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Deciphering Chickpea Breeding Lines through Genetic Potential and Trait Association Analysis

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ABSTRACT

Exploring the genetic potential of chickpeas is imperative for strategic parent selection, targeted hybridization, and effective trait integration, resulting in development of resilient and high-yielding varieties. Hence, the current study aims to uncover the genetic potential and character associations of advanced breeding lines in chickpea, conducted at the Seed Breeding Farm, Department of Plant Breeding and Genetics, JNKVV, Jabalpur during the *rabi* season of 2021-22. The assessment of forty advanced chickpea breeding lines encompassed an analysis of genetic parameters, correlation, and path coefficients. The findings unveiled that, across all observed traits, the phenotypic coefficient of variation (PCV %) exceeded the genotypic coefficient of variation (GCV %). The examination of genetic potential, utilizing phenotypic and genotypic coefficients of variability, heritability, genetic advance, and genetic gain, demonstrates a significant degree of variability within the genotypes for traits including total number of pods per plant, number of effective pods per plant, biological yield per plant, and seed yield per plant. The seed yield per plant exhibited high positive and direct effect and significant positive correlation with biological yield per plant and total number of pods per plant. Consequently, prioritizing these traits in future breeding programs could lead to the development of chickpea varieties with enhanced yield potential.

Key words: *Association, Chickpea, Path, Variability, Yield*

Introduction

Chickpea (*Cicer arietinum* L.) is a significant pulse crop belongs to family *Leguminosae*. It is widely recognized by various names including Gram, Chana, Garbanzo bean, Egyptian pea, Bengal gram, Hommes, Hamaz, Shimbra and Nohud and Loblebi. Originating in Southeastern Turkey, chickpea was later introduced to India. It is grown in temperate as well as subtropical regions across the globe. In India, it constitutes a significant 70 percent of the cultivated *rabi* pulses. The major states in India for chickpea cultivation include Madhya Pradesh, Rajasthan, Andhra Pradesh, Bihar, Uttar Pradesh, Maharashtra, Haryana, and Karnataka. In India, chickpea is cultivated approximately 11.20 million hectares of area, resulting in an annual production of 13.98 million metric tons and an average productivity of 1249 kg/ha. The primary districts for chickpea cultivation in Madhya Pradesh are Sagar, Raisen, Narsinghpur, Ujjain, Dewas, Ashok Nagar, Damoh, Rajgarh, Sehore, Shajapur, Chhatarpur,

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Guna, Dhar, and Panna. Madhya Pradesh encompasses a chickpea cultivation area of 2.80 million hectares, yielding a production of 3.61 million metric tons, and achieving a productivity rate of 1291 kg/ha (Annual Report, DPD 2021-22).

Adequate genetic variability is crucial for successful crop improvement (Arshad *et al.*, 2013). Therefore, it is imperative for a plant breeder to quantitatively measure this variability through genetic parameters like GCV, PCV, heritability and genetic advance. Studying seed yield directly can be challenging due to its low heritability. Relying solely on yield for selection of parent can be misleading. Understanding the relationship between yield and contributing traits is crucial for efficient selection and developing economically superior varieties. Correlation analysis for seed yield assesses the relationship between traits, offering insights for effective selection based on yield and its component (Yucel *et al*., 2006). Path coefficient analysis, a statistical tool, precisely quantifies direct and indirect effects of traits on yield, providing deeper insights in cases with multiple factors, surpassing traditional correlations. Path coefficient analysis elucidates direct trait effects and their indirect contributions through other characters (Singh *et al*. 1990). Knowledge of correlation and path coefficient analysis is indispensable for plant breeders in devising a proficient selection program and developing genotypes with enhanced yield potential. Hence, this study aims to unravel the genetic variability, assess character associations, and conduct path coefficient analysis in advanced chickpea breeding lines.

Materials and Method

During the *rabi* season of 2021-22, forty chickpea advanced breeding lines were planted in a randomized block design with three replications at Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur. Each genotype was allocated in a four-row plot, each with a length of 4.0 meters and a plant-to-plant spacing of 30.0×10.0 cm. In each replication, the genotypes were allocated randomly to individual plots. All advised agronomic cultivation practices were diligently followed to ensure the successful growth of the crop. Observations were recorded based on data gathered from five randomly selected plants per replication for fourteen traits, including plant height (PH), height of the first fruiting node (HFFN), stem thickness (ST), number of primary branches per plant (NPBPP), number of secondary branches per plant (NSBPP), total number of pods per plant (TNPPP), number of effective pods per plant (NEPPP), number of seeds per pod (NSPP), hundred seed weight (HSW), biological yield per plant (BY), harvest index (HI), and seed yield per plant (SYPP), with the exception of days to 50% flowering(DFF) and days to maturity (DTM), which were noted on a per-plot basis. The phenotypic and genotypic coefficient of variation was calculated using the methodology proposed by Burton and De Vane (1953). Heritability (bs) and genetic advance were computed based on the procedures outlined by Hanson *et al.* (1956) and Johnson *et al.* (1955) respectively. Correlation was determined following the methodologies of Miller *et al.* (1958), while path coefficient analysis was conducted according to the approaches of Dewey and Lu (1959) and Wright (1921). The statistical analysis of data was conducted utilizing R software, version 4.3.

Results and Discussion

Estimates of genetic variability

Table 1 and Figure 1 displays the computed values for the mean, range, GCV (%), PCV (%), ECV (%), heritability (bs), genetic advance, and genetic advance as a percentage of the mean for fourteen distinct traits under investigation. The magnitude of the phenotypic coefficient of variation (PCV %) surpassed the genotypic coefficient of variation (GCV%) for all the observed traits. The highest genotypic and phenotypic coefficient of variation were observed for number of effective pods per plant (33.8% and 38.9%), total number of pods per plant (31.8% and 36.6%), seed yield per plant (27.7% and 30%), and biological yield per plant (28% and 29.8%). In contrast, the lowest genotypic coefficient of variation was found for days to maturity (4.7% and 5.1%), followed by plant height (8.0% and 8.8%) and days to 50% flowering (10.1% and 10.8%). The results were consistent with the findings reported in the studies conducted by Awasthi *et al.* (2017), Upadhyay *et al.* (2022), Vikram *et al.* (2022) and Ningwal *et al.* (2023). The number of effective pods per plant exhibited the highest environmental coefficient of variation (19.3%), whereas days to maturity displayed the lowest (2.0%). The heritability in broad sense ranged from 58.4% to 95.6% across the traits. The highest heritability values were observed for hundred seed weight (95.6%), stem thickness (90.4%), biological yield (87.0%), and days to 50% flowering (84.4%). These findings indicate that a significant portion of the observed phenotypic variation for these traits can be attributed to genetic factors, with less influence from environmental conditions. Likewise, the range of genetic advance as a percentage of the mean extended from 9.0% to 60.5%. The traits that exhibited notably high values of genetic advance as a percentage of the mean included number of effective pods per plant (60.5%), total number of pods per plant (56.9%), biological yield per plant (54.4%), and seed yield per plant (52.7%). Conversely, days to maturity (9.0%), plant height (15.0%), and days to 50% flowering (19.4%) displayed lower value. The traits encompassing total number of pods per plant, number of effective pods per plant, biological yield per plant, and seed yield per plant displayed a distinctive combination of high GCV, substantial heritability, and significant genetic advance as a percentage of the mean. This signifies the presence of abundant variability within the population for these traits, predominantly driven by additive gene action. Consequently, these characteristics emerge as pivotal genetic parameters for the enhancement and selection of high-yielding genotypes. The outcomes resonated with the investigations carried out by Stuti and Babbar (2014), Jakhar *et al.* (2016), Awasthi *et al.* (2017), Gautam *et al.* (2021), Singh *et al.* (2021), Kumawat *et al.* (2021),

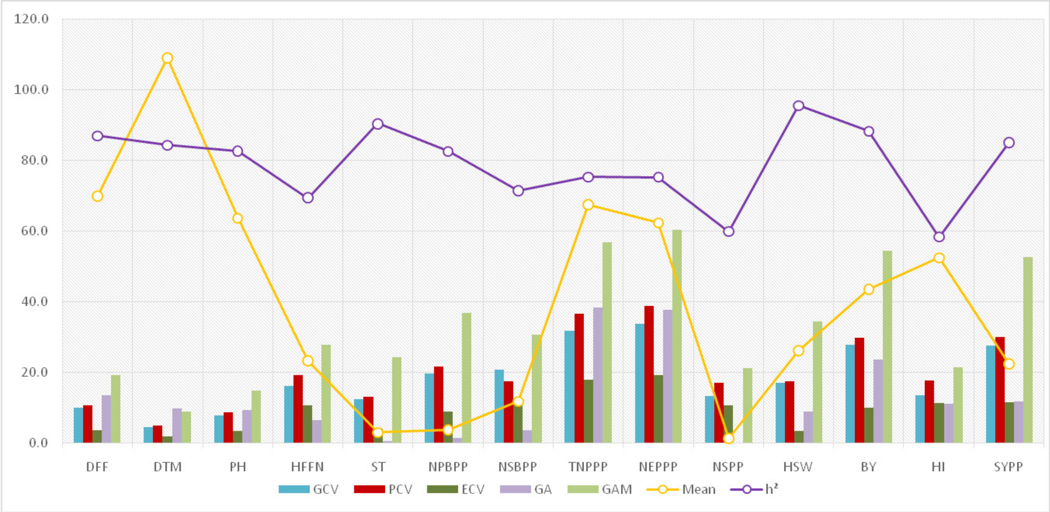

Fig. 1. Graphical representation of genetic variability for quantitative traits in advanced breeding lines of chickpea

Table 1. Genetic factor of variation for yield and its attributing traits in the advanced breeding lines of chickpea

Characters	Mean	Range		GCV (%)	PCV (%)	ECV (%)	h^2 (bs) (%)	GA at 5%	GAM at 5%
		Min.	Max.						
DFF	70.0	49.0	81.0	10.1	10.8	3.8	87.0	13.6	19.4
DTM	109.1	96.0	125.0	4.7	5.1	2.0	84.4	9.8	9.0
PH	63.7	50.0	73.0	8.0	8.8	3.6	82.7	9.5	15.0
HFFN	23.4	13.3	32.4	16.2	19.4	10.7	69.4	6.5	27.8
ST	3.05	2.0	3.6	12.4	13.0	4.0	90.4	0.74	24.4
NPBPP	3.8	2.0	5.45	19.6	21.6	9.0	82.6	1.4	36.8
NSBPP	11.8	5.0	15.8	20.8	17.6	11.1	71.4	3.6	30.7
TNPPP	67.5	27.0	139.0	31.8	36.6	18.1	75.4	38.4	56.9
NEPPP	62.4	19.0	125.0	33.8	38.9	19.3	75.3	37.7	60.5
NSPP	1.37	1.0	1.9	13.3	17.2	10.8	59.9	0.2	21.2
HSW	26.2	15.9	37.4	17.1	17.5	3.6	95.6	9.0	34.5
BY	43.6	17.6	69.3	28.0	29.8	10.1	88.4	23.7	54.4
HI	52.5	33.5	77.1	13.7	17.9	11.5	58.4	11.3	21.6
SYPP	22.5	10.0	36.4	27.7	30.0	11.6	85.1	11.9	52.7

Ram *et al.* (2021), and Xalxo *et al.* (2021).

Character association

Table 2 and Figure 2 display the phenotypic correlation coefficients for all the examined traits. Seed yield per plant demonstrated a strong significant positive correlation with biological yield per plant (r= 0.8388) followed by total number of pods per plant (r= 0.8053), number of effective pods per plant (r= 0.7902), number of secondary branches per plant (r= 0.6494), hundred seed weight (r= 0.4419), days to maturity (r= 0.3828), days to 50% flowering (r= 0.3488) and harvest index (r= 0.2547). However, it had a significant negative correlation with height of the first fruiting node (r = -0.3114). The results were in accordance with the findings of Jakhar *et al.* (2016), Bhanu *et al.* (2017), Kumawat *et al.* (2021) and Meena *et al.* (2021). Days to 50% flowering displayed a strong and significant positive correlation with days to maturity (r= 0.505) and hundred seed weight (r= 0.332). It also exhibited a significant negative correlation with number of seeds per pod (r= -0.230). Days to maturity showed significant positive correlations with biological yield per plant (r= 0.453) and number of secondary branches per plant (r= 0.358). Conversely, it is significantly negatively correlated with height of first fruiting node (r= -0.435) and number of seeds per pod (r= -0.239). Plant height showed a significant and positive correlation with stem thickness (r= 0.427) and hundred seed weight (r= 0.381). On the other hand, it exhib-

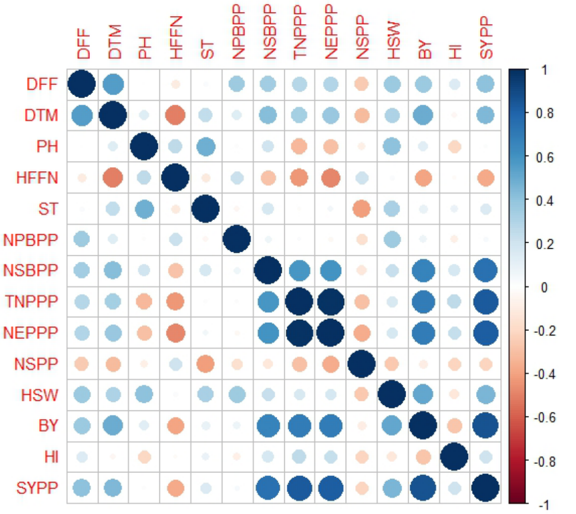

Fig. 2. Correlation for seed yield and its attributing traits in the advanced breeding lines of chickpea

Table 2. Phenotypic correlation coefficients among 14 quantitative traits in the advanced breeding lines of chickpea

	DFF	DTM	PH	HFFN	ST	NPBPP	NSBPP	TNPPP	NEPPP	NSPP	HSW	BY	HI	SYPP
DFF	1.000	0.505**	0.003	-0.093	0.025	0.305**	0.325**	0.246**	0.256**	-0.230*	0.332**	0.322**	0.116	0.3488 **
DTM		1.000	0.107	-0.435**	0.213*	0.146	0.358**	0.290**	0.315**	-0.239**	0.301**	0.453**	-0.062	0.3828 **
PH			1.000	0.328**	0.427**	0.010	0.203*	-0.269**	-0.247**	-0.051	0.381**	0.117	-0.154	0.0276
HFFN				1.000	-0.102	0.187*	-0.177	-0.337**	-0.387**	0.180*	0.024	-0.337**	-0.011	-0.3114 **
ST					1.000	-0.053	0.170	-0.001	0.054	-0.369**	0.306**	0.087	0.083	0.1504
NPBPP						1.000	0.064	0.048	-0.004	-0.128	0.328**	0.064	-0.038	0.0406
NSBPP							1.000	0.521**	0.501**	-0.074	0.206*	0.577**	0.158	0.6494 **
TNPPP								1.000	0.967**	-0.246 **	0.156	0.647**	0.2584 **	0.8053 **
NEPPP									1.000	-0.349**	0.164	0.642**	0.2509 **	0.7902 **
NSPP										1.000	-0.231*	-0.041	-0.2154 *	-0.1568
HSW											1.000	0.486**	-0.076	0.4419 **
BY												1.000	-0.2883 **	0.8388 **
HI													1.000	0.2547 **
SYPP														1.000

**** Significant at 5%, ***highly significant at 1%**

Where, DTF: Days to 50% flowering, DTM: Days to maturity, PH: Plant height, HFFN: Height of first fruiting node, ST: Stem thickness, NPBPP: Number of primary branches per plant, NSBPP: Number of secondary branches per plant, TNPPP: Total number of pods per plant, NEPPP: Number of effective pods per plant, NSPP: Number of seeds per pod, HSW: Hundred seed weight, BY: Biological yield per plant, HI- Harvest index, SYPP: Seed yield per plant its significant and negative correlation with total number of pods per plant (r= -0.269) and number of effective pods per plant (r= -0.247). Height of first fruiting node observed significant and positive correlation with number of primary branches per plant (r= 0.187) and number of seeds per pod (r= 0.180). Conversely, it showed significant and negative correlation with number of effective pods per plant (r = -0.387), total number of pods per plant (r = -0.337) and biological yield per plant (r = -0.337). Stem thickness exhibited a significant and positive correlation with hundred seed weight (r = 0.306) and significant and negative correlation with number of seeds per pod (r= -0.369). The number of primary branches per plant demonstrated a significant and positive correlation with hundred seed weight (r = 0.328). Number of secondary branches per plant displayed a significant and positive correlation with biological yield per plant (r = 0.577) and total number of pods per plant (r = 0.521). Total number of pods per plant recorded significant and positive correlation with number of effective pods per plant (r = 0.967) and biological yield per plant (r= 0.647). Notably, it showed a significant and negative correlation with number of seeds per pod (r = -0.246). Number of effective pods per plant expressed a significant and positive correlation with biological yield per plant (r = 0.642) and harvest index (r = 0.250). However, it exhibited a significant and negative correlation with number of seeds per pod (r = -0.349). Number of seeds per pod found a significant and negative correlation with hundred seed weight (r = -0.231) and harvest index (r = -0.215). Hundred seed weight showed a significant and positive correlation with biological yield per plant (r= 0.486). Biological yield per plant observed a significant and negative correlation with harvest index (r= 0.288).

Path coefficient analysis

The examination of path coefficient analysis demonstrated that the highest direct positive effect on seed yield per plant was exerted by biological yield per plant (1.1906), followed by harvest index (0.4944), height of the first fruiting node (0.0932), stem thickness (0.0435), and total number of pods per plant (0.0105). Similar results were also reported by Bala *et al.* (2015) and Meena *et al.* (2021) for biological yield per plant and harvest index, Bhanu *et al.* (2017), Jakhar *et al.* (2016) for pods per plant. In contrast, the number of effective pods per plant (-0.1180) showed the highest negative direct effect on seed yield per plant succeeded by plant height (-0.0857), number of seeds per pod (-0.0805), days to 50% flowering (-0.0612), hundred seed weight (-0.0472), number of primary branches per plant (-0.0122), number of secondary branches per plant (-0.0043) and days to maturity (-0.0001). The most substantial positive indirect effect was illustrated by biological yield per plant through number of effective pods per plant (0.8725) followed by total number of pods per plant (0.8616), number of secondary branches per plant (0.8529) and hundred seed

Table 3. Estimation of direct and indirect effect at genotypic level for yield attributing traits

	DFF	DTM	PH	HFFN	ST	NPBPP	NSBPP	TNPPP	NEPPP	NSPP	HSW	BY	HI	SYPP
DFF	-0.0612	-0.0001	-0.0007	-0.0104	0.0013	-0.0046	-0.0015	0.0033	-0.0379	0.0221	-0.0178	0.4587	0.0841	0.4353
DTM	-0.0360	-0.0001	-0.0125	-0.0509	0.0113	-0.0016	-0.0020	0.0039	-0.0478	0.0292	-0.0148	0.6208	-0.0203	0.4791
PH	-0.0005	0.0000	-0.0857	0.0194	0.0225	0.0004	-0.0009	-0.0037	0.0386	0.0088	-0.0199	0.1529	-0.1214	0.0107
HFFN	0.0068	0.0001	-0.0178	0.0932	-0.0052	-0.0028	0.0016	-0.0052	0.0658	-0.0184	-0.0015	-0.5158	-0.0169	-0.4162
ST	-0.0018	0.0000	-0.0444	-0.0112	0.0435	0.0005	-0.0008	-0.0003	-0.0062	0.0360	-0.0158	0.1221	0.0408	0.1622
NPBPP	-0.0233	0.0000	0.0030	0.0217	-0.0016	-0.0122	-0.0003	0.0001	0.0072	0.0151	-0.0180	0.1018	-0.0570	0.0365
NSBPP	-0.0217	-0.0001	-0.0170	-0.0344	0.0081	-0.0007	-0.0043	0.0067	-0.0774	0.0126	-0.0112	0.8529	0.0937	0.8072
TNPPP	-0.0190	-0.0001	0.0304	-0.0463	-0.0012	-0.0001	-0.0028	0.0105	-0.1170	0.0272	-0.0077	0.8616	0.1232	0.8591
NEPPP	-0.0196	-0.0001	0.0280	-0.0520	0.0023	0.0008	-0.0028	0.0104	-0.1180	0.0310	-0.0082	0.8725	0.1076	0.8538
NSPP	0.0168	0.0001	0.0094	0.0213	-0.0194	0.0023	0.0007	-0.0035	0.0455	-0.0805	0.0139	-0.1633	-0.1035	-0.2604
HSW	-0.0231	0.0000	-0.0360	0.0029	0.0145	-0.0047	-0.0010	0.0017	-0.0206	0.0237	-0.0472	0.6309	-0.0764	0.4648
BY	-0.0236	-0.0001	-0.0110	-0.0404	0.0045	-0.0010	-0.0031	0.0076	-0.0865	0.0110	-0.0250	**1.1906**	-0.1361	0.8869
HI	-0.0104	0.0000	0.0210	-0.0032	0.0036	0.0014	-0.0008	0.0026	-0.0257	0.0169	0.0073	-0.3277	**0.4944**	0.1794

Residual effect= 0.0112

Where, DTF: Days to 50% flowering, DTM: Days to maturity, PH: Plant height, HFFN: Height of first fruiting node, ST: Stem thickness, NPBPP: Number of primary branches per plant, NSBPP: Number of secondary branches per plant, TNPPP: Total number of pods per plant, NEPPP: Number of effective pods per plant, NSPP: Number of seeds per pod, HSW: Hundred seed weight, BY: Biological yield per plant, HI- Harvest index, SYPP: Seed yield per plant weight (0.6309). Conversely the most significant negative indirect effect was noted for biological yield per plant through height of first fruiting node (-0.5158), harvest index (-0.3277) and number of seeds per pod (-0.1633). The outcomes in Table 3 provide an estimation of the direct and indirect effects of various traits on seed yield per plant. At the genotypic level, the residual effect is minimal (0.0112), suggesting that the study incorporated a maximum number of independent variables concerning the dependent variable.

Conclusion

Higher genotypic coefficient of variation and heritability coupled with genetic advance as percentage of mean was observed for total number of pods per plant, number of effective pods per plant, biological yield per plant, and seed yield per plant. The seed yield per plant displayed a high positive and direct effect, along with significant positive correlation with both biological yield per plant and total number of pods per plant. Thus, emphasizing direct selection for these traits is the most effective strategy for enhancing seed yield in chickpea.

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Conflicts of interest

The authors declare that they have no conflict of interest.

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