

AZERBAIJANI WILD CHERRY PLUM (*Prunus cerasifera* Ehrh.): PHENOLOGICAL AND MORPHOLOGICAL CHARACTERISTICS

 Shahmar Hajiye¹,  Sabina Hajiye^{2,3},  Elchin Hajiye^{2,4,5*}

¹Department of General Agriculture, Genetics and Breeding, Azerbaijan State Agricultural University, Ganja, Azerbaijan

²Department of Immunogenetics, Genetic Resources Institute, Ministry of Science and Education, Baku, Azerbaijan

³Department of Natural Sciences, Western Caspian University, Baku, Azerbaijan

⁴International Center for Biodiversity and Genomics, Baku Eurasian University, Baku, Azerbaijan

⁵Department of Life Sciences, Khazar University, Baku, Azerbaijan

Abstract. This research examines the species *Prunus cerasifera* Ehrh., which is widespread in Azerbaijan, with the aim of investigating its genetic resources, identifying potential genetic resources by assessing phenological and morphological diversity and contributing to scientific understanding of the richness of Azerbaijan's wild flora. A total of 100 distinct genotypes collected in situ from various regions of Azerbaijan were comprehensively analyzed at the Department of General Agriculture, Genetics and Selection of the Azerbaijan State Agrarian University. In phenological studies, the flowering period of genotypes occurred in the second 10 days of March through the first 10 days of April, lasting 7-12 days. Leaf formation was observed in early April and fruit formation in late April. The fruit ripening period lasted from the end of July to the beginning of September, depending on the genotype and growing conditions. The morphological characteristics of the tree, especially the diameter and height of the trunk, significantly influence the formation of both vegetative organs and the size of the fruit. The results of the correlation analysis can be used as reliable statistical indicators in the selection of more productive and high-quality varieties in breeding programs. The results of cluster analysis showed that phenotypic diversity among wild cherry plum genotypes is high and is based on key characteristics such as tree structure, fruit morphometric parameters and fruit pulp percentage. Morphological and fruit characteristics observed in different clusters are important in terms of identifying potential donor genotypes for use in breeding programs. In particular, clusters G1 and D1 can be assessed as promising genotypes selected for high fruit quality and balanced structural parameters. Principal component analysis showed that the majority of the total variance was explained by the first three components. This proves that the selected morphological characters are effective in explaining the structure of variability. The results confirm that *Prunus cerasifera* Ehrh. has significant genetic and morphological diversity, representing a rich genetic resource base for future breeding programs and the creation of productive varieties suitable for local conditions.

Keywords: *Prunus cerasifera* Ehrh., genetic resources, phenotypic variation, cluster.

***Corresponding Author:** Elchin Hajiye, Department of Immunogenetics, Genetic Resources Institute, Ministry of Science and Education; International Center for Biodiversity and Genomics, Baku Eurasian University; Department of Life Sciences, Khazar University, Baku, Azerbaijan,
e-mail: elchinhajiye85@gmail.com

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1. Introduction

Genetic resources provide people with a variety of products and the global economy, livelihoods and health of individuals significantly rely on these resources (Hajiye^{et al.}, 2024). The Rosaceae family has 20-40 plum species, several of which intergrade in the wild (Heidari ^{et al.}, 2022). *Prunus cerasifera* Ehrh., also known as

cherry plum, is a member of the genus *Prunus*. It is native to western and central Asia (Ternjak *et al.*, 2024). Wild cherry plum trees are found in Azerbaijan, a small Asian country known for its varied climate. They are mainly concentrated in the regions of Lankaran-Astara, Guba-Khachmaz, Sheki-Zagatala, Karabakh and Mil plain, as well as the Nakhchivan Autonomous Republic (Karyagin, 1954). Prior studies on wild cherry plums from the Caspian coast have examined *Prunus divaricata* and *Prunus cerasifera* (Wöhrmann *et al.*, 2011; Paunović *et al.*, 2011). Morphological traits can be used to identify genetic differences between and within plant species (Nikolić *et al.*, 2007). Some phenotypic variables can be influenced by environmental factors (Tucić *et al.*, 2018). To prevent genetic erosion, research, collection, conservation and sustainable use of wild plant genetic resources are needed, both as selection material and for low-impact fruit production (Shashidhara *et al.*, 2023). Natural populations of this species are extremely diverse in growth strength, temperature tolerance, ripening time and resistance to diseases and pests (Petrov *et al.*, 2024). It grows well on gravelly, sandy, calcareous and nutrient-poor soils, but it does not do well on dense soils (Dunaevskaya *et al.*, 2021). Due to these properties, it is often used as a rootstock for commercially important *Prunus* species such as almonds, apricots, plums and peaches (Das *et al.*, 2011). In addition, this species has high potential for carbon sequestration and the accumulation of heavy metals (Petrov *et al.*, 2024). In some regions such as the Caucasus, Central Asia, Belarus and Ukraine, *Prunus cerasifera* is also known as a medicinal plant (Liu *et al.*, 2020). The fruits are consumed both fresh and dried (Cosmulescu *et al.*, 2018). Analysis of *Prunus cerasifera* fruits collected from different regions showed that they are rich in polyphenols, flavonoids, anthocyanins, carotenoids, alkaloids and essential amino acids (Liu *et al.*, 2020). At the same time, they have high antioxidant activity (Wang *et al.*, 2012).

In recent decades, a number of investigations have conducted morphological assessments of wild and cultivated cherry plums (Khadivi *et al.*, 2020; Heidari *et al.*, 2022). The aim of these studies was to collect important information for the conservation and use of this species. In some investigations, the assessment of morphological characteristics was combined with the analysis of the fruits' biochemical properties. Miletic *et al.* (2005) investigated the pomological and technological characteristics of 19 genotypes selected from spontaneous populations in Serbia, attempting to isolate valuable material for conservation and commercial cultivation. Similarly, Nikolić *et al.* (2007) evaluated 17 genotypes selected from local *Prunus cerasifera* populations, investigating their cultivation potential and the phenotypic variability of key morphological and chemical traits such as fruit and drupe weight, soluble dry matter, total sugar content and acidity. In China, Liu *et al.* (2008) examined the genetic diversity of 47 wild *Prunus cerasifera* from the Xinjiang region for phenotypic traits and found that there was a wide range of genetic variation in this area, supporting the need for conservation and use. In Romania, Cosmulescu *et al.* (2018) assessed morphological characteristics, total dry matter, soluble dry matter, sugars and acidity in 20 semi-cultivated genotypes of *Prunus cerasifera* and found high genetic diversity in both phenotypic and biochemical traits.

The main goal of this investigation is to research the genetic resources of the widespread *Prunus cerasifera* Ehrh. species in Azerbaijan, to identify potential genetic resources by evaluating their phenological and morphological diversity and to contribute to scientific understanding of the richness of Azerbaijan's wild flora.

2. Materials and methods

Plant material

Plant material for this research was collected and evaluated at the Department of General Agriculture, Genetics and Selection of Azerbaijan State Agrarian University, based on 100 in situ-distributed genotypes of *Prunus cerasifera* Ehrh. gathered from various regions of Azerbaijan. The areas where the evaluated genotypes were collected are shown in Figure 1. The fruits were collected at full ripeness, at intervals of 1 to 2 weeks, from July to September. It was not possible to collect all the investigated genotypes simultaneously due to their belonging to different regions and having significant differences in the timing of development and maturation. Phenological observations began from the moment of shoot swelling in pre-determined genotypes. To evaluate the morphological characteristics, 10 fruits were collected from each tree.

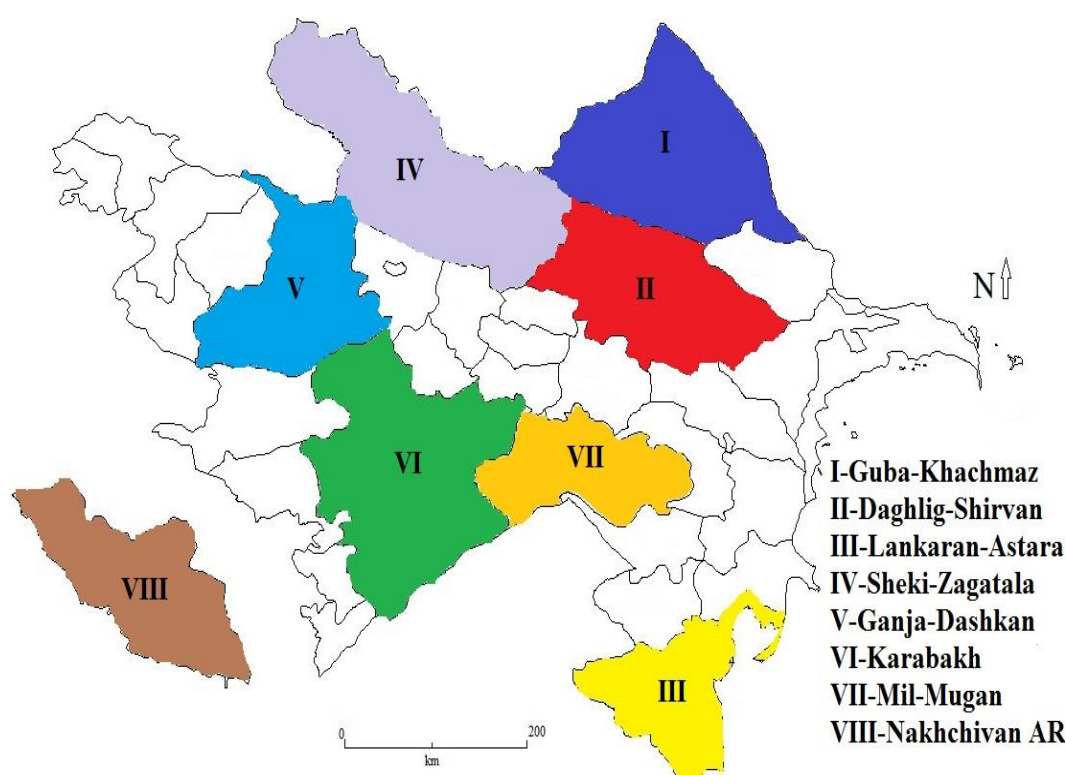


Figure 1. Regions where *Prunus cerasifera* genotypes were collected

Phenological analysis

As part of the research, phenological observations were carried out on the phases of flowering, leaf fall, fruit formation and the ripening of tree fruits. The flowering stage was determined by the number of days from bud opening to petal shedding (Sadigov, 2023). The period of leaf formation was defined as the period from the day the leaf buds began to open until the day the fully formed leaves appeared. The time of fruit formation was calculated based on the time from the fall of flower petals to the appearance of the first fruits. The fruit maturation period was observed and recorded from fruit emergence to full maturity (Tzoner & Yamaguchi, 1999).

Morphological analysis

A total of 38 morphological characters related to tree, flower, leaf and fruit were assessed in the investigation (Sadigov, 2023). These assessments were researched in 10

samples for each of the quantitative characteristics and a result was obtained. Quality characteristics were given separately. The following characteristics were investigated in the research: tree shape, tree trunk diameter, tree height, tree canopy diameter, leaf shape, leaf tip, leaf margins, leaf base shape, leaf width, leaf length, leaf length to width ratio, leaf petiole length, flower group type, pedicel color, pedicel length, flower axis length, flower axis direction, flower color, flower scent, sepal position, sepal shape, sepal length, sepal surface, pistil to tube ratio, flower color, corolla to sepal ratio, fruit type, fruit shape, fruit color, fruit length, fruit width, fruit shape index, fruit flavor, drupe length, drupe width and drupe weight. The investigated features are presented in Table 2.

Statistical analysis

All measurements were performed on 30 plants from each population at the plant maturity stage and average values were calculated. IBM SPSS software (version 25.0) was used to conduct correlation analysis of morphological features. To group genotypes according to morphological characteristics, a two-factor cluster analysis was performed using the Euclidean method in the PAST program (version 4.11) (Hammer *et al.*, 2001).

3. Results and Discussion

Phenological assessment

Although all of the genotypes were extremely early flowering and susceptible to spring-frost damage, the phenological traits of the plant previously showed that the blossoming period differed across them (Shamsolshoara *et al.*, 2021). It should be noted that phenological studies of the genetic resources of wild cherry plum in the world and in our republic are limited. *Prunus cerasifera* Ehrh. (cherry plum) is one of the species of drupe fruit trees with an early growing season. Our research established that although the phenological phases of cherry plum differ somewhat depending on climatic conditions and genotype characteristics, the general sequence of development is stable. This stability may make it important in breeding research. As part of the investigation, phenological observations of wild cherry plum genotypes were carried out and the onset time and duration of each development stage were precisely determined (Table 1).

Table 1. Main phenological phases of *Prunus cerasifera* Ehrh.

Phenological stage	Start time	End time	Note
Flowering	March 12	April 10	Flowering before leaves appear; duration of 7-12 days
Formation of the leaf	April 2	April 14	Starts immediately after flowering
Formation of the fruit	April 22	May 18	Fertilization stage, depends a lot on weather conditions
Fruit ripening	June 25	September 2	Varies depending on genotype and climatic conditions

The investigation showed that the flowering stage of this species occurs very early. Flowering was observed from the second 10 days of March and continued through the first 10 days of April. The flowering phase lasted 7-12 days depending on weather conditions. The flowering process occurred earliest in genotypes common in the Upper Shirvan region and it occurred later in the Karabakh region. It has been noted that after a short winter dormancy, cherry plum blossoms begin to bloom in early spring, usually in March-April (Ternjak *et al.*, 2024).

Leaf formation began shortly after flowering ended. The first leaves were fully developed by early to mid-April. Rapid leaf formation prepares the soil for the next stages of vegetation - photosynthesis and the accumulation of nutrients.

The fruit formation phase was observed from the end of April. Fertilization began immediately after the flowers fell and the fruits gradually formed throughout May. At this stage, air temperature and humidity have a serious impact on the quality of fermentation. Fruit ripening times varied depending on genotype and environmental conditions. Early ripening forms bear fruit from the end of June, while mid- and late ripening forms bear fruit from mid-July to early September. Due to differences in maturity between genotypes, it was not possible to collect all the samples at the same time. Cherry plum fruits are reported to ripen between July and September (Sadigov, 2023).

In conclusion, *Prunus cerasifera* Ehrh. can be considered a productive and promising fruit species both in natural ecosystems and in agriculture, with early flowering and medium or high fruit ripening periods.

Morphological assessment

The flora of Azerbaijan is rich in diversity (Qurbanova *et al.*, 2024). Of the 4,961 species of higher plants common in Azerbaijan, 4,557 species are found in the wild flora of the republic. Since the flora of Azerbaijan was formed in conditions where various elements of the world flora converged in different climatic and soil conditions, the natural plant species common here have complex resistance characteristics (to cold, heat, drought, salinity, disease, pests, etc.). These characteristics can also be successfully used as a valuable resource in selection and hybridization research. The modern vegetation of Azerbaijan was greatly influenced by the flora of Western Asia (Guvendiyev *et al.*, 2025). As *Prunus cerasifera* Ehrh. is a common drupe fruit plant belonging to the *Rosaceae* family, morphological diversity increases its potential for adaptation and selection in this context.

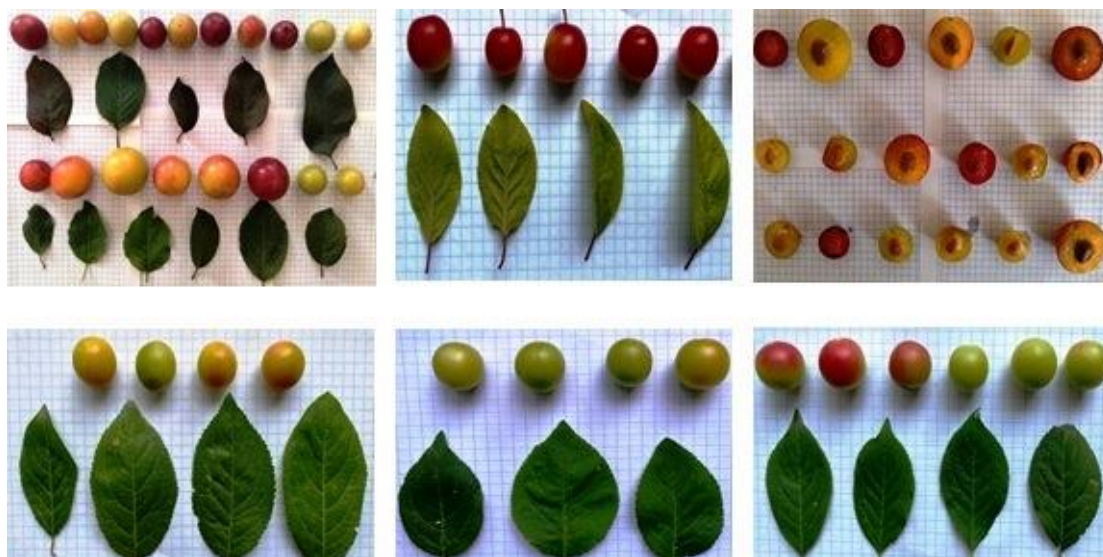


Figure 2. Photographs of fruits and leaves from various wild cherry plum genotypes

This investigation assessed the main morphological characteristics of the species (Figure 2). It has been established that *Prunus cerasifera* has a widespread and multi-branched tree-like form. Descriptive statistics of pomological and morphological traits used in the investigation of wild cherry plum genotypes are presented in detail in Table 2. Some researchers reported that their studies did not find significant differences for

certain variables (CV = 0.00%), prompting them to exclude these variables from their analyses (Goodarzi *et al.*, 2018; Mostafa *et al.*, 2020; Elwakil *et al.*, 2021; Khadivi *et al.*, 2022). The tree trunk diameter ranged from 12 cm to 16.9 cm, averaging 15.6 cm. The standard deviation was 3.87 cm and the coefficient of variation was 24.8%. This indicates a moderate level of variability in trunk diameter, which may indicate potential differences in selection. Tree heights ranged from 740 cm to 970 cm, with an average recorded height of 902.2 cm. The coefficient of variation for this parameter was 25.5%, indicating that there were some non-constant differences that could be explained by genetic or environmental influences. The canopy diameter varied from 312 cm to 369.9 cm, with an average of 344.1 cm. The volatility coefficient here was 6.4%, which indicates the high stability of this indicator. *Prunus cerasifera* is a deciduous, often productive shrub or small tree (4-8 m tall) (Ternjak *et al.*, 2024).

Table 2. Descriptive statistics of the studied morphological traits in *Prunus cerasifera* Ehrh. Genotypes

	Min	Max	Mean	SE	SD	Mode	CV%
DTT	12	16,9	15,6	0,39	3,87	NA	24,8
HT	740	970	902,2	23,0	230,3	870	25,5
DTC	312	369,9	344,1	2,20	21,9	NA	6,4
LC	1	3	1,8	0,08	0,76	NA	43,3
LW	3,3	3,8	5,0	0,09	0,90	NA	18,3
LL	5,3	5,8	7,1	0,11	1,11	NA	15,7
LWR	0,6	0,7	0,7	0,01	0,13	0,7	18,6
LSI	1,3	1,8	2,1	0,06	0,64	NA	30,4
PC	1	1	1,4	0,05	0,50	1	34,6
PL	0,6	0,8	1,0	0,04	0,38	NA	39,0
LFA	1,9	2,2	3,2	0,13	1,34	NA	42,0
FC	2	1	1,3	0,05	0,47	NA	35,5
CL	0,5	0,3	0,5	0,01	0,10	NA	21,3
FSC	1	2	2,6	0,14	1,39	NA	54,0
FL	1,9	1,2	2,8	0,10	0,97	4	34,3
FW	1,9	1,2	2,8	0,10	0,97	4	34,4
FSI	1	1	1,0	0,00	0,05	1	4,9
FWt	5,7	10	7,8	0,17	1,73	NA	22,2
FFW	3,5	8,2	6,2	0,17	1,70	NA	27,5
FT	1	1	1,6	0,05	0,50	2	31,7
SL	0,9	1,3	1,1	0,01	0,12	NA	11,4
SW	0,6	1	0,8	0,01	0,13	0,8	15,8
SSI	0,7	0,8	0,7	0,00	0,05	NA	6,7
SWt	1,5	2,6	2,0	0,04	0,43	NA	21,2
FCPF	61,6	81,5	78,3	0,84	8,40	NA	10,7

Note: DTT – Diameter of the Tree Trunk, HT – Height of the Tree, DTC – Diameter of the Tree Canopy, LC – Leaf Color, LW – Leaf Width, LL – Leaf Length, LWR – Length-to-Width Ratio (of the Leaf), LSI – Leaf Shape Index, PC – Pedicel Color, PL – Pedicel Length, LFA – Length of the Floral Axis, FC – Flower Color, CL – Calyx Length, FSC – Fruit Skin Color, FL – Fruit Length, FW – Fruit Width, FSI – Fruit Shape Index, FWt – Fruit Weight, FFW – Flesh (Fresh) Fruit Weight, FT – Fruit Taste, SL – Stone Length, SW – Stone Width, SSI – Stone Shape Index, SWt – Stone Weight, FCPF – Flesh Content Percentage of the Fruit

Leaf-related parameters were also analyzed. The leaves were described as ovate-lanceolate, thin and pointed. The edges are wavy and the base is long and slightly narrow. The width and length of the leaf were 5.0 cm and 7.1 cm, respectively. The volatility coefficients were 18.3% and 15.7%, respectively. The leaf shape index was determined to be 2.1 and the coefficient of variation for this parameter was 30.4%, indicating that the trait is more genetically variable. The coefficient of variation of leaf color was 43.3%.

Heidari et al. (2022) found that leaf length ranged from 19.10 mm to 44.60 mm with a mean of 31.50 mm, standard deviation of 6.80 mm and CV of 21.50%; leaf width ranged from 8.43 mm to 26.80 mm with a mean of 17.30 mm, standard deviation of 4.30 mm and CV of 25.00% and leaf length-to-width ratio ranged from 1.18 to 2.47 with a mean of 1.87, standard deviation of 0.30 and CV of 15.50%. Cherry plum tree leaves are elliptical to ovate (2-7 cm) and range in color from green to purple (Ternjak *et al.*, 2024). The color of the leaves was light green, dark green and reddish. Kyparissis et al. (2007) investigated the morphological and physiological characteristics of red leaves of *Prunus cerasifera*, finding that thinner red leaves and fewer stomata facilitate selective light absorption and regulation of photosynthetic processes. In this research, as in another investigation conducted on *Prunus cerasifera* (Liu *et al.*, 2023), specific adaptations of red leaves to the light spectrum were investigated, with red leaves showing high tolerance to blue light but low tolerance to red light. Liu et al. (2023) noted that these features are important for optimizing photosynthesis processes. The fruits of genotypes with reddish leaves also had a darker color.

The pedicel length varied between 0.6 cm and 0.8 cm, averaging 1.0 cm and the length of the flower axis ranged from 1.9 to 2.2 cm, averaging 3.2 cm. The coefficients of variation for these indicators were 39.0% and 42.0%, respectively. The observation of high variability in both parameters indicates the presence of genetic diversity in the flower structure. The coefficient of variation for the characteristics of flower color and pedicel color was 35.5% and 34.6%, respectively. The high variability of these parameters indicates that these traits are sensitive to the environment and the characteristics of the genetic structure. Ternjak et al. (2024) note that white hermaphroditic flowers appear before the leaves.

Fruit size has a significant impact on customer preferences and marketability in the production of premium table fruit (Miranda *et al.*, 2023). Larger fruits are typically regarded as higher quality, which has a substantial impact on fruit quality determination and purchase decisions along with characteristics like color, shape and defect-free status (Ni *et al.*, 2024). Fruit quality is also determined by flavor, taste, texture and skin color, which influence customer preferences for different fruits (Cetin & Saraçoğlu, 2023; Ranganath, 2022). In a similar vein, consumers of sweet cherries tend to choose big, sweet, crimson or dark-red fruits with a mesocarp that is medium-firm to firm (Paunović *et al.*, 2022). The fruits are drupe-shaped, mostly round or oval. The taste is sweet and slightly sour. The color range turned out to be very wide, as genotypes with fruits in shades of red, pink and purple were identified.

Among the fruit-related parameters, the highest variability was recorded for fruit skin color (CV = 54.0%). This indicates that the genetic diversity of fruit skin color is very wide and that it has high breeding potential. Heidari et al. (2022) evaluated fruit color on a scale of 1 to 7, with a mean value of 3.74, standard deviation of 1.80 and CV of 46.80%. The coefficients of variation of fruit length and width were similar: 34.3% and 34.4%, respectively. These figures show that fruit sizes vary considerably. Meanwhile, fruit length ranged from 10.90 mm to 16.40 mm, with a mean of 14.30 mm, standard deviation of 1.60 mm and CV of 10.90%; fruit width ranged from 9.09 mm to 16.70 mm, with a mean of 13.20 mm, standard deviation of 1.80 mm and CV of 13.40% (Heidari *et al.*, 2022). The fruit shape index was very stable at 1.0 and the coefficient of variation was only 4.9%. This indicates that the shape of the fruit is genetically stable. Heidari et al. (2022) classified fruit shape on a scale of 1 to 3, with a mean score of 2.35, standard deviation of 1.00 and CV of 40.40%. Fruit weight ranged from 5.7 to 10.0 grams, averaging 7.8 grams. The coefficient of variation here was 22.2%, indicating a moderate level of variability. In addition to this parameter, the traits that stand out in terms of

variability also include the mass of the fruit pulp (mean value = 6.2 grams, CV = 27.5%) and the taste of the fruit (mean value = 1.6, CV = 31.7%). The weight of 10 fruits ranged from 5.53 g to 33.50 g, with a mean of 17.70 g, standard deviation of 6.00 g and CV of 33.70% (Heidari *et al.*, 2022). The percentage of fruit pulp ranged from 61.6 to 81.5%, averaging 78.3%. The volatility coefficient is only 10.7%, which indicates the high stability of this indicator. They note that the peel color varies from yellow and orange to red, blue or purple and the fruit flesh is greenish, yellow, orange or red and ripens to varying degrees (Sadigov, 2023). The fruits ripen from July to September and are usually sweet and juicy, but tasteless genotypes sometimes occur (Sadigov, 2023). A study conducted by Ternyak *et al.* (2024) noted that the length of the fruits ranged from 2.19 cm to 2.82 cm and the width ranged from 2.18 cm to 2.99 cm. Khadivi *et al.* (2020) reported a fruit length range of 11.48-28.40 mm and fruit width range of 10.33-29.23 mm in *Prunus divaricata*. Heidari *et al.* (2022) also investigated wild cherry plum fruits in Iran and recorded even smaller fruits (length: 1.09-1.6 cm, width: 0.9-1.67 cm). These results indicate the wide phenotypic diversity that exists within the species across different regions.

Our results are consistent with those of other investigations (Horvath *et al.*, 2008; Miletic *et al.*, 2005; Liu *et al.*, 2008). Cosmulescu *et al.* (2018) found that the fruit weight of the cherry plum ranged from 5.86 g to 15.39 g, while Čolić *et al.* (2003) determined that the fruit weight ranged from 5.6 g to 15.34 g. However, Horvath *et al.* (2008) reported slightly higher values (6.56-17.5 g). Similarly, Miletic *et al.* (2005), assessing the morphological characteristics of spontaneous populations of *Prunus cerasifera* in eastern Serbia, found that fruit weight ranged from 4.8 g to 24.3 g. Khadivi *et al.* (2020) showed that the fruit weight of wild mirabolan from Iran ranged from 1.79 g to 14.09 g. Heidari *et al.* (2022) also researched wild mirabolan fruits in Iran and recorded even smaller fruits (0.6-3.3 g). This is also consistent with the results of other studies (Horvath *et al.*, 2008; Miletic *et al.*, 2005; Liu *et al.*, 2008). Fruit size is an important factor in the production of high-quality table fruits, influencing consumer preferences and marketability (Miranda *et al.*, 2023). According to Heidari *et al.* (2022), stone width (CV = 9.99%), stone length (CV = 10.20%) and fruit length (CV = 10.90%) were the characteristics with the least variability.

The morphological characteristics of the *Prunus* species' stones are an important tool for distinguishing between different types and varieties (Ropelewska, 2022). The length of the drupe was 0.9-1.3 cm, the width was 0.6-1.0 cm and the weight was 1.4-2.8 g. These findings indicate that nuclear morphology also exhibits genetic variability. The coefficients of variation of the length, width and weight of stones were 11.4%, 15.8% and 21.2%, respectively. These indicators reflect the morphological stability of the stone as well as a certain genetic diversity. The coefficient of variation of the stone shape index was 6.7%, which indicates the high stability of the indicator. Heidari *et al.* (2022), the weight of 10 stones ranged from 1.82 g to 5.05 g, with a mean of 3.34 g, standard deviation of 1.00 g and CV of 28.40%; the length of the stone ranged from 8.44 mm to 12.20 mm, with a mean of 10.50 mm, standard deviation of 1.10 mm and CV of 10.20%; the width of the stone ranged from 6.88 mm to 9.93 mm, with a mean of 8.51 mm, standard deviation of 0.90 mm and CV of 9.99%. Colic *et al.* (2003) found that cherry plum fruit and stone diameters exhibited little variation. Increased variety is indicated by higher CV values, which make such qualities ideal for selection (Mohammadi & Prasanna, 2003). Khadivi-Khub and Barazandeh (2015), examining farmed plums of the *P. domestica* species, found a significant degree of variability.

According to the analysis results, a significant portion of the traits showed moderate and high levels of variability. This demonstrates that a wide range of genetic diversity

was observed among the samples investigated. In particular, high variability was observed for parameters such as fruit skin color, flower structure, fruit taste and leaf shape index, which allows them to be assessed as promising traits for breeding and genetic research. In contrast, indices such as fruit shape index, stone shape index and the percentage of the fruit pulp showed remarkable stability. This indicates that these traits have stable heredity and may be preferable during selection. These results can serve as a starting point for subsequent stages of selection, identifying the most promising samples among the researched genotypes.

The KMO index is set at 0.594 (Table 3). The KMO test measures the strength of partial correlations between variables, assessing their suitability for factor and principal component analysis. An index below 0.5 indicates low reliability of the analysis (Khargharia *et al.*, 2015), while a range of 0.6-0.7 indicates a “satisfactory” level. Thus, the obtained result allows us to conclude that the data are suitable for principal component analysis.

Table 3. KMO and Bartlett’s test

Kaiser-Meyer-Olkin (KMO) measure of sampling adequacy		0.594
Bartlett’s test of sphericity	Approximate chi-square	4803.626
	Degrees of freedom (df)	300
	Significance (<i>p</i> -value)	0.000

Bartlett’s test (1950) checks whether the correlation matrix is an identity matrix, which would indicate that the variables are unrelated and unsuitable for structure detection. The chi-square value of the Bartlett test was 4803.626 and the degree of freedom (df) was 300. The significance level of the test ($p < 0.001$) indicates high statistical significance (Sarma *et al.*, 2024). This result confirms that the correlation matrix is not an identity matrix, which means that there are statistically significant correlations between the variables. Thus, the result of Bartlett’s test indicates that the data are suitable for factor analysis and principal components analysis.

The combination of the KMO index and Bartlett’s sphericity test results indicates that the set of variables under investigation is suitable for principal component analysis. A KMO index of 0.594 indicates a sufficient level of fit for the analysis, but it may also indicate weakness in the factor structure of some variables. The high statistical significance of Bartlett’s test confirms the presence of a strong correlation structure between the variables and confirms the reliability of the principal component analysis results. Therefore, the presented statistical tests provide a sufficient basis for conducting principal component analysis based on the data selected for the study.

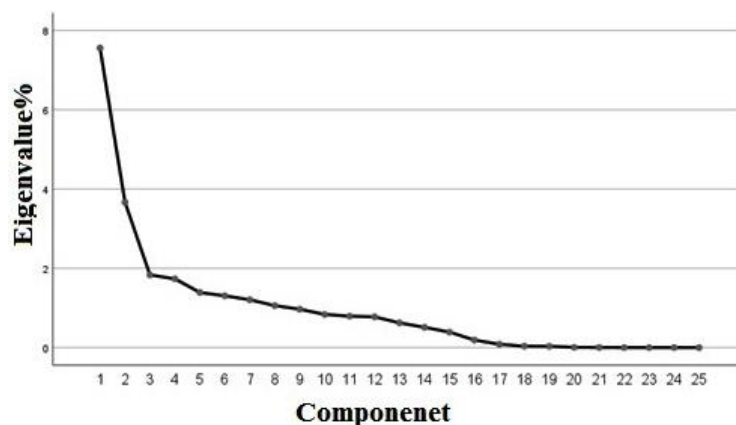


Figure 3. Principal component-based scree plot

Figure 3 shows the distribution of eigenvalues for each component obtained from the principal component analysis (PCA). Here, the x axis indicates the serial number of the component and the y axis indicates the values of those components. Eigenvalues reflect the extent to which the principal components explain the variation in the data.

The graph shows that the eigenvalues of the first two components are significantly higher than those of the others: the eigenvalue of the first component is approximately 7.7 and that of the second component is 3.7. This suggests that the majority of the total variation in the dataset (approximately 48-50%) is mainly explained by these two components. Thus, the first two components are of particular importance for understanding the structure of the data.

Traditionally, only components with an eigenvalue greater than 1 are considered significant. The analysis showed that 8 components had eigenvalues greater than 1, indicating that additional components also play a role in explaining the underlying variation in the data. Based on the presented PCA results, it is reasonable to retain 8 components, since these components explain approximately 79% of the data (Table 4). This means a high level of data presentation and analysis efficiency. Thus, the first two components indicate the main source of the plants' phenotypic variability and the other components reveal additional morphological and qualitative parameters. This information provides researchers with a scientific basis for the efficient management of genetic resources, grouping different phenotypes and optimizing breeding programs.

Table 4. Results of principal component analysis for each trait investigated

	PCA1	PCA2	PCA3	PCA4	PCA5	PCA6	PCA7	PCA8
DTT	0,131		0,504	0,49		-0,195	0,248	-0,139
HT				0,11	0,32	0,524	0,229	0,559
DTC	0,945	0,229		-0,103				
LC		-0,165		0,266	-0,31	0,497	0,186	
LW		0,662	0,413	-0,199	0,205	0,168	-0,301	-0,129
LL	0,155	0,214	0,42	0,616	0,193	-0,115	-0,343	
LWR	-0,143	0,48		-0,698		0,283		-0,132
LSI	-0,42	0,733		0,108		-0,117	0,257	0,176
PC		0,158	0,378		-0,383	-0,156	0,31	
PL	-0,414	0,746	0,149	0,134		-0,16	0,214	0,127
LFA	-0,395	0,794					0,153	
FC	-0,123		0,173	-0,355	0,35	-0,39	-0,343	0,122
CL			-0,189		0,619	-0,152	0,401	
FSC		-0,104		0,152	0,65	0,319		-0,355
FL	-0,127	0,677	-0,526	0,317	-0,101	0,132	-0,196	
FW	-0,132	0,664	-0,574	0,301			-0,138	-0,137
FSI			-0,372	-0,114		-0,341	0,434	-0,401
FWt	0,975	0,131						
FFW	0,975	0,178						
FT			-0,459			-0,271		0,552
SL	0,972	0,126						
SW	0,982	0,132						
SSI	0,943	0,15				0,104		
SWt	0,971	0,119						
FCPF	0,61	0,262		-0,295		0,179	0,257	
Eigenvalue	7,558	3,665	1,833	1,734	1,39	1,306	1,207	1,058
Variance (%)	30,231	14,659	7,333	6,936	5,559	5,224	4,829	4,233
Σ variance (%)	30,231	44,89	52,222	59,158	64,717	69,941	74,77	79,003

Note: DTT – Diameter of the Tree Trunk, HT – Height of the Tree, DTC – Diameter of the Tree Canopy, LC – Leaf Color, LW – Leaf Width, LL – Leaf Length, LWR – Length-to-Width Ratio (of the Leaf), LSI – Leaf Shape Index, PC – Pedicel Color, PL – Pedicel Length, LFA – Length of the Floral Axis, FC – Flower Color, CL – Calyx Length, FSC – Fruit Skin Color, FL – Fruit Length, FW – Fruit Width, FSI – Fruit Shape Index, FWt – Fruit Weight, FFW – Flesh (Fresh) Fruit Weight, FT – Fruit Taste, SL – Stone Length, SW – Stone Width, SSI – Stone Shape Index, SWt – Stone Weight, FCPF – Flesh Content Percentage of the Fruit

The conducted PCA allowed for the assessment of a set of various morphological and phenotypic indicators explaining the overall variability. The PCA orthogonally translates the observable qualities that could be associated with a numerical value. PCA reduces characteristics to distinguish different genotypes and the correlations it reveals may indicate pleiotropic effects or genetic links between loci governing the observed features (Iezzoni, 2008). Phenotypic trait associations are a great way to identify differences across plum species (Heidari *et al.*, 2022). The analysis revealed 8 principal components that explained more than 79.00% of the data, indicating that the model effectively reflects the data.

The first principal component accounted for 30.23% of the total variance and showed a high positive correlation, mainly with the size and mass characteristics of fruits and stones (e.g., fruit weight: 0.975, stone length: 0.972, stone width: 0.982). In addition, the percentage of fruit pulp also had a positive correlation (0.61). This result shows that PC1 mainly reflects overall fruit size and yield and these indices are closely related to each other. The second component explained 14.66% of the total variance. This component closely correlates with the structural features of vegetative and reproductive organs, such as leaf size (width: 0.662, shape index: 0.733) and pedicel length (0.746). Moreover, a positive correlation was observed with the length (0.677) and width (0.664) of the fruit. This indicates that PC2 is associated with vegetative development and plant structural form. The third component accounted for 7.33% of the total variance and the fourth component accounted for 6.94%. PC3 is mainly related to leaf length and pedicel color, reflecting the aesthetic and visual characteristics of the plant. Meanwhile, PC4 expresses plant shape and symmetry, showing a positive correlation with measurements such as leaf length and tree trunk diameter and a negative correlation with length-to-width ratio. Although the latter components account for only a small percentage of the variation, they explain certain phenotypic traits such as fruit taste, flower color and calyx length. These components may be particularly interesting in the selection process, as they highlight different morphological and qualitative characteristics. In a principal component analysis by Heidari *et al.* (2022), seven principal components with eigenvalues ≥ 1 explained 69.93% of the total variance. The first three components (PC1-PC3) together explained 44.33% of the variation, where PC1 (21.61%) was related to fruit and seed size, PC2 (11.66%) was related to fruit and leaf morphology and PC3 (11.06%) was related to traits such as fruit shape, seed tip shape and leaf underside color.

The analysis shows that the greatest influence on morphological variability is exerted by the fruit size, weight and stone characteristics. These indicators act as the main factors determining the quality and quantity of products. The PCA results are important in terms of grouping multiple and interrelated morphological features and identifying the main factors (Hajiyev *et al.*, 2025). This provides a scientific basis for managing genetic resources, planning breeding programs and creating new varieties.

The correlation between the two features was calculated. Correlation analysis can provide valuable information about the most important traits when evaluating genotypes (Norman *et al.*, 2011). The technique used most often for determining the strength of the linear relationship between two continuous variables is the Pearson correlation coefficient (r), which has a value between -1 and 1 (Pearson, 1900). By identifying features that have a significant correlation, it is possible to predict in advance the ratio of one feature to another, which can facilitate the selection of suitable genotypes. The results of the correlation analysis are presented in Figure 4.

The investigation found that there was a very strong positive correlation between tree trunk diameter and tree height ($r = 0.965$, $p < 0.01$), indicating that trees with thicker trunks tend to be taller. This may reflect a coevolutionary mechanism associated with the

influence of genetic or environmental factors (Brock & Weinig, 2007). A strong correlation was also found between stem diameter and flower axis length ($r = 0.984$, $p < 0.001$). This is an important indicator of the influence of vegetative development on the development of generative organs. A very high correlation was observed between leaf length and flower axis length ($r = 0.970$, $p < 0.001$). This result confirms the possibility of synchronous development of vegetative and generative organs, suggesting that there is a close relationship between leaf size and the structures that support it (Lal *et al.*, 2019). A significant positive correlation was also observed between leaf width and length ($r = 0.870$, $p < 0.01$), indicating a predominance of leaves with a balanced shape. A moderately strong positive correlation was recorded between trunk diameter and fruit weight ($r = 0.449$, $p < 0.05$), which also shows that trees with larger trunks can produce heavier fruit. Moreover, there was an almost perfect positive correlation between tree height and fruit taste ($r = 0.982$, $p < 0.001$), showing that product quality can be related to tree height. There is a strong positive correlation between fruit length and weight ($r = 0.864$), indicating a direct influence of fruit size on total weight. This also highlights the geometric symmetry present in the fruit's morphology (Ghahremani *et al.*, 2023).

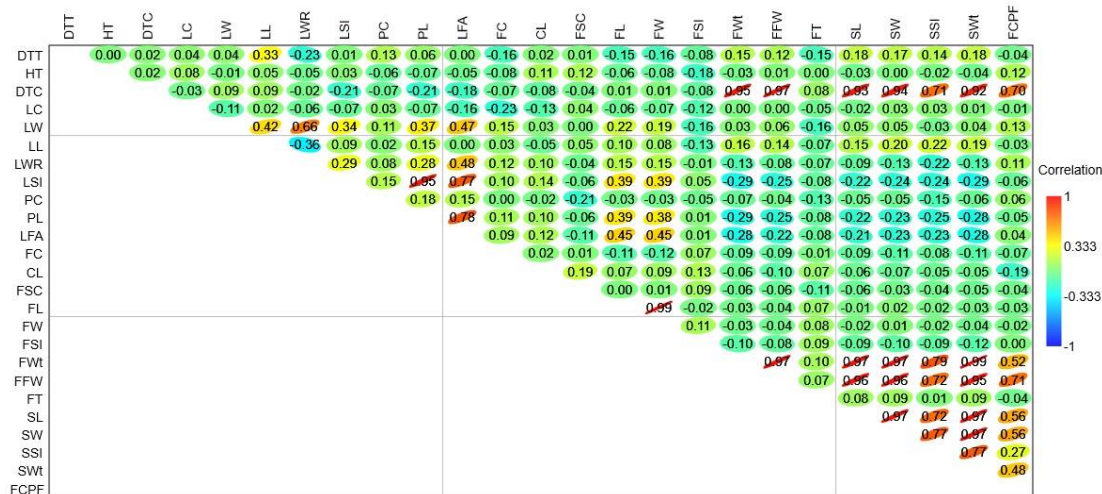


Figure 4. Pearson correlation among studied morphological traits

Note: DTT – Diameter of the Tree Trunk, HT – Height of the Tree, DTC – Diameter of the Tree Canopy, LC – Leaf Color, LW – Leaf Width, LL – Leaf Length, LWR – Length-to-Width Ratio (of the Leaf), LSI – Leaf Shape Index, PC – Pedicel Color, PL – Pedicel Length, LFA – Length of the Floral Axis, FC – Flower Color, CL – Calyx Length, FSC – Fruit Skin Color, FL – Fruit Length, FW – Fruit Width, FSI – Fruit Shape Index, FWT – Fruit Weight, FFW – Flesh (Fresh) Fruit Weight, FT – Fruit Taste, SL – Stone Length, SW – Stone Width, SSI – Stone Shape Index, SWt – Stone Weight, FCPF – Flesh Content Percentage of the Fruit

Furthermore, a strong positive correlation was observed between fruit weight and stone weight ($r = 0.991$, $p < 0.001$), indicating that stones play an important role in total fruit weight. A high correlation ($r = 0.971$) was observed between fruit weight and fruit pulp weight, indicating that the total fruit weight mainly consists of pulp. Khadivi *et al.* (2025) noted that fruit length showed a high positive correlation with fruit weight ($r = 0.85$, $p < 0.01$), fruit skin thickness ($r = 0.52$, $p < 0.01$) and stone length ($r = 0.46$, $p < 0.01$). These results indicate that both internal tissue development and stone size increase proportionally with increasing fruit size. This emphasizes the existence of structural and functional relationships between the morphological characteristics of the fruit (Khadivi *et al.*, 2025). There is a weak correlation between the leaf shape index and fruit length, taste and weight ($r < 0.2$). This indicates that vegetative forms do not have a direct influence on fruit characteristics (Flore & Lakso, 1989). Additionally, no statistically

significant relationships were found between organoleptic indicators such as flower color and fruit taste ($p > 0.05$). Heidari et al. (2022) found significant statistical relationships between various morphological characteristics using Pearson correlation analysis. The results of the investigation revealed a strong positive correlation between the weight of the fruit and its length ($r = 0.81$) and width ($r = 0.73$), as well as the thickness of the fruit pulp ($r = 0.62$). Moreover, a moderate positive correlation was also recorded between fruit weight and stone length ($r = 0.70$), stone width ($r = 0.62$) and stone weight ($r = 0.62$) (Heidari *et al.*, 2022).

The results of the analysis showed that the morphological features of the tree, especially the diameter and height of the trunk, significantly affect the formation of both vegetative organs (leaves and flowers) and the size of the fruit. There was a very high correlation between the fruit weight and the weight of stones and fruit pulp, which is important in terms of yield and crop quality. The influence of leaf shape and indices on fruit characteristics was weak. Overall, these results can be used as reliable statistical indicators when selecting more productive and high-quality varieties in breeding programs.

To assess the relationship between the 100 studied cherry plum genotypes, a two-factor cluster analysis was used for 25 traits. The dendrogram was constructed using the Euclidean method in the PAST 4.11 statistical software package (Figure 5). This analysis facilitates the visual observation of genotype grouping (Mammadova *et al.*, 2024). One of the most precise ways to express relationships between data is to use the Euclidean distance, which is the linear distance between two points (Hajiyev *et al.*, 2025; Khadivi *et al.*, 2025).

Ward's approach is used to create clusters based on the distance matrix that was collected. By reducing the variation across groups, Ward's technique guarantees the creation of homogenous subgroups. This approach is especially recommended for classification analyses where inter-cluster differences must be kept to a minimum (Kaufman & Rousseeuw, 2009; Ward, 1963). The analysis findings are displayed using a cluster, which also aids in comprehending the connections between quantitative variables and observations (samples). The degree of similarity or distance between the data points is shown by color intensity on the cluster. For instance, separate samples are displayed with more distinct color tones, whereas comparable samples are depicted with closer color shades (Wilkinson & Friendly, 2009). Because it swiftly and efficiently visualizes the data's clustering structure, this approach is particularly favored for analyzing big and complicated datasets. As a result, the samples' similarities, differences and groups may be determined. In this investigation, the similarities and differences between the analyzed samples were visualized using a cluster made using Ward's approach and Euclidean distance coefficients. Quantitative data were used for the analysis procedure and the findings show which samples are more closely connected to one another and how the data are organized into groups (Figure 5).

In the first part of the dendrogram, constructed using the Euclidean distance index, the variables were initially divided into three main groups. Group A includes the DTC (diameter of tree canopy) feature. Group B combined most traits related to tree trunk, fruit size, leaves, seeds and flowers (DTT – Diameter of the Tree Trunk, LC – Leaf Color, LW – Leaf Width, LL – Leaf Length, LWR – Length-to-Width Ratio (of the Leaf), LSI – Leaf Shape Index, PC – Pedicel Color, PL – Pedicel Length, LFA – Length of the Floral Axis, FC – Flower Color, CL – Calyx Length, FSC – Fruit Skin Color, FL – Fruit Length, FW – Fruit Width, FSI – Fruit Shape Index, FWt – Fruit Weight, FFW – Flesh (Fresh) Fruit Weight, FT – Fruit Taste, SL – Stone Length, SW – Stone Width, SSI – Stone Shape

Index, SWt – Stone Weight, FCPF – Flesh Content Percentage of the Fruit). In Group C, only one trait concerns tree height.

The samples were divided into four main groups: D, E, F and G. Then, each of them was divided into two subgroups (D1, D2; E1, E2; F1, F2 and G1, G2). Subgroup D1 included a total of nine genotypes (PCE8, PCE39, PCE51, PCE60, PCE81, PCE87, PCE93, PCE96 and PCE100). The canopy diameter of these genotypes was 340-368 cm and the trunk diameter was 14-18 cm. The tree structures were medium-large in size and developed proportionally. The fruits measured 3-6 cm in length and 1-4 cm in width and they weighed 7-10 grams. The fruit set percentage of genotypes in this cluster ranged from 78% to 84% and the fruits were generally symmetrical in shape. Subgroup D2 included two genotypes (PCE57 and PCE65). The canopy diameter of these genotypes was 272-302 cm and the trunk diameter was 12-27 cm. The percentage of fruit pulp was relatively low, amounting to 55-57%. These differences, observed in morphological and fruit characteristics, determined the location of this cluster outside the other clusters.

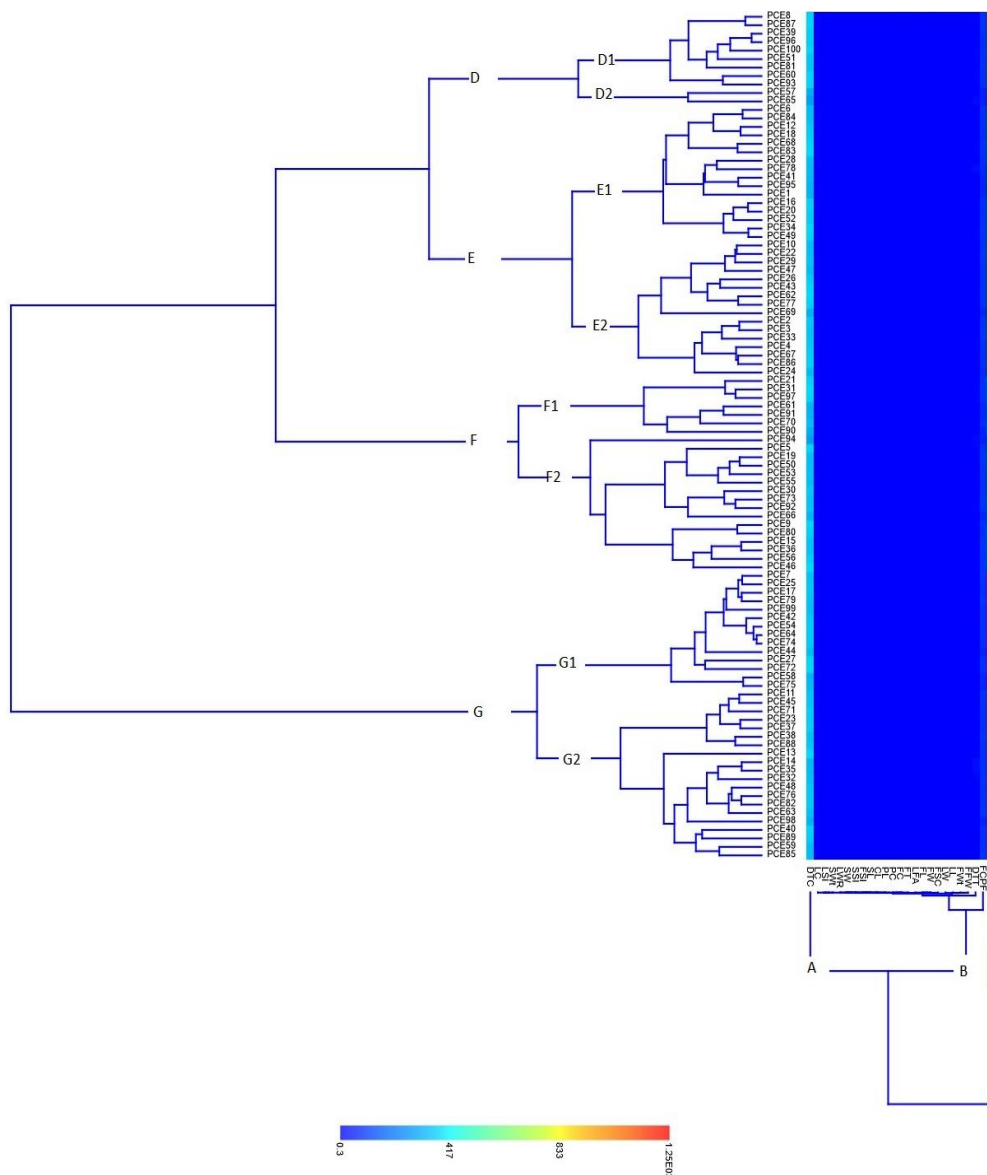


Figure 5. Dendrogram of *Prunus cerasifera* Ehrh. genotypes performed using 25 morphological characteristics

Subgroup E1 included 13 genotypes (PCE1, PCE6, PCE12, PCE16, PCE18, PCE20, PCE28, PCE34, PCE41, PCE49, PCE52, PCE68 and PCE83). The canopy diameter of these genotypes was 312-376 cm and the trunk diameter was 11.8-17.6 cm. The length of the fruits was 3-6 cm and the width was 2-4 cm. The percentage of pulp in the fruits varied from 56% to 84%. The genotypes of cluster E1 were medium in size and had balanced structural characteristics. The E2 subgroup included a total of 16 genotypes (PCE2, PCE3, PCE4, PCE10, PCE22, PCE24, PCE26, PCE29, PCE33, PCE43, PCE47, PCE62, PCE67, PCE69, PCE77 and PCE86). The canopy diameter of the genotypes was 326-375 cm and the trunk diameter was 12-17 cm. The pulp percentage of the fruits was 74-86%. Genotypes in this cluster exhibited more stable and similar characteristics in terms of fruit size and fruit pulp percentage.

Subgroup F1 included six genotypes (PCE21, PCE31, PCE61, PCE70, PCE90 and PCE91). The canopy diameter of the genotypes was 300-380 cm and the trunk diameter was 12-18 cm. The length of the fruits ranged from 3 to 6 cm and the percentage of fruit pulp varied widely - from 55% to 82%. This cluster was selected due to its phenotypically intermediate characteristics. The F2 subgroup was represented by 15 genotypes (PCE5, PCE9, PCE15, PCE19, PCE30, PCE36, PCE46, PCE50, PCE53, PCE55, PCE56, PCE66, PCE73, PCE80 and PCE92). The canopy diameter of these genotypes was 271-378 cm and the trunk diameter was 12-19 cm. The fruit pulp percentage was recorded between 54% and 86%. The F2 cluster showed wide phenotypic variability, making this cluster important for genetic and breeding investigations.

Subgroup G1 included 14 genotypes (PCE7, PCE17, PCE25, PCE27, PCE42, PCE44, PCE54, PCE58, PCE64, PCE72, PCE74, PCE75, PCE79 and PCE99). The canopy diameter of the genotypes was 324-373 cm and the trunk diameter was 12-17 cm. The percentage of fruit pulp was 63-87% and this indicator distinguishes the cluster in terms of fruit quality. The last subgroup, G2, included 18 genotypes (PCE11, PCE13, PCE14, PCE23, PCE32, PCE35, PCE37, PCE38, PCE40, PCE45, PCE48, PCE59, PCE63, PCE71, PCE76, PCE82, PCE85 and PCE88). The canopy diameter of the genotypes varied within the range of 311-377 cm and the trunk diameter within the range of 11.9-32.7 cm. The pulp percentages of the fruit ranged from 55% to 86% and a relatively high level of diversity was observed within this cluster.

The results of cluster analysis showed that phenotypic diversity among wild cherry plum genotypes is high and is based on key characteristics such as tree structure, fruit morphometric parameters and the pulp percentage of the fruit. Morphological and fruit characteristics observed in different clusters are important in terms of identifying potential donor genotypes for use in breeding programs. In particular, clusters G1 and D1 can be assessed as promising genotypes selected for high fruit quality and balanced structural parameters.

The use of Euclidean distance is one of the main methodological approaches to the quantitative assessment of morphometric differences between plant samples. In this study, the morphological variability of 100 tree samples was estimated using the Euclidean distance. The analysis of cluster E (E1, E2) shows that this group contains the largest number of points of the researched objects. In particular, in subgroup E2, the average distance between points fluctuates within 12-50 units, which indicates a high group density. Group E had a more homogeneous and cohesive structure compared to other clusters. In cluster F (F1, F2), the situation is somewhat different. Here, subgroup F2 not only covers more points, but the average intra-group distance also varies between 70 and 120 units. These indicators demonstrate that the group is clustered with medium density. The analysis of cluster G (G1, G2) gives interesting results. Although subgroup G2 showed closer clustering, some points located in G1 (especially PCE7) appeared to

be located relatively far from other members of the group. The average distance between these points reaches 162 units, which means they can be considered as “outliers” of the group. Cluster D (D1, D2) is one of the most interesting results of the investigation. This group, in addition to connecting the fewest points, is completely independent, with an average distance of over 400 units from other clusters. Of particular note is the fact that point PCE57 has minimal connections with other clusters. Analysis of inter-cluster distances shows that the average distance between clusters E and F varies in the range of 150-300 units. Between clusters E and G, this indicator is recorded in the range of 200-400 units. The most interesting case concerns cluster D, whose average distance from all other clusters is more than 400 units. The native cherry plum genotypes in this region exhibit significant morphological variety, according to research on the phenotypic variability of the wild cherry plum (Čolić *et al.*, 2003; Khadivi *et al.*, 2020).

This comparative study was conducted to examine the factors and the genotypes both alone and in relation to one another. This method not only made the unique characteristics of each variable and accession clear, but it also made it easier to comprehend how several qualities interact with one another. The thorough examination carried out at the individual and group levels made it possible to interpret the data in a more thorough manner. Additionally, this approach improved the precision and dependability of the results by graphically illustrating how the pomological and morphological traits of each accession either match or diverge. This made it possible to gain a deeper understanding of the general dynamics and structure of the dataset. The cluster analysis was a powerful technique for visualizing intricate information, making it possible to clearly identify links within and across clusters. The investigation provided a thorough understanding of the dataset structure by classifying variables and genotypes according to common characteristics. The results establish a strong basis for further research in addition to improving the understanding of the connections between genotypes. An important tool for comprehending phenotypic variance and assisting with future research goals, this method might direct the identification of genotypes with desired features for breeding programs or additional genetic investigations.

Prunus cerasifera Ehrh. has high ecological plasticity and can successfully grow in various soil and climatic conditions. The natural habitat of the cherry plum mainly includes forest edges, shrub zones, river valleys, valley and hillside slopes and foothills and plains. The plant grows particularly well on riverbanks and in damp valleys, but it also adapts to areas with low humidity and sunlight. This is explained by the fact that it is an ecologically versatile plant (Table 6).

Table 6. Genotypes, habitat, ecological group and distribution

Species	Habitat	Ecological group	Distribution
<i>Prunus cerasifera</i> Ehrh.	Forest edges and bushes Riverbanks and valleys Foothills and plains	Mesophilic Sero-mesophilic Heliophilous Nitrophilous	Guba-Khachmaz Mountainous-Shirvan Lankaran-Astara Sheki-Zagatala Ganja-Dashkasan Karabakh Mil-Mugan Nakhchivan Autonomous Republic

The species *Prunus cerasifera* is represented in various ecological groups. It is predominantly mesophilic, meaning it thrives in moderately humid conditions, especially at forest edges and in semi-shaded areas. At the same time, it also acts as a sero-

mesophilic (partially adapted to arid climate) plant; this feature allows the species to remain viable even on rocky soils with low moisture content. However, cherry plum is a light-loving species and grows best in open areas and roadsides. The species also has nitrophilous (thriving in nitrogen-rich soils) characteristics, leading to its occurrence in some anthropogenic ruderal areas. Researching the drupe fruit plants of the Nakhchivan Autonomous Republic, Talibov and Ibrahimov (2023) noted that cherry plum is widespread in forests, thickets, clearings, mountain slopes and river valleys in Gilanchay and Dyrnys of the Ordubad district; Kirne, Goydar and Alinja of the Julfa district; Garabaglar of the Kengerli district; Vaykhir of the Babek district; Garabab, Kulus of the Shahbuz district and other areas. Nabiyeve et al. (2023) examined the state of flora and vegetation in the Agsu district, investigating meadows, forest-meadows, forests, mountain xerophytes and tugay forests, as well as conducting observations of early spring vegetation, especially in the mountain villages of Kalva, Khatman, Dilman and Khadzhiman. They found a widespread distribution of cherry plum and other tree-shrub species (Nabiyeve *et al.*, 2023).

The distribution area of the *Prunus cerasifera* species in Azerbaijan is quite wide and covers various physical and geographical regions of the country. The densest distribution is observed in the Lankaran-Astara zone, especially in the foothills of the Talysh Mountains. Here, cherry plum trees grow on the edges of natural forests. Semi-natural forms of cherry plum are often found in the Guba-Khachmaz region, in foothill and forest areas. In the Sheki-Zagatala and Gakh regions, it is widespread in the shrub-forest landscapes of the southern foothills of the Greater Caucasus. In lowland regions such as Karabakh and the Mil plain, cherry plums mainly grow on plains and in irrigated fields. Wild forms of cherry plum are widespread in the Nakhchivan Autonomous Republic, especially in river valleys and foothill areas. While conducting a botanical-geographical and phytocoenological research of rare trees and shrubs in Azerbaijan, Iskenderov and Mustafayeva (2011) noted that the cherry plum species is widespread at an altitude of 600-1,100 m in the Astara region of Lankaran. They also emphasized that this species is widespread in the Karabakh region (Iskenderov & Mustafayeva, 2011). Talibov and Ibrahimov (2023), investigating drupe fruits in the Nakhchivan Autonomous Republic, noted the spread of cherry plum in these territories. While investigating the current state of the Goygol National Park, located on the northeastern slopes of the Lesser Caucasus, Mirzoyev and Sadikhova (2016) noted that the cherry plum species is widespread in the park's forests.

Thus, *Prunus cerasifera* Ehrh. is an important fruit plant of Azerbaijan, which easily adapts to various environmental conditions, is widely distributed in natural landscapes and has genetic diversity. These characteristics make it a promising genetic resource both for biodiversity conservation and for selection and introduction into agriculture.

4. Conclusion

Research has confirmed that *Prunus cerasifera* Ehrh. has a wide range of ecological plasticity. The results revealed valuable scientific and practical implications in several areas. The high coefficient of variation of morphological traits - especially fruit weight, skin color, taste and percentage of pulp - indicates the high genetic diversity of this species. This variability creates a rich source material base for breeding programs. In particular, high yield, large fruits and adaptability can be considered priority traits for selection. Genotypes with high yield potential can be used as the main breeding initial forms when creating new cherry plum varieties in the future. These genotypes may play a role in developing varieties adapted for both local markets and export-oriented

horticultural systems. The results obtained using principal component analysis and clustering methods show that there are relationships between different morphological parameters and that these relationships are important for predicting fruit quality, vegetative development and adaptive capacity. This approach provides a scientific basis for developing more targeted selection strategies in the future. It should be noted that there are few existing studies on the distribution of genotypes of Azerbaijani wild cherry plum only on the territory of the Republic and there is no research on the specific focus examined in the present study. Thus, this study makes a significant contribution to the existing literature with its analytical approach.

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