

Article

Comparative Analysis of Agronomic Traits and Total Phenolic Components of Three Wine Grape Cultivars Across Three Production Sites in Northern China

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Abstract

Phenolic compounds are critical components that determine the processing quality of wine grapes, and their accumulation is jointly affected by environmental conditions and genotype. However, the respective contributions of production site and cultivar, as well as the response differences in various phenolic components to environmental changes, remain unclear in northern China. In this study, three major red wine grape cultivars (*Vitis vinifera* L. cvs. Marselan, Cabernet Franc, Cabernet Sauvignon) were sampled from three typical producing areas, including Turpan, the Hexi Corridor, and Huailai in 2024. Botanical characteristics, quantitative agronomic traits, physicochemical indexes, and five phenolic components in berry skins and seeds were determined with three biological replicates. A general linear model (GLM) was used to quantify the effects of production site and genotype on berry quality, and principal component analysis (PCA) and Pearson correlation analysis were performed to explore the relationships between quality indicators. Our results indicate that clear quality differences were observed among the three studied production sites, which were the main source of variation in this dataset, accounting for 65.7% to 82.1% of total variance across most traits. Three distinct regional patterns were observed: grapes from Xinjiang had the highest sugar content, those from Gansu had the highest phenolic levels, and those from Zhangjiakou were richest in anthocyanins. The responsiveness of individual phenolic components to ecological conditions varied markedly, with anthocyanins being the most sensitive, followed by proanthocyanidins, tannins, total phenolics, and flavonoids. Marselan maintained a stable genotypic advantage in proanthocyanidin accumulation across all three sites, with skin levels 12.5–230.5% higher than other cultivars under the same growing conditions. Additionally, a potential tissue-specific association between cluster weight and phenolic components was preliminarily observed: higher cluster weight was associated with lower concentrations of late-accumulating anthocyanins and proanthocyanidins, but did not negatively affect total phenolics and tannins that form in early fruit development. Based on the above results, preliminary suggestions for cultivar–site matching were provided for reference. This study provides preliminary baseline data for cultivar selection and viticultural management in northern China, pending further multi-year validation.



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Keywords: wine grapes; agronomic traits; phenolic compounds; cultivar–site matching; ecological factors; tissue specificity

1. Introduction

China ranks third in the world in grape cultivation area, and is also the world's eighth largest wine consumer and largest producer of table grapes [1]. Environmental conditions, including climate, soil, and terrain in different wine-producing regions, directly affect grape growth, development, and secondary metabolism, and further form unique fruit quality characteristics [2]. In recent years, the development of China's wine grape industry has shifted from scale expansion to quality improvement. It is particularly important to select suitable varieties for different regions and realize the matching of varieties and producing areas.

Phenolic compounds are key secondary metabolites that determine the processing quality of wine grapes, and their content and composition affect antioxidant capacity, storage properties, and winemaking characteristics of berries [3]. Volatile flavour compounds, another important class of secondary metabolites, directly shape the sensory quality of both table and wine grapes, and also show rich genotypic diversity among different cultivars [4]. Phenolic accumulation is affected by both environmental factors and genetic characteristics and is also closely coupled with the fruit development process. Fruit set, as the first key node of grape yield and quality formation, is precisely regulated by a conserved transcription regulatory network at the transcriptome level [5]. UV radiation, accumulated temperature, and diurnal temperature difference are the main environmental factors affecting phenolic synthesis. Precipitation and wind speed also indirectly affect agronomic characters and fruit quality by regulating water status and microclimate [6]. Different varieties differ greatly in phenolic synthesis ability and component distribution [7]. In addition, phenolic components in seeds and skins vary greatly: seeds are rich in tannins and proanthocyanidins, while skins mainly contain anthocyanins and flavonoids [8].

Worldwide, many studies have focused on the relationship between terroir and grape quality. In Mediterranean regions, Venios et al. [9] reported that diurnal temperature range (DTR) can significantly promote anthocyanin accumulation in grape skins, and higher DTR helps deepen fruit color. High temperature inhibits anthocyanin synthesis, while low night temperature helps maintain fruit acidity and color, which is weakened by global warming [10]. In northern China, He et al. [11] studied Cabernet Sauvignon from 12 producing regions and found that UV intensity was extremely significantly positively correlated with total phenols in skins ($r = 0.83$, $p < 0.01$). High altitude and strong UV help improve the accumulation of total phenols, anthocyanins, and flavonols in skins.

However, current studies still have limitations. Most studies focus on single region or single variety, and lack comparative analysis of the main varieties in Xinjiang, Gansu, and Zhangjiakou [12]. Many studies only determine total phenols in whole fruit and ignore the differences between seeds and skins [13,14]. Few studies have clarified the sensitivity differences in various phenolic components to ecological factors, which makes it difficult to support variety–region matching [15,16]. Moreover, most previous PCAs used mean values instead of biological replicates, which cannot accurately reflect the experimental repeatability and group differences.

Therefore, three main wine grape varieties from three typical producing regions in northern China were selected for this study. Botanical characteristics, quantitative agronomic traits, physicochemical indexes, and five phenolic components in seeds and skins were measured with three biological replicates. The effects of environment and variety

on fruit quality were clarified, and the response of phenolic components to ecological factors was analyzed. Preliminary suggestions for cultivar–site matching were provided. The results provide baseline data for cultivar selection and regional production planning for wine grapes in northern China.

2. Materials and Methods

2.1. Experimental Sites and Materials

This field experiment was conducted in three main wine grape regions of northern China during the 2024 growing season: the Turpan Basin in Xinjiang (42°56′ N, 89°12′ E), the Hexi Corridor in Gansu (39°42′ N, 98°30′ E), and Huailai County in Hebei (40°24′ N, 115°30′ E). Meteorological data from April to October 2024 were obtained from the official China Meteorological Data Network.

Three red wine grape cultivars were used: Marselan, Cabernet Franc, and Cabernet Sauvignon. All vines were 5 years old, grafted onto SO4 rootstock, trained on a single cordon, and spur-pruned to retain 10–12 buds per vine. The planting density was 1.0 m × 3.0 m, and drip irrigation was applied. Standard viticultural practices, including pest and disease control and fertilization, were uniformly implemented across all experimental sites.

All three vineyards are located on well-drained sandy loam soils with a pH range of 7.8–8.5. Standardized viticultural practices were uniformly implemented across all sites: 300 kg·ha^{−1} compound fertilizer (N:P:K = 15:15:15) was applied at budbreak, drip irrigation was scheduled based on evapotranspiration estimates with 250–300 mm total irrigation during the growing season, and no cluster thinning was performed in 2024. At the commercial harvest stage (when total SSC reached 20–27 °Brix), samples were collected from 30 randomly selected healthy vines per cultivar per site, with a spacing of at least 5 m between sampled vines to avoid spatial autocorrelation. A total of 30 healthy clusters were collected for each cultivar at each site and divided into three independent biological replicates (10 clusters per replicate, each from 10 separate vines). All samples were immediately frozen in liquid nitrogen and stored at −80 °C until analysis.

2.2. Determination of Indicators and Methods

2.2.1. Botanical Characteristics

Botanical characteristics, including cluster shape, secondary clusters, shoulder type, cluster compactness, berry shape, skin color, skin thickness, skin astringency, bloom thickness, flesh texture, flesh aroma, juice color, flesh color, and seed development status, were investigated according to the national standard GB/T 15038-2006 [17].

2.2.2. Quantitative Agronomic Traits

Average cluster weight was measured using an electronic balance (Sartorius, Göttingen, Germany; precision 0.01 g). Average berry weight was determined by weighing 100 randomly selected berries. Juice yield was calculated as the percentage of juice weight to berry weight. Seed length and width were measured using a digital vernier caliper (Mitutoyo, Kawasaki, Japan; precision 0.01 mm). All determinations were performed with three technical replicates for each biological sample.

2.2.3. Physicochemical Quality Analysis

SSC was measured using a PAL-1 handheld refractometer (Atago, Tokyo, Japan). Titratable acidity (TA) was determined by acid–base titration with 0.1 mol·L^{−1} NaOH and expressed as g·L^{−1} of tartaric acid. pH was measured using a PHS-3C digital pH meter (Leici, Shanghai, China). SSC was measured and reported in °Brix. The sugar–acid

ratio was calculated as the ratio of SSC (°Brix) to TA ($\text{g}\cdot\text{L}^{-1}$) [18]. All measurements were performed in triplicate.

2.2.4. Phenolic Compound Analysis

Frozen berry skins and seeds were separated manually and ground into powder in liquid nitrogen. For each sample, 0.5 g of powder was extracted with 5 mL of 80% methanol containing 0.1% HCl. The mixture was incubated at 4 °C in the dark for 24 h with intermittent shaking three times. After extraction, the mixture was centrifuged at $4000\times g$ for 10 min at 4 °C using a high-speed refrigerated centrifuge (Eppendorf, Hamburg, Germany), and the supernatant was filtered through a $0.45\text{ }\mu\text{m}$ organic membrane filter. Each extraction was carried out in triplicate for every biological replicate.

Total phenolic content: Folin–Ciocalteu method with gallic acid as standard, expressed as $\text{mg GAE}\cdot\text{g}^{-1}$ FW. Tannin content: Folin–Denis method with tannic acid as standard, expressed as $\text{mg TAE}\cdot\text{g}^{-1}$ FW [19]. Total flavonoid content: AlCl_3 colorimetric method with rutin as standard, expressed as $\text{mg RE}\cdot\text{g}^{-1}$ FW [20]. Anthocyanin content: pH differential method with cyanidin-3-glucoside as standard, expressed as $\text{mg C3GE}\cdot 100\text{ g}^{-1}$ FW [21]. Proanthocyanidin content was determined by the n-butanol-hydrochloric acid method [22], with procyanidin B1 as the calibration standard, detected at 550 nm. The calibration curve showed good linearity with $R^2 > 0.99$, and the average spiked recovery rate ranged from 92.5% to 96.8%. Results were expressed as $\text{mg}\cdot\text{g}^{-1}$ FW.

All standards were purchased from Sigma-Aldrich (St. Louis, MO, USA). All calibration curves showed good linearity ($R^2 > 0.99$), with average spiked recovery rates ranging from 92.5% to 97.2% across all phenolic indices.

2.3. Data Analysis

All statistical analyses were performed using SPSS 26.0 (IBM, Armonk, NY, USA). A two-way factorial general linear model (GLM) with Type III sums of squares was applied to each trait, with production site and cultivar set as fixed effects, to test main effects and interaction effects. One-way ANOVA followed by Duncan’s multiple range test was used for pairwise comparisons among the nine cultivar–site combinations, with a significance level set at $p < 0.05$. Variance contribution rates were calculated as the ratio of each factor’s sum of squares to the total sum of squares. All main effects and interaction effects were statistically significant ($p < 0.05$). Principal component analysis (PCA) and Pearson correlation analysis were performed using Origin 2023 (OriginLab, Northampton, MA, USA). For PCA, all 14 quality indicators from 27 biological replicates were standardized using Z-scores before analysis. PCA was used as an exploratory visualization method for sample clustering patterns and does not imply causal inference. Bonferroni correction was applied for multiple comparisons in correlation analysis.

3. Results

3.1. Differences in Agronomic Traits

3.1.1. Botanical Characteristics

All three cultivars showed typical conical cluster shape and round berry shape (Table 1). Significant regional differences were observed in skin color, skin thickness, and cluster compactness. Gansu-grown grapes generally had multiple shoulders and compact clusters, while Zhangjiakou-grown grapes had double shoulders and loose clusters. GS-CF showed a unique reddish-purple skin color, while all other samples had blue-black skin. All seeds were fully developed across all samples.

Table 1. Botanical characteristics of three wine grape cultivars grown in different regions of northern China.

Cultivar	XJ-M	GS-M	ZJK-M	XJ-CF	GS-CF	ZJK-CF	XJ-CS	GS-CS	ZJK-CS
Cluster Shape	Conical	Conical	Conical	Conical	Conical	Conical	Conical	Conical	Conical
Secondary Cluster	Present	Present	Present	Present	Present	Present	Present	Present	Present
Shoulder	Single	Multiple	Double	Single	Multiple	Double	Single	Multiple	Double
Cluster Compactness	Medium	Compact	Loose	Medium	Medium	Medium	Medium	Loose	Medium
Berry Shape	Round	Round	Round	Round	Round	Round	Round	Round	Round
Skin Color	Blue-black	Blue-black	Blue-black	Blue-black	Reddish-purple	Blue-black	Blue-black	Blue-black	Blue-black
Skin Thickness	Thick	Medium	Thick	Thick	Medium	Thin	Medium	Medium	Thick
Skin Astringency	Present	Slight	Present	Present	Absent	Slight	Present	Absent	Present
Bloom Thickness	Thick	Thin	Thick	Thick	Thin	Thick	Thick	Thin	Thin
Flesh Texture	Soft	Soft	Soft	Soft	Soft	Soft	Soft	Soft	Soft
Flesh Aroma	Absent	Foxy odor	Absent	Absent	Absent	Absent	Absent	Absent	Absent
Juice Color	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent
Flesh Color	Absent	Absent or very light	Absent	Absent	Absent or very light	Absent	Absent	Absent or very light	Absent
Seed Development	Fully developed	Fully developed	Fully developed	Fully developed	Fully developed	Fully developed	Fully developed	Fully developed	Fully developed

3.1.2. Quantitative Agronomic Traits

Significant regional differences were observed in quantitative agronomic traits among the same cultivar grown in different regions ($p < 0.05$; Table 2). Grapes cultivated in Gansu exhibited significantly heavier cluster weights compared with those from Xinjiang and Zhangjiakou. Among all samples, Cabernet Franc grown in Gansu achieved the highest cluster weight, with an average value of 603.22 g. In contrast, berries from Xinjiang were the smallest; for instance, the average berry weight of Marselan was only 0.88 g. Grapes harvested from Zhangjiakou showed higher juice yield. Both Cabernet Franc and Cabernet Sauvignon from Zhangjiakou presented juice yields exceeding 68%, among which Cabernet Franc reached the highest value of 72%. Seeds of Marselan from Gansu displayed the maximum seed length (6.8 mm), whereas seeds of Cabernet Sauvignon from Zhangjiakou had the largest seed width (0.40 mm).

Table 2. Quantitative agronomic traits of three wine grape cultivars (mean $\pm$ SD, $n = 3$).

Sample	Average Cluster Weight (g)	Average Berry Weight (g)	Juice Yield (%)	Seed Length (mm)	Seed Width (mm)
XJ-M	135.56 $\pm$ 6.78 b	0.88 $\pm$ 0.04 d	54 $\pm$ 2 c	6.1 $\pm$ 0.3 b	0.39 $\pm$ 0.02 b
GS-M	547.16 $\pm$ 22.35 a	1.17 $\pm$ 0.05 c	56 $\pm$ 2 c	6.8 $\pm$ 0.3 a	0.41 $\pm$ 0.02 a
ZJK-M	188.00 $\pm$ 9.42 b	1.44 $\pm$ 0.06 b	59 $\pm$ 2 b	5.5 $\pm$ 0.2 c	0.37 $\pm$ 0.02 c
XJ-CF	177.54 $\pm$ 8.91 b	1.11 $\pm$ 0.05 c	56 $\pm$ 2 c	5.8 $\pm$ 0.2 b	0.37 $\pm$ 0.02 c
GS-CF	603.22 $\pm$ 24.16 a	1.74 $\pm$ 0.08 a	62 $\pm$ 3 b	6.0 $\pm$ 0.3 b	0.32 $\pm$ 0.01 d
ZJK-CF	224.52 $\pm$ 11.23 b	1.54 $\pm$ 0.07 b	72 $\pm$ 3 a	5.2 $\pm$ 0.2 d	0.36 $\pm$ 0.02 c
XJ-CS	101.11 $\pm$ 5.05 c	0.96 $\pm$ 0.04 d	53 $\pm$ 2 c	6.7 $\pm$ 0.3 a	0.39 $\pm$ 0.02 b
GS-CS	470.23 $\pm$ 18.81 a	1.93 $\pm$ 0.09 a	68 $\pm$ 3 a	5.7 $\pm$ 0.2 c	0.33 $\pm$ 0.01 d
ZJK-CS	205.52 $\pm$ 10.31 b	1.67 $\pm$ 0.08 b	68 $\pm$ 3 a	5.7 $\pm$ 0.2 c	0.40 $\pm$ 0.02 a

Note: Different lowercase letters indicate significant differences between samples ($p < 0.05$). The same below.

3.1.3. Meteorological Conditions

The three producing regions showed distinct meteorological characteristics during the 2024 growing season (Table 3). Xinjiang had the highest average temperature, accumulated temperature, sunshine duration, and wind speed, but the lowest precipitation. Zhangjiakou had the lowest average temperature and accumulated temperature, but the highest precipitation. Gansu showed intermediate meteorological conditions between Xinjiang and Zhangjiakou.

Table 3. Main meteorological indicators of the three producing regions during the 2024 growing season (April–October).

Producing Region	Average Temperature (°C)	Accumulated Temperature ≥ 10 °C (°C)	Growing Season Precipitation (mm)	Growing Season Sunshine Duration (h)	Average Wind Speed (m·s ^{−1})
Turpan, Xinjiang	22.6	4520	16.4	3210	2.8
Hexi Corridor, Gansu	16.8	4010	158.2	3050	2.5
Zhangjiakou, Hebei	12.5	3680	420.5	2780	1.6

Note: Data were obtained from the China Meteorological Data Network.

3.2. Differences in Physicochemical Quality

Significant regional differences in physicochemical quality were observed among the same cultivar grown in different regions ($p < 0.05$; Table 4). Grapes cultivated in Xinjiang displayed significantly higher SSC than those from Gansu and Zhangjiakou. Specifically, Cabernet Franc from Xinjiang showed the highest SSC value of 27.2 °Brix. In comparison, grapes harvested in Gansu exhibited the highest TA, ranging from 7.50 to 12.75 g·L^{−1}, with corresponding pH values ranging from 3.40 to 3.61. Marselan from Gansu showed the highest TA and the lowest pH, while Cabernet Franc and Cabernet Sauvignon from Gansu had moderate acidity levels. Xinjiang-grown cultivars had sugar–acid ratios close to or slightly above the widely accepted optimal range of 5–7 for red winemaking, among which Cabernet Franc from Xinjiang had the highest ratio (8.05). By contrast, Marselan from Gansu showed the lowest ratio (1.65) due to its high acidity.

Table 4. Physicochemical quality of three wine grape cultivars (mean ± SD, n = 3).

Sample	SSC (°Brix)	TA (g·L ^{−1})	pH	Sugar–Acid Ratio
XJ-M	26.3 ± 0.4 a	3.68 ± 0.15 d	3.80 ± 0.05 a	7.15
GS-M	21.1 ± 0.3 c	9.75 ± 0.39 b	3.40 ± 0.04 cd	1.65
ZJK-M	22.3 ± 0.4 b	9.75 ± 0.39 b	2.96 ± 0.03 e	2.29
XJ-CF	27.2 ± 0.5 a	3.38 ± 0.13 d	3.90 ± 0.05 a	8.05
GS-CF	20.3 ± 0.3 d	7.50 ± 0.30 c	3.59 ± 0.04 bc	2.71
ZJK-CF	22.4 ± 0.4 b	8.25 ± 0.33 bc	3.36 ± 0.04 d	2.72
XJ-CS	26.7 ± 0.4 a	4.20 ± 0.17 d	3.80 ± 0.05 a	6.36
GS-CS	21.2 ± 0.3 c	7.50 ± 0.30 c	3.61 ± 0.06 b	2.83
ZJK-CS	22.2 ± 0.3 b	9.75 ± 0.39 b	3.16 ± 0.03 de	2.28

Note: Different lowercase letters in the same column indicate significant differences at $p < 0.05$ by Duncan’s multiple range test. The sugar–acid ratio was calculated from the mean SSC and the mean TA, without standard deviation. Abbreviations: XJ, Turpan, Xinjiang; GS, Hexi Corridor, Gansu; ZJK, Huailai, Zhangjiakou; M, Marselan; CF, Cabernet Franc; CS, Cabernet Sauvignon.

3.3. Differences in Phenolic Compound Contents

3.3.1. Total Phenolics and Tannins

Total phenolic and tannin contents followed a descending order: Gansu > Zhangjiakou > Xinjiang (Figures 1 and 2). Cabernet Sauvignon in Gansu had the highest skin total phenolic content (32.84 mg GAE·g^{−1} FW) and seed total phenolic content (20.15 mg GAE·g^{−1}

FW), which were 3.41 and 4.86 times those of Cabernet Franc in Xinjiang, respectively ($p < 0.05$, $n = 3$).

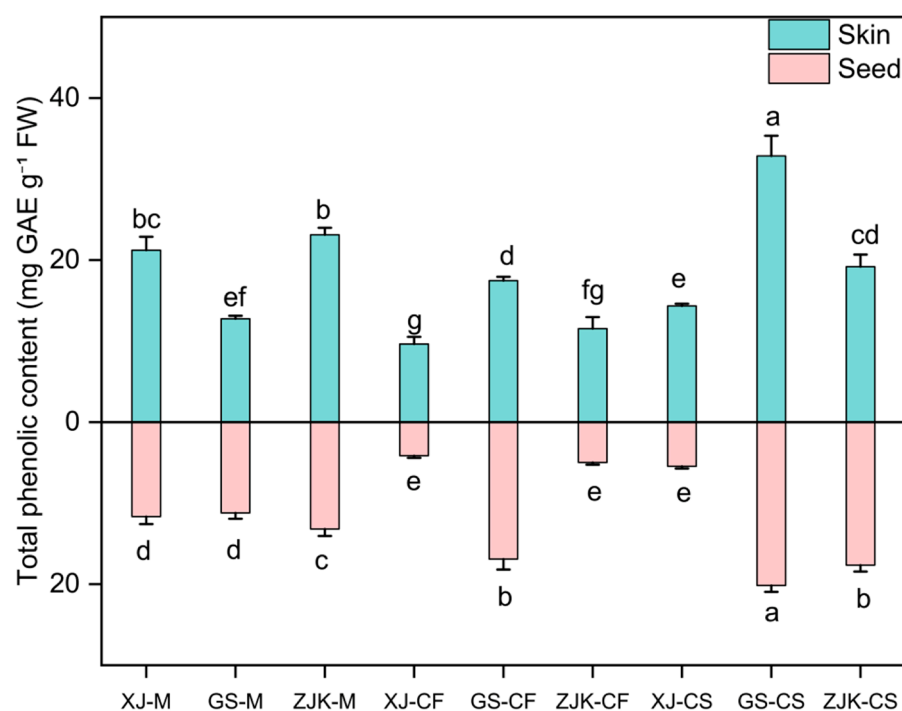


Figure 1. Total phenolic contents in skins and seeds of three wine grape cultivars from different producing regions. Note: Different lowercase letters indicate significant differences between different samples of the same tissue ($p < 0.05$).

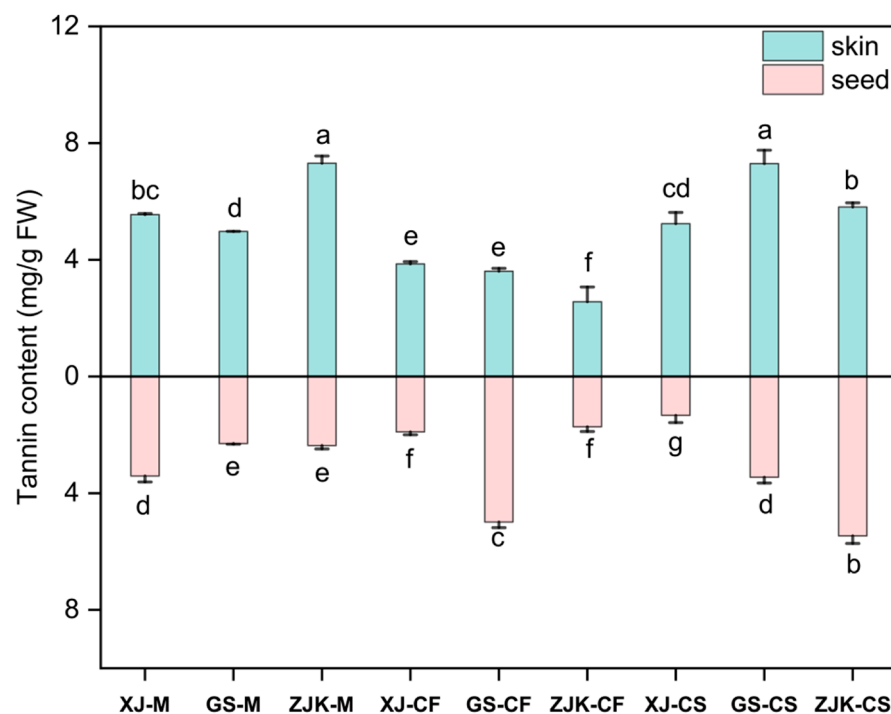


Figure 2. Tannin contents in skins and seeds of three wine grape cultivars from different producing regions. Note: Different lowercase letters indicate significant differences between different samples of the same tissue ($p < 0.05$).

The tannin content trend mirrored that of total phenolics (Figure 2). Marselan from Zhangjiakou had the highest skin tannin content ($7.31 \text{ mg TAE} \cdot \text{g}^{-1} \text{ FW}$), while Cabernet

Sauvignon from the same region exhibited the highest seed tannin content ($5.47 \text{ mg TAE} \cdot \text{g}^{-1} \text{ FW}$) ($p < 0.05$, $n = 3$). On a fresh weight basis, tannin concentrations were consistently higher in skins than in seeds across all samples, with a mean skin-to-seed ratio of 2.1.

3.3.2. Proanthocyanidins and Anthocyanins

Marselan exhibited a notable genotypic advantage in proanthocyanidin biosynthesis (Figure 3). Its skin proanthocyanidin levels were significantly higher than those of Cabernet Franc across all three sites, and significantly higher than Cabernet Sauvignon at the Zhangjiakou and Xinjiang sites ($p < 0.05$). Within each region, Marselan's skin proanthocyanidin content was 12.5–29.1% higher than Cabernet Sauvignon and 189.7–230.5% higher than Cabernet Franc. Zhangjiakou's Marselan had the highest skin proanthocyanidin content ($12.26 \text{ mg} \cdot \text{g}^{-1} \text{ FW}$), while Xinjiang's Cabernet Franc had the lowest ($2.81 \text{ mg} \cdot \text{g}^{-1} \text{ FW}$).

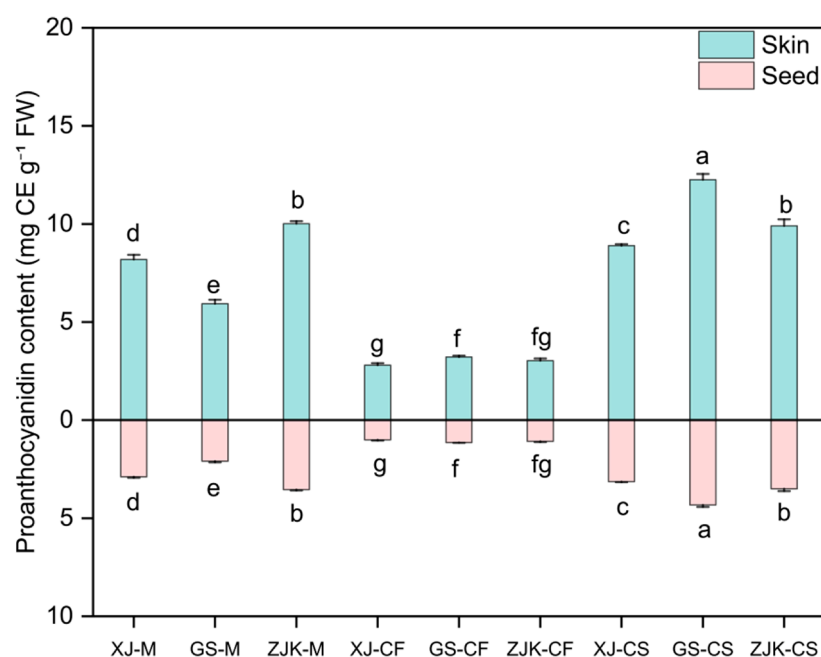


Figure 3. Proanthocyanidin contents in skins and seeds of three wine grape cultivars from different producing regions. Note: Different lowercase letters indicate significant differences between different samples of the same tissue ($p < 0.05$).

Across all samples, proanthocyanidin concentrations were consistently higher in skins than in seeds, with skin-to-seed ratios ranging from 2.3 to 9.9, suggesting that skins are the primary site of proanthocyanidin accumulation in these cultivars.

Anthocyanins were only detected in grape skins, and showed the most significant regional differences among all phenolic compounds (Figure 4). The highest skin anthocyanin level reached $12.26 \text{ mg C3GE} \cdot 100 \text{ g}^{-1} \text{ FW}$ in Marselan grapes from Zhangjiakou, while Cabernet Franc from Xinjiang had the lowest value ($1.42 \text{ mg C3GE} \cdot 100 \text{ g}^{-1} \text{ FW}$), representing an 8.47-fold difference between regions. The regional trend for anthocyanins was: Zhangjiakou > Gansu > Xinjiang.

3.3.3. Flavonoids and Tissue Specificity

Flavonoid levels followed the same pattern as total phenolics (Figure 5). Cabernet Sauvignon seeds from Gansu had the highest flavonoid content ($9.45 \text{ mg RE} \cdot \text{g}^{-1} \text{ FW}$), while Cabernet Franc seeds from Zhangjiakou had the lowest ($0.29 \text{ mg RE} \cdot \text{g}^{-1} \text{ FW}$).

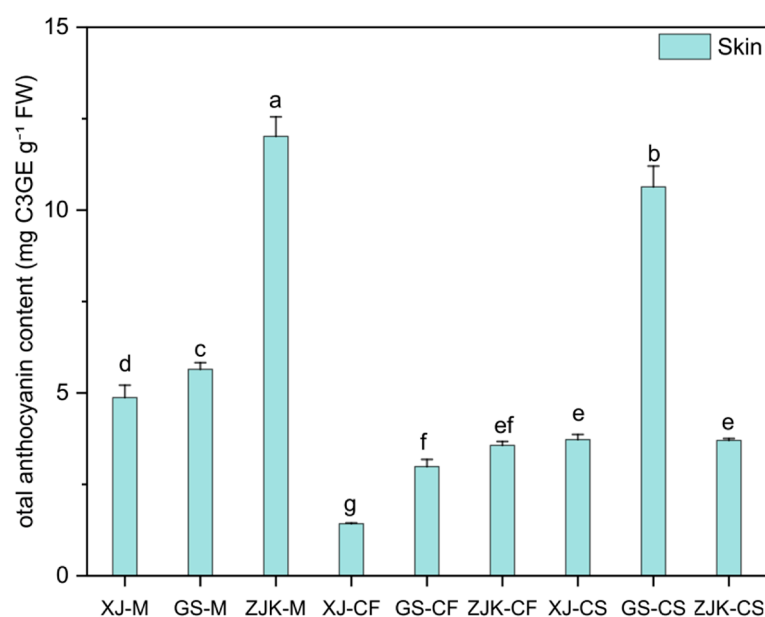


Figure 4. Anthocyanin contents in skins of three wine grape cultivars from different producing regions (mg C3GE·100 g⁻¹ FW). Note: Anthocyanins were only detected in grape skins, not in seeds. Different lowercase letters indicate significant differences between different samples of the same tissue ($p < 0.05$).

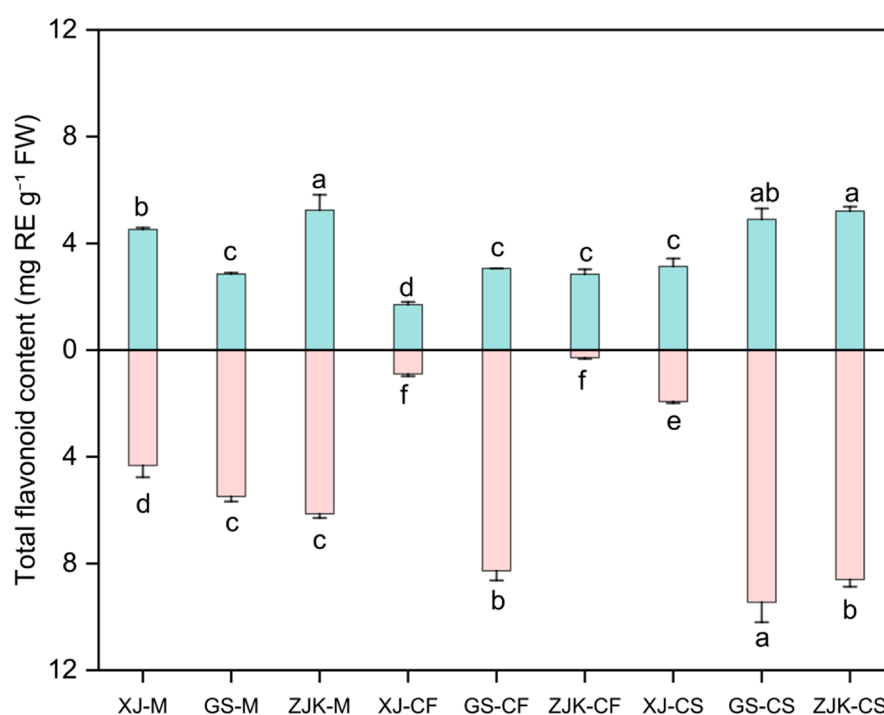


Figure 5. Total flavonoid contents in skins and seeds of three wine grape cultivars from different producing regions (mg RE·g⁻¹ FW). Note: Different lowercase letters indicate significant differences between different samples of the same tissue ($p < 0.05$).

Significant tissue specificity was observed in the phenolic compositions of grape seeds and skins (Table 5). Proanthocyanidins showed the highest tissue specificity, with skin/seed ratios ranging from 2.3 to 9.9. Anthocyanins were exclusively distributed in the skin, making them the most distinctive marker for tissue differentiation. On a fresh weight basis, total phenolics, proanthocyanidins, and anthocyanins were mainly concentrated in berry skins. Flavonoids showed a similar distribution between the two tissues.

Table 5. Tissue-specific differences in phenolic composition between seeds and skins (mean $\pm$ SD, n = 9).

Phenolic Indices	Content Range in Skin	Content Range in Seed	Skin/Seed Ratio
Total phenolics	9.64–32.84 mg GAE·g ^{−1} FW	4.15–20.15 mg GAE·g ^{−1} FW	1.7 $\pm$ 0.3
Tannins	2.56–7.31 mg TAE·g ^{−1} FW	1.33–5.47 mg TAE·g ^{−1} FW	2.1 $\pm$ 0.5
Proanthocyanidins	2.81–12.26 mg g ^{−1} FW	1.00–4.33 mg g ^{−1} FW	4.2 $\pm$ 1.8
Total flavonoids	1.71–5.25 mg RE·g ^{−1} FW	0.29–9.45 mg RE·g ^{−1} FW	2.8 $\pm$ 1.2
Anthocyanins	1.42–12.26 mg C3GE·100 g ^{−1} FW	–	–

3.4. Variance Decomposition and Multivariate Analysis

3.4.1. Variance Component Analysis

Variance decomposition based on the two-way GLM (Type III sums of squares) showed that production site was the dominant source of variation in wine grape quality (Table 6). Variance contribution rates were calculated as the ratio of each factor's sum of squares to the total sum of squares, and all main effects and interaction effects were statistically significant ($p < 0.05$). Production site explained 65.7–82.1% of the total variation in most quality traits, with the highest contribution to average cluster weight (82.1%) and anthocyanin content (75.4%). Genotype contributed 7.2–14.2% of the variation, with the highest contribution to flavonoid content (14.2%). The interaction between site and cultivar accounted for 8.5–16.1% of the variation.

Table 6. Variance component contributions of production site, cultivar, and their interaction to main quality indicators (%).

Quality Indices	Production Site	Cultivar	Site $\times$ Cultivar Interaction	Error
Total phenolics	68.2	12.5	15.3	4.0
Tannin	71.4	10.8	13.7	4.1
Proanthocyanidin	73.6	9.7	12.9	3.8
Anthocyanin	75.4	8.3	12.5	3.8
Flavonoid	65.7	14.2	16.1	4.0
Average cluster weight	82.1	7.2	8.5	2.2
SSC	79.3	8.5	9.2	3.0
TA	76.8	9.1	11.3	2.8

Variance contribution rates were calculated as the ratio of Type III sum of squares of each factor to the total sum of squares.

Phenolic compounds showed a clear gradient of sensitivity to ecological factors, following the order: anthocyanins (75.4%) > proanthocyanidins (73.6%) > tannins (71.4%) > total phenolics (68.2%) > flavonoids (65.7%).

3.4.2. Principal Component Analysis

Principal component analysis was performed on 14 quality indicators from 27 biological replicates. The first two principal components explained 66.2% of the total variation (PC1: 40.1%, PC2: 26.1%), which was sufficient to represent the overall quality differences between samples (Figure 6).

PC1 was mainly positively correlated with phenolic compounds (anthocyanins, proanthocyanidins, total phenolics, and tannins) and TA, and negatively correlated with SSC, sugar–acid ratio, and pH. It represented the trade-off between sugar accumulation and phenolic biosynthesis. PC2 was mainly positively correlated with average berry weight and phenolic compounds, and negatively correlated with average cluster weight and juice yield. It reflected the trade-off between yield and berry size, which is a common phenomenon in vineyard production systems [23]. The score plot showed clear regional clustering: all Xinjiang cultivars clustered on the negative side of PC1, characterized by high sugar and

low acid; all Gansu cultivars clustered in the lower right quadrant, characterized by high yield and high total phenolics; and all Zhangjiakou cultivars clustered in the upper right quadrant, characterized by high anthocyanins and proanthocyanidins. This indicated that the production site was the main source of sample separation in this exploratory analysis.

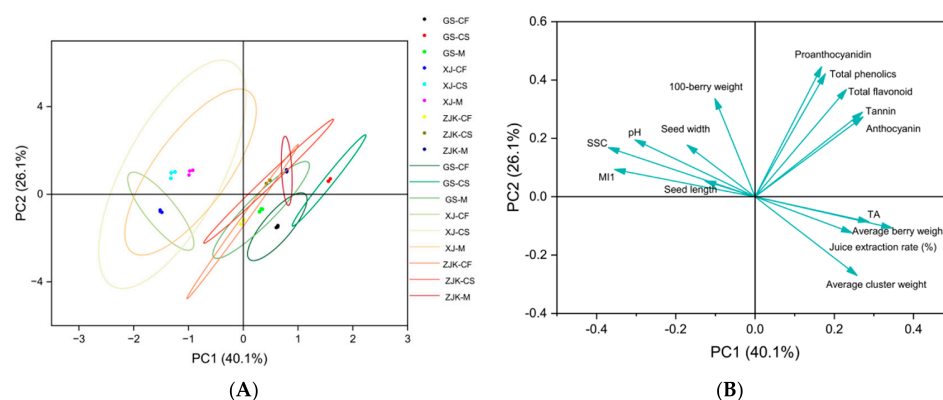
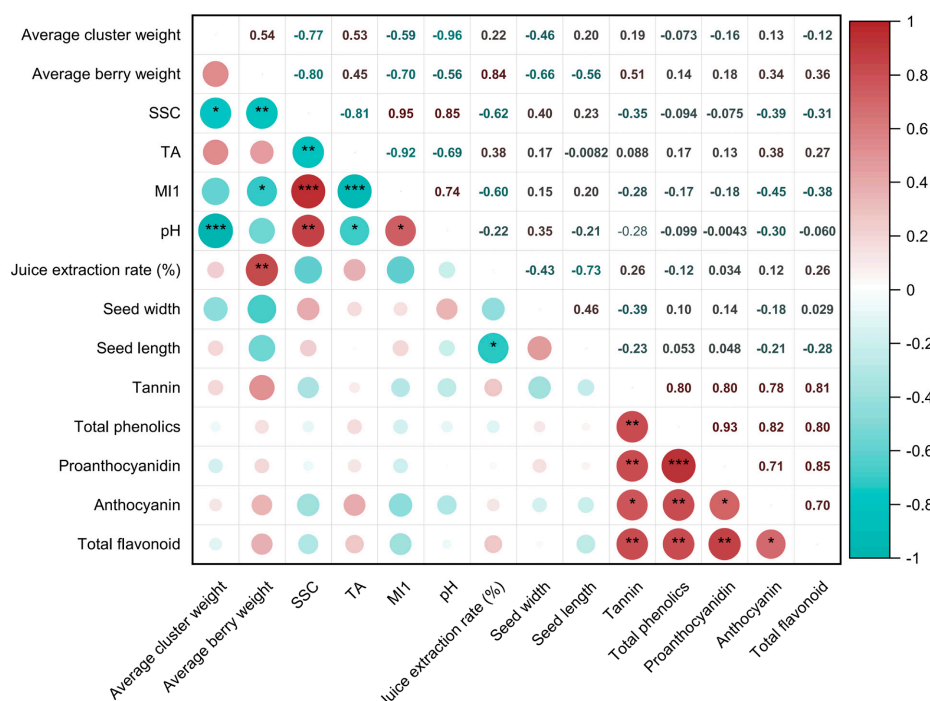


Figure 6. Principal component analysis of grape quality indicators. (A) Score plot with 95% confidence ellipses for each cultivar; (B) Loading plot showing the contribution of each quality indicator to the first two principal components. Abbreviations: SSC, soluble solids content; TA, titratable acidity; MI, sugar–acid ratio. Note: 95% confidence ellipses are for exploratory visualization only and should be interpreted with caution due to the limited number of replicates per group.

3.4.3. Correlation Analysis

Pearson correlation analysis revealed significant relationships between different quality indicators (Figure 7). Extremely strong positive correlations were observed among phenolic compounds: total phenolics vs. tannins ($r = 0.93$, $p < 0.001$), proanthocyanidins vs. anthocyanins ($r = 0.85$, $p < 0.001$), and total phenolics vs. proanthocyanidins ($r = 0.82$, $p < 0.001$), indicating coordinated accumulation of phenolic compounds in grape skins.



* $p < 0.05$ ** $p < 0.01$ *** $p < 0.001$

Figure 7. Pearson correlation heatmap of grape quality indicators. Red indicates positive correlation; blue indicates negative correlation. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

SSC was positively correlated with the sugar–acid ratio ($r = 0.95$, $p < 0.001$) and pH ($r = 0.85$, $p < 0.001$), but negatively correlated with all phenolic compounds. Average cluster weight was positively correlated with juice yield ($r = 0.73$, $p < 0.001$) and total phenolics ($r = 0.20$), but negatively correlated with anthocyanins ($r = -0.12$) and proanthocyanidins ($r = -0.16$), indicating a weak negative association between cluster weight and late-accumulating phenolics, which requires further validation by controlled yield trials.

4. Discussion

4.1. Differential Regulation of Grape Quality by Ecological Factors

Ecological factors regulate grape phenotypic traits and quality by modulating photosynthesis and secondary metabolism [24]. In the present study, grapes from Gansu exhibited the highest average cluster weight and total phenolic content. This could be attributed to the moderate accumulated temperature ($\approx 4000\text{ }^{\circ}\text{C} \geq 10\text{ }^{\circ}\text{C}$) and long growing season, which prolonged fruit development and phenolic accumulation. The large diurnal temperature range has been reported to upregulate phenylalanine ammonia-lyase (PAL) activity and promote phenolic biosynthesis in grape berries, which may partly explain the high phenolic levels observed in Gansu [25,26].

The higher SSC and total sugar content in Xinjiang are attributed to the large diurnal temperature range of $15\text{--}20\text{ }^{\circ}\text{C}$: abundant sunlight during the day promotes sugar synthesis, while low night temperatures greatly reduce respiratory consumption, which is conducive to sugar accumulation in berries. Although Xinjiang had the longest sunshine duration and strongest UV-B radiation, its total phenolic content was lower than that of Gansu because of the higher growing season temperature, which led to fruit maturation 10–15 days earlier than in Gansu and thus a relatively shorter accumulation time of phenolic substances.

The higher anthocyanin accumulation in Zhangjiakou may be attributed to moderate UV-B radiation and an appropriate diurnal temperature range, which is consistent with the report by He et al. [11] that UV radiation intensity was significantly and positively correlated with anthocyanin biosynthesis in grape skins. Significant gradient differences were observed in the sensitivity of different phenolic compounds to ecological factors, specifically anthocyanins > proanthocyanidins > tannins > total phenolics. This gradient could be explained by the differential sensitivity of phenolic pathways to climatic conditions. As reported in previous studies, the anthocyanin biosynthesis pathway contains multiple UV-B response elements [27], which may underlie its stronger responsiveness. In contrast, the synthesis of tannins and total phenolics mainly occurs in the early stage of fruit development and is relatively less affected by late UV-B radiation [28].

The pH values of Gansu grapes (3.40–3.61) fall within the generally accepted optimal pH range (3.3–3.7) for red winemaking, which may contribute to wine microbial stability and sensory balance. It should be noted that samples were harvested at commercial maturity with variable SSC levels. Since phenolic accumulation progresses with berry ripening, differences in ripening stage may contribute to part of the observed site variation. This confounding effect cannot be fully separated in the current dataset.

4.2. Tissue-Specific Yield Dilution Effect

Although only a weak negative association between cluster weight and late-accumulating phenolics was observed in this dataset, the tissue-specific pattern of yield dilution has been widely documented in previous studies. This pattern is driven by the asynchronous synthesis periods of different phenolic components: total phenolics and tannins are mainly synthesized in the early stage of fruit development (before veraison), when yield formation is not yet finalized; in contrast, anthocyanins and proanthocyanidins are mainly accumulated after veraison, when yield is already determined, so higher

cluster weight may dilute the concentration of these late-synthesized compounds. From a metabolic perspective, increased yield essentially reduces the carbon supply per berry and induces a carbon limitation state. An integrated metabolomics and enzyme activity study on Cabernet Sauvignon confirmed that grape berries have strong plasticity in central carbon metabolism under carbon limitation: they prioritize maintaining basic sugar metabolism and early-formed structural substances, while carbon flux allocated to late-stage secondary metabolism such as anthocyanin synthesis is significantly reduced [29]. This metabolic priority allocation mechanism, combined with the asynchrony of synthesis periods, jointly drives the tissue-specific yield dilution pattern of different phenolic components.

This result has important guiding significance for cultivation management. For varieties and regions aiming to produce high-anthocyanin wines (such as Marselan in Zhangjiakou), appropriate cluster thinning may be considered to reduce crop load and potentially improve anthocyanin accumulation. In addition, regulated deficit irrigation can be applied at the veraison stage to moderately induce drought stress, which promotes anthocyanin accumulation through the ABA-miR156b-VvSBP regulatory pathway [30], so as to further enhance the phenolic quality of berries on the basis of regional ecological advantages. For varieties and regions aiming to produce high-tannin wines (such as Cabernet Sauvignon in Gansu), moderate high yield can be maintained without significantly reducing tannin content [31]. The haplotype-specific expression patterns of phenolic synthesis genes found in Malbec genome research also provide a possible genetic explanation for this tissue-specific and development-stage-specific accumulation pattern [32], which is worthy of in-depth verification through transcriptomic analysis in subsequent studies.

4.3. Genotypic Effects on Phenolic Composition

Genotype is an important factor shaping the phenolic composition of grape berries. Different cultivars vary considerably in phenolic biosynthesis capacity and component profiles [33]. In this study, Marselan exhibited a distinct advantage in proanthocyanidin accumulation, which was consistent with previous findings reported by Li et al. As a hybrid of Cabernet Sauvignon and Grenache, Marselan inherits favorable traits from both parents. This advantage is closely related to the regulatory characteristics of key transcription factors such as VvMYBPA1 in the proanthocyanidin biosynthesis pathway of Marselan, as well as its consistently high phenylalanine ammonia-lyase (PAL) activity inherited from Cabernet Sauvignon, which has been widely reported in previous studies [34]. Due to these genetic advantages, Marselan maintains stable and efficient proanthocyanidin biosynthesis under diverse environmental conditions. Cabernet Sauvignon showed strong adaptability to Gansu's climate, with the highest total phenolic and tannin contents among all varieties in this region. This is attributed to its robust secondary metabolism and strong stress resistance. Cabernet Franc yields grapes with the most balanced sugar–acid ratio in Xinjiang, which confirms its excellent climatic adaptability in high-heat and high-light production areas.

4.4. Preliminary Cultivar–Site Matching Recommendations

Based on the comprehensive quality evaluation, preliminary cultivar–site matching suggestions are proposed for reference:

At the Turpan site in Xinjiang, Cabernet Franc showed the most balanced sugar–acid ratio among the three cultivars in 2024, making it a promising candidate for further evaluation. It maintains well-balanced sugar and acid levels and favorable flavor coordination under the local high-temperature and strong-light conditions.

At the Hexi Corridor site in Gansu, Cabernet Sauvignon achieved the highest phenolic content and yield among the tested cultivars, showing good application potential.

It achieves a favorable balance among high yield, abundant phenolic compounds and moderate acidity. At the Huailai site in Zhangjiakou, Marselan exhibited the highest proanthocyanidin and anthocyanin contents, which is worthy of further validation in multi-year trials. Its genetic advantage in proanthocyanidin biosynthesis can be fully exploited under the local moderate temperature and UV conditions, yielding grapes with excellent phenolic quality.

4.5. Study Limitations

This study has several limitations. First, all data were collected from a single growing season (2024) and one representative vineyard per site, so the observed differences cannot be generalized to broader ecological regions, and vintage and site-specific effects cannot be fully separated. Second, samples were harvested at commercial maturity with variable SSC levels, and ripening stage may confound phenolic accumulation. Third, detailed soil properties, precise irrigation volumes, and UV radiation data were not systematically monitored, limiting mechanistic interpretation. Finally, only total phenolic groups were quantified, and individual phenolic profiles were not characterized. Long-term multi-site trials with standardized harvest maturity will be conducted to verify these findings.

5. Conclusions

This study systematically investigated the quality characteristics of three major red wine grape cultivars across three typical producing regions in northern China.

First, production site was identified as the main source of quality variation in this dataset, accounting for 65.7% to 82.1% of the total variation across most quality traits, and three distinct site-specific quality patterns were clearly distinguished: grapes from Xinjiang were characterized by high sugar accumulation, those from Gansu by abundant total phenolics, and those from Zhangjiakou by high anthocyanin content.

Second, individual phenolic components differed markedly in their responsiveness to ecological conditions, forming a clear sensitivity gradient from anthocyanins (highest) to flavonoids (lowest), with proanthocyanidins, tannins and total phenolics falling in between.

Third, Marselan exhibited a notable genotypic advantage in proanthocyanidin biosynthesis, and this trait remained stable across all three growing environments tested in this study.

Fourth, a weak tissue-specific association between cluster weight and phenolic components was preliminarily observed: higher cluster weight was associated with lower concentrations of late-synthesized anthocyanins and proanthocyanidins, but showed little negative effect on early-formed total phenolics and tannins.

Finally, preliminary suggestions for cultivar–site matching were provided based on the comprehensive quality evaluation, which can provide reference for the scientific layout of wine grape production in northern China.

Long-term multi-location trials will be carried out to verify the stability of these findings, and the effects of soil properties and cultivation measures on grape phenolic composition will be further explored to optimize the matching scheme in future work.

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