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Assessment of genetic diversity in *Kabuli* chickpea (*Cicer arietinum* L.) Germplasm under late sown condition

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Abstract
During the Rabi season of 2017-18, an experiment was conducted at the Seed Breeding Farm of Jawaharlal Nehru Krishi Vishwa Vidyalaya to investigate the genetic diversity present in 50 kabuli chickpea genotypes under normal sowing conditions. The study aimed to assess genetic variability, correlation, path coefficients, and genetic diversity in yield and its contributing traits. The experiment employed a Randomized Block Design with three replications. Analysis of variance revealed that genotypes were highly significant for all traits except the number of primary branches per plant and the number of seeds per pod. Phenotypic variance was found to be higher in magnitude than genotypic variance, a trend observed consistently across all the characters investigated. Notably, high genotypic and phenotypic coefficients of variance were recorded for the number of effective pods per plant, total number of pods per plant, biological yield, and seed yield per plant. Traits such as total number of pods per plant, total number of seeds per plant, seed yield per plant, biological yield per plant, and number of effective pods per plant exhibited high heritability coupled with a high genetic advance as a percentage of the mean, suggesting that heritability is predominantly due to additive gene actions, making selection based on these traits effective. Correlation coefficients among yield and component characters indicated significant positive correlations with biological yield, total number of pods per plant, number of effective pods per plant, plant height, days to maturity, number of secondary branches per plant, days to flower initiation, days to 50% flowering, and days to pod initiation. Path coefficient analysis revealed that biological yield per plant had the highest positive direct effect on seed yield per plant, followed by the number of effective pods per plant, total number of pods per plant, total number of seeds per pod, harvest index, and days to maturity. The percentage contribution of various characters toward total divergence showed that the total number of pods per plant contributed the most, followed by biological yield, 100-seed weight, seed yield per plant, harvest index, days to pod initiation, days to 50% flowering, days to maturity, number of primary branches per plant, number of effective pods per plant, number of seeds per pod, days to flower initiation, number of secondary branches per plant, and plant height. The evaluation of fifty kabuli chickpea genotypes for genetic divergence resulted in the grouping of genotypes into eight clusters. Clusters I, III, V, VII, and VIII were poly-genotypic, while clusters II, IV, and VI were mono-genotypic. The highest inter-cluster distance was observed for cluster VIII, followed by clusters III, I, VII, and V. Meanwhile, three clusters, namely II, IV, and VI, showed zero values for intra-cluster distance in the present investigation.

Keywords: ANOVA, Genetic variability, correlation, path analysis, D^2 and *Kabuli* Chickpea

Introduction
The term "Cicer" finds its origin in the Greek word "kiros," which is associated with the well-known Roman family Cicero. Meanwhile, "Arietinum" is derived from the Latin word "arise," meaning ram, which alludes to the ram's head shape of the chickpea (Singh, 1985) [53]. Chickpea (*Cicer arietinum* L.), known by various names such as gram, Chana, Bengal gram, and Kadle in different countries, holds significance as a vital legume in the Rabi season with a widespread geographical distribution. Being a diploid species with a chromosome number 2n=2x=14, chickpea is self-pollinated and belongs to the subfamily Papilionoideae and tribe Cicereae of the leguminaceae family. Initially considered to belong to the tribe Viceae Alef, chickpea is the third most crucial pulse crop globally, following beans and peas, covering an area of 12 million hectares with an annual production of 8.9 million tons. The phenotypic variance is higher than the genotypic variance across various traits, indicating the significance of additive gene actions.
Chickpea, believed to have originated from South Eastern Turkey and adjacent areas of Syria, serves as a major grain legume crop globally, particularly in semi-arid tropics and warm

temperate zones. India leads in both area and production, contributing to 67 percent of the global chickpea production. Despite this, chickpea production and productivity in India have stagnated for decades, with the crop covering 10.56 million hectares and yielding 11.23 million tons, resulting in an average productivity of 1078 Kg/ha (Agriculture statistics at a glance, 2022) [2]. Chickpea is predominantly cultivated in states like Madhya Pradesh, Rajasthan, Maharashtra, Uttar Pradesh, Karnataka, and Andhra Pradesh, which collectively account for 91 percent of total production and 90 percent of the total area in the country.

Kabuli chickpea holds a significant place in Indian cuisine, particularly as 'chhole.' It serves as an excellent source of protein and minerals, especially for the vegetarian population, with approximately 23% protein content, 64% total carbohydrates, 5% fat, and various essential minerals and amino acids. This study focuses on evaluating morphological diversity among chickpea varieties and local populations based on quantitative characters for developing candidate varieties as per the DUS descriptor.

While chickpea is an important pulse crop in India, its productivity is relatively low compared to other growing countries. This may be attributed to factors such as the lack of improved high-yielding varieties, a narrow genetic base of released varieties, the use of poor-quality seeds, and limited irrigation availability. A critical analysis of genetic variability is essential for initiating crop improvement programs and selecting appropriate breeding techniques. Parameters like heritability and genetic advance play crucial roles in the selection process, providing insights into the magnitude of genetic and environmental variations and helping determine breeding procedures.

Correlation coefficient analysis in plant breeding helps identify characters suitable for genetic improvement in yield by assessing the mutual relationships between variables. The genotypic and phenotypic paths are estimated to understand the impact of various characters on yield-contributing traits. Path coefficient analysis, introduced by Wright (1921) [65], is used to determine direct and indirect effects of traits on yield, aiding in trait selection. This investigation includes germplasm lines of Kabuli chickpea to study genetic components and Euclidean distance cluster analysis for yield and its attributing traits. The goal is to identify genetically divergent parents for hybridization programs through genetic divergence analysis, measuring the degree of diversification at both inter-cluster and intra-cluster levels. This approach provides reliable estimates of genetic diversity, enabling the evaluation of a large number of germplasm lines simultaneously. The results can be visually represented through a cluster diagram.

Materials and Methods

The plant material comprised 50 kabuli chickpea genotypes obtained from AICRP on Chickpea, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, ICRISAT, Patencheru, and ICARDA, Morocco. All genotypes were cultivated in a Randomized Complete Block Design with three replications during the Rabi season of 2017-18 at the Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur (M.P.), M.P., India. Each genotype was planted in a plot consisting of two rows of 4-meter length, spaced 45 cm apart between rows and 10 cm between plants. Protective irrigations and recommended agricultural practices were applied throughout the growing season. For data collection, five randomly selected plants from each treatment were marked to observe parameters such as days to flower initiation, days to 50% flowering, days to pod initiation, days to maturity, plant height (cm), number of primary branches, number of secondary branches, total number of pods per plant, number of effective pods per plant, number of seeds per pod, 100-seed weight (g), biological yield (g), harvest index (%), and seed yield per plant (g).

Statistical analysis utilized the mean values of each genotype. Genotypic (GCV) and phenotypic coefficient of variation (PCV) were calculated following Burton's formula. Broad-sense heritability (h^2 (b)) and expected genetic advance were computed using Allard's formula (1960) [3]. Correlation and path coefficient analysis followed the methods proposed by Wright (1921; 1934) [65] and further detailed by Dewey and Lu (1959) [12]. Genetic divergence was assessed using Mahalanobis D2 statistic (1936) [38], as outlined by Rao (1952) [44]. Inter and intra-cluster distances were determined using Tocher's method, as suggested by Rao (1952) [44], to establish the clusters.

Results and Discussion

Understanding the extent of variability and genetic diversity is crucial when aiming to enhance a complex trait like yield. Consequently, in the pursuit of improving seed yield, the selection of parents with broad genetic divergence for multiple characters becomes paramount. This selection process is evaluated using D2-statistics, as developed by Mahalanobis (1936) [38].

In the current investigation, the analysis of variance underscored the significance of genotypes for all examined traits, including days to flower initiation, days to 50% flowering, days to pod initiation, days to maturity, plant height, number of secondary branches per plant, total number of pods per plant, number of effective pods per plant, 100 seeds weight, biological yield, harvest index, and seed yield per plant. Notably, there was a substantial variation among genotypes for all characters, as indicated in Table 1. This observation implies that the existing gene pool for yields and its components offers a considerable selection space for identifying promising lines.

In general, the phenotypic variance must be higher in magnitude than genotypic variance. The same trend was observed in the investigation of all the characters. This shows that the current gene pool for yields and its components has a large enough selection space for promising lines. Thus, it suggests that there is a lot of scope for choosing various quantitative traits to improve *Kabuli* chickpea. High genotypic and phenotypic coefficient of variance were recorded number of effective pods per plant, total number of pod per plant, biological yield and seed yield per plant (Table 2). Similar findings were also reported by Jivani *et al*., (2013) [24], Nizama *et al*., (2013) [40] Kuldeep *et al*., (2014) [34], Dhuria and Babbar (2015) [14], Shakya *et al*., (2017) [47], Desai *et al*., (2015) [13], Joshi *et al*., (2018) [26] Babbar and Tiwari (2018) [8] and Hailu *et al*., (2020) [19]. This implies that substantial phenotypic variation is present in the genotypes with respect to these traits indicating the scope of exploiting variability for further improvement of these traits.

Heritability serves as a valuable indicator of the transmission of diverse traits from parents to offspring. Assessing heritability aids breeders in selecting superior genotypes from diverse populations. It's important to note that the heritability of the same trait can vary significantly among different populations. Estimates of heritability, combined with genetic

advances, prove particularly helpful in reassessing the gains achievable through selection (Kumawat *et al*., 2022) [36].

High heritability recorded for number of effective pods per plant, seed yield per plant, total number of pods per plant, biological yield, 100 seeds weight, days to pod initiation, days to 50% flowering, days to flower initiation, harvest index, days to maturity, plant height, number of seeds per pod and number of seeds per pod (Table 2). High heritability coupled with high genetic advance as percentage of mean was observed for total number of pods per plant, total number of seeds per plant, seed yield per plant, biological yield per plant, number of effective pods per plant (Table 2). It showed that mostly the heritability is because of additive gene actions and selection based on that can be effective. Hence, direct selection for such traits would be more effective. High heritability is being showed due to favorable effect of environment rather than the genotype and selection based on such traits cannot be effective. The results in line with the earlier findings of Shweta *et al*., (2014) [50], Hussain *et al*., (2017) [22], Honappa *et al*., (2018) [21], Pithiya *et al*., (2019) [42], Tsehaye *et al*., (2020) [63].

The coefficient of variation does not encompass the entire scope of heritable variation. Assessing heritability and genetic progress in conjunction enhances the accuracy of determination. When contemplating character improvement through selection, it is imperative to consider both heritability and genetic advancement. Relying solely on heritability is less advantageous in predicting gains under selection compared to considering estimates of high heritability combined with rapid genetic progress.

When establishing a robust selection criterion to assess the reciprocal interaction among diverse attributes, the measurement of correlation coefficients proves highly beneficial. This data can be applied to both indirect selection and the anticipation of the corresponding response to direct selection. In the case of Kabuli chickpea, similar to other crops, seed yield exhibits considerable variability and complexity due to a range of interconnected contributing characters. Direct selection for yield may, therefore, lack effectiveness. The intricacies of this trait underscore the importance of adopting a component-based approach in developing an efficient breeding program aimed at enhancing yield. Moreover, it has been proposed that, instead of specific genes solely for yield, there might exist genes influencing various components. Examining the genetic foundation of the relationship between two qualities, Falconer (1960) [16] posited that pleiotropy or full linkage could account for the linear association. In instances of pleiotropy or linkage, a gene exerts a general influence on both aspects (positive correlation), while other genes may enhance one feature while diminishing the other (negative correlation).

Correlation provides the measure of the linear association between pairs of characters and serves as the foundation for a selection index, thereby assisting breeders in crop improvement programs through the simultaneous manipulation of paired traits. Genetic correlation among traits may arise due to either linkage or pleiotropy, playing a crucial role in indirect selection. Understanding phenotypic correlation among the factors contributing to yield leads to the most effective method of selection by utilizing favorable combinations of characters, where coefficients for most of the characters are higher than the phenotypic correlation coefficients. This suggests a robust inherent association between the various studied characters, with less influence from environmental effects.

In present investigation, correlation coefficient showed strong significant and positive association with each other. Correlation coefficients among yield and component characters showed significant positive correlation with biological yield (r= 0.8275), total number of per plant (r= 0.6398), number of effective pod (r= 0.6344), plant height (r= 0.4446), days to maturity (r= 0.4035), number of secondary branches per plant (r= 0.2725), days to flower initiation (r= 0.2548), days to 50% flowering (r= 0.2404) days to pod initiation (r= 0.2202), whereas significant negative correlation of seed yield with Number of primary branches per plant (r= -0.3684) was observed. (Table 3). These results are in agreement with the findings of Monpara and Dhamelia (2013) [39], Malik *et al*., (2014) [38], Tadesse *et al*., (2016) [57], Thakur *et al*., (2018) [59], Kousar *et al*., (2019) [31], Shanmugam and Kalaimagal (2019) [48] and Kumawat *et al*., (2022) [36]. Shown similarity with the findings of Babbar *et al*., (2012) [7-9], Monpara and Dhamelia (2013) [39], Shafique *et al*., (2016) [46], Solanki *et al*., (2017) [54], Sharma and Saini (2019) [45] and Kumawat *et al*., (2021) [35]. Therefore breeding strategies for improvement of yield potential in chickpea would be to select plants having biological yield, total number of per plant, number of effective pod, plant height, days to maturity, number of secondary branches per plant, days to flower initiation, days to 50% flowering, days to pod initiation. In the present investigation, positively correlated characters can be suggested to improve simultaneously and enhancement of in one will automatically enhance the other. However, such simultaneous manipulations are not possible for those traits which are negatively associated. Thus, indirect selection can be adopted to improve such traits.

Path analysis allows the division of the observed correlation coefficient into two distinct causal components, which are unit-less and, as a result, are adaptable and easy to interpret. In the current study, path coefficient analysis has been conducted with yield as the dependent variable.

Path coefficient analysis revealed that positive direct effects was manifested by biological yield per plant followed by number of effective pods per plant, total number of pods per plant, total number of seeds per pod, harvest index and days to maturity on seed yield per plant. However, maximum negative direct effect on seed yield per plant was noted for days to flower initiation and 100 seed weight (Table 6). Thus, direct selection based biological yield per plant, number of effective pods per plant, total number of pods per plant, total number of seeds per pod, harvest index and days to maturity would be effective in improving the yield. This implies that these components are important yield determinants in chickpea. Similar result was reported by Dhuria and Babbar (2015) [14], Joshi and Yasin (2015) [25], Shafique (2016) [46], Paneliya *et al*., (2017) [41], Agrawal *et al*., (2018) [1], Shanmugam and Kalaimagal (2019) [48], Solanki *et al*., (2019) [55], Thakur and Sirohi (2020) [60], Kobraee *et al*., (2021) [32].

Therefore, both correlation and path analysis emphasize that characters with a high direct positive effect and significant correlation with seed yield should be prioritized when selecting for improvements in seed yield. Similarly, as with direct effects, indirect effects also contribute to seed yield per plant through different traits. The majority of indirect effects from various independent traits via other traits were found to be extremely low in magnitude and of varying signs.

Based on path analysis, characters such as biological yield per plant, number of effective pods per plant, total number of pods per plant, total number of seeds per pod, harvest index, and days to maturity have been identified as highly effective,

displaying substantial positive direct effects on seed yield per plant. These crucial yield-contributing traits can be incorporated into selection strategies for the development of high-yielding varieties of Kabuli chickpea.

The D2 statistic has been instrumental in elucidating the association between the number of agricultural plants, their diverse breeding systems, and geographical dispersion. This statistic is closely linked, indicating a direct relationship. The observed diversity extends beyond mere geographical differences, stemming from genetic drift and selective pressures in various environments. In the realm of crop species, the comprehension of genetic divergence plays a pivotal role in parental selection. This concept facilitates the distinction of well-defined populations (Arunachalam, 1981) [6]. In the current study, D2 analysis was conducted on 50 genotypes of Kabuli chickpea, considering various yield attributing components. The outcome revealed the formation of eight distinct clusters, signifying substantial genetic divergence. The clustering pattern strongly indicates that there is significant divergence, allowing for the establishment of well-defined clusters. The Mahalanobis D2 analysis of quantitative traits proves to be a potent tool for evaluating genetic divergence among choices originating from the same geographic region. The characters showing more contribution (%) towards the divergence should be considered important during selection. The percentage contribution of various characters toward the total divergence was recorded highest for Total number of pods per plant followed by Biological yield, 100seed weight, Seed yield per plant, Harvest index, Days to pod initiation, Days to 50% flowering, Days to maturity, Number of primary branches per plant, Number of effective pods per plant, Number of seeds per pod, Days to flower initiation, Number of secondary branches per plant and Plant height (Table 6). These characters were liable for expressing maximum diversity among the clusters. These findings were similar to the findings of Sreelakshmi *et al*., (2010) [56] and Gediya *et al*., (2018) [18] Prakash *et al*., (2012) [66], Pandey *et al*., (2013) [67], Jayalakshmi *et al*., (2014) [68], Tiwari and Babbar (2017) [61], Johnson *et al*., (2019) [27], Janghel *et al*., (2020) [23], Tomar *et al*., (2021) [62] and Biswal and Babbar (2022) [11]. Fifty *kabuli* chickpea genotypes which were evaluated for nature and magnitude of genetic divergence were grouped into eight clusters (Table 7). Cluster I, III, V, VII and VIII were poly-genotypic and cluster II, IV and VI were found mono-genotypic under present investigation, this confirmed the diversity present in the material. Cluster I was the largest among all the clusters comprised 33 genotypes *viz*., ICCV 14308, ICCV 14501, ICCV 14511, ICCV 14509, ICCV 14508, ICCV 14313, ICCV 14314, ICCV 14510, ICCV 14500, ICCV 14513, ICCV 14512, ICCV 171314, ICCV 06303, FLIP 09-348C, FLIP 08-986, FLIP11-51C, FLIP11-53C, FLIP11-64C, FLIP11-65C, FLIP11-78C, FLIP11-84C, FLIP11-87C, FLIP11-156C, FLIP11-164C, FLIP11-180C, FLIP11-195C, FLIP11-197C, FLIP11-232C, ILC482, FLIP88-85C, JGK 32-1, JGK 3 and JGK 5 followed by cluster III consisted 8 genotypes *viz*., ICCV 171301, ICCV 171305, ICCV 171315, ICCV 171312, FLIP11-183C, FLIP11-211C, FLIP11-93C, FLIP11-220C. Cluster V (ICCV 171306 and ICCV 171309,), cluster VII (JGK 1 and JGK 2) and cluster VIII (ICCV 171308 and ICCV 171313) had 2 genotypes. On the other hand, cluster II, cluster IV and cluster VI comprised only one genotype *viz*., FLIP11-91C, FLIP93-93C and ICCV 6301 respectively. The D^2 values of the genotypes and clustering pattern suggested that the material is highly diverse and has no relationship between the geographical diversity and genetic diversity, while there is presence of some homologous correspondence between closely situated clusters.

Intra cluster distance was recorded maximum for cluster VIII (D^2 = 390.3) followed by cluster III (D^2 = 253.3), cluster I (D^2 = 230.3), cluster VII (D^2 = 126.9) and cluster V (D^2 = 75.5), whereas three clusters *viz*., cluster II, cluster IV and cluster VI showed zero value for intra cluster distance. The maximum inter cluster distance was noted between genotypes of Cluster II and cluster VIII followed by cluster IV and cluster VIII, cluster VI and cluster VIII, cluster II and cluster V, cluster IV and cluster V, cluster V and cluster VI, cluster I and cluster III (Table 9). High heterotic combinations will obtain when genotypes of these distinctly placed clusters were crossed would give high heterosis or heterotic segregants. Inter cluster distance was lowest between cluster IV and cluster VI indicating closeness between these clusters. The results indicated that inclusion of genotypes grouped in cluster VIII and cluster VI in the crossing program in chickpea is expected to give useful recombinants in subsequent generations as diverse parents could generate good amount of genetic variability. Highest cluster mean for days to 50% flowering, days to pod initiation, Number of primary branches per plant and Number of seeds per pod was observed in cluster IV, whereas cluster VII had high values of mean for, plant height, Total number of pods per plant, Number of effective pods per plant and Seed yield per plant which indicated that genotypes having high seed yield and tall plants were concentrated in these clusters (Table 8). These findings confirm in earlier studies of Babbar and Thakur (2012) [7-9], Jivani *et al*., (2013) [24],Johnson *et al*., (2015), Dhuria and Babbar (2016) [15], Tiwari and Babbar (2017) [61], Thakur *et al*., (2018) [59], Gediya *et al*., (2018) [18], Johnson *et al*., (2019) [27], Ponnuru *et al*., (2019) [43], Janghel *et al*., (2020) [23] and Katkani *et al*., (2022) [30]. On the basis of these characters superior genotypes are selected and used in hybridization program as a donor parent.

Table 1: Analysis of Variance

Source of variation	DF	DFI	DF50%	DPI	DM	PH	PB	SB
Replication	2	2.32*	0.14	2.58*	6.16*	0.74	0.14	0.18
Treatments	49	157.4***	181.4***	197.45***	101.82***	20.72**	0.40	2.87*
Error	98	2.94*	3.11*	3.26*	3.30*	0.781	0.19	0.33
Source of variation		TNP	NEP	NSP	100 SW	BY	HI	SYP
Replication	2	0.72	1.6	0.24	4.56*	0.09	21.12**	1.64
Treatments	49	816.10***	803.15***	0.02	251.13***	691.12***	303.66***	142.2**
Error	98	0.63	4.18*	0.02	4.01*	0.62	6.45*	0.7

* Significant at 5% and ** Significant at 1%

Where,

DFI: Days to flower initiation, DFF: Days to 50% flowering, DPI: Days to pod initiation, DM: Days to maturity, PH: Plant height, PB: Number of primary branches per plant, SB: Number of secondary branches per plant, TNP: Total number of pods per plant, NEP: Number of effective pods per plant, NSP: Number of seeds per pod,100SW:100seed weight, BY: Biological yield, HI: Harvest index, SY: Seed yield per plant.

Table 2: Genetic parameters of variability for yield and its component traits for chickpea genotypes

Characters	GCV (%)	PCV (%)	h^2 (b)%	GA as% of mean at 5%
DFI	15.3	15.8	94.6	30.8
DF 50%	14.1	14.5	95	28.4
DPI	12.9	13.2	95.2	26
DM	5.7	6	90.8	11.2
PH	14.7	15.5	89.5	28.6
PB	14.3	28	66.1	15
SB	25	29.5	71.6	43.6
TNPP	43.6	45.6	97.8	68.7
NEP	45	46.4	98.5	62.1
NSP	1.9	11.6	82.9	68.2
100SW	21.2	21.7	95.4	42.6
BY	41.7	42.8	97.7	65.8
HI	19.4	20	93.9	38.7
SYP	37.7	38	98.2	67.2

Where,
DFI: Days to flower initiation, DFF: Days to 50% flowering, DPI: Days to pod initiation, DM: Days to maturity, PH: Plant height, PB: Number of primary branches per plant, SB: Number of secondary branches per plant, TNP: Total number of pods per plant, NEP: Number of effective pods per plant, NSP: Number of seeds per pod,100SW:100seed weight, BY: Biological yield, HI: Harvest index, SY: Seed yield per plant.

Table 3: Correlation coefficient for yield and its attributing traits in *kabuli* chickpea genotypes

Char.	DFI	DF 50%	DPI	DM	PH	PB	SB	TNPP	NEP	NSP	100 SW	BY	HI	SYP
DFI	1	0.8742**	0.8037**	0.2608**	0.5029**	0.2385**	0.0116	0.0348	0.0303	0.0707	-0.2697**	0.3868**	-0.3012**	0.2548**
DF 50%		1	0.9338**	0.0954	0.5117**	0.2241**	0.0071	-0.0492	-0.0592	0.0853	-0.1497	0.3431**	-0.2646**	0.2404**
DPI			1	0.0757	0.5081**	0.1943*	0.1151	0.003	-0.0067	0.072	-0.1941*	0.3439**	-0.2640**	0.2202**
DM				1	0.1755*	-0.2105**	0.087	0.5858**	0.5854**	-0.0026	0.0397	0.5528**	-0.2127**	0.4035**
PH					1	0.1082	0.1165	0.2922**	0.2820**	-0.0271	-0.1163	0.6037**	-0.3684**	0.4446**
PB						1	0.1082	0.1165	0.2922**	0.2820**	-0.0271	-0.1163	0.6037**	-0.3684**
SB							1	0.3290**	0.3269**	0.0958	-0.1757*	0.2630**	-0.0635	0.2725**
TNPP								1	0.9950**	0.0145	-0.0178	0.7212**	-0.1841*	0.6398**
NEP									1	0.0232	-0.013	0.7140**	-0.1767*	0.6344**
NSP										1	0.0293	0.0615	-0.0259	0.0348
100 SW											1	0.0043	0.1478	0.0072
BY												1	-0.3790**	0.8275**
HI													1	0.127
SYP														1

* Significant at 5% and ** Highly Significant at 1%

Where,
DFI: Days to flower initiation, DFF: Days to 50% flowering, DPI: Days to pod initiation, DM: Days to maturity, PH: Plant height, PB: Number of primary branches per plant, SB: Number of secondary branches per plant, TNP: Total number of pods per plant, NEP: Number of effective pods per plant, NSP: Number of seeds per pod,100SW:100seed weight, BY: Biological yield, HI: Harvest index, SY: Seed yield per plant.

Table 5: Path coefficient analysis for yield and its component traits in *kabuli* chickpea genotypes

Cha.	DFI	DF 50%	DPI	DM	PH	PB	SB	TNP	NEP	NSP	100SW	BY	HI	SYP
DFI	-1.1281	-0.9989	-0.917	-0.2861	-0.603	-0.5778	-0.0117	-0.0395	-0.0375	-0.5974	0.3215	-0.4477	0.3706	0.2589
DF 50%	0.1869	0.211	0.1992	0.015	0.1157	0.0985	0.0007	-0.0106	-0.0117	0.1001	-0.0336	0.0742	-0.0599	0.2457
DPI	0.0958	0.1113	0.1179	0.0049	0.0638	0.0505	0.0168	0.0005	0.0046	0.0512	-0.0242	0.0417	-0.0342	0.2228
DM	0.135	0.0379	0.0223	0.5322	0.0971	-0.2296	0.0536	0.3271	0.3321	0.0175	0.0261	0.3095	-0.1235	0.4267
PH	0.2619	0.2685	0.2653	0.0894	0.4899	0.1801	0.0878	0.1493	0.145	-0.0249	-0.0546	0.311	-0.1932	0.4726
PB	0.1175	0.1071	0.0983	-0.099	0.0843	0.2294	0.0031	-0.0562	-0.0564	0.0899	-0.0333	0.0039	0.0013	0.098
SB	-0.0042	-0.0013	-0.0586	-0.0413	-0.0735	-0.0055	0.4103	0.1604	-0.1621	-0.2235	0.0793	0.1294	0.0391	0.3235
TNP	0.1981	-0.2842	0.0219	0.4757	1.7229	-1.3849	2.211	0.6554	0.6603	0.4512	-0.103	0.086	-1.0823	0.6445
NEP	-0.1888	0.3153	-0.0006	-3.5469	-1.6824	1.3977	-2.2461	0.6893	0.6844	0.3788	0.0682	1.0955	1.0526	0.6441
NSP	0.341	0.3053	0.2799	0.0212	-0.0328	0.2523	0.3508	0.0514	0.0429	0.6439	0.1692	0.1851	-0.0575	0.154
100SW	0.1414	0.0791	0.1017	-0.0243	0.0553	0.0722	0.0959	0.009	0.006	-0.1304	-0.4962	-0.0025	-0.0761	0.0063
BY	0.2813	0.2493	0.2505	0.4122	0.4501	0.0121	0.2236	0.5122	0.5107	0.2038	0.0035	0.7089	-0.2756	0.8335
HI	-0.1789	-0.1547	-0.1579	-0.1264	-0.2148	0.0031	-0.0519	0.1042	0.1008	-0.0486	0.0835	-0.2117	0.5446	0.1058

Where,
DFI: Days to flower initiation, DFF: Days to 50% flowering, DPI: Days to pod initiation, DM: Days to maturity, PH: Plant height, PB: Number of primary branches per plant, SB: Number of secondary branches per plant, TNP: Total number of pods per plant, NEP: Number of effective pods per plant, NSP: Number of seeds per pod,100SW:100seed weight, BY: Biological yield, HI: Harvest index, SY: Seed yield per plant.

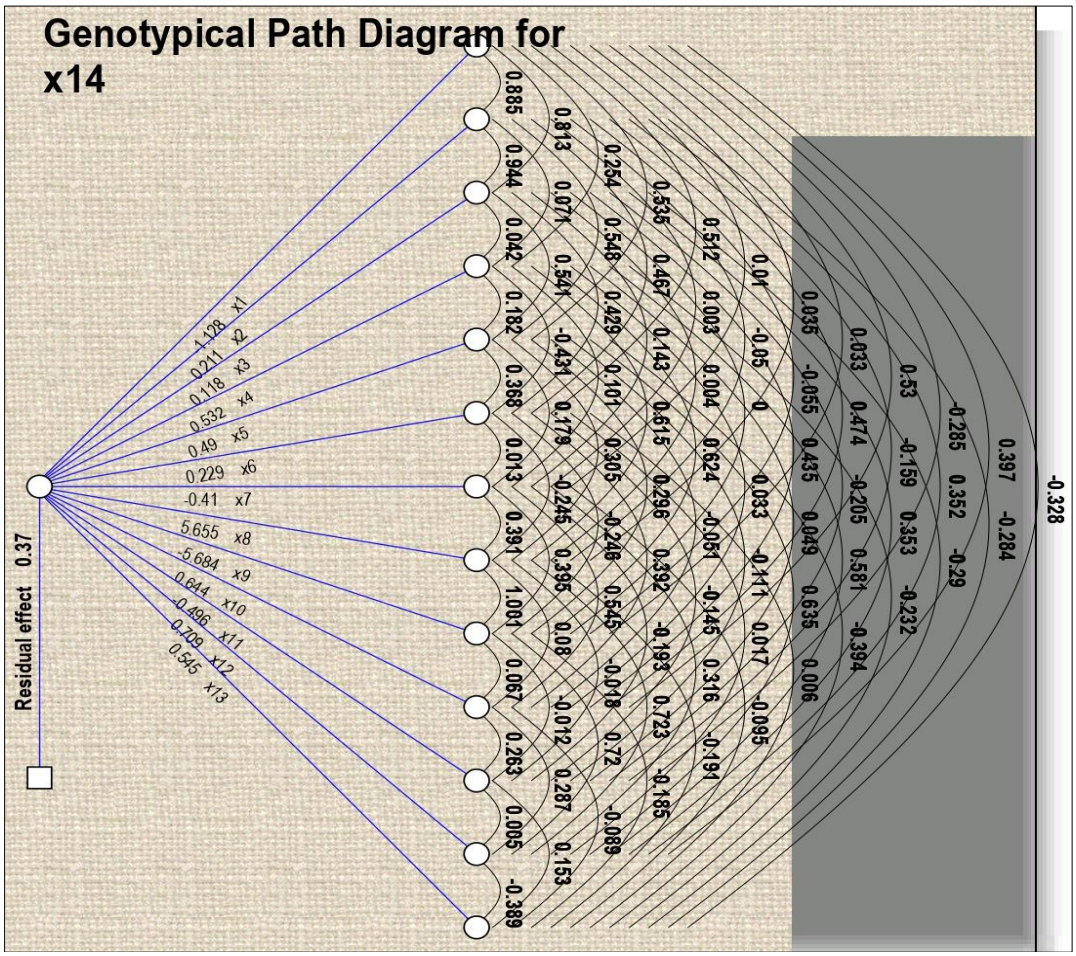

Fig 1: Path diagram for 14 characters in *kabuli* chickpea genotypes

Table 7: Contribution of Various traits towards clustering in *Kabuli* Chickpea Genotypes

Days to flower initiation	0.57%
Days to 50% flowering	1.06%
Days to pod initiation	1.31%
Days to maturity	1.06%
Plant height	0.08%
Number of primary branches per plant	0.01%
Number of secondary branches per plant	0.33%
Total number of pods per plant	49.68%
Number of effective pods per plant	0.01%
Number of seeds per pod	0.01%
100seed weight	3.51%
Biological yield	36.90%
Harvest index	2.69%
Seed yield per plant	2.78%
Total	100%

Table 8: Cluster Mean for Yield and its Component Traits of Chickpea Genotypes: Tocher's Method

Cluster	DFI	DF50%	DPI	DM	PH	PB	SB	TNP	NEP	NSP	100 SW	BY	HI	SY
I	44	53	60	98	17	1.83	3.4	31.6	30	1.36	43.6	30	51.5	15.4
II	52	54	61	92	15.2	2.11	3.3	12.7	11.7	1.37	44.2	12.7	44.1	5.6
III	53	60	68	103	19.6	1.87	4.5	48.6	46.7	1.36	38.2	53.2	52.6	27.8
IV	52	66	74	97	15.2	2.11	3.4	15.7	14.2	1.44	34.1	13.4	63.3	8.5
V	54	61	70	113	20.7	1.44	3.2	57.6	56.1	1.43	48.1	73.7	29.4	21.6
VI	38	43	53	98	14.6	1.67	3	20	18.6	1.23	55.8	19.3	79.6	15.4
VII	33	40	48	104	13.4	1.72	5.3	64.1	63	1.4	39.2	36.1	48	17.4
VIII	52	58	67	106	21.4	2.06	4.1	82.8	81.1	1.37	41.7	66.6	49.7	33.3

Where,

DFI: Days to flower initiation, DFF: Days to 50% flowering, DPI: Days to pod initiation, DM: Days to maturity, PH: Plant height, PB: Number of primary branches per plant, SB: Number of secondary branches per plant, TNP: Total number of pods per plant, NEP: Number of effective pods per plant, NSP: Number of seeds per pod,100SW:100seed weight, BY: Biological yield, HI: Harvest index, SY: Seed yield per plant.

Table 9: Inter and Intra Cluster D^2Values for Different Clusters

Cluster	I	II	III	IV	V	VI	VII	VIII
I	230.3	501.6	723.2	479.8	1654.1	408.2	874.1	2452.4
II		0.0	1817.9	111.2	3260.2	265.4	1958.0	4486.3
III			253.3	1715.2	637.0	1493.6	639.6	998.1
IV				0.0	2978.6	206.4	1864.4	4283.0
V					75.5	2513.1	1255.0	949.8
VI						0.0	1629.0	3922.4
VII							126.9	945.1
VIII								390.3

Table 10: Distribution of *kabuli* Chickpea Genotypes into Different Clusters

Cluster	No. of genotypes	Genotypes included in the cluster
I	33	ICCV 14308, ICCV 14501, ICCV 14511, ICCV 14509, ICCV 14508, ICCV 14313, ICCV 14314, ICCV 14510, ICCV 14500, ICCV 14513, ICCV 14512, ICCV 171314, ICCV 06303, FLIP 09-348C, FLIP 08-986, FLIP11-51C, FLIP11-53C, FLIP11-64C, FLIP11-65C,FLIP11-78C, FLIP11-84C, FLIP11-87C, FLIP11-156C, FLIP11-164C, FLIP11-180C, FLIP11-195C,FLIP11-197C, FLIP11-232C, ILC482, FLIP88-85C, JGK 32-1, JGK 3, JGK 5
II	1	FLIP11-91C
III	8	ICCV171301, ICCV171305, ICCV171315, ICCV 171312, FLIP11-183C, FLIP11-211C, FLIP11-93C, FLIP11-220C
IV	1	FLIP93-93C
V	2	ICCV 171306, ICCV 171309
VI	1	ICCV 6301
VII	2	JGK 1, JGK 2,
VIII	2	ICCV 171308, ICCV 171313

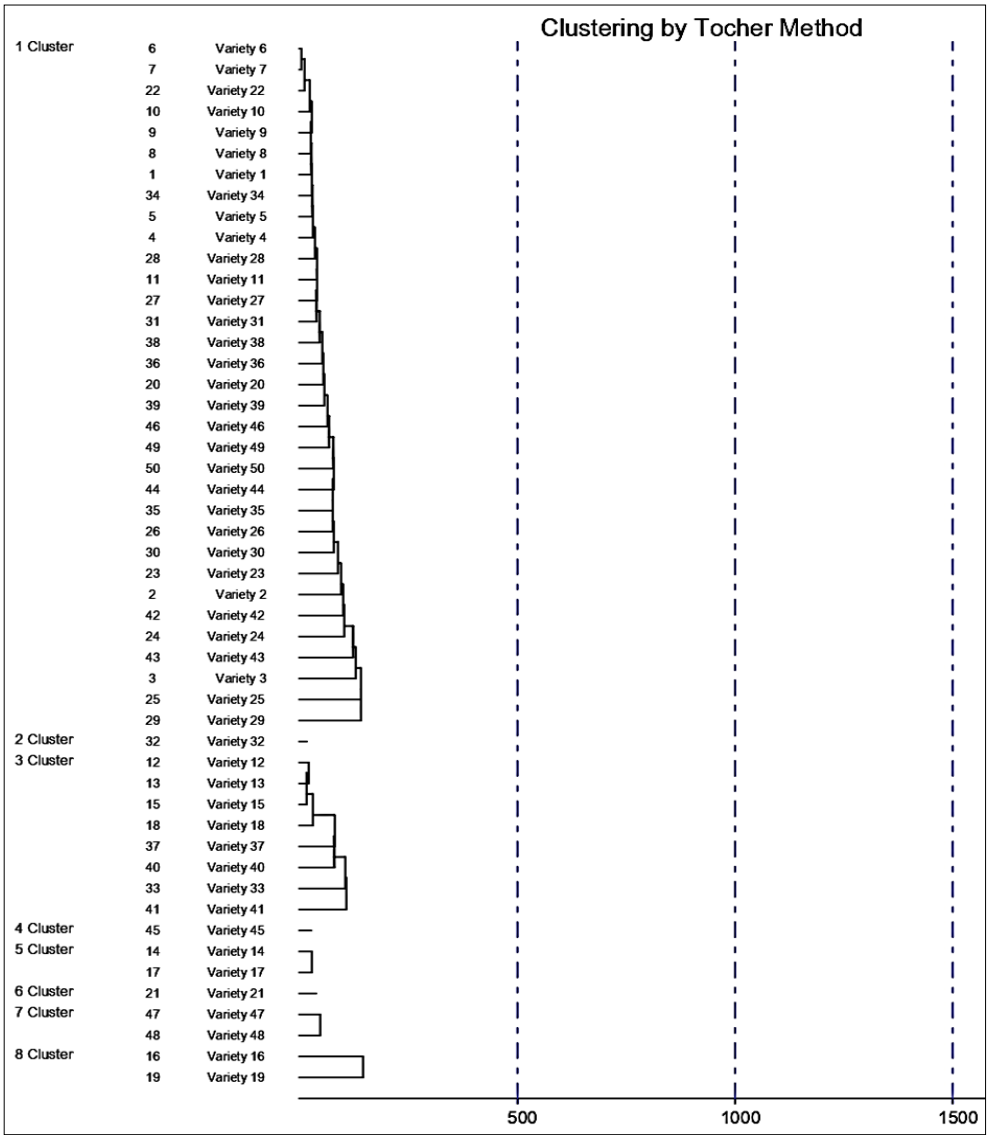

Fig 2: Cluster diagram of diverse chickpea genotypes based on D^2 analysis

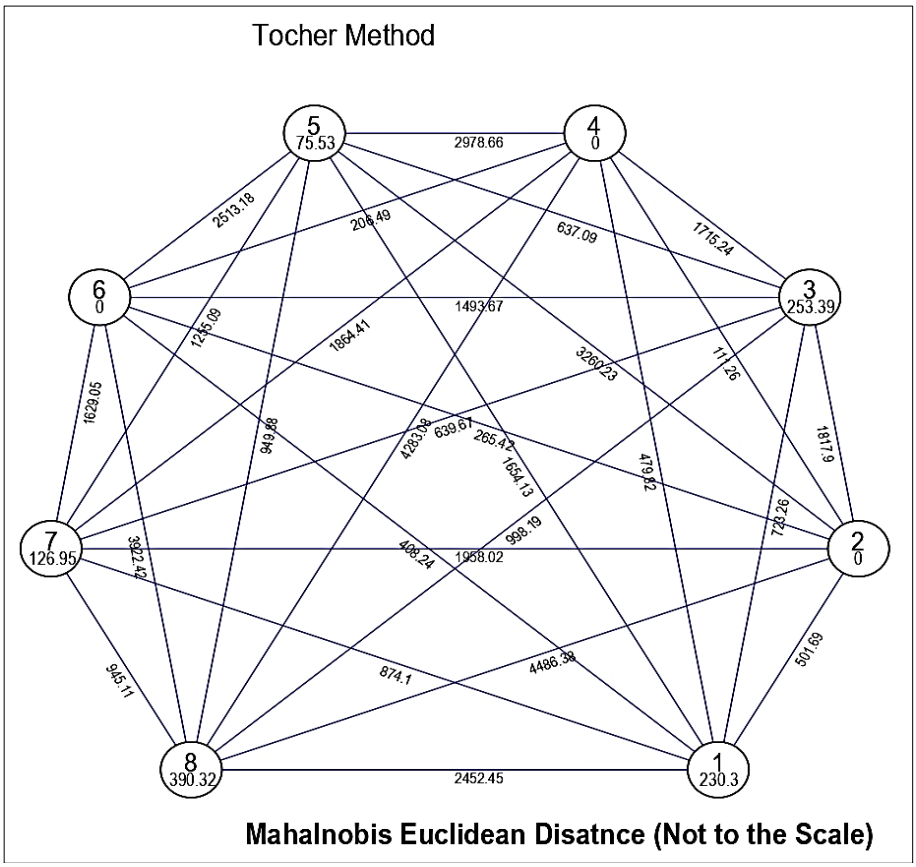

Fig 3: Euclidean distance of *kabuli* chickpea genotypes based on D^2 analysis

Conclusion

Based on the present investigation, it can be concluded that the values of PCV were higher than GCV but in a narrow range for almost all the studied characters indicating the least influence of the environment. Traits such as total number of pods per plant, total number of seeds per plant, seed yield per plant, biological yield per plant, and number of effective pods per plant exhibited high heritability coupled with a high genetic advance as a percentage of the mean. Correlation coefficients among yield and component characters indicated significant positive correlations with biological yield, total number of pods per plant, number of effective pods per plant, plant height, days to maturity, number of secondary branches per plant, days to flower initiation, days to 50% flowering, and days to pod initiation. Path coefficient analysis revealed that biological yield per plant had the highest positive direct effect on seed yield per plant, number of effective pods per plant, total number of pods per plant, total number of seeds per pod, harvest index, and days to maturity. The percentage contribution of various characters toward total divergence showed that the total number of pods per plant contributed the most, followed by biological yield, 100-seed weight, seed yield per plant, harvest index, days to pod initiation, days to 50% flowering, days to maturity, number of primary branches per plant, number of effective pods per plant, number of seeds per pod, days to flower initiation, number of secondary branches per plant, and plant height. The grouping of genotypes into eight clusters. Clusters I, III, V, VII, and VIII were poly-genotypic, while clusters II, IV, and VI were mono-genotypic.

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