

Assessment of Genetic Diversity among Chickpea Varieties and Associations of Some Yield-Related Agro-Morphological Traits Through Correlation, Cluster and Principal Component Analyses

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ABSTRACT

Twenty-one chickpea (*Cicer arietinum* L.) cultivars were comprehensively evaluated based on 15 agro-morphological traits through multivariate approaches, including principal component analysis (PCA) and cluster analysis. The experiment was conducted in a completely randomized design with ten replications. The objectives were to (i) assess genetic relationships among cultivars, (ii) identify key traits for breeding prioritization, and (iii) examine the consistency among PCA, clustering, and correlation analyses. The first five principal components (PCs) with eigenvalues >1 explained 86.5% of the total variance, indicating that the dataset structure was well captured. PC1 and PC2 together accounted for 51.82% of the total variation (33.50% and 18.32%, respectively). PC1 was primarily associated with yield-related traits, including seed width (SW), seed length (SL), seed number per plant (SN), plant seed yield (PSY), pod number per plant (PN), and stem weight per plant (PSW), along with days to emergence (DE), all showing strong positive loadings. PC2 was characterized by positive contributions from harvest index (HI), plant height (PH), first pod height (FPH), average seed weight (ASW), SN, PSY, SW, SL, days to flowering (DF), and days to first pod setting (DPS), whereas root weight per plant (PRW) and PSW exhibited negative loadings. Hierarchical heat map clustering classified the varieties into four main groups; (i) Akça, Sarı-98, Aksu, Hasanbey, Sezenbey, Çağatay, Seçkin, and İnci, indicating substantial similarity among these genotypes, (ii) Diyar-95 formed a distinct cluster alone, (iii) ILC-482, Aziziye, and Arda and (iv) İzmir, Çakır, Zuhul, Gülümser, Cevdetbey, Hisar, Uzunlu, Işık-05, and Sağel. The pronounced divergence of genotypes such as Diyar-95 and İnci suggests their strong potential as parental lines in chickpea breeding programs to improve yield. Overall, the concordance among PCA, cluster, and correlation analyses identified seed yield per plant, seed number, seed width, seed length, pod number, and stem weight as the most influential traits.

Keywords: chickpea, *Cicer arietinum* L., cluster analysis, principal component analysis, multivariate analysis.

INTRODUCTION

Chickpea (*Cicer arietinum* L.), a pulse crop defined as the dried seeds of legumes, is an essential component of human nutrition. Globally, chickpea ranks third by total cultivated area and second by production volume among pulse crops. The major chickpea-producing countries are India, Australia, Türkiye, the Russian Federation, Ethiopia, Myanmar, Pakistan, the United States of America, Iran, and Mexico, which together account for approximately 96.6% of global production. In 2024, chickpea was cultivated at 14.12 million hectares worldwide, producing 16.88 million tons and an average yield of 1195.2 kg/ha. In the same year, Türkiye recorded a harvested

area of 459,430 ha, with a total production of 575,000 tons and an average yield of 1251.6 kg/ha (FAOSTAT, 2025). The global population is projected to continue increasing over the coming decades, reaching approximately 10.3 billion by the mid-2080s, up from 8.2 billion in 2024 (United Nations, 2024). A substantial proportion of the world's population currently faces food insecurity due to socio-economic challenges, urbanization, and increased reliance on centralized food production systems (Babagil, 2010). It is evident that chickpeas are still not fully utilized, despite their promising potential for cultivation in the face of climate change. This potential is due to several advantageous traits identified by researchers, such as resistance to drought, adaptability to both high and low temperatures and various

types of soil, relative resilience against diseases and pests, beneficial biochemical properties, and significant health advantages for both humans and animals when used as food and fodder (Dimitrova, et al., 2026). In this context, edible grain legumes play a critical role in human nutrition, especially in developing countries, serving as an affordable and high-protein source that helps mitigate protein deficiencies and address broader nutritional challenges.

One of the primary objectives of plant breeding programs is to increase productivity per unit area. Understanding the factors affecting yield, selecting genotypes adapted to specific environments, and evaluating genetic diversity are critical to developing improved cultivars (Torun and Köycü, 1999). Agro-morphological traits, observable characteristics such as leaf morphology, plant height, and flowering time, provide essential information for assessing plant performance, adaptability, and yield potential under diverse environmental conditions. Based on plant traits, several studies have been conducted to evaluate variability in chickpea using cluster analysis (Malik et al., 2014; Tesfamichael et al., 2015; Kahraman et al., 2016; Garg et al., 2017; Arbissie et al., 2025; Kumar et al., 2025) and to distinguish genotypes under stress conditions and identify genetically distant clusters as promising parental sources (Yücel and Mart, 2014; Jha and Shil, 2015; Kumar et al., 2020a).

Cluster analysis is a crucial technique for classifying data, enabling the division of genetic material into distinct homogeneous groups. It facilitates the grouping of genotypes based on morphogenetic traits. Cluster analysis helps minimize variance within groups while maximizing variance between groups, thereby aiding in the identification of outliers (Jain et al., 2023). In addition, multivariate techniques such as principal component analysis (PCA) allow researchers to identify key traits contributing to variation and to select genotypes with desirable characteristics. PCA, first introduced by Pearson (1901) and developed by Hotelling (1933), is widely used alongside discriminant, cluster, and correlation analyses to study

genetic diversity and guide plant breeding strategies (Cowen and Frey, 1987; Jolliffe, 2002; Sharifi et al., 2018).

This study was conducted to evaluate selected chickpea cultivars from Türkiye's national variety list using correlation, cluster analysis, and PCA for agronomic, morphological, and phenological traits. The objectives were to (i) assess genetic relationships among cultivars, (ii) identify key traits to prioritize in breeding programs, and (iii) examine the consistency of cluster and PCA results alongside correlation analyses. The study aimed to compare the practical reliability of these multivariate approaches for selecting genotypes and principal traits to guide the improvement of new chickpea varieties.

MATERIAL AND METHODS

Plant material

Twenty-one chickpea (*Cicer arietinum* L.) varieties that were released in Türkiye, including Aksu, Işık-05, Aziziye, ILC-482, Sağel, İzmir, Sarı-98, Çağatay, Zuhall, Hisar, Arda, Hasanbey, Diyar-95, Seçkin, Sezenbey, Cevdetbey, Uzunlu, Gülümser, Çakır, İnci, and Akça were evaluated in this study.

Experimental site and climate

The experiment was conducted at the experimental area of the Faculty of Agriculture, Department of Field Crops, OMÜ Kurupelit Campus, Samsun, Türkiye, in 2020.

Climate data were recorded for both the experimental year and the long-term period (1929-2020) (Table 1). The lowest average air temperatures occurred in February (7.1 and 5.2°C, respectively), while the highest temperatures were observed in July and August. Total precipitation in July was notably low (1.4 mm) compared to the long-term average (34.9 mm).

Soil properties

Soil samples were collected from the 0-20 cm soil layer and analyzed at the Soil Science and Plant Nutrition Department Laboratory, Faculty of Agriculture, Ondokuz Mayıs

University, to determine the physical and chemical properties of the soil. Soil analysis indicated that the experimental site had a clayey texture, a slightly acidic pH, non-saline conditions, low organic matter content, and was slightly calcareous. Soil nutrient analysis

revealed adequate levels of total nitrogen (N), available phosphorus (P_2O_5), and magnesium (Mg), whereas potassium (K) was present at an extremely high concentration in the experiment soil (Table 2).

Table 1. Meteorological data during the chickpea growing period in 2020 and the long-term (1929-2020) period belong to Samsun city of Türkiye*

Months	Average temperature (°C)		Total precipitation (mm = kg/m ²)		Relative humidity (%)	
	1929-2020	2020	1929-2020	2020	1929-2020	2020
February	7.1	5.2	58.4	61.0	78.00	66.37
March	8.1	7.2	66.6	46.3	79.00	76.65
April	11.3	10.6	56.9	36.6	74.50	77.50
May	15.6	15.0	48.4	42.7	72.30	78.35
June	20.2	19.3	45.4	33.3	72.10	76.88
July	23.2	22.0	34.9	1.4	73.60	71.96
August	23.6	22.7	37.3	22.8	74.60	68.24

*Data was obtained from the Records of Samsun Meteorology Regional Directorate.

Table 2. Some physical and chemical properties of the experimental area soil

Feature	Value	Degree
Texture (%)	30.03% sand, 23.10% loam, 46.80% clay	Clayey
pH	6.69	Slightly acidic
Total salt (mmhos/cm)	0.58	Non-saline
Lime $CaCO_3$	1.96	Less chalky
Organic matter (%)	1.00	Low
Total nitrogen (%)	0.15	Sufficient
Available phosphorus (P_2O_5)	11.70	Sufficient
Potassium (mg/kg)	310.37	Very high
Magnesium (mg/kg)	1.89	Sufficient

Field preparation, sowing and cultural practices

The soil plowed to a depth of 15-20 cm and harrowed prior to sowing. Rows were opened using a hand hoe. Sowing was carried out by hand on February 13, 2020, in plots consisting of three rows, each 3 m in length, with 50 cm inter-row spacing. Based on soil analysis, a basal fertilizer consisting of 20 kg/ha N and 60 kg/ha P_2O_5 was applied as diammonium phosphate at sowing. Weed control was performed by hand hoeing. No irrigation was applied during the growing period. Plants were harvested manually at physiological maturity and left to dry under field conditions on the soil surface for one week prior to threshing.

Plant traits, data collection and experimental design

Data were recorded for the following plant traits: seed yield per plant (PSY; g/plant), plant height (PH; cm), first pod height (FPH; cm), number of pods per plant (PN; pod/plant), number of seeds per plant (SN; seed/plant), average seed weight (ASW; g/seed), seed width (SW; mm), seed length (SL; mm), root weight per plant (PRW; g/plant), stem weight per plant (PSW; g/plant), harvest index (HI; %), days to emergence (DE; days), days to first flowering (DF; days), days to first pod setting (DPS; days), and pod setting duration (PSD; days, calculated as the interval between first and last fruit formation). Plants were hand-

harvested at seed maturity. Data on plant traits and seed yield were obtained from ten randomly selected plants, with each plant representing one replication. The experiment was conducted in the field as a completely randomized design with ten replications.

Statistical analysis

Seed yield data were analyzed by analysis of variance (ANOVA) using SPSS under a completely randomized design. Cluster analysis was performed to group the varieties and plant traits, and a clustered heatmap (double dendrogram) was generated using NCSS 12 (2018) statistical software. Principal component analysis (PCA) and correlation analyses were conducted using Jamovi (2025) to identify the most influential traits for single-plant selection in breeding programs and to examine associations among

traits. A heatmap of the correlation matrix was also plotted using Jamovi (2025).

RESULTS AND DISCUSSION

Descriptive statistics

Basic descriptive statistics for fifteen agro-morphological and phenological traits showed considerable diversity among chickpea genotypes (Table 3). The coefficients of variation (CVs) for the traits ranged from 4.73% to 34.62%. The largest CV was observed for plant root weight (PRW; g/plant), which varied between 1.01 and 4.05 g/plant. This was followed by PSD, PSW, HI, PSY, and SN. Among the examined traits, the lowest CVs were observed for the first flower appearance (DF), the first pod setting (DPS), plant height (PH), and average seed weight (ASW) (Table 3).

Table 3. Descriptive statistics for seed yield and yield-related agro-morphological traits determined in chickpea cultivars

Traits	Range	Minimum	Maximum	Mean ($\bar{x}$)	Standard error of the mean ($S\bar{x}$)	Variance (S^2)	Standard deviation (S)	Coefficient of variation (%)
PSY	2.56	1.82	4.38	3.14	0.13	0.36	0.60	19.21
PH	15.90	33.60	49.50	41.30	0.86	15.35	3.92	9.49
FPH	14.70	20.70	35.40	27.31	0.84	14.92	3.86	14.14
PN	3.90	4.90	8.80	7.21	0.20	0.83	0.91	12.64
SN	5.30	4.50	9.80	6.87	0.29	1.71	1.31	19.05
ASW	0.17	0.37	0.54	0.46	0.01	0.00	0.04	9.61
SW	4.02	3.15	7.17	5.74	0.22	1.04	1.02	17.76
SL	4.21	3.59	7.80	6.28	0.23	1.11	1.05	16.73
PRW	3.04	1.01	4.05	2.34	0.18	0.66	0.81	34.62
PSW	8.88	3.08	11.96	7.48	0.40	3.32	1.82	24.34
HI	37.93	20.67	58.60	42.68	1.93	78.26	8.85	20.73
DE	9.00	11.00	20.00	15.76	0.59	7.39	2.72	17.25
DF	11.00	50.00	61.00	54.81	0.69	9.86	3.14	5.73
DPS	11.00	60.00	71.00	63.57	0.66	9.06	3.01	4.73
PSD	10.00	5.00	15.00	8.76	0.52	5.59	2.36	26.99

PSY: Plant seed yield (g/plant), PH: plant height (cm), FPH: first pod height (cm), PN: number of pods per plant (pod/plant), SN: number of seeds per plant (seed/plant), ASW: average seed weight (g/seed), SW: seed width (mm), SL: seed length (mm), PRW: Plant root weight (g/plant), PSW: Plant stem weight (g/plant), HI: harvest index (%), DE: Days to emergence days (days), DF: Days to first flowering (days), DPS: Days to first pod setting (days), PSD: Pod setting duration (days), n=21.

Variations sourced from genetic diversity are primary criteria to evaluate the genetic potential of genetic materials as they externalize trait-related characteristics (Zhang et al., 2014). The extent of genetic variability in a given population determines the success of genetic improvement of the trait under consideration. The wide genetic variability

present in the population could be associated with a genetic basis and may reveal variation in resistance to major diseases, insects and adverse climatic changes, higher yield and quality traits which could help to select parents for developing desired varieties (Arbissie et al., 2025). High genetic divergence and CV were noted regarding all morphological

characters in chickpea (Kumar et al., 2020b). Yu et al. (2021) evaluated 12 agronomic traits in 181 chickpea accessions and determined the coefficients of variation (CV) ranged from 7.47% to 85.26%. Traits including hundred-seed weight, branch number, pod number, flowering time, overall yield, yield per plant, and number of unfilled pods, showed CV values above 30%, indicating a strong potential for improvement. Generally, selecting genotypes with high variability for a particular trait as parents increases the likelihood that crosses and subsequent selection will produce novel combinations.

Seed yield (g/plant)

Figure 1 shows the seed yields of chickpea cultivars. A horizontal green line on the seed

yield chart indicates the overall mean seed yield, which is 3.14 g/plant. Among the chickpea varieties, Akça, Çağatay, Sarı-98, Hasanbey, Hisar, Diyar-95, Sezenbey, İnci, and Aksu produced seed yields below the overall mean, whereas the remaining varieties produced yields above the mean. The Aziziye variety produced the highest plant seed yield; this was followed by Gülümser, Işık-05, Cevdetbey, Arda, Sağel, Çakır, ILC-482, Uzunlu, Seçkin, and Zuhul varieties. Erden et al. (2021) conducted a study to determine the adaptation of Gökçe, Küsmen 99, Akçin 91, Uzunlu 99, Hisar, Canıtez 87, Yaşa 05, Işık-05, Diyar 95, Güney Sarısı (ILC 482), İnci, Çağatay, Aksu and Aziziye 94 cultivars to Siirt, Türkiye conditions. Seed yield in the study ranged from 857 to 2005 kg/ha.

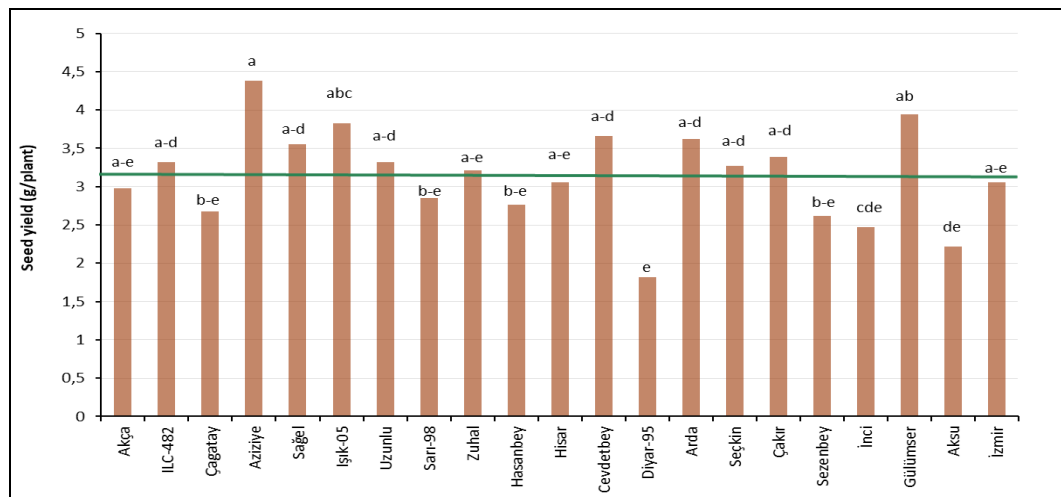


Figure 1. Plant seed yields (g/plant) of chickpea cultivars used in the experiment (No statistical difference among the seed yields indicated with the same letter, with a probability of $p < 0.05$)

Correlations among agro-morphological and phenological traits

The Correlation network plot, showing the possible relationships among all traits, and the heatmap correlation matrix illustrating only significant relationships at the $p < 0.05$ level, are given in Figure 2a and 2b, respectively. SN, SW and SL were the traits most strongly and positively correlated with PSY. PN and PSW also exhibited slightly lower, yet positive and significant relationships with PSY. Seed yield was greatly enhanced by increases in SN, SW, SL, PN and PSW. The relationships between PSY and other agro-morphological and phenological traits were not statistically

significant. PN and SN were positively and significantly associated with SW and SL. PSW was negatively and significantly correlated with PH, FPH, and HI (Figure 2a and 2b).

Several studies have identified key traits that substantially influence seed yield in chickpea. According to Kayan and Adak (2012), harvest index, number of pods per plant, biological yield, and plant height are among the most important contributors on seed yield. Similarly, Zali et al. (2011) found seed yield to be positively and strongly associated with number of seeds per plant, secondary branch number, 100-seed weight, pod number per plant, primary branch

number, and plant height. Malik et al. (2014) observed significant positive correlations between yield per plant and biological yield, number of primary and secondary branches, number of pods per plant, number of seeds per pod, and harvest index. Kumar et al. (2018) informed that seed yield per plant positively and highly significantly correlated with biological yield per plant, 100-seed

weight, harvest index and pods per plant. Erdemci et al. (2016) found that while seed yield exhibited highly significant positive associations ($p < 0.01$) with plant height, number of primary branches per plant, number of pods with seed settled per plant, and number of seeds per plant, it was significantly negatively correlated ($p < 0.05$) with 100-seed weight.

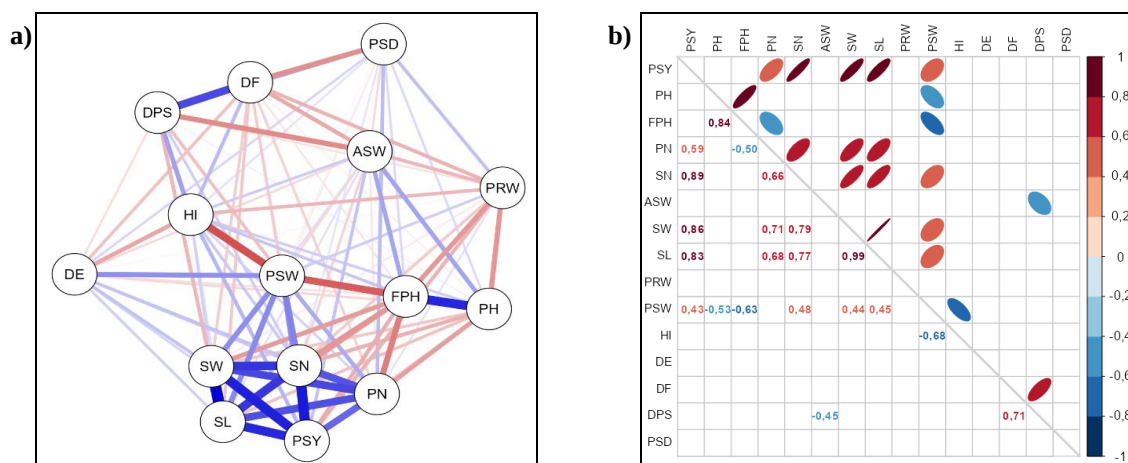


Figure 2. a) Correlation network illustrates the relationship between seed yield and all investigated agro-morphological and phenological traits studied in the present study. Each node surrounded by a ring represents one trait and lines with blue and red color indicate positive and negative correlation between two traits, respectively. b) Heatmap correlation matrix based on the Pearson correlation coefficients illustrates just correlations with statistically significant at $p < 0.05$ level. PSY: plant seed yield (g/plant), PH: plant height (cm), FPH: first pod height (cm), PN: number of pods per plant (pod/plant), SN: number of seeds per plant (seed/plant), ASW: average seed weight (g/seed), SW: seed width (mm), SL: seed length (mm), PRW: plant root weight (g/plant), PSW: plant stem weight (g/plant), HI: harvest index (%), DE: days to emergence days (days), DF: days to first flowering (days), DPS: days to first pod setting (days), PSD: pod setting duration (days), $n=21$.

Principal component analysis (PCA)

Agro-morphological and phenological (observable) traits cover the measurable and observable physical characteristics, including features such as leaf morphology, plant height, and flowering time. These traits are critical for evaluating plant performance,

adaptability, and yield potential under diverse environmental conditions.

Figure 3 shows a scree plot of the 15 principal components revealed by principal component analysis, indicating the number of explanatory factors to consider when accounting for the total variation among cultivars.

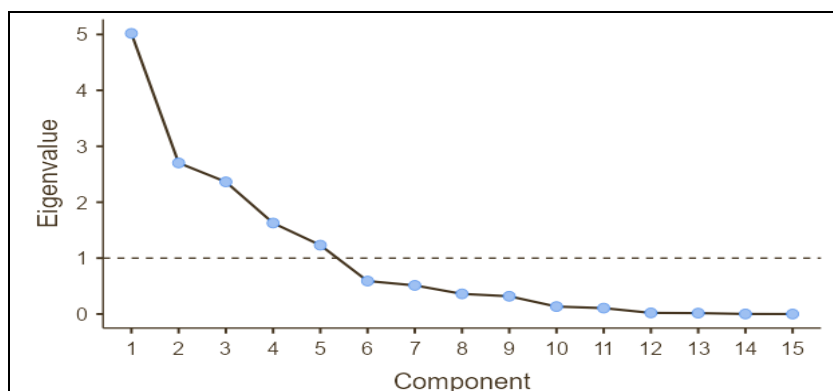


Figure 3. Scree plot exhibiting the variability determined by each component based on its own eigenvalues

Principal component analysis (PCA) revealed substantial genetic differences among the varieties. PCA resulted in 15 principal components (PCs) corresponding to the different traits. In PCA, Kaiser's rule, based on eigenvalues, was used to determine the optimal

number of PCs to retain. PC1, PC2, PC3, PC4 and PC5 had eigenvalues greater than 1, and these first five PCs explained 86.5% of the total variation. PC1 and PC2 explained 51.82% of the total variation, contributing 33.50% and 18.32%, respectively (Table 4).

Table 4. Principal components of chickpea varieties for examined traits

	PC1	PC2	PC3	PC4	PC5
Eigenvalue	5.0247	2.7475	2.3251	1.6258	1.2495
Variance explained (%)	33.50	18.32	15.50	10.84	8.33
Cumulative variance explained (%)	33.50	51.82	67.32	78.16	86.49
Traits					
PSY	0.372	0.281	-0.023	-0.073	0.069
PH	-0.237	0.322	-0.237	0.129	0.251
FPH	-0.294	0.284	-0.244	0.137	0.236
PN	0.351	0.064	0.052	0.256	-0.138
SN	0.382	0.194	0.143	0.042	0.146
ASW	-0.033	0.241	-0.461	-0.149	-0.167
SW	0.402	0.176	-0.122	-0.001	-0.054
SL	0.398	0.153	-0.138	-0.034	-0.092
PRW	0.029	-0.400	0.050	0.269	-0.444
PSW	0.308	-0.317	-0.050	-0.136	0.269
HI	-0.015	0.482	0.150	0.143	-0.344
DE	0.155	-0.171	-0.112	0.143	0.596
DF	-0.067	0.171	0.521	-0.354	0.116
DPS	-0.064	0.177	0.550	0.220	0.185
PSD	0.008	-0.002	0.009	0.750	0.082

PSY: plant seed yield (g/plant), PH: plant height (cm), FPH: first pod height (cm), PN: number of pods per plant (pod/plant), SN: number of seeds per plant (seed/plant), ASW: average seed weight (g/seed), SW: seed width (mm), SL: seed length (mm), PRW: plant root weight (g/plant), PSW: plant stem weight (g/plant), HI: harvest index (%), DE: days to emergence days (days), DF: days to first flowering (days), DPS: days to first pod setting (days), PSD: pod setting duration(days), n=21.

Kumar et al. (2021) examined 25 characteristics in 25 chickpea cultivars and determined that the first nine principal components explained 84.10% of the total variation. In the study conducted with 25 chickpea genotypes, Sharifi et al. (2018) revealed that the first three main components accounted for 69.69% of the total variability. Malik et al. (2014) studied genetic diversity of 113 desi chickpea genotypes through multivariate analysis including PCA and cluster analysis. The first four PCs accounted for 71.99% of total variation. The first principal component (PC1) showed positive associations with plant height, seed yield per plant, biological yield, secondary branches per plant, number of pods per plant, whereas the second principal component (PC2) was positively correlated with hundred-seed

weight, days to flowering, and days to maturity.

According to the PCA results, the first principal component (PC1), which explained 33.50% of the total variance, exhibited positive strong loadings for seed width (0.402), seed length (0.398), number of seeds per plant (0.382), plant seed yield (0.372), number of pods per plant (0.351), and plant stem weight (0.308), indicating that this component was mainly associated with seed size and yield-related traits. The second principal component (PC2), accounting for 18.32% of the total variance, was characterized by positive loadings for harvest index (0.482) and plant height (0.322), and negative loadings for plant root weight (-0.400) and plant stem weight (-0.317) (Table 4).

Loading plot, between PC1 and PC2, based on the correlation coefficients of the traits shows the clustered traits and their

contribution to total variance among the chickpea varieties (Figure 4).

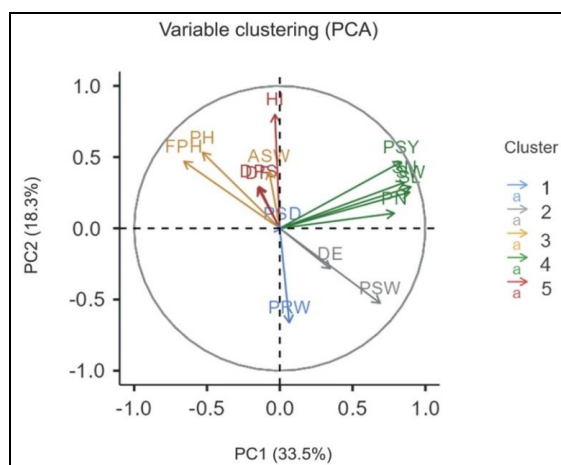


Figure 4. Loading plot between PC1 and PC2 that showing clustered traits in chickpea
 PSY: plant seed yield (g/plant), PH: plant height (cm), FPH: first pod height (cm), PN: number of pods per plant (pod/plant), SN: number of seeds per plant (seed/plant), ASW: average seed weight (g/seed), SW: seed width (mm), SL: seed length (mm), PRW: plant root weight (g/plant), PSW: plant stem weight (g/plant), HI: harvest index (%), DE: days to emergence days (days), DF: days to first flowering (days), DPS: days to first pod setting (days), PSD: pod setting duration (days), n=21.

PCA variable clustering plot illustrates trait interrelations via vector angles; positive correlations were indicated by acute angles, negative associations by obtuse angles, and very low relationships by right angles. PCA variable clustering partitioned the evaluated traits into five distinct groups with respect to 15 agronomic traits. The first cluster included PRW and PSD. PSW and DE were grouped in the second cluster. The third cluster consisted of PH, FPH and ASW. The fourth cluster comprised PSY, SN, SW, SL, and PN, indicating a close association among yield and yield-related components. Finally, DF, DPS

and HI formed the fifth cluster (Figure 4). Those relationships have also been confirmed by the correlation network plot and the correlation analysis (Figure 2a and 2b). In a study involving 25 chickpea genotypes, there were positive and important relationships between seed yield, number of pods per plant, plant canopy width, harvest index and biological yield (Sharifi et al., 2018).

Considering PC1 and PC2, chickpea varieties have been separated into four groups based on their agro-morphological and phenological characteristics (Figure 5).

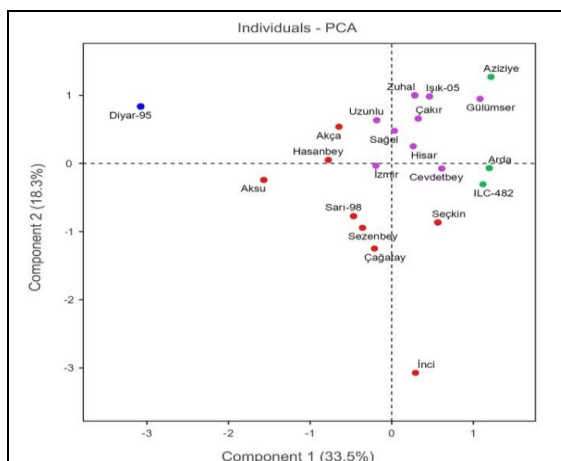


Figure 5. Distribution of chickpea varieties based on PC1 and PC2

In the scatter plot based on factor scores for PC1 and PC2, chickpea cultivars were distributed across all four quadrants of the plot, revealing genetic variation among varieties from different clusters (Figure 5). Varieties that are close together and indicated by the same-colored dot on the graph are similar regarding the examined traits while different from those in the other group. Especially, Diyar-95 and İnci were not placed in close position to the other varieties on the scatter plot. Genotypes that were not placed within the same or near cluster may have genetic variations regarding the examined traits. Therefore, it is highly possible that these varieties can be used as parents in crossing to generate new combinations in chickpea breeding.

Two-way (double heatmap) hierarchical clustering analysis

The 21 chickpea varieties were divided into four distinct groups by hierarchical heatmap clustering through the Ward technique and Euclidean distance based on standardized data regarding 15 agro-morphological and phenological traits. Hierarchical heatmap dendrogram plotted to reveal the similarities of chickpea varieties based on their agro-morphological and phenological characteristics is presented in Figure 6.

Cluster covering different chickpea varieties were indicated with red, blue, green and lilac colors for Cluster 1, 2, 3 and 4, respectively. A relative homogeneity within Cluster 1 (red-labeled varieties namely Akça, Sarı-98, Aksu, Hasanbey, Sezenbey, Çağatay, Seçkin, and İnci) was observed from the heatmap. In this cluster, trait values tend to follow similar color patterns across multiple variables. This suggests a shared phenotypic architecture, potentially reflecting similar selection histories or adaptation to comparable agro-ecological conditions. However, İnci stands out within this cluster

due to localized deviations in color intensity across several traits, indicating that while it is grouped within Cluster 1, it retains a degree of phenotypic distinctiveness that may be masked in purely hierarchical grouping.

Diyar-95 variety, which stood alone in cluster 2, was completely distinct from all other varieties with respect to the traits. This was strongly supported by its distinct color profile across numerous traits. Although Cluster 3, included in ILC-482, Aziziye, and Arda with green labeled varieties, had trait values that were more similar within the group, it was clearly differentiated from Clusters 1 and 4. This cluster hosts varieties with balanced or moderate trait expressions rather than extreme ones. Cluster 4 (purple-labeled genotypes such as İzmir, Çakır, Zuhul, Gülümser, Cevdetbey, Hisar, Uzunlu, Işık-05, and Sağel) exhibits wide internal variability that is indicated by high heterogeneity for color distributions across traits. Even though these genotypes were together in the same cluster, they may have a wider range of phenotypic expressions, possibly reflecting diverse adaptation abilities or genetic bases.

The combination of dendrogram topology with heatmap intensity patterns provides a big opportunity to interpret clustering results. A clear separation of clusters indicates that the selected traits are effective in capturing meaningful variation. In the present study, separation of clusters clearly indicates that the selected traits are effective in capturing meaningful variation. The evident differentiation of Diyar-95 and the relative distinctness of İnci varieties indicate their strategic importance as parental lines. Crosses between these genotypes, especially with the members of distant clusters such as Cluster 4, seem to enhance genetic recombination and increase the probability of obtaining transgressive segregants with improved agronomic performance.

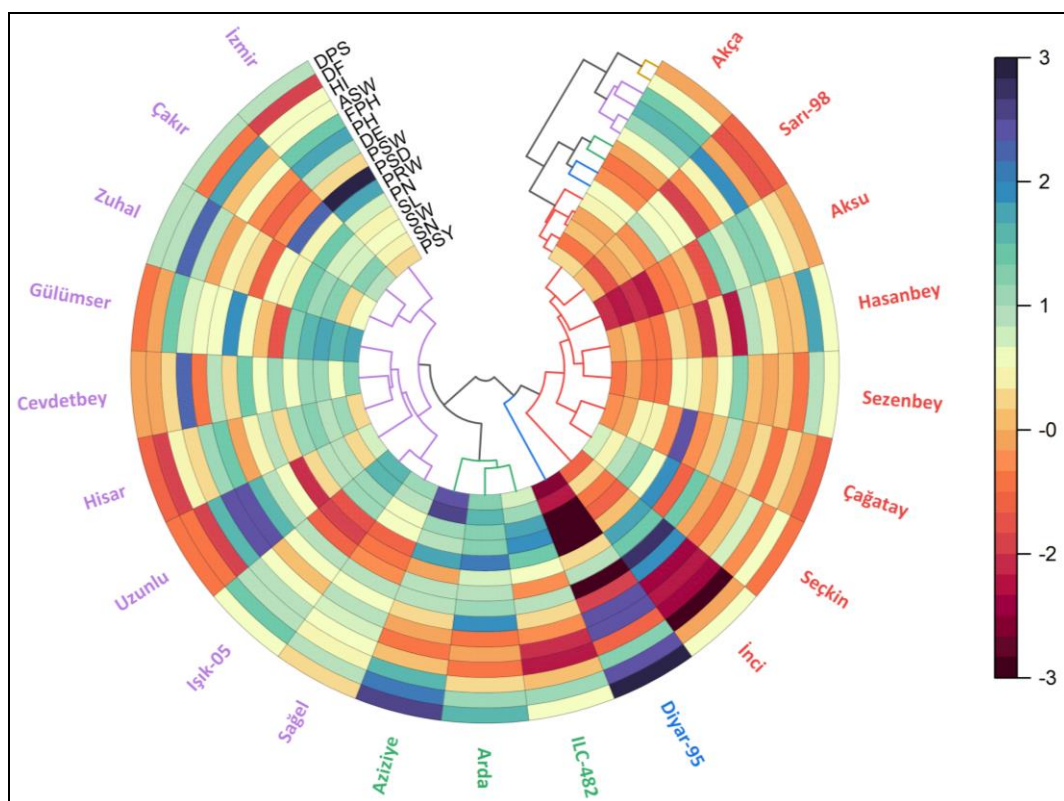


Figure 6. Circular clustered heatmap with dendrogram illustrated hierarchical clustering of chickpea varieties and agro-morphological and phenological traits. PSY: plant seed yield (g/plant), PH: plant height (cm), FPH: first pod height (cm), PN: number of pods per plant (pod/plant), SN: number of seeds per plant (seed/plant), ASW: average seed weight (g/seed), SW: seed width (mm), SL: seed length (mm), PRW: plant root weight (g/plant), PSW: plant stem weight (g/plant), HI: harvest index (%), DE: days to emergence days (days), DF: days to first flowering (days), DPS: days to first pod setting (days), PSD: pod setting duration (days), n=21.

Eser-87, Akçin-91, Canitez-87, Diyar-95, ILC-482, AK 7112, ILC-5566, Leblebik Red Chickpea, 4N-495/2, and Spanish chickpea varieties were subjected to cluster analysis to determine the level of similarity among genotypes. Eser-87, ILC-482, ILC-5566, and AK 7112 were grouped within the same cluster, clearly distinguishing them from the other genotypes. The greatest genetic distance was observed between Eser-87 and Leblebik Red Chickpea, whereas the closest relationship was found between Canitez-87 and Leblebik Red Chickpea. It has been reported that genotypes within the same cluster may be used as alternatives to each other, while crosses between genetically distant genotypes may generate novel and highly variable progenies (Karasu and Vural, 2006). Malik et al. (2014) evaluated 113 desi chickpea genotypes using descriptive statistics, principal component analysis (PCA), and cluster analysis based on morpho-genetic traits. Cluster analysis grouped the genotypes into four clusters.

Cluster I was characterized by genotypes with early flowering early maturing. Similarly, Hamayoon et al. (2011) identified three main clusters and two sub-clusters among 20 chickpea genotypes based on various traits. Mahmood et al. (2018) reported that 15 chickpea genotypes were divided into three clusters by cluster analysis according to their similarities, and very important genetic variation was found among the genotypes regarding various characteristics. It was found that these diverging genotypes have the potential to be used in chickpea breeding programs.

Heatmap clustering analysis (Figure 6) grouped the variables into five distinct clusters, relying on 15 agro-morphological and phenological traits, like PCA trait clustering (Figure 4). The first cluster included PSY, SN, SW, SL, and PN; the second cluster comprised PRW and PSD; the third cluster included PSW and DE; the fourth cluster consisted of PH, FPH, ASW, and HI; and the fifth cluster contained DF and DPS. The traits included in the clusters and the number of clusters

determined in the heatmap clustering dendrogram (Figure 6) on both variables and varieties were fully consistent with the variable clustering (Figure 4), and also variety distribution plot (Figure 5) in PCA analysis. Thus, the relationships among traits previously determined through variable clustering (Figure 4) and the grouping patterns observed in PCA (Figure 5) were confirmed once again by the double heatmap cluster analysis.

CONCLUSIONS

Multivariate analysis methods, including correlation analysis, principal component analysis, and cluster analysis, were employed to comprehensively characterize the genetic structure of the chickpea varieties. In addition, traits that contribute to increased yield in chickpea have been revealed. Seed yield per plant showed positive and significant correlations with SN, SW, SL, PN, and PSW. The correlation analysis indicated that these traits should be considered during plant selection to improve seed yield. The results of basic descriptive statistics, especially the coefficients of variation (CV), which varied between 4.73% and 34.62%, showed that there was considerable diversity among chickpea genotypes with respect to the studied traits. PSY and yield-associated traits (SN, SW, SL, and PN) clustered in the heatmap-based clustering analysis, indicating their coordinated contribution to productivity, whereas phenological traits such as DF and DPS formed a separate group, emphasizing their joint role in developmental timing. Selecting parents from genetically distant clusters, particularly those that differ in yield and phenological traits, could enhance the efficiency of breeding programs by increasing the probability of obtaining superior and diverse progeny. The current positions of both Diyar-95 and İnci within their clusters indicate that these genotypes deviate markedly from other genotypes. While Diyar-95 stands alone as an outlier, İnci appears to contribute to intra-cluster variability. These genotypes can be exploited as parents in hybridization

programs to enhance genetic diversity and improve target traits, as their divergence may reflect valuable adaptive traits or allelic combinations. The consistency among the results from double heatmap hierarchical clustering, PCA variable clustering, and genotype distribution based on PC1 and PC2 demonstrates the reliability of the multivariate methods used in this study. These results confirm that the identified trait associations and genotype clusters reflect stable and reliable patterns.

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