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Evaluation of Selenium Enrichment Capacity and Screening of Selenium-Rich Varieties in 77 Sweetpotato Germplasm Resources

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Abstract

Selenium is a beneficial trace element for humans, animals, and plants, and adequate intake contributes to health, growth, and development. Selenium accumulation in sweet potato varies among genotypes. In this study, 77 sweet potato germplasm resources were planted in the Wuming natural selenium-rich soil region and the Mingyang low-selenium soil region. The differences and correlations in major agronomic traits, quality traits, and tuber selenium content between the two regions were analyzed, and natural selenium-enriched germplasm were screened. The results showed that yield, vine length, branch number, and fresh vine and leaf weight per plant in the Mingyang low-selenium region were higher than those in the Wuming selenium-rich region, while storage root number per plant was similar between the two sites. Dry matter rate and total flavonoid content in Wuming were higher than those in Mingyang. Tuber selenium content in Wuming ranged from 0.034 to 0.319 mg/kg DW, with a mean of 0.070 mg/kg; in Mingyang, it ranged from 0.025 to 0.068 mg/kg DW, with a mean of 0.040 mg/kg. Zhenghong 163, Longzi 9, and Guangzishu 9 exhibited the highest selenium enrichment multiples and were identified as the optimal selenium-enriched candidate varieties. Principal component analysis and cluster analysis further revealed the structural differences in trait variation between the two regions and the significant influence of soil selenium level on germplasm classification. This study provides core germplasm resources for selenium-enriched sweet potato breeding and industrial development.

1. Introduction

Selenium (Se) is an essential trace element for humans. It participates in the synthesis of 25 selenoproteins, including glutathione peroxidase and thioredoxin reductase, and plays critical roles in development and immune responses[1, 2].Se is considered a special micronutrient, with a recommended daily intake of 50–60 μg[3].Unfortunately, many regions suffer from insufficient soil selenium levels, which fail to produce crops that meet the recommended daily intake. Selenium deficiency has been linked to health issues such as epilepsy, liver cirrhosis, and immune dysfunction[4].Dietary selenium intake largely depends on the total concentration and bioavailability of selenium in food sources, highlighting the importance of research on plants[5].

Sweet potato (*Ipomoea batatas L.*) is an annual or perennial trailing herbaceous plant of the Convolvulaceae family, characterized by high and stable yield and rich nutritional value[6, 7].It is widely cultivated in more than 100 countries worldwide, particularly in tropical and subtropical regions of Asia and Africa. Asia contributes over 90 million tons to global annual production, with China as the largest producer, making sweet potato one of the most important, versatile, and underutilized food crops in the world[8].Sweet potato storage roots are rich in starch, dietary fiber, vitamins, and minerals. Orange-fleshed varieties are particularly high in β-carotene, while purple-fleshed varieties are rich in anthocyanins[9].Sweet potato also contains abundant phenolic compounds and dietary fiber, exhibiting high antioxidant activity, and is considered to have potential in improving micronutrient deficiencies and regulating intestinal function[10, 11].Additionally, sweet potato is rich in mineral elements such as iron and zinc[12], Notably, sweet potato has a certain capacity for selenium bioaccumulation, converting inorganic selenium into organic forms and storing them in storage roots[13], which makes sweet potato a high-quality dietary source for natural selenium supplementation.

However, significant differences in selenium enrichment capacity exist among sweet potato varieties, and there is currently a lack of systematic evaluation of selenium enrichment capacity in germplasm resources. Therefore, this study comprehensively evaluated the selenium enrichment capacity of 77 sweet potato germplasm resources, aiming to screen natural selenium-enriched varieties and provide a theoretical basis for germplasm innovation, development, and utilization of selenium-enriched sweet potato.

2. Materials and Methods

2.1 Plant Materials

A total of 77 sweet potato germplasm resources were provided by the Maize Research Institute, Guangxi Academy of Agricultural Sciences. The field experiments were conducted in 2023 and 2024 at two sites: Ganwei Town, Wuming District, Nanning City, Guangxi (soil pH = 4.8, organic matter content = 21.40 g/kg, total selenium content = 0.78 mg/kg) and the Mingyang Base of Guangxi Academy of Agricultural Sciences (soil pH = 6.38, organic matter content = 19.40 g/kg, total selenium content = 0.30 mg/kg). According to the Guangxi local standard DB45/T 2578—2022 "Identification and Classification of Natural Selenium-Rich Agricultural Products", the Wuming site was designated as a natural selenium-rich soil region, and the Mingyang site as a low-selenium soil region. At each site, 10 plants per genotype were planted with three replicates, and field management followed standard agricultural practices. The details of the 77 sweet potato germplasm resources are listed in Table S1.

2.2 Measurement Items

2.2.1 Agronomic Traits

The 77 sweet potato germplasm resources were grown in both the Wuming natural selenium-rich soil region and the Mingyang low-selenium soil region. At harvest, agronomic traits including vine length, stem diameter, branch number, storage root number per plant, and fresh storage root weight per plant were measured.

2.2.2 Quality Traits

At harvest, fresh storage roots of the 77 germplasm resources were collected. Part of the fresh root samples were cut into pieces, sealed in tubes, treated with liquid nitrogen, and stored at − 80°C for subsequent analyses. The remaining root samples were cut into strips, oven-dried at 105°C for 30 min for enzyme deactivation, and then dried at 80°C to constant weight. The dried samples were ground and used to calculate dry matter rate. The ground samples were passed through a 0.2 mm sieve and stored in sealed bags.

All quality trait assays were performed using commercial kits (Suzhou Grace Biotechnology Co., Ltd., China). Soluble sugar content was determined by the anthrone method, reducing sugar content by the dinitrosalicylic acid (DNS) method, total phenolic content by the Folin–Ciocalteu method, total flavonoid content by the $NaNO_2$–$Al(NO_3)_3$–NaOH colorimetric method, crude starch content by the acid hydrolysis method, and crude protein content by the BCA method.

2.2.3 Selenium Content Determination

Selenium content in sweet potato was determined using atomic fluorescence spectrometry according to the national standard GB 5009.93—2017 "National Food Safety Standard – Determination of Selenium in Foods". The detailed procedure was as follows:

(1) **Sample pretreatment**. Leaves, stems, and storage roots of sweet potato were washed with purified water, surface-dried, cut into strips, oven-dried at 105°C for 30 min for enzyme deactivation, and then dried at 80°C to constant weight. The dried samples were ground, sealed in bags, and stored for analysis.

(2) **Microwave digestion**. An aliquot of 0.30 g of dried sweet potato powder was weighed into a clean digestion tube, and 5.0 mL of nitric acid was added. After mixing, the tube was placed in a microwave digestion system for digestion. Two blank controls (digestion tubes containing 5.0 mL nitric acid only) were prepared simultaneously. The digestion was carried out at 120°C for 30 min. After cooling, 1.0 mL of hydrogen peroxide was added, and the tubes were capped and placed in a Mars6 microwave digestion system using program 109-40Jh. After digestion, the tubes were removed and cooled in a fume hood. Then, 2.5 mL of 50% hydrochloric acid was added, and the tubes were heated at 150°C for 40 min, followed by 180°C for approximately 20 min, until the remaining liquid volume was reduced to 1.0–2.0 mL. After cooling to room temperature, the solution was transferred to a 10 mL glass tube, mixed with 2.5 mL of potassium ferricyanide solution, and diluted to the mark with 5% HCl. The resulting solution was stored at low temperature for analysis.

(3) **Total selenium determination**. A dual-channel atomic fluorescence spectrometer was preheated for at least 30 min. Before sample measurement, the instrument was ignited and rinsed with purified water and carrier solution. Instrument conditions were set as follows: carrier gas flow rate = 400 mL/min, shield gas flow rate = 900 mL/min. Standard curves were established using selenium standard solutions at concentrations of 0, 10, 20, 40, 60, 80, and 100 μg/L. Blank solutions were measured first, followed by the standard solutions and then the sample solutions. After measurement, the instrument was thoroughly rinsed with purified water and turned off.

(4) **Calculation**.

$$X = \frac{(c - c_0) \times V}{W \times 1000} \times D$$

X= total selenium content in the sweet potato sample (mg/kg DW)

C= selenium concentration in the sample solution (μg/L)

C_0 = selenium concentration in the blank solution (μg/L)

V = volume of the sample solution (mL)

W= weight of the sweet potato sample (g)

D = dilution factor

3.3 Statistical Analysis

Statistical calculations, analysis of variance (ANOVA), and correlation analyses were performed using Microsoft Excel 2016, GraphPad Prism 8, and Origin 2024 software. Graphs were generated using GraphPad Prism 8 and TBtools-II. Independent-sample t-tests and one-way ANOVA were used to determine significant differences, with a significance threshold of $P < 0.05 P < 0.05$. All data are presented as mean ± standard deviation (SD).

3. Results

3.1 Agronomic Traits of Sweet Potato Under Different Soil Selenium Environments

For the 77 sweet potato germplasms planted in the Wuming selenium-rich and Mingyang low-selenium regions, seven agronomic traits (vine length, branch number, stem diameter, storage root number per plant, fresh vine weight per plant, fresh leaf weight per plant, and fresh storage root weight per plant) are presented in Fig. 1 and Tables S2.

In the Wuming high-selenium region, the coefficients of variation (CV) for the seven traits ranked as follows: stem diameter (15.48%), branch number (24.43%), storage root number per plant (33.54%), vine length (33.13%), fresh storage root weight per plant (48%), fresh vine weight per plant (70%), and fresh leaf weight per plant (75%). Vine length ranged from 36.00 to 174.25 cm, with a mean of 89.91 cm. Fresh storage root weight per plant ranged from 0.05 to 0.61 kg, with a mean of 0.25 kg.

In the Mingyang low-selenium region, the CVs for the seven traits ranked as follows: stem diameter (17.56%), vine length (30.77%), branch number (35.49%), storage root number per plant (36.74%), fresh storage root weight per plant (45.71%), fresh vine weight per plant (53.49%), and fresh leaf weight per plant (75%). Vine length ranged from 84.50 to 396.83 cm, with a mean of 217.39 cm. Fresh storage root weight per plant ranged from 0.16 to 1.47 kg, with a mean of 0.7kg.

3.2 Quality Traits of Sweet Potato Under Different Soil Selenium Environments

For the 77 sweet potato germplasms planted in the Wuming selenium-rich and Mingyang low-selenium regions, seven quality traits (dry matter rate, crude starch, reducing sugars, soluble sugars, crude protein, total flavonoids, and total phenolics) are presented in Fig. 2 and Tables S3.

In the Wuming high-selenium region, dry matter rate ranged from 18.2% to 36.53%, with a mean of 29.6%; crude starch ranged from 45.45% to 66.81% (mean = 55.71%); reducing sugars ranged from 2.86% to 17.52% (mean = 7.98%); soluble sugars ranged from 6.79% to19.28% (mean = 12.08%); crude protein ranged from 7.22% to 13.31% (mean = 9.39%); total flavonoids ranged from 1.04 to 26.31 mg/g DW (mean = 5.01 mg/g DW); and total phenolics ranged from 1.22 to 19.62 mg/g DW (mean = 3.78 mg/g DW).

In the Mingyang low-selenium region, dry matter rate ranged from 17.17% to 33.08%, with a mean of 25.72%; crude starch ranged from 38.88% to 64.41% (mean = 54.19%); reducing sugars ranged from 1.49% to 16.15% (mean = 6..96%); soluble sugars ranged from 4.03% to 17.03% (mean = 10.86%); crude protein ranged from 6.14% to 13.14% (mean =8.95%); total flavonoids ranged from 0.20 to 16.41 mg/g DW (mean = 3.34 mg/g DW); and total phenolics ranged from 1.32 to 14.63 mg/g DW (mean = 3.29 mg/g DW).

3.3 Principal Component Analysis of Sweet Potato Germplasm Resources

Principal component analysis (PCA) was performed on 14 traits of 77 sweet potato germplasm resources from two distinct regions. As shown in Figures 3A and 3B, the eigenvalues of the first five principal components were greater than 1.0 in the Wuming high-selenium region, while in the Mingyang low-selenium region, the eigenvalues of the first six principal components exceeded 1.0, indicating their statistical significance. The PCA biplot in Figure 3C revealed that in the Wuming region, PC1 and PC2 accounted for 20.2% and 18.2% of the total variance, respectively, with a cumulative contribution of 38.4%. Similarly, the biplot in Figure 3D showed that in the Mingyang region, PC1 and PC2 explained 22.5% and 18.5% of the variance, respectively, together accounting for 41.0% of the total variation. Both biplots simultaneously displayed sample scores and variable loadings, with a 95% confidence ellipse included.

After data standardization, principal components with eigenvalues greater than 1.0 were retained. As presented in Table 1, five principal components were extracted in the Wuming region, with a cumulative contribution rate of 70.7%, indicating that these components effectively captured the major information of the traits in sweet potato germplasm from this region. The third principal component had an eigenvalue of 2.0 and a cumulative contribution rate of 52.75%, with soluble sugar showing the highest loading. As shown in Table 2, six principal components were obtained in the Mingyang region, with a cumulative contribution rate of 79.42%, suggesting that these

components could adequately represent the primary trait information of the germplasm in this area. Notably, total flavonoids exhibited the highest loading on the third principal component in the Mingyang region.

Table 1 Principal component analysis of germplasm resources from the Wuming high-selenium region

traits	PC1	PC2	PC3	PC4	PC5
Vine length (cm)	-0.284031435	0.491381538	-0.38928479	0.152927887	-0.234863893
Number of branches	-0.505714844	0.34129632	-0.285086554	-0.302407699	0.121200234
Stem diameter (mm)	0.005076661	0.442306126	0.351551704	0.564061444	0.179226467
Number of tubers per plant	-0.30264266	0.292851712	-0.295338146	-0.310722828	0.719055197
Fresh vine weight per plant (kg)	-0.419210808	0.497613391	-0.203798878	0.271981295	-0.310304656
Fresh leaf weight per plant (kg)	-0.188008548	0.458023001	-0.084095817	0.52134646	-0.009037077
Fresh tuber weight per plant (kg)	-0.55014491	0.583634744	-0.131179357	-0.120084502	0.058340114
Dry matter rate (%)	0.669104741	0.123404962	-0.248433998	0.315515369	-0.022224719
Crude starch (%)	0.59481953	0.669027652	0.109875175	-0.187594249	-0.059138217
Reducing sugar (%)	-0.700035166	-0.384369116	0.203577096	0.24380001	-0.094452155
Soluble sugar (%)	-0.750902543	-0.312347053	0.324448984	-0.105401201	-0.204933368
Crude protein (%)	-0.11145982	-0.417934043	-0.07747985	0.579193668	0.524648998
Total flavonoids (mg/g DW)	0.124918803	-0.332138922	-0.792360702	0.028570477	-0.074672119
Total phenolics (mg/g DW)	-0.072518121	-0.346439296	-0.800306017	0.102647149	-0.130339656
Eigenvalue	2.83	2.55	2	1.44	1.07
Contribution (%)	20.22%	18.21%	14.32%	10.30%	7.65%
Cumulative contribution (%)	20.22%	38.43%	52.75%	63.05%	70.70%

Table2 Principal component analysis of germplasm resources from the Mingyang low-selenium region

traits	PC1	PC2	PC3	PC4	PC5	PC6
Vine length (cm)	-0.097816492	0.565900007	-0.006340215	0.216705218	-0.219762434	0.517070174
Number of branches	-0.228199884	0.390650345	-0.456809249	-0.015023768	-0.222368974	-0.592498598
Stem diameter (mm)	0.226259003	0.114127804	-0.280389352	-0.350825866	0.433967152	0.473454061
Number of tubers per plant	-0.328654249	0.365711566	-0.381544319	0.419999104	0.460055981	-0.171960609
Fresh vine weight per plant (kg)	-0.174823796	0.776765115	-0.309382762	-0.273389309	-0.268507221	0.098319943
Fresh leaf weight per plant (kg)	-0.063922313	0.694934928	-0.18530563	-0.461405361	-0.128600262	-0.020188822
Fresh tuber weight per plant (kg)	-0.276781859	0.310999553	-0.316120449	0.556475901	0.302031632	0.183368924
Dry matter rate (%)	0.588724862	0.361021874	0.403884945	-0.05282852	-0.103239155	0.034598087
Crude starch (%)	0.921627022	0.159909254	-0.053813193	0.237698701	-0.053742407	0.019303286
Reducing sugar (%)	-0.803411302	-0.256617129	0.020165048	-0.10961881	-0.20963473	0.226980093
Soluble sugar (%)	-0.655005655	-0.477157848	-0.267723421	0.017352402	-0.273622237	0.165617406
Crude protein (%)	-0.274579817	0.021337271	0.118591445	-0.541386688	0.590841005	-0.128571649
Total flavonoids (mg/g DW)	-0.351480286	0.456742127	0.712926566	0.167874171	0.026322809	-0.104853928
Total phenolics (mg/g DW)	-0.58445008	0.35429194	0.657792831	0.072557516	0.096924849	0.001874158
Eigenvalue	3.14	2.59	1.86	1.34	1.17	1.02
Contribution (%)	22.43	18.48	13.26	9.59	8.35	7.31
Cumulative contribution (%)	22.43	40.91	54.17	63.76	72.11	79.42

3.5 Differences in Tuber Selenium Content and Screening of Selenium-Enriched Varieties

The selenium contents of the 77 sweet potato varieties grown in the two different geographical regions are summarized in Table S4. In the Wuming high-selenium region, tuber selenium content ranged from 0.034 to 0.319 mg/kg DW, with a mean of 0.070 mg/kg DW and a coefficient of variation (CV) of 66.11%. Among these, 41 varieties had selenium content below 0.06 mg/kg DW, 28 varieties had selenium content between 0.06 and 0.10 mg/kg DW, and 10 varieties had selenium content ≥ 0.10 mg/kg DW. Zhenghong 163 exhibited significantly higher selenium content than the other varieties, being approximately 3.19 times that of Qianshu 15.

In the Mingyang low-selenium region, tuber selenium content ranged from 0.025 to 0.068 mg/kg DW, with a mean of 0.040 mg/kg DW and a CV of 24.87%. Among these, five varieties had selenium content below 0.03 mg/kg DW, 58 varieties had selenium content between 0.03 and 0.05 mg/kg DW, and 16 varieties had selenium content between 0.05 and 0.07 mg/kg DW. All varieties had selenium content below 0.10 mg/kg DW. Ranked from highest to lowest selenium content, the top five varieties were Zhanxie 12, Yushu 27, Longshu 14, Yinggehong, and Ganshu 6; the bottom five varieties were Jishu 7, Guangzishu 10, Qinzi 2, Longzi 9, and Yanshu 25. Zhanxie 12 had the highest selenium content (0.068 mg/kg DW), while Jishu 7, Guangzishu 10, and Qinzi 2 had the lowest (0.025 mg/kg DW).

To further screen selenium-enriched varieties, the 10 varieties with the highest selenium content in Wuming were selected, and their tuber selenium content in Mingyang was compared (Fig. 5). All varieties showed higher selenium content in Wuming than in Mingyang. Among them, Zhenghong 163 (0.319 mg/kg in Wuming vs. 0.036 mg/kg in Mingyang), Longzi 9 (0.255 vs. 0.030 mg/kg), and Guangzishu 9 (0.221 vs. 0.034 mg/kg) exhibited the largest differences between the two sites, with selenium enrichment multiples of 8.86, 8.50, and 6.50, respectively. Guangshu 22, Qinzi 2, Xiaobinlang, Guishu 6, and Qianshu 15 showed moderate differences. Ziluolan and Wanshu 10 showed the smallest differences, with Wanshu 10 having the highest selenium content (0.052 mg/kg) among the 10 varieties in Mingyang.

3.4 Cluster Analysis of Sweet Potato Germplasm Resources

The cluster analysis results of sweet potato germplasm resources are presented in Figure 4. In the Wuming region, the 77 sweet potato germplasm resources were classified into three groups: Group I comprised 40 germplasms, Group II comprised 27 germplasms, and Group III comprised 10 germplasms. In the Mingyang region, the 77 sweet potato germplasm resources were also divided into three groups: Group I consisted of 51 germplasms, Group II consisted of 18 germplasms, and Group III consisted of 8 germplasms.

3.6 Correlation Analysis of Tuber Selenium Content with Other Traits

The relationships between tuber selenium content and agronomic and quality traits were analyzed in 77 sweet potato germplasm resources.

In the Wuming high-selenium region, tuber selenium content showed positive correlations with storage root number per plant, stem diameter, and crude protein content, and negative correlations with dry matter rate, starch content, sugar content, total flavonoids, and total phenolics. Fresh storage root weight per plant was positively correlated with vine length, branch number, storage root number per plant, and fresh vine weight per plant, and negatively correlated with dry matter rate, crude protein content, and total phenolics. Fresh vine weight per plant was positively correlated with vine length, branch number, and fresh leaf weight per plant, and negatively correlated with dry matter rate, crude protein content, total flavonoids, and total phenolics. Storage root number per plant was positively correlated with branch number, and negatively correlated with stem diameter, dry matter rate, and sugar content. Vine length was positively correlated with branch number and negatively correlated with stem diameter. Starch content was negatively correlated with branch number, sugar content, crude protein content, total flavonoids, and total phenolics, and positively correlated with dry matter rate. Dry matter rate was negatively correlated with branch number and soluble sugar content.(Fig.6)

In the Mingyang low-selenium region, tuber selenium content showed positive correlations with stem diameter, storage root number per plant, fresh storage root weight per plant, dry matter rate, and starch content, and negative correlations with vine length, branch number, and fresh vine weight per plant. Fresh storage root weight per plant was positively correlated with storage root number per plant, and negatively correlated with dry matter rate, starch content, and crude protein content. Fresh vine weight per plant was positively correlated with vine length, branch number, and fresh leaf weight per plant, and negatively correlated with starch content, sugar content, and crude protein content. Storage root number per plant was positively correlated with branch number, and negatively correlated with dry matter rate. Vine length was positively correlated with branch number and negatively correlated with stem diameter. Dry matter rate was positively correlated with starch content, and negatively correlated with reducing sugar and soluble sugar content. Starch content was negatively correlated with sugar content, crude protein content, total flavonoids, and total phenolics(Fig.7).

4. Discussion

Selenium (Se) is a beneficial element for plants, and studying its role and mechanisms in plants is of great significance[14]. Se is a trace element essential for plant growth, development, and stress responses. Its physiological functions are primarily attributed to its antioxidant activity, which enhances plant tolerance to various abiotic stresses, including heavy metal toxicity, salinity, drought, and low temperature[15, 16]. Notably, the beneficial effects of Se are dose-dependent and vary among plant species and environmental conditions[17]. Studies have shown that appropriate concentrations of exogenous Se enhance plant antioxidant capacity and reduce malondialdehyde (MDA) content, whereas excessive Se exacerbates oxidative damage[18]. Thus, Se exhibits a dual effect on plants. Excessive Se has been reported to exert toxic effects, negatively impacting vegetative growth and yield formation[19]. In the present study, the mean values of most vegetative growth and yield-related traits in the Mingyang low-selenium region were significantly higher than those in the Wuming high-selenium region. In particular, the mean fresh storage root weight per plant in Mingyang (0.7 kg) was approximately three times that in Wuming (0.25 kg). This phenomenon may be attributed to the fact that although the soil selenium content in Wuming favors selenium accumulation, other limiting factors such as lower organic matter content, poor soil structure, or water stress may inhibit overall sweet potato growth. Notably, the mean storage root number per plant was similar between the two environments (4.92 vs. 5.09), suggesting that soil environment has a relatively minor effect on root number, while root expansiois more sensitive to environmental conditions. Furthermore, stem diameter consistently showed the lowest coefficient of variation in both environments, indicating that it is a relatively conserved and stable agronomic trait in sweet potato. This stability facilitates variety identification and field management. In contrast, fresh vine weight and fresh leaf weight exhibited high levels of variation in both environments, reflecting the rich genetic diversity of vegetative growth traits in sweet potato, which provides a solid foundation for germplasm screening and breeding selection.

Selenium is an essential trace element for both animals and plants and can improve the quality of various crops. Se participates in regulating plant photosynthesis and respiration, protects plants from free radical damage, increases the content of macro- and micro-elements, and enhances adaptation to environmental changes and abiotic stresses, thereby improving crop quality[20, 21]. Se has been reported to increase the expression of enzymes involved in sucrose and starch biosynthesis in rice, leading to increased sucrose and starch contents, early maturation, and higher grain yield[22]. In wheat, Se significantly enhances the accumulation of flavonoids, six anthocyanins, dihydroquercetin (a precursor of anthocyanin biosynthesis), and catechin[23]. Additionally, Se application significantly increased soluble sugar, crude protein, crude fat, and starch contents in grains by 9.48%, 6.59%, 1.56%, and 4.82%, respectively, indicating that appropriate Se supply not only increases grain Se content but also improves major nutritional quality indicators[24]. In the present study, the mean values of

most quality traits (dry matter rate, crude starch, total flavonoids, total phenolics, reducing sugars, and soluble sugars) in the Wuming high-selenium region were higher than those in the Mingyang low-selenium region. Among these, dry matter rate and crude starch content showed the most pronounced differences, consistent with previous studies.

Different crop varieties exhibit inherent differences in selenium uptake and accumulation capacity. Studies in rice have shown that the selenium distribution pattern in Jiahua 1 and Wuyou 29 follows: straw > polished rice > brown rice > milled rice, whereas in Nanjing 9108, the pattern is: straw > brown rice > polished rice > milled rice, indicating that variety is a key intrinsic factor determining selenium distribution in grain processing fractions[25]. In the present study, tuber selenium content varied significantly among sweet potato varieties and between soil environments. In the Wuming high-selenium region, tuber selenium content ranged from 0.034 to 0.319 mg/kg DW, with a CV of 66.11%, further confirming that selenium enrichment capacity is a strongly genotype-controlled trait. Among the varieties, Zhenghong 163, Longzi 9 and Guangzishu 9 exhibited the strongest selenium enrichment capacity, with selenium contents 3.19-fold, 2.55-fold, and 2.21-fold higher than that of Qianshu 15, respectively. This magnitude of variation is comparable to that reported for selenium enrichment in rice and wheat. In the Mingyang low-selenium region, all varieties had selenium content below 0.10 mg/kg DW, but still showed approximately 2.7-fold variation among varieties. Notably, the top 10 varieties with the highest selenium content in Wuming all showed reduced selenium content in Mingyang. Among them, Zhenghong 163, Longzi 9, and Guangzishu 9 exhibited the largest reductions, while Wanshu 10 and Ziluolan showed relatively smaller reductions. These results indicate a significant genotype-by-environment interaction for tuber selenium content in sweet potato. Based on their phenotypic responses to changes in soil selenium level, the varieties can be classified into two types: sensitive genotypes that exhibit high selenium accumulation in selenium-rich environments but are highly dependent on selenium supply; and insensitive genotypes that maintain relatively stable selenium content across different environments, demonstrating strong phenotypic plasticity. Based on these differences, sensitive genotypes are more suitable for direct cultivation in natural selenium-rich regions to fully realize their selenium enrichment potential, whereas insensitive genotypes may require exogenous selenium application for biofortification to achieve selenium enrichment when grown in low-selenium regions.

Principal component analysis, as a multivariate statistical method, reduces the dimensionality of multiple original trait indicators into a few independent composite indicators, thereby minimizing data complexity while preserving as much of the original information as possible[26]. The PCA results further elucidated the structure of trait variation between the two environments. In the Wuming high-selenium region, PC1 and PC2 together accounted for 38.4% of the total variance, with soluble sugar exhibiting the highest loading on PC3, which is consistent with the previously observed increase in soluble sugar content under selenium-rich conditions. In contrast, in the Mingyang low-selenium region, total flavonoids showed the highest loading on PC3. Previous studies have reported that selenium application significantly promotes the accumulation of flavonoids in crops[23], suggesting that flavonoid metabolic pathways may be particularly sensitive to selenium availability under low-selenium conditions, thereby serving as an important trait for discriminating germplasm variation in this environment. Meanwhile, cluster analysis classified the 77 germplasms from both regions into three groups, indicating that environmental conditions influenced the grouping patterns—Group I in Wuming comprised 40 germplasms, whereas Group I in Mingyang comprised 51 germplasms, suggesting that certain genotypes shifted their trait performance in response to soil selenium levels. This genotype-by-environment interaction is consistent with the observed variation in selenium enrichment capacity among varieties.

This study systematically evaluated, for the first time, the agronomic traits, quality traits, and selenium enrichment capacity of 77 sweet potato germplasm resources in both natural selenium-rich and low-selenium regions. Varieties with outstanding natural selenium enrichment capacity, such as Zhenghong 163, Longzi 9, and Guangzishu 9, as well as varieties with strong environmental adaptability, such as Wanshu 10, were identified, providing direct material support for selenium-enriched sweet potato breeding and promotion. The multiple correlations between selenium enrichment and yield and quality traits were revealed, and two selenium enrichment strategies ("environment-sensitive" and "environment-stable") were proposed, providing phenotypic evidence and germplasm materials for future research on the molecular mechanisms of selenium metabolism.

5. Conclusion

This study systematically evaluated 77 sweet potato germplasm resources from a natural selenium-rich region (Wuming) and a low-selenium region (Mingyang), and revealed that soil selenium environment significantly affects the agronomic and quality traits of sweet potato. In the selenium-rich region, dry matter rate, starch content, and antioxidant compound content were higher, while tuber yield was lower than that in the low-selenium region, indicating an environment-dependent trade-off between yield and quality. Principal component analysis and cluster analysis further confirmed the structural differences in trait variation between the two environments, and revealed the significant influence of soil selenium level on germplasm classification. Tuber selenium content varied significantly among varieties. Zhenghong 163, Longzi 9, and Guangzishu 9 were identified as the varieties with the strongest natural selenium enrichment capacity, among which Zhenghong 163 exhibited a selenium content of 0.319 mg/kg DW, demonstrating high potential for natural selenium-enriched

development. The selenium-enriched varieties screened in this study provide important germplasm resources for breeding, promotion, and future research on selenium metabolism mechanisms in functional selenium-enriched sweet potato.

Declarations

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Author information

All authors contributed to the study conception and design. Material preparation, data collection, and analysis were carried out by Jinfeng Hua, Zhenwei Li, Yongmei Huang, and Yanqing Li. The first draft was written by Yixuan Zhang, and Huifeng Li and Dong Xiao contributed to conceptualization, methodology, project administration, and manuscript revision. All authors reviewed previous versions of the manuscript and approved the final version.

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Ethics declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare no competing interests.

Availability of data and materials

A total of 77 sweet potato germplasm resources were provided by the Maize Research Institute, Guangxi Academy of Agricultural Sciences. The field experiments were conducted in 2023 and 2024 at two sites: Ganwei Town, Wuming District, Nanning City, Guangxi (soil pH = 4.8, organic matter content = 21.40 g/kg, total selenium content = 0.78 mg/kg) and the Mingyang Base of Guangxi Academy of Agricultural Sciences (soil pH = 6.38, organic matter content = 19.40 g/kg, total selenium content = 0.30 mg/kg). All other data generated or analysed during this study are presented in the main tables or supplementary tables (Table S1–S4) of this published article.

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Figures

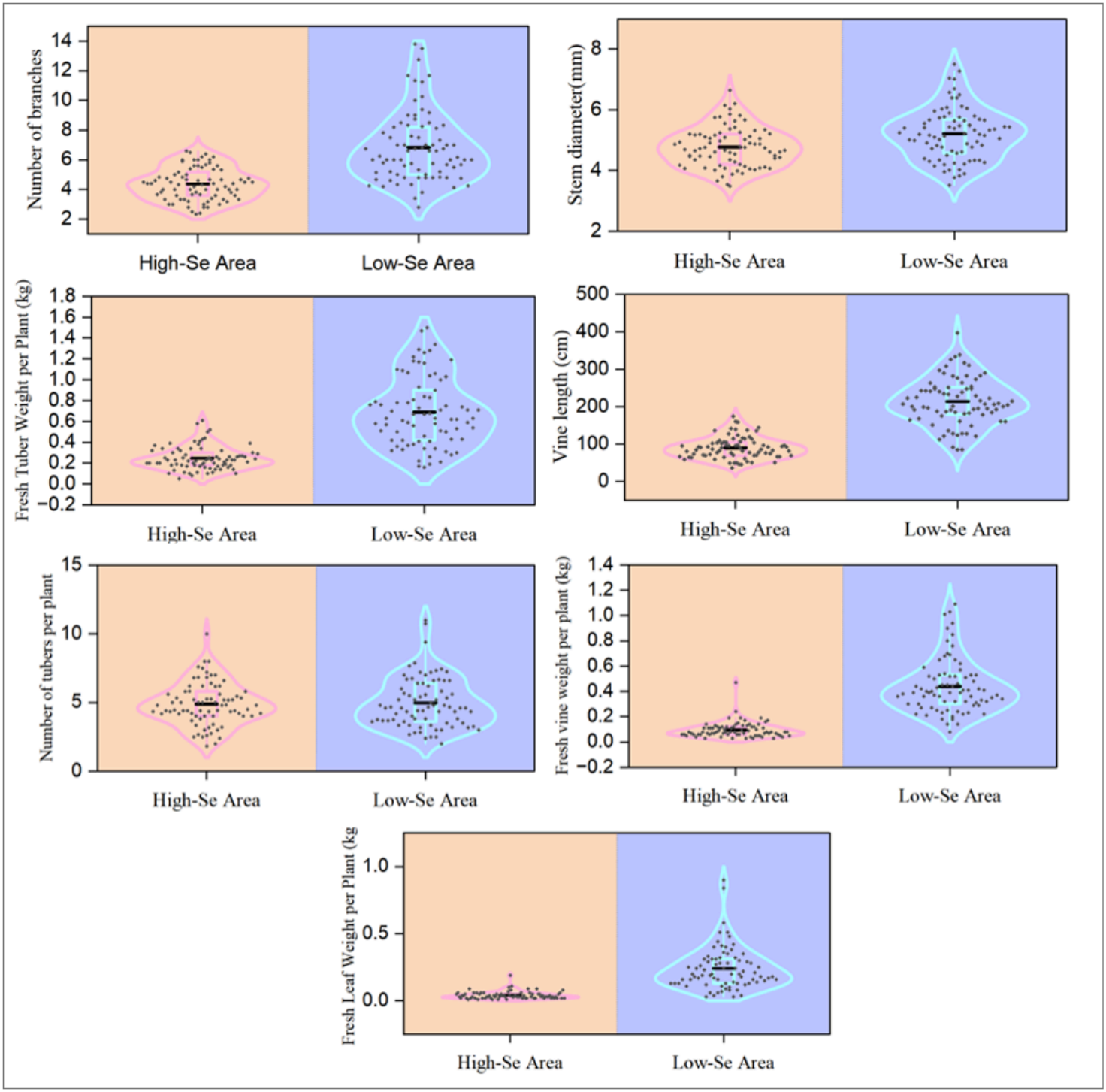


Figure 1

Violin plots showing the distribution of seven agronomic traits (branch number, stem diameter, fresh storage root weight per plant, vine length, storage root number per plant, fresh vine weight per plant, and fresh leaf weight per plant) in 77 sweet potato germplasms. The Wuming high-selenium region is shown on the left, and the Mingyang low-selenium region on the right. Within each violin plot, the black line represents the median, the box represents the interquartile range, and the black dots represent individual data points.

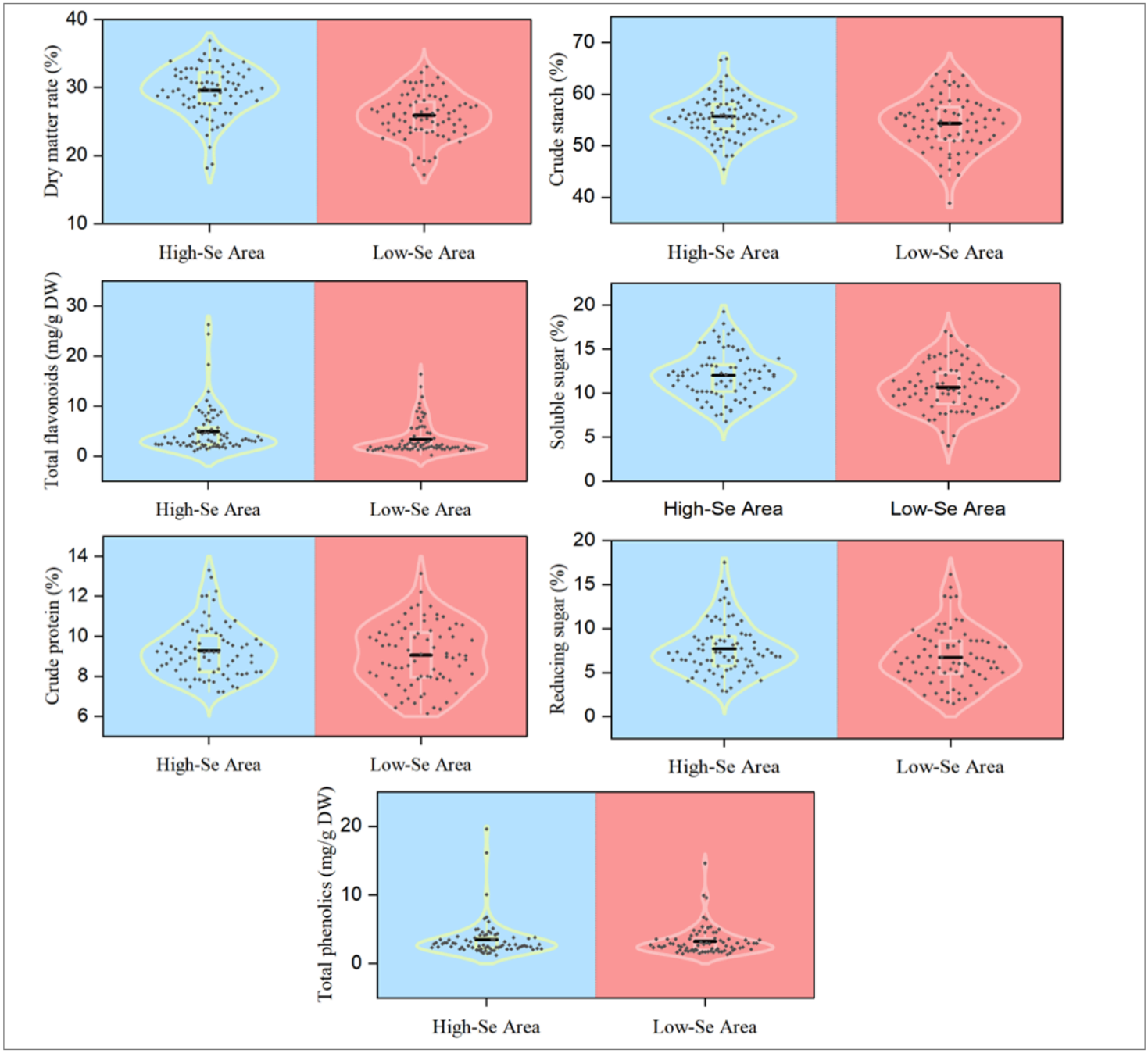


Figure 2

Violin plots showing the distribution of seven quality traits (dry matter rate, crude starch, total flavonoids, soluble sugars, crude protein, reducing sugars, and total phenolics) in 77 sweet potato germplasms. The Wuming high-selenium region is shown on the left, and the Mingyang low-selenium region on the right. Within each violin plot, the black line represents the median, the box represents the interquartile range, and the black dots represent individual data points.

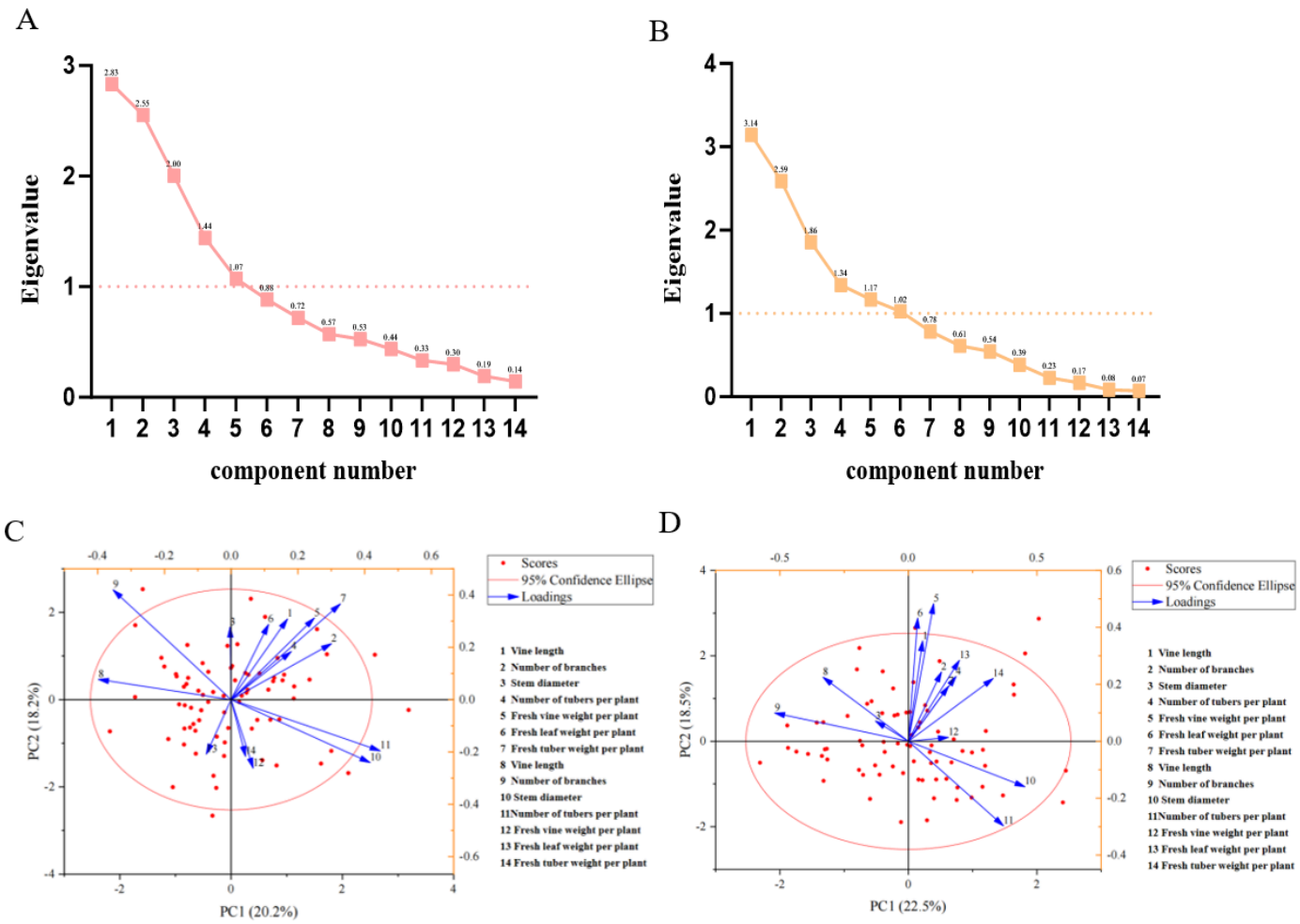


Figure 3

Principal component analysis plots of sweet potato germplasm from two regions.
A: Scree plot of principal components for the Wuming high-selenium region;B: Scree plot of principal components for the Mingyang low-selenium region;C: Biplot of principal components for the Wuming high-selenium region;D: Biplot of principal components for the Mingyang low-selenium region.

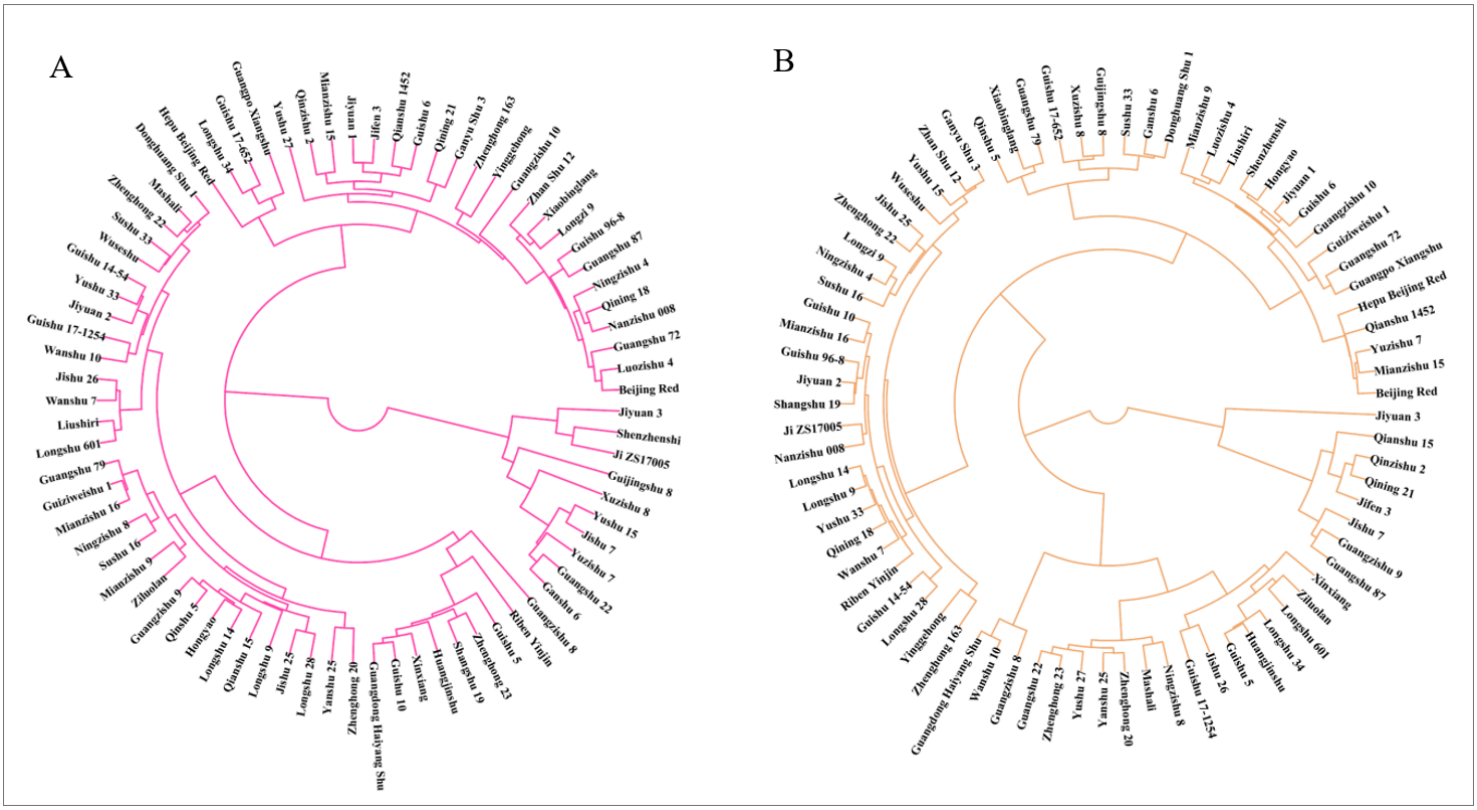


Figure 4

Cluster analysis of sweet potato germplasm resources from two regions.
A: Cluster analysis for the Wuming region;B: Cluster analysis for the Mingyang region.

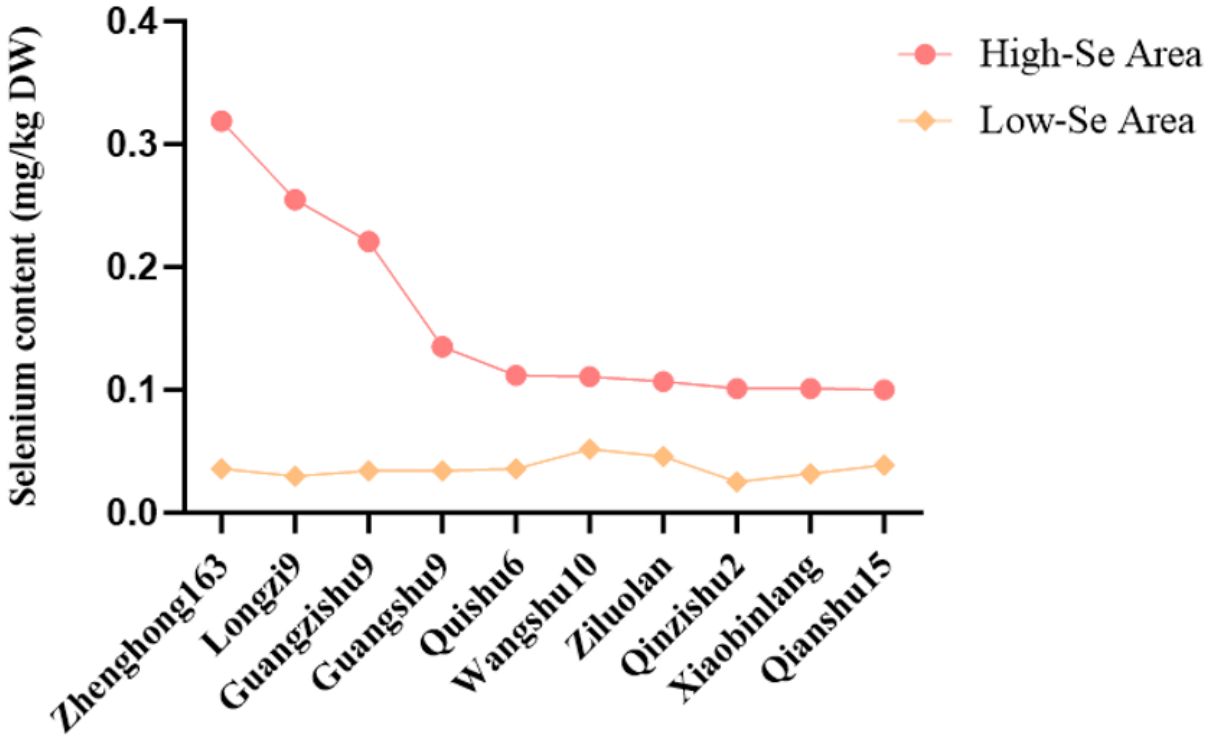


Figure 5

Top 10 sweet potato varieties with the highest selenium enrichment multiples.

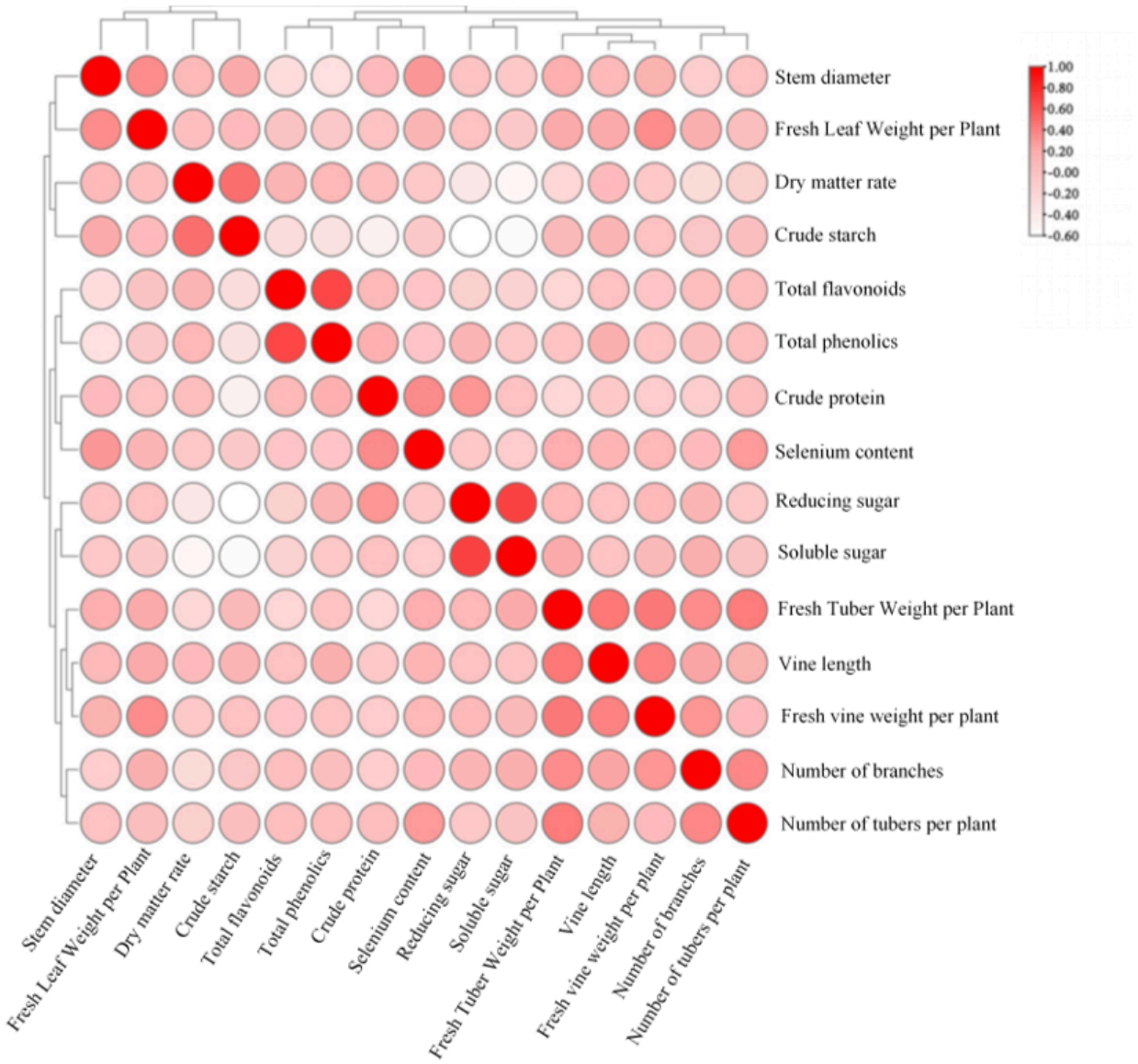


Figure 6

Correlation analysis of various traits of sweet potato germplasm grown in the Wuming natural selenium-rich soil region.

Note: The intensity of the color reflects the magnitude of the correlation coefficient. Red denotes a positive correlation, while white denotes a negative correlation. Darker shades indicate stronger correlations.

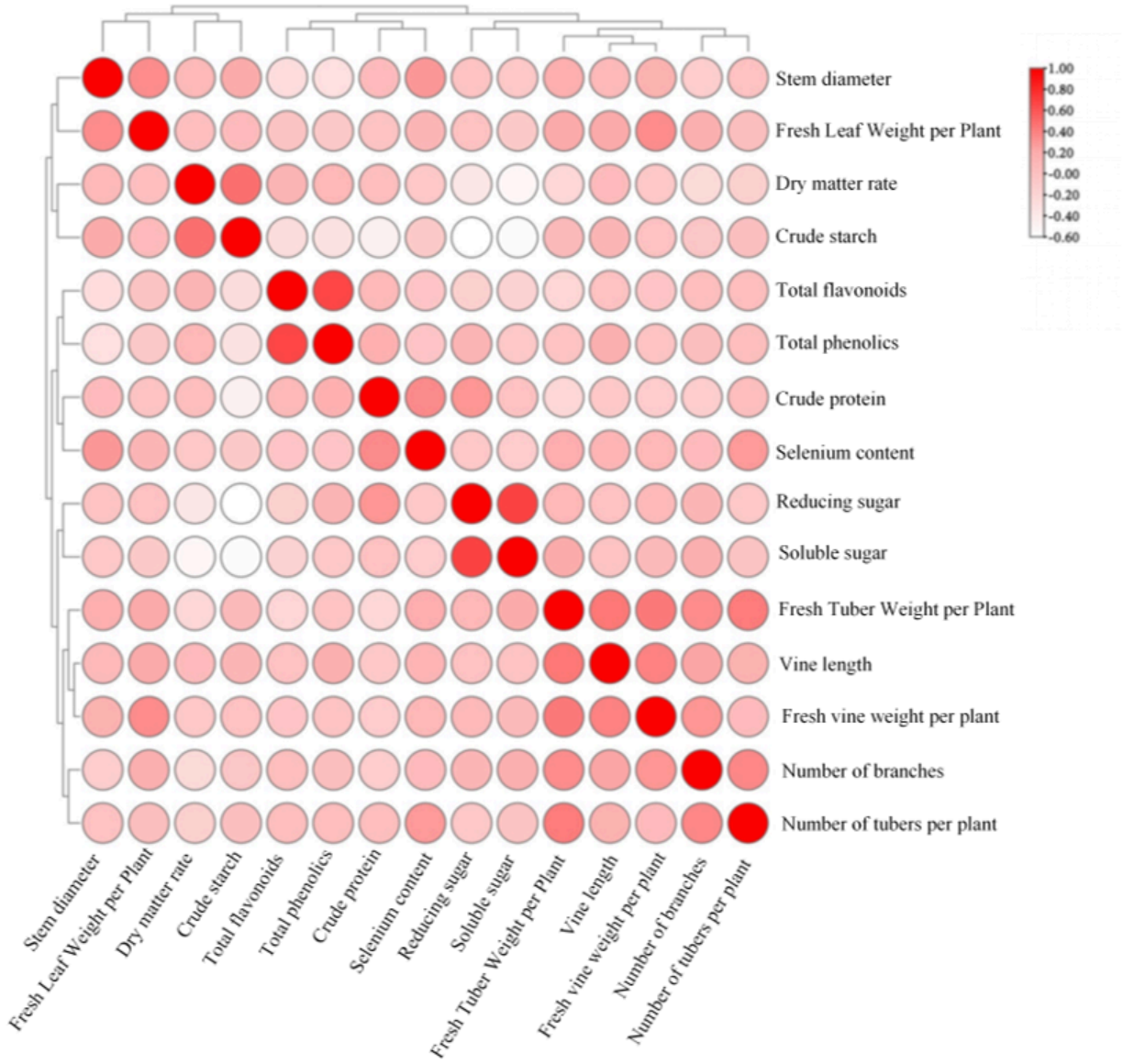


Figure 7

Correlation analysis of various traits of sweet potato germplasm grown in the Mingyang low-selenium soil region.

Note: The intensity of the color reflects the magnitude of the correlation coefficient. Red denotes a positive correlation, while white denotes a negative correlation. Darker shades indicate stronger correlations.

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