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Study of genetic variability, correlation and path analysis for yield and yield attributing traits in early maturing chickpea (*Cicer arietinum* L.) Lines

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Abstract

A field experiment to study the genetic variability, correlation and path analysis for seven quantitative characters in early maturing thirty-one desi Chickpea lines was conducted at Agricultural Research Station, Adilabad, Professor Jayashankar Telangana State Agricultural University, Hyderabad. All the characters under study i.e., Days to 50% flowering, plant height, number of primary branches, number of secondary branches, number of pods per plant, test weight and grain yield showed significant mean sum of squares indicating the presence of significant variability among the test genotypes. The estimates of genotypic and phenotypic coefficients of variability were high for the traits, number of pods per plant and grain yield. High phenotypic coefficient of variability and moderate genotypic coefficient of variability was observed for the trait, number of secondary branches. Moderate levels of Phenotypic and Genotypic Coefficients of Variability were observed for the trait, number of primary branches. Moderate Phenotypic Coefficient of Variability and low Genotypic Coefficient of Variability were recorded for the traits, plant height and test weight. Low Phenotypic and Genotypic Coefficients of Variability was observed for the character, days to 50% flowering. High heritability coupled with high genetic advance over mean was observed for the traits, number of primary branches, Number of secondary branches, Number of pods per plant and grain yield per hectare. High heritability coupled with high genetic advance over mean indicates the presence of additive gene action for the traits, and their response to selection. Grain yield was significantly and positively correlated at genotypic and phenotypic levels with the traits; days to 50% flowering, number of secondary branches, number of pods per plant and test weight. Genotypic Path analysis revealed that, the characters; plant height (0.09797), number of primary branches per plant (0.12687), number of pods per plant (0.40957) and test weight (0.77133) showed positive direct effects.

Keywords: Chickpea, correlation, genetic advance, genetic variability, heritability and path analysis

Introduction

Chickpeas (*Cicer arietinum*) are one of the earliest known cultivated legumes, tracing their ancestry back at least 7,000 years to the dawn of agriculture. Chickpea, a normally cold season legume is grown on more than 10 million hectares in 45 countries in a wide range of environments and cropping systems. Desi chickpeas account for close to 80% of global production. Desi varieties are cultivated primarily on the Indian Subcontinent and in Ethiopia, Mexico and Iran. Desi types can tolerate cooler temperatures and mature more quickly making them suitable for a wider range of production environments. India, the world's largest producing (60% area) & consuming nation, produces nearly 70% of all global production. Other major producers include Pakistan, Turkey, Australia, Iran, Myanmar, Canada, Ethiopia, Mexico and the USA. Chickpeas are low in fat, and rich both in protein and in zinc, a micronutrient essential to the health of pregnant women and children. An important component to be considered for crop adaptation to the different environments is phenology (the time to flowering, podding and maturity). Chickpea can mature in a wide timeframe ranging from 80 to 180 days depending on the genotype, growing conditions and environments. However, in at least two-thirds of the chickpea growing areas, the available crop growing season is short (90-120 days) due to risk of drought or temperature extremities towards the end of the crop season, which coincides with the pod filling stage of the crop. Therefore, to enable the crop to escape stress at the end of the season, it is important to cultivate early maturing varieties for these areas. During the past four decades, the chickpea area declined by 3.2 m ha in northern India (cooler long-season environments) and increased by 2.5 m ha in central and southern India (warmer short season environments), thus further necessitating cultivation of early maturing varieties.

Generating information about the genetic variability, genetic diversity relationships and inheritance of the genetic traits involved is the key task in genetic improvement of any crop plant. The genotypic and phenotypic coefficients of variation are helpful in understanding the existing variability in the populations whereas, the estimates of heritability and genetic advance provide the indices of transmissibility of characters. Thus, estimates of variability like coefficients of variation, heritability and genetic advance are very useful for devising suitable selection strategy for developing high yielding genotypes in Chickpea crop. Absolute variability values of different characters do not reveal which characters are showing high variability. This could only be accessed through standardized values of the phenotypic and genotypic variance estimates by obtaining the coefficients of variability. Heritability is a useful quantitative parameter, which considers the role of heredity and environment in determining the expression of a trait. Effective selection can be achieved only when additive effects are substantial and environmental effects are small. Expected genetic advance indicates the expected genetic progress for a particular trait under selection cycles and measures the extent of its stability under selection pressure. The heritability estimates along with genetic advance will be more useful than heritability value alone, in selecting best individuals. Broad sense heritability gives an idea about the portion of observed variability attributable to genetic differences. The difference between PCV and GCV estimates indicates the relative influence of environment on the character, which in turn decides the extent of their heritability. Keeping this in view, a field experiment was conducted to assess the genetic variation present in the advance chickpea lines.

Materials and Methods

The present investigation was carried out with thirty-one (31) genotypes that included twenty-seven (27) advance lines and four (4) checks *viz.*, NBeG 47, NBeG 3, JG 11 and JG 14; in a randomized complete block design with two replications in preliminary varietal trial; during *rabi*, 2020-2021 at Agricultural Research Station, Adilabad, Professor Jayashankar Telangana State Agricultural University, Hyderabad. Each entry was grown at a spacing of 30 x 5 cm, in a plot size of two rows with 4 m length. Two seeds were dibbled per hill and later thinned to retain one seedling per hill. The observations *viz.*, days to 50 percent flowering, plant height (cm), number of primary branches per plant, number of secondary branches per plant, test weight (g), grain yield per plot (g) were recorded on five randomly selected competitive plants. The mean of five observations were computed for all the characters. The data obtained were subjected to the biometrical analysis that included analysis of variance and genetic variability parameters. Genotypic coefficient of variation (GCV%), phenotypic coefficient of variation (PCV%), broad sense heritability (h^2) and genetic advance as percent mean (GAM) were estimated. Genotypic and phenotypic coefficient of variation were calculated using the method suggested by Burton (1953) [1] and were categorized as low, moderate and high by following Shivasubramanian and Menon (1973) [2]. The heritability in broad sense was calculated by using the formula proposed by Allard (1960) [3] and was categorized as suggested by Robinson *et al.* (1949) [4]. The expected genetic advance as expressed in per cent of mean was calculated by the method suggested by Johnson *et al.* (1955) [5] and categorized by adopting the method of Johnson *et al.*, 1955. For estimating correlation coefficients, analysis of covariance for all possible pairs of seven characters was carried out using the procedure of Panse and Sukhatme (1978) [6]. The genotypic (r_g) and phenotypic (r_p) correlation coefficients were calculated by adopting the procedure explained by Miller *et al.* (1958) [7]. The genotypic and phenotypic correlations were tested using the method (t-test) suggested by Fisher and Yates (1963) [8]. The cause-and-effect relationship between two variables cannot be known from simple correlation coefficient. Therefore, path analysis suggested by Wright (1921) [9] and Dewey and Lu (1959) [10] was adopted in order to partition the genotypic correlation between variables with seed yield into direct and indirect effects of those variables on yield. Genotypic correlation coefficients of six variables with yield were used to estimate the path coefficients for the direct effect of various independent characters on the dependent character, grain yield. The analysis of the data was carried out using the R package “variability: Genetic Variability Analysis for Plant Breeding Research” version 0.1.0. of Raj Popat *et al.* (2020) [11].

Results and Discussion

The data was recorded for seven quantitative characters which is presented here under and thoroughly discussed. The analysis of variance revealed that mean sum of squares due to genotypes (Table 2) was significant for all the seven characters under study. This confirms the presence of adequate amount of genetic variability in the advance breeding lines for all the characters studied and it offers a strong chance of improving the chickpea breeding program. High magnitude of variability in a population provides an opportunity for selection so as to evolve a high yielding variety with desirable characters. Range, variance, coefficient of variation, heritability and genetic advance are biometrical components that can be used to measure the genetic variation in any breeding program.

The parameters like mean, range, GCV, PCV, heritability in broad sense and percent genetic advance over mean for seven yield attributing traits are presented in Table 2. The mean value for days to 50 per cent flowering was 41.3 days with a range of 38 to 47 days. The genotypes ADBG 228 and ADBG 170 were early to flower (38.5 days to 50% flowering). The mean value for plant height was 46.7 cm with a range of 34.0 to 63.4 cm. The number of primary branches ranged from 1.0 to 3.2 with a mean of 2.3. The mean number of secondary branches per plant was 6.7 and the range was 4.2 to 10.4. The number of pods per plant ranged from 18.6 to 65.2 with a mean of 33.2. The test weight of the genotypes ranged from 18.0 g to 27.2 g (ADBG 300) with a mean of 22.7 g.

The estimates of phenotypic and genotypic coefficients of variability were high (20% and above) for number of pods per plant (26.2% and 24.4% respectively) and grain yield (26.2% and 25.18% respectively). The results are in conformity with the earlier findings of Sharma *et al.* (2005) [12]. High PCV (20% and above) and moderate GCV (10 -20%) was observed for the trait; number of secondary branches (20.06% and 17.1% respectively). Moderate levels (10 -20%) of PCV and GCV were observed for the trait; number of primary branches (16.4% and 12.76% respectively). Moderate PCV (10 -20%) and low GCV (0-10%) was recorded for the traits; plant height (12.03% and 8.3% respectively) and test weight (10.67% and 9.7% respectively). Low (0-10%) PCV and GCV was observed for the character; days to 50% flowering

(5.04% and 4.23% respectively). Low GCV and PCV values for the trait, days to 50% flowering, indicate the difficulty of improvement for this trait through selection because of the influence of environment on the expression of the trait. The magnitude of GCV was lower than PCV for all the characters under study, indicating that the variability was not only due to genotype but also influenced by environment.

The genotypic coefficient of variation alone is insufficient for determining genetic variability. Estimates of heritability and genetic advance are critical for predicting genetic improvement of any quantitative trait. High heritability estimates along with high genetic advance is more useful for selection (Johnson *et al.*, 1955) [5]. High heritability coupled with high genetic advance over mean was observed for the traits; number of primary branches, number of secondary branches, number of pods per plant and grain yield. High heritability coupled with high GAM indicates the presence of additive gene action for the traits, and these characters could be improved more easily than other characters in this study. The genotypic coefficient of variation and heritability estimates combined give a better understanding of the extent of genetic advance that may be predicted as a result of selection (Burton and De Vane, 1953) [1].

In the present investigation, heritability in broad sense ranged from 47.7% for plant height to 92.38% for grain yield**.** High heritability was observed for all of the traits studied, except plant height; showing that all the traits have a strong genetic basis. Maximum values were observed for grain yield (92.38%), followed by number of pods per plant (86.8%), test weight (82.5), number of secondary branches (72.6%), days to 50% flowering (70.3%), and number of primary branches (60.6%); whereas, medium heritability was observed for plant height (47.7%), indicating that desired improvement through exploitation of traits having high heritability can be achieved. Therefore, the observed variance was mostly under genetic control and was less impacted by environmental factors and there is likelihood of selection progress. These findings are in accordance with the results of Singh and Rao (1991) [13], Chavan *et al*., (1994) [14] and Samal and Jagadev (1994) [15]. Genetic advance as per cent of mean was observed to be maximum for grain yield (49.87%), followed by number of pods per plant (46.87%), number of secondary branches (30.03%), number of primary branches (20.47%), test weight (18.15%), plant height (11.82%) and days to 50% flowering (7.3%). Ali *et al*. (2011) [16] found higher values of genetic advance for number of pods per plant, plant height.

It's important to understand the association that exists between the traits in terms of influence of one trait over the other, in a positive or negative way. Because correlation provides a clear, complete association between characters, we employ correlation methods to learn about the characters that impact yield directly or indirectly. Grain yield is the end result of its constituents which directly or indirectly influence on yield. We can improve our trait of interest by indirectly selecting the characters which are positively correlated with the trait of interest. In the present study, the correlation coefficients for the characters analyzed were found to be significant and non-significant (Table 3). The genotypic correlation coefficients were in general, observed to be greater than phenotypic correlation coefficients, indicating the strong inherent association for the traits; thereby pointing out the possibility of effective phenotypic selection. The trait, plant height showed significant and negative genotypic correlation with number of secondary branches (-0.4*), non-significant and positive genotypic correlation with grain yield (0.1335), and non-significant and negative genotypic correlation with number of primary branches (-0.1391), number of pods per plant (-0.0906), test weight (-0.0714) and days to 50% flowering (-0.3069). The trait, number of primary branches per plant showed non-significant and positive genotypic correlation with number of secondary branches (0.2652), number of pods per plant (0.0066), test weight (0.056) and grain yield (0.0716). It showed non-significant and negative correlation with days to 50% flowering (-0.0873). The trait, number of secondary branches per plant showed significant and positive genotypic correlation with number of pods per plant (0.6687**), test weight (0.6294**), days to 50% flowering (0.4297*) and grain yield (0.4153*). The trait, number of pods per plant showed significant and positive genotypic correlation with test weight (0.8724**), days to 50% flowering (0.5*) and grain yield (0.8486**). The character, test weight showed significant and positive genotypic correlation with days to 50% flowering (0.5123**) and grain yield (0.9159**). The trait, days to 50% flowering showed significant and positive genotypic correlation with grain yield (0.4091*). In the present study, grain yield was found to be significantly and positively correlated with the traits; number of secondary branches, number of pods per plant, test weight, days to 50% flowering at both genotypic and phenotypic levels. Thus, these traits influence grain yield in chickpea and therefore could be used as indicators for improving grain yield in chickpea. Sharma and Saini (2010) [17] reported highly significant correlation of grain yield with number of branches per plant and number of pods per plant. Sarviyayal & Goyal (1994) [18] and Ali *et al*., (1991) [19] proposed pods per plant and 100-seed weight as selection criteria for high yielding genotypes

The genotypic and phenotypic correlation coefficients of the six characters with grain yield were partitioned into direct and indirect effects at genotypic and phenotypic levels through path coefficient analysis (Table 4). Direct and positive effect on grain yield at genotypic level was exhibited by test weight (0.77133) and number of pods per plant (0.40957) and also their genotypic correlations with grain yield were highly significant (0.91** & 0.84** respectively). The correlation therefore explains the true relationship and a direct selection through these traits will be effective. The characters, number of primary branches (0.12687) and plant height (0.09797) also showed positive direct effects but their correlations with grain yield were positive but non-significant. Genotypic Path analysis also revealed that, though the characters; number of secondary branches (-0.33258), and days to 50% flowering (-0.00686) showed negative direct effects, their correlation coefficients (0.4153* & 0.4091* respectively) with grain yield were positive and therefore; the indirect effects seem to be the cause of correlation. Hence, these indirect causal factors are to be considered simultaneously for selection for grain yield. The estimate of residual effect being of very low magnitude (0.0648), the variables included in the study explain most of the variability for the trait, grain yield.

Table 1: Analysis of variance (ANOVA) for different yield attributing traits of Chickpea

Source	Mean Sum of Square due to Genotypes	Mean Sum of Square due to Replications	Mean Error Sum of Square
df	30	1	30
DFF	7.41**	2.72	1.29
PH	46.72**	64.83	16.54
NPB	0.24**	0.74	0.05
NSB	3.128***	0.036	0.495
NPP	142.25***	1.249	10.04
TW	10.74***	0.883	1.498
GY	488664***	292474	97940

DFF: Days to 50 percent flowering
PH: Plant height (cm)
NPB: Number of primary branches per plant
NSB: Number of secondary branches per plant
NPP: Number of pods per plant
TW: Test weight (g)
GYP: Grain yield per hectare (Kg)

Table 2: Variability parameters of the advance lines evaluated in Preliminary varietal trial for different yield attributing traits of Chickpea

Character	Mean	Range		PCV (%)	GCV (%)	h^2 (bs)	GAM (%)
		Max	Min				
DFF	41.3	47.0	38.0	5.04	4.23	70.31	7.3
PH	46.7	63.4	34.0	12.03	8.3	47.7	11.82
NPB	2.3	3.2	1.0	16.4	12.76	60.6	20.47
NSB	6.7	10.4	4.2	20.06	17.1	72.6	30.03
NPP	33.3	65.2	18.6	26.2	24.4	86.8	46.87
TW	22.7	27.2	18.0	10.67	9.7	82.5	18.15
GY	1923.3	2708.3	875.0	26.2	25.18	92.38	49.87

*, **, *** Significant at 5%, 1% and 0.1% levels, respectively
DFF: Days to 50 percent flowering
PH: Plant height (cm)
NPB: Number of primary branches per plant
NSB: Number of secondary branches per plant
NPP: Number of pods per plant
TW: Test weight (g)
GYP: Grain yield per hectare (Kg)

Table 3: Genotypic and Phenotypic correlation coefficients among seven characters in Chickpea

Character	Genotypic (r_g) & Phenotypic (r_p) correlation	PH	NPB	NSB	NPP	TW	DFF	GY
PH	r_g	1	-0.1391^{NS}	-0.4305*	-0.0906 ^{NS}	-0.0714 ^{NS}	-0.3069 ^{NS}	0.1335 ^{NS}
	r_p	1	0.1106 NS	-0.0866 ^{NS}	-0.015 ^{NS}	-0.0783 ^{NS}	-0.1269 ^{NS}	0.1738 ^{NS}
NPB	r_g		1	0.2652 ^{NS}	0.0066 ^{NS}	0.056 ^{NS}	-0.0873 ^{NS}	0.0716 ^{NS}
	r_p		1	0.3316**	0.1017 ^{NS}	0.0348 ^{NS}	-0.1158 ^{NS}	0.0733 ^{NS}
NSB	r_g			1	0.6687**	0.6294**	0.4297*	0.4153*
	r_p			1	0.5704**	0.4626**	0.2553**	0.3832**
NPP	r_g				1	0.8724**	0.5**	0.8486**
	r_p				1	0.7544**	0.3592**	0.7593**
TW	r_g					1	0.5123**	0.9159**
	r_p					1	0.4309**	0.7598**
DFF	r_g						1	0.4091*
	r_p						1	0.3071**
GY	r_g							1
	r_p							1

*, ** Significant at 5% and 1% levels, respectively
DFF: Days to 50 percent flowering
PH: Plant height (cm)
NPB: Number of primary branches per plant
NSB: Number of secondary branches per plant
NPP: Number of pods per plant
TW: Test weight (g)
GYP: Grain yield per hectare (Kg)

Table 4: Path-coefficient analysis showing matrix of direct and indirect effects of six characters on seed yield per hectare in chickpea

Characters		PH	NPB	NSB	NPP	TW	DFF	Correlation coefficient with seed yield per hectare (r_g)
PH	P_g	0.09797	-0.01764	0.14318	-0.03709	-0.05505	0.00211	0.1335
	P_p	0.20843	0.00129	0.00661	-0.00673	-0.03741	0.00161	
NPB	Pg	-0.01362	0.12687	-0.08820	0.00271	0.04319	0.00060	0.0716

	Pp	0.02305	0.01164	-0.02534	0.04570	0.01677	0.00148	
NSB	Pg	-0.04218	0.03364	-0.33258	0.27387	0.48551	-0.00295	0.4153*
	Pp	-0.01805	0.00386	-0.07636	0.25607	0.22093	-0.00325	
NPP	Pg	-0.00887	0.00084	-0.22239	0.40957	0.67287	-0.00343	0.8486**
	Pp	-0.00313	0.00118	-0.04356	0.44893	0.36044	-0.00457	
TW	Pg	-0.00699	0.00710	-0.20934	0.35729	0.77133	-0.00351	0.9159**
	Pp	-0.01632	0.00041	-0.3531	0.33867	0.47783	-0.00548	
DFF	Pg	-0.03007	-0.01107	-0.14290	0.20477	0.39518	-0.00686	0.4091*
	Pp	-0.02647	-0.00135	-0.01950	0.16126	0.20588	-0.01271	

Residual Effect: 0.0648
*, ** Significant at 5% and 1% levels, respectively
DFF: Days to 50 percent flowering
PH: Plant height (cm)
NPB: Number of primary branches per plant
NSB: Number of secondary branches per plant
NPP: Number of pods per plant
TW: Test weight (g)
GYP: Grain yield per hectare (Kg)

Conclusion

In the present investigation, high heritability coupled with high genetic advance over mean was observed for the traits; number of primary branches, number of secondary branches, number of pods per plant and grain yield, indicating the presence of additive gene action for the traits, which plays an important role in selection programs. In the studied traits, grain yield was found to be significantly and positively correlated with the traits; number of secondary branches, number of pods per plant, test weight and days to 50% flowering at both genotypic and phenotypic levels. Thus, these traits influence grain yield in chickpea and therefore could be used as indicators for improving grain yield. Genotypic path analysis of grain yield indicated that the characters; test weight and number of pods per plant that showed direct positive effects and highly significant correlations with grain yield; and the characters number of secondary branches and days to 50% flowering that showed negative direct effects but significant correlations with grain yield need to be considered simultaneously for selection for grain yield.

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