

Article

Comprehensive Evaluation of Fruit Quality in 142 Pomegranate Accessions from China

Zhen Cao ¹, Jiyu Li ¹, Cong He ¹, Bo Deng ^{2,*} and Gaihua Qin ^{1,*} 

¹ Key Laboratory of Horticultural Crop Germplasm Innovation and Utilization (Co-Construction by Ministry and Province), Key Laboratory of Horticultural Crop Genetic Improvement and Eco-Physiology of Anhui Province, Institute of Horticulture, Anhui Academy of Agricultural Sciences, Hefei 230031, China; hazelcz@163.com (Z.C.)

² College of Horticulture, Anhui Agricultural University, Anhui 230001, China

* Correspondence: bdeng2008@sohu.com (B.D.); qghahstu@163.com (G.Q.)

Abstract

Pomegranate (*Punica granatum* L.) is widely valued for its rich nutritional profile and distinctive sensory characteristics. As one of the oldest cultivated fruits, it has an extensive history of cultivation in China and possesses abundant germplasm resources. Nevertheless, systematic evaluation of these resources remains inadequate, limiting progress in germplasm innovation and utilization. In this study, we analyzed 16 fruit quality traits across 142 pomegranate accessions. Most traits showed wide phenotypic variation, with coefficients of variation (CVs) ranging from 2.10% to 108.83%. Notably, titratable acidity (TA) and anthocyanin content showed high variability (coefficient of variation, CV > 78%), while fruit shape index and total soluble solids (TSS) showed relatively low variability (CV < 10%). Cluster analysis delineated three distinct phenotypic groups. The first group comprised accessions characterized by large fruit size, thick peel, high acidity, and soft seeds. The second group exhibited high seed hardness, low acidity, and elevated sugar-acid and TSS–acid ratios. The third group displayed reduced levels of bioactive compounds such as tannins, phenols, and anthocyanins, combined with high seed hardness. Correlation analysis followed by principal component analysis (PCA) extracted six principal components, and based on comprehensive scoring, SXXA23, AHHB13, SD41, SXXA27, AHHB40, HS1, AHHB8, HY22, HN4, and AH27 were identified as priority accessions for further evaluation within this repository panel.

Keywords: *Punica granatum* L.; Phenotypic evaluation; Principal component analysis; Cluster analysis; breeding selection



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1. Introduction

The pomegranate (*Punica granatum* L.) is a perennial fruit tree belonging to the genus *Punica* in the family Lythraceae [1]. Its excellent edible qualities, combined with notable nutritional and medicinal values, have led to its global consumption [2,3]. It originated in Central Asia and is traditionally believed to have been introduced by Zhang Qian's missions to the Western Regions during the Western Han Dynasty (c. 119 BC) [4,5], with the earliest textual evidence for the fruit appearing in Li You's "Rhapsody on the Deyang Hall" (ca. 1st–2nd century CE) [6]. In China, pomegranate has been cultivated for over 2000 years, during which extensive ecotypes and local cultivars have developed through long-term cultivation practices [7]. Pomegranate breeding in China began in the early 1980s [8]. Notably, the introduction of the 'Tunisian Soft-Seed' pomegranate in 1986 ended China's lack of soft-seeded germplasm [5]. China is now one of

the world's leading pomegranate producers, with a cultivation area of approximately 120,000 hectares and an annual output exceeding 1.2 million tons [5,7,8]. The major production regions include Sichuan, Yunnan, Shaanxi, Henan, Shandong, Anhui, and Xinjiang [7]. The 'Tunisian Soft-Seed' cultivar currently dominates the market, alongside other elite local cultivars such as 'Taishan Hong', 'Yushiliu', and 'Tianlvzi' [7,9].

The phenotypic variation of pomegranate accessions, including most Chinese cultivars, has been evaluated, revealing high polymorphism, with 218 accessions classified into three distinct groups [10]. A comprehensive study involving 30 samples from 11 Tunisian cultivars utilized principal component analysis (PCA) and UPGMA clustering methods, revealing that key distinguishing characteristics included fruit size, peel coloration, and juice pH levels [11]. A study of 78 Turkish accessions using microsatellite markers demonstrated significant genetic differentiation by origin [12], supporting the value of geographically diverse collections for understanding germplasm structure, although the present panel represents the current holdings of a regional repository rather than a nationwide survey.

Building on germplasm resource surveys and analyses, researchers have systematically characterized pomegranate accessions from different regions, focusing on fruit quality and bioactive compounds [13], morphological and nutraceutical characteristics [14], and yield and salt tolerance [15,16], as well as other agronomic traits, including storability, cold resistance, commercial appearance, fruit weight, chemical properties, and seed hardness. Genetic analysis using six SSR primers identified 41 alleles, with an average of 4.6 alleles per locus and a mean probability of identity (PI) value of 0.366, demonstrating significant genetic polymorphism within the examined pomegranate germplasm [12]. A comprehensive two-year evaluation was conducted on 25 morphological and fruit-related traits across 221 pomegranate genotypes [17]. Through the application of PowerCore software's maximization strategy, 12 representative accessions were selected to establish a novel core collection. This study marked the first successful development of a core germplasm repository for Iranian pomegranates based exclusively on phenotypic characterization data.

Various comprehensive evaluation methods are employed in horticultural plant assessment, including grey correlation analysis [18], membership function method [19], factor analysis method [20], and PCA [21]. While factor analysis, grey correlation analysis, and membership function analysis each have distinct advantages, these methods require manual weight assignment to traits or the artificial establishment of ideal values, introducing subjectivity and limitations. In contrast, PCA transforms multiple observed variables into a few independent principal components without requiring subjective weight allocation or predefined ideal values, thereby simplifying data structure. Furthermore, PCA employs weighted summation to calculate composite scores, ensuring complete and objective consideration of all data while maintaining a high level of analytical objectivity [22]. Additionally, cluster analysis serves as another important statistical method for genotype screening. For example, Iranian researchers selected 18 pomegranate accessions with soft seeds, low acidity, and high soluble sugar content (SSC) from 100 pomegranate accessions through PCA and cluster analysis [23]. Similarly, Indian researchers also divided 40 pomegranate accessions into eight clusters by cluster analysis [24]. In Shandong Province, China, PCA and cluster analysis were employed to evaluate 45 pomegranate cultivars, leading to the identification of 10 promising accessions suitable for high-quality breeding programs [9].

Although regional evaluations of pomegranate fruit quality have been reported in China, comprehensive assessment of a large repository-based germplasm collection based on multiple sensory and physicochemical traits remains limited. To address this gap, the present study evaluated 142 pomegranate accessions from the germplasm repository at the Anhui Academy of Agricultural Sciences using 16 fruit quality traits, including morphological, flavor, and biochemical characteristics. The specific objectives of this study were to (1) characterize

phenotypic variation in fruit quality traits among the 142 accessions; (2) determine inter-trait relationships and classify accessions into phenotypic groups with distinct quality profiles; and (3) identify the principal components of quality variation and select elite accessions for breeding and commercial utilization through comprehensive evaluation. We hypothesized that substantial phenotypic variation exists among the evaluated accessions for the 16 fruit quality traits; physical, flavor, and biochemical traits are significantly correlated, enabling quality evaluation and indirect selection in breeding programs; and multivariate analysis can classify accessions into distinct quality types and objectively identify elite germplasm for further utilization. The results of this study provide a scientific reference for the evaluation, conservation, and utilization of pomegranate germplasm resources in China.

2. Materials and Methods

2.1. Plant Materials

The 142 pomegranate accessions used in this study were collected from the Pomegranate Germplasm Resource Bank of Anhui Academy of Agricultural Sciences (31°51′9.05″ N, 117°06′34.33″ E), located in Gangji Town, Changfeng County, Hefei City, Anhui Province, China. These accessions were collected from local landraces, farmer-selected ecotypes, and commercially used cultivars in China, with detailed information for each sample provided in Supplementary Table S1. These accessions, originating from Anhui (86 accessions), Shandong (29), Henan (13), Shaanxi (13), and the Xinjiang Autonomous Region (1) (Figure 1), were introduced into the repository over several years through continuous field collection from major pomegranate-growing areas in China. The purpose of this effort was germplasm conservation, identification, and utilization. The soil type of the experimental orchard was sandy loam. The trees were 10 years old, grown under uniform management, and planted at a spacing of 4.0 m × 2.5 m. During the fruit maturation period, three healthy and well-growing trees were selected for each accession, and 10 mature, disease-free fruits were harvested from each tree. This study reports fruit-quality phenotyping conducted in a single growing season (2023) under common-garden conditions.

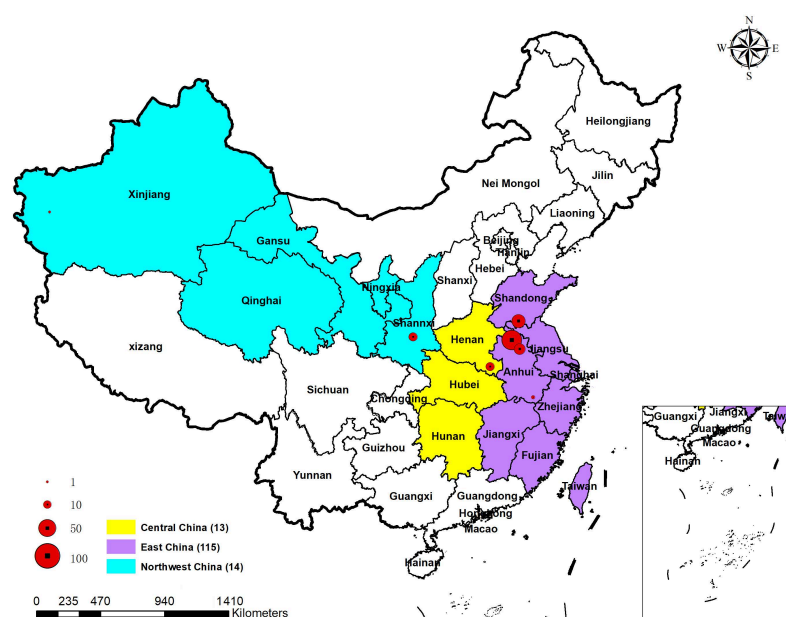


Figure 1. Distribution of 142 collected domestic accessions of pomegranates from different regions in China; 115 accessions were collected from East China, 13 from Central China, and 14 from Northwest China.

2.2. Fruit Quality Measurement

2.2.1. Morphological Characteristics

The fruit weight of mature fruits was measured by an electronic balance (Yongkang Molin Trading Co., Ltd., Yongkang, China). Fruit length, diameter, and peel thickness were measured using a digital vernier caliper (0–200 mm, MNT, Munich, Germany) [25]. Fruit shape index was calculated as fruit length divided by fruit diameter and classified as flat-round (index ≤ 0.7), near-round ($0.7 < \text{index} < 1.0$ or > 1.0), or round (index ≈ 1) [26].

The 100-seed weight was measured by manually extracting the seeds, randomly selecting 100 seeds for weighing using an electronic balance (0–210 g, $d = 0.001$ g, AUY220, Shimadzu, Kyoto, Japan), then hand-squeezing those 100 seeds to obtain the kernels and weighing all the obtained kernels using the same balance [23]. Juice yield was calculated per fruit as $(100\text{-seed weight} - 100\text{-kernel weight}) / 100\text{-seed weight} \times 100\%$. Seed hardness was measured using a texture analyzer (TA.XT PLUS, Stable Micro Systems, Godalming, Surrey, UK) equipped with an HDP/VB probe, and the average hardness of 30 individual seeds was calculated [27] and classified into four categories: very soft (< 2.20 kg/cm²), soft ($2.20\text{--}4.5$ kg/cm²), semi-soft ($4.5\text{--}7.5$ kg/cm²), and hard (> 7.5 kg/cm²) [26]. Each accession had three replicates. A summary of all measurement methods for morphological and internal quality traits is provided in Supplementary Table S2.

2.2.2. Internal Quality

Juice was extracted from fresh seeds. Total soluble solids (TSS) was measured employing a digital refractometer (PAL-1, ATAGO, Tokyo, Japan). SSC was analyzed by anthrone colorimetry [28], and the absorbance was measured at 620 nm using a UV spectrophotometer (T6 New Century, Puxi Tongyong Apparatus Ltd., Beijing, China). Titratable acidity was determined by acid–base titration [29]. Phytochemical content, including total phenolics, tannins, vitamin C, and anthocyanins, was measured as follows: Total phenolics were determined using the Folin–Ciocalteu method [30], and the absorbance was measured at 765 nm using the same spectrophotometer against a gallic acid standard curve. Tannins were measured using the Folin–Denis method [31], and the absorbance was measured at 760 nm using the same spectrophotometer. Vitamin C was quantified using the molybdenum blue method [32], and the absorbance was measured at 723 nm using the same spectrophotometer. The total anthocyanin content was determined by mixing the juice with methanol containing 1% HCl, and measuring absorbance at 530, 620 and 650 nm using the same spectrophotometer. Anthocyanin content was calculated using the formula $OD = (A_{530} - A_{620}) - 0.1(A_{650} - A_{620})$ and expressed as nmol per gram of juice [27]. Sugar–acid and TSS–acid ratios were calculated based on initial measurements. All analyses were performed in triplicate with appropriate controls.

2.3. Statistical and Analytical Methods

Numerical data analysis, correlation analysis, PCA, and normality tests for all sample data were executed via SPSS 21.0 Statistics (IBM, Chicago, IL, USA). Normality was tested using the Shapiro–Wilk test (Supplementary Table S3). Pairwise correlations among traits were analyzed using Pearson’s correlation for normally distributed traits (100-kernel weight, juice yield and seed hardness) and Spearman’s rank correlation for all other trait pairs.

For cluster analysis, accession-level mean values of the 16 fruit-quality traits were standardized to zero mean and unit variance (z-score transformation). Pairwise Euclidean distances among accessions were calculated from the standardized data, and a neighbor-joining (NJ) tree was constructed from the distance matrix. The resulting tree was visualized and annotated using iTOL (<https://itol.embl.de/>, accessed on 22 July 2025). Accessions were assigned to three phenotypic groups according to the major partitions of the NJ

dendrogram and the biological interpretability of group-specific trait profiles. Correlation and PCA plots were created using the online platform (<https://www.chiplot.online/>, accessed on 5 July 2025). Principal component analysis (PCA) was performed on the 16 quality traits. Principal components with eigenvalues >1 were retained. Factor scores for each principal component were calculated for all 142 accessions. A comprehensive evaluation model was established based on the principal component scores and their respective variance contribution rates:

$$F = \sum_{k=1}^6 F_k X_k$$

where F_k represents the score of the k -th principal component, and X_k denotes its contribution rate. Accessions were then ranked based on their comprehensive scores.

Cluster analysis and PCA were both applied to the standardized quality data, but they addressed different questions: cluster analysis was used to define quality-based accession groups, whereas PCA was used to reduce trait dimensionality and calculate composite scores for accession ranking. PCA was not used as an independent clustering method.

3. Results

3.1. Physical Indexes of Pomegranate Fruit

Among the 142 studied accessions, fruit weight exhibited considerable variation (Table 1). The heaviest fruit was recorded in SD43, while HY3 displayed the lowest weight. Notably, 64.79% of the samples ($n = 92$) fell within the 200–300 g range (Figure 2).

The 100-seed weight varied considerably among accessions (Table 1), with HY21 and AHHB29 having the highest and lowest values, respectively. The majority of accessions (66.90%) had 100-seed weights between 35 and 50 g. Similarly, the 100-kernel weight showed moderate variation, with SD35 and HY2 representing the extremes. Juice yield showed minimal variation among accessions. Peel thickness also showed considerable variation, with SD41 and AH69 showing the thickest and thinnest peels, respectively. Approximately 61.27% of accessions had peel thicknesses between 4.00 and 5.50 mm.

Seed hardness showed moderate variation among accessions, with AHHB58 and SXXA26 representing the hardest and softest seeds, respectively. The majority (87.32%; $n = 124$) were classified as semi-soft, while only 18 samples (12.68%) fell within the soft-seed category. For fruit shape index, most samples clustered between 0.85 and 1.00 (Figure 2), indicating a predominance of near-round or round fruits.

Table 1. Coefficient of variation of pomegranate fruit quality indicators.

Index	Abbreviation	Sample Number	Minimum	Maximum	Average Value	Standard Deviation	Variable Coefficient/%
Fruit weight (g)	FW	142	145.92	483.68	248.76	62.27	25.03
Peel thickness (mm)	PT	142	2.10	8.46	4.45	0.93	20.91
Fruit shape index	FSI	142	0.75	1.20	0.91	0.06	6.31
100-seed weight (g)	SW	142	23.00	67.40	43.84	8.80	20.08
100-kernel weight (g)	KW	142	3.38	6.37	4.70	0.58	12.39
Juice yield (%)	JY	142	83.39	92.88	88.93	1.87	2.10
Seed hardness (Kg/cm ²)	SH	142	3.08	7.48	5.23	0.74	14.13
Total soluble solids (%)	TSS	142	11.70	18.70	14.68	1.10	7.46
Soluble sugar content (%)	SSC	142	8.68	16.35	13.01	1.57	12.09
Titrateable acidity (%)	TA	142	0.25	5.68	0.88	0.95	108.83
Sugar–acid ratio	SAR	142	1.96	62.07	21.74	8.62	39.66
TSS–acid ratio	RTT	142	2.38	68.80	24.36	9.28	38.08
Anthocyanin (nmol/g)	ANT	142	1.36	124.53	34.81	27.42	78.75
Tannin (mg/mL)	TAN	142	2.88	9.11	4.47	0.93	20.72
Total phenol (mg/mL)	TP	142	0.82	3.29	1.79	0.40	22.45
Vitamin C (mg/mL)	Vc	142	0.33	0.85	0.52	0.08	16.09

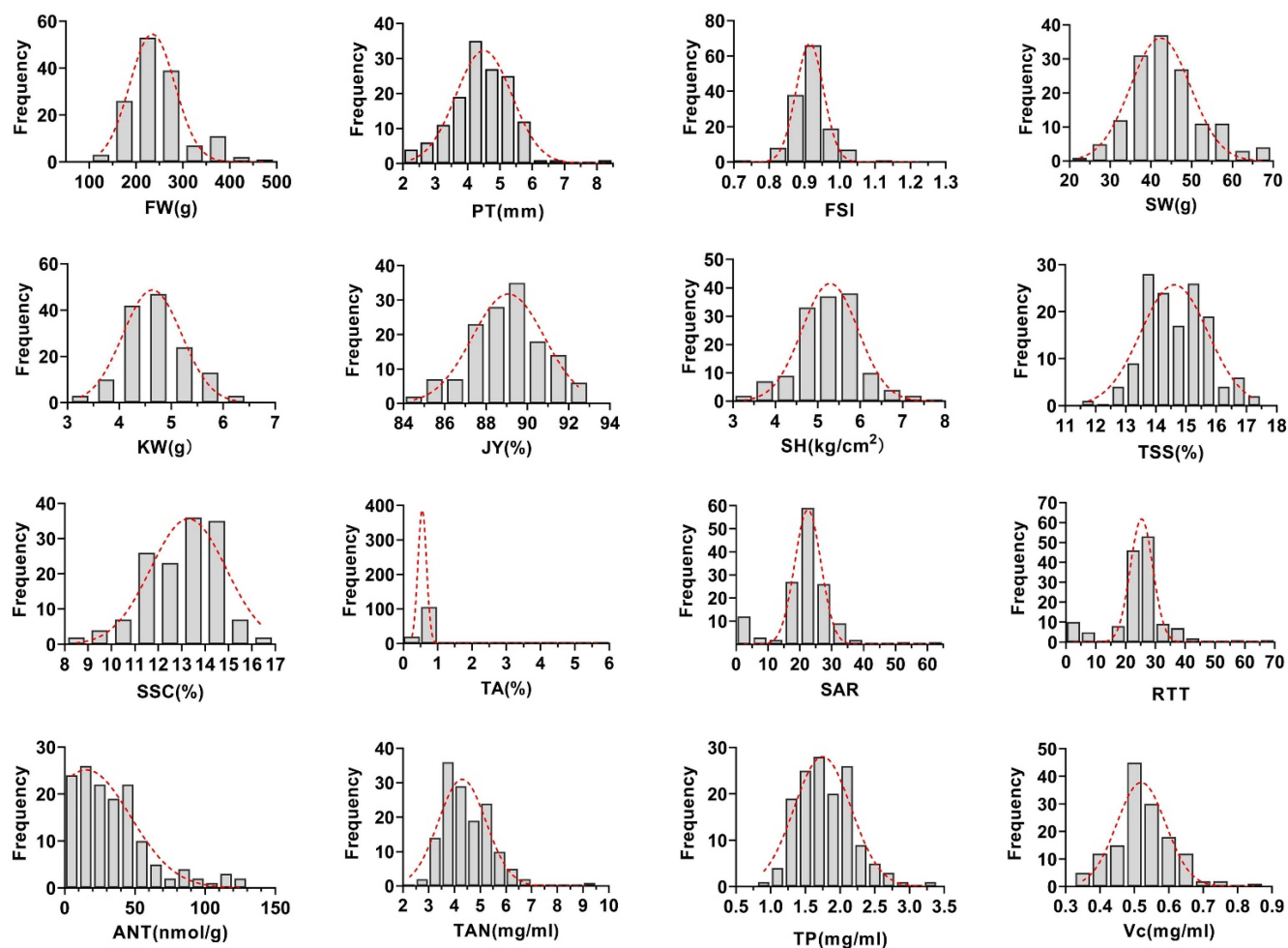


Figure 2. Frequency distribution of pomegranate fruit quality indicators. The red dotted line represents the Gaussian fitting curve. Fruit weight (FW), Peel thickness (PT), Fruit shape index (FSI), 100-seed weight (SW), 100-kernel weight (KW), Juice yield (JY), Seed hardness (SH), Total soluble solids (TSS), Soluble sugar content (SSC), Titratable acidity (TA), Sugar–acid ratio (SAR), TSS–acid ratio (RTT), Anthocyanin (ANT), Tannin (TAN), Total phenol (TP), Vitamin C (Vc).

3.2. Flavor and Biochemical Attributes of Pomegranate Fruit

TSS showed relatively low variation among accessions, with the majority of accessions (80.28%) falling between 13.5% and 16.0%. SSC exhibited moderate variation, with SD31 and SXXA23 having the highest TSS and SSC, respectively. TA had extreme variability, with 74.65% of samples ranging between 0.5% and 1.0%. SAR and RTT showed high variation among accessions, with AHHB24 and SD36 being the most acidic, while SD41 was the sweetest.

Among biochemical traits, anthocyanin content varied most widely, followed by total phenolics and tannins, whereas vitamin C was comparatively stable.

3.3. Correlation Analysis

Significant correlations were observed among quality traits (Figure 3). For morphological characteristics, fruit weight showed a positive correlation with peel thickness but a negative correlation with fruit shape index. The 100-seed weight was strongly positively correlated with both 100-kernel weight and juice yield.

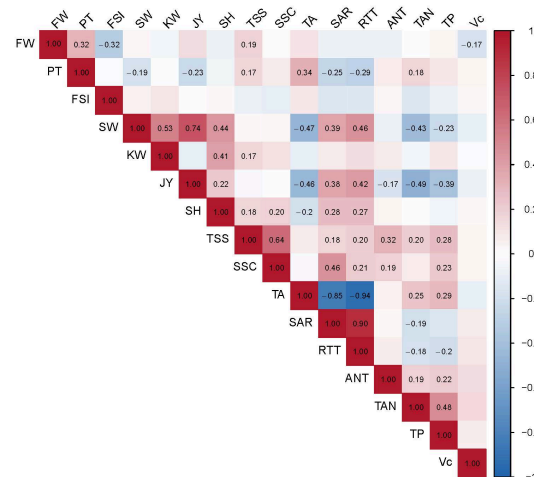


Figure 3. Correlation heatmap of 16 phenotypic traits across 142 accessions. Cell color indicates correlation strength and direction (blue, negative; red, positive; white, weak). Correlation coefficients are displayed only when $p \leq 0.05$. Pearson correlation was used for pairwise comparisons among KW, JY, and SH, as these traits were normally distributed; Spearman correlation was used for all other pairs.

For internal quality traits, TSS was strongly positively correlated with SSC. SSC showed positive correlations with SAR and RTT, but a negative correlation with TA. TA was negatively correlated with SAR and RTT, and positively correlated with tannins. SAR and RTT showed a strong positive correlation. Among phytochemicals, tannins exhibited a strong positive correlation with total phenols. Anthocyanin was positively correlated with tannin and total phenol.

3.4. Cluster Analysis of Pomegranate Accessions Based on Quality Traits

The cluster analysis of 16 quality traits across 142 pomegranate accessions resulted in three distinct groups (Figure 4), with Group 3 being the largest and Groups 1 and 2 representing smaller subsets of the collection.

Group 1 exhibited the largest fruit size (287.72 g) and thickest peel (5.09 mm), but the lowest juice yield (87.86%) and seed hardness (4.94 kg/cm²). Biochemically, this group showed the highest TA (1.96%) and phenolic content (tannins: 5.01 mg/mL; total phenols: 1.95 mg/mL), along with elevated anthocyanins (41.93 nmol/g). However, it had the lowest SAR (13.60) and RTT (15.01) and vitamin C concentration (0.47 mg/mL). These findings suggest Group 1 accessions are particularly suitable for processing (especially phytochemical extraction and juice production) but less ideal for fresh consumption due to their high acidity.

Group 2 was characterized by an exceptionally favorable sugar–acid balance (SAR: 27.30; RTT: 30.91) and the lowest TA (0.51%). While this group exhibited the highest seed hardness (5.61 kg/cm²), which is generally less desirable for fresh consumption, its moderate fruit size (243.64 g) and outstanding sweetness position these accessions as strong candidates for the fresh fruit market, particularly appealing to consumers who prioritize flavor over seed softness.

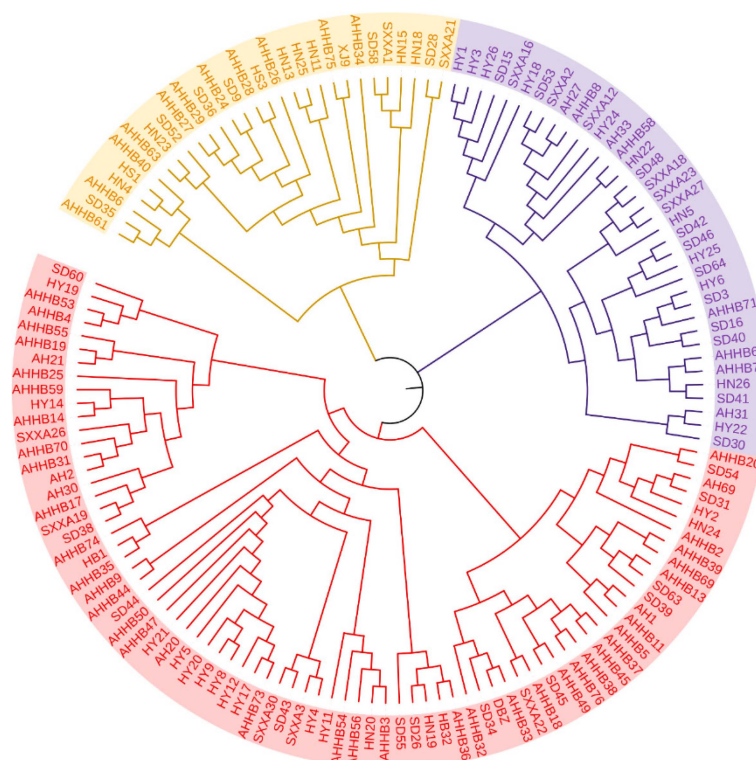


Figure 4. Cluster analysis of 142 pomegranate accessions. Yellow represents Group 1, comprising 29 accessions; red represents Group 2, comprising 36 accessions; and purple represents Group 3, comprising 77 accessions.

Group 3 displayed intermediate values for most parameters: fruit weight (236.49 g), peel thickness (4.21 mm), and TA (0.64%). Notably, it contained the lowest concentrations of bioactive compounds (tannins: 4.01 mg/mL; total phenols: 1.61 mg/mL; anthocyanins: 27.89 nmol/g), though with slightly higher vitamin C (0.53 mg/mL) than Group 1. This cluster likely represents commercial accessions bred for yield stability rather than nutritional superiority.

3.5. PCA and Comprehensive Evaluation of Pomegranate Quality Traits

The first six principal components together explained 72.78% of the total variance (Table 2). The first principal component (PC1), accounting for 24.26% of the variance, was strongly correlated with taste-related parameters, particularly the SAR and the RTT. PC2 primarily represented sweetness components, with TSS contributing most significantly. PC3 was predominantly influenced by seed physical characteristics, particularly kernel weight. Fruit morphological traits, especially the fruit shape index (FSI), were the major contributors to PC4. PC5 was associated with antioxidant properties, with anthocyanin content exhibiting the highest loading. Finally, PC6 (6.28% of variance) was strongly linked to peel thickness. To assess the relationship between PCA and cluster analysis, accessions in Figure 5 are colored according to the three groups defined in Section 3.4. Although Groups 2 and 3 overlapped substantially in the PC1–PC2 plane (39.97% of total variance), Group 1 showed partial separation along PC1, which is consistent with its distinct acidity and taste profile. Based on the composite scores (Supplementary Table S4), the top 10 accessions identified were: SXXA23, AHHB13, SD41, SXXA27, AHHB40, HS1, AHHB8, HY22, HN4, and AH27.

Table 2. The matrix of each principal component in fruit quality indicators.

Index	Principal Component					
	PC1	PC2	PC3	PC4	PC5	PC6
Fruit weight	−0.033	0.135	0.342	−0.711	−0.050	0.271
Peel thickness	−0.170	0.396	0.099	−0.313	0.169	0.714
Fruit shape index	−0.027	−0.110	0.010	0.493	0.731	0.215
100-seed weight	0.706	−0.270	0.534	0.080	−0.010	−0.041
100-kernel weight	0.275	0.187	0.596	0.503	−0.153	0.172
Juice yield	0.665	−0.399	0.185	−0.306	0.132	−0.120
Seed hardness	0.471	0.151	0.401	0.334	−0.194	0.195
Total Soluble Solids	0.117	0.765	0.221	−0.200	0.233	−0.222
Soluble sugar content	0.342	0.646	0.142	−0.124	0.058	−0.221
Titrate acidity	−0.802	−0.113	0.289	−0.085	0.091	−0.107
Sugar–acid ratio	0.844	0.266	−0.317	−0.068	−0.060	−0.008
TSS–acid ratio	0.842	0.226	−0.343	−0.047	−0.043	0.021
Anthocyanin	0.024	0.505	−0.039	0.019	0.464	−0.239
Tannin	−0.522	0.506	−0.038	0.115	−0.276	−0.068
Total phenol	−0.354	0.562	0.150	0.260	−0.206	−0.096
Vitamin C	0.137	0.272	−0.549	0.247	−0.114	0.335
Eigenvalue	3.881	2.514	1.658	1.523	1.063	1.005
Variance contribution rate (%)	24.258	15.711	10.364	9.519	6.644	6.282
Cumulative variance contribution rate (%)	24.258	39.969	50.333	59.852	66.496	72.778

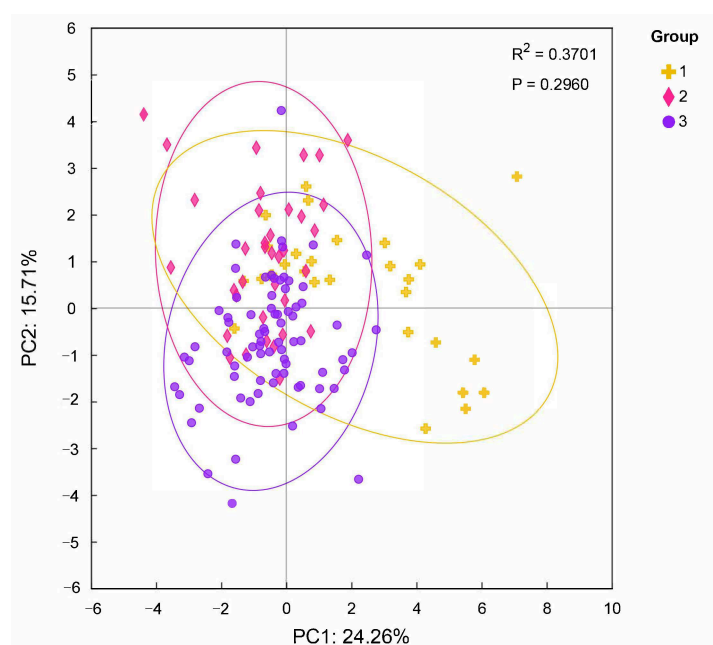


Figure 5. Two-dimensional principal component analysis (PCA) plot of the 16 index and 142 pomegranate accessions. PC1 and PC2 explained 24.26% and 15.71% of the total variance, respectively. Symbols are colored according to the three phenotypic groups defined by cluster analysis (Figure 4): Group 1 (yellow plus), Group 2 (red diamond), and Group 3 (purple circle). Ellipses represent 95% confidence intervals. PCA was used for ordination and comprehensive evaluation, not as an independent clustering method.

4. Discussion

Under common-garden conditions with conventional cultivation and management, the 142 accessions showed wide phenotypic variation in several key quality traits, particularly titratable acidity and anthocyanin content. Compared with published ranges from Iran [25], Turkey [33], and Spain [14], the present repository panel encompassed comparable fruit-weight and TSS ranges, whereas acidity and anthocyanin spanned particularly broad values. Although many previous pomegranate quality evaluations in China were conducted on smaller regional panels [9,23], phenotyping 142 accessions with a multi-trait framework enabled examination of how quality variation is organized within this repository rather than through accession-by-accession description alone. However, this panel should be interpreted as a repository-based phenotypic dataset rather than as a

geographically balanced representation of Chinese pomegranate diversity, and its implications for breeding should be considered preliminary until supported by genetic and multi-environment evidence.

4.1. Phenotypic Variation in Fruit Quality Traits

The observed variation in fruit weight, 100-seed weight, peel thickness and biochemical composition indicates that the evaluated collection retains considerable phenotypic differentiation in commercially relevant characters. Wide ranges of titratable acidity and anthocyanin content, in particular, suggest that the repository contains accessions with contrasting sugar–acid balance and pigmentation profiles. This pattern is consistent with previous reports of large cultivar-to-cultivar differences in pomegranate anthocyanin accumulation [34–36] and with the known importance of acidity and pigment traits in determining fresh-market acceptability and processing suitability [14,23]. At the same time, relatively low variation in juice yield and fruit shape index indicates that some quality attributes are more uniform in this collection than others. The broad phenotypic ranges observed here confirm that this repository harbors substantial trait variation, but they do not by themselves demonstrate the genetic basis of that variation. From a germplasm-management perspective, the broad phenotypic ranges observed here are useful for accession classification, core collection design, and prioritization of materials for further testing. They should not, however, be equated automatically with broad genetic diversity or with directly selectable breeding gain, because phenotypic differentiation may reflect genetic, environmental, and management effects, as well as the historical composition of the repository.

4.2. Phenotypic Associations Among Quality Traits

Fruit quality traits in pomegranate do not develop independently; coordinated phenotypic variation among physical and biochemical characters is therefore expected during germplasm evaluation [23,27]. The associations observed among seed weight, juice yield, sweetness indicators, and acidity-related traits are broadly consistent with earlier reports that taste and seed physical traits are linked at the phenotypic level in this species [9,14,23]. For example, the strong association between 100-seed weight and juice yield suggests that larger seeds contribute to higher juice extraction efficiency, whereas the relationship between 100-seed weight and 100-kernel weight likely reflects seed composition rather than an independent breeding target. Likewise, the positive association between TSS and SSC supports the practical use of TSS as a field indicator of sweetness during large-scale screening [37,38].

These phenotypic associations are valuable for identifying trait combinations that may be useful in preliminary germplasm screening. Nevertheless, they should be interpreted cautiously when extrapolated to genetic improvement. Phenotypic correlations integrate genetic, environmental, and residual components, and numerous studies in perennial crops have shown that phenotypic and genetic correlations may differ in magnitude and, in some cases, even in direction [39,40]. Therefore, the correlations reported here describe coordinated quality profiles within this collection at the phenotypic level, but they do not confirm that the same relationships would hold among genetic values or that indirect selection on one trait would reliably improve another in a breeding population.

4.3. Multivariate Classification and Accession Ranking

Cluster analysis separated the 142 accessions into three quality-based groups, providing a practical framework for germplasm organization and targeted utilization. The processing-oriented group aligns with previous reports that high-acidity and phytochemical-rich pomegranates are suitable for juice and functional product

development [23], whereas the fresh-market-oriented group is consistent with selections emphasizing sugar–acid balance in Iran, India, and Shandong Province [9,17,24]. The large intermediate group likely reflects commercial genotypes selected for yield stability rather than maximal nutritional quality. Importantly, these quality groups were not strictly congruent with province of origin because accessions from different provinces occurred in all three clusters. This suggests that utilization type in this collection was associated more closely with end-use quality profiles than with geographic source alone.

PCA and comprehensive scoring reduced 16 traits to six principal components that together explained 72.78% of the total variance and enabled objective comparison and ranking of accessions. The dominance of sugar–acid ratio, TSS–acid ratio, and titratable acidity on PC1 indicates that taste balance is the primary axis of quality differentiation in this collection, whereas anthocyanin content and peel thickness contributed mainly to secondary axes [9,17,23]. Cluster analysis and PCA were complementary rather than redundant: the former defined discrete utilization-oriented groups using overall multivariate similarity, whereas the latter identified the main quality axes and supported ranking of elite accessions. The partial overlap between cluster groups and PCA ordination further suggests that taste-related traits were major but not exclusive drivers of group separation.

The ten top-ranked accessions therefore represent candidate materials for follow-up evaluation, not finalized commercial or parental recommendations. Accessions such as SXXA23, SXXA27, SD41, and HY22 may warrant further testing for fresh-market quality, whereas AHHB13, HS1, and AH27 may be useful for pigment-oriented evaluation. HN4 and AHHB40, combining large fruit size with high composite scores, may be prioritized for multi-environment and agronomic validation. In all cases, their breeding value remains to be confirmed.

4.4. Cautions for Application to Genetic Improvement

Although this study provides useful phenotypic information for pomegranate germplasm evaluation, its direct application to genetic improvement requires caution. All variation, group differences, and correlations reported here are phenotypic and estimated from mature fruit evaluated in a single orchard during one growing season. Consequently, they reflect the combined effects of genotype, environment, and measurement error rather than genetic effects alone.

For breeding purposes, the most informative parameters are genetic variation, genetic correlations among traits, and the degree of genetic control (e.g., heritability or breeding value estimation) of key quality characters [39,40]. Without such information, it is not possible to determine whether desirable trait combinations can be improved simultaneously through selection, or whether gains in one trait would be offset by unfavorable responses in another. Recent genomic and genetic studies in pomegranate have begun to uncover the genetic architecture of fruit quality and pigmentation [10,36,38], but the present dataset does not estimate genetic parameters and therefore cannot conclusively translate phenotypic patterns into breeding strategy.

Accordingly, the phenotypic groups identified here should be viewed as hypothesis-generating classifications for germplasm management, and the observed trait associations should be treated as candidate relationships requiring confirmation through progeny testing, parent–offspring analysis, multi-location trials, or molecular QTL/genomic analyses. Likewise, the top-ranked accessions should be considered priority candidates for genetic and agronomic validation rather than as proven breeding parents. This cautious interpretation does not diminish the value of the present study; rather, it defines its appropriate scope as a large-scale phenotypic baseline for repository screening, accession prioritization, and the design of subsequent genetic experiments.

4.5. Limitations and Future Perspectives

This study was conducted at a single location during one season under common-garden conditions; therefore, genotype-by-environment interaction, year-to-year stability, and yield-related performance remain unknown. In addition, the panel represents the current holdings of a regional repository rather than a nationally representative sample of Chinese pomegranate germplasm. Future research should therefore combine the present phenotypic framework with multi-environment evaluation, yield and adaptability assessment, and genetic analyses of quality traits. Such integrated studies will be necessary to determine whether the phenotypic variation and trait associations identified here can be effectively exploited in pomegranate breeding and cultivar development in China.

5. Conclusions

Evaluation of 16 fruit-quality traits in 142 pomegranate accessions under common-garden conditions revealed substantial phenotypic variation in this repository-based collection. Titratable acidity and anthocyanin content were the most discriminatory traits, whereas juice yield and fruit shape index were comparatively stable, indicating that the collection retains marked contrasts in taste balance and pigmentation, while some commercially relevant traits are more uniform.

Significant phenotypic associations were detected among seed-related, sweetness-related, and acidity-related traits, supporting the utility of multivariate quality profiling for repository-scale screening. However, because these associations are phenotypic rather than genetic, their implications for breeding should be interpreted with caution and verified through further genetic studies.

Cluster analysis and PCA provided complementary perspectives on the collection: cluster analysis resolved three quality-based groups with distinct utilization-oriented profiles, whereas PCA identified the main axes of quality variation and enabled composite ranking of accessions. Together, these analyses offer a practical phenotypic framework for germplasm classification, accession prioritization, and candidate selection within this repository.

Overall, this study establishes a repository-scale phenotypic baseline for quality-oriented evaluation of Chinese pomegranate germplasm. The ten top-ranked accessions and the three phenotypic groups identified here should be regarded as priority candidates for further genetic, agronomic, and multi-environment validation rather than as finalized breeding recommendations. Such follow-up studies are essential to determine whether the observed phenotypic patterns can be effectively translated into pomegranate improvement and cultivar development.

Supplementary Materials: The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/horticulturae12070827/s1>. Table S1: Origin on pomegranate accessions; Table S2: Summary of assessed fruit quality traits and measurement methods; Table S3: Shapiro–Wilk normality test results for 16 fruit quality indicators; Table S4: Principal component score and comprehensive score pomegranate accessions.

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Conflicts of Interest: The authors declare that they have no conflicts of interest.

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