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Genotypic Variability, Correlation and Path Coefficient Analysis for Elite Genotypes of Chickpea (*Cicer arietinum* L.)

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ABSTRACT

The study was conducted during the *rabi* season (October, 2021–April, 2022) at the Crop Research Centre, Department of Genetics and Plant Breeding, School of Agriculture, ITM University, Gwalior, Madhya Pradesh, focused on 30 chickpea genotypes to evaluate genetic variability, heritability, genetic advance, correlations and path analysis among quantitative traits. Utilizing a randomized block design, the study found that the number of pods plant^{-1} exhibited the highest variability, while pod length showed the least variability. Significant phenotypic and genotypic coefficients of variation highlighted substantial variability among the genotypes, with shoot length, root length, and the number of secondary branches displaying high genetic advance and heritability. This suggested the predominant influence of additive gene action on these traits, making them suitable for selection-based improvements. Genotypic and phenotypic correlations were generally similar, indicating minimal environmental influence on most traits. Positive correlations were identified between the number of primary branches, number of secondary branches, pods plant^{-1}, seeds pod^{-1}, seed index and other dependent traits, indicating their potential for enhancing crop yield through selection. The study further revealed significant direct associations among traits, emphasizing the presence of additive gene action and the feasibility of effective selection for improving chickpea characteristics. In conclusion, the findings offer valuable insights into the genetic variability and heritability of chickpea traits, guiding future breeding and selection programs for enhanced genotypes.

KEYWORDS: Chickpea, PCV, GCV, heritability, correlations and path analysis

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1. INTRODUCTION

Chickpea (*Cicer arietinum* L.) is a leguminous crop, belonging to Fabaceae family. It isa self-pollinated with chromosomal number 2n=14. It is an Indian native crop with other names for chickpea include Egyptian pea, Bengal gram and gram. Chickpea has a taproot with root nodules where, strong roots extend most of the way down to 60 cm, yet they can extend as far as 3 m Sajja et al. (2017). The stem's pubescence is glandular andit might be dark green, bluish green or olive in colour. The leaves are pinnately compound, imparipinnate, glandular, hairy, stipulate, alternating, with 3–8 pairs of leaflets and a top leaflet (rachis ending in a leaflet) the leaflets shape range from ovate to elliptic (Shaheen et al., 2020). The chickpea flower has a normal aestivation which is complete, bisexual, zygomorphic, hypogynous, pentamerous solitary and polypetalous. The odd petal is composed of a posterior standard, two lateral wings and two anterior wings that form a keel (enclosing the pistil and stamens) (Yeo, 2012). Diadelphous has 10 stamens (nine anthers united and one free) and its ovary is superior, sessile, inflated and hairy Sajja et al. (2017). The majority of buds start to open between 8 and 11 in the morning. In 5 to 6 days following fertilization and pod development begins.

One of the most popular pulses grown and consumed in India is chickpea. Chickpea seeds contain on an average 23% protein, 64% total carbohydrates (47% starch, 6% soluble sugar), 5% fat, 6% crude fiber and 3% ash and also contain micro nutrients like phosphorus (340 mg 100 g^{-1}), calcium (160 mg 100 g^{-1}), magnesium (140 mg 100 g^{-1}), iron (5 mg 100 g^{-1}), zinc (4.1 mg 100 g^{-1}) Kaur et al. (2019). The protein content of chickpeas is relatively lower than that of other pulses, but they have higher biological value and protein digestibility (Gu et al., 2023). Malic acid (90–96%) and oxalic acid are secreted in liquid form by the granular hair on leaves and pods (4–10%). It is the third most important pulse crop in the world, after dry bean and field pea Jagadish and Jayalakshmi (2014). It is most important pulse crop of India contributing about 30% of total pulse acreage and about 40% of total pulse production of the nation. India ranked first in area and production in the world with cultivated area of 9.55 mha and production of 9.94 mt with productivity of 1041 kg ha^{-1}. In Madhya Pradesh, it covers an area of 31.03 lakh ha with production of 39.97 lakh t and productivity of 1288 kg ha^{-1} (Anonymous, 2019–20).

The success of any crop improvement programme largely depends on the genetic variability present in the population. Estimates of heritability are used to assess the variability in the population. Heritability combined with genetic advance will bring out the genetic gain predicated from selection (Kumar et al., 2012). Estimates of genotypic and phenotypic coefficients are required to understand the impact of the environment on various traits. The knowledge ofcorrelation between different characters, direct and indirect selection of characters that are not easily measured and those with low heritability is important in breeding Earline by several workers (Yadav et al., 2002); (Yucel et al., 2006) and (Singh, 1997) therefore, the present investigation has been taken. Although chickpea has less diversity and self-pollinating crop. According to studies on the chickpea, there is a significant genetic variation in terms of the number of secondary branches $plant^{-1}$, number of pods $plant^{-1}$, seed index (Malik et al. (2014). The aim of this research was to understand the genetic variability, heritability, genetic advance, genetic advance as a percent of mean, correlation coefficients and path analysis of various features and their associations with seed yield in chickpea.

2. MATERIALS AND METHODS

The present experiment was conducted during the *rabi* season from October 2021-April 2022 at Crop Research Centre, Department of Genetics and Plant Breeding, School of Agriculture, ITM University, Gwalior, Madhya Pradesh, India. The 30 genotypes for research were procured from Department of Genetics and Plant Breeding, Sam Higginbottom Institute of Agriculture, Technology and Sciences, Deemed to be University, Prayagaraj (Uttar Pradesh) Listed in Table 1.

Observations were recorded including germination percentage, root length, shoot length, days to 50% flowering, plant height, number of primary branches, number of

Table 1: List of 30 genotypes of chickpea

Sl. No.	Genotype	S. No.	Genotype
1.	C-1044	16.	IPC-97/29
2.	ECSI-6270	17.	ICC -1205
3.	C -115	18.	C -137
4.	IPC-10-134	19.	GNG-1958
5.	C-128	20.	C-210
6.	C-1027	21.	C-1013
7.	C-205	22.	IPC-04-52
8.	C-1014	23.	C-1011
9.	C -1014	24.	JG-24
10.	C-136	25.	C-1023
11.	C-126	26.	CSG-8962
12.	C-223	27.	C-127
13.	C-1022	28.	AVTI-G5
14.	NBG-47	29.	C -1021
15.	C-1025	30.	C -133

secondary branches, number of pods plant^{-1}, number of seeds pod^{-1}, pod length, seed index and yield plant^{-1}.

Analysis of variance was carried out by using standard statistical methods Panse and Sukhatme (1989). Variability parameters were determined as per methods described by Burton and de vane (1953). Correlation analysis was done as per the procedure described by Singh and Chaudhary (1979). The estimates of direct and indirect effects were calculated by the path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959). All statistical analyses were done using by R package Doebioresearch (Popat and Banakara, 2020) and O.P. Sheoran Programmer, Computer Section, CCS HAU, Hisar. The genotypic correlation coefficient provides a measure of genotypic association between different characters, while the phenotypic correlation coefficient includes both genotypic as well as environmental influences Ali- Jibouri et al. (1958).

2.1. *Estimation of GA and GAM*

The genetic advance (GA) for selection intensity (K) at 5% was calculated by the formula suggested by Allard (1960).

$GA=(K)\ (\sigma_p)\ (H^2)$

Where,

GA=Expected genetic advance at 5% selection intensity, σ_p=Phenotypic standard deviation.

H^2=Heritability and K=Selection differential (K=2.063 at 5% selection intensity).

The genetic advance as percent of the mean (GAM) was calculated by formula given by Johnson et al. (1955).

$GAM=(GA/X)\times100$

Where,

GAM=Genetic advance as percent of mean

GA=Genetic advance at 5% selection intensity

X=Population mean

Heritability (H^2) was computed by formula developed by Allard (1960).

$H^2=\sigma^2g/\sigma^2p\times100$

Where,

σ^2p=Phenotypic variance σ^2g=Genotypic variance H^2=Heritability in broad sense

The genotypic and phenotypic correlation coefficients were calculated from the genotypic and phenotypic components of variance and covariance as described by Singh and Chaudhary (1979) and as per formula given by Johnson et al. (1955). The following statistical parameters were calculated for the presentation of data on different quantitative attributes.

2.2. *Estimating of correlation*

Now, genotypic and phenotypic correlation coefficients were calculated using formula

Phenotypic correlation (rp)=$\mathrm{PCov.\ xy}/\sqrt{\mathrm{PVx.PVy}}$

Genotypic correlation (rg)=$\mathrm{GCov.\ xy}/\sqrt{\mathrm{GVx.GVy}}$

$rxy=\mathrm{Cov}\ (x,y)/\sqrt{V(x)}\times\sqrt{V\ (y)}$

Where,

r_{xy}=Correlation coefficient between character x and y

$\mathrm{Cov}_{x,y}$=Co-variance of character x and y

V_x=Variance of character x, and

V_y=Variance of character y

rp=Phenotypic correlation

rg=Genotypic correlation.

2.3. *Path analysis*

Path analysis splits te correlation coefficient into the measures of direct and indirect effects and measures contribution of each independent variable on the dependent variable and estimates residual effects. It helps in determining the yield and yield contributing characters.

To estimate various direct and indirect effects, the following equations were used

$r1y=P1y+r12P2y+r13P3y+\ldots+r1IPIy$

$r2y=r2yP1y+P2y+r23P3y+\ldots+r2IPIy$

$rIy=rI1P1y+rI2P2y+rI3P3y+\ldots+PIy$

Where,

r_{1y} to r_{Iy}=Coefficient of correlation between factor 1 to I and dependent character y

r_{12} to $r_{I-1,I}$=Coefficient of correlation among causal factors themselves

P_{1y} to P_{Iy}=Direct effects of characters 1 to I on character y.

2.4. *Residual effect*

Residual effect, which measures the contribution of the characters not considered was obtained as:

$(PRY)=\sqrt{1-R^2}$

Where,

$R^2=\sum_{ij}P_i{}^2Y+2\sum_{i>j}^{i\neq j}P_{iy}\ P_{jy}R_{ij}$

3. RESULTS AND DISCUSSION

3.1. *Analysis of variance*

The analysis of variance for different characters was presented in Table 2 and Plate 1. Analysis of variance revealed that the difference among 30 genotypes were highly significant for all the characters *viz.* germination percentage (41.198**), root length (14.605**), shoot length

Table 2: Analysis of variance for 12 characters among 30 genotypes of chickpea during *rabi* 2021–2022

Sl. No.	Characters	Mean sum of squares		
		Replication	Treatments	Error
1.	Germination%	2.016	41.198**	0.706
2.	Root length (cm)	0.001	14.605**	0.126
3.	Shoot length (cm)	0.014	13.954**	0.1000
4.	Days to 50% flowering	6.016	121.051**	0.292
5.	Plant height (PH) (cm)	3.630	77.338**	2.504
6.	No. of primary branches	0.065	1.009**	0.059
7.	No. of secondary branches	0.005	13.224**	0.050
8.	No. of pods plant^{-1}	0.312	419.560**	0.258
9.	No. of seeds pod^{-1}	0.303	0.095**	0.007
10.	Pod length (cm)	0.306	0.056**	0.014
11.	Seed index	0.164	21.312**	0.027
12.	Yield plant^{-1} (g)	79.180	60.764**	1.733

Level of significance at (p=0.05)

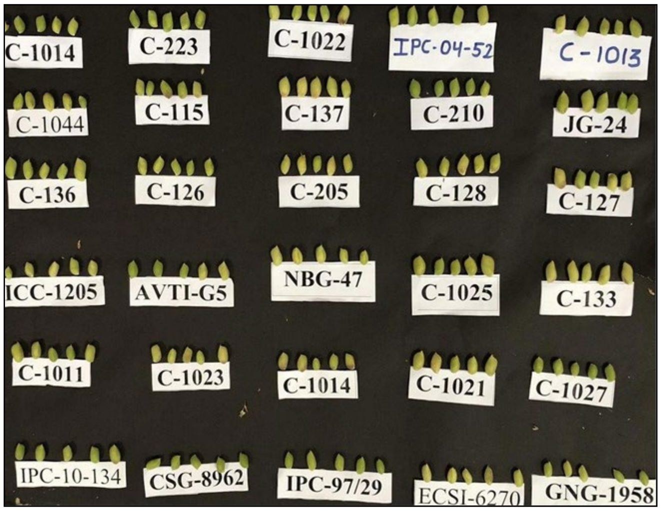

Plate 1: Variation in pod length, pod shape and pod colour among 30 genotypes of chickpea

(13.954**), days to 50% flowering (121.051**), plant height (77.338**), number of primary branches (1.009**), number of secondary branches (13.224**), number of pods plant^{-1} (419.560**), number of seeds pod^{-1} (0.095**), pod length(0.056**), seed index (21.312**) and yield plant^{-1} (60.764**).

3.2. Phenotypic and genotypic coefficient of variation

Magnitude of genetic variability in a gene pool is the pre-requisite of a breeding programme. Variability measures the genotypic variance phenotypic variance, genotypes co-efficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability the broad sense (H) are expected genetic advance at 5% selection index (GA) for grain yield and other attributing characters. The estimations are explained here as under Estimation of Phenotypic and Genotypic Coefficient of Variation. The Estimates of Phenotypic Coefficient of Variation (PCV) for all the 12 character were found to be higher than the Estimates of Genotypic Coefficient of Variation (GCV) Table 3, indicating the influence of environment on the expression of these characters which was also reported by Raju et al. (2017), Mohammed et al. (2019).

Table 3: Estimates of PCV, GCV and ECV for 12 characters in 30 chickpea genotypes

Sl. No.	Characters	PCV	GCV	ECV
1.	Germination %	5.04	4.95	0.92
2.	Root length	51.61	51.16	6.75
3.	Shoot length	108.31	107.53	12.93
4.	Days to 50% flowering	8.54	8.52	0.59
5.	Plant height	9.62	9.32	2.41
6.	No. of primary branches	22.41	21.11	7.50
7.	No. of secondary branches	20.50	20.43	1.79
8.	No. of pods plant^{-1}	17.49	17.48	0.61
9.	No. of seeds pod^{-1}	12.24	11.38	4.52
10.	Pod length	9.46	7.22	6.12
11.	Seed index	19.23	19.21	0.97
12.	Yield plant^{-1}	21.79	21.14	5.25

As per the data displayed in the Table 4 and Plate 2 it is clearly visible that there is nominal difference between PCV and GCV in the characters root length, days to 50% flowering, number of secondary branches, number of pod plant^{-1}, seed index and yield plant^{-1}, indicating very small Environment Coefficient of Variation (ECV) for this character. PCV and GCV values more than 20% are consider to be high, values between 10–20% as medium and values less than 10% low Sivasubramanian and Menon (1973). Highest value of PCV and GCV (108.31 and 107.5) was recorded in the character shoot length followed by root length (51.61 and 51.16), number of primary branches (22.4 and 21.11), yield plant^{-1} (21.79 and 21.14) and number of secondary branches (20.50 and 20. 43), indicating the presence of wide variability among the genotypes studied for these traits, on the other hand character such as germination percentage (5.04 and 4.95), days to 50% flowering (8.54 and 8.52), pod length. (9.46 and 7.22) and plant height (9.62 and 9.32) showed low

Table 4: Estimates of heritability and genetic advance as percent mean for 12 character in 30 chickpea genotypes

Sl. No.	Characters	H^2 (bs) %	GA (%)	GAM (%)
1.	Germination %	96.63	9.11	10.04
2.	Root length	98.29	5.50	104.50
3.	Shoot length	98.57	5.38	219.94
4.	Days to 50% flowering	99.52	15.97	17.51
5.	Plant height	93.73	12.20	18.59
6.	No. of primary branches	88.80	1.34	41.00
7.	No. of secondary branches	99.23	5.27	41.93
8.	No. of pods plant^{-1}	99.80	29.80	35.98
9.	No. of seeds pod^{-1}	86.30	0.40	21.79
10.	Pod length	58.20	0.23	11.36
11.	Seed index	99.70	6.71	39.52
12.	Yield plant^{-1}	94.10	10.81	42.27

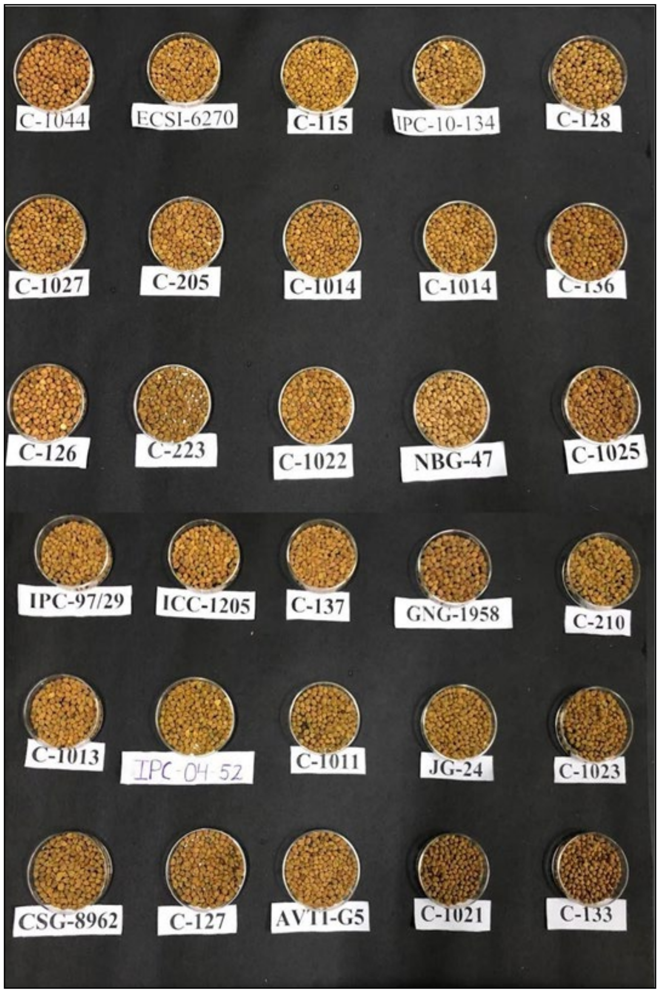

Plate 2: Variation in seed shape, size and colour among 30 genotypes of chickpea

level of PCV and GCV signifying very limited scope for future genetic improvement through selection.

The trait seed index (19.23 and 19.21), number of pod plant^{-1} (17.79 and 17.48), number of seed pod^{-1} (12.24 and 11.38) showed moderate magnitude of PCV and GCV indicating medium variability for these traits in the genotype present under study. This finding is in conformity with finding of Jayalakshmi et al. (2018) for shoot length, root length, yield plant^{-1}. Banik et al. (2018), Mohammed et al. (2019), Thonta et al. (2023), also reported similar trend of moderate magnitude of PCV and GCV for days to 50% flowering, plant height, pod length and germination percent.

3.3. Heritability

Heritability measures the possibility of joint transmission of two characters in two correlated characters through selection of one character. It is measures of the relationship between parents and progeny and has been widely used to assess the degree to which a character may be transmitted from parent to progeny. It also indicates the relative importance of heritability and environment in the expression of character.

3.3.1. Heritability (broad sense) and genetic advance as percent of mean

High heritability in broad sense estimated was observed in Table 4 for the characters *viz.* number of pods plant^{-1} (98%), seed index (99.7%), days to 50% flowering (99.52%), number of secondary branches (99.23%), shoot length (98.57%.), root length (98.29%) germination percent (96.93%), yield plant^{-1} (94.1%) and plant height (93.73%) and thus indicated by the presence of total genetic variance with fixable and non-fixable variance. Moderate heritability estimates were recorded for number of primary branches (88.8%), number of seed pod^{-1} (86.3%) and pod length (58.2%). Desai et al. (2015), Raju et al. (2017), Banik et al. (2018) and Singh et al. (2018) for number of primary branches also reported similar findings.

Genetic advance as per cent of mean was high for shoot length (219. 94%) followed by root length (104.50%), yield plant^{-1} (42.27%), number of secondary branches (41.92%) and number of primary branches (40.99%) thus showed that these characters were governed by Additive gene and selection will be rewarding for improvement of this character. The trend of the result was similar as reported by Saleem et al. (2005), Yucel et al. (2006), Atta et al. (2008) and Singh et al. (2024).

Low genetic advance as percent of mean was observed for the characters germination percent (10.04%), pod length (11.36%) and days to 50% flowering (17.51%) indicating that non-additive genes govern these characters. Raju et al. (2017) and Singh et al. (2018) reported similar trend for higher germination percent. Singh et al. (2018) reported this for days to 50% flowering. Jayalakshmi et al. (2018) reported similar trend for the character pod length.

3.4. Correlation studies

Correlation is a statistical measure, which is used to find out the degree and diversion of relationship between the grain yield with other characters was estimated by phenotypic and genotypic correlation coefficients which are discussed in Table 5 and Table 6 respectively. The knowledge regarding relative contribution of individual traits to yield may be accomplished by correlation studies.

The character germination percentage displayed a positive correlation at both phenotypic and genotypic levels for the character root length (rp: 0.401, rg: 0.408) on the other

Table 5: Estimates of phenotypic correlation coefficient between yield plant^{-1} and its attributes traits in 30 chickpea genotypes

	Ger %	RL	SL	DTF	PH	NPB	NSB	NPP	NSP	PL	SI	YPP
Ger %	1											
RL	0.401**	1										
SL	0.247$^{\text{NS}}$	-0.125$^{\text{NS}}$	1									
DTF	0.181$^{\text{NS}}$	0.120$^{\text{NS}}$	-0.152$^{\text{NS}}$	1								
PH	-0.291*	0.181$^{\text{NS}}$	-0.091$^{\text{NS}}$	-0.110$^{\text{NS}}$	1							
NPB	-0.263*	-0.002$^{\text{NS}}$	-0.174$^{\text{NS}}$	-0.084$^{\text{NS}}$	0.156$^{\text{NS}}$	1						
NSB	-0.169$^{\text{NS}}$	0.003$^{\text{NS}}$	-0.256*	0.277*	0.054$^{\text{NS}}$	0.639**	1					
NPP	-0.109$^{\text{NS}}$	-0.097$^{\text{NS}}$	-0.330*	0.173$^{\text{NS}}$	-0.225$^{\text{NS}}$	0.529**	0.592**	1				
NSP	-0.151$^{\text{NS}}$	0.205$^{\text{NS}}$	0.267*	-0.139$^{\text{NS}}$	0.444**	0.053$^{\text{NS}}$	0.095$^{\text{NS}}$	-0.101$^{\text{NS}}$	1			
PL	-0.190$^{\text{NS}}$	0.062$^{\text{NS}}$	-0.392**	-0.063$^{\text{NS}}$	0.140$^{\text{NS}}$	0.248$^{\text{NS}}$	0.030$^{\text{NS}}$	0.228$^{\text{NS}}$	0.089$^{\text{NS}}$	1		
SI	-0.136$^{\text{NS}}$	-0.133$^{\text{NS}}$	-0.148$^{\text{NS}}$	-0.224$^{\text{NS}}$	-0.018$^{\text{NS}}$	-0.094$^{\text{NS}}$	-0.178$^{\text{NS}}$	-0.191$^{\text{NS}}$	-0.331**	0.023$^{\text{NS}}$	1	
YPP	-0.269*	-0.042$^{\text{NS}}$	-0.210$^{\text{NS}}$	-0.131$^{\text{NS}}$	0.073$^{\text{NS}}$	0.366**	0.364**	0.561**	0.237$^{\text{NS}}$	0.219$^{\text{NS}}$	0.484**	1

Ger %: Germination percentage; RL: Root length; SL: shoot length; DTF: Days to 50% flowering; PH: Plant height; NPB: No. of primary branches; NSB: No. of secondary branches; NPP: No. of pods plant^{-1}; NSP: No. of seeds pod^{-1}; PL: Pod length; SI: Seed index; YPP: Yield plant^{-1}

Table 6: Estimates of genotypic correlation coefficient between yield per plant and its attributes traits in 30 chickpea genotypes

	Ger%	RL	SL	DTF	PH	NPB	NSB	NPP	NSP	PL	SI	YPP
Ger %	1											
RL	0.408**	1										
SL	0.252$^{\text{NS}}$	-0.124$^{\text{NS}}$	1									
DTF	0.184$^{\text{NS}}$	0.122$^{\text{NS}}$	-0.152$^{\text{NS}}$	1								
PH	-0.299*	0.196$^{\text{NS}}$	-0.107$^{\text{NS}}$	-0.111$^{\text{NS}}$	1							
NPB	-0.248$^{\text{NS}}$	0.007$^{\text{NS}}$	-0.180$^{\text{NS}}$	-0.091$^{\text{NS}}$	0.185$^{\text{NS}}$	1						
NSB	-0.164$^{\text{NS}}$	0.005$^{\text{NS}}$	-0.255*	0.279*	0.059$^{\text{NS}}$	0.658**	1					
NPP	-0.110$^{\text{NS}}$	-0.097$^{\text{NS}}$	-0.332**	0.174$^{\text{NS}}$	-0.232$^{\text{NS}}$	0.555**	0.593**	1				
NSP	-0.172$^{\text{NS}}$	0.223$^{\text{NS}}$	0.276*	-0.148$^{\text{NS}}$	0.483**	0.062$^{\text{NS}}$	0.098$^{\text{NS}}$	-0.110$^{\text{NS}}$	1			
PL	-0.240$^{\text{NS}}$	0.066$^{\text{NS}}$	-0.497**	-0.081$^{\text{NS}}$	0.228$^{\text{NS}}$	0.277*	0.023$^{\text{NS}}$	0.296*	0.166$^{\text{NS}}$	1		
SI	-0.137$^{\text{NS}}$	-0.133$^{\text{NS}}$	-0.150$^{\text{NS}}$	-0.225$^{\text{NS}}$	-0.017$^{\text{NS}}$	-0.112$^{\text{NS}}$	-0.182$^{\text{NS}}$	-0.192$^{\text{NS}}$	-0.360**	0.016$^{\text{NS}}$	1	
YPP	-0.284*	-0.040$^{\text{NS}}$	-0.227$^{\text{NS}}$	-0.132$^{\text{NS}}$	0.071$^{\text{NS}}$	0.392**	0.371**	0.576**	0.172$^{\text{NS}}$	0.306*	0.495**	1

Ger %: Germination percentage; RL: Root length; SL: shoot length; DTF: Days to 50% flowering; PH: Plant height; NPB: No. of primary branches; NSB: No. of secondary branches; NPP: No. of pods plant^{-1}; NSP: No. of seeds pod^{-1}; PL: Pod length; SI: Seed index; YPP: Yield plant^{-1}

hand shoot length and days to 50% flowering showed non-significant positive correlation and other characters displayed negative correlation with germination percentage.

The character days to 50% flowering displayed a positive correlation at both phenotypic and genotypic levels. The character number of secondary branches (r_p: 0.277, r_g: 0.279) and number pod plant^{-1} showed a non-significant positive correlation on the other characterrevealed non-significant negative correlation with days to 50% flowering. Akhtar et al. (2011), Gohil et al. (2010) and Gaikwad et al. (2011), observed similar Trend of correlation for the character days to 50% flowering with number of secondary branches and number of pods plant^{-1}. The character plant height displayed a positive correlation at both phenotypic and genotypic levels for the character number of seeds pod^{-1} (r_p: 0.444, r_g: 0.483) on other hand number of primary branches, number of secondary branches, pod length, yield plant^{-1} showed non-significant positive correlation. Other character showed non-significant negative correlation with plant height. Akhtar et al. (2011) have worked in the coincidence with the present finding for the character plant height.

The character number of primary branches showed a positive correlation at both phenotypic and genotypic levels for the character number of secondary branches (rp: 0.639, rg: 0.658), number of pod plant^{-1} (rp: 0.529, rg: 0.555), yield plant^{-1} (rp: 0.366, rg: 0.392) on the other hand number of seeds pod^{-1} and pod length showed non-significant positive correlation. Seed index was non-significantly negatively correlation with number of primary branches. Similar trend of correlation was observed by Akhtar et al. (2011), Kumar et al. (2023) for the character number ofprimary branches with number of secondary branches, number of pods plant^{-1} and yield plant^{-1}.

The character number of secondary branches showed a positive correlation at both phenotypicand genotypic levels for the character number of pod plant^{-1} (r_p: 0.592, r_g: 0.593) and yield plant^{-1} (r_p: 0.364, r_g: 0.371). Number of seeds pod^{-1} and pod length showed non-significantpositive correlation. Seed index shows non-significant negative correlation with number of secondary branches. Malik et al., (2010), reported similar trend finding. The character number of pod plant^{-1} showed a positive correlation at both phenotypic and genotypic levels for the character yield plant^{-1} (rp: 0.561, rg: 0.576) and in phenotypic correlation, pod length displayed non-significant positive correlation whereas genotypic correlation pod length showed positive correlation. Other character showed non significant negative correlation. Bicer and sarkar (2008), Ali et al. (2011) and Babber et al. (2012) produced similar finding for the character number of pods plant^{-1} with yield plant^{-1}.

The character number of seeds plant^{-1} showed a non-significant positive correlation at both phenotypic and genotypic levels for the character pod length and yield plant^{-1} and seed index showed significantly negative correlation. Bicer and sarkar (2008), Ali et al. (2011) and Babber et al. (2012) produced similar finding for the character number of seed plant^{-1}. The character pod length showed a non-significant positive correlation at both phenotypic and genotypic levels for the character seed index and in phenotypic correlation yield plant^{-1} displayed

Table 7: Estimates of direct and indirect effects between yield plant^{-1} and its attributes traits in 30 chickpea genotypes at phenotypic level

	Ger %	RL	SL	DTF	PH	NPB	NSB	NPP	NSP	PL	SI
Ger %	0.005	0.010	0.001	0.001	-0.003	-0.005	0.005	-0.088	-0.089	0.007	-0.114
RL	0.002	0.025	-0.001	0.0005	0.002	-0.00004	-0.0001	-0.078	0.121	-0.002	-0.111
SL	0.001	-0.003	0.004	-0.001	-0.001	-0.003	0.007	-0.264	0.158	0.015	-0.124
DTF	0.001	0.003	-0.001	0.004	-0.001	-0.002	-0.008	0.139	-0.082	0.002	-0.187
PH	-0.002	0.005	-0.0004	-0.0005	0.009	0.003	-0.002	-0.180	0.262	-0.005	-0.015
NPB	-0.001	-0.0001	-0.001	-0.0003	0.001	0.018	-0.018	0.424	0.031	-0.010	-0.079
NSB	-0.001	0.00007	-0.001	0.001	0.0005	0.012	-0.028	0.475	0.056	-0.001	-0.149
NPP	-0.001	-0.002	-0.001	0.001	-0.002	0.010	-0.017	0.801	-0.060	-0.009	-0.159
NSP	-0.001	0.005	0.001	-0.001	0.004	0.001	-0.003	-0.081	0.591	-0.003	-0.276
PL	-0.001	0.002	-0.002	-0.0003	0.001	0.005	-0.001	0.183	0.053	-0.039	0.020
SI	-0.001	-0.003	-0.001	-0.001	-0.0002	-0.002	0.005	-0.153	-0.195	-0.001	0.836

Ger %: Germination percentage; RL: Root length; SL: shoot length; DTF: Days to 50% flowering; PH: Plant height; NPB: No. of primary branches; NSB: No. of secondary branches; NPP: No. of pods plant^{-1}; NSP: No. of seeds pod^{-1}; PL: Pod length; SI: Seed index non-significant positive correlation where as genotypic correlation yield plant^{-1} showed significant positive correlation. Similar finding for the present character were observed also reported by Sanjay et al. (2019). Pod length showed a positive correlation at both phenotypic and genotypic levels for the character yield plant^{-1} (rp: 0.484, rg: 0.495). Similar trend of correlation was also observed by Gohil et al. (2010), Tutlani et al. (2023), Garikwad et al. (2011) for the character seed index with yield plant^{-1}.

3.5. *Path coefficient analysis*

Simple correlation does not provide the adequate information about the contribution of each factor towards yield. Therefore, the technique of path coefficient analysis is utilized to have a direct and indirect contribution of a trait towards the yield the end product. The results by the path coefficient analysis are presented in Table 7 and 8, Figure 1 and 2. The earlier studies for direct effect on yield plant^{-1}. With all the independent character under study *viz.*, germination percentage, root length, shoot length, days to 50% flowering, plant height, number of primary branches, number of secondary branches, number pod plant^{-1}, no. of seeds plant^{-1}, pod length, seed index. Were in agreement with the studies reported by Tadessa et al. (2016), Thonta et al. (2023), Naveed et al. (2012), Babber and Patel (2005) found positive indirect effect on pod length and seed index.

Table 8: Estimates of direct and indirect effects between yield plant^{-1} and its attributes traits in 30 chickpea genotypes at genotypic level

	Ger %	RL	SL	DTF	PH	NPB	NSB	NPP	NSP	PL	SI
Ger %	0.013	0.006	-0.010	0.004	0.002	-0.016	0.012	-0.092	-0.105	0.020	-0.119
RL	0.005	0.014	0.005	0.002	-0.001	0.0004	-0.0004	-0.080	0.136	-0.006	-0.116
SL	0.003	-0.002	-0.038	-0.003	0.001	-0.011	0.019	-0.275	0.168	0.042	-0.130
DTF	0.002	0.002	0.006	0.020	0.001	-0.006	-0.021	0.144	-0.090	0.007	-0.196
PH	-0.004	0.003	0.004	-0.002	-0.006	0.012	-0.004	-0.192	0.294	-0.019	-0.015
NPB	-0.003	0.0001	0.007	-0.002	-0.001	0.063	-0.050	0.460	0.038	-0.023	-0.097
NSB	-0.002	0.0001	0.010	0.005	-0.0003	0.041	-0.075	0.492	0.060	-0.002	-0.158
NPP	-0.001	-0.001	0.013	0.003	0.001	0.035	-0.045	0.830	-0.067	-0.025	-0.167
NSP	-0.002	0.003	-0.010	-0.003	-0.003	0.004	-0.007	-0.091	0.610	-0.014	-0.314
PL	-0.003	0.001	0.019	-0.002	-0.001	0.017	-0.002	0.246	0.101	-0.084	0.014
SI	-0.002	-0.002	0.006	-0.004	0.0001	-0.007	0.014	-0.159	-0.220	-0.001	0.871

Ger %: Germination percentage; RL: Root length; SL: shoot length; DTF: Days to 50% flowering; PH: Plant height; NPB: No. of primary branches; NSB: No. of secondary branches; NPP: No. of pods plant^{-1}; NSP: No. of seeds pod^{-1}; PL: Pod length; SI: Seed index

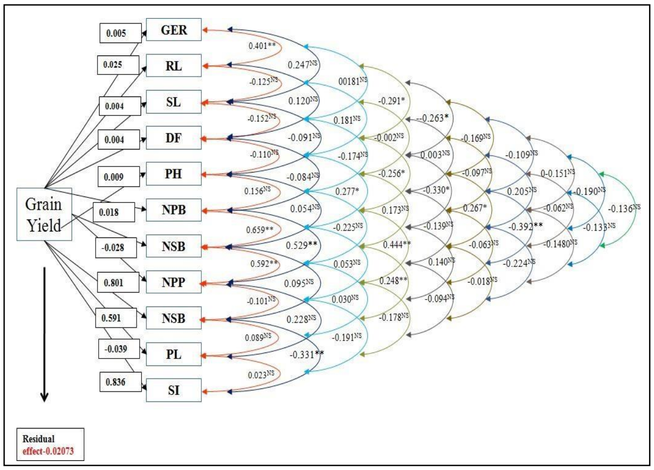

Figure 1: Estimates of direct and indirect effects between yield plant^{-1} and its attributes traits in 30 chickpea genotypes at phenotypic level

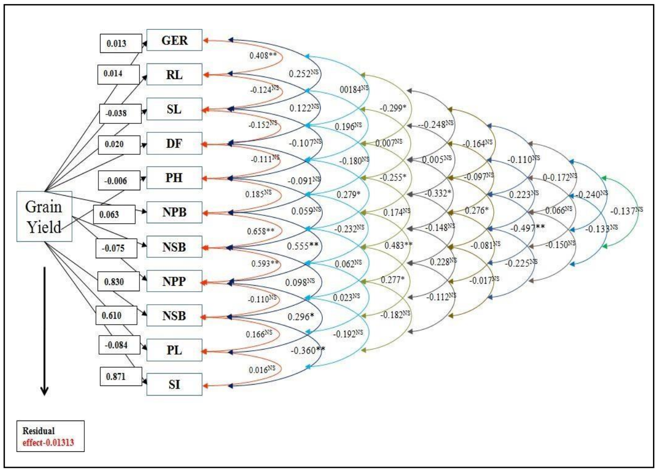

Figure 2: Estimates of direct and indirect effects between yield plant^{-1} and its attributes traits in 30 chickpea genotypes at genotypic level

4. CONCLUSION

High estimates of PCV and GCV indicates significant variability among 30 genotypes under study. High genetic advance coupled with high heritability indicating additive gene action, which makes selection conducive for such traits. Selection will prove high degree of improvement under such condition were the correlation of the dependent character is significantly positive with independent traits *viz.,* number primary branches, number of secondary branches, number of pods plant^{-1}, number of seeds pod^{-1} and seed index.

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