

## GENETIC DIVERSITY AND ASSOCIATION STUDIES IN CHICKPEA (*Cicer arietinum* L.)

Rahul J. Parmar<sup>1</sup>, Vikas Pali<sup>2</sup> and Hardik H. Patel<sup>3</sup>

### ABSTRACT

Chickpea stands out as a crucial winter crop among various legumes, being widely accepted and utilized. To assess the diversity among chickpea plants, a total of 48 different chickpea genotypes were analyzed with respect to 11 distinct characteristics at Agricultural Research Station, AAU, Dahod during *rabi* 2022-23. Based on mean performance, genotypes ACP 13 (39.06 g), ACP 21 (33.38 g) and BGT 211 (32.13 g) were promising with respect to seed yield plant<sup>-1</sup>, whereas for protein content, genotypes GJG 6 (26.71%), Varantha (26.38%) and GAG 0622 (25.47%) were found promising. Significant values of genetic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were noted for traits such as the number of pods plant<sup>-1</sup>, weight of 100 seeds, individual plant seed yield, and harvest index. Traits like pods plant<sup>-1</sup>, 100 seed weight, seed yield plant<sup>-1</sup>, harvest index, and protein content exhibited both high heritability and substantial genetic advancement as a percentage of the mean. This suggests that these characteristics are primarily influenced by additive genetic factors, indicating promising potential for enhancing these attributes through selective breeding strategies. The correlation coefficient estimations suggested that three variables, namely pods plant<sup>-1</sup>, 100 seed weight, and harvest index, had a substantial and positive link with seed yield plant<sup>-1</sup> and were the most important yield contributing characters for enhancing chickpea seed production. Path analysis based on genotypic correlation revealed a high direct effect of days to 50 per cent flowering, pods plant<sup>-1</sup>, and 100 seed weight, as well as moderate to low indirect effects of primary branches plant<sup>-1</sup> and harvest index on seed yield plant<sup>-1</sup>, indicating the potential for using these traits to impose selection pressure to improve chickpea yield.

(Key words: Chickpea, variability, phenotypic coefficient of variation, heritability, genetic advance, correlation coefficient, path analysis)

### INTRODUCTION

Chickpea (*Cicer arietinum* L.) has chromosomal number 2n=16, also known as Gramme, Bengal gramme, Chana or Kabuli chana and Chhola. Among the earliest leguminous crops to be cultivated by humans in the ancient world, this plant falls under the genus *Cicer* within the *Papilionaceae* sub-family of the *Leguminoceae* family, which is now more commonly referred to as *Fabaceae*. The roots of the crop can be traced back to Western Asia, and subsequently, it expanded to regions like India and other parts of the world (Rathore and Sharma, 2003). Chickpea seeds are abundant in nutrients such as protein and phosphorus, calcium and fiber content as well as relatively low in anti-nutritional factors such as tripsin inhibitors. It comprises approximately 17.21% protein, 61.5% carbohydrates, 4.5% fat, along with approximately 0.49% lysine, and 0.04% tryptophan.

The significance of legumes holds greater prominence within our nation, given that their role in providing nutrients to the Indian diet surpasses their contribution to diets in Asia and the global context.

Chickpeas, specifically, serve as *dal* when split, while their whole seeds are consumed boiled or fried. Additionally, young, green chickpeas find use as a vegetable, and their flour constitutes a key component in Indian and Pakistani snacks and desserts. Furthermore, the straw of chickpea plants proves to be excellent fodder for animals.

Currently, chickpeas are cultivated across approximately 147 lakh hectares worldwide, yielding an annual production of 151 lakh tones. In India, chickpeas are cultivated on a total area of 99.9 lakh hectares, resulting in an annual output of 119.1 lakh tones and a yield rate of 1192 kg hectare<sup>-1</sup>. Gujarat encompasses a landmass of 11.01 lakh hectares, yielding 21.01 lakh tones of produce, and achieving a productivity level of 1568 kg hectare<sup>-1</sup> (Anonymous, 2022).

India's yield increase is low in comparison to the rest of the worldwide, and it needs to be promoted by intensive efforts on producing high yielding better varieties and assuring their availability to farmers through an active seed system. Genetic diversity within a population holds significant value for biodiversity, as the absence of diversity can render a population unable to adjust to shifts in its environment, increasing its vulnerability to extinction.

1 and 3. Res. Scholar, Dept. of Genetics and Plant Breeding, B. A. College of Agriculture, AAU, Anand  
2. Asstt. Res. Scientist, Agricultural Research Station, AAU, Dahod

Assessing genetic variability, particularly in essential yield-related characteristics of chickpeas, is crucial for determining its suitability as a foundational resource for genetic enhancement efforts. Moreover, the direct choice based on intricate characteristics like seed yield proves to be inefficient; thus, a solid selection framework necessitates an understanding of the linkage involving easily heritable traits, which are minimally affected by environmental factors (Kumar and Bisen, 2016).

## MATERIALS AND METHODS

The present study was conducted at the Agricultural Research Station, AAU, Muvaliya Farm, Dahod, during the winter *rabi* season of 2022-23. The experimental site's soil ranged from dark black to heavy black in texture. It was very deep, with good water-holding capacity moisture retentivity. A group of 48 different chickpea genotypes were chosen for field testing and produced in a Randomised Complete Block Design (RCBD) by sowing seeds in three replications. Each genotype was planted in a single 4 m

long line with 30 cm × 10 cm inter-row and intra-row spacing. The standard set of chickpea farming practices were utilised to grow a healthy crop. Data collection involved recording observations for days 50 per cent flowering and days to maturity, plant height in centimeters, primary and secondary branches plant<sup>-1</sup>, pod and seed counts plant<sup>-1</sup>, individual seed yield plant<sup>-1</sup> in grams, 100-seed weight in grams, harvest index as a percentage, protein content as a percentage. Mean values were then utilized for the purpose of statistical analysis, with each genotype being represented by observations from five competitive plants in each replication. Days to 50 per cent flowering, days to maturity and protein content were recorded on plot basis. The contents of total nitrogen in each variety were estimated by using the Kjeldahl procedure (Anonymous, 1990). The percentage of crude proteins was calculated by multiplying the per cent nitrogen by 6.25.

Johnson *et al.* (1955) proposed a formula for calculating genotypic and phenotypic variations. The calculation of PCV and GCV was performed using the method introduced by Burton (1952).

**Table 1. List of best performing genotypes recognized for chickpea seed yield and constituent traits**

Sr. No.	Characters	Name of the genotypes		
1.	Days to 50 per cent flowering	VMG-1	DBGP-1	ACP-24
2.	Days to maturity	VMG-1	DBGP-1	ACP-24
3.	Pods plant <sup>-1</sup>	ACP-21	ACP-13	ACP-16
4.	Seeds pod <sup>-1</sup>	Dahod Yellow	DBGP-1	BGT-211
5.	100 seed weight (g)	ICC-10945	ACP-13	ACP-21
6.	Seed yield plant <sup>-1</sup> (g)	ACP-13	ACP-21	BGT-211
7.	Harvest index (%)	ACP-13	ACP-28	ICC-10945
8.	Protein content (%)	GJG-6	Varantha	GAG-0622

The estimation of heritability followed the approach outlined by Allard (1960), while genetic advance was calculated utilizing the formula developed by Johnson *et al.* (1955). The analysis of correlation and path coefficients was conducted in accordance with the methodologies described by Dewey and Lu (1959) and Falconer (1960).

## RESULTS AND DISCUSSION

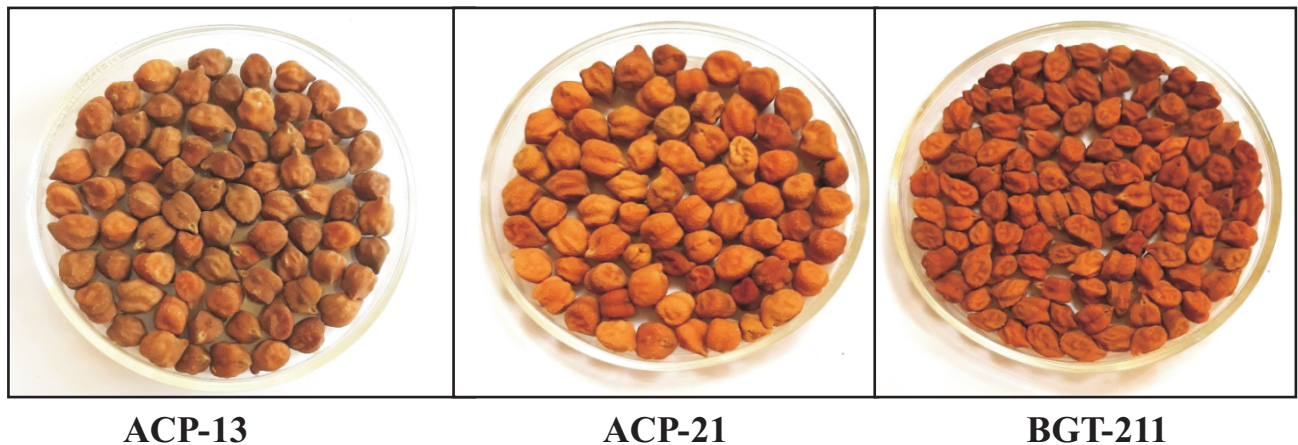
### Mean and range

The mean serves as a basic statistical tool in plant breeding for assessing phenotypic diversity and establishing a basis to identify desirable genotypes through screening. Table 2 shows the mean values of 48 chickpea genotypes for all 11 quantitative attributes, as well as the standard error of mean (SEm), critical difference (CD), and coefficient of variation (CV%). To find early maturing genotypes, days to 50 per cent flowering and days to maturity are appropriate selection standards in chickpea. In

current investigation, genotype VMG-1 (105.00 days) followed by DBGP-1 (105.67 days) and ACP-24 (106.00 days) were matured early. The late-maturing genotypes were identified as Narmada Late and GNG-1581, with a duration of 120.00 days, while genotypes Bavsar and GAG-0622 exhibited a slightly shorter duration of 118.33 days (Table 1).

Greater pods plant<sup>-1</sup> is sought after due to its direct correlation with elevated seed yield plant<sup>-1</sup>. The highest number of pods plant<sup>-1</sup> was expressed by genotype ACP-21 (95.53) which was at par with ACP-13 (89.93) and ACP-16 (88.17). The genotype Dahod Yellow displayed the greatest number of seeds pod<sup>-1</sup> (1.70), which was notably better than all the others. Following closely were DBGP-1 with 1.67 seeds pod<sup>-1</sup> and BGT-211 with 1.63 seeds pod<sup>-1</sup>.

The weight of 100 seeds serves as an indicator of seed boldness and a higher average performance is considered as desirable. The genotype, ICC-10945 (35.18 g) had significantly bolder seeds followed by ACP 13 (33.06 g)



**Figure 1.** Top performing genotypes in chickpea based on seed yield plant<sup>-1</sup>

and ACP 21 (31.98 g). Out of the genotypes examined, ACP 13 demonstrated the greatest seed yield at 39.06 g, a significantly superior outcome compared to all the other genotypes. Following behind were ACP 21 with a seed yield of 33.38 g and BGT 211 with 32.13 g (Figure 1). The average seed yield plant<sup>-1</sup> across all genotypes was 19.88 g. Genotype ACP 13 displayed the highest harvest index (61.95%) which was statistically at par with genotypes ACP 28 (57.12%) and ICC 10945 (54.72%).

Chickpeas with higher protein content are preferable in terms of quality. Significant differences between genotypes were found, ranging from 16.03% to 26.71%. Genotype GJG 6 exhibited the highest protein content (26.71%) followed by Varantha (26.38%) and GAG 0622 (25.47%). The average protein content was 20.68 %.

#### **Genetic variability, heritability and genetic advance**

The outcomes of the variance analysis for different characteristics are displayed in Table 2. These findings demonstrated notable variations among the genotypes across all 11 traits. The analysis of variance also allowed the determination of genotypic and phenotypic variances for each trait. Variability parameters are presented in Table 3.

The assessments of genotypic and phenotypic variances revealed variations in characteristics such as the duration to reach 50 per cent flowering, time to maturity, number of pods plant<sup>-1</sup>, seeds pod<sup>-1</sup>, weight of 100 seeds, yield of seeds plant<sup>-1</sup>, harvest index and protein content. Genetic variance played a more substantial role in the overall phenotypic variance, suggesting that the impact of environmental factors on the manifestation of these traits was comparatively limited. Conversely, attributes like plant

height, primary branches plant<sup>-1</sup>, and secondary branches plant<sup>-1</sup> displayed reduced contributions of genotypic variance to the overall phenotypic variance. This indicates a more prominent role of environmental factors in shaping the expression of these characteristics.

High levels of GCV were observed in traits including pod count plant<sup>-1</sup> (20.25%), 100-seed weight (29.53%), individual seed yield pod<sup>-1</sup> (34.24%), and harvest index (22.05%). Joshi *et al.* (2018), Dadas *et al.* (2020), Bukke *et al.* (2022), Pravalika *et al.* (2022) and Thapa *et al.* (2022) were also reported high GCV with a high estimate of heritability for this trait.

Elevated GCV figures accompanied by slightly elevated PCV values indicated substantial inter-accession differences and indicated that these traits were relatively less influenced by environmental factors. Conversely, attributes such as days to reach 50 per cent flowering (7.02%), days to maturity (3.35%), plant height (8.47%) and secondary branches plant<sup>-1</sup> (9.07%) demonstrated limited GCV values. The results of the study aligned with the research conducted by Pravalika *et al.* (2022) and Thapa *et al.* (2022), they also found low GCV. The limited variability among genotypes is indicated by the modestly low GCV values and the low PCV values, suggesting that these factors exhibit a subdued response to selection. The remaining parameters, such as primary branches plant<sup>-1</sup>, seeds pod<sup>-1</sup>, and protein content, had low GCV and PCV (10-20%). Ingle *et al.* (2021) and Pawar *et al.* (2018) also found low GCV and PCV in their experiment. This means that there is a larger chance of improving these features through selection. The small differences in GCV and PCV estimations for each trait suggest that environmental influences have only a minor impact in the development of these traits.

**Table 2. Evaluation of average performance, analysis of variance (ANOVA) and estimation of genetic variability for 11 distinct traits in chickpea**

Traits	Mean performance				Source of variation and mean squares (ANOVA)			
	Mean	Range	SEm.(-±)	CD at 5%	CV%	Replication (df = 02)	Genotypes (df = 47)	Error (df = 94)
Days to 50 per cent flowering	52.05	45.00 - 60.00	0.59	1.65	1.96	2.86	41.13**	1.04
Days to maturity	112.33	105.00 - 120.00	0.74	2.07	1.14	2.33	44.11**	1.64
Plant height (cm)	47.46	38.46 - 59.33	1.85	5.20	6.76	2.09	58.79**	10.31
Primary branches plant <sup>-1</sup>	3.07	2.33 - 4.03	0.18	0.50	9.95	0.02	0.44**	0.09
Secondary branches plant <sup>-1</sup>	10.56	7.67 - 12.60	0.47	1.33	7.77	0.45	3.43**	0.67
Pods plant <sup>-1</sup>	65.43	34.67 - 95.53	2.86	8.04	7.58	19.99	551.12**	24.59
Seeds pod <sup>-1</sup>	1.43	1.13 - 1.70	0.054	0.15	6.60	0.01	0.08**	0.01
100 seed weight (g)	20.15	9.57 - 35.18	0.63	1.76	5.40	1.14	107.40**	1.18
Seed yield plant <sup>-1</sup> (g)	19.88	7.72 - 39.06	1.24	3.47	10.78	7.61	143.64**	4.59
Harvest index (%)	38.53	22.44 - 61.95	2.93	8.23	13.17	0.72	242.35**	25.77
Protein content (%)	20.68	16.03 - 26.71	0.39	1.10	3.29	0.92	26.83**	0.46

**Table 3. Variability parameters for 11 chickpea characteristics**

Characters	$\delta^2_g$	$\delta^2_p$	GCV (%)	PCV (%)	H <sup>2</sup> <sub>b</sub> (%)	GA % Mean
Days to 50 per cent flowering	13.37	14.40	7.02	7.29	92.79	13.94
Days to maturity	14.16	15.80	3.35	3.54	89.63	6.53
Plant height (cm)	16.16	26.47	8.47	10.84	61.05	13.63
Primary branches plant <sup>-1</sup>	0.11	0.21	10.99	14.83	54.93	16.78
Secondary branches plant <sup>-1</sup>	0.92	1.59	9.07	11.95	57.65	14.19
Pods plant <sup>-1</sup>	175.51	200.10	20.25	21.62	87.71	39.06
Seeds pod <sup>-1</sup>	0.02	0.03	10.50	12.40	71.66	18.31
100 seed weight (g)	35.41	36.59	29.53	30.02	96.77	59.83
Seed yield plant <sup>-1</sup> (g)	46.35	50.94	34.24	35.90	90.98	67.28
Harvest index (%)	72.19	97.96	22.05	25.69	73.69	39.00
Protein content (%)	8.79	9.25	14.34	14.71	94.99	28.79

**Table 4. Correlation between genotype (above diagonal) and phenotypic (lower diagonal) traits in chickpea**

Cha.	DF	DM	PH	PBPP	SBPP	PPP	SPP	SW	HI	PC	SYPP
DF	1.000	0.999 **	0.331 *	-0.122	0.087	0.029	-0.252	-0.070	0.140	0.226	0.028
DM	0.987 **	1.000	0.348 *	-0.111	0.089	0.036	-0.224	-0.081	0.141	0.212	0.029
PH	0.263 **	0.273 **	1.000	-0.248	-0.085	0.369 **	-0.190	0.234	0.258	0.040	0.182
PBPP	-0.073	-0.059	-0.155	1.000	0.777 **	-0.227	0.075	-0.093	-0.046	-0.027	-0.068
SBPP	0.058	0.043	-0.094	0.429 **	1.000	-0.115	-0.083	0.108	0.133	-0.050	0.004
PPP	0.031	0.026	0.258 **	-0.119	-0.084	1.000	0.035	0.803 **	0.590 **	-0.529 **	0.949 **
SPP	-0.218 **	-0.185 *	-0.113	0.001	-0.035	0.036	1.000	0.067	-0.007	0.225	0.041
SW	-0.07	-0.078	0.189 *	-0.06	0.076	0.737 **	0.054	1.000	0.425 **	-0.464 **	0.872 **
HI	0.132	0.131	0.182 *	-0.115	0.088	0.466 **	-0.045	0.346 **	1.000	-0.595 **	0.622 **
PC	0.213 *	0.196 *	0.036	-0.001	-0.03	-0.465 **	0.195 *	-0.454 **	-0.489 **	1.000	-0.617 **
SYPP	0.017	0.016	0.136	-0.03	0.021	0.837 **	0.065	0.806 **	0.485 **	-0.561 **	1.000

\*, \*\* significant at 0.05 and 0.01 level of probability, respectively



**Table 5. Analysis of genotypic path coefficients reveals direct and indirect impacts of various traits on chickpea seed yield**

Cha.	DFE	DM	PH	PBPP	SBPP	PPP	SPP	SW	HI	PC	Correlation coefficient with SYPP ( $r_g$ )
DFE	<b>0.305</b>	-0.172	-0.056	-0.030	-0.017	0.019	0.005	-0.025	0.015	-0.014	0.028
DM	0.304	<b>-0.172</b>	-0.059	-0.027	-0.017	0.024	0.004	-0.029	0.015	-0.014	0.029
PH	0.101	-0.060	<b>-0.170</b>	-0.061	0.017	0.242	0.004	0.085	0.027	-0.003	0.182
PBPP	-0.037	0.019	0.042	<b>0.247</b>	-0.152	-0.149	-0.001	-0.034	-0.005	0.002	-0.068
SBPP	0.026	-0.015	0.014	0.191	<b>-0.196</b>	-0.076	0.002	0.039	0.014	0.003	0.004
PPP	0.009	-0.006	-0.063	-0.056	0.023	<b>0.656</b>	-0.001	0.292	0.062	0.034	0.949 **
SPP	-0.077	0.039	0.032	0.019	0.016	0.023	<b>-0.019</b>	0.024	-0.001	-0.014	0.041
SW	-0.021	0.014	-0.040	-0.023	-0.021	0.527	-0.001	<b>0.363</b>	0.045	0.030	0.872 **
HI	0.043	-0.024	-0.044	-0.011	-0.026	0.387	0.000	0.154	<b>0.105</b>	0.038	0.622 **
PC	0.069	-0.037	-0.007	-0.007	0.010	-0.347	-0.004	-0.169	-0.062	<b>-0.064</b>	-0.617 **

\*, \*\* significant at 0.05 and 0.01 levels of probability, respectively, Residual factor = 0.0023 DFE=Days to 50% flowering, DM=Days to maturity, PH=Plant height, PBPP=Primary branches plant<sup>-1</sup>, SBPP=Secondary branches plant<sup>-1</sup>, PPP= Pods plant<sup>-1</sup>, SPP=Seeds pod<sup>-1</sup>, SW=100 seed weight, HI=Harvest index, PC=Protein content, SYPP= Seed yield plant<sup>-1</sup>

A plant breeder has to understand heritability since it reveals the probability and extent of improvement through selection. traits like time taken to reach 50 per cent flowering (92.79%), duration to maturity (89.63%), plant height (61.05%), pods plant<sup>-1</sup> (87.71%), seeds pod<sup>-1</sup> (71.66%), 100-seed weight (96.77%), individual seed yield plant<sup>-1</sup> (90.98%), harvest index (73.69%), and protein content (94.99%) exhibited high heritability estimates. High heritability estimates for majority traits indicating major contribution of genetic variance to phenotypic variance and thereby little role of environment on their expression. High heritability estimates were reported by Uikay *et al.* (2018) and Navghare *et al.* (2019) for seed yield plant<sup>-1</sup> seeds pod<sup>-1</sup> and 100-seed weight. Primary branches plant<sup>-1</sup> (54.93%) and secondary branches plant<sup>-1</sup> (57.65%) heritability estimates were moderate, indicating that selection based on phenotypic performance would be beneficial in terms of environmental variance partitioning. Ingle *et al.* (2021) and Pawar *et al.* (2018) also reported moderate estimates of heritability.

The combination of heritability estimates and genetic advance offers more comprehensive insights compared to using heritability alone for identifying the most promising individuals. When the heritability estimates are primarily influenced by non-additive gene effects, the potential gain tends to be limited. Conversely, if the heritability is driven by additive gene effects, a significant genetic advance can be anticipated. Genetic gain serves as an indicator of the anticipated progress in a particular trait through a suitable selection procedure.

Regarding traits such as pods plant<sup>-1</sup>, weight of 100 seeds, seed yield plant<sup>-1</sup>, harvest index, and protein content, notable heritability was observed alongside substantial genetic advancement relative to the mean. This suggests a significant potential for enhancement through

selection, as these characteristics are primarily influenced by additive genetic variance. High heritability with higher genetic advance for pods plant<sup>-1</sup>, seed yield plant<sup>-1</sup> and harvest index also found by Alemu *et al.* (2017) and Joshi *et al.* (2018).

#### Correlation coefficients analysis

Before initiating any crop enhancement initiative aimed at achieving greater yields, it is essential to gather insights into the interconnectedness of various traits with yield and their mutual associations. This process expedites the evaluation of high-yield genotypes in selection schemes. Table 4 shows the phenotypic and genotypic relationships for all potential combinations.

The seed yield plant<sup>-1</sup> displayed significant and positive correlations with the pod count plant<sup>-1</sup> ( $r_g = 0.949$  and  $r_p = 0.837$ ), 100-seed weight ( $r_g = 0.872$  and  $r_p = 0.806$ ), and harvest index ( $r_g = 0.622$  and  $r_p = 0.485$ ) at both assessed levels. Deshmukh *et al.* (2020) and Yadav *et al.* (2023) observed that seed yield plant<sup>-1</sup> shows positive correlations with pod count plant<sup>-1</sup> and 100-seed weight at genotypic level. The harvest index demonstrated positive and significant correlation with pods count plant<sup>-1</sup> ( $r_g = 0.590$  and  $r_p = 0.466$ ), 100-seed weight ( $r_g = 0.425$  and  $r_p = 0.346$ ) and seed yield plant<sup>-1</sup> ( $r_g = 0.622$  and  $r_p = 0.485$ ) across both levels of evaluation. Positive and significant correlation between harvest index and seed yield plant<sup>-1</sup> reported by Barde *et al.* (2023) and Yadav *et al.* (2023). 100-seed weight had significant and positive genotypic as well as phenotypic correlation with pods plant<sup>-1</sup> ( $r_g = 0.803$ ,  $r_p = 0.737$ ), harvest index ( $r_g = 0.425$ ,  $r_p = 0.346$ ) and seed yield plant<sup>-1</sup> ( $r_g = 0.872$ ,  $r_p = 0.806$ ), while plant height ( $r_p = 0.182$ ) had positive and significant association at phenotypic level only. Plant height ( $r_g = 0.369$ ,  $r_p = 0.258$ ), 100-seed weight ( $r_g = 0.803$ ,  $r_p = 0.737$ ), harvest index ( $r_g = 0.590$ ,  $r_p = 0.466$ ) and seed yield plant<sup>-1</sup> ( $r_g = 0.949$ ,  $r_p = 0.837$ ) showed positive and significant correlation

with pods count plant<sup>-1</sup> at both levels. Yadav *et al.* (2023) also documented that 100 seed weight displayed positive and significant correlation with seed yield plant<sup>-1</sup> and harvest index in their respective studies.

Protein content exhibited significant and negative correlation with pods count plant<sup>-1</sup> ( $r_g = -0.529, r_p = -0.465$ ), 100-seed weight ( $r_g = -0.464, r_p = -0.454$ ), harvest index ( $r_g = -0.595, r_p = -0.489$ ) and seed yield plant<sup>-1</sup> ( $r_g = -0.617, r_p = -0.561$ ) at both levels (Table 4). Protein content showed negative correlation with pods plant<sup>-1</sup>, harvest index and seed yield plant<sup>-1</sup> founded in experiment was carried out by Padmavathi *et al.* (2013) and Babbar *et al.* (2015). Hence, as a result, simultaneous improvement of protein content and seed yield is not achievable, while it is advised that the breeding methods for improving chickpea quality by appropriately structured.

**Path coefficients analysis**

The study centered on seed yield plant<sup>-1</sup> as the outcome of interest, with the remaining quantitative traits serving as independent variables in the analysis of path coefficients (Table 5 and Figure 2).

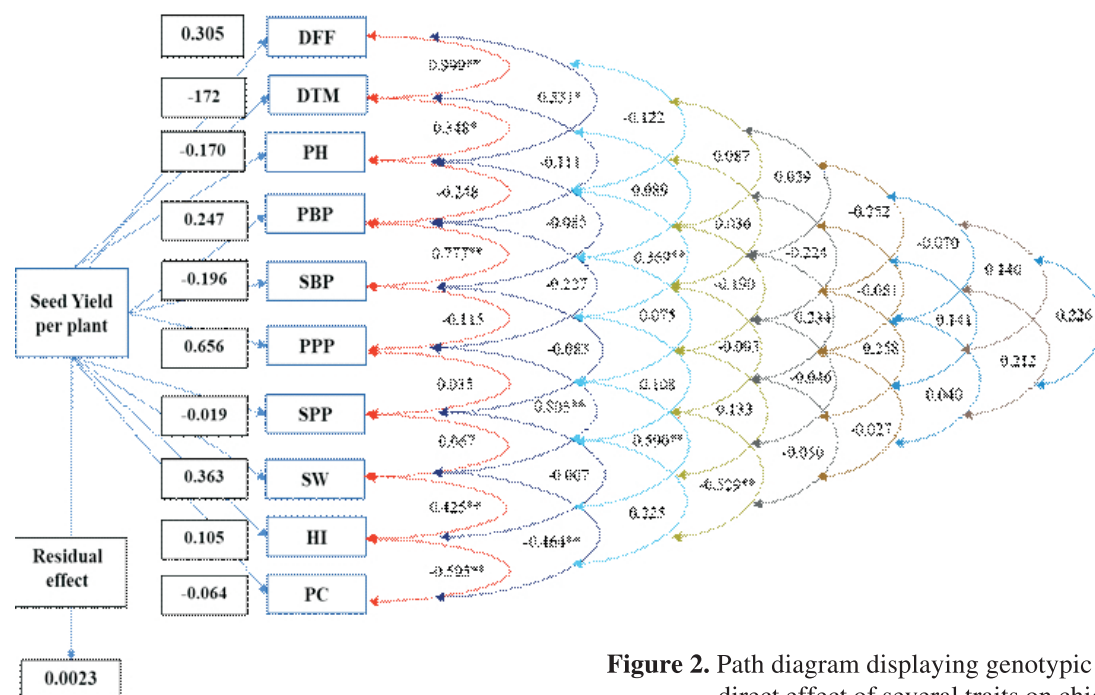
Path coefficient research found that pods count plant<sup>-1</sup> (0.656) and 100-seed weight (0.363) were prominent characteristics with significant positive direct effects and a high association with seed yield plant<sup>-1</sup>. The outcomes concurred with the discovery reported by Barde *et al.* (2023), who also reported pods plant<sup>-1</sup> and 100 seed weight exhibited positive direct effect and significantly correlated with seed yield plant<sup>-1</sup>. As a result, applying selection pressure to these traits would increase chickpea seed production.

Harvest index (0.105) exhibited minimal direct effects and supplemented yield indirectly through pods

count plant<sup>-1</sup>, resulting in a strong and positive connection of these parameters with seed production. Barde *et al.* (2023) and Yadav *et al.* (2023) also showed harvest index exhibited low direct effect and significantly correlated with seed yield plant<sup>-1</sup>. Protein content had a small and negative direct effect (-0.064), but their indirect effect *via* pods count plant<sup>-1</sup> was moderate and negative, resulting in a negative and significant genotypic correlation of this variable with seed yield plant<sup>-1</sup>. Babbar *et al.* (2015) reported negative direct effect of protein content on seed yield. The study also demonstrated that the trait secondary branches plant<sup>-1</sup> (-0.196) had a negative direct effect on seed yield plant<sup>-1</sup>, but due to the low and positive indirect effect *via* primary branches plant<sup>-1</sup>, there was a positive genotypic association with seed yield plant<sup>-1</sup>. Similar results determine by Yadav *et al.* (2023) that secondary branches plant<sup>-1</sup> exhibited a negative direct effect on seed yield plant<sup>-1</sup>.

The residual effect assesses the extent to which the causal factors contribute to the fluctuations in seed yield. In this investigation, the residual effect at the genetic level was minimal (0.0023), suggesting that the traits examined in this study sufficiently account for the diversity in chickpea seed yield plant<sup>-1</sup>.

The outcomes of the present study indicate that within the examined genotypes, it is feasible to identify strains with elevated seed yield and favourable quality. Notably, traits such as pods count plant<sup>-1</sup>, weight of 100 seeds, seed yield plant<sup>-1</sup>, harvest index and protein content exhibited substantial diversity, heritability, and genetic advancement. Consequently, these attributes are largely influenced by additive genetic factors and can be enhanced through selective breeding.



**Figure 2.** Path diagram displaying genotypic association and direct effect of several traits on chickpea seed yield plant<sup>-1</sup>

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