60%

(g) Genetic advance (GA):

Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. Expected genetic advance for each character at 5% selection intensity was computed using the methodology described by Johnson *et al.* (1955).

GA= K.$\sqrt{\sigma^2 p} . h^2$

Where,

GA = expected genetic advance

K = constant (selection differential) 2.056 at 5% selection intensity

$\sqrt{\sigma^2 p}$ = square root of phenotypic variance

h^2 = heritability in broad sense

Genetic advance as percent of mean was calculated to compare the extent of predicted advance of different traits under selection, using the following formula.

The range of genetic advance (G.A.) was categorized as suggested by Johnson *et al.* (1955).

Low = < 10

Moderate = 10-20

High = > 20

RESULT AND DISCUSSION

The analysis of variances of 31 backcross derived lines along with their parents (Digvijay and ICC4958) and checks for all the characters studied showed significant differences in the material as presented in Table 1. Phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for almost all the traits in both irrigated and drought stress condition which indicates role of environment for these characters (Table 2 and 3).

In irrigated condition, GCV ranged from 0.92 per cent (days to maturity) to 15.39 per cent (seed yield per plant) for different characters under study. High GCV was not found for any character. The moderate values of GCV were recorded for seed yield per plant (15.39%) followed by biomass per plant (14.92%), number of pods per plant (14.1%) and proline (11.26%). The lowest values were observed for days to maturity (0.92%) preceded by protein (1.63%), days to 50% flowering (2.55%), days to first flowering

(3.17%), plant height (3.27%), chlorophyll content index (3.67%), number of primary branches per plant (6.05%), number of secondary branches per plant (7.48%), yield per plot (9.05%) and 100 seed weight (9.60%).

In drought stress condition, GCV ranged from 0.83 per cent (days to maturity) to 18.04 per cent (seed yield per plant). The moderate values of GCV was observed for seed yield per plant (18.04%) followed by yield per plot

(17.02%), biomass per plant (15.85%), proline (15.61%) and number of pods per plant (14.59%). The lowest values of GCV were recorded for number of secondary branches per plant (9.74%), 100 seed weight (9.22%), number of primary branches per plant (5.72%), chlorophyll content index (3.93%), plant height (3.27%), days to 50% flowering (2.81%), days to first flowering (2.56%), protein (2.17%) and days to maturity (0.83) with least GCV.

Table 1: Analysis of variance for BC₂F₄ lines of non-irrigated and irrigated trials for grain yield and its component traits in chickpea.

Sr. No.	Name of characters	Irrigated		Non-Irrigated	
		Mean sum of squares		Mean sum of squares	
		Treatments	Error	Treatments	Error
	Df	34	34	34	34
1.	Days to 1st flowering	6.45**	2.51	3.86**	1.56
2.	Days to 50% flowering	6.72*	3.11	6.88*	3.12
3.	Days to maturity	3.85**	1.64	2.75**	0.85
4.	Plant height (cm)	16.93**	6.10	15.64**	8.46
5.	No. of primary branches per plant	0.11**	0.04	0.09**	0.04
6.	No. of secondary branches per plant	3.91*	1.83	6.22*	3.19
7.	Biomass per plant (g)	238.23**	89.94	99.32**	27.11
8.	No. of pods per plant	681.70**	247.69	440.52**	162.94
9.	100 seed weight (g)	10.80**	1.35	9.19**	0.35
10.	Seed yield per plant (g)	42.87**	12.39	38.80**	9.48
11.	Yield per plot (g)	12625.68**	5237.95	14600.04**	4158.78
12.	Chlorophyll content index	9.42**	4.16	6.50**	2.30
13.	Proline (μmole g⁻¹ fresh weight)	1.09*	0.61	15.15**	4.48
14.	Protein (%)	0.28*	0.12	0.43**	0.16

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

For irrigated condition, PCV ranged from 1.21 per cent (days to maturity) to 18.91 per cent (biomass per plant) for various characters under study. Moderate PCV were noted for biomass per plant (18.91%) followed by seed yield per plant (18.25%), number of pods per plant (17.68%), proline (16.92%), yield per plot (11.84%), 100 seed weight (10.27%) and number of secondary

branches per plant (10.25%). The lowest values were recorded for days to maturity (1.21%) preceded by protein (2.20%), days to 50% flowering (3.49%), days to first flowering (4.06%), plant height (4.09%), chlorophyll content index (4.87%) and number of primary branches per plant (7.99%).

Table 2: Genetic parameters under normal irrigated condition.

Sr. No.	Characters	GCV (%)	PCV (%)	Heritability (%)	Genetic advance (%)
1.	Days to 1st flowering	3.17	4.06	61.1	5.11
2.	Days to 50% flowering	2.55	3.49	53.8	3.86
3.	Days to maturity	0.92	1.21	57.2	1.43
4.	Plant height (cm)	3.27	4.09	64.0	5.40
5.	No. of primary branches per plant	6.05	7.99	57.4	9.45
6.	No. of secondary branches per plant	7.48	10.25	53.2	11.23
7.	Biomass per plant (g)	14.92	18.91	62.2	24.25
8.	No. of pods per plant	14.10	17.68	63.7	23.19
9.	100 seed weight (g)	9.60	10.27	87.4	18.50
10.	Seed yield per plant (g)	15.39	18.25	71.1	26.73
11.	Yield per plot (g)	9.05	11.84	58.5	14.27
12.	Chlorophyll content index	3.64	4.87	55.8	5.60
13.	Proline (μmole g⁻¹ fresh weight)	11.26	16.92	44.3	15.45
14.	Protein (%)	1.63	2.20	54.9	2.49

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

The PCV in drought stress condition ranged from 1.04 per cent (days to maturity) to 20.75 per cent (seed yield per plant) for different characters under study. The highest PCV were recorded for seed yield per plant

(20.75%) and yield per plot (20.13%). Whereas, the moderate PCV was observed for proline (18.60%) followed by biomass per plant (18.59%), number of pods per plant (18.39%) and number of secondary

branches per plant (13.97%). The lowest values of PCV were recorded for 100 seed weight (9.40%), number of primary branches per plant (7.60%), plant height (5.26%), chlorophyll content index (4.89%), days to 50% flowering (3.81%), days to first flowering (3.32%), protein (2.74%) and days to maturity (1.04%). The narrow differences between PCV and GCV were recorded in both the environments. The present findings suggested less influence of external environmental factors on the traits under study. Parameshwarappa *et al.* (2012) reported narrow differences for PCV (%) and GCV (%) for the traits days to 50% flowering and plant height indicating absence of environmental factor. High PCV was recorded in drought stress trial for seed yield per plant and yield per plot. Biomass per plant, number of pods per plant and proline recorded moderate GCV and PCV. While, number of secondary branches per plant in both condition; 100 seed weight, seed yield per plant and yield per plot in normal trial were found to have moderate PCV. Also, seed yield per plant in both environment and yield per plot in drought stress trial recorded moderate GCV. This indicates that there is preponderance of additive gene action and selection based on these traits may be rewarding.

Johnson *et al.* (2018) estimated the high values of GCV and PCV for secondary branches per plant, pods per plant, hydration index, seed yield per plant, biological yield, primary branches per plant, swelling index. Moderate values were recorded for seed volume and 100 seed weight and lowest values were noted for days to 50% flowering, protein content, days to maturity. Kumar *et al.* (2019) reported that traits number of primary branches per plant, 100 seed weight, grain yield per plant and biomass yield per plant showed high estimates of PCV and GCV.

Traits *viz.,* days to first flowering, days to 50% flowering, days to maturity, plant height, number of primary branches per plant, chlorophyll content index and protein (%) in both environments and 100 seed weight in drought stress condition recorded low GCV and PCV. Whereas, low GCV was observed for number of secondary branches per plant in both environment and for 100 seed weight and yield per plot in irrigated condition. It shows that selection for such traits may not be effective for crop improvement. Mohan and Thiyagarajan (2019) found that 100 seed weight had high GCV and PCV. While, low estimates was recorded for number of days to 50 percent flowering and days to harvest maturity. Tsehaye *et al.* (2020) investigated that in chickpea phenotypic and genotypic variance were lowest for number of seeds per pod and number of primary branches.

The proportion of genetic variability which is transmitted from parents to offspring is reflected by heritability (Lush, 1940). Heritability estimates indicate effectiveness of selection for phenotypic performance but it is alone not enough to make sufficient improvement through selection. The high heritability estimates coupled with high genetic advance is more useful for the selection (Johnson *et al.*, 1995).

Table 3: Genetic parameters under drought stress condition.

Sr. No.	Characters	GCV (%)	PCV (%)	Heritability (%)	Genetic advance (%)
1.	Days to 1st flowering	2.56	3.32	59.5	4.07
2.	Days to 50% flowering	2.81	3.81	54.6	4.28
3.	Days to maturity	0.83	1.04	63.7	1.37
4.	Plant height (cm)	3.56	5.26	45.9	4.97
5.	Primary branches per plant	5.72	7.60	56.6	8.86
6.	Secondary branches per plant	9.74	13.97	48.6	13.98
7.	Biomass per plant (g)	15.85	18.59	72.7	27.84
8.	No. of pods per plant	14.59	18.39	63.0	23.87
9.	100 seed weight (g)	9.22	9.40	96.1	18.62
10.	Seed yield per plant (g)	18.04	20.75	75.6	32.31
11.	Yield per plot (g)	17.02	20.13	71.5	29.66
12.	Chlorophyll content index	3.93	4.89	64.6	6.51
13.	Proline (µmole g^{-1} fresh weight)	15.61	18.60	70.4	26.98
14.	Protein (%)	2.17	2.74	62.8	3.54

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

High heritability with high genetic advance was exhibited by biomass per plant, number of pods per plant, seed yield per plant in both environment, while yield per plot and proline in drought stress trial indicate that the traits are governed by additive gene action and selection would be effective. Babbar and Tiwari (2018) reported high heritability coupled with high genetic advance as percentage of mean for biological yield per plant, seed yield per plant and total number of pod per plant under three diverse environments. Also, Joshi *et al.* (2018) noticed biological yield, seed yield, harvest index and 100 seed weight exhibited high heritability coupled with high genetic advance as percent of mean in 35 chickpea genotypes.

High heritability with moderate genetic advance was exerted by 100 seed weight in both environments. Whereas, yield per plot and proline in irrigated trial and number of secondary branches per plant in both conditions exhibited moderate heritability with moderate genetic advance. This also indicates the presence of additive gene action and selection of these characters may be rewarding.

CONCLUSION AND FUTURE SCOPE

Hence, from the present finding it is concluded that the advanced chickpea backcross derived BC_2F_4 lines used in the present study has plenty of variability for most of the traits and these traits should be taken into account while selecting superior plants for further improvement of yield and yield attributing traits in chickpea.

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