



Exploring Variability, Character Association and Path Analysis in Chickpea (*Cicer arietinum* L.) Accessions in the Northwestern Region of India

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

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ABSTRACT

Assessing genetic variability makes it easier to identify stronger genotypes, allowing to produce high-yielding crops that are climatically resilient and promote efficient crop improvement. The present study aimed to assesses the genetic variability, association study & path analysis of 51 chickpea [*Cicer arietinum* (L.)] genotypes on 12 characteristics. The experiment utilized Randomized complete block design with three replications conducted in Phagwara, Punjab. The ANOVA recorded significant variance at the 1% level for all traits, indicating considerable variability amongst germplasm. SY expressed comparatively high Genotypic coefficient of variance and

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heritability with other traits, indicating that it is the most heritable trait and has the highest potential for improvement through selective breeding. Positive correlation with SY was revealed by PH, NPB, NSB, NPP, NFP, TW, BY, HI. Path analysis revealed that NFP had highest positive effect on SY followed by NUFP, HI, BY, NSB, TW, DFF & DM suggesting selection from any of these traits would be beneficial. When selecting traits to improve yield in chickpea through breeding, it is essential to focus on specific characteristics that directly contribute to higher production. This research will help understand yield-influencing factors for resilient chickpea varieties in Punjab environmental conditions.

Keywords: Chickpea; variability; correlation coefficient; path coefficient; environmental conditions; yield; *cicer reticulatum*; phytochemicals.

1. INTRODUCTION

Chickpea (*Cicer arietinum* L.) is a traditional grown in crop among various regions of the world for thousands of years, including in Asia and Europe. Self-pollinated, annual, cleistogamous, and diploid ($2n=16$) grain legume crop that can grow in diverse environments belonging to genus *Cicer* and Fabaceae family. There are a total of 9 annual and 35 perennial species known for chickpea Van der Maesen et al., [1]. Cultivated chickpea's wild progenitor is believed to be *Cicer reticulatum*, confirmed by electrophoresis of seed protein, and the centre of origin for the crop is thought to be Southeastern Turkey, according to Ladizinsky & Adler [2]. It is a major cold season pulse crop in India, during 2022-23, a domestic produce of 13.75 million tonnes in 10.91 million ha. with a productivity of 12.6 q./ha [3]. The crop is primarily cultivated under rainfed conditions on marginal lands, with almost 90% of the crop being grown in this way Koul et al., [4]. Cultivated chickpeas are classified into two main classes, Desi, and Kabuli, with Kabuli seeds being larger, cream-colored, less fibrous, and more desired for food purposes Huntrods [5]. In addition to being a healthy source of minerals, vitamins, fiber (18–20%), proteins (12.02–24.91%), and carbohydrates (52.61–67.66%), chickpeas also include phytochemicals that may be healthful Yegrem [6]. Understanding the genetic variability is important for the development of improved cultivars. Genetic variability allows breeders to select parents with desirable traits and to create new hybrid varieties that combine desirable traits from different parental lines. By analysing the genetic variability of different chickpea varieties, breeders can also identify unique genes and alleles that are important for crop improvement, such as genes that confer resistance to pests or diseases or genes that improve yield or quality, Bhandari et al., [7]. This information can be used to develop new breeding strategies and to guide the development of new chickpea varieties that

are adapted to specific agro-climatic conditions. Genetic variability among the parents of chickpea is essential for establishing selection strategies and identifying diverse parents that lead to a wide spectrum of gene combinations. The parental selection for breeding programs is of utmost importance, and genetic variability and divergence among the parents play a crucial role in crop improvement. Plant breeders generally select parents based on phenotypic divergence, but knowledge about genetic variability amongst parents is necessary for effective breeding, particularly with respect to traits needing improvement, Begna [8]. This present study involves above mentioned components to the study the variability among the entries which helps in selection of genotypes for utilization in future breeding agendas.

2. MATERIALS AND METHODS

2.1 Methodology

The study employed a complete randomized block design, incorporating 51 chickpea genotypes. It was carried out during *rabi* of 2019-2020 at the School of Agriculture, Lovely Professional University, Punjab. Seeds were sown by dibbling. Each genotype was sown in 3 replicates in RCBD (Randomized complete block design) spaced at 45 x 10 cm.

Yield-contributing factors were seen in five plants per entry from all three replications, viz., DFF- days to first flowering, D50%F- days to 50% flowering, DM- days to maturity (Chronological traits- observed and recorded on plot basis). Vegetative and yield related characters viz., PH- plant height (cm), NPB- number of primary branches plant⁻¹, NSB- number of secondary branches plant⁻¹, NPP- number of pods plant⁻¹, NFP- number of filled pods plant⁻¹, NUFP- number of unfilled pods plant⁻¹, NSP- number of seeds pod⁻¹, TW- test weight, BY- biological yield,

HI- harvest index and SY- seed yield were observed and recorded from five randomly selected and tagged plants from each entry.

2.2 Statistical Analysis

The study computed the mean values from each replication and employed a randomized block design to assess the variance among germplasms, Panse and Sukhatme [9]. To explore the relationships between various attributes, Pearson's correlation coefficients were calculated for pairs of variables. To investigate path coefficient analysis, proposed by Wright [10] and further expanded by Dewey and Lu [11] was employed to estimate the direct and indirect effect of various traits on yield. Every analysis was performed employing statistical software R-Studio using the packages agricolae, Mendiburu [12] for ANOVA, metan (multi-environment trials analysis), Olivoto et al., [13] for correlation coefficients, variability package, Popat et al., [14] for path analysis.

3. RESULTS AND DISCUSSION

3.1 ANOVA

The ANOVA results on 51 chickpea genotypes, focusing on 12 characteristics, displayed that the mean sum of squares had significant variance at the 1% level, indicating considerable variability among the germplasm across all 12 traits (Table-1). These results were compatible with previous studies on chickpea, as reported by Jayalakshmi et al., [15] for 64 chickpea genotypes and Jayalakshmi et al., [16] for 100 chickpea advance breeding lines.

3.2 Genetic Parameters

3.2.1 GCV and PCV

The highest Genotypic & phenotypic coefficient of variance (Fig- 1) was recorded for the trait SY (22.21, 22.42) whereas, moderate estimates for NSP (17.72, 18.62), TW (17.22, 17.27), HI (13.62, 13.89), NUFP (11.22, 11.50) and BY (10.20, 10.28). Corresponding results were observed previously by Ningwal et al., [17] in 57 chickpea genotypes & Upadhyay *et al.*, [18] in 30 chickpea genotypes for SY, NSP & HI, Bharathi et al., [19] for BY in 26 chickpea genotypes. Giving much emphasis to aforementioned characters while breeding would be beneficial but, it is important to be cautious during selection, as PCV estimates were also on the

higher side for these characters and environmental variations can mislead results.

3.2.2 Heritability and genetic advance as % to mean

Every trait in the study recorded very high heritability (Fig- 1), several studies have suggested that traits with high heritability and genetic advance over mean are be good targets for selection as underlying genetic mechanisms are primarily additive in nature. High heritability coupled with genetic advance were noted for SY (98.15, 45.33), TW (99.42, 35.37), NSP (90.53, 34.73), HI (96.24, 27.53), NUFP (95.17, 22.54) and BY (98.49, 20.85). Similar reports were made in earlier studies by Ningwal et al., [17] in 57 and Khade et al., [20] in 18 genotypes of chickpea for SY, HI, Gulwane et al., [21] in 44 chickpea genotypes and Karthikeyan et al., [22] in 20 genotypes for TW, Kishore et al., [23] in 240 chickpea lines & Pravallika et al., [24] in 23 genotypes for NSP, Kumar et al., [25] for BY in 50 chickpea genotypes, Tare et al., [26] for NUFP in 28 chickpea germplasm. These results suggest that these traits could be considered as tools for crop improvement involving selection, which could be possibly due to additive gene action, meaning that they can be improved by adapting selection excluding progeny testing.

3.3 Correlation Coefficient Analysis

The genotypic and phenotypic correlation coefficients between seventeen traits are presented in (Fig- 2). PH ($r_G = 0.571$, $r_P = 0.551$), NPB ($r_G = 0.278$, $r_P = 0.264$), NSB ($r_G = 0.347$, $r_P = 0.319$), NPP ($r_G = 0.404$, $r_P = 0.391$), NFP ($r_G = 0.458$, $r_P = 0.445$), TW ($r_G = 0.819$, $r_P = 0.806$), BY ($r_G = 0.860$, $r_P = 0.854$), HI ($r_G = 0.912$, $r_P = 0.910$) demonstrated statistically significant associations with SY. Corresponding results were observed previously by Jayalakshmi et al., [15] in 64 genotypes & Tutlani et al., [27] in 20 genotypes for PH, TW & BY, Nikhitha & Walia [28] in 27 genotypes and 3 checks and Meena et al., [29] in 25 chickpea genotypes for NPB, NSB & NPP. Singh et al., [30] for NFP in 15 chickpea genotypes. Understanding the connections between the factors' affecting yield is crucial for developing a selection-based plant breeding program to boost yield. Yield, being a dependent trait, is influenced by numerous characteristics. Plant breeders can derive substantial advantages from positive associations among desirable traits. Positive correlations indicate that

enhancing one specific trait often leads to the simultaneous improvement of related characteristics.

3.4 Path Coefficient Analysis

The breeder primarily aims to minimize production potential while having specific defects. Some are significant constituents that directly impact yield, while others have an indirect effect through the development and behavior of other traits. Therefore, it is better to understand how other factors, directly and indirectly, affect yield. Path analysis has been used to identify each feature's relative value and limit the total number of characteristics used in selection program. Genotypic level path analysis can reveal how plant parts work together to produce yield by studying both the direct and indirect effects of genotypic features on yield.

The estimates for the path coefficient matrix, are tabulated in Table- 2 and represented in Fig. 3. The direct positive impact on yield was achieved by the NFP (107.93), NUFP (39.00), HI (0.606), BY (0.486), NSB (0.036), TW (0.035), DFF (0.016), days to maturity (0.009). Similarly, Atieno et al., [31] conducted genotypic path analysis on 267 landraces, 13 advanced lines, 7 wild accessions and 13 unknown accessions revealed positive association of NUFP, Nikhitha & Walia [28] in 27 genotypes and 3 checks for TW, BY, and HI, Jayalakshmi et al., [16] for DFF & NSB in 64 genotypes, Xalxo et al., [32] for DM in 56 genotypes (16 parents & 40 F1 population). Direct selection in plant breeding involves choosing plants for further breeding based on their performance regarding the desired traits so plant breeders can establish a clear link between the selected traits and the desired outcome, such as improved yield in chickpea [33].

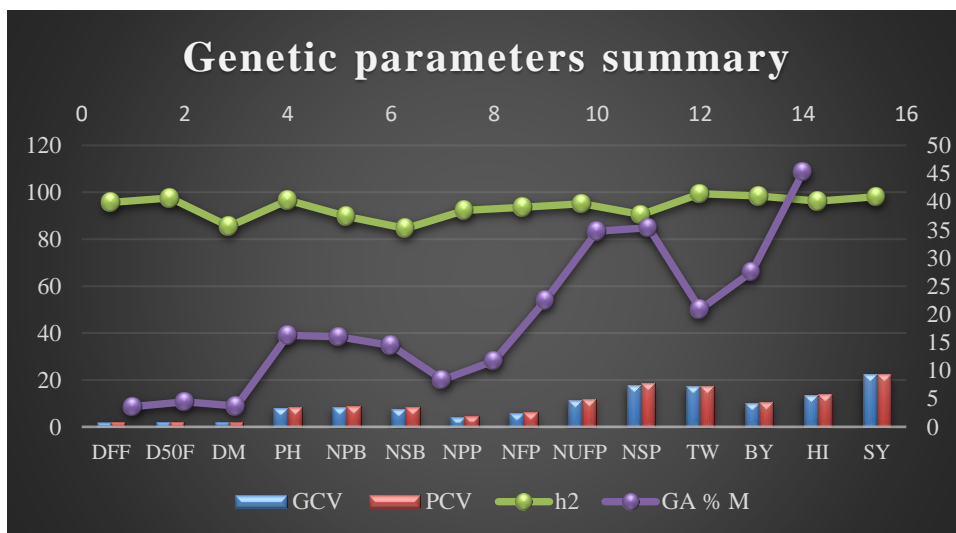


Fig. 1. Illustration of genetic parameters for yield and contributing traits

Table 1. ANOVA illustrating the significance for yield and corresponding traits in chickpea

Characters	Replication d.f.=2	Treatments d.f.=50	Error d.f.=100
DFF	0.634	10.494**	0.447
D50%F	0.399	17.551**	0.412
DM	10.477	37.857**	5.490
PH (cm)	1.131	33.110**	1.131
NPB	0.014	0.331**	0.034
NSB	0.104	0.873**	0.134
NPP	5.987	32.872**	2.539
NFP	6.176	44.391**	2.842
NUFP	0.348	5.701**	0.275
NSP	0.002	0.309**	0.029
TW	0.067	9.228**	0.054
BY	0.143	11.447**	0.173
HI	3.697	100.747**	3.793
SY	0.179	9.623**	0.178

Table 2. Path coefficients (genotypic) for SY and corresponding traits

Character	DFF	D50F	DM	PH	NPB	NSB	NPP	NFP	NUFP	NSP	TW	BY	HI
DFF	0.0168	0.0153	0.0123	0.0003	-0.0017	-0.001	-0.0031	-0.0018	-0.0023	-0.0003	-0.0018	-0.0019	0.0008
D50F	-0.0101	-0.0112	-0.0081	-0.0002	-0.0002	-0.0009	0.0013	0.0008	0.0009	-0.0015	-0.0001	0.0011	-0.0005
DM	0.0066	0.0066	0.0091	0.0001	-0.0024	-0.0013	0.0001	0.0002	-0.0002	0.0002	-0.0001	-0.0005	0.0003
PH	-0.0007	-0.0006	0.0002	-0.0353	-0.0094	-0.0084	-0.0168	-0.0208	0.018	0.0023	-0.0167	-0.0203	-0.0166
NPB	0.0005	-0.0001	0.0013	-0.0013	-0.0048	-0.0042	-0.002	-0.0019	0.0006	-0.0027	-0.0015	-0.0007	-0.0015
NSB	-0.0022	0.003	-0.0051	0.0086	0.0313	0.036	0.0075	0.0069	-0.0015	0.0235	0.0118	0.0044	0.016
NPP	17.1638	10.5087	-0.9855	-43.8244	-37.5923	-19.1418	-92.1925	-86.2909	20.8062	-18.0559	-25.4367	-38.794	-27.1567
NFP	-11.7403	-7.4226	1.9663	63.6915	42.3731	20.7502	101.0243	107.9336	-59.8159	18.0932	26.7266	50.1106	38.6089
NUFP	-5.4286	-3.0893	-0.9804	-19.8516	-4.7684	-1.6021	-8.8016	-21.6135	39.0001	-0.0315	-1.2817	-11.3034	-11.4427
NSP	0.0006	-0.004	-0.0006	0.002	-0.0167	-0.0197	-0.0059	-0.0051	0.0001	-0.0303	-0.0054	-0.0004	-0.0107
TW	-0.0038	0.0004	-0.0005	0.0166	0.0111	0.0115	0.0097	0.0087	-0.0012	0.0062	0.0351	0.0258	0.025
BY	-0.054	-0.0481	-0.0264	0.2797	0.073	0.0597	0.2046	0.2258	-0.1409	0.0059	0.357	0.4863	0.2837
HI	0.0294	0.029	0.0179	0.2854	0.1864	0.2698	0.1786	0.2169	-0.1779	0.2142	0.4325	0.3537	0.6063
SY	-0.0219	-0.0128	0.0004	0.5713	0.2789	0.3477	0.404	0.4587	-0.3142	0.2233	0.8191	0.8607	0.9123

R Square = 0.9972 Residual Effect = 0.0527

4. CONCLUSION

The present study assesses the genetic variability of 51 chickpea [*Cicer arietinum* (L.)] genotypes on 12 characteristics displayed ANOVA recorded significant variance at the 1% level for all traits, indicating considerable variability amongst germplasm. The study found that SYper plant expressed comparatively high GCV and heritability with other traits, indicating that it is the most heritable trait and has the highest potential for improvement through selective breeding. Positive correlation with SY was revealed by PH, NPB, NSB, NPP, NFP, TW, BY, HI. Path analysis revealed that NFP had highest positive effect on SY followed by NUFP, HI, BY, NSB, TW, DFF & DM suggesting selection from any of these traits would be beneficial. Overall, the results of this study provide important information in respect to crop improvement programs, highlighting the importance of selecting for traits such as NSB, NFP, NUFP, TW, BY, HI for improving seed yield.

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