



original scientific paper

Ratar. Povrt. 2026, 63(2): 105-115

doi: 10.5937/ratpov63-66827

Manuscript submitted: 28 April 2026

Manuscript accepted: 27 June 2026

Published online: 19 August 2026

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Assessment of phenotypic diversity in source collection of *Cicer arietinum* L.

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Summary: Phenotypic divergence between parental forms is important for the varietal improvement. The present study aimed to find the degree of phenotypic diversity among 22 chickpea collection cultivars and to identify accessions with valuable breeding traits. The experiment was conducted during the period 2023-2025 at the Institute of Forage Crops (Pleven). Genetic distance, heritability coefficient, genetic advance, and genotypic and phenotypic variation coefficients were determined. The highest PCV and GCV were found for the traits of seeds number (49.37%, 34.05%) and pods number/plant (36.53%, 28.99%). Estimates for broad-sense heritability ranged from 5.73% for 1000-seed mass to 88.28% for plant height. High heritability coupled with high genetic advance was established for plant height ($H^2 = 88.28\%$, $GA = 9.49$) and number of pods per plant ($H^2 = 62.77\%$, $GA = 13.01$), indicating the predominance of additive gene action and the potential for successful direct phenotypic selection. Hierarchical cluster analysis and principal component analysis classified the cultivars into distinct groups based on their agro-morphological profiles. The genotypes Garbanzo 4, Alfa, Caqui, Garbanzo 1, and Blanco Lechoso exhibited the highest genetic divergence, marking them as valuable parental components for hybridization programs aimed at improving chickpea productivity and environmental adaptability.

Key words: chickpea, phenotypic diversity, cluster analysis, heritability, genetic advance

Introduction

The use of plant genetic resources to develop improved cultivars adapted to the specific conditions of agroecosystems is a key element to ensuring food security and sustainable crop production. Legumes have great potential for realization, the most common among them being beans, peas, and chickpeas. Legumes are widely considered as “thrifty and economical” plant species and excellent predecessors for many crops (Shikhalieva et al., 2016; Wang et al. 2021).

Among legumes, chickpea (*Cicer arietinum* L.) takes second position worldwide in terms of harvested area and third position in seed production. The seeds are a good source of energy, protein, minerals, vitamins, fiber, and beneficial phytochemicals. Among annual legumes, chickpea is the most hypocholesterolemic agent. Sprouted chickpea seeds are effective in regulating cholesterol levels. In regions where it is grown, chickpeas are widely used for food and feed purposes, as well as raw material for the canning and food industries (Germantseva, 2019; Duarte, 2022). However, modern chickpea varieties are sensitive to disease and drought. One of the ways to improve this crop is the introgression of adaptability genes from old varieties, especially from sites of phenotypic diversity and the centers

of the species' origin, primary – Turkey and secondary – Ethiopia (Shikhalieva et al., 2016; Kalve & Tadege, 2017).

In Bulgaria, chickpea has been an old traditional crop with various uses. It is used not only in animal husbandry, but in many countries around the world it is a staple food in vegetarian diets. Seeds are a major source of food and, when combined with cereals, provide a nutritionally balanced amino acid composition with a ratio close to the ideal for humans (Leterme, 2002; Petrova & Angelova, 2021). Compared to other legumes, the improvement of chickpea varietal composition began later in time and on a very limited scale. Increased interest has been observed in recent years with the introduction of a vaster range of cultivars, which has led to the production of diverse and healthy products (Mihov et al., 2001; Petrova et al., 2011).

Genetic diversity is the basis of plant survival in nature and crop improvement. It has been a subject of scientific interest among researchers who have studied the relative contributions of different divergence traits, the model of genotype clustering, and breeding effectiveness (Bisht et al., 2005; Thakur et al., 2018). Genetic divergence between parental forms plays a vital role in cultivar improvement due to a greater variability in hybrid generations, which can be used to improve some crop characteristics (Nimbalkar et al., 2017). The present study aimed to reveal the extent of genetic diversity among chickpea cultivars, and to identify accessions with valuable breeding traits.

Materials and Methods

The field experiment was conducted at the Institute of Forage Crops (Pleven, Bulgaria) located at 43°25' N latitude and 24°37' E longitude in the period 2023–2025, on a leached chernozem soil type with an organic matter content of approximately 2.5–3.0%. The experiment followed a long plot design method with three replications. Each experimental plot consisted of 2 meters in length, with a harvest plot area of 2.0 m². Sowing was performed manually during the optimum spring period (late March to early April) at a sowing density of 40 viable seeds per m². The inter-row spacing was maintained at 50 cm, with an intra-row spacing of 5–7 cm between plants. No chemical fertilizers or irrigation were applied, and weed control was managed mechanically by hand hoeing. Vegetative activities related to chickpea cultivation were carried out according to the technology of growing the crop.

A collection of 22 chickpea cultivars was used including genotypes from the types “desi”, “kabuli,” and an intermediate type, “pea grain” (Table 1). A comparative varietal evaluation was carried out according to 9 main quantitative characteristics: aboveground biomass/plant (g), number of basal branches/plant, height/plant (cm), 1st pod height (cm), pods number/plant, seeds number/plant, seed weight/plant (g), 1000 seeds mass (g), pod length (mm) (Table 4).

The following statistical methods were used to process the results: factor analysis using the principal components method (PC1 and PC2) (Vandev, 2003), hierarchical cluster analysis (Ward, 1963) – for grouping genotypes based on similarity as a measure of differences (genetic distance). The Euclidean distance was defined as a measure of divergence, as the data were standardized.

The phenotypic and genotypic components of variation, including heritability and genetic advance, were calculated based on the pooled data averaged across the three experimental years during which this study was conducted in (2023–2025). Data from individual years were combined into a grand mean for each genotype to minimize the influence of annual environmental fluctuations and to obtain more stable and representative phenotypic values for the evaluated chickpea collection.

Genotypic (σ^2_g) and phenotypic (σ^2_p) variances as well as genotypic (GCV) and phenotypic coefficients of variation (PCV) were calculated according to Singh & Chaudhary (1985). Genetic advance (GA) was calculated according to the method of Johnson et al. (1955). The genotypic (GCV, %) and phenotypic coefficient of variation (PCV, %) were determined using the following formulas:

$$GCV\% = \frac{\sqrt{\sigma^2_g}}{\bar{X}} \cdot 100$$

$$PCV\% = \frac{\sqrt{\sigma^2_p}}{X} \cdot 100$$

, where X is the grand mean of the population for each specific trait.

Broad-sense heritability (H^2) was estimated as the ratio of genotypic variance to phenotypic variance:

$$H^2 = \sigma^2_g / \sigma^2_p \cdot 100$$

The expected genetic advance (GA) and genetic advance as a percentage of the mean (GAM) under selection (at 5% selection intensity, $k = 2.06$) were calculated according to Allard (1960) and Johnson et al. (1955):

$$GA = k \cdot \sigma_p \cdot H^2$$

$$GAM (\%) = GA / X \cdot 100$$

Table 1. Source collection of chickpea cultivars

Cultivar	Origin	Type
Alfa	Slovak Republic	pea grain
Beta	Slovak Republic	pea grain
Businsky	Slovak Republic	pea grain
Irenka	Slovak Republic	desi
Krajova z Kralovej	Slovak Republic	pea grain
Maskovsky Bagovec	Slovak Republic	pea grain
Slovak	Slovak Republic	pea grain
FLIP84- 149 C	Slovak Republic	pea grain
VSP 11	Slovak Republic	pea grain
Progres	Bulgaria	pea grain
Balkan	Bulgaria	pea grain
Garbanzo 1	Spain	kabuli
Blanco Lechoso	Spain	kabuli
Caqui	Spain	desi
Garbanzo negro	Spain	desi
Tadzkikij 10	Tajikistan	desi
Sovhoznyj 14	Russia	desi
Dneprovskij 1	Ukraine	pea grain
Garbanzo 2	Spain	pea grain
Garbanzo 3	Spain	pea grain
Garbanzo 4	Spain	pea grain
Plovdiv8	Bulgaria	pea grain

Multivariate statistical analyses, including Principal Component Analysis (PCA) and Cluster Analysis (Hierarchical Cluster Analysis using Ward's method and Euclidean distance), were performed to assess the phenotypic diversity among the cultivars. Data processing was carried out using the STATGRAFS 2.1 program and SPSS 13 software product. The statistical significance of the differences among the evaluated chickpea cultivars for all quantitative traits was verified by analysis of variance with probability level $p < 0.05$.

Results and Discussion

Phenotypic diversity in breeding is essential for it to be effective. The use of genetically distant accessions as parental forms in combinative breeding creates adequate prerequisites and opportunities for the manifestation of heterosis and transgressions in hybrid offspring. It is considered that the

assessment of genetic distance between genotypes is determined by the phenotypic expression of quantitative and qualitative traits. If genotypes differ phenotypically in many traits, they would also be genetically and genomically distant (Gocheva, 2020).

Cluster analysis

To identify the similarity and proximity of chickpea cultivars, hierarchical cluster analysis was applied. The clustering was based on the complex action of 9 variables corresponding to the 9 quantitative traits. The resulting dendrogram displays a clustering of the variants into 2 main groups (A and B) (Figure 1).

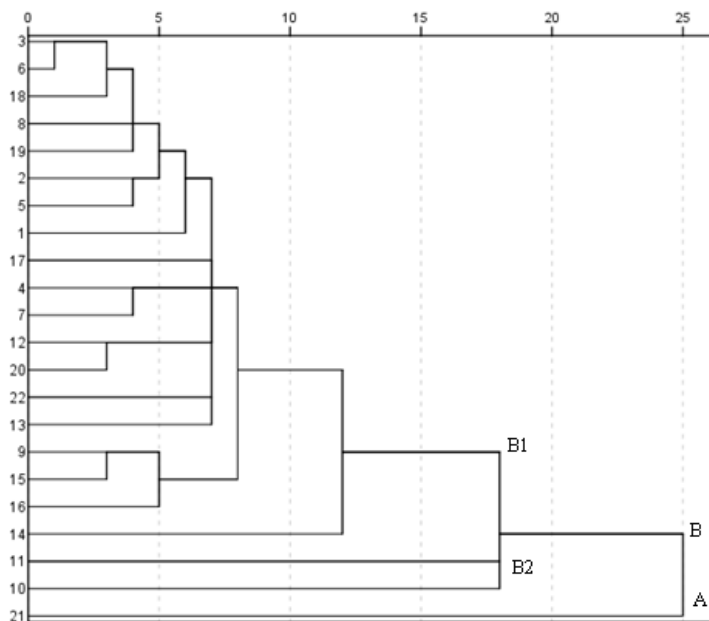


Figure 1. Dendrogram of chickpea cultivars

1-Alfa; 2-Beta; 3-Businsky; 4-Irenka; 5-Krajova z Kralovej; 6-Maskovsky Bagovec; 7-Slovak; 8-FLIP 84-149 C; 9-VSP 11; 10-Progres; 11-Balkan; 12-Garbanzo 1; 13-Blanco Lechoso; 14-Caqui; 15-Garbanzo negro; 16-Tadziksij 10; 17-Sovhoznyj 14; 18-Dneprovskij 1; 19-Garbanzo 2; 20-Garbanzo 3; 21-Garbanzo 4; 22-Plovdiv 8

Cluster A included only Garbanzo 4, which was characterized by an increased number of seeds per plant, small pods, low mass per 1000 seeds, and high seed productivity.

Cluster B was represented by two subclusters: B1 and B2. The first subcluster (B1) was formed by a larger group of cultivars. The Caqui genotype was located alone at the bottom of the dendrogram within subcluster B1 because it had the highest seed productivity compared to the other cultivars, as well as increased values for the number of pods and seeds per plant and the number of basal branches. Caqui was also characterized by lower values for 1000-seed mass and pod length.

The next group from subcluster B1, located at the top of the dendrogram, was the most numerous and consisted of several subgroups. Alfa, Beta, Businsky, Krajova z Kralovej, Maskovsky Bagovec, FLIP 84-149 C, Dneprovskij 1, and Garbanzo 2 were distinguished by similarity in the characteristics of height/plant, number of pods and pod length. Another subgroup included Irenka, Slovak, Garbanzo 1, Blanco Lechoso, Sovhoznyj 14 and Garbanzo 3. They were characterized by shorter stems, a lower formation of 1st pods, and a relatively small number of pods per plant. In most cases, the studied traits, the differences between them, and the remaining accessions from other subclusters were statistically insignificant. A separate subgroup was formed by VSP 11, Garbanzo negro and Tadziksij 10. Except for two traits (number of pods and seeds/plant), they were inferior to the other cultivars in their ability to manifest traits.

The obtained results partially support the studies of Kuz'mina et al. (2022), who, after evaluating chickpea varieties based on the studied traits using the Euclidean distance method, found that the collection accessions were divided into 5 groups with different breeding value. The authors pointed out that the most promising varieties, in practical and breeding terms, were those belonging to the IVth cluster of the Kabuli morphotype. In comparative testing of 27 chickpea varieties and after applying cluster analysis, Syed et al. (2012) found the formation of five main groups of genotypes by quantitative and qualitative traits. Cluster II included the largest number of genotypes, and cluster I contained the smallest number of genotypes, characterized by an increased number of pods/plants. The effectiveness of cluster analysis as a method for assessing phenotypic diversity has also been reported by Vus et al. (2020). When analyzing a large collection of chickpea accessions, they noted that cluster analysis based on many parameters allowed for the choice of suitable parental pairs. The authors found out that genotypes from cluster IV have been good donors of desirable traits and can be used in specialized breeding programs.

In another study, Meena et al. (2025) assessed the phenotypic diversity of 40 chickpea cultivars using cluster analysis. The genotypes were grouped into eight clusters, suggesting a high level of phenotypic diversity. Cluster III, which included ten genotypes, was the most numerous. The authors noted that seed productivity/plant (18.07%) and pod number (3.26%) had the maximum contribution to divergence. They concluded that these characteristics should be given greater attention in breeding for high-yielding chickpea varieties. Janghel et al. (2020) and Katkani et al. (2022) summarized that systematic selection of parental lines shows that genotypes from clusters with maximum distance between them can be used as starting forms for creating varieties with improved productive potential and good seed quality. These findings were in accordance with earlier studies by Vural & Karasu (2007), Aarif et al. (2017), and Haralayya et al. (2017).

Principal component analysis

The principal component analysis aims to establish which of the analyzed traits have a determining influence on the cultivar clustering. The analysis was conducted up to the third principal component with an eigenvalue above one, which explains over 77% of the total variation. Approximately 2/3 of the total variation of phenotypic expression of genotypes for the studied traits was due to the first two principal components – PC1 and PC2. This value indicated considerable diversity of the genotypes for the studied traits.

The first principal component (Table 2, Figure 2) explains 38.66% of the total variation, where the traits of seed weight/plant, biomass/plant, number of pods, and seeds/plant had the greatest relative weight value for the indicated clustering. The positive value for seed weight/plant and the negative value for height/plant, 1st pod height and 1000 seed mass indicated that there is a favorable opportunity for breeding genotypes with shorter stems, lower mass per 1000 seeds, and high productivity. Regarding the second principal component, the traits of 1000 seeds mass, pod length, and biomass/plant had a determining role. On the other side, height/plant and 1st pod height had less importance. The third principal component (PC3), with a weight above 1, explained 13.417% of the total variation. Positive values of PC3 for 1000 seeds mass and number of branches showed the possibility of breeding to increase productivity by improving these parameters.

The differences among cultivars (Table 3) are reflected by their grouping by the values of the principal components, which indicate that they respond specifically to changing environmental conditions. The Caqui variety received the highest PC1 score (3.79), followed by Garbanzo 4 (2.98), Krajova z Kralovej (2.49), and Beta (1.63). This indicates that these genotypes possess high values for biomass/plant, seeds number/plant and seed productivity.

In PC2, the highest results were obtained for Garbanzo 1 and Blanco Lechoso, whose results were mainly related to 1000 seeds mass, longer pods, and a smaller number of pods and seeds per plant. Regarding PC3, the highest results were found in FLIP 84-149 C, Slovak, Businsky, and Maskovsky Bagovec, where most of the traits exhibited medium manifestation. The same cultivars can be characterized as small-seeded and low-yielding.

Multivariate analysis methods are widely used to assess the phenotypic diversity of various plant breeding materials. Figure 3 presents the arrangement of genotypes according to their values for the principal components PC1 and PC2.

Table 2. Principal component analysis for quantitative traits in chickpea cultivars

Traits	PC1	PC2	PC3
Aboveground biomass/plant	0.434	0.337	-0.0005
Number of basal branches/plant	0.384	0.273	0.142
Height/plant	-0.073	0.135	-0.832
1st pod height	-0.310	0.119	-0.241
Pods number/plant	0.402	-0.296	-0.092
Seeds number/plant	0.403	-0.266	-0.203
Seed weight/plant	0.485	0.139	-0.130
1000 seeds mass	-0.046	0.546	0.319
Pod length	-0.038	0.549	-0.245
Eigenvalue	3.479	2.315	1.21
Percent of Variance	38.663	25.729	13.417
Cumulative Percentage	38.663	64.39	77.81

The biplot graph of the genotypes shows that they were quite different from each other and distributed across the four quadrants. By comparing the two figures (Figure 2 and Figure 3), the association of genotypes into groups according to certain characteristics can be assessed. The closer the points of the genotypes in Figure 3 are located to those of the corresponding traits in Figure 2, the more decisive this trait is in their grouping.

The 22 evaluated chickpea cultivars were distributed into four distinct groups across the quadrants defined by the positive and negative coordinates of PC1 and PC2 on the biplot. The first group, located in Quadrant I, clustered together a specific set of genotypes, including Alfa, Beta, Krajova z Kralovej, and Garbanzo 2. These cultivars exhibited a strong positive association with PC1 loading vectors, primarily being characterized by high values for yield-related traits such as biomass per plant, plant height, and pods number per plant. The third group was the most numerous, clustering 8 cultivars: Businsky, Irenka, Maskovsky Bagovec, Slovak, FLIP 84-149 C, Sovhoznoj 14, Dneprovskij 1, and Plovdiv 8. These genotypes were distinguished by an optimal architecture defined by increased plant height and 1st pod height, along with stable expressions for number and weight of seeds per plant. The fourth group comprised only of 4 cultivars (Progress, Garbanzo 1, Blanco Lechoso, and Garbanzo 3), which were phenotypically characterized by an increased number of basal branches and longer pods, while demonstrating a comparatively lower number of pods and seeds per plant. This spatial alignment of genotypes perfectly corresponds with the underlying factor loadings, providing a robust biological interpretation of the diversity within the source collection.

These results can be used to suggest precise breeding criteria, the intensity of which can be determined by the variability explained by each principal component. In principle, a high PC score for a given genotype in a particular component means high values for the variables (traits) in that genotype. Similar findings had been reported by Hailu (2020) and Ningwal et al. (2023), who recorded considerable trait variability in chickpea accessions. The authors had obtained high values of genotypic and phenotypic coefficients of variation for height/plant, pods/plant, seed weight/plant and 1000 seeds mass. The investigations of Dixit et al. (2022) and Karimizadeh et al. (2021) were in line with the results of the study conducted. The researchers found that the studied chickpea genotypes had very high phenotypic variability in the following traits: 1000 seeds mass, number and weight of seeds per plant. According to the authors, these are some of the most important characteristics for evaluating grain productivity in chickpeas.

Table 3. Principal component analysis for chickpea cultivars

Cultivars	PC1	PC2	PC3
Alfa	1.26	0.85	0.17
Beta	1.63	1.15	-0.33
Businsky	-0.62	-0.40	0.34
Irenka	-3.01	-1.48	-0.34
Krajova z Kralovej	2.49	1.61	0.02
Maskovsky Bagovec	-0.33	-0.19	0.31
Slovak	-1.87	-1.03	0.45
FLIP 84-149 C	-0.20	-0.37	0.53
VSP 11	0.38	-2.82	0.19
Progres	-0.84	2.11	-4.17
Balkan (st)	0.81	-0.15	0.66
Garbanzo 1	-1.03	3.12	0.55
Blanco Lechoso	-0.68	2.82	2.01
Caqui	3.79	-0.55	-0.38
Garbanzo negro	0.66	-1.31	0.07
Tadziskij 10	0.81	-2.17	-0.38
Sovhoznyj 14	-1.37	-0.36	0.101
Dneprovskij 1	-1.37	-1.09	0.004
Garbanzo 2	0.81	0.46	0.20
Garbanzo 3	-1.65	0.92	1.08
Garbanzo 4	2.98	-0.83	-0.39
Plovdiv8	-4.09	-0.31	-0.69

Heritability coefficient and genetic advance

The values of genotypic (GCV) and phenotypic (PCV) coefficient of variation, genotypic (σ^2_g) and phenotypic variance (σ^2_p), genetic advance (GA), and broad sense heritability (H^2) are presented in Table 4. High values of GCV and PCV were found for seeds number (49.37%, 34.05%) and pods number (36.53%, 28.99%). Therefore, the variation between the studied cultivars was greatest for these parameters.

For all investigated traits, the phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV), confirming that phenotypic variation is composed of genetic components and environmental influences. The highest PCV (53.86%) and lowest GCV (5.65%) were recorded for 1000 seed mass. Essential differences between GCV and PCV were also found in pod length and seed/plant weight, indicating the considerable influence of the environment on their formation.

Genetic advance (GA) is a crucial indicator in plant breeding, serving as a valuable supplement to the heritability coefficient for predicting the expected progress under selection. In the present study, the highest genetic advance was calculated for seeds number per plant (15.82), aboveground biomass per plant (13.88), and number of pods per plant (13.01). Conversely, a moderate genetic advance was recorded for plant height (9.49) and seed weight per plant (3.31), while low genetic advance values were observed for all other investigated traits, including number of basal branches (0.54) and pod length (0.11).

Similar genetic variability trends in chickpea genotypes have been discussed by Durgarani et al. (2025), who noted that significant morphological variation forms the basis for effective selection. However, the exact heritability and genetic progress values often vary depending on the specific breeding collections used.

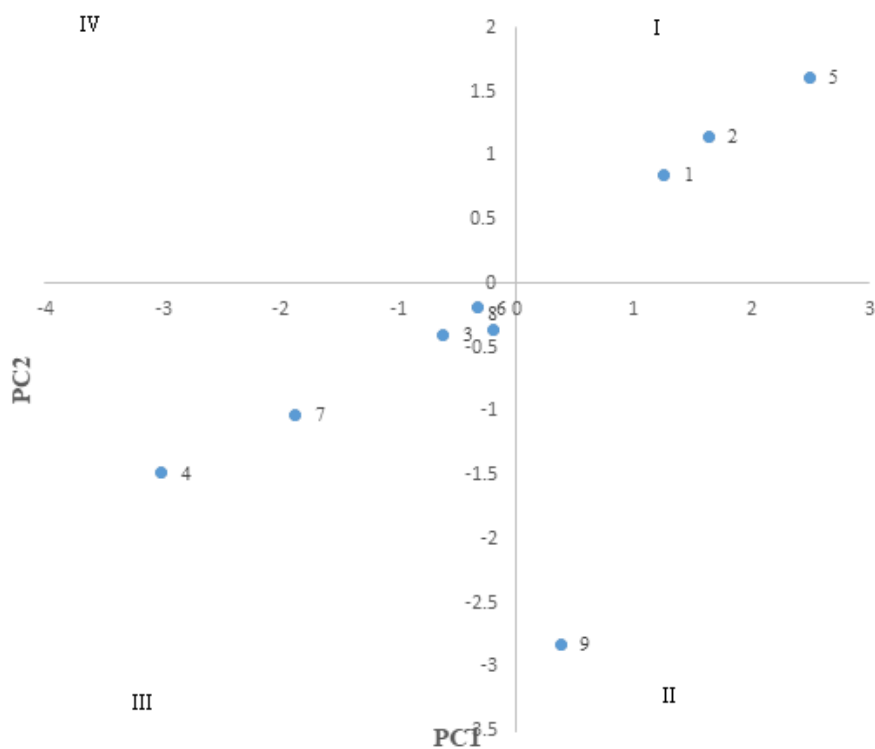


Figure 2. Projection of the studied traits in the factor plane / Слика 2.

1 - aboveground biomass/plant, 2 - number of basal branches/plant, 3 - height/plant, 4 - 1st pod height (cm), 5 - pods number/plant, 6 - seeds number/plant, 7 - seed weight/plant, 8 - 1000 seeds mass, 9 - pod length

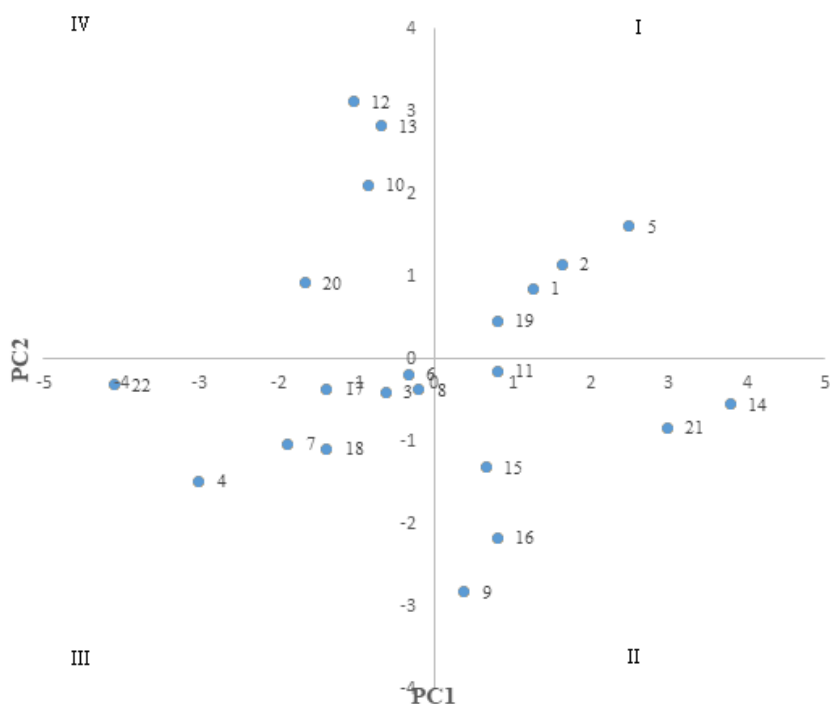


Figure 3. Projection of chickpea cultivars in factor plane

1-Alfa, 2-Beta, 3-Businsky, 4-Irenka, 5-Krajova z Kralovej, 6-Maskovsky Bagovec, 7-Slovak, 8-FLIP 84-149 C, 9-VSP 11, 10-Progres, 11-Balkan, 12- Garbanzo 1, 13-Blanco Lechoso, 14-Caqui, 15-Garbanzo negro, 16-Tadzikskij 10, 17-Sovhoznyj 14, 18-Dneprovskij 1, 19-Garbanzo 2, 20 Garbanzo 3, 21-Garbanzo 4, 22-Plovdiv 8

It is well established that high heritability combined with high genetic advance indicates the presence of additive gene effects, making phenotypic selection highly effective. In our study, robust additive gene actions were predominantly expressed for plant height ($H^2=88.28\%$, $GA=9.49$) and number of pods per plant ($H^2=62.77\%$, $GA=13.01$). The heritability of productivity and its components remains a central focus for breeders. Our results revealed that broad-sense heritability ranged from 5.73% for 1000-seed mass to 88.28% for plant height. Traits exhibiting moderate to high heritability included number of pods per plant (62.77%), number of basal branches (57.14%), aboveground biomass per plant (50.01%), and seeds number per plant (47.41%).

Table 4. Phenotypic and genotypic components of variation in chickpea cultivars

Trait/parameter	ABP	NBBP	HP	FPP	PNP	SNP	SWP	1000SM	PL
Min	28.80	1.20	31.00	15.80	26.40	32.40	9.67	10.28	1.29
Max	102.24	4.40	76.00	40.80	258.60	434.40	39.31	585.00	4.06
PCV (%)	20.20	14.47	8.56	12.83	36.53	49.37	31.02	53.86	18.08
GCV (%)	14.33	11.13	8.05	7.37	28.99	34.05	13.31	12.85	6.82
σ^2_p	181.06	0.21	27.31	13.14	100.28	262.64	59.54	139.28	0.156
σ^2_g	90.54	0.12	24.11	4.32	62.95	124.51	10.98	7.98	0.022
H^2 (%)	50.01	57.14	88.28	32.88	62.77	47.41	18.44	5.73	14.10
GA	13.88	0.54	9.49	2.45	13.01	15.82	3.31	1.39	0.11

ABP – aboveground biomass per plant (g); NBBP – number of basal branches per plant; HP – plant height (cm); FPP – first pod height (cm); PNP – number of pods per plant; SNP – number of seeds per plant; SWP – seed weight per plant (g); 1000SM – 1000-seed mass (g); PL – pod length (mm); GCV (%) - genotypic coefficient of variation; PCV (%) - phenotypic coefficient of variation; σ^2_g - genotypic variance; σ^2_p - phenotypic variance; GA - genetic advance; H^2 - broad sense heritability

It is known that high heritability, combined with high genetic progress, indicates the presence of additive gene effects, whereas high heritability, combined with low genetic progress, is an indicator of the manifestation of non-additive gene effects in the trait expression.

The heritable nature of yield components is always a central focus for breeders. Our updated results demonstrated that broad-sense heritability estimates ranged from a low of 5.73% (for 1000-seed mass) to a high of 88.28% (for plant height). Under the specific experimental conditions, relatively high to moderate heritability values were also recorded for number of pods per plant (62.77%), number of basal branches (57.14%), aboveground biomass per plant (50.01%), and seeds number per plant (47.41%). Singh et al. (2020) and Srijia et al. (2022) similarly emphasized that when heritability is coupled with substantial genetic advance, selection success can be achieved more efficiently due to the prominent correspondence between phenotype and genotype driven by additive gene actions.

Conclusions

The study demonstrated significant agro-morphological diversity among the 22 evaluated chickpea cultivars, highlighting their substantial potential for future breeding programs. High estimates of heritability coupled with steady genetic advance for plant height, number of pods per plant, and seeds number per plant indicate that these traits are governed predominantly by additive gene action and can be effectively improved through direct phenotypic selection.

The pronounced genetic distance identified between Garbanzo 4, Alfa, Caqui, Garbanzo 1, and Blanco Lechoso suggests that these distinct genotypes should be prioritized as parental components in hybridization schemes. Utilizing these divergent sources will maximize transgressive segregation, thereby driving significant progress in chickpea yield components and environmental adaptability.

Author contributions: Conceptualization, data curation, formal analysis and investigation - G.B., Methodology - V.K., N.G. and S. N., Resources - V.K, N. G. and S. N., Validation - V.K. and N.G. Visualization and Writing - original draft - M. G., Writing - review & editing -G.B..

Competing interests statement: No competing interests were disclosed.

Funding statement: No external funding was disclosed.

Data availability statement: All data gathered in this study are included in this article and are available from the corresponding author upon reasonable request.

Ethical issues statement: This research did not involve human or animal subjects. Ethical approval was therefore not required. All experimental procedures adhered to institutional and scientific guidelines for plant research. No AI tools were used in the preparation of this manuscript.

References

- Aarif, M., Rastogi, N. K., Johnson, P. L., & Yadav, S. K. (2017). Genetic divergence analysis in kabuli chickpea (*Cicer arietinum* L.). *Journal of Pharmacognosy and Phytochemistry*, 6(4), 1775-1778.
- Allard, R. W. (1960). *Principles of Plant Breeding*. John Wiley & Sons, New York, USA.
- Bisht, I. S., Bhat, K. V., Lakhanpaul, S., Latha, M., Jayan, P. K., Biswas, B. K., & Singh, A. K. (2005). Diversity and genetic resources of wild Vigna species in India. *Genetic Resources and Crop Evolution*, 52(1), 53-68. <https://doi.org/10.1007/s10722-005-0286-0>
- Dixit, G. P., Srivastava, A. K., Jayalakshmi, V., Bindra, S., & Singh, S. (2022). Chickpea Breeding. In Yadava, D. K., Dikshit, H. K., Mishra, G. P., & Tripathi, S. (Eds.), *Fundamentals of Field Crop Breeding* (pp. 1009–1062). Singapore: Springer Nature Singapore. https://doi.org/10.1007/978-981-16-9257-4_20
- Duarte, I. (2022). Chickpea breeding program and research in Portugal. *Open Journal of Plant Science*, 7(2), 034-042. <https://doi.org/10.17352/ojps.000049>
- Durgarani, M., Rathod, R., Ravinder, J., Bhargavi, B. M., & Sri, G. D. (2025). Multivariate Analysis in Chickpea (*Cicer arietinum* L.) Cultivars. *Journal of Scientific Research and Reports*, 31(6), 503–512. <https://doi.org/10.9734/jsrr/2025/v31i63147>
- Germantseva, N. I. (2019). Rezultaty i perspektivy selektsii nuta na Krasnokutskoi stantsii [The results and perspectives of chickpea breeding at Krasnokutskaya station]. *Agrarnyi vestnik Yugo-Vostoka*, 1(21), 9-14.
- Gocheva, M. (2020). Otsenka na genetichnoto raznoobrazie na obraztsi prolethen echemik ot Severnoamerikanski proizkhod [Assessment of the genetic diversity of spring barley samples from North American origin]. *Rastenievadni nauki*, 57(3), 3-8.
- Hailu, F. (2020). Genetic Variability, Heritability and Genetic Advance of Kabuli Chickpea (*Cicer arietinum* L.) for Agronomic Traits at Central Ethiopia. *International Journal of Plant Breeding and Crop Science*, 7(1), 710-714.
- Haralayya, D., Salimath, P. M., Aghora, T. S., Adivappar, N., & Ganga, P. S. (2017). Genetic diversity analysis by D2 clustering of yield and yield attributing traits in French bean (*Phaseolus vulgaris* L.). *J. Pharmacogn. Phytochem*, 6(6), 1331-1335.
- Janghel, D. K., Kumar, K., Sunil, R., & Chhabra, A. K. (2020). Genetic diversity analysis, characterization and evaluation of elite chickpea (*Cicer arietinum* L.) genotypes. *International Journal of Current Microbiology and Applied Sciences*, 9(1), 199-209. <https://doi.org/10.20546/ijcmas.2020.901.023>
- Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of genetic and environmental variability in Soybeans. *Agronomy Journal*, 47(7), 314-318. <https://doi.org/10.2134/agronj1955.00021962004700070009x>
- Kalve, S., & Tadege, M. (2017). A comprehensive technique for artificial hybridization in Chickpea (*Cicer arietinum* L.). *Plant Methods*, 13(1), 52. <https://doi.org/10.1186/s13007-017-0202-6>
- Karimizadeh, R., Keshavarzi, K., Karimpour, F., & Sharifi, P. (2021). Analysis of Screening Tools for Drought Tolerance in Chickpea (*Cicer arietinum* L.) Genotypes. *Agricultural Science Digest*, 41(4), 531-541. <https://doi.org/10.18805/ag.D-255>
- Katkani, D., Babbar, A., Upadhyay, S., & Goyal, V. (2022). Computation of Genetic Variability and Divergence Analysis in Advance Breeding Lines of Chickpea. *Biological Forum – An International Journal*, 14(2), 611-617.
- Kuz'mina, S. P., Kazydub, N. G., Bulyntsev, S. V., & Vlasova, A. A. (2022). Primenenie klasternogo analiza dlia opredeleniia selektsionnoi tsennosti nuta (*Cicer arietinum* L.) [Application of cluster analysis to determine the breeding value of chickpeas (*Cicer arietinum* L.)]. *Vestnik Omskogo gosudarstvennogo agrarnogo universiteta*, 2(46), 13-21. https://doi.org/10.48136/2222-0364_2022_2_13
- Leterme, P. (2002). Recommendations by health organizations for pulse consumption. *British Journal of Nutrition*, 88(S3), 239–242. <https://doi.org/10.1079/BJN2002712>
- Meena, V. K., Verma, P., Jajoriya, R., & Sharma, R. (2025). Genetic Diversity Analysis in Chickpea (*Cicer arietinum* L.) Genotypes in South-Eastern Rajasthan, India. *Journal of Experimental Agriculture International*, 47(4), 16-22. <https://doi.org/10.9734/jeai/2025/v47i43353>
- Mihov, M., Mehandeziev, A., & Stoyanova, M. (2001). Achievement in the breeding of cool grain legume crops. Anniversary Scientific Session. *Breeding and farming equipment for field crops*, 1, 283-286.
- Nimbalkar, R. D., Katre, Y. Y., & Phad, D. S. (2017). Genetic diversity in Chickpea (*Cicer arietinum* L.). *Bioinfolet*, 14(1), 60-63.
- Ningwal, R., Tripathi, M. K., Tiwari, S., Yadav, R. K., Tripathi, N., Solanki, R. S., Asati, R., & Yasin, M. (2023).

- Assessment of genetic variability, correlation and path coefficient analysis for yield and its attributing traits in chickpea (*Cicer arietinum* L.). *Pharma Innovation Journal*, 12(3), 4851-4859.
- Petrova, S., & Angelova, S. (2011). Status of the national chickpea collection in Bulgaria. *Bulletin of the Transilvania University of Braşov. Series VI: Medical Sciences*, 4(53) No. 2, 73-80.
- Petrova, S., Ivanova, I., & Angelova, S. (2011). Characterization of local and introduced samples from the collection of chickpea (*Cicer arietinum*). *Scientific Researches of the Union of Scientists in Bulgaria – Plovdiv*, 8, 218-221.
- Shikhalieva, K. B., Akperov, Z. I., Amirov, L. A., Gasanova, S. K., & Babaeva, S. M. (2016). Rol' genofonda nuta (*Cicer arietinum* L.) iz koleksii zernobobovykh kul'tur v reshenii zadach selektsii v Azerbaidzhane [Role of chickpea (*Cicer arietinum* L.) gene pool from grain legume collection in solving breeding problems in Azerbaijan]. *Uspekhi sovremennogo estestvoznaniya*, 7, 101-105.
- Singh, R. K., & Chaudhary, B. D. (1985). *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani Publishers. New Delhi.
- Singh, V., Vimal, S. C., Shrivastav, S. P., Maurya, V., & Singh, N. (2020). Genetic variability, heritability and genetic advance for yield and its contributing traits in chickpea (*Cicer arietinum* L.). *Int. J. Curr. Microbiol. App. Sci.* 9(9), 445-452. <https://doi.org/10.20546/ijemas.2020.909.056>
- Srija, K., Lal, G. M., Snehapriya, P., & Lavanya, G. R. (2022). Estimation of Genetic Variability and Correlation Analysis for Quantitative Traits in Chickpea (*Cicer arietinum* L.). *International Journal of Environment and Climate Change*, 12(11), 3641-3649.
- <https://doi.org/10.9734/ijecc/2022/v12i111412>
- Syed, M. A., Islam, M. R., Hossain, M. S., Alam, M. M., & Amin, M. N. (2012). Genetic divergence in chickpea (*Cicer arietinum* L.). *Bangladesh Journal of Agricultural Research*, 37(1), 129-136.
- <https://doi.org/10.3329/bjar.v37i1.11184>
- Thakur, N. R., Toprope, V. N., & Phanindra, K. S. (2018). Genetic diversity analysis in chickpea (*Cicer arietinum* L.). *International Journal of Current Microbiology and Applied Sciences*, 6, 904-910.
- Vandev, D. L. (2003). *Zapiski po Prilozhna statistika 1* [Notes on Applied Statistics 1]. Veroyatnosti, Operatsionni izsledvaniya i statistika. Sofiyski universitet „Sv. Kliment Ohridski“, Fakultet po matematika i informatika., 92
- Vural, H., & Karasu, A. (2007). Agronomical characteristics of several chickpea ecotypes (*Cicer arietinum*) grown in Turkey. *Notulae Botanicae Horti Agrobotanici Cluj-Napoca*, 35(2), 33-38.
- Vus, N. A., Kobzyeva, L. N., & Bezuglaya, O. N. (2020). Determination of the breeding value of collection chickpea (*Cicer arietinum* L.) accessions by cluster analysis. *Vavilov Journal of Genetics and Breeding*, 24(3), 244–251. <https://doi.org/10.18699/VJ20.617>
- Wang, T., Liu, Y., Wang, M., Fan, Q., Tian, H., Qiao, X., & Li, Y. (2021). Applications of UAS in crop biomass monitoring: A review. *Frontiers in Plant Science*, 12, 616689. <https://doi.org/10.3389/fpls.2021.616689>
- Ward, Jr. J. H. (1963). Hierarchical grouping to optimize an objective function. *Journal of the American Statistical Association*, 58(301), 236-244. <https://doi.org/10.1080/01621459.1963.10500845>

Genetička raznolikost i fenotipska varijabilnost u kolekciji genotipova leblebije (*Cicer arietinum* L.)

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Sažetak: Genetička divergencija između roditeljskih oblika je važna za poboljšanje sorti. Cilj ove studije bio je da se utvrdi stepen genetske raznolikosti među 22 kolekcijske sorte leblebije i da se identifikuju prikupljanja sa vrednim osobinama oplemenjivanja. Eksperiment je sproveden u periodu 2023-2025. u Institutu za krmno bilje (Pleven). Određeni su genetska udaljenost, koeficijent heritabilnosti, genetski napredak i koeficijenti genotipske i fenotipske varijacije. Najveći PCV i GCV pronađeni su za osobine broja semena (49,37%, 34,05%) i broja mahuna/biljci (36,53%, 28,99%). Procene za heritabilnost u širem smislu kretale su se od 5,73% za masu 1000 semena do 88,28% za visinu biljke. Visoka heritabilnost zajedno sa visokim genetskim napretkom utvrđena je za visinu biljke ($H^2 = 88,28\%$, $GA = 9,49$) i broj mahuna po biljci ($H^2 = 62,77\%$, $GA = 13,01$), što ukazuje na prevlast aditivnog delovanja gena i potencijal za uspešnu direktnu fenotipsku selekciju. Hijerarhijska klaster analiza i analiza glavnih komponenti klasifikovale su kultivare u različite grupe na osnovu njihovih agromorfoloških profila. Genotipovi Garbanzo 4, Alfa, Caqui, Garbanzo 1 i Blanco Lechoso pokazali su najveću genetsku divergenciju, što ih označava kao vredne roditeljske komponente za programe hibridizacije usmerene na poboljšanje produktivnosti leblebije i prilagodljivosti životnoj sredini.

Ključne reči: genetski napredak, heritabilnost, klaster analiza, fenotipska varijabilnost, leblebija