

Article

Comprehensive Evaluation of Phenotypic Diversity and Nutritional Properties of Mango Leaves

Jing Zhang , Changli Mao , Ni Liu, Ziyang Liu, Xiaoran Qian , Xiaoping Zhu , Jin Liu *  and Yingfeng Niu * 

Molecular Biology Research Center, Yunnan Institute of Tropical Crops, Jinghong 666100, China; zhashoveljing@163.com (J.Z.); maokangwan@163.com (C.M.); liuni3710@163.com (N.L.); liuziyan90@163.com (Z.L.); mosaiclaw@163.com (X.Q.); zhu_xiaoping123@163.com (X.Z.)

* Correspondence: liujin06@126.com (J.L.); niuyingfeng@163.com (Y.N.)

Highlights

What are the main findings?

- The mature leaf stage is confirmed as the optimal period for Guifei-mango-leaf deep processing with superior nutritional traits.
- Elite mango germplasms for high-value leaf utilization including Sri Lanka No.811 are screened via comprehensive evaluation.

What are the implications of the main findings?

- It fills the research gap in identifying the optimal sampling period for Guifei mango leaves and unifies the leaf collection time for all germplasms.
- It establishes a standardized evaluation system for mango-leaf resources integrating leaf phenotypic diversity and nutritional characteristics.
- It supports targeted germplasm screening and breeding for high-value mango-leaf utilization.

Abstract

Mango is a globally vital tropical commercial fruit crop boasting a sizable industry and remarkable economic benefits. Nevertheless, mango leaves, abundant in carbohydrates, polyphenols and other nutrients, remain underdeveloped in comprehensive resource exploitation. First, comparative analysis of leaf phenotypic traits and nutritional quality at different developmental stages of the Guifei cultivar showed that mature leaves possessed significantly higher contents of soluble sugar, total polyphenols, and total flavonoids, as well as better comprehensive traits, indicating that the mature leaf stage is optimal for deep processing. Subsequent assays of 70 mango germplasms detected obvious differences in leaf phenotypic characteristics and nutritional quality among materials, with the coefficient of variation values ranging from 2.35% to 50.38%. Correlation analysis revealed significant intra-group correlations for leaf phenotypic indicators and antioxidant indicators, whereas the five basic nutritional indices were mutually independent. Cluster analysis classified the tested germplasms into four distinct groups with clear trait divergence and unique functional features. Five principal components were extracted from 11 leaf quantitative indices to construct a comprehensive evaluation system, which pinpointed elite accessions including Sri Lanka No.811, Nam Dok Mai, and Shuoshuai Mango, with Sri Lanka No.811 exhibiting the highest total polyphenol content. This study determines the optimal harvest period and elite germplasms for high-value utilization of mango leaves, facilitating special-purpose germplasm screening and targeted breeding.



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Keywords: mango; leaf; phenotypic traits; nutritional quality; correlation analysis; principal component analysis; diversity

1. Introduction

Mango (*Mangifera indica* L.), also known as the ‘King of Fruits’, is an evergreen tree in the genus *Mangifera* of the family Anacardiaceae [1]. As the world’s second most important tropical fruit crop, mango is extensively cultivated in tropical and subtropical zones across more than 103 countries on all continents except Antarctica, with a long cultivation history and considerable economic significance [2]. With its unique flavor and high nutritional value, the fruit contains ample vitamin C, carotenoids and a range of minerals, making it highly favored by consumers [3]. Ranked second globally in mango production, China comes next only to India, with a planting area of around 988,000 acres and an annual yield of 3 million tons [4]. This vast industry supports the exploitation of germplasm resources and high-value development of mango by-products.

Long-term natural evolution and artificial domestication have contributed to over a thousand preserved mango germplasms globally with rich genetic variations. However, substantial differences in genetic background and phylogenetic relationships exist among germplasms from different producing regions, making precise identification and in-depth exploitation of mango germplasms persistent research hotspots [5]. In plant germplasm evaluation, phenotypic trait-based genetic diversity analysis is a key strategy to explore elite germplasms and superior genetic resources [5,6]. For instance, investigations on 70 phenotypic and biochemical leaf and fruit traits from 58 mango germplasm accessions uncovered abundant genetic diversity and obvious fruit quality variations, screened superior genotypes such as Kancha Mitha, classified all tested accessions into five distinct clusters, and provided solid reference data for mango breeding and germplasm resource utilization [6]. Current studies have also systematically investigated commercially important mango traits, including aroma and flavor, stress tolerance, antioxidant capacity, and forage nutritional components [7–12], laying a solid germplasm and theoretical foundation for the diversified exploitation and utilization of mango resources.

As a vital organ for nutrient biosynthesis and assimilation, mango leaves constitute the fundamental basis for vegetative and reproductive growth [13]. With diverse morphology and firm texture, they are a highly valuable resource with great utilization potential. They are abundant in flavonoids, polyphenols, terpenoids and other bioactive compounds, as well as nutrients such as proteins and crude fiber, which confer antioxidant, anti-inflammatory and antibacterial activities with broad application prospects in medicine, health products and cosmetics [14–17]. In addition, mango leaves have favorable palatability and can be processed into high-quality mango-leaf beverages, livestock feed and natural dyes, supporting ecological circular agriculture [18–20]. With rising interest in natural bioactive products, mango leaves exhibit great market potential and are poised to serve as a novel economic driver for the mango industry.

Global studies on mango-leaf traits have provided fundamental support for the selective breeding of specialized mango cultivars. Leaf morphology and texture are reliable indicators for germplasm discrimination, with abundant phenotypic diversity observed in leaf shape, color, apex and margin among different mango genotypes [21]. As a vital organ for photosynthesis and transpiration, the leaf anatomical structure closely correlates with plant stress tolerance. Previous research has evaluated the drought resistance of various mango germplasms, and superior drought-tolerant cultivars (Jinhuang and Dashehari) have been screened to support local mango breeding [9]. Furthermore, mango leaves

contain abundant polyphenols and flavonoids with bioactive properties, enabling them to be developed as functional feed additives for enhancing the stress resistance of livestock. For instance, Guifei mango leaves have been recognized as high-quality raw materials for fish feed due to their outstanding feeding performance [11].

Despite the verified application potential of mango leaves, critical research gaps remain in current studies. First, existing germplasm evaluations prioritize fruit traits, while leaf resource research is fragmented and lacks unified evaluation criteria. Second, while numerous studies have analyzed multiple indicators of mango germplasms separately, few have conducted a comprehensive integrated assessment that simultaneously combines phenotypic and nutritional traits across diverse germplasm resources. Third, uniform-stage leaf sampling is standard practice for mango germplasm evaluation. Still, the leaf developmental gradient matching this sampling time is rarely quantified based on a representative cultivar, hindering reliable interpretation of trait differences among germplasms.

To fill these research gaps, this study builds on prior findings to develop a standardized evaluation framework for mango-leaf resources. Previous research has demonstrated that leaves of Guifei mango exhibit the best comprehensive nutritional properties among five mango cultivars [11]. Using Guifei mango as the material, we characterized leaf trait dynamics across three growth stages and defined a unified representative sampling stage. All leaf samples from 70 mango germplasms were uniformly collected at this stage to eliminate growth-stage interference and ensure reliable inter-germplasm comparability. By integrating leaf morphological, physiological and nutritional indices, we systematically analyzed phenotypic variation and phenotype-nutrition correlations among mango germplasms. This study established a standardized evaluation system for mango-leaf germplasms under consistent growth conditions, screened elite germplasms, and clarified synergistic variation patterns of leaf phenotypic and nutritional traits. The findings provide theoretical and technical support for mango germplasm exploitation and high-value utilization of mango-leaf resources.

2. Materials and Methods

2.1. Plant Materials

The experimental materials consisted of 70 cultivated mango accessions originating from 11 countries, which were preserved at the Yunnan Innovation Base of Mango Germplasm Resources, Ministry of Agriculture (Xishuangbanna, Yunnan, China; 22°1'12" N, 100°47'15" E) (Table 1). From each germplasm, three healthy fruiting trees with uniform growth were selected. A total of 15 healthy leaves without obvious diseases, insect damage and mechanical injury were collected from four directions (east, south, west, and north) of the middle branches to minimize microenvironmental errors. These leaves were used for morphological characterization and component determination.

Table 1. Information on 70 mango germplasm resources.

No.	Variety	Origin	No.	Variety	Origin
1	Chok Anand	Thailand	36	Xiamao Mango	China
2	Nam Dok Mai	Thailand	37	Myanmar No.5	Myanmar
3	Siji Mi Mango	China	38	Yunmang No.4	China
4	Banana Mango	Myanmar	39	Hong Xiangya	China
5	Guire No.10	China	40	Xiao Xiangya	Thailand
6	Hubaoya	China	41	India No.905	India
7	Nan Klang Wan	Thailand	42	Guifei	China
8	Dasannian	China	43	Haden	America
9	Liandao Mango	China	44	Guangnong No.2	China

Table 1. Cont.

No.	Variety	Origin	No.	Variety	Origin
10	Jinsui	China	45	Tainong No.1	China
11	Renong No.1	China	46	Zihua Mango	China
12	Guire No.3	China	47	Sensation	America
13	Gaozhou Lvsung	Philippines	48	Keitt	America
14	Sri Lanka No.811	Sri Lanka	49	Longjin	China
15	Naiyou Xiang Mango	Vietnam	50	Kent	America
16	Yunmang No.1	China	51	Tom	America
17	Yunmang No.2	China	52	Dongzhen Hong Mango	China
18	Big Neelum	India	53	Irwin	America
19	Ai Mango	China	54	Daxiangya	China
20	Hongyun	India	55	Hongyun No.5	China
21	Yunmang No.3	China	56	Long Mango	China
22	Myanmar No.4	Myanmar	57	Neelum	India
23	Baiyu Mango	Malaysia	58	Tainong No.2	China
24	Liuzhou Lvsung	China	59	Shengchi Mango	China
25	India No.90-15	India	60	Lvsung	Philippines
26	Myanmar No.3	Myanmar	61	Dashehari	India
27	Shuoshuai Mango	Thailand	62	Dabaiyu	Thailand
28	Siam Mango	Thailand	63	Jinlong	China
29	Yuxi No.1	China	64	Myanmar Qiu Mango	Myanmar
30	Guiqi Mango	China	65	Longyan Xiang Mango	China
31	Hongyin Mango	India	66	Liuxiang Mango	Sri Lanka
32	Macheso	Myanmar	67	Anning Hong Mango	China
33	Jinhuang	China	68	Ru Mango	China
34	Taohong Mango	Cuba	69	Thai Mango	Thailand
35	Macheso Variant	Myanmar	70	Sannian Mango	China

Previous research has demonstrated that leaves of Guifei mangos exhibit the best comprehensive nutritional properties among five mango cultivars [11]. Accordingly, leaves of the Guifei mango at three representative developmental stages, namely young leaves (Y1), adult leaves (Y2) and mature leaves (Y3), were sampled to comprehensively determine the optimal leaf stage for deep processing and utilization. Following the identification of this optimal stage from Guifei mangos, leaf samples at the corresponding developmental stage were collected from all other tested accessions for comparative analysis.

2.2. Measurement of Leaf Phenotype

Leaf phenotypic measurements were performed according to the Agricultural Industry Standard of the People's Republic of China, Descriptors for Mango Germplasm Resources (NY/T 1808-2022). For each germplasm, three healthy individual trees were chosen as three biological replicates, and five intact, pest- and disease-free mature leaves without mechanical damage were randomly sampled from each tree. Following the principle of maximum morphological similarity, leaf shape (LS), leaf apex (LA), leaf base (LB), leaf margin (LM), leaf length (LL), and leaf width (LW) were systematically investigated, and the leaf shape index (LL/LW, LI) was calculated accordingly.

2.3. Determination of Leaf Nutritional and Antioxidant Properties

After phenotypic measurement, leaves from each individual tree were pooled as one biological replicate. For each germplasm, three biological replicates were prepared, with each replicate measured in three technical repeats. All indices were determined using 0.1 g of crushed leaf samples with micro-detection kits from Suzhou Grace Biotechnology Co., Ltd., (Suzhou, China) and the contents were calculated via corresponding standard curves.

The detection parameters of each index are listed below. Amino acids (AA, G0415W) were determined at 570 nm using the ninhydrin colorimetric method. Triglycerides (TG, G0190W) were quantified at 510 nm through the glycerol-3-phosphate oxidase reaction. Soluble sugars (SS, G0501W) and cellulose (CCL, G0715W) were diluted 20-fold and measured at 620 nm by anthrone colorimetry. Amylase (AM, G0507W) was diluted 10-fold and detected at 620 nm via enzymatic hydrolysis. Total flavonoids (TF, G0118W) were diluted 10-fold and assayed at 510 nm with the $\text{NaNO}_2\text{-Al}(\text{NO}_3)_3\text{-NaOH}$ colorimetric method. Total phenols (TP, G0117W) were diluted 10-fold and determined at 760 nm using the Folin–Ciocalteu method. DPPH radical scavenging activity (DPPH, G0128W) was diluted 10-fold and tested at 517 nm by colorimetric method.

2.4. Statistical Analysis

Origin 2024 (OriginLab Corporation, Northampton, MA, USA) was used for basic statistical analysis including maximum (Max), minimum (Min), mean, standard deviation (SD), coefficient of variation (CV), skewness (S) and kurtosis (K), as well as frequency distribution sorting and graph plotting. IBM SPSS v.26 (International Business Machines Corporation, Armonk, NY, USA) was applied for one-way analysis of variance (ANOVA), and significant differences were evaluated at $p < 0.05$. R v.4.1.3 (University of Auckland, Auckland, New Zealand) was used for further data analysis and visualization. Pearson correlation analysis was conducted to evaluate pairwise relationships among indices, while the mantel test was adopted to assess associations between different trait groups. All datasets were standardized by Z-score prior to hierarchical clustering based on genetic distance. Principal component analysis was performed to establish a comprehensive evaluation system, and the final comprehensive scores were calculated according to corresponding weighting coefficients.

3. Results

3.1. Mature Leaves of Guifei Cultivar Are the Preferred Material for Mango-Leaf Deep Processing

Significant differences were observed in the morphological characteristics of Guifei mango leaves at different growth stages (Figure 1A). Y1 were light yellowish-brown to pale yellow-green, Y2 were bright emerald green, and Y3 were dark green, with leaf texture gradually changing from tender to thick and tough as growth proceeded. Marked differences were also detected in the component accumulation of leaves at different growth stages (Figure 1B). Y3 showed the highest content in most indicators, including TF, TP, DPPH, SS, AM, and CCL, with significant advantages in antioxidant activity and nutrient accumulation; Y2 exhibited intermediate levels for all indicators; except for AA, Y1 had the lowest overall content. In conclusion, Y3 has the optimal comprehensive properties and is the best period for deep processing and utilization of Guifei mango leaves.

Correlation analysis was conducted on eight key indicators of Guifei mango leaves at three developmental stages (Table S1). Except for AA, all other indices displayed positive correlations. Within nutritional indicators (AA, TG, SS, AM and CCL), significant correlations were only detected between TG and AM, and between CCL and SS. In contrast, all pairwise combinations of the antioxidant indicators (TF, TP, and DPPH) showed significant positive correlations, indicating a synchronized trend between the accumulation of antioxidant substances and the enhancement of antioxidant activity. Inter-group correlation analysis revealed that SS and CCL in the nutritional group were significantly positively correlated with all antioxidant indicators. These results suggested that soluble sugar and cellulose metabolism might synergistically promote the synthesis of flavonoids and phenolics, thereby regulating leaf antioxidant capacity.

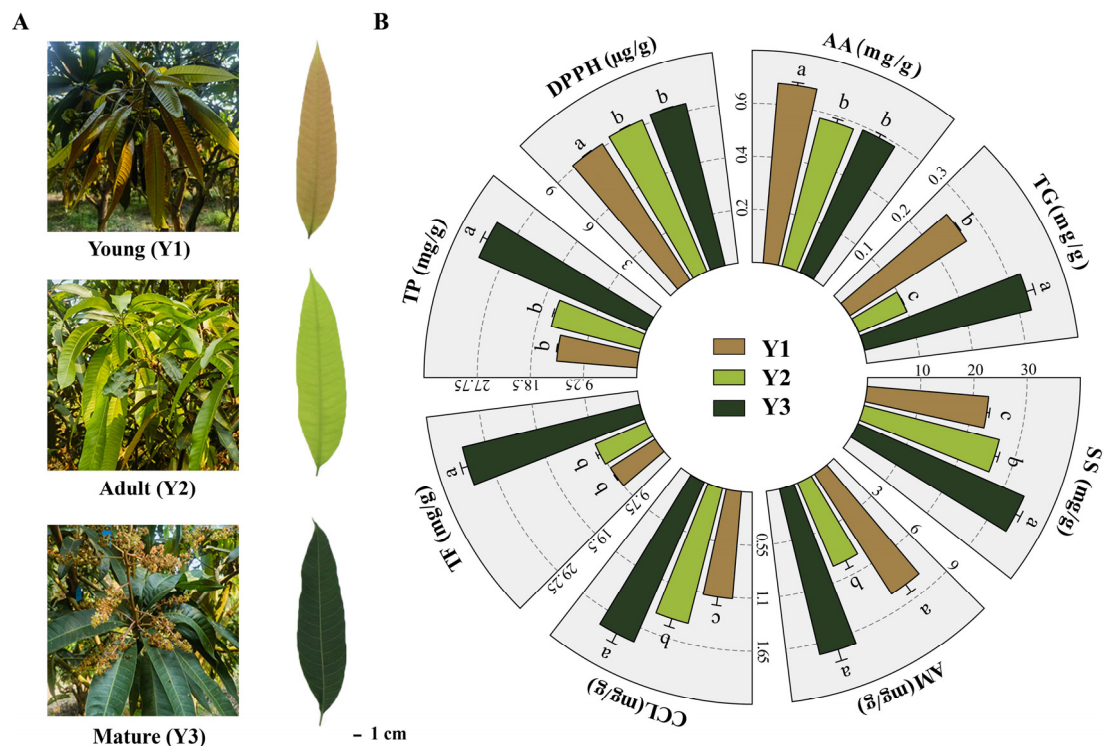


Figure 1. Morphology (A) and component differences (B) of mango leaves at three growth stages. Different lowercase letters in (B) show significant differences by one-way ANOVA followed by Duncan's multiple range test.

3.2. Diversity Analysis of Leaf Morphological Traits in 70 Mango Germplasms

As shown in Figure 2A, significant differences were observed in qualitative leaf traits among the 70 mango germplasms. LS was dominated by long elliptic type, followed by lanceolate, while elliptic and oblanceolate types accounted for a relatively low proportion. LB was mainly cuneate, with the obtuse type being the rarest. LA was predominantly acuminate (81.43%), and the remaining accessions were acute. Flat LM were prevalent, and only one accession had revolute margins.

According to the distribution characteristics, leaf width, leaf length and leaf shape index were divided into six grades (Table S2). Figure 2B indicated that all three quantitative traits displayed an approximately normal distribution. The CV of LW (12.7%) was slightly higher than that of LL (12.5%), suggesting richer variation among germplasms. LI had the lowest CV (10.4%), indicating higher stability across accessions. Overall, the leaf quantitative traits showed moderate variation, providing important morphological evidence for mango germplasms identification and genetic diversity evaluation.

3.3. Analysis of Leaf Nutritional Components and Antioxidant Activities

Descriptive statistical analysis was conducted on eight physiological indices of 70 mango germplasms (Table 2), and the results showed significant differences among various traits. SS, TF and TP exhibited relatively high contents, with mean values all exceeding 20 mg/g, and the CV were 16.25%, 39.45%, and 31.35%, respectively. DPPH showed the lowest content, ranging from 8.12 to 9.05 µg/g, and had the smallest coefficient of variation at only 2.35%, indicating extremely high stability. In contrast, TG ranked second lowest in content among all indices, but had the highest coefficient of variation at 50.38%, showing the most abundant variation among germplasms. The CV of AM, AA and CCL were 46.35%, 33.36% and 28.14%, respectively, all presenting moderate to high genetic diversity.

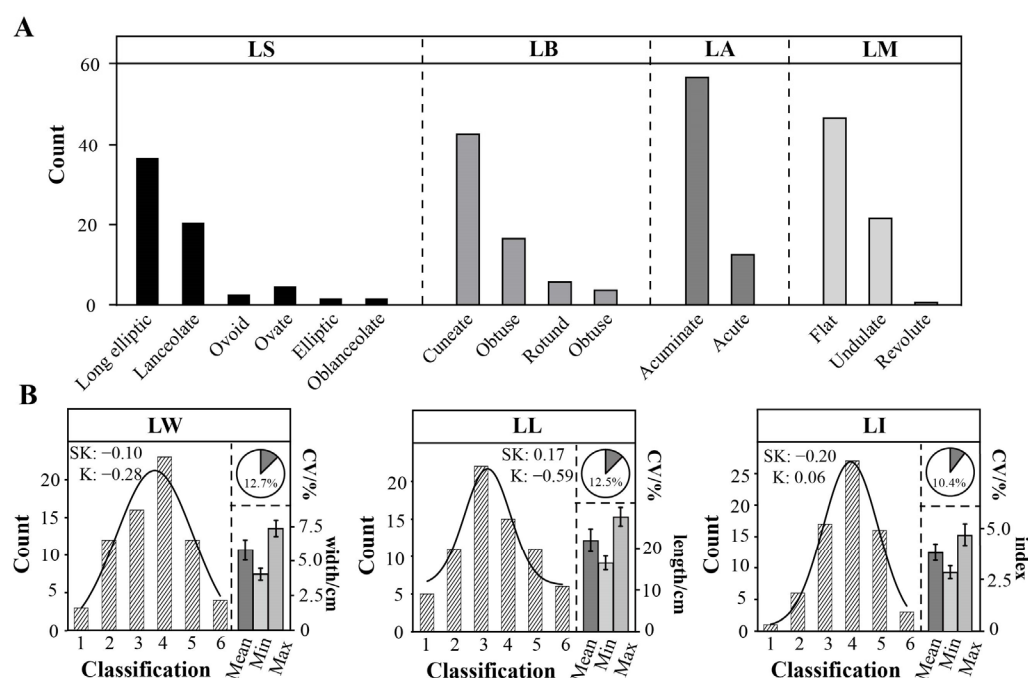


Figure 2. Type distribution and variation analysis of leaf morphological traits in 70 mango germplasms. (A) Counts of leaf shape (LS), leaf base (LB), leaf apex (LA), and leaf margin (LM) types. (B) Histograms of leaf width (LW), leaf length (LL) and leaf shape index (LI) are shown on the left; the black fitted nonlinear curve is overlaid on the plots. SK stands for skewness and K stands for kurtosis. The shaded sectors at the upper right display the coefficient of variation (CV) of each trait, while the minimum (Min), maximum (Max) and mean values of all indicators are presented at the lower right.

Table 2. Descriptive statistics of leaf nutritional and antioxidant indexes in 70 mango germplasms.

Index	Mean	SD	Min	Max	CV (%)
AA (mg/g)	0.96	0.32	0.27	1.94	33.36
TG (mg/g)	0.38	0.19	0.07	0.92	50.38
SS (mg/g)	23.08	3.75	14.19	34.82	16.25
AM (mg/g)	7.19	3.33	2.70	18.37	46.35
CCL (mg/g)	1.49	0.42	0.38	2.25	28.14
TF (mg/g)	21.87	8.63	6.96	44.93	39.45
TP (mg/g)	21.54	6.75	10.19	40.53	31.35
DPPH (μg/g)	8.73	0.21	8.12	9.05	2.35

Frequency distribution analysis of eight leaf nutritional and antioxidant traits in 70 mango germplasms was performed (Figure S1 and Table S2). Most traits, including AA, TG, CCL, and SS, followed an approximately normal distribution. By contrast, AM showed a strong right-skewed pattern, with most individuals concentrated in grade 2, while DPPH exhibited a pronounced left-skewed distribution, peaking in grade 5. AA and SS shared a similar frequency distribution trend, with the majority of germplasms clustered in grade 3. AM and TF displayed a flat, dispersed distribution with high variation, demonstrating abundant genetic diversity. Collectively, the tested mango germplasms exhibited rich phenotypic differentiation in leaf nutritional and antioxidant traits, providing a solid foundation for germplasm evaluation and breeding utilization.

3.4. Correlation Analysis of Leaf Phenotypic and Nutritional Quality Traits

To clarify the interrelationships among leaf traits in mangos, 11 indicators were divided into three groups: leaf phenotypic (LW, LL and LI), nutrients (AA, TG, SS, AM and CCL),

and antioxidants (TF, TP and DPPH). As shown in Figure 3, complex correlations were observed among these traits. Specifically, leaf width and leaf length were significantly correlated with the three antioxidant indicators and CCL, and the antioxidant indicators were also significantly correlated with SS and CCL. At the group level, the nutrients group was significantly correlated only with SS, AM, and CCL within the group, whereas the leaf phenotype group and antioxidants group showed strong correlations not only among intra-group indicators but also with some extra-group indicators to varying degrees. For instance, the leaf phenotype group was extremely significantly correlated with TG, and the antioxidants group was extremely significantly correlated with CCL. These results indicate that leaf phenotypic development, nutrient metabolism, and the antioxidant system in mangos are closely coordinated and regulated.

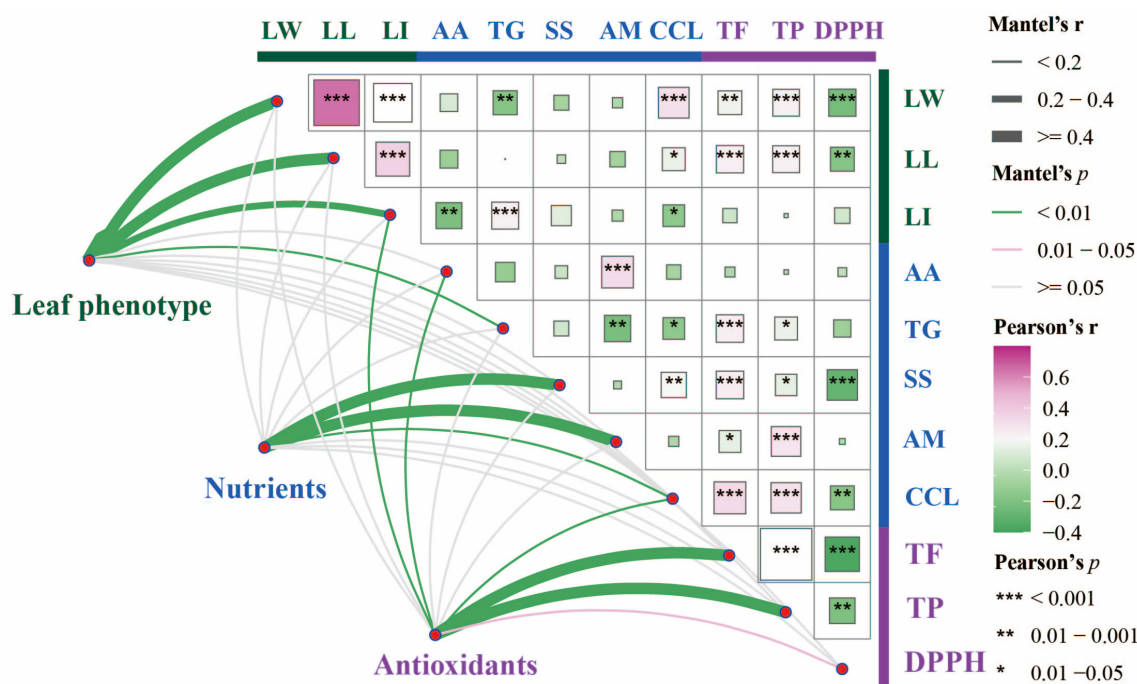


Figure 3. Correlation analysis of leaf traits in different mango germplasms. Leaf phenotypic traits include LW, LL, and LI; nutritional indices include AA, TG, SS, AM, and CCL; antioxidant indices include TF, TP, and DPPH. Traits from the same category are displayed in the same color.

3.5. Cluster Analysis of Leaf Phenotypic and Nutritional Quality Traits

Hierarchical clustering analysis based on 11 leaf traits classified 70 mango germplasms into four distinct groups, exhibiting a clear pattern of trait differentiation and functional specialization (Figure 4). Group I comprised seven germplasms, characterized by small leaf morphology, high leaf index, and significantly superior TG and DPPH activities. Group II, the largest group with 27 germplasms, showed low contents of most indicators including TF and TP, except for relatively high DPPH activity. Group III and Group IV both exhibited elevated overall physiological activity and complex variation across evaluated indicators; the former (14 germplasms) was characterized by outstanding AA and AM contents, whereas the latter (22 germplasms) possessed large leaves, a low leaf index, and remarkably accumulated TF and TP. The evident phenotypic divergence across clusters reflects adaptive differentiation among mango germplasms, providing reliable phenotypic support for germplasm classification, identification and targeted genetic improvement.



Figure 4. Cluster analysis of leaf traits in different mango germplasms. The right color bar represents standardized trait values; red denotes high values, and green denotes low values.

3.6. Principal Component Analysis and Comprehensive Evaluation

Five principal components were extracted based on eigenvalues greater than one, with a cumulative variance contribution of 76.11%, effectively explaining the overall variation of 11 leaf traits among mango germplasms (Table 3). PC1 explained 25.46% of the total variance and primarily reflected differences in antioxidant accumulation and leaf morphology, showing high positive loadings for TF, TP, LW, LL and CCL and an obvious negative loading for DPPH. In comparison, PC2 accounted for 17.18% of the variance and represented variations in leaf index and basic physiological indicators, with prominent positive loadings of LI and TG and negative loadings of LW and AA. PC3 contributed 13.69% of the variance and further revealed correlations between antioxidant activity and leaf morphology, as indicated by positive loadings of AA and AM and negative loadings of LL and LW. Meanwhile, PC4 (10.34%) supplemented integrated variation in morphological and physiological traits via positive loadings of LL, LI and AM and a negative loading of CCL. PC5 (9.45%) was dominated by SS, with negative loadings for TG and TP. Overall, these components covering morphological, nutritional and antioxidant indices fully summarized the core leaf phenotypic information of the tested mango materials.

A comprehensive evaluation model was established using scores of five principal components to rank leaf-related traits of 70 mango germplasms (Table S3). Significant variations in overall performance were observed, with Sri Lanka No.811, Nam Dok Mai, and Shuoshuai Mango ranking top three. These elite germplasms had diverse leaf morphology, high TF and TP contents and balanced basic nutrients, with 811 having the highest TP content. Most intermediate germplasms showed a comprehensive score (TS) of 0.10–0.84,

with stable performance and slight trait variation. Kent's TS approached 0, consistent with the population average. Lower-ranked germplasms mostly had negative TS values, with Myanmar Qiu Mango, India No.905, and Tainong No.2 performing poorest, exhibiting inferior leaf morphology, nutritional quality and antioxidant capacity relative to the other tested accessions. In conclusion, principal component-derived comprehensive scores effectively distinguish leaf trait superiority among mango germplasms, and elite resources (e.g., Sri Lanka No.811 and Nam Dok Mai) provide a reliable basis for screening and evaluating high-quality tropical mango germplasms.

Table 3. Principal component analysis loadings and eigenvalues of leaf traits and nutrients in 70 mango germplasms.

Index	PC1	PC2	PC3	PC4	PC5
LW	0.32	−0.45	−0.37	0.14	−0.14
LL	0.34	0.03	−0.44	0.56	0.07
LI	0.00	0.57	−0.06	0.49	0.24
AA	−0.02	−0.33	0.40	0.22	0.10
TG	0.07	0.48	0.04	−0.17	−0.40
SS	0.22	0.20	0.17	−0.17	0.70
AM	0.08	−0.20	0.56	0.38	0.06
CCL	0.33	−0.16	−0.09	−0.30	0.33
TF	0.51	0.16	0.24	−0.07	−0.22
TP	0.48	0.07	0.30	0.04	−0.30
DPPH	−0.34	−0.01	0.12	0.28	−0.11
Eigenvalue	2.80	1.89	1.51	1.14	1.04
Contributionrate (%)	25.46	17.18	13.69	10.34	9.45
Cumulative contributionrate (%)	25.46	42.64	56.32	66.66	76.11

All data were rounded to two decimal places, and values below 0.01 were recorded as 0.00 following standard rounding criteria.

4. Discussion

Mango germplasms have been globally introduced and domesticated via selective breeding in China, forming multiple standardized germplasm nurseries characterized by abundant genetic diversity [22]. Widely planted as landscape trees across Yunnan, Guangxi and Fujian, mangos supply abundant raw materials for by-product exploitation [23]. Owing to the absence of a systematic evaluation framework for the forage potential of mango leaves, the present study assessed leaf phenotypic traits and nutritional compositions simultaneously. Leaf morphological traits including shape, base, apex, margin, LL, LW and LI facilitate germplasm discrimination and prediction of nutrient accumulation, supporting preliminary screening of superior forage germplasm [24,25]. AA, TG, SS, AM and CCL dominate core nutritional properties by regulating nitrogen supply, energy level, palatability and dietary fiber content, while TF, TP and DPPH activity reflect antioxidant capacity to promote animal health and elevate feed economic value [26–31]. Integrative analysis of these indices enables quantitative assessment of forage performance and offers theoretical guidance for future utilization of mango-leaf resources.

Leaf developmental maturity governs the accumulation and transformation of primary nutrients and secondary antioxidants, whose contents vary regularly across leaf ontogeny. Given that Guifei mangos exhibit the best nutritional profile among five cultivars [11], this cultivar served to establish the optimal harvest stage via evaluation of nutritional and antioxidant dynamics across the three leaf ages, after which the same stage was adopted for comparative validation in other accessions. Results showed that concentrations of SS, CCL, TP, TF and DPPH in Guifei mango leaves all increased progressively with leaf age, peaking at the Y3 stage. This ontogenetic trajectory aligns with findings in tea (*Camellia sinensis*),

coix (*Coix lacryma*), new wheat grass (*Psathyrostachys juncea*), mulberry (*Morus alba*) and fig (*Ficus carica*) [27,28,32–34], suggesting a conserved pattern across diverse plant taxa in which leaf maturation drives the directional accumulation of both primary and secondary metabolites. This progressive increase is likely due to enhanced photosynthetic carbon fixation in mature leaves, which provides more substrates for both sugar and phenolic synthesis, while prolonged leaf age also allows greater time for the accumulation and storage of these metabolites in vacuoles.

Leaf phenotype serves as the most intuitive external manifestation of genetic differentiation in plant germplasms, and its trait variation directly reflects inter-germplasm genetic differences. Morphological indicator-based evaluation of germplasm diversity has been widely applied in multiple plant species, such as ancient tea and *Eucommia ulmoides* [35,36], and relevant studies on mango germplasms have also been increasingly reported. In this study, seven leaf phenotypic traits of 70 mango germplasms were measured and analyzed. The results revealed abundant leaf morphological variation among the tested germplasms, which were predominantly characterized by elongated elliptical leaves with wedge-shaped bases, acuminate apices, and entire straight margins. These phenotypic characteristics are consistent with previous evaluations of mango germplasms in Pakistan and India [6,21]. A prior study with a small sample size of six mango germplasms documented similar variation ranges for LL, LW, and LI, but differed substantially in coefficients of variation [37]. Compared with the aforementioned small-sample investigation, the larger germplasm population and wider sample coverage in this study enable a more objective and comprehensive characterization of the natural phenotypic variation and genetic diversity of mango leaves. Collectively, these findings provide a solid and reliable morphological foundation for germplasm identification, classification, and genetic diversity assessment of mango resources.

Studies on nutritional components and bioactive substances in mango leaves have laid a solid foundation for their resource utilization. Xu et al. determined leaf nutrients and antioxidants of five mango accessions and confirmed that Guifei leaves possess excellent nutritional quality and aquatic disease resistance, showing great potential for forage application [11]. A previous study on 13 accessions revealed that Lu Mango had the highest leaf flavonoid content [38]. Huang assessed 40 accessions through multiple antioxidant assays, defined late winter to early spring as the optimal harvest period, and screened elite cultivars including Jinhuang and Jinxing [10]. Based on these achievements, we standardized sampling procedures considering spring harvest and superior metabolite accumulation in old leaves and expanded the germplasm to 70 accessions to analyze genotypic variation in leaf nutritional and antioxidant traits. Significant genotypic differences and rich genetic diversity were detected across all traits. SS, TF and TP were present at high contents and displayed large coefficients of variation, reflecting considerable genetic and environmental influences on their biosynthetic pathways. By contrast, DPPH radical scavenging activity maintained low variability and high stability across accessions, which may be attributed to the functional redundancy and compensatory interactions among various antioxidant compounds. This pattern is consistent with the observations of earlier studies [10]. Further research integrating various antioxidant evaluation systems is thus suggested. Additionally, distinct frequency distribution patterns were observed for all traits using the trait classification system proposed by Liu et al. [39]. This variation reflects the diverse genetic underpinnings across traits, from polygenic to major-gene control, and provides a broad allelic pool for targeted parental selection in future breeding programs.

The correlation, clustering, and principal component comprehensive evaluation are widely applied in mango germplasm screening, and related research mainly focuses on plant growth traits, fruit quality, and stress-responsive phenotypes [9,21,40–43]. In plants

such as mulberry and *Bromus inermis*, researchers have combined leaf phenotype with nutritional quality indicators to conduct trait correlation analysis, forming a mature research approach [44,45]. Liao et al. verified strong correlations among leaf phenotypic traits but relative independence of nutritional indicators in plants [44], which is consistent with the findings of the present study. This study also found that the accumulation of TF and TP in mango leaves and the DPPH antioxidant activity showed synchronous positive changes at different growth stages, which aligns with previous findings in mulberry [33]. Within a single genotype, leaf metabolic flux shifts uniformly with developmental rhythm, and TP and TF act as the dominant DPPH-scavenging substances with little interference from other antioxidants. In the analysis of 70 mango germplasms, TF and TP content co-accumulated, but showed a significant negative correlation with DPPH activity. Such discrepancies may stem from genetic divergence in carbon allocation for secondary metabolism, diverse structural modification forms of phenols and flavonoids, and distinct levels of non-phenolic and non-flavonoid antioxidants among different mango germplasms.

The clustering analysis of different germplasm using the same method varies with material properties and evaluation indicators. For example, Ansari et al. clustered 89 mango germplasms based on quantitative and qualitative traits, yielding five and six groups, respectively, which reflected geographical origin and morphological phylogenetic similarity [21]. In this study, 70 mango germplasms were divided into four groups, showing clear trait differentiation and functional specialization. The small-leaf type (Group I) tended to accumulate flavonoids, likely as an adaptive strategy to environmental stress through enhanced secondary metabolism, while the large-leaf type (Group IV) achieved growth advantage through expanded leaf area, reflecting a trade-off between defensive investment and carbon assimilation efficiency. Notably, Groups II and IV further defined subpopulations where DPPH activity was negatively correlated with TF and TP content. The former showed low DPPH activity but high TF/TP content, suggesting a predominance of simple phenolics with higher radical-scavenging efficiency per unit, whereas the latter exhibited the opposite, implying a greater proportion of complex polyphenols with lower DPPH activity per unit mass, or the involvement of alternative antioxidant systems. These subgroup divergences are likely attributed to differential metabolic flux allocation and genetic heterogeneity among accessions, possibly shaped by distinct ecological origins or breeding histories. Overall, these clustering results clarify differences in trait differentiation and antioxidant characteristics among mango germplasms, providing a reference for elite germplasm screening, antioxidant mechanism studies, and innovative germplasm utilization.

To simplify multi-index data analysis and achieve comprehensive evaluation of germplasm resources, many studies use principal component analysis to reduce trait dimensionality while retaining core variation. Nong et al. [31] measured 16 indicators of the peels and seeds of seven mango varieties, extracted four principal components, and evaluated their potential for feed development. The top three varieties were Yu Mango, Jinhuang and Keitt. In this study, five principal components extracted from 11 mango-leaf quantitative traits sufficiently captured phenotypic variation among germplasm accessions, with Sri Lanka No.811, Nam Dok Mai and Shuoshuai Mango ranking highest in the comprehensive evaluation. These results confirm that leaf traits effectively assess mango germplasm and reveal tissue-specific phenotypic differences tied to usage. Leaf-based markers offer a rapid, non-destructive tool for preliminary screening, significantly boosting evaluation efficiency in large-scale germplasm work.

Growing demand for natural plant feed has driven rising interest in valorization of mango-leaf by-products. This study determined the optimal harvest stage of Guifei mango leaves and established phenotypic, nutritional, and bioactive datasets of 70 mango

germplasms, providing a solid experimental basis for the development of mature mango-leaf feed. To further enrich the biological understanding of mango-leaf feed value, future studies should integrate multi-omics platforms, with a particular emphasis on metabolomics, for thorough profiling and accurate quantification of signature bioactive metabolites. Further refined stage-specific analysis of leaves from elite mango germplasm can be carried out to enrich relevant trait data. In parallel, targeted molecular experiments should be conducted to validate candidate functional genes, thereby elucidating the regulatory mechanisms underlying feeding-related traits in mango leaves. Such efforts will also facilitate germplasm innovation and directional breeding, refine evaluation and breeding systems, and promote genetic improvement for the high-value utilization of mango leaves.

5. Conclusions

This study confirmed Y3 as the optimal leaf stage for deep processing of Guifei mango leaves due to its high nutrient and antioxidant accumulation. The 70 tested mango germplasms possessed rich diversity in mature leaf phenotypes and nutrients, with SS, TP and TF as the primary functional components, and long elliptic leaf was the major morphological characteristic. Leaf morphological and antioxidant traits exhibited synergistic correlations, and all germplasms were divided into four distinct clusters via hierarchical clustering. Sri Lanka No.811 was screened as the outstanding germplasm with high polyphenols and balanced nutrition by principal component analysis. This study fills the gap in systematic evaluation of mango germplasms for leaf utilization, offering theoretical and practical support for elite germplasm screening, high-value leaf processing, and targeted mango breeding.

Supplementary Materials: The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/horticulturae12070881/s1>, Figure S1: Frequency distribution of leaf nutritional and antioxidant traits in 70 mango germplasms. The black line represents the fitted nonlinear regression curve; Table S1: Correlation of component indicators in mango leaves at three growth stages; Table S2: Classification of mango-leaf characteristics and nutritional quality parameters; Table S3: Comprehensive evaluation results of mango germplasm leaf traits.

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Abbreviations

The following abbreviations are used in this manuscript:

Y1	young leaves
Y2	adult leaves
Y3	mature leaves
LS	leaf shape
LA	leaf apex
LB	leaf base
LM	leaf margin
LL	leaf length
LW	leaf width
LI	leaf shape index
AA	amino acids
TG	triglycerides
SS	soluble sugars
AM	amylase
CCL	cellulose
TF	total flavonoids
TP	total phenols
DPPH	2,2-diphenyl-1-picrylhydrazyl

References

- Ahmad, B.; Su, Y.; Arshad, R.; Razzaq, T.; Zhang, Y.; Hou, T.; Li, C.; Jin, Z.; Chen, C.; Wang, P.; et al. Integrative genomics for mango genetics and breeding. *Hortic. Res.* **2026**, *13*, uhaf260. [[CrossRef](#)] [[PubMed](#)]
- FAO. *Major Tropical Fruits: Market Review 2020*; Food and Agriculture Organization of the United Nations: Rome, Italy, 2021.
- Burton-Freeman, B.M.; Sandhu, A.K.; Edirisinghe, I. Mangos and their bioactive components: Adding variety to the fruit plate for health. *Food Funct.* **2017**, *8*, 3010–3032. [[CrossRef](#)] [[PubMed](#)]
- Liu, B.; Xin, Q.; Zhang, M.; Chen, J.; Lu, Q.; Zhou, X.; Li, X.; Zhang, W.; Feng, W.; Pei, H.; et al. Research progress on mango post-harvest ripening physiology and the regulatory technologies. *Foods* **2023**, *12*, 173. [[CrossRef](#)] [[PubMed](#)]
- Kassa, A.; Alcaraz, L.; Larranaga, N.; de Meyer, E.; Hormaza, I.; de la Peña, E. Evaluation of genetic diversity of Ethiopian mango genotypes and comparison with a worldwide germplasm collection. *Sci. Hortic.* **2025**, *348*, 114211. [[CrossRef](#)]
- Jena, R.C.; Agarwal, K.; Chand, P.K. Fruit and leaf diversity of selected Indian mangoes (*Mangifera indica* L.). *Sci. Hortic.* **2021**, *282*, 109941. [[CrossRef](#)]
- Ge, Y.; Lu, H.; Wu, J.; Liang, Q.; Yu, X.; Lao, F. Analysis of aroma and flavor characteristics of different species of mango. *China Fruit Veg.* **2026**, *46*, 6–16. [[CrossRef](#)]
- Adikshita; Sharma, I.M.; Sharma, M. Screening of mango germplasm under natural epiphytotic conditions against anthracnose (*Colletotrichum gloeosporioides*). *Indian Phytopathol.* **2018**, *71*, 285–289. [[CrossRef](#)]
- Lei, Y.; Lin, Y.; Gao, A.P.; Liu, F.Z.; Liu, Q.G.; Zhang, Z.X. Anatomical leaf structure characteristics and comprehensive drought resistance evaluation of 14 mango germplasm resources. *Southwest China J. Agric. Sci.* **2025**, *38*, 250–258. [[CrossRef](#)]
- Huang, L.Y. Evaluation and Analysis of Leaf Antioxidant Activity in 40 Mango Germplasm Resources. Master's Thesis, Chinese Academy of Agricultural Sciences, Beijing, China, 2025.
- Xu, C.; Ma, T. Analysis of nutritional components and active substances in leaves of different mango cultivars. *Cereal Feed Ind.* **2022**, 53–56. [[CrossRef](#)]
- Feng, M. Preliminary study on cell structure and cold tolerance of mango leaf tissues. *Trop. Agric. Sci. Technol.* **2003**, 5–7+18. [[CrossRef](#)]
- Asrey, R.; Patel, V.B.; Barman, K.; Pal, R.K. Pruning affects fruit yield and postharvest quality in mango (*Mangifera indica* L.) cv. Amrapali. *Fruits* **2013**, *68*, 367–380. [[CrossRef](#)]
- Wei, K.; Liang, L.; Wang, M.; Liao, D.; Jiang, Q. Study on Antioxidant and Anti-Ultraviolet Capacities of Mangiferin in Mango Leaves. *Food Saf. Guide* **2024**, 80–82+86. [[CrossRef](#)]
- Selim, D.A.; Shams Eldin, S.M.; González, F.P.; Ghareeb, D.A.; Shawky, E. Metabolomics and chemometrics-driven valorisation of mango leaves: Unveiling putative α -amylase and α -glycosidase inhibitory metabolites. *Food Biosci.* **2024**, *61*, 104652. [[CrossRef](#)]
- Pan, J.; Yi, X.; Zhang, S.; Cheng, J.; Wang, Y.; Liu, C.; He, X. Bioactive phenolics from mango leaves (*Mangifera indica* L.). *Ind. Crops Prod.* **2018**, *111*, 400–406. [[CrossRef](#)]

17. Aderibigbe, A.O.; Emudianughe, T.S.; Lawal, B.A.S. Antihyperglycaemic effect of *Mangifera indica* in rat. *Phytother. Res.* **1999**, *13*, 504–507. [CrossRef]
18. Cai, H.; Zhang, H.; Lu, R.; Feng, S.; Lin, M. Efficacy of Mango Leaf-Based Feed Additive on Growth Performance, Antioxidant Status and Digestive Enzyme Activities in *Litopenaeus vannamei*. *Fishes* **2025**, *10*, 524. [CrossRef]
19. Sunarya, I.K.; Ismadi, I.; Wahyono, W.; Dianita, N.K.; Nain Febri, I.W. Kembar mayang and ronce as motif ideas in natural dye batik of keci beling leaves and honey mango leaves. *Open Cult. Stud.* **2025**, *9*, 20240044. [CrossRef]
20. Alasvand, S.; Crane, J.; Haley-Zitlin, V. Chemical Characteristics of Mango Leaf Tea Prepared From Different Varieties of *Mangifera indica* L. Leaves. *Curr. Dev. Nutr.* **2022**, *6*, 263. [CrossRef]
21. Ansari, W.Z.; Mukhtar, H.; Ali, A.; Arif, M.; Iqbal, J.; Henry, R.J. Evaluation of mango (*Mangifera indica* L.) germplasm for phenotypic diversity and breeding potential in Pakistan. *Sci. Rep.* **2026**, *16*, 3693. [CrossRef] [PubMed]
22. Zhang, J.; Qian, X.; Tian, L.; Zhang, H.; Mao, C.; Zhu, X.; Liu, J.; Niu, Y. Comparative study on pigments and quality-related enzymes in young fruits of mango germplasm resources from yunnan. *Trop. Agric. Sci. Technol.* **2025**, *48*, 6–15. [CrossRef]
23. Lin, Y. Selection and application of ornamental fruit plants in landscape greening engineering. *Mod. Hortic.* **2020**, *43*, 99–101. [CrossRef]
24. Wright, I.J.; Ackerly, D.D.; Bongers, F.; Harms, K.E.; Ibarra-Manriquez, G.; Martinez-Ramos, M.; Mazer, S.J.; Muller-Landau, H.C.; Paz, H.; Pitman, N.C.A.; et al. relationships among ecologically important dimensions of plant trait variation in seven neotropical forests. *Ann. Bot.* **2007**, *99*, 1003–1015. [CrossRef] [PubMed]
25. Ni, X.; Sun, L.; Cai, Q.; Ma, S.; Feng, Y.; Sun, Y.; An, L.; Ji, C. Variation and determinants of leaf anatomical traits from boreal to tropical forests in eastern China. *Ecol. Indic.* **2022**, *140*, 108992. [CrossRef]
26. Du, Z.; Lin, W.; Zhu, J.; Li, J. Amino acids profiling and transcriptomic data integration demonstrates the dynamic regulation of amino acids synthesis in the leaves of *Cyclocarya paliurus*. *PeerJ* **2022**, *10*, e13689. [CrossRef] [PubMed]
27. Zhou, C.; Yun, L.; Ai, Q.; Li, B.; He, Y.; Ren, N.; Li, Z. Core regulatory pathways and genes regulating soluble sugar accumulation in psathyrostachys juncea during different growth stages. *J. Plant Genet. Resour.* **2026**, 1–16. [CrossRef]
28. Shang, K.; Fu, Y.; Li, X.; Zhou, X.; Meng, Q.; Ao, M. Determination of triglyceride content and genetic diversity analysis of coix lacryma-jobi core germplasm. *Mol. Plant Breed.* **2022**, *20*, 4765–4771. [CrossRef]
29. Vieira, P.A.F.; Queiroz, J.H.d.; Albino, L.F.T.; Moraes, G.H.K.d.; Barbosa, A.d.A.; Müller, E.S.; Viana, M.T.d.S. Effects of inclusion of mango residues on performance of broilers chickens from 1 to 42 days. *Rev. Bras. Zootec.* **2008**, *37*, 2173–2178. [CrossRef]
30. Nong, S.; Liao, Y.; Wan, R.; Lei, L.; Lu, L.; Wei, X.; Shen, S. Biological functions of mango extracts and its application prospect in poultry production. *Feed Res.* **2023**, *46*, 158–162. [CrossRef]
31. Nong, S.; Wang, Y.; Mei, Y.; Wang, F.; Xu, X.; Huang, J.; Zhang, C.; Yang, Z.; Liu, C.; Wan, R. Comparison and analysis of nutritional and active components in peel and kernel of different mango cultivars. *Feed Ind.* **2025**, *47*, 166–173. [CrossRef]
32. Deng, H.; Liang, Z.; Dong, F.; Li, J.; Liang, Z.; Zhong, D. Effects of leaf maturity and brewing methods on free amino acid, tea polyphenol contents and antioxidant capacity of aquilaria leaf tea. *China Food Saf. Mag.* **2025**, *19*, 130–134. [CrossRef]
33. Zhang, X.; Liu, Y.; Zhu, Z.; Du, L.; Li, M. Study on polyphenols, flavonoids and antioxidant activity in mulberry fruits and leaves at different maturity stages. *J. Fruit Sci.* **2014**, *31*, 660–666. [CrossRef]
34. Nadeem, M.; Zeb, A. Impact of maturity on phenolic composition and antioxidant activity of medicinally important leaves of *Ficus carica* L. *Physiol. Mol. Biol. Plants* **2018**, *24*, 881–887. [CrossRef] [PubMed]
35. Li, Y.; Xu, F.; Dong, Z.; Yang, C.; Liang, S.; Guo, Y.; Guo, C.; Chen, Z. Phenotypic diversity analysis and excellent germplasm screening of 66 ancient tea plant germplasms in guizhou province. *Guizhou Agric. Sci.* **2026**, *54*, 23–34. [CrossRef]
36. Gong, H.; Yang, M.; Wang, C.; Tian, C. Leaf phenotypic variation and its response to environmental factors in natural populations of *Eucommia ulmoides*. *BMC Plant Biol.* **2023**, *23*, 562. [CrossRef] [PubMed]
37. Liao, H.; Li, L.; Li, R.; Chen, Y.; Luo, S.; Wu, J.; Li, X.; Huang, G. Analysis of vegetative and reproductive organ traits of mango germplasms with different flesh colors based on DUS testing. *Agric. Res. Appl.* **2026**, *39*, 196–210. [CrossRef]
38. Deng, J.; Yu, C.; Wang, F.; Wang, M. Determination of flavonoid content in leaves of different mango cultivars by high performance liquid chromatography. *Food Ind.* **2015**, *36*, 273–275. Available online: https://kns.cnki.net/kcms2/article/abstract?v=MKd1fMAWOtUhSV3-rocGs_lfIVOTXtlq2q_EmhNjNZpuQJl6vfQp8u7KoBAembjc2g8z5Bsa7LrHJGN3SmzQMatMIAiQremGpeFRTx8DzNjB788Alxt5PpPb8hyjT0VtIpiguyt5JlIa_wjFxtqP7pYISUenAIYAD7OmSAPvY98=&uniplatform=NZKPT&language=CHS (accessed on 12 July 2026).
39. Liu, J.; Niu, Y.; Kong, G.; Li, K.; Ni, S. Variation analysis of fruit quality traits of cultivated mango germplasms in yunnan province. *Southwest China J. Agric. Sci.* **2018**, *31*, 582–586. [CrossRef]
40. Pang, Y.; Zhao, Z.; Huang, L.; Wang, J.; Luo, R.; Gao, A. Optimization of mango pollen medium and observation of germination characteristics of 33 germplasm resources. *China Fruits* **2025**, 52–58. [CrossRef]
41. Khadivi, A.; Mirheidari, F.; Saeidifar, A.; Moradi, Y. Identification of the promising mango (*Mangifera indica* L.) genotypes based on morphological and pomological characters. *Food Sci. Nutr.* **2022**, *10*, 3638–3650. [CrossRef] [PubMed]

42. Qian, X.; Zhang, J.; Tian, L.; Zhang, H.; Yan, P.; Mao, C.; Liu, J.; Niu, Y. Analysis of fruit quality characteristics of 55 mango germplasm resources at young fruit stage. *South China Fruits* **2026**, *55*, 89–95. [[CrossRef](#)]
43. Raj, R.S.; Thakur, S.V.; Vyas, Y.S.; Patel, K.M.; Patel, P.V.; Joshi, M.N.; Tyagi, S.N.; Bagatharia, S.B. Diversity analysis, pathogen load and gene expression studies of mango cultivars infected by mango malformation disease. *Plant Growth Regul.* **2016**, *81*, 117–130. [[CrossRef](#)]
44. Liao, Y.; Zheng, Z.; Zhang, Z.; Chen, L.; Xia, C.; Ren, J.; Tan, L. Analysis of phenotypes and leaf nutritional quality of 42 mulberry germplasm resources. *Chin. Agric. Sci. Bull.* **2026**, *42*, 105–116. [[CrossRef](#)]
45. Gu, X.; Wang, G.; Xie, Z.; Qin, F.; Yang, Y.; He, C. genetic diversity analysis of nutritional quality, phenotypic and agronomic traits in 37 bromus inermis germplasm resources. *Feed Res.* **2026**, *49*, 132–136. [[CrossRef](#)]

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