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GENETIC DIVERSITY OF AZERBAIJANI GARLIC (*ALLIUM SATIVUM* L.) GERMPLASM RESOURCES: PHENOLOGICAL, AGROMORPHOLOGICAL, AND BIOCHEMICAL INVESTIGATION

F.R. GULMALIYEVA¹, Z.A. GULIYEVA², B.S. BAYRAMOV³, R.T. ALIYEV¹, and
 E.S. HAJIYEV^{1*}

¹Genetic Resources Institute, Baku, Azerbaijan

²Research Institute of Vegetable Growing, Public Legal Entity, Baku, Azerbaijan

³Nakhchivan State University, Nakhchivan, Azerbaijan

*Corresponding author's email: elchinhajiyev85@gmail.com

Email addresses of co-authors: ferqane.rafiq@gmail.com, zeyneb.quliyeva@gmail.com,
 behruzbayramov67@gmail.com, aliyeqramiz37@gmail.com

SUMMARY

This study evaluated 26 garlic (*Allium sativum* L.) genotypes for phenological, agromorphological, and biochemical traits to identify those with high genetic diversity and selection potential. Descriptive statistics revealed extensive variations in earliness, bulb and clove mass, root mass, and yield-related traits, while the biochemical traits were relatively stable. Overall, the bulb yield in garlic genotypes ranged from 16.9 to 69.1 t/ha (CV = 33.51%), indicating substantial genotypic diversity, and showed moderate positive correlations with bulb diameter, bulb and clove weight, and plant height ($r = 0.55-0.67$). Principal component analysis (PCA) identified seven components explaining 81.09% of the total variation, with PC1 related to vegetative growth and yield, PC2 to biochemical traits, and PC3 to bulb shape. Cluster analysis grouped the garlic genotypes into early and low-yielding; medium-vegetation with large bulbs; and late, high-yielding genotypes. An analysis of variance confirmed significant ($P \leq 0.000$) differences among garlic genotypes for all traits. Overall, the results enunciated substantial genetic diversity and provide a robust basis for targeted selection in terms of earliness, yield, bulb quality, and biochemical traits.

Keywords: Garlic (*A. sativum* L.), germplasm, genetic diversity, principal component analysis, phenological, morpho-biological, biochemical traits

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Key findings: Garlic (*A. sativum* L.) genotypes revealed significant genetic diversity and greater potential for selection. Bulb yield showed a positive association with other bulb traits and plant height. Variation in sugar and nitrate content enables the selection of high-quality garlic genotypes with good yield and improved flavor.

INTRODUCTION

Garlic (*Allium sativum* L.) belongs to the family Amaryllidaceae and is a recognized second most important bulb crop worldwide, extensively used as a spice and flavoring agent. Garlic is a diploid species with $2n = 16$ chromosomes (Figliuolo *et al.*, 2001). With its wide adaptability and highest morphological variability, garlic cultivation occurs across a wide range of climatic zones, from subtropical to cold temperate regions (Kindie and Mengistu, 2022). Central Asia, believed to be the center of garlic origin, includes countries, such as Turkmenistan, Tajikistan, Uzbekistan, and Kyrgyzstan, which are considered influential reservoirs of genetic diversity (Ali *et al.*, 2006).

Despite vegetative reproduction, garlic expressed considerable phenotypic plasticity and variations in both morphological and biochemical traits among and within the ecotypes. The key morphological traits comprised clove size, clove number, skin color, and leaf traits, while biochemically important traits involved organic acids and sugars (Polyzos *et al.*, 2019). Moreover, the stress-tolerant genotypes appeared viable for sustainable agriculture and climate adaptation (Khar *et al.*, 2020).

Garlic genetic diversity reflects adaptation to diverse environmental conditions (Shaaf *et al.*, 2014). This is particularly relevant to Azerbaijan, which has diverse agroecological zones, ranging from arid plains to humid subtropical and mountainous regions. Such climatic and geographical variability develops robust selection pressures that shape local adaptation and highlight the importance of conserving local populations and their genetic resources for sustainable productivity. Additionally, biochemical profiling is also crucial for determining quality traits based on scientific and industrial perspectives.

Although the genetic diversity and local adaptation of garlic genotypes under Azerbaijani conditions are of considerable importance, studies on the agromorphological and biochemical characterization of these genotypes remain relatively limited within the country. This research gap highlights the need for further investigations to systematically evaluate the Azerbaijan's garlic gene pool and support the improvement of breeding programs.

Previous studies primarily focused on commercial cultivars (Abdelrahman *et al.*, 2021), and limited information exists on broader genetic resources, particularly in Azerbaijani genotypes, which are increasingly under threat due to intensive selection and cultivation practices. This trend contributes to the narrowing of the garlic genetic base. Therefore, the pioneering study aimed to comprehensively evaluate the phenological, agromorphological, and biochemical traits of the local and introduced garlic genotypes preserved in the Azerbaijani gene pool. A total of 26 garlic genotypes, including local and foreign accessions, received analysis to capture a wide range of genetic diversity. In this context, the study aimed to characterize and compare the garlic genotypes from different regions and identify valuable genetic material for utilization in future breeding programs.

MATERIALS AND METHODS

Experimental procedure

An evaluation of the garlic (*A. sativum* L.) genotypes totaled 26, including local accessions (AS1–AS24) collected from different regions of Azerbaijan, as well as introduced genotypes from China (AS25) and Iran (AS26), two major contributors to global garlic production. The experiments took place during

2022 to 2025 in the field located on the Absheron Peninsula, Azerbaijan. All the garlic genotypes succeeded in growing under identical agronomic conditions, ensuring reliable comparison of phenological, agromorphological, and biochemical traits. Garlic bulb harvesting occurred at their full maturity and served as the primary material for assessing morphological traits and biochemical composition under laboratory conditions.

Traits measurement

Within the framework of this study, comprehensive observational and measurement methods used sought to assess the phenological, agromorphological, and biochemical traits of garlic genotypes. Phenological observations continued throughout the vegetation period, recording the number of days from sowing to mass emergence, from sowing to the 2–3 leaf stage, and from sowing to the 4–5 leaf stage for each genotype. In addition, the determination of duration from mass emergence to technical maturity and from sowing to harvest succeeded. For agromorphological evaluation, the samples collected came from mature garlic plants. Plant height (cm), leaf length and width, the number of leaf tiers, and stem diameter (cm) incurred measurement for each garlic genotype. At the end of the growing season, harvested bulbs underwent the laboratory analysis. The detection of the average bulb weight (g), bulb height and diameter (mm), and bulb index ensued. Internal bulb structure, as assessed, measured the average clove weight (g) and the number of cloves per bulb. Root system development reached evaluation by determining the total root mass (g) and root dry matter content (%), with the bulb dry matter content (%) also analyzed. Bulb color recording proceeded through visual assessment. Biochemical analyses employed standard laboratory methods. Determining sugar content (%) and extractive substances engaged an Atago LI-3100 refractometer. Total acidity (%) measurement was by the titrimetric method (Ermakov, 1972) using an acidity titrator.

Nitrate content (mg/kg) detection used a SOEKS nitrate meter. In each garlic genotype, the tuber yield entailed calculation as an agronomic trait (t/ha). For each genotype, measurements transpired on 10 randomly selected plants, with three replications for each plant, thereby ensuring the reliability and statistical robustness of results.

Statistical analysis

For statistical analysis, the study used IBM SPSS (v25.0) for correlation analysis of morphological traits. Two-way cluster analysis, as performed in PAST (v4.11), used Euclidean distances and Ward's method (Hammer *et al.*, 2001). Ward's approach sought to create clusters based on the distance matrix collected (Hajiyev *et al.* 2026). By reducing the variation across groups, Ward's technique guarantees the creation of homogenous subgroups. This approach is especially a recommendation for classification analyses where inter-cluster differences must remain to a minimum (Hajiyev *et al.* 2025). The principal component analysis (PCA), conducted in SPSS, utilized both quantitative and coded qualitative traits, with qualitative variables treated as ordinal, retaining components with eigenvalues >1.0 (Jolliffe, 2002).

RESULTS AND DISCUSSION

The main descriptive statistics revealed considerable variations among the garlic (*A. sativum* L.) genotypes across phenological, agromorphological, and biochemical traits (Table 1). The period from sowing to mass germination (DME) ranged from 16 to 38 days (mean 24.9; CV = 27.43%), indicating high genetic variability and strong potential for selecting early-maturing genotypes. Moderate variation resulted in early leaf development stages (CV = 17.11%–17.47%), while the total vegetation period remained relatively stable (CV = 5.13%), reflecting similar developmental patterns among the genotypes. Morphological traits also showed moderate variability. Plant height ranged from 40.8 to 83.0 cm (CV = 18.99%), while leaf length (28.3–55.2 cm) and

Table 1. Descriptive statistical parameters of the phenological, agromorphological, and biochemical traits recorded in garlic genotypes.

Traits	Abbrev.	Min.	Max.	Mean	CV (%)
Days to mass emergence	DME	16	38	24.9	27.43
Days to 2–3 leaves	D2–3L	24	43	30.6	17.11
Days to 4–5 leaves	D4–5L	30	53	39	17.47
Days from emergence to technical maturity	DMTM	132	185	149	12.48
Days to harvest maturity	DHM	214	250	222.7	5.13
Plant height (cm)	PH	40.8	83	49.71	18.99
Leaf length (cm)	LL	28.3	55.2	36.39	16.22
Leaf width (cm)	LW	1.8	4	2.31	14.97
Number of leafs	NL	6	9	7.10	11.48
Stem diameter (cm)	SD	4.1	7.1	5.25	12.73
Average bulb weight (g)	ABW	34	98.4	63.84	23.84
Bulb height (mm)	BH	30.1	60.2	40.63	16.53
Bulb diameter (mm)	BD	43.8	77.1	54.20	11.80
Bulb index	BI	0.48	1.21	0.76	18.14
Average clove weight (g)	ACW	3.20	10.15	6.20	27.52
Number of cloves per bulb	NCB	10.00	18.00	12.72	16.32
Root mass (g)	RM	1.00	7.54	4.58	42.25
Bulb dry matter content (%)	BDM	29.24	36.94	34.13	5.39
Root dry matter content (%)	RDM	90.00	97.10	92.88	2.04
Total sugars (%)	TS	27.70	35.29	30.85	5.25
Extractive substances (%)	ES	28.20	36.37	32.27	6.38
Nitrate content (mg/kg)	NO ₃ ⁻	33.30	60.80	46.50	13.31
Total acidity (%)	TA	0.14	0.35	0.25	19.73
Sugars	S	89.90	199.4	131.2	22.71
Yield (t/ha)	Y	16.90	69.10	34.98	33.51

leaf width (1.8–4.0 cm) exhibited moderate variation (CV = 16.22% and 14.97%, respectively). These results emerged as comparable with the findings reported in earlier studies (Tiwari *et al.*, 2020), with similar variability patterns also observed by Khadi *et al.* (2022).

In garlic genotypes, leaf number remained relatively stable (CV = 11.48%), indicating a strong genetic control. In contrast, bulb weight showed a wide variation (34.0–98.4 g; CV = 23.84%), highlighting its importance as a key selection trait. Average clove weight (CV = 27.52%) and root mass (CV = 42.25%) exhibited the highest variability, reflecting substantial differences in nutrient uptake efficiency and plant vigor among genotypes. Bulb yield also varied considerably, ranging from 16.9 to 69.1 t/ha (mean 34.98; CV = 33.51%), demonstrating a strong genotypic influence and a high potential for selecting superior, high-yielding garlic lines. Moreover, the bulb shape index displayed

moderate-to-high variability, and these results were consistent with previous reports of significant differences in agronomic traits (Jabbes *et al.*, 2012; Popa and Cosmulescu, 2024).

Biochemical traits were notably comparatively stable. The coefficient of variation for bulb dry matter (BDM), total sugars, and extractives was low (5%–6%), while root dry matter (RDM) evinced the highest stability (CV = 2.04%). Bulb dry matter ranged from 29.24% to 36.94%, aligning with findings of Pasupula *et al.* (2024). Nitrate content (NO₃⁻) showed moderate variation; however, it remained within safe limits. Overall, the garlic genotypes revealed significant genetic diversity in terms of phenological, agromorphological, yield, and biochemical traits. Earliness, bulb and clove weight, and productivity showed distinction as key selection criteria, providing a robust basis for developing high-yielding and high-quality garlic genotypes.

Table 2. Descriptive statistical parameters of the phenological, agromorphological, and biochemical traits recorded in garlic genotypes.

Traits (Abbrev.)	1	2	3	4	5	6	7
DME	0.897	-0.160		-0.108			
DHM	0.816		0.263		0.232		
D4-5L	0.793	-0.276	0.269				
D2-3L	0.784	-0.218			0.298		
Y	0.773	-0.181	-0.313	0.419			
LL	0.721				-0.555	-0.109	
PH	0.642				-0.638	-0.192	
DMTM	0.577		0.237	-0.566	0.148		
LW	0.555				0.325		
SD	0.546						0.280
ACW	0.513	-0.189	-0.507	0.130	0.333		
S	0.221	0.759		0.318	0.177		-0.262
ES		0.736	-0.256				0.348
TS		0.706	0.136				0.566
TA	-0.247	-0.677		-0.271	-0.162	0.388	
RM	0.460	0.645					
BI		-0.141	0.792		-0.141	-0.171	
BD		0.160	-0.660			0.311	-0.123
ABW		-0.251	-0.563	0.621			
BH				0.589			
RDM				0.516		-0.103	0.280
NLL				0.466	0.636		0.175
BDM						0.573	
NO ₃ ⁻					-0.102		-0.186
NCB						0.476	
Eigenvalue	6.552	3.571	2.892	2.600	2.002	1.479	1.177
Variance (%)	26.209	14.282	11.569	10.402	8.007	5.914	4.706
Σ variance (%)	26.209	40.491	52.060	62.462	70.469	76.383	81.089

Note: For abbreviations, see Table 1.

Principal component analysis (PCA) enabled a comprehensive interpretation of the interactions among the phenological, agromorphological, and biochemical traits in 26 garlic genotypes. As a key multivariate analysis, PCA reduced the correlated variables into independent components that explain overall variability (Azimi *et al.*, 2025). In the presented study, seven principal components with eigenvalues > 1 explained 81.09% of the total variation (Table 2), indicating the highest reliability of the selected traits. Azimi *et al.* (2025) also reported the first two components explained 79.11% of the total variation.

The first principal component (26.21%) signified an association with phenological stages, plant height, leaf length, and bulb yield, detailing that garlic genotypes with longer vegetation periods and robust

vegetative growth produced higher yields. The second component (14.28%) has mainly an association with biochemical traits, with positive loadings for sugars, extractives, and root mass, while the negative loading was for total acidity, indicating considerable variations in nutritional quality. The third component (11.57%) reflected bulb shape traits, where the bulb index had the major contribution and showed an inverse relationship with bulb diameter and mass, highlighting shape as an important distinguishing and economically relevant trait. Panthee *et al.* (2006) also identified the bulb mass, diameter, and clove number as key yield-related traits.

Overall, the PCA results revealed genetic variability among garlic genotypes had the primary influence from growth dynamics, yield potential, biochemical quality, and the

Table 3. Analysis of variance of the phenological, agromorphological, and biochemical traits recorded in garlic genotypes.

Traits (Abbrev.)	Sum of squares	Mean square	F	p (same)
DME	3422.2	136.9	40.6	0.000
D2-3L	1947.3	77.9	24.8	0.000
D4-5L	3520.9	140.8	109.9	0.000
DMTM	26521.0	1060.8	384.9	0.000
DHM	9963.1	398.5	201.9	0.000
PH	6773.3	270.9	158.5	0.000
LL	2626.7	105.1	96.2	0.000
LW	7.9	0.3	13.1	0.000
NLL	50.5	2.0	157.6	0.000
SD	31.2	1.2	20.1	0.000
ABW	17582.7	703.3	144.1	0.000
BH	3424.6	137.0	141.7	0.000
BD	3041.3	121.7	59.9	0.000
BI	1.4	0.1	111.8	0.000
ACW	213.6	8.5	41.4	0.000
NCB	317.8	12.7	47.2	0.000
RM	287.6	11.5	804.8	0.000
BDM	177.8	7.1	4.4	0.000
RDM	217.7	8.7	7.6	0.000
TS	160.5	6.4	8.1	0.000
ES	282.0	11.3	13.1	0.000
NO ₃ ⁻	2904.7	116.2	137.7	0.000
TA	0.2	0.0	34.6	0.000
S	68207.7	2728.3	811.1	0.000
Y	10447.4	417.9	164.9	0.000

Note: For abbreviations, see Table 1

bulb's morphological traits. Thus, PCA provides an effective tool for simplifying complex trait interactions, enabling objective genotype evaluation and more targeted breeding decisions, which serves as a considerable scientific basis for developing high-yielding, and high-quality garlic cultivars.

The analysis of variance revealed significant ($P \leq 0.000$) differences among the 26 garlic genotypes for phenological, agromorphological, and biochemical traits, confirming that the observed variations were predominantly genetic in origin rather than random environmental variation (Table 3). In phenological traits, such as days from emergence to technical maturity and days to harvest maturity, the significant differences were particularly evident, revealing clear variations in the vegetation period and maturity. Morphological traits, including plant height and leaf dimensions, as well as bulb, clove, root mass, and yield-related traits, also

showed considerable significance, revealing their importance in genotype discrimination and selection. Additionally, biochemical traits, such as sugar content, nitrate levels, and dry matter, exhibited highly significant variations, emphasizing their relevance for both quality assessment and breeding improvement. These results were consistent with the findings reported in studying the genetic variability in garlic genotypes (Vatsyayan *et al.*, 2013). Overall, analysis of variance confirmed the substantial genetic diversity among garlic genotypes, providing a solid basis for targeted breeding focused on earliness, yield, bulb quality, and biochemical traits.

The relationship among various traits, as evaluated in the study, used Pearson's correlation coefficient (Figure 1). Correlation analysis revealed both positive and negative associations among phenological, agromorphological, and biochemical traits, with coefficients ranging from -0.87 to +0.86,

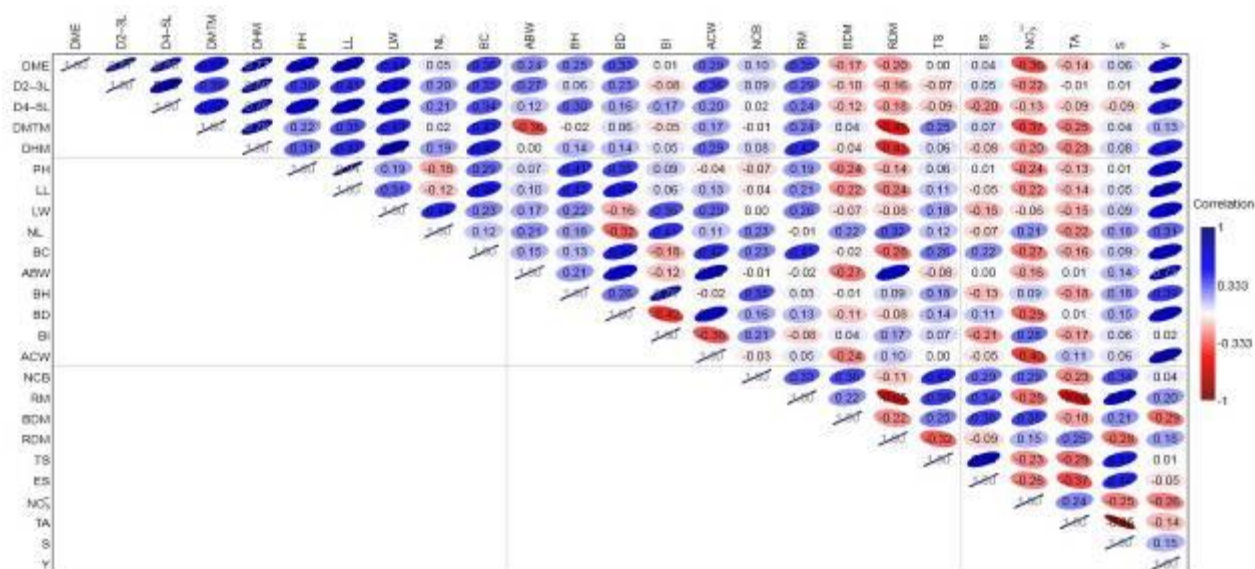


Figure 1. Pearson correlation matrix reflecting the relationships between phenological, agromorphological, and biochemical traits of garlic genotypes (for abbreviations, see Table 1).

revealing complex trait interactions. The significant positive correlations were evident among phenological traits, where DME has a high association with later developmental stages and total vegetation period ($r = 0.82$ – 0.88), suggesting consistent developmental timing across the growth stages. Phenological traits also indicated positive correlations with plant height and leaf length ($r = 0.60$ – 0.64). Bulb yield showed moderate positive correlations with bulb weight, clove weight, and bulb diameter ($r = 0.55$ – 0.67), confirming that better-developed bulbs considerably contribute to higher productivity. These results received support from previous studies reporting similar associations between the bulb yield and key morphological traits (Azimi *et al.*, 2025).

Among the biochemical traits, significant positive correlations were notable among the traits, such as sugars, total sugars, and extractives ($r = 0.64$ – 0.86), while total acidity showed a considerable negative correlation with sugars ($r = -0.87$). Nitrate content has a negative association with dry matter and sugars, stating that high-quality garlic genotypes tend to accumulate lower nitrate levels. A moderate positive relationship

between root mass and bulb yield suggested that robust root systems contribute to improved productivity. Overall, correlation analysis revealed yield formation in garlic had the influences from a complex interaction of phenological, vegetative, bulb-related, and biochemical traits. These relationships provide a robust basis for indirect selection in breeding programs.

The analysis of 26 garlic genotypes (AS1–AS26) revealed remarkable variations in phenological, agromorphological, and biochemical traits, summarized through PCA (Figure 2). The distribution of accessions indicates that both morphological and yield-related traits played a significant role in the differentiation of genotypes. Group I included accessions such as AS1, AS10, AS19, AS20, AS25, AS26, and AS4. These genotypes displayed primary associations with phenological and morphological traits, including days to 2–3 leaves (D2–3L), days to 4–5 leaves (D4–5L), and bulb diameter (BD). Group II consisted of AS13 and AS21. These genotypes were characteristic of superior growth and productivity performance. AS21 exhibited some of the highest values recorded in the study, including plant height (54.3 cm),

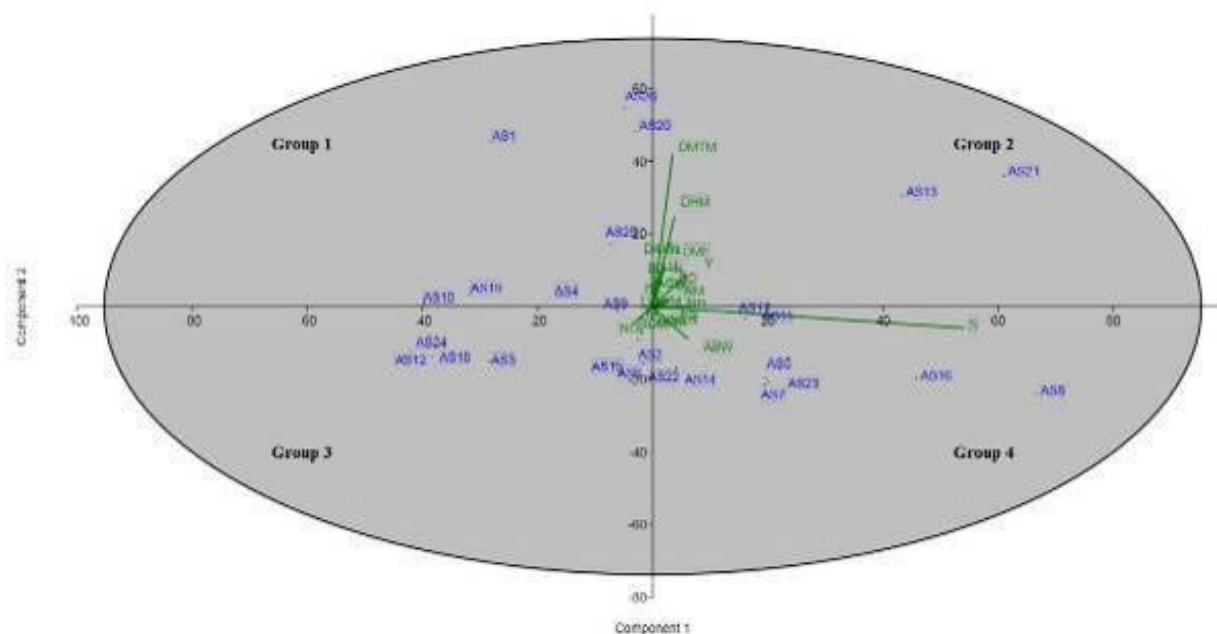


Figure 2. PCA biplot (PC1 vs. PC2) illustrating the distribution of garlic genotypes and trait vectors based on phenological, agromorphological, and biochemical traits (for abbreviations, see Table 1).

leaf length (44.2 cm), bulb index (77.0), average clove weight (10.1 g), and yield (60 g), confirming its outstanding agronomic performance. AS13 also showed relatively high values for days from emergence to technical maturity (179) and days to harvest maturity (245), supporting its placement in this group. Group III, located in the lower-left quadrant, comprised AS12, AS18, AS24, AS9, AS15, AS6, AS2, and AS3. These genotypes had features generally of moderate or relatively low values for most traits. They were in association mainly with biochemical traits, such as nitrate content and root dry matter content. Group IV represented the largest cluster and included AS5, AS7, AS8, AS11, AS14, AS16, AS17, AS22, and AS23. These genotypes were in association mostly with average bulb weight and the number of cloves per bulb. Previous studies by Jabbes *et al.* (2012), who investigated Tunisian garlic landraces, and Panthee *et al.* (2006), who studied Nepalese garlic accessions, reported similar patterns, although differences existed in the number of accessions, their geographic origins, and the traits evaluated.

Overall, the PCA results indicate the observed variation among garlic accessions has the control of the complex interaction of vegetative, phenological, yield-related, and biochemical traits. The grouping of genotypes clearly reflects their functional similarities and distinct agronomic characteristics. In particular, AS21 and AS13 showed distinction as promising genotypes due to their superior growth and yield performance, while AS20, AS25, and AS26 demonstrated strong vegetative development and stable performance. In contrast, AS8, AS14, and AS23 were mainly notable for quality-related and yield-structure traits.

Thus, the results confirm the presence of substantial genetic diversity within the garlic germplasm, which provides valuable potential for breeding programs aimed at improving both yield and quality. Accordingly, the identified promising accessions could serve as important genetic resources for future breeding and hybridization efforts.

Cluster analysis further supported genotype differentiation by grouping them based on similarity. Using Ward's method and

Euclidean distance, the dendrogram (Figure 3) illustrated the relationship among the garlic genotypes, where shorter distances revealed the highest similarity, and longer distances reflected the greater divergence (Khan *et al.*, 2021). The two-way hierarchical cluster analysis disclosed substantial variability among the 26 accessions (AS1–AS26) based on the evaluated morphological, biometric, and

quality-related traits. The heatmap and dendrogram simultaneously classified both the accessions and the measured variables according to their degree of similarity, providing a comprehensive overview of relationships among genotypes and traits. The clustering pattern indicated the separation of accessions into two major groups (Cluster 1 and Cluster 2). Each further underwent

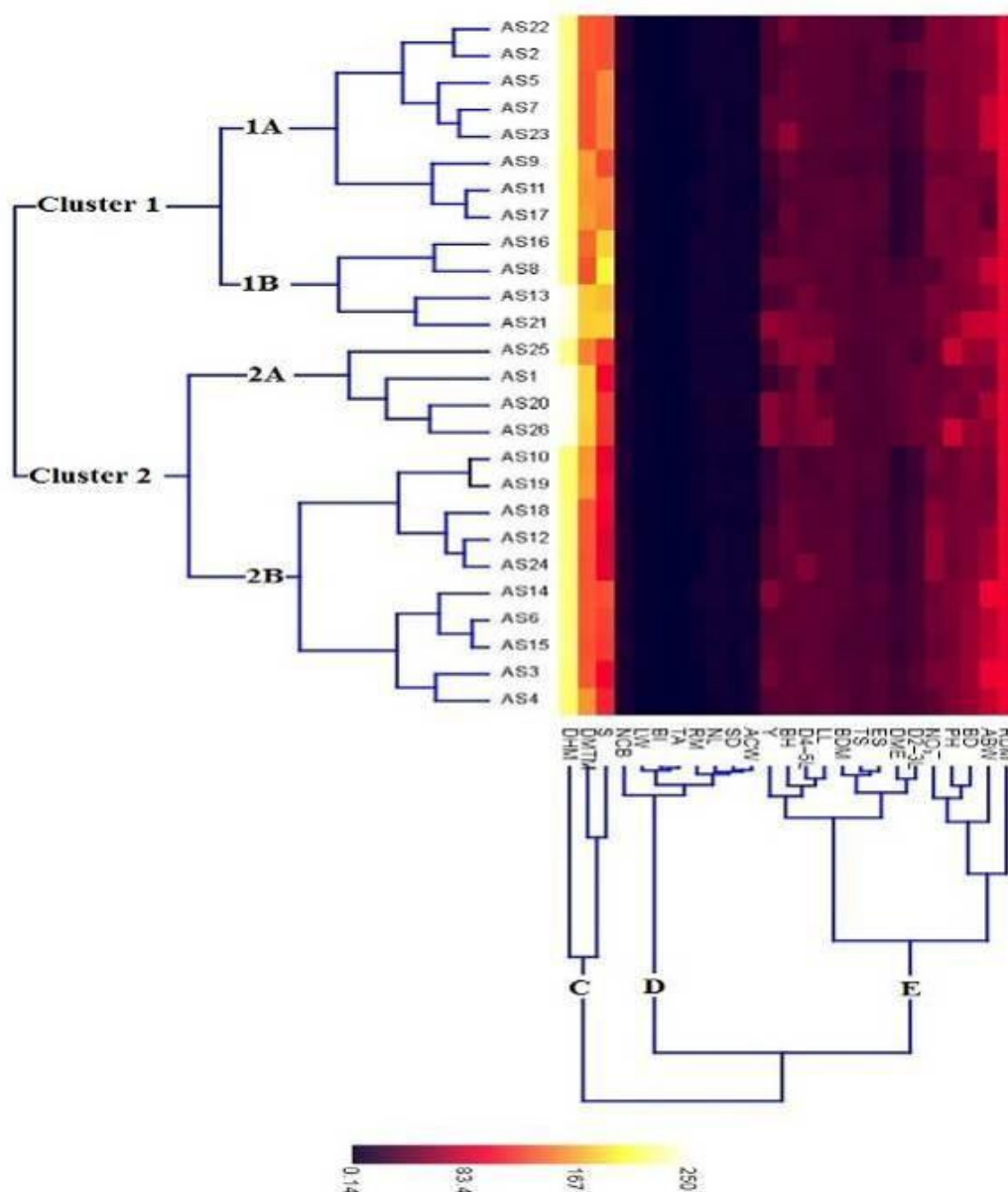


Figure 3. Dendrogram constructed based on phenological, agromorphological, and biochemical traits of garlic genotypes (for abbreviations, see Table 1).

subdivision into two subclusters, reflecting differences in growth, yield, and quality characteristics. Cluster 1 has divided into two subclusters (1A and 1B). Subcluster 1A (AS22, AS2, AS5, AS7, AS23, AS9, AS11, AS17, and AS16) displayed characteristics of low-to-moderate values for key phenological traits. Meanwhile, yield and quality parameters were generally at moderate levels, indicating a relatively homogeneous phenotypic profile. In contrast, subcluster 1B (AS8, AS13, and AS21) exhibited higher vegetative growth and productivity. Notably, AS21 showed superior performance in plant height (PH), leaf length (LL), average bulb weight (ABW), bulb index (BI), average clove weight (ACW), and yield (Y), whereas AS8 revealed distinct superiority in high yield and total sugars (TS).

Cluster 2 also entailed division into two subclusters (2A and 2B). Subcluster 2A (AS25, AS1, AS20, and AS26) had characteristics of high phenological and morphometric trait values, particularly days to mass emergence, days to 4–5 leaves, days from emergence to technical maturity, days to harvest maturity, plant height, and leaf length. Accessions AS25 and AS26 exhibited the highest plant height and leaf length, while AS20 and AS26 showed high-yield potential. Subcluster 2B (AS10, AS19, AS18, AS12, AS24, AS14, AS6, AS15, AS3, and AS4) displayed moderate morphometric traits but considerable variation in yield and quality parameters. For example, AS14 was superior for high bulb weight and yield, whereas AS3 and AS15 showed elevated biomass-related traits.

The clustering of variables revealed clear functional differentiation among the identified groups. One group was in primary association with phenological development and its relationship with biochemical characteristics, indicating that growth duration influences quality formation. Another group reflected vegetative growth and structural features, describing overall plant vigor and its contribution to yield formation. The third group represented a complex integration of developmental, morphological, and biochemical traits, collectively determining both yield

quantity and quality. Similar clustering patterns were in reports of past studies that grouped 36 Tunisian garlic genotypes based on morpho-agronomic traits, identifying high-performing groups with superior yield and bulb traits (Ayed *et al.*, 2019).

Overall, the two-way hierarchical cluster analysis demonstrated a clear separation of accessions according to their morphological, vegetative, and productivity-related characteristics. Accessions AS20, AS21, AS25, and AS26 emerged as particularly promising genotypes due to their superior vegetative growth and yield potential, whereas AS3, AS14, and AS15 were distinguishably favorable for fruit quality and biomass-related traits. The observed clustering pattern highlights the importance of morphometric and yield-related parameters in determining phenotypic diversity among the evaluated accessions and provides valuable information for germplasm characterization, breeding programs, and future selection strategies.

CONCLUSIONS

The study revealed significant genetic diversity among the 26 garlic (*A. sativum* L.) genotypes across the phenological, agromorphological, and biochemical traits. Earliness, bulb and clove mass, root mass, and yield showed the highest variability, which were identified as key selection traits. Bulb yield has a positive association with bulb diameter, bulb and clove weight, and plant height, supporting indirect selection approaches. The PCA and cluster analyses grouped the garlic genotypes into early and low-yielding; medium-vegetation with large bulbs; and late, high-yielding types, and the genotypes AS21, AS20, AS26, and AS14 were leading with superior performance. The biochemical traits proved relatively stable, with variations in sugar and nitrate content providing additional opportunities for selecting the high-quality and safe genotypes. Overall, the results provided a robust basis for developing high-yielding, high-quality, and environmentally adapted garlic cultivars.

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