



Genetic Variability and Association Analysis in Chickpea (*Cicer arietinum* L.) for Seed Yield Characters

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Authors' contributions

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

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ABSTRACT

During Rabi, 2019-2020, the present trial was carried out at the field experimentation centre of the Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad to assess genetic variability, correlation and path analysis in twenty-six chickpea genotypes, including one check variety Uday for twelve quantitative traits. The analysis of variance revealed significant variations across genotypes for all of the features under investigation, demonstrating a high level of genetic variability in the experimental material. The genotypes C-224, C-201, ICC-16693, C-1028, C-129, C-213, C-130 and C-1025 have been identified as the top performing lines among the genotypes studied. PCV values were found to be higher than GCV for all of the traits investigated, indicating that environmental variables influence the characters. The fact that biological yield per plant has a high PCV and GCV implies that there is a lot of genetic variability in the material for these qualities. Plant height, days to 50% flowering, harvest index, biological yield per plant, hundred seed weight, seed yield per plant and number of pods per plant were all found to have high heritability. For the traits of biological yield per plant, seed index, harvest index, number of pods per plant, seed yield per plant and plant height, high heritability was observed along with high genetic advance as percent of mean, indicating that these characters were primarily governed by additive gene effects. As a result of the accumulation

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of more additive genes, direct selection of these features using a simple selection strategy would be efficient, leading to further development of chickpea genotypes. Number of seeds per plant, number of pods per plant, biological yield per plant, number of primary branches per plant, number of secondary branches per plant and plant height all had positive significant genotypic and phenotypic associations with grain yield per plant. At the phenotypic level, biological yield per plant and number of seeds per plant both had a strong positive direct effect on grain yield per plant and contributed the most to yield per plant.

Keywords: Chickpea; PCV; GCV; heritability; genetic advance; correlation and path coefficient.

1. INTRODUCTION

Pulses are an essential group of food crops due to their high protein content and an imperative part of the Indian diet, provided that roughly 30% of the daily protein ingestion. Chickpea (*Cicer arietinum* L.), a foremost winter crop. This crop is vital part of our daily nourishment because it is an admirable source of protein, adapts well to farming techniques, and can resist drought. It generates 126 kg of protein per hectare on average, building it the most protein-rich legume after groundnut and soybean. Chickpea is identified by a variety of names in India, counting Chana, Gram, Bengalgram, Chani, Chhole, Chola, Harbara, Boot, Sanagalu, Kadalai, and Kadala. Chickpea is an autogamous crop with chromosome number of $2n=16$ belongs to the fabaceae family. Southwest Asia and the Mediterranean were predictable as primary centres of diversity by Vavilov [1], while Ethiopia was designated as a secondary centre of diversity. Chickpeas are grown extensively in Pakistan, Mexico, Turkey, Canada, Iran, Australia, Tanzania, Ethiopia, Spain and Burma. The principal chickpea-growing states in our country are Madhya Pradesh, Uttar Pradesh, Rajasthan, Maharashtra, Andhra Pradesh, Telangana and Karnataka, which primarily cultivate in rainfed conditions. Chickpea is principally grown in India through the *rabi* season, on the other hand there has recently been substantiation of chickpea production extending from Northern India's cool season to the warm climates of Central and Southern India Kuldeep et al. [2]. Chickpeas are a high-protein crop that can be used to supplement cereal-based diets. Chickpeas are high in both protein and carbohydrates. Chickpea protein is higher than that of pigeonpea, blackgram, and greengram legumes Kaur and Singh [3]. On average, chickpea seeds contain 23 percent protein, 64 percent total carbohydrates (47 percent starch, 6 percent soluble sugar), 5 percent fat, 6 percent crude fibre and 2 percent ash, as well as micronutrients like phosphorus

(340 mg/100 g), calcium (160 mg/100 g), magnesium (140 mg/100 g), iron (5 mg/100 g), zinc (4.1 mg/100 g) and zinc (4.1 mg/100 g) Jukanti and colleagues [4]. Cereals and pulses make up a large portion of the diets of billions of people around the world and chickpeas are being targeted in many countries to help battle malnutrition to some extent.

The quantity of genetic variability included in the breeding material, as well as the degree to which yield and yield-related qualities are transferred from generation to generation, are the most important determinants in crop development. To understand the influence of the environment on specific phenotypes, estimates of genotypic and phenotypic coefficients are required. In the selection programme, heritability and genetic progress expressed as a percent of the mean is a useful tool for estimating the amount to which particular qualities can be enhanced through selection. Breeders can use the identification of high-yielding chickpea genotypes to find donors for future breeding programmes. Yield is a dynamic variable that is influenced by a variety of circumstances it would be beneficial to intend enhanced genotypes by identifying vital characters and their interrelationships. As a result, selection based on yield component traits can result in a significant raise in yield. Correlation collective with path coefficient analysis is the finest approach to measure the inter-relationship among essential yield components. These strategies were engaged in the breeding programme to take full advantage of the yield prospective of chickpeas in order to enhance efficiency and produce. The interrelation among the variables is known as correlation, and it contributes in establishing the most efficient procedures for genotype selection. When there is a positive connection between major yield components, breeding procedures are generally effective, but choosing becomes extremely difficult when there is a negative correlation. Estimates of correlation coefficients alone may be confusing due to reciprocal

termination of component characters. As a result, correlation analysis paired with path analysis is a more effective technique in the research of yield contributing features. The path coefficient analysis technique is useful for determining the direct and indirect impacts of the causative components on the complex component of the correlation coefficient. One of the most essential breeding objectives, according to previous research, is to analyse genetic variability. Number of pods per plant, followed by biological yield per plant, number of seeds per plant, seed yield per plant, number of major branches per plant and 100-seed weight had large phenotypic and genotypic coefficients of variation, according to Kishore et al. [5]. Harvest index, seeds per pod, total number of pods per plant, seed yield per plant and days to maturity were all found to have strong heritability, according to Akanksha et al. [6]. Grain yield, number of pods per plant and biomass output all demonstrated high heritability, as well as high genetic progress as a percentage of the mean, according to Mohammed et al. [7]. According to Astereki et al. [8], the number of pods per plant and the harvest index had a highly substantial and favourable relationship with seed yield per plant. According to Tiwari et al. [9], the harvest index, 100 seed weight, seeds per pod and total number of pods per plant all had a strong positive direct effect on seed yield per plant.

2. MATERIALS AND METHODS

The current study includes twenty-six genotypes of chickpea in Rabi 2019-2020 at SHUATS, Prayagraj's experimentation centre of Genetics and Plant Breeding. During Rabi 2019-2020, the experiment was conducted in a randomised complete block design with three replications, with the indicated packages and practises for a healthy crop included. Days to 50% flowering, days to 50% pod setting, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of days to maturity, number of pods per plant, number of seeds per plant, seed index (gm), biological yield per plant (gm), harvest index (gm) and seed yield per plant were all recorded. Plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per plant, seed index (gm), harvest index (gm), biological yield per plant (gm) and seed yield per plant (gm) were all predictable from a random sample of plants, as were days to 50% flowering, days to 50% pod

setting and days to maturity. As per established methods, data were statistically analysed to determine genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), heritability, genetic advance and genetic advance as a percent mean. For the analysis of variance, genotypic coefficient of variation and phenotypic coefficient of variation, standard statistical methods were utilised Burton [10], heritability Burton and Devane [11] and genetic advance Johnson et al. [12]. Ai Jibouri et al. [13] used genotypic and phenotypic variances and co-variances to calculate genotypic and phenotypic correlation coefficients. The path coefficient study was carried out using the technique proposed by Dewey and Lu [14].

3. RESULTS AND DISCUSSION

For all of the traits studied, the analysis of variance indicated substantial differences between the genotypes (Table 1). As a result, it revealed a significant level of genetic heterogeneity among twenty-six chickpea genotypes. Evaluation of genetic characteristics, correlation and path coefficient analysis aid in the examination of significant traits during the selection process for optimizing chickpea productivity. Table 2 displays the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance (GA) and genetic advance as a percent of mean GA (percent) for all yield contributing characteristics.

For all of the characters, PCV was higher than the matching GCV, indicating that the environment had an impact. The highest GCV and PCV were found for biological yield per plant (26.833 and 32.118) and moderate GCV and PCV for number of pods per plant (14.277, 18.306), seed index (14.128, 17.061), harvest index (13.186, 15.457), seed yield per plant (12.427, 15.735), number of seeds per plant (11.651, 15.100), number of primary branches per plant (11.621, 16.712) and plant height (11.621, 16.712). GCV and PCV estimations ranging from high to moderate (10.316, 10.942) reveal that there is a lot of variation across these traits, implying that there is extent for genetic improvement through effective selection. Thakur and Sirohi [15], Shweta and Yadav [16] and Tsehaye et al. [17] all observed similar findings. The genotypic coefficient of variation estimations reflect the overall amount of genotypic variability present in the material.

Table 1. ANOVA for various traits in chickpea

S. No.	Characters/traits	Mean sum of squares		
		Replication (df =02)	Treatments (df = 25)	Error (df = 50)
01	Days to 50% Flowering	2.71	33.74**	2.15
02	Days to 50% pod setting	0.17	29.23**	3.95
03	Plant height	3.83	91.04**	3.64
04	Number of primary branches per plant	0.20	0.84**	0.22
05	Number of secondary branches per plant	0.22	0.89**	0.25
06	Days to maturity	10.76	10.08**	1.93
07	Number of pods per plant	193.59	125.13**	22.11
08	Number of seeds per plant	134.59	135.93**	25.11
09	Seed index	12.26	34.24**	4.54
10	Biological yield per plant	16.80	132.00**	16.64
11	Harvest index	7.63	87.10**	9.66
12	Seed yield per plant	1.82	4.23**	0.71

** indicates 1% level of significance

Table 2. Evaluation of genetic characters for twelve quantitative traits

Traits	GCV	PCV	h^2 h (Broad Sense)	GA	GAM
Days to 50% flowering	4.900	5.377	83.000	6.092	9.199
Days to 50% pods setting	3.218	3.899	68.100	4.935	5.470
Plant height	10.316	10.942	88.900	10.482	20.035
Number of primary branches per plant	11.621	16.712	48.300	0.652	16.645
Number of secondary branches per plant	9.092	13.449	45.700	0.644	12.663
Number of days to maturity	1.382	1.807	58.400	2.595	2.176
Number of pods per plant	14.277	18.306	60.800	9.414	22.938
Number of seeds per plant	11.651	15.100	59.500	9.660	18.519
100 seed weight	14.128	17.061	68.600	5.368	24.102
Biological yield per plant	26.833	32.118	69.800	10.672	46.179
Harvest index	13.186	15.457	72.800	8.928	23.172
Seed yield per plant	12.427	15.735	62.400	1.762	20.219

PCV: Phenotypic Coefficient of Variation, GCV: Genotypic Coefficient of Variation, h^2 : heritability (Broad sense), GA: Genetic Advance, GAM: Genetic Advance as Percent of Mean

Heritability, on the other hand, reflects the fraction of this genotypic polymorphism that is passed down from parents to offspring. Lush [18] proposed the broad sense heredity idea. It influences how effective genotypic variability may be used in a breeding programme. Table 2 shows the heritability estimates obtained during the current investigation. The heritability of the qualities is moderate to high, ranging from 45.7 percent to 88.9 percent. Plant height (88.900), days to 50% flowering (83.000), harvest index (72.800), biological yield per plant (69.800), seed index (68.600), seed yield per plant (62.400) and number of pods per plant were the traits with the highest heritability among the traits evaluated (60.800). The high heritability values of the qualities examined in this study revealed that they were less influenced by the environment, allowing for successful selection of traits based on phenotypic appearance using a simple

selection strategy and indicating the possibility of genetic progress. Ali et al. [19], Borate et al. [20], Khan et al. [21], Gaikwad et al. [22], Babbar et al. [23] and Yucel et al. [24] have all reported similar findings.

Genetic progress is useful in estimating the true gain expected under selection, whereas heritability evaluation offers information on the degree of inheritance of features from parents to offspring. In this study, high heritability and medium genetic advance was observed for biological yield per plant (69.800, 10.672) and plant height (88.900, 10.482), indicating that both attributes were influenced by both additive and dominant gene effects. As a result, careful selection may lead to the advancement of these features in chickpea. The percent mean evaluation of genetic progress aids in understanding the sort of gene action involved in

Table 3. Genotypic and phenotypic association analysis for yield and yield related qualities in chickpea genotypes

Traits	r	DFF	D50%P	PH	PB/ P	SB/ P	DM	Pods/ P	Seeds/ P	SI	BY/ P	HI	SYPP
DF50%	G	1.000	0.977**	0.034	0.346**	0.170	-0.143	0.345**	0.330**	0.001	0.291**	-0.179	0.192
	P	1.000	0.8920 **	0.054	0.172	0.087	-0.071	0.2610 *	0.2422 *	0.004	0.218	-0.086	0.135
DP50%	G		1.000	0.016	0.271*	-0.017	0.089	0.399**	0.353**	-0.013	0.229*	-0.080	0.196
	P		1.000	0.076	0.084	-0.006	0.112	0.218	0.166	-0.037	0.103	-0.009	0.068
PH	G			1.000	0.253*	0.237*	0.114	0.580**	0.535**	0.046	0.389**	-0.208	0.596**
	P			1.000	0.202	0.189	0.113	0.4372 **	0.4522 **	0.047	0.3242 **	-0.153	0.515**
NPBP	G				1.000	0.846**	-0.106	0.880**	0.788**	-0.232*	0.839**	-0.503**	0.812**
	P				1.000	0.7572 **	-0.051	0.6810 **	0.6155 **	-0.117	0.5169 **	-0.2382 *	0.633**
NSBP	G					1.000	-0.305**	0.660**	0.544**	-0.334**	0.660**	-0.526**	0.719**
	P					1.000	-0.136	0.5295 **	0.3999 **	-0.207	0.4669 **	-0.3057 **	0.533**
DM	G						1.000	0.082	-0.087	-0.082	-0.253*	0.281*	-0.095
	P						1.000	0.101	-0.031	-0.026	-0.165	0.205	0.019
NPP	G							1.000	0.959**	-0.165	0.823**	-0.486**	0.983**
	P							1.000	0.8327 **	-0.121	0.5718 **	-0.2392 *	0.781**
NSP	G								1.000	-0.081	0.864**	-0.504**	0.985**
	P								1.000	-0.019	0.6444 **	-0.2643 *	0.833**
SI	G									1.000	0.026	-0.241*	-0.107
	P									1.000	0.080	-0.195	-0.045
BYP	G										1.000	-0.872**	0.830**
	P										1.000	-0.6693 **	0.687**
HI	G											1.000	-0.490**
	P											1.000	-0.212
SYP	G												1.000
	P												1.000

*,** Significant at $P < 0.05$, $P < 0.01$, respectively. DF50%: Days to 50% flowering, DP50%: Days to 50% pod setting, PH: Plant height, NPBP: Number of primary branches per plant, NSBP: Number of secondary branches per plant, DM: Days to maturity, NPP: Number of pods per plant, NSP: Number of seeds per plant, SI: Seed index, BYP: Biological yield per plant, HI: Harvest index, SYP: Seed yield per plant

Table 4. Direct (diagonal) and indirect (off diagonal) effect of 12 characters on grain yield evaluated in chickpea germplasm

Traits	DF50%	DP50%	PH	NPBP	NSBP	DM	NPP	NSP	SI	BY/P	HI	SYP
DF50%	-0.063	-0.056	-0.003	-0.011	-0.005	0.004	-0.016	-0.015	0.000	-0.014	0.005	0.135
DP50%	-0.024	-0.027	-0.002	-0.002	0.000	-0.003	-0.006	-0.005	0.001	-0.003	0.000	0.068
PH	0.008	0.011	0.142	0.029	0.027	0.016	0.062	0.064	0.007	0.046	-0.022	0.515**
NPBP	-0.003	-0.002	-0.004	-0.020	-0.015	0.001	-0.014	-0.012	0.002	-0.010	0.005	0.633**
NSBP	0.016	-0.001	0.036	0.142	0.188	-0.026	0.100	0.075	-0.039	0.088	-0.058	0.533**
DM	-0.003	0.005	0.005	-0.002	-0.006	0.040	0.004	-0.001	-0.001	-0.007	0.008	0.019
NPP	0.033	0.028	0.056	0.086	0.067	0.013	0.127	0.106	-0.015	0.073	-0.030	0.781**
NSP	0.101	0.070	0.189	0.258	0.168	-0.013	0.349	0.419	-0.008	0.270	-0.111	0.833**
SI	0.000	-0.001	0.001	-0.003	-0.006	-0.001	-0.004	-0.001	0.029	0.002	-0.006	-0.045
BYP	0.094	0.045	0.140	0.223	0.202	-0.072	0.247	0.279	0.035	0.432	-0.289	0.687**
HI	-0.024	-0.003	-0.044	-0.068	-0.087	0.058	-0.068	-0.075	-0.056	-0.191	0.285	-0.212

Residual effect: 0.407. ** Significant at $P < 0.01$, respectively. DF50%: Days to 50% flowering, DP50%: Days to 50% pod setting, PH: Plant height, NPBP: Number of primary branches per plant, NSBP: Number of secondary branches per plant, DM: Days to maturity, NPP: Number of pods per plant, NSP: Number of seeds per plant, SI: Seed index, BYP: Biological yield per plant, HI: Harvest index, SYP: Seed yield per plant

the manifestation of a trait. Table 2 shows the estimates of genetic advance as a percentage of the mean for the current study. Heritability and genetic advance as a percentage of mean were estimated to be the highest for biological yield per plant (69.800, 46.179), seed index (68.600, 24.102), harvest index (72.800, 23.172), number of pods per plant (60.800, 22.938), seed yield per plant (62.400, 20.219) and plant height (88.900, 20.035), indicating that these traits are most likely controlled by additive gene action and selection will be effective. Vaghela et al. [25], Parameshwarappa et al. [26], Jakhar et al. [27], Srivastava et al. [28], Chopdar et al. [29], Thakur et al. [30], Arora et al. [31] and Anusha et al. [32] have all reported similar findings. Because the inclusion of more additive genes leads to greater enlargement, direct selection of these traits based on phenotypic expression by a simple selection procedure would be efficient. Shivashish et al. [33] reported similar findings.

During the correlation study, associations between yield and yield contributing features were investigated under study. Table 3 shows the phenotypic and genotypic correlation coefficients between the investigated features of 26 chickpea genotypes on different quantitative traits. According to Bhattacharyya et al. [34], correlation analysis between yield and its causal features revealed that genotypic correlation coefficients were generally greater than phenotypic correlation coefficients, indicating that the bond was mostly attributable to genetic factors. In several cases, the phenotypic correlation coefficients were larger than the genotypic correlation coefficients, indicating that the environment has a restraining influence on the expression of characteristics at the phenotypic level. Number of seeds per plant (0.985**, 0.833**), number of pods per plant (0.983**, 0.781**), biological yield per plant (0.830**, 0.687**), number of primary branches per plant (0.812**, 0.633**), number of secondary branches per plant (0.719**, 0.533**) and plant height (0.596**, 0.515**) all had positive significant genotypic and phenotypic correlations with grain yield per plant. At both genotypic and phenotypic levels, number of seeds per plant had a substantial positive association with biological yield per plant (0.864**, 0.644**), but a significant negative correlation with harvest index (-0.504**, -0.264*). At both genotypic and phenotypic levels, biological yield per plant demonstrated a substantial negative relation with harvest index (-0.872**, -0.669**). Grain yield per plant had

significant and positive correlations with the number of seeds per plant, the number of pods per plant, the biological yield per plant, the number of primary branches per plant, the number of secondary branches per plant and plant height at both genotypic and phenotypic levels, according to a correlation study (Table 3). Babbar et al. [35], Meena et al. [36], Gul et al. [37], Kuldeep et al. [38], Vartika singh et al. [39] and Manasa et al. [40] have all found similar findings.

Path analysis is one of the most accurate statistical techniques for determining the interdependence of features and the degree of control of independent characters on seed production, either directly or indirectly. Mushtaq et al. [41]. When it comes to choosing high yielding germplasm, the idea of direct and indirect influence of yield contributing traits on the final end product yield in any crop is crucial. Table 4 depicted the direct and indirect effects of twelve different quantitative characters. The path analysis revealed that biological yield per plant (0.432) and number of seeds per plant (0.419) had the most positive direct effects on seed yield, followed by harvest index (0.285), number of secondary branches per plant (0.188), plant height (0.142), number of pods per plant (0.127), days to maturity (0.040) and seed index (0.029), implying that direct selection for seed yield is important in future breeding programme. Number of seeds per plant is influenced by number of pods per plant (0.349), biological yield per plant (0.27), number of primary branches per plant (0.258), plant height (0.189), number of secondary branches per plant (0.168), days to 50% flowering (0.101) and days to 50% pod setting (0.07), as well as a negative indirect effect via harvest index (-0.111), days to maturity (-0.013), seed index (-0.008). The parameters biological yield per plant and number of seeds per plant had substantial positive direct influences on seed yield per plant, according to the path analysis. Both of these traits have a strong and positive relationship with seed yield per plant. Renukadevi and Subbalakshmi [42], Naveed et al. [43], Dehal et al. [44], Tadesse et al. [45] and Agarwal et al. [46] have all found similar findings.

4. CONCLUSION

Biological yield per plant, number of seeds per plant, number of pods per plant, number of primary branches per plant, number of secondary branches per plant, harvest index, seed index

and plant height all these characters contribute to higher seed yield per plant, according to genetic variability, correlation and path analysis in this study. As a result, selecting chickpea germplasm based on these characteristics should be prioritised in order to improve production potential.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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