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The first assessment of phenotypic diversity in four quinoa (*Chenopodium quinoa* Willd.) populations cultivated in Algeria based on morphological traits

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ABSTRACT

In the present study, the morphological variation among seventeen accessions from four quinoa populations (Giza 01, Q101, Q102, and Black) cultivated in a semi-arid region of Algeria was investigated using 26 morphological descriptors established by the International Union for the Protection of New Varieties of Plants (UPOV), along with descriptors from FAO, PROINPA, INIAF, and FIDA. The study aimed to determine which of these descriptors serve as robust estimators of phenotypic diversity within quinoa populations accessions and to analyze the patterns of morphological diversity in cultivated quinoa in Algeria. To address these objectives, principal component analysis (PCA), hierarchical cluster analysis, and the Shannon-Weaver diversity index (H') were employed. The selected 26 descriptors covered plant structural traits, leaf characteristics, inflorescence features, stem properties, panicle attributes, and seed traits to assess the overall degree of polymorphism among the studied accessions. The computed H' index values ranged from 0.38 for plant height (PH) to a maximum of 0.98 for branching type (TB), leaf size, and foliage color (FC). The average diversity index among all traits and populations was 0.59, reflecting a substantial level of genetic diversity within the collection. The relative magnitude of the first two PCA eigenvectors indicated that 11 out of the 26 descriptors were the most significant for populations classification. Multivariate analyses, including factorial correspondence analysis and cluster analysis based on morphological descriptors, facilitated the classification of the quinoa accessions into three discrete groups. The first group consisted of four accessions (Giza 01), while the second group was subdivided into two subgroups: the first, a major subgroup comprising eight accessions (Q102), and the second, a minor subgroup with a single accession (Q101). The third group included four accessions (Black). The findings of this study represent a crucial step toward the efficient selection of promising quinoa accessions and their optimal management and conservation.

Keywords: Quinoa, diversity index, multivariate analysis, morphological descriptors.

INTRODUCTION

Quinoa (*Chenopodium quinoa* Willd.) is an annual plant species belonging to the dicotyledons, and gynomonoecious plant classified as a pseudo-cereal within the Amaranthaceae family. It figures among the oldest cultivated crops in the Andes, with evidence of domestication dating back to before 5000 BCE (Lallouche and Hadj Kouider, 2024). Quinoa has attracted significant scientific and commercial interest worldwide owing to the remarkable nutritional composition of its seeds, which contain high-quality protein (14–20%), fats, and antioxidants. Notably, its nutritional profile is at least five times higher than that of conventional cereal flours (Bhargava et al., 2006; Jacobsen, 2003). Quinoa seeds contain up to 48.5–69.8% carbohydrates, up to 4.0

to 7.6% fat (which remains relatively stable), and up to (7.0 to 14.1% fiber, making them an excellent functional food (Pathan and Siddiqui, 2022). Additionally, Quinoa is a highly nutritious food, offering a rich supply of dietary fiber along with significant levels of minerals, iron, vitamins and calcium (Maradiniu-Filho et al., 2017). In the absence of gluten proteins, quinoa is suitable for the production of gluten-free cereal-based products, making it appropriate for individuals with celiac disease and wheat sensitivities (Chillo et al., 2009; Gambus et al., 2002).

This crop thrives under a wide range of environmental conditions, tolerating relative humidity levels from 40% to 88% and soil pH between 4.8 and 8.5. It can survive temperatures ranging from -8 °C to 38 °C and is capable of growing from sea level to the Andean highlands (Bazile et al., 2016). Tolerant of low soil moisture and capable of yielding acceptable results even with with annual precipitation levels between 100 and 200 mm. Furthermore, it is an optional plant parasite (Panuccio et al., 2014) with a notable resistance to saline conditions, enduring NaCl concentrations of up to 200 mM (Lallouche and Hadjkouider, 2024).

Quinoa demonstrates a remarkable level of genetic diversity, with different varieties thriving across a wide spectrum of environments, from areas at sea level to elevations above 4000 meters, and from cool highland zones to warmer subtropical areas. This broad genetic range supports the selection and development of cultivars that can adapt to diverse environmental conditions, such as dry or humid regions, extreme temperatures, and soils with varying pH levels (Jacobsen, 2003).

Following the release of the quinoa reference genome (Jarvis et al., 2017), global interest in quinoa cultivation has grown substantially, accompanied by a notable increase in related scientific research. This trend suggests a likely global expansion of quinoa farming in the near future. To date, more than a thousand studies have explored how climate variability impacts quinoa production, with particular emphasis on its genetic traits, growth stages, physiological responses, yield potential, and the nutritional properties of its seeds. Leading contributors to quinoa-related publications include the USA, UK, Italy, Germany, and France. In South America, key research contributions have come from Chile, Argentina, and Brazil (Bazile et al., 2016; Ruiz et al., 2014).

In recent years, numerous countries have launched research initiatives aimed at advancing quinoa cultivation. Algeria is among those that have embraced this crop, benefiting from support provided by the FAO in terms of scientific and technical expertise. This collaboration helped assess quinoa's adaptability after its introduction to Algeria during the 2013–2014 period.

For the initial evaluation, eight experimental locations were chosen to reflect the country's varied agro-ecological zones. These sites included Baïnem (Algiers), Sétif, Tiaret, Relizane, Guelma, Biskra, El Oued, and Adrar.

Through international collaboration led by the FAO, an evaluation was carried out to assess 16 quinoa genotypes (including Q21, Q12, Q29, Q18, Q26, Q22, Q27, Giza1, Giza2, Sajama, Santamaria, Amarilla Marangani, Amarilla Sacaca, Blanca de Junin, Kancolla, and Salcedo Inea) under arid and semi-arid climate conditions. The goal of this study was to analyze the phenological development of these genotypes and assess key yield-related traits across different varieties and test locations. The first phase of the trials began in the autumn of 2014 at seven sites, Baïnem (Algiers), Sétif, Tiaret, Biskra, El Oued, Adrar, and Relizane, Further trials were carried out in Guelma and Relizane in the spring of 2015.

Introducing quinoa to Algeria primarily aims to find alternative crops suitable for cultivation on marginal lands impacted by salinity, drought, and extreme temperatures. The focus is on determining whether quinoa has the resilience to endure both current and anticipated challenges within the Saharan agricultural landscape, especially as desert conditions become more severe. Nonetheless, quinoa farming in Algeria is still in its initial phases and has yet to achieve the scale or national visibility required for widespread adoption.

To improve the understanding and optimization of quinoa cultivation techniques in Algeria, several studies have been conducted across different agro-ecological regions (Maamri et al., 2022; Oustani et al., 2023). Additionally, the study by Lallouche and Hadjkouider (2024) examines the influence of hydropriming, halopriming, and hormopriming methods on seed performance on quinoa (*Chenopodium quinoa* Willd.) and their impact on salt stress tolerance in Algerian conditions.

Although efforts have been made, the morphological and genetic diversity of quinoa in Algeria has not been thoroughly explored. This gap in research has prompted our study to examine the morphological and phenological variation within quinoa species, aiming to identify key traits that

can be used to distinguish and characterize this genetic diversity.

The objective of this study is to assess the morphological diversity of four quinoa populations, which may have significant agro-ecological value for human consumption, cultivated in Algeria's semi-arid regions. A set of 26 morphological traits was documented from different plant structures such as the stem, panicle, flowers, and seeds, in accordance with the guidelines provided by the International Union for the Protection of New Varieties of Plants (UPOV) and descriptors from organizations like FAO, PROINPA, INIAF, and FIDA. Phenotypic diversity was evaluated both within and between populations to identify key traits driving morphological variation. To classify the genotypes based on their morphological features, principal component analysis (PCA), hierarchical clustering, and the Shannon-Weaver diversity index (H') were used.

MATERIAL AND METHODS

Plant material

This study investigates the morphological diversity within and between four quinoa (*Chenopodium quinoa* Willd.) populations: Giza 01, Q101, Q102, and Black (Fig. 1), These populations were provided by the Technical Institute for the Development of Saharan Agriculture (ITDAS), located in Ain Ben Naoui, Biskra, Algeria. with the seeds initially obtained from the United States Department of Agriculture (USDA).

The experiment began in October 2023 at the experimental station of the Department of Agronomic Sciences at Mohammed Boudiaf University in M'Sila, located in Algeria's semi-arid region (35° 74' N, 04° 55' E; elevation: 512 m). Prior to sowing, the seeds underwent disinfection by soaking in a 1% sodium hypochlorite solution for five minutes, then were thoroughly rinsed with distilled water three to five times.

The crop was sown in sandy clay soil using a completely randomized design with a single-factor approach and five replications. Sowing was performed in rows spaced 100 cm apart, with a 50 cm interplant spacing to facilitate crop management and monitoring. Each experimental unit consisted of a single-row crop representing one population. Throughout the cultivation period, agronomic practices, including irrigation and weeding, were applied uniformly across all plots as needed. This study involved the identification of 17 accessions following the sowing of four quinoa populations, Giza 01, Q101, Q102, and Black, as illustrated in Figure 1. Specifically, the Giza 01 population comprised four accessions, Q102 consisted of eight accessions, Q101 included one accession, and the Black population contained four accessions.

All identified quinoa accessions were evaluated based on 26 quantitative and qualitative traits related to the plant, leaf, stem, inflorescence, panicle, and seed (Fig. 1). In each replication, five central plants from each accession were selected for sampling. Trait selection was based on the descriptor lists Supplied by the International Union for the Protection of New Varieties of Plants (UPOV, 2018), as well as FAO, PROINPA, INIAF, and FIDA (2013) (Table 1).

Morphological descriptors and data collection

Twenty-six key quantitative and qualitative traits were assessed, selected from the UPOV descriptor list (UPOV, 2018) and the guidelines of FAO, PROINPA, INIAF, and FIDA (2013).

The evaluated traits comprised 14 qualitative and 12 quantitative characteristics. The qualitative traits included foliage color (FC), leaf base angle (LAB), inflorescence color (IC), stem color (SC), stem stripes (SS), stem stripe color (SCS), panicle color (PC), seed color without tegument (SCwT), seed color (SeC), growth type (TG), branching type (TB), leaf shape (SL), panicle shape (SP), and seed shape (SSp).

The quantitative traits measured were saponin content in seeds (SSC), foliage glaucosity (FG), leaf size (LS), leaf dentation (LD), flowering time (TF), panicle density (PD), panicle width (PW), maturity time (TM), plant height (PH), 1000-seed weight (MSW), presence of branching (PB), and germinative vigor (GV) (Table 1).

These traits covered descriptors related to various plant structures, including the plant as a whole, leaves, stem, inflorescence, panicle, and seeds, and were used to construct a numerical data matrix (Table 1).

Morphological diversity was evaluated for five individuals per accession based on the 26 selected descriptors. To minimize variability and ensure consistency in data collection, all measurements were conducted by the same two researchers.

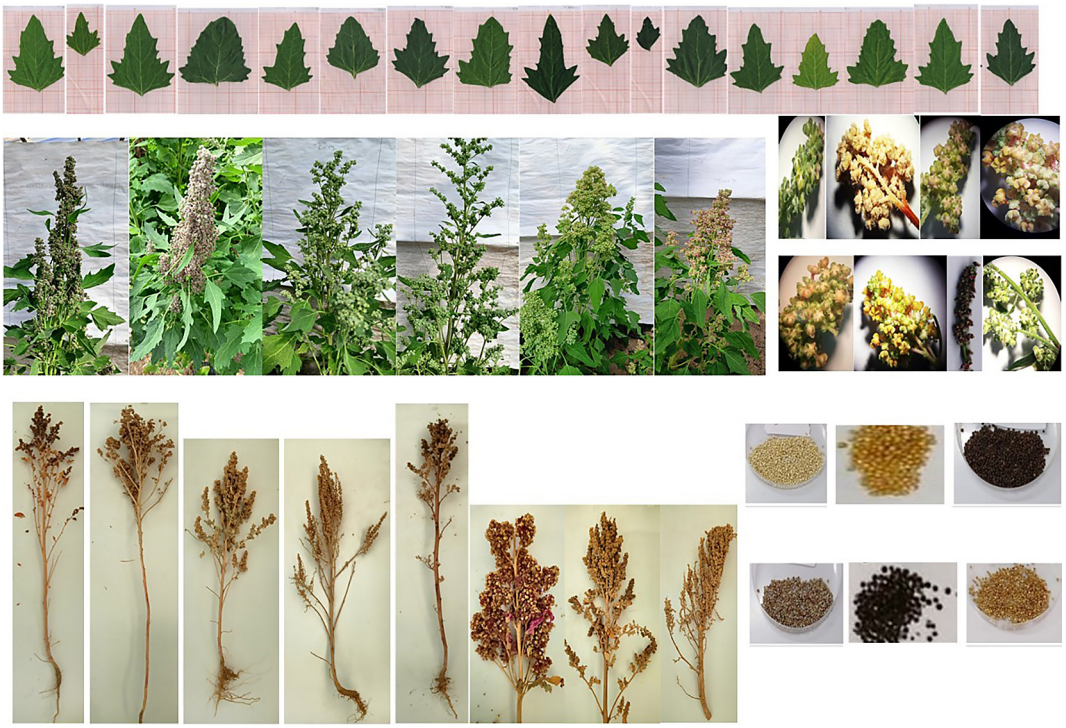

Figure 1. Illustration of the morphological diversity and the various quinoa plant organs sampled for experimental analysis mentioned in Table 1

Data analysis

Data analysis was performed to assess the morphological diversity of intra- and inter-populations based on plant, leaf, inflorescence, stem, panicle, and seed traits (Table 1).

Morphological and phenological data were examined using multivariate statistical methods and clustering techniques, processed through XLSTAT software (Addinsoft, www.xlstat.com). PCA was conducted to group accessions within the population and to pinpoint the primary axes and traits that played a significant role in morphological variation. During this process, a similarity matrix was applied to calculate eigenvalues and accession scores. The first two principal components, that captured the most variation, were employed to create two-dimensional scatter plots.

hierarchical cluster analysis (HCA) was carried out using Ward's minimum variance approach (Williams, 1976) for clustering, with squared Euclidean distances employed as the metric for dissimilarity (Ward, 1963).

Each trait' variability was quantified with the standardized Shannon-Weaver diversity index (H') (Shannon and Weaver, 1949, as cited by (Al Khanjari et al., 2008). The index is determined using the formula: H' = -P pi (log2 pi)/log2 n, in which pi represents the proportion of each descriptor state, and n refers to the total number of states for each descriptor. Microsoft Excel (2013) was employed to produce frequency distributions for all morphological traits. The Shannon-Weaver diversity index has a scale from 0 to 1, with 0 reflecting an absence of diversity and 1 indicating the highest possible level of diversity (Table 1).

RESULTS

Assessment of variation through the Shannon-Weaver diversity index

As shown in Table 1, The diversity index values for quantitative and qualitative traits varied from 0.38 for plant height (PH) to 0.98 for traits such as type of branching (TB), leaf size (LS), and foliage color, with an average diversity value of 0.59. The lowest variation was observed in plant height (0.38), whereas high phenotypic variability was detected across multiple traits. The highest diversity values were recorded for FC (0.98), LS (0.98), and TB (0.98), followed by SC (0.97), panicle width PW (0.94), foliage glaucosity (FG) (0.86), TF (0.86), maturity (TM) (0.86), seed shape (SSp) (0.86), panicle shape (SP) (0.85),

Table 1. Morphological descriptors used to characterize the morphology of four distinct quinoa populations cultivated in Algeria

Descriptor acronym	Type of expression	Descriptor state and class	Population Giza 01				Population Q102								Population Q101	Population black				Frequency (%)	Diversity index (H')
			Giza 01-1	Giza 01-2	Giza 01-3	Giza 01-4	Q102 -1	Q102 -2	Q102 -3	Q102 -4	Q102 -5	Q102 -6	Q102 -7	Q102 -8	Q101	Black-1	Black-2	Black-3	Black-4		
SSC	QN MG	Absent or low: 1; medium: 2; high: 3	3	3	2	3	3	2	3	2	1	1	3	3	1	3	3	2	3	17.64; 23.52; 58.82	0.80
FGC	PQ VG	Light green: 1; medium green:2; dark green:3; Red : 4; purple : 5	3	2	2	2	1	1	2	3	2	3	1	3	3	3	3	3	3	17.64; 29.41; 52.94; 0; 0	0.98
FG	QN	Absent or weak: 1; medium :3; strong : 5	3	3	3	3	3	1	1	1	1	1	1	1	5	3	3	3	3	41.17; 52.94; 5.88	0.86
LS	QN	Small: 3 ; medium:5 ; large:7	5	5	5	5	7	7	7	7	7	3	7	7	7	7	3	3	5	17.64; 29.41; 52.94	0.98
LD	QN VG	Absent or weak: 1; medium:3; strong:5	3	3	3	3	3	5	3	5	5	5	5	3	5	3	3	3	3	0; 64.70; 35.29	0.64
LAB	PQ	Acute: 1 ; obtuse:2 Truncate:3	2	2	2	1	1	1	2	2	2	2	2	2	3	2	2	2	2	17.64; 76.47; 5.88	0 .66
TF	QN	Early: 3 ; medium:5 Late:7	3	3	3	3	5	5	5	5	5	5	5	5	7	3	3	3	3	47.05; 47.05; 5.88	0.86
IC	PQ VG	White: 1; green: 2 Yellow: 3; orange: 4 Pink: 5; purple: 6	2	3	5	2	4	1	2	5	2	6	6	4	2	2	2	2	2	5.88; 52.94; 5.88; 11.76 11.76; 11.76	0.49
SC	PQVG	White:1; green:2 Yellow:3; purple:4	3	4	4	4	2	2	2	2	2	2	2	2	2	2	4	4	4	0; 58.82; 17.64; 35.29	0.97
SS	QLVG	Absent:1; present:9	1	1	1	1	1	1	1	1	1	1	1	1	1	9	9	9	9	76. 47; 23.52	0.54
SCS	PGVG	Green;1; yellow:2 Pink:3;r:4; purple:5	/	/	/	/	/	/	/	/	/	/	/	/	/	2	5	5	5	0; 5.88; 0; 0; 17 ;64	0.46
PD	QN VG	Sparse: 3 ; medium: 5 ; dense: 7	3	3	3	3	7	7	7	7	7	7	7	7	7	7	7	7	7	23.52; 0; 76.47	0.54
PW	QN MG/VG	Narrow:3;mediu m:5; broad:7	3	7	5	5	7	7	7	7	7	7	7	7	3	3	3	3	3	35.29; 11.76; 52.94	0.94
PC	PQ VG	Light yellow brown:1; brown:2; black:3	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	3	76.47; 0; 0; 23.52	0.54
PH	QN MG/VG	Short: 3 ; medium: 5 ; tall:7	7	7	3	3	5	3	5	5	3	5	3	7	7	5	5	5	7	29.41; 41.17; 29.41	0.38
SCwT	PQ VG	White: 1; yellow: 2 Red: 3; grey: 4	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	100; 0; 0; 0	0
SeC	PQ	Whitish:1; yellow:2 Red: 3; light brown: 4; grey: 5; black: 6	1	2	4	1	2	2	2	1	2	2	3	5	5	6	3	6	3	17.64; 35.29; 17.64; 5.88; 11.76; 11.76	0.47
TM	QN MG	Early: 3 ; medium: 5 ; Late: 7	3	3	3	3	5	5	5	5	5	5	5	5	7	3	3	3	3	47.05; 47.05; 5.88	0.86
MSW	QN	Very low: 1; low:3 medium:5; high:7 Very high: 9	9	9	9	9	7	7	7	7	7	7	7	7	7	9	9	9	9	0; 0; 0; 52.94; 47.05	0.68
TG	QL	Herbaceous:1; shrub :2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	100; 0	0
PB		Absent : 0 ; présent : 1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0;100	0
TB	QL	Simple:1;branch ing to lower third:2; twigs to second third:3; branching with undefined main panicle: 4	4	1	2	1	2	2	2	2	2	1	2	1	1	2	3	2	2	29.41; 58.82; 5.88; 5.88	0.98
SL	QL	Rhomboid : 1, triangular : 2	2	2	2	2	2	1	1	1	1	2	2	1	2	1	1	1	2	47.05; 52.94	0.68
SP	QL	Glomeriform:1 intermediate:2 (presence of both shapes); Amarantiform: 3	1	2	2	1	1	1	2	1	1	2	1	1	2	2	3	2	1	52 ;94; 41.17; 5.88	0.85
SSp	QL	Lenticulaire: 1 ; cylindrical: 2 ; ellipsoidal: 3; Conical: 4	3	3	2	2	3	3	2	2	2	1	3	2	3	3	2	3	2	5.88; 47.05; 47.05; 0	0.86
GV	QN	Poor: 1 ; average: 2 ; good: 3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	0; 0; 100	0

Note: seed: saponin content (SSC); foliage: color (FC); foliage: glaucosity (FG); leaf: size; leaf: dentation (LD); leaf: angle of base (LAB); time of flowering (TF); inflorescence: color (IC); stem: color (SC); stem: stripes (SS); stem: color of stripes (SCS): panicle: density (PD): panicle: width (PW); panicle: color (PC); plant: height (PH); seed: color without tegument (SCwT); seed: color (SeC); time of maturity (TM); 1000 seed weight (MSW); type of growth (TG); presence of branching (PB); type of branching (TB); shape of leaf (SL); shape of panicle (SP); seed shape (SSp); germinative vigour (GV).

and seed saponin content (GSC) (0.80). Moderate variability was observed for leaf shape (SL) (0.68), MSW (0.68), and leaf angle at the base (LAB) (0.66). All other traits exhibited intermediate variation (0.46–0.54), including seed color (SeC), PC, panicle density (PD), stem stripe color (SCS), SS, and inflorescence color (IC). Low variation indicated the predominance of a single character state, whereas a high level of variation suggested a more uniform representation of the various trait states, as demonstrated by the frequency distribution.

Correlation analysis between all traits

Pearson correlation coefficients (r) were computed to assess the associations between all quantitative and qualitative variables. A total of 11 traits exhibited significant correlations at $p < 0.05$. Time of flowering (TF) showed a strong positive correlation with leaf dentation (LD) (r = 0.71), as well as with AHI and LHI (r = 0.88). Additionally, a strong positive correlation was found between AP and DT (r = 0.91), as well as between 1000-seed weight (MSW) and stem color (SC) (r = 0.86).

Conversely, significant negative correlations were found between 1000-seed weight and time of flowering (r = - 0.92), stem color and time of flowering (r = - 0.79), and panicle width (PW) and panicle color (PC) with stem stripes (SS) and foliage color (FC) (r = - 0.70 and r = - 0.75, respectively).

Principal component analysis (PCA)

PCA showed a considerable level of morphological variation across the four quinoa populations examined. The first two principal components (PCA) explained a total of 49.757% of the overall variation, with the first principal component (PC1) contributing 33.520% and the second principal component (PC2) contributing 16.237% of the total variation (Fig. 2).

Among the 26 morphological descriptors analyzed. four were identified as the most discriminative and essential for classifying the quinoa populations. The contributions of all parameters to the first two PCA axes are presented in Figure 2. The traits that contributed most significantly to the variability of the first principal component included SSp (0.129). TB (0.352). SP (0.468). PH (0.301). SeC (0.323). SC (0.815). SS (0.760). PC (0.760). MSW (0.945). TF (0.849). LS (0.641). LD (0.739). IC (0.407). PW (0.799). and TM (0.849). Conversely. in the second principal component. the most strongly correlated traits were PH (0.354). LAB (0.707). PD (0.694). SeC (0.670). FGC (0.583). SSC (0.434) and SL (0.414) (Fig. 2).

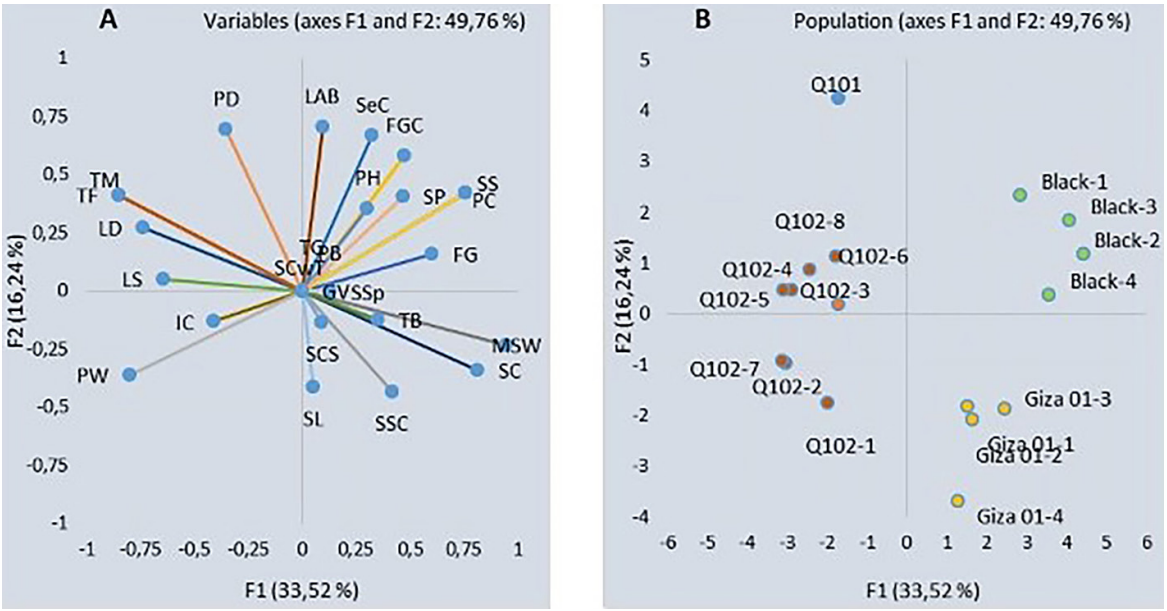

Figure 2. Principal component analysis illustrating: (a) the contribution of UPOV descriptors along with those from FAO. PROINPA. INIAF. and FIDA (1 to 26. see Table 1) to the observed morphological variation; (b) the differentiation among the studied quinoa populations

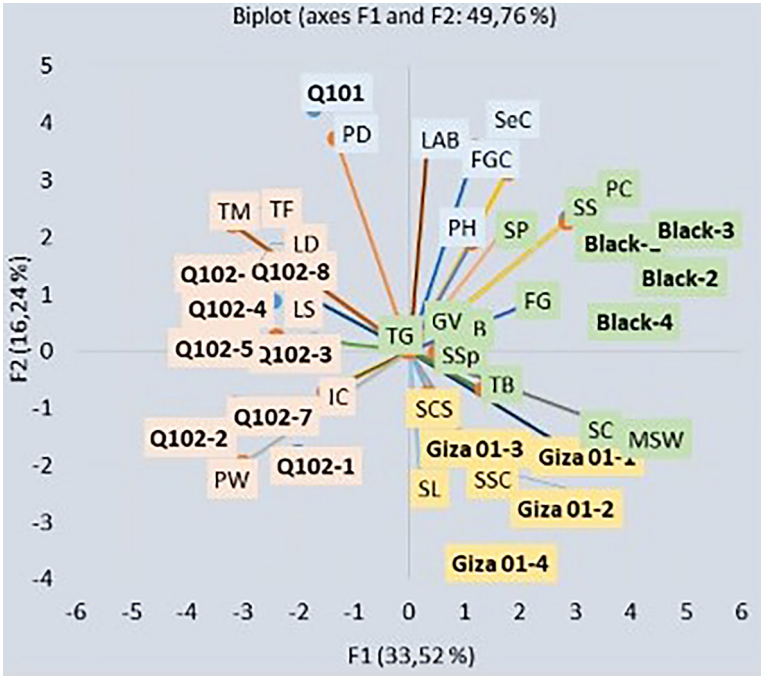

Figure 3. Biplot representation of quinoa accessions intra- and inter-populations based on the first and second principal component axes

The projection of quinoa populations onto the plot defined by the first two PCA axes revealed a clear classification into four distinct groups (Fig. 3). The first group (a) consists of the Black population. comprising accessions Black-1. Black-2. Black-3. and Black-4. The second group (b) includes the Q102 population. with eight accessions (Q102-1 to Q102-8). positioned on the negative side of the plot. The third group (c) is represented by the Q101 population. The fourth group (d) consists of the Giza 01 population. including accessions Giza 01-1. Giza 01-2. Giza 01-3. and Giza 01-4.

Cluster analysis

A dendrogram incorporating both quantitative and qualitative traits was constructed to assess the overall variance pattern and to determine the relationships among the four quinoa populations (Fig. 4). The accessions were grouped into three primary clusters.

The first cluster (C1) consisted of the Giza 01 population. which included four accessions: Giza 01-1. Giza 01-2. Giza 01-3. and Giza 01-4. Within this cluster. Giza 01-3 was distinguished by its medium seed saponin content. while Giza 01-1. Giza 01-2. and Giza 01-4 exhibited the closest similarity.

The second cluster (C2) was split into two separate subgroups:

- Subgroup C2-1: this subgroup comprised the Q102 population. which included eight accessions (Q102-1. Q102-2. Q102-3. Q102-4. Q102-5. Q102-6. Q102-7. and Q102-8). The accessions Q102-5 and Q102-6 were characterized by absent or low seed saponin content. whereas Q102-2 and Q102-4 exhibited medium saponin levels. In contrast. accessions Q102-1. Q102-3. Q102-7. and Q102-8 displayed high seed saponin content. Leaf morphology also varied within this subgroup. with accessions Q102-2. Q102-3. Q102-4. and Q102-5 exhibiting rhomboid-shaped leaves. while Q102-1. Q102-6. and Q102-7 presented triangular leaf shapes.
- Subgroup C2-2: this subgroup included the Q101 population. which was distinguished by its dark green foliage. truncate leaf base angle. dense panicle structure. and gray seed color.

The Black population. comprising four accessions. constituted the third cluster (C3): Black-1. Black-2. Black-3. and Black-4. Within this group. the Black-2 accession exhibited distinct characteristics. notably its branching pattern extending to the second and third nodes and an amaranti-form panicle shape. In contrast. Black-1 and Black-3 shared the highest degree of similarity.

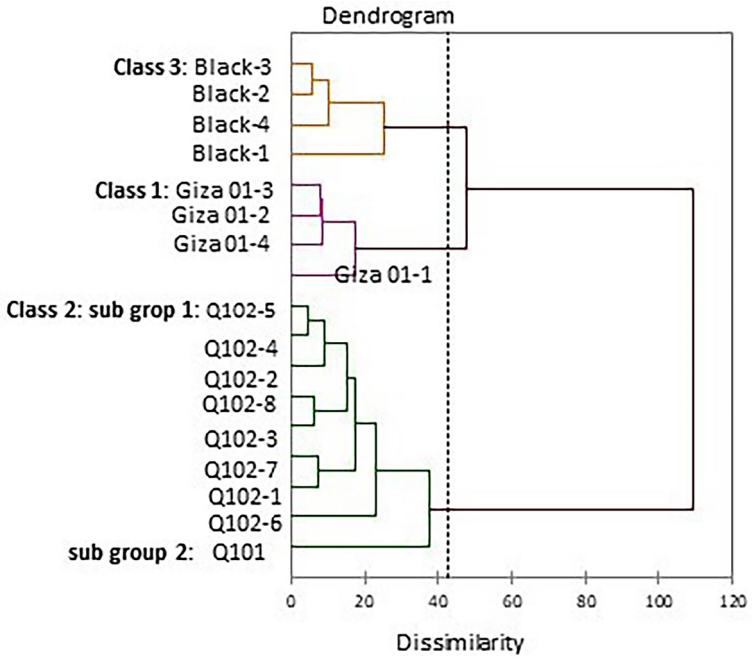

Figure 4. Dendrogram illustrating the relationships among seventeen accessions from four quinoa populations cultivated in Algeria, based on 26 morphological descriptors

both displaying a branching pattern limited to the lower third. an intermediate panicle shape. and ellipsoidal seed morphology.

DISCUSSION

To date. no studies have been conducted in Algeria to characterize the morphological diversity of a broad range of quinoa accessions using international standards (UPOV. 2018; FAO. PROINPA. INIAF. and IFAD. 2013). The plant. leaf. stem. and seed traits evaluated in this study revealed significant diversity within a quinoa collection cultivated in "M'sila". Algeria. as indicated by an average diversity index of 0.59. These findings confirm Algeria's role as a key center for quinoa adaptation and diversification within the Mediterranean region. This study offers important insights into both intra- and inter-population quinoa's variation cultivated in the semi-arid regions of Algeria.

The application of multivariate factorial correspondence analysis and cluster analysis on plant. leaf. stem. and seed descriptors facilitated the classification of the studied quinoa populations into three distinct morphological groups. The analysis revealed that only a limited number of descriptors exhibited effective discriminative capacity. Specifically. four quantitative traits. 1000 seed weight. plant height. foliage glaucosity. and seed saponin content. along with seven qualitative descriptors. including stem color. panicle color. leaf angle of base. stem stripes. panicle shape. branching type. and seed shape. were identified as key differentiating parameters among the quinoa accessions across the four populations (Table 1; Fig. 3).

These descriptors align with the primary characterization criteria established according to the guidelines set by the International Union for the Protection of New Varieties of Plants (UPOV, 2018), as well as FAO, PROINPA, INIAF, and IFAD (2013) for quinoa accession assessment. The classification results were consistent with the established criteria for the morphological classification of quinoa varieties and accessions. as previously reported in various countries (EL-Harty et al., 2021; Hafeez et al., 2022; Madrid et al., 2018; Manjarres-Hernández et al., 2021).

Accordingly. the first identified group consisted of four accessions of Giza 01. characterized by medium leaf size. triangular leaf shape. light yellow-brown panicle color. and sparse panicle density. The second and largest group comprised the Q102 population. which was subsequently separated into two subgroups. The first subgroup comprised Q102-1. Q102-2. Q102-3. Q102-4. Q102-5. Q102-6. Q102-7. and Q102-8. exhibiting medium time of flowering. broad panicle width. and

medium time of maturity. The second subgroup contained the Q101 accession. distinguished by yellow stem stripes. strong foliage glaucosity. and late time of flowering. The third group corresponded to the Black population. which included four accessions (Black-1. Black-2. Black-3. and Black-4) characterized by the presence of stem stripes and a black panicle color.

Data also revealed that phenotypic differences between populations have been attributed to both environmental and genetic factors (Hadjkouider et al., 2017; Moskalets et al., 2024). Furthermore. Madrid et al., (2018). Manjarres-Hernández et al., (2021) and Hafeez et al., (2022) have highlighted the extensive inherent variation of quinoa in characteristics like inflorescence type. panicle density. seed color and size. production cycle length, tolerance to drought and salinity, and the nutritional value of the grain. This inherent variability has positioned quinoa cultivation as a key strategy for mitigating the effects of climate change while simultaneously serving as an alternative for enhancing food security across various regions worldwide. Variations in research findings may arise due to differences in genetic material used. as well as variations in the environmental conditions under which experiments are conducted.

The utilization of morphological descriptors encompassing plant. leaf. inflorescence. stem. and seed traits resulted in a high level of morphotypic diversity. enabling clear discrimination among the studied quinoa populations. Previous studies have reported similar levels of discrimination. comparable to those obtained using molecular markers for quinoa (Jarvis et al., 2008; Mizuno et al., 2020).

Multivariate analyses based on morphological traits continue to provide valuable insights. facilitating the selection and improvement of species adapted to specific geographical regions (Hadjkouider et al., 2017). Such techniques have been widely applied in quinoa for morphological and agronomic characterization (Bhargava et al., 2007; EL-Harty et al., 2021; Manjarres-Hernández et al., 2021). In the present study. multivariate analyses revealed that the highest degree of variation was captured through leaf. stem. panicle. and seed descriptors (Table 1, Fig. 1 and 2). These traits have been previously identified as key parameters for quinoa variety characterization (Bhargava and Ohri, 2016; EL-Harty et al., 2021).

CONCLUSION

The present study emphasizes plants' utility. stem. leaf. panicle. and seed traits in assessing the genetic diversity of quinoa populations cultivated in Algeria. The findings contribute to improving the selection process and can aid in the conservation and management of quinoa genetic resources for future breeding initiatives. The morphological data presented here offer valuable insights for distinguishing quinoa accessions within each population of this taxonomically complex genus.

Additional germplasm gathering y efforts are needed to obtain more accessions. enriching the existing repository with ensuring comprehensive identification of quinoa diversity in Algeria. Future research will integrate both morphological and molecular approaches to validate the observed diversity and enhance the management of quinoa genetic resources.

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