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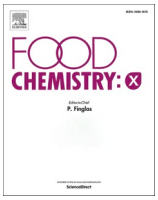

Comprehensive quality assessment of 296 sweetpotato core germplasm in China: A quantitative and qualitative analysis

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ABSTRACT

The potential for improving sweetpotato quality remains underutilized due to a lack of comprehensive quality data on germplasm resources. This study evaluated 296 core germplasms, revealing significant phenotypic diversity across 24 quality traits in both stem tips and roots. Landraces had higher sugar content in roots, while wild relatives showed increased total flavonoid and phenol contents. Accessions with red-orange flesh were rich in sugars and carotenoids, whereas those with purple flesh had higher dry matter, flavonoids, and phenols. The accessions were classified into three clusters: high sugars and carotenoids, high phenolic compounds, and high starch. A comprehensive quality scoring model identified SP286 and SP192 as superior for stem tips and roots, respectively. Near-infrared spectroscopy, combined with a random forest algorithm, enabled rapid screening of superior germplasm, achieving prediction accuracies of 97 % for stem tips and 98 % for roots. These findings offer valuable resources and high-throughput models for enhancing sweetpotato quality.

1. Introduction

Sweetpotato (*Ipomoea batatas* L.) is a major root crop renowned for its high yield potential and significant role in global food security. As a nutritious and adaptable crop, it contributes to diversified diets and serves as a staple in many regions, particularly in Africa and Asia (FAOSTAT, 2023). Beyond its storage roots, the young stem tips (leaves) of sweetpotato are also prized for their health benefits, including antioxidant properties and potential anticancer effects (Alam, 2021; Tang et al., 2021). This underscores the dual utility of sweetpotato, serving both as a robust root crop and a nutrient-rich leafy vegetable. In this context, breeders and food scientists advocate for the breeding of sweetpotato varieties with enhanced nutritional profiles, aiming to improve public health in developing regions (Laurie, Naidoo, Magwaza, Shimelis, & Laing, 2020; Rosero et al., 2022). Breeding and cultivation strategies are now equally focused on maximizing root yield and optimizing the nutritional quality of stem tips and roots (Tang et al., 2023). The development of high-quality varieties is crucial to satisfy the escalating demand for nutritious food and to guide breeding programs toward enhancing the nutritional value of sweetpotatoes, thereby promoting sustainable development within the industry.

Genetic diversity is a fundamental prerequisite for successful plant breeding. With the continual expansion of sweetpotato germplasm collections, the growing number of accessions provides a rich genetic basis and diversity for enhancing quality traits. As sweetpotatoes are typically propagated asexually, nutritional improvements can be achieved through classical hybrid breeding or genetic engineering (Lu, Huang, & Zhang, 2006). Whether through traditional or modern methods, a detailed characterization of quality traits in both stem tips and roots is a crucial step in the effective utilization of germplasm, which is of great significance for breeding nutrient-rich varieties (Laurie et al., 2020). However, current sweetpotato germplasm suffers from a scarcity of quality data and a lack of a systematic evaluation framework, necessitating a comprehensive, large-scale quality evaluation. Although previous studies have characterized nutrients in sweetpotato (Laurie et al., 2020; Rosero et al., 2022; Sun, Mu, Xi, Zhang, & Chen, 2014), most have focused on a limited number of commonly grown varieties and quality indicators. This restricted scope hampers a broader understanding of the nutritional components in the stem tips and roots of most accessions, thus limiting efforts to breed sweetpotato varieties with enhanced and balanced nutritional profiles. Consequently, evaluating a wide range of germplasm resources and identifying elite parental materials are paramount tasks in quality-focused breeding practices.

Carbohydrates, proteins, carotenoids, and phenolic compounds are

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major nutrients in sweetpotato stem tips and roots (Wang, Nie, & Zhu, 2016). Proximate components such as dry matter, cellulose, crude protein, starch (including both amylose and amylopectin), and sugars display considerable variation across different accessions (Alam, 2021). Additionally, bioactive compounds like anthocyanins, carotenoids, chlorogenic acid, flavonoids, and phenols serve as key antioxidant indicators, playing a pivotal role in the selection and breeding of health-oriented sweetpotato varieties (de Albuquerque, Sampaio, & de Souza, 2019; Tang et al., 2024). These quality traits not only contribute to the nutritional profile of sweetpotatoes but also influence sensory attributes, which are critical for consumer acceptance (Mello et al., 2022; Zhang et al., 2023). Despite the importance of these traits, a comprehensive approach that integrates multiple quality indicators for selecting parental materials is lacking. This limitation slows the process of identifying elite hybrids. Currently, germplasm screening focuses predominantly on external characteristics and root biomass, with minimal attention to internal nutritional qualities (Sanchez, Hashim, Shamsudin, & Mohd Nor, 2020; Tang et al., 2023). Moreover, existing methods often target specific utilization purposes (e.g., high yield or starch processing), which limits their effectiveness in selecting germplasm suitable for multiple end-uses. To address these challenges and enhance germplasm screening efficiency, it is imperative to develop a comprehensive quality scoring model with standardized indices that enable the identification of elite sweetpotato germplasm for leaf-vegetable and root utilization purposes.

The application of multi-criteria decision-making (MCDM) methods, such as principal component analysis (PCA), the entropy weight (EW) method, and the technique for order preference by similarity to an ideal solution (TOPSIS), plays a crucial role in the comprehensive quality analysis of agricultural products (Song et al., 2022; Wang et al., 2021). These methods have significantly contributed to superior variety screening, product grade classification, and processing method optimization in the fields of agriculture and food science (Adainoo, Thomas, & Krishnaswamy, 2023; Bao et al., 2023; Zhang et al., 2023). Besides, the development of qualitative models for rapid screening of superior germplasm based on comprehensive quality scores is urgently needed, supporting the efficient breeding of high-quality varieties and the advanced processing of sweetpotatoes. Near-infrared spectroscopy (NIRS), with its rapid, non-destructive nature and absence of chemical reagents, is an ideal tool for large-scale and high-throughput germplasm screening. NIRS has proven effective for qualitative analysis, classification, and origin identification across various crops (Schütz, Riedl, Achten, & Fischer, 2022; Yang et al., 2022; Yang et al., 2022). However, to date, qualitative quality characterization of sweetpotato stem tips and roots, and the potential for NIRS coupled with machine learning algorithm (e.g., random forest (RF)) for rapid screening of sweetpotato germplasm resources, remains unexplored.

In response to these challenges, this study conducted a comprehensive quantitative and qualitative assessment of 296 core sweetpotato accessions cultivated in China. The objectives were to: (1) elucidate variations in 24 major quality traits in stem tips and roots; (2) establish a comprehensive quality scoring model for evaluating each accession and selecting superior germplasms; and (3) develop a rapid screening model for superior germplasms using NIRS and the RF algorithm. Overall, this research provides valuable insights into nutrient-driven comprehensive quality assessments, offers a framework for high-throughput screening of elite germplasm resources, and promotes the sustainable growth and high-quality development of the sweetpotato industry.

2. Materials and methods

2.1. Plant materials

To represent the broad genetic diversity and geographical distribution of sweetpotato, we selected 296 core germplasms from a collection of over 2500 accessions preserved at the Chinese National Sweetpotato Germplasm Resource Nursery in Guangzhou. These selected accessions constitute a core collection that epitomizes rich genetic diversity in both phenotypic and genotypic aspects (Chen et al., 2023), spanning 30 years of breeding endeavors. Originating from 12 countries (Fig. 1), this core collection includes 126 landraces, 96 released varieties, 44 introduced accessions, 24 breeding lines, and 6 wild relatives (Table S1). The flesh colors of these sweetpotatoes vary widely across genotypes, encompassing shades of white (61), cream (76), yellow (50), orange (47), red-orange (31), and purple (31).

2.2. Planting and sample preparation

All selected germplasms were planted on July 8, 2020, at the Baiyun Experimental Station (23°23′N, 113°26′E) of the Guangdong Academy of Agricultural Sciences, Guangzhou, China. The planting was organized in a randomized complete block design with three replicates. Each plot covered an area of 4.4 m^2, arranged in two rows each 2 m long oriented north-south. The spacing was 20 cm between plants and 110 cm between rows. Field management practices, including fertilization, irrigation, and pest control, adhered to local agricultural standards.

Sixty days after planting, fresh stem tip samples from each germplasm were collected and promptly preserved on dry ice. Samples were processed in duplicate using two distinct drying methods, as informed by our laboratory data and previous findings (Tang et al., 2024). One set was oven-dried at 45 °C until constant weight, then pulverized, sieved through a 40–80 mesh screen, and stored at 4 °C for proximate components analysis (i.e., cellulose, crude protein, and soluble sugar). The other set was freeze-drying, ground in a liquid nitrogen grinder (A10 basic, IKA, Staufen, Germany), and stored at −80 °C for functional composition analysis, including chlorogenic acid, total anthocyanin, total flavonoid, and total phenol content.

At 140 days post-planting, five medium-sized roots (100–250 g) from each germplasm were harvested and processing immediately in the laboratory. Root samples were prepared in duplicate, analyzed for starch, amylose, crude protein, soluble sugar, and reducing sugar using hot-air drying, and for sucrose, fructose, glucose, maltose, total carotenoid, total anthocyanin, total flavonoid, and total phenol content using freeze-drying, consistent with protocols from Tang et al. (2023).

2.3. Chemical assays

2.3.1. Stem tip quality components

The dry matter content of stem tips was measured using the oven drying method. Cellulose content was determined at 620 nm using a microassay kit (Solarbio, Beijing, China) in combination with a spectrophotometer (Varioskan Flash, Thermo Scientific, Inc., Madison, WI, USA). Crude protein was analyzed using the Kjeldahl distillation method according to the AOAC standard, employing a nitrogen-to-protein conversion factor of 6.25. Soluble sugar content was quantified via the anthrone sulfuric acid colorimetric method (Hansen & Møller, 1975). Chlorogenic acid content was determined using high-performance liquid chromatography (HPLC) in accordance with Chinese National Standard GB/T 43733–2024. Total anthocyanin, flavonoid, and phenol contents were assessed using the pH differential, aluminum chloride colorimetric, and Folin-Ciocalteu colorimetric methods, respectively, following protocols described by Tang et al. (2024). All assays were performed in triplicate and the results were expressed on a dry weight basis.

2.3.2. Root quality components

Dry matter and total starch contents were quantified using oven drying and the Megazyme assay kit (K-TSTA-100 A, Wicklow, Ireland), respectively. Amylose content was determined using the Megazyme assay kit (K-AMYL, Wicklow, Ireland), and amylopectin content was obtained by subtracting the amylose value. The ratio of amylose to amylopectin was computed from these values. Soluble sugar content was measured using the anthrone sulfuric acid method at 620 nm (Hansen &

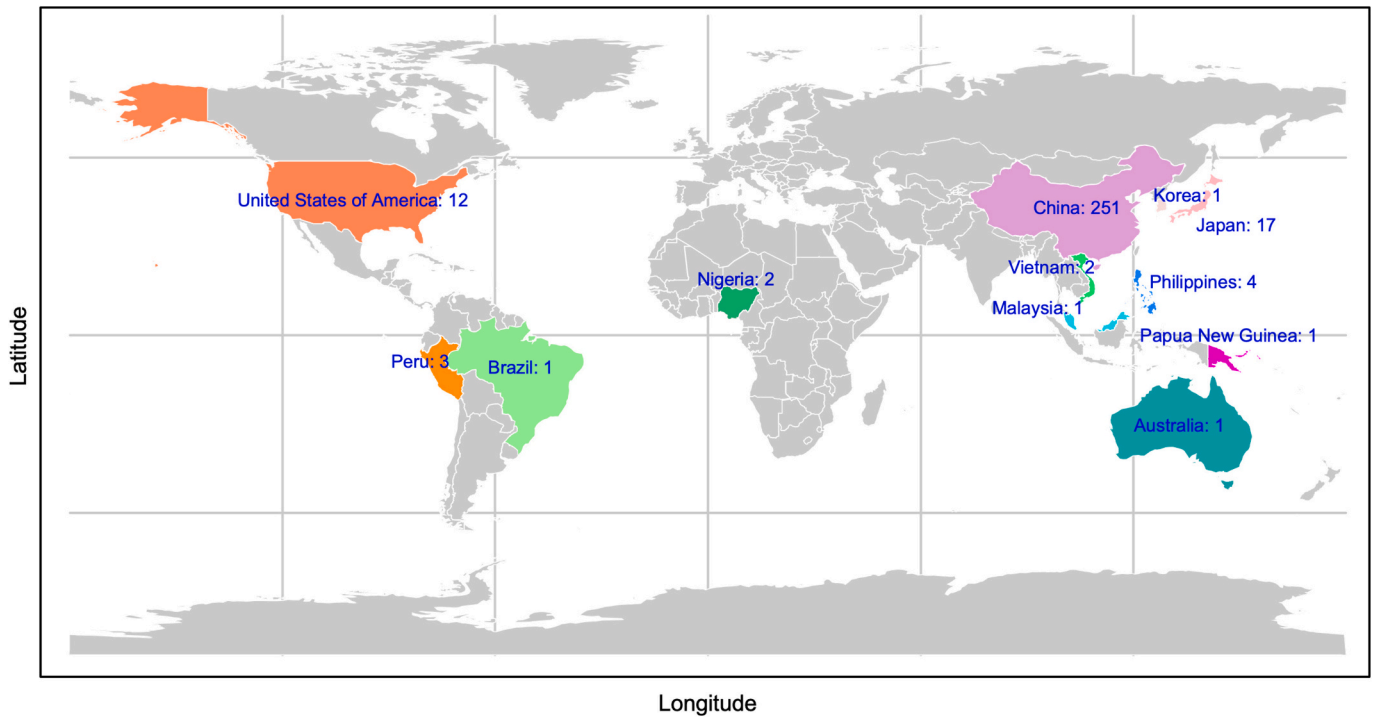

Fig. 1. Distribution map of 296 sweetpotato core germplasm sources.

Møller, 1975). Crude protein content was assessed using the Kjeldahl method, while reducing sugar content was determined via the 3,5-dinitrosalicylic acid colorimetric method. Total anthocyanin content was determined using the pH difference method, with only 31 germplasm accessions found to contain detectable levels of this compound. Total carotenoid content in the roots was analyzed using HPLC as described by Jia, Chen, Zhang, Tang, and Wang (2023); notably, 84 germplasm accessions did not contain measurable carotenoids. Following the protocols of Tang et al. (2023), total flavonoid and phenol contents were quantified using the aluminum nitrate colorimetric and Folin-Ciocalteu colorimetric methods, respectively. The composition of sugars, including fructose, glucose, sucrose, and maltose, was analyzed through ultra-performance liquid chromatography with an evaporative light scattering detector (UPLC-ELSD) (Koh, Park, Lim, Yea, & Bang, 2018). All above assays were performed in triplicate, and results were reported on a dry weight basis.

2.4. Spectral acquisition and preprocessing

Spectral data for stem tips and roots were acquired using a PerkinElmer FT-9700 NIR spectrometer equipped with an InGaAs detector at room temperature (25 °C). Approximately 6 g of each sample was placed into a mini-sample cup and scanned in reflectance mode. Spectra were collected from 10,000 to 4000 cm^{-1} at a resolution of 8 cm^{-1}, with each spectrum averaged across 64 scans, resulting in 751 data points per spectrum. Subsequently, PCA was performed using Unscrambler v10.4 software (CAMO, Corvallis, USA) to examine spectral structures and identify outliers. Preprocessing was performed using ChemDataSolution v3.5 software (Dalian ChemData Solution Technology Co. Ltd., Dalian, China), employing standard normal variate to mitigate scattering effects, and the Savitzky–Golay algorithm was employed for smoothing and derivative processing.

2.5. Comprehensive quality scoring models

To objectively select optimal germplasms based on multiple quality indicators, this study employed the PCA-EW-TOPSIS analysis method. We evaluated 296 sweetpotato germplasms across three dimensions: 24 overall quality traits, 8 stem tip quality traits, and 16 root quality traits. The top 5 % of the rankings (corresponding to the top 15 germplasms) were defined as superior germplasms, while the remained were classified as mediocre. Steps for the analysis were as follows:

Step 1: Standardization of all data using *Z*-score normalization to eliminate scale effects among variables.

$$Z_{ij} = \frac{X_{ij} - \mu_j}{\sigma_j} \tag{1}$$

where Z_{ij} is the standardized value, X_{ij} is the original value, μ_j is the mean of the *j*-th variable, and σ_j is the standard deviation of the *j*-th variable.

Step 2: Application of PCA to the standardized data to reduce dimensionality and extract the principal components (PCs). Only PCs with eigenvalues greater than 1 were retained for further analysis. This threshold ensured that the retained components captured the majority of variance in the data.

Step 3: Use of the EW method to calculate the weight of each indicator based on its information entropy, enhancing the representation of diverse data.

$$e_j = \frac{1}{log(n)} \sum_{i=1}^{n} p_{ij} log\left(p_{ij}\right) \tag{2}$$

where $p_{ij} = \frac{x_{ij}}{\sum_{i=1}^{n} x_{ij}}$ is the proportion of the *j*-th attribute of the *i*-th object, and *n* is the number of objects. The weight w_j for each attribute was then determined using:

$$w_j = \frac{1 - e_j}{\sum_{j=1}^{m}(1 - e_j)} \tag{3}$$

Step 4: Weighting of each standardized attribute by its entropy-derived weight and determination of the ideal (best) and negative ideal (worst) solutions using the maximal and minimal values for each attribute across all alternatives. The distance of each alternative from the ideal solution (D_i^+) and the negative ideal solution (D_i^-) was calculated using Euclidean distance.

$$D_i^+ = \sqrt{\sum_{j=1}^{m} w_j \left(x_{ij} - x_j^+\right)^2} \quad (4)$$

$$D_i^- = \sqrt{\sum_{j=1}^{m} w_j \left(x_{ij} - x_j^-\right)^2} \quad (5)$$

where w_j represents the weight of the j-th attribute, x_{ij} is the weighted standardized value of the j-th attribute for the i-th alternative, x_j^+ is the ideal value of the j-th attribute, x_j^- is the negative ideal value of the j-th attribute.

Step 5: Calculation of the relative closeness (C_i) to the ideal solution for each germplasm, using it as the comprehensive score for ranking based on their comprehensive quality scores (CQS).

$$C_i = \frac{D_i^-}{D_i^+ + D_i^-} \quad (6)$$

$$CQS_i = \frac{C_i - min(C)}{max(C) - min(C)} \times 100 \quad (7)$$

where C_i is the original relative closeness, min(C) is the minimum value among all relative closeness values, max(C) is the maximum value among all relative closeness values.

2.6. NIRS modeling and performance evaluation

The spectral dataset of stem tips and roots was partitioned into calibration and prediction sets in a 4:1 ratio using the Kennard-Stone algorithm to ensure representativeness. The Random Frog algorithm was employed to filter irrelevant spectral information and extract feature bands (Li, Xu, & Liang, 2012). After sample partitioning and variable selection, the Python v3.12 software and RF algorithm was employed to develop NIRS-based qualitative models for the rapid screening of superior sweetpotato germplasm in both stem tips and roots dimensions. The constructed RF model, comprising 500 trees with a maximum depth of 20, utilized one-third of the available features at each node to balance computational efficiency with model accuracy. Model performance was evaluated using accuracy (i.e., recognition rate, %), calculated as the ratio of correctly identified samples to the total number of samples. In addition, the confusion matrix of the RF classifier was used to display the relationship between the true labels of each category and the predicted labels of the model.

2.7. Data analysis

Descriptive statistics, including maximum, minimum, mean value, standard deviation (SD), coefficient of variation (CV), and Shannon-Weiner index, were computed using Microsoft Excel 2024. Statistical analyses were performed using the SPSS 29.0 analytical software package (IBM, SPSS Inc., Chicago, IL, USA). One-way analysis of variance (ANOVA) followed by least significant difference (LSD) posthoc tests was conducted to assess differences among means at $p < 0.05$. Pearson's correlation coefficients were calculated to quantify relationships among quality indicators, and hierarchical clustering was performed using Ward's method based on squared Euclidean distance.

3. Results and discussion

3.1. Stem tip and root quality components of sweetpotato germplasm

A concise step-by-step flowchart illustrating the quantitative and qualitative analysis is provided in Fig. 2. First, the analysis of 296 core germplasms highlighted significant variability and broad diversity across all quality components (Fig. 3). In stem tips, dry matter content ranged from 8.08 g/100 g (SP017) to 17.79 g/100 g (SP129), cellulose from 6.11 g/100 g (SP156) to 21.65 g/100 g (SP270), crude protein from 12.24 g/100 g (SP036) to 25.14 g/100 g (SP212), and soluble sugar from 3.86 g/100 g (SP176) to 37.72 g/100 g (SP091). The corresponding mean values were 11.37 g/100 g, 12.75 g/100 g, 18.25 g/100 g, and 18.83 g/100 g, respectively (Fig. 3a). The range for chlorogenic acid, total anthocyanin, total flavonoid, and total phenol content varied widely, ranging from 1.21 g/kg (SP093) to 5.56 g/kg (SP077), 0.06 g/kg (SP173) to 1.33 g/kg (SP286), 10.97 g/kg (SP090) to 35.68 g/kg (SP037), and 0.03 g/kg (SP263) to 66.86 g/kg (SP153), with their means recorded at 3.35 g/kg, 0.38 g/kg, 20.15 g/kg, and 27.69 g/kg, respectively (Fig. 3b). These findings align with Sun et al. (2014), who reported comparable ranges of 11.08–15.91 g/100 g for dry matter,

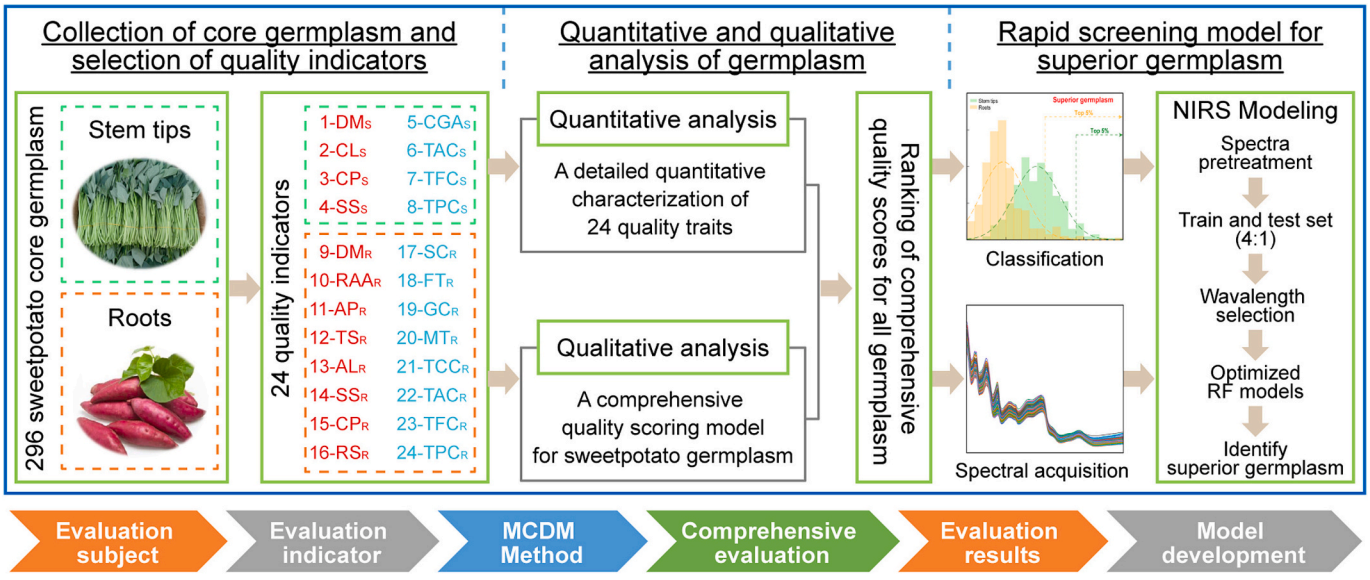

Fig. 2. Flowchart for comprehensive quantitative and qualitative analysis of 296 core sweetpotato accessions. Note: The subscript S and R represents the trait of the stem tips and roots, respectively. DM: dry matter; CL: cellulose; CP: crude protein; SS: soluble sugar; CGA: chlorogenic acid; TAC: total anthocyanin content; TFC: total flavonoid content; TPC: total phenol content; TS: total starch; AL: amylose; AP: amylopectin; RAA: ratio of amylose to amylopectin; RS: reducing sugar; SC: sucrose; FT: fructose; GC: glucose; MT: maltose; TCC: total carotenoid content; NIRS: near-infrared spectroscopy; RF: random forest.

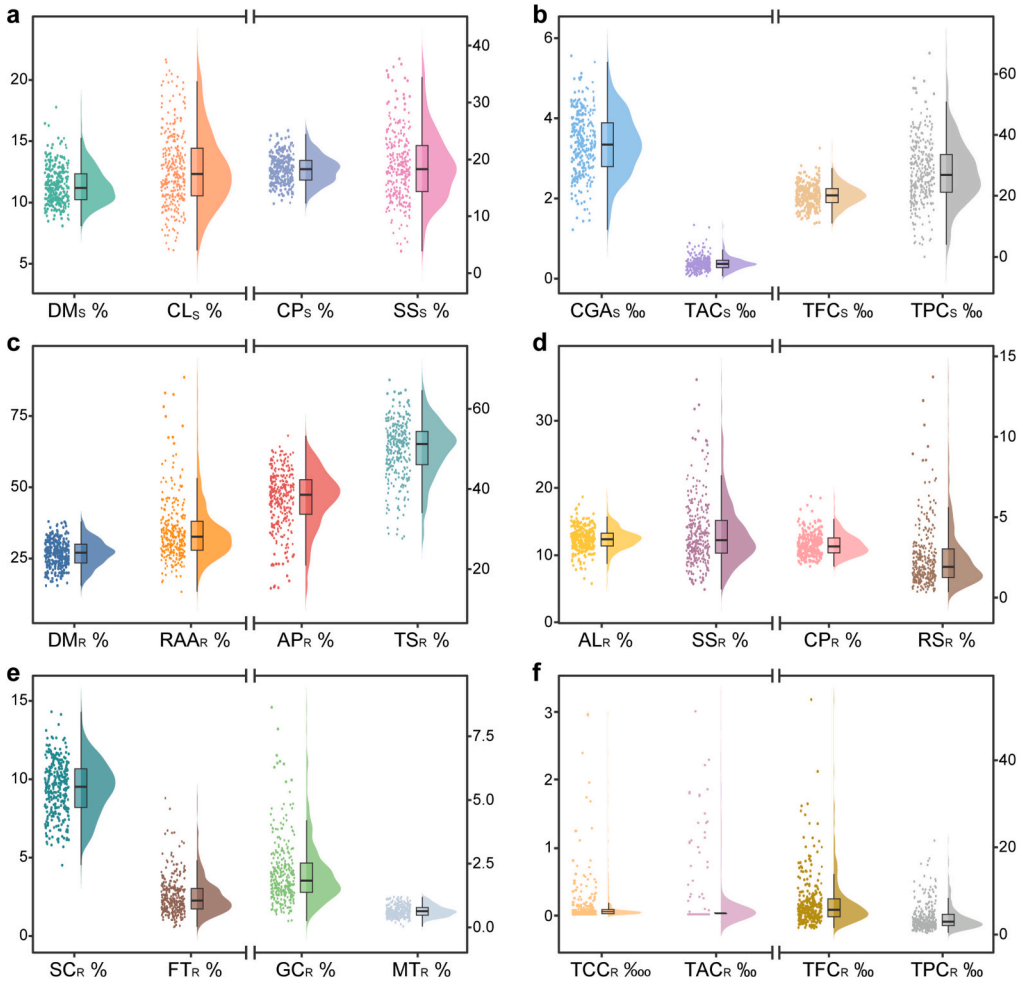

Fig. 3. Variations in 24 quality components among 296 sweetpotato core germplasm sources. (a-b) 8 stem tip quality traits. **(c-f)** 16 root quality traits. Note: The two indicators on the left of each subplot correspond to the left axis, while the two indicators on the right correspond to the right axis. The subscript S and R represents the trait of the stem tips and roots, respectively. DM: dry matter; CL: cellulose; CP: crude protein; SS: soluble sugar; CGA: chlorogenic acid; TAC: total anthocyanin content; TFC: total flavonoid content; TPC: total phenol content; TS: total starch; AL: amylose; AP: amylopectin; RAA: ratio of amylose to amylopectin; RS: reducing sugar; SC: sucrose; FT: fructose; GC: glucose; MT: maltose; TCC: total carotenoid content.

16.69–31.08 g/100 g for crude protein, and 9.15–14.26 g/100 g for crude fiber from 40 common sweetpotato varieties. Additionally, high CVs were observed for total anthocyanin (45.78 %), total phenol (37.73 %), and soluble sugar (32.17 %), while dry matter and crude protein exhibited relatively low variability (CV: 13.45 % and 13.79 %, respectively). Notably, the stem tip quality traits possess rich genetic diversity, with Shannon-Weiner index ranging from 5.61 to 5.69 (Table S2).

Regarding the 16 root quality indicators, significant variability was observed. Dry matter content ranged from 15.47 g/100 g (SP188) to 37.96 g/100 g (SP056), total starch from 27.70 g/100 g (SP116) to 67.16 g/100 g (SP025), amylopectin from 15.22 g/100 g (SP192) to 53.27 g/100 g (SP025), and amylose from 5.76 g/100 g (SP227) to 18.67 g/100 g (SP035), with the ratio of amylose to amylopectin varying from 13.29 % (SP227) to 88.61 % (SP192) (Fig. 3c). These results are consistent with previous studies reporting average levels of amylose and amylopectin (22 % and 78 %, respectively) in sweetpotato starches utilized by the Chinese starch industry (Abegunde, Mu, Chen and Deng, 2013) and the variation in amylose content (0–34.16 %) across different sweetpotato genotypes (Zhu & Wang, 2014). The soluble sugar content ranged from 4.89 g/100 g (SP025) to 36.10 g/100 g (SP192), crude protein from 1.95 g/100 g (SP088) to 6.30 g/100 g (SP291), and reducing sugar from 0.35 g/100 g (SP161) to 13.71 g/100 g (SP192) (Fig. 3d). These findings align with Laurie et al. (2020), who reported similar ranges for crude protein (2.65–6.45 g/100 g) in sweetpotato accessions. Furthermore, the sucrose varied from 4.52 g/100 g (SP141) to 14.30 g/100 g (SP116), fructose varied from 0.58 g/100 g (SP003) to 8.80 g/100 g (SP192), glucose varied from 0.25 g/100 g (SP056) to 8.64 g/100 g (SP192), while maltose varied from 0.04 g/100 g (SP192) to 1.19 g/100 g (SP210) (Fig. 3e). The total carotenoid content ranged from 0 to 29.40 mg/100 g (SP267), total anthocyanin content from 0 to 2.99 g/kg (SP002), total flavonoid content from 1.47 g/kg (SP249) to 53.91 g/kg (SP116), and total phenol content from 0.37 g/kg (SP229) to 21.58 g/kg (SP116), with correspondingly high CVs (Fig. 3f). In contrast, amylose, total starch, dry matter, sucrose, and amylopectin exhibited relatively low variability (Table S2). The Shannon-Wiener index for root quality traits ranged from 4.43 to 5.69, except for total anthocyanin (0.69), which was lower due to the limited presence of anthocyanins in non-purple-fleshed sweet potato varieties. This aligns with earlier reports indicating that roots with white, yellow, or orange flesh typically have little to no anthocyanin content (de Albuquerque et al., 2019; Grace et al., 2014; Ji, Zhang, Li, & Li, 2015).

To sum up, the significant variation (average of 57.93 %) and extensive diversity (average of 5.41) of 24 quality components in stem tips and roots, probably linked to self-incompatibility and the prolonged domestication history of sweetpotato species (Baccichet et al., 2022). Germplasm with extreme values for quality components may serve as potential material for genetic mechanism analysis, and the observed genetic variation allows breeders to exploit additive and non-additive

gene effects for improving nutritional profiles (Pfeiffer & McClafferty, 2007; Wang et al., 2022). Traits with high CV, such as total anthocyanin, total carotenoid, total phenol, and total flavonoid content, could be improved through selective breeding.

3.2. Correlation analysis of stem tip and root quality traits

Correlation analysis is crucial for understanding the accumulation and variation of quality components, as well as for enhancing their utilization (Wang et al., 2022). In stem tips, crude protein content was significantly negatively correlated with soluble sugar ($r = -0.59$, $p < 0.001$) and chlorogenic acid ($r = -0.42$, $p < 0.001$), while total phenol content showed positive correlations with chlorogenic acid ($r = 0.67$, $p < 0.001$) and total flavonoid content ($r = 0.34$, $p < 0.001$) (Fig. 4). In roots, total starch was positively correlated with dry matter content ($r = 0.52$, $p < 0.001$) but negatively correlated with sugars, including soluble sugar, reducing sugar, fructose, and glucose, which were themselves positively intercorrelated. Additionally, total phenol content exhibited a strong positive correlation with both total flavonoid ($r = 0.94$, $p < 0.001$) and total anthocyanin ($r = 0.66$, $p < 0.001$). These findings are consistent with the results of Xiong et al. (2024), who observed similar correlations between starch, sugars, and dry matter content in sweetpotato roots. However, weak correlations between the traits of above-ground (stem tips) and below-ground (roots) parts offer limited insight into the physiological trade-offs involved in resource allocation between different plant tissues (Fig. 4).

3.3. Comparison of quality components among various germplasm types and flesh colors

Significant differences in quality traits of stem tips and roots were observed among different sweetpotato germplasm types (Table 1). Wild relatives exhibited the highest total flavonoid and total phenol contents in both stem tips (22.80 and 31.38 g/kg) and roots (20.53 and 9.28 g/kg), but had the lowest cellulose (10.92 g/100 g) and crude protein (16.73 g/100 g) contents in stem tips, as well as the lowest total starch (38.87 g/100 g) and maltose (0.45 g/100 g) contents in roots. Breeding lines had the highest crude protein content (18.84 g/100 g) in stem tips, while landraces showed the highest soluble sugar (13.94 g/100 g), reducing sugar (2.92 g/100 g), fructose (2.80 g/100 g), and glucose (2.43 g/100 g) contents in roots. Released varieties had the highest cellulose content (13.08 g/100 g) in stem tips and total carotenoid content (2.23 mg/100 g) in roots. Introduced accessions, meanwhile, exhibited the highest total anthocyanin content (0.40 g/kg) in stem tips, though this was not significantly difference from other germplasm types. Sugars such as sucrose, fructose, glucose, and maltose are key

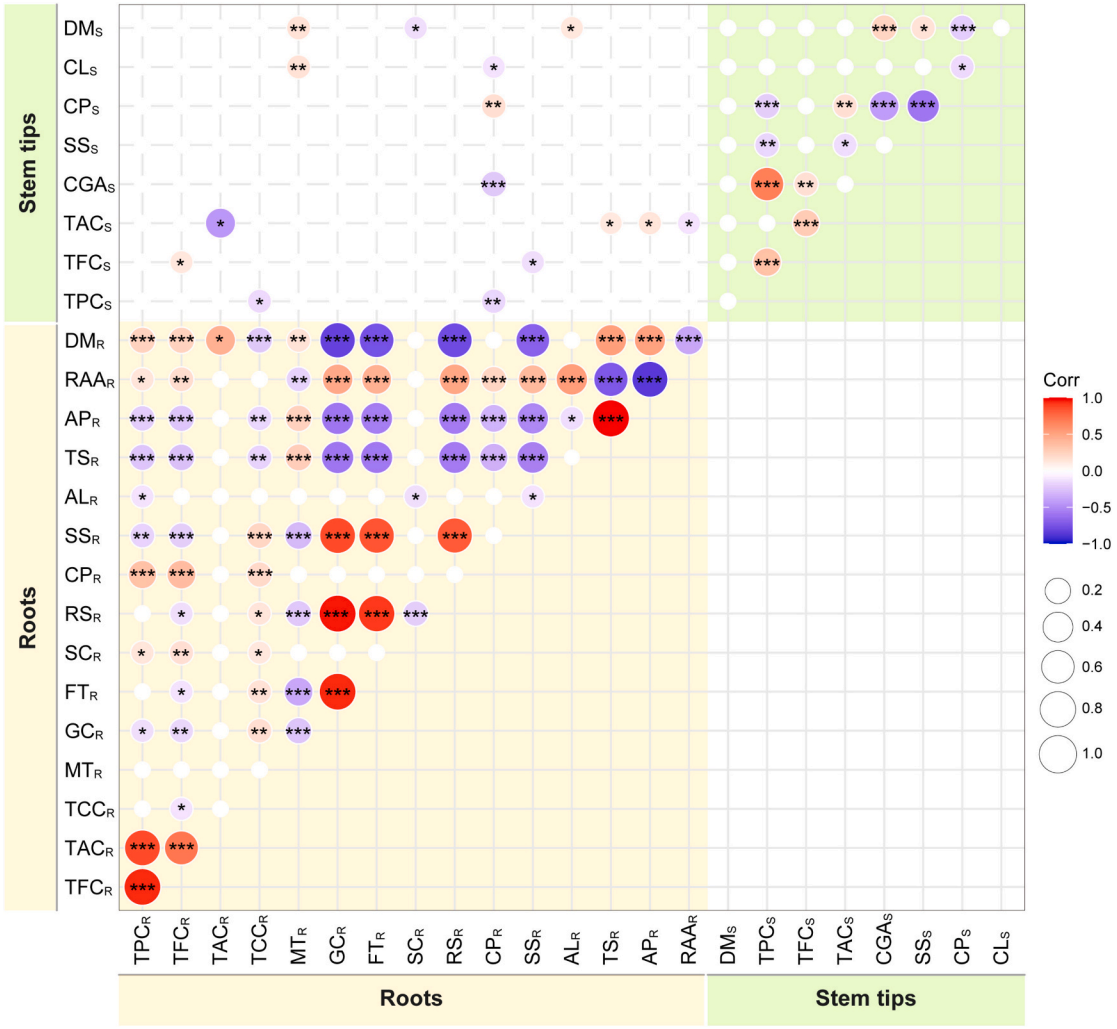

Fig. 4. Correlation analysis between 24 quality traits. Note: The subscript S and R represents the trait of the stem tips and roots, respectively. DM: dry matter; CL: cellulose; CP: crude protein; SS: soluble sugar; CGA: chlorogenic acid; TAC: total anthocyanin content; TFC: total flavonoid content; TPC: total phenol content; TS: total starch; AL: amylose; AP: amylopectin; RAA: ratio of amylose to amylopectin; RS: reducing sugar; SC: sucrose; FT: fructose; GC: glucose; MT: maltose; TCC: total carotenoid content.

Table 1
Characterization data of 8 stem tip quality traits and 16 roots quality traits of different sweetpotato germplasm types.

Organ	Type	DM_S	CL_S	CP_S	SS_S	CGA_S	TAC_S	TFC_S	TPC_S
		(g/100 g)				(g/kg)	(g/kg)		
Stem tips	BL	10.86 ± 1.33 b	11.44 ± 2.26 ab	18.84 ± 2.27 a	17.60 ± 5.20	3.00 ± 0.62	0.39 ± 0.16	18.95 ± 3.18 b	22.42 ± 7.90 b
	IA	11.63 ± 1.59 ab	12.91 ± 3.17 ab	17.76 ± 2.70 ab	19.33 ± 5.11	3.50 ± 0.81	0.40 ± 0.18	20.85 ± 4.26 ab	30.24 ± 9.93 a
	LR	11.46 ± 1.62 b	12.77 ± 3.06 ab	18.14 ± 2.29 ab	18.56 ± 6.00	3.45 ± 0.79	0.38 ± 0.18	19.32 ± 3.50 b	29.59 ± 9.54 a
	RV	11.17 ± 1.33 b	13.08 ± 3.18 a	18.55 ± 2.72 a	19.16 ± 6.65	3.23 ± 0.76	0.36 ± 0.17	21.04 ± 3.32 ab	25.11 ± 9.60 ab
	WR	12.52 ± 2.13 a	10.92 ± 1.06 b	16.73 ± 2.65 b	20.35 ± 7.65	3.53 ± 0.46	0.33 ± 0.16	22.80 ± 3.63 a	31.38 ± 9.96 a
Roots	Type	DM_R (g/100 g)	RAA_R	AP_R	TS_R	AL_R	SS_R	CP_R	RS_R
	BL	31.325 ± 3.86 a	29.89 ± 10.01 b	41.20 ± 5.51 a	53.25 ± 5.64 a	12.05 ± 1.70	11.64 ± 3.35	3.34 ± 0.69 b	1.40 ± 0.66 b
	IA	28.93 ± 4.39 a	33.06 ± 10.26 b	39.31 ± 6.83 a	51.74 ± 6.63 a	12.43 ± 1.79	11.86 ± 3.37	3.35 ± 0.63 b	1.68 ± 1.32 ab
	LR	25.67 ± 4.25 b	35.26 ± 11.70 b	37.02 ± 7.25 a	49.35 ± 7.32 a	12.33 ± 1.66	13.94 ± 5.28	3.17 ± 0.63 b	2.92 ± 2.22 a
	RV	26.12 ± 4.19 b	35.38 ± 10.77 b	37.11 ± 6.96 a	49.59 ± 6.85 a	12.48 ± 1.80	13.70 ± 4.79	3.36 ± 0.68 b	2.58 ± 1.77 ab
	WR	29.70 ± 6.22 a	47.13 ± 15.13 a	26.79 ± 4.78 b	38.87 ± 3.91 b	12.08 ± 1.83	11.20 ± 4.56	4.58 ± 1.61 a	2.28 ± 1.72 ab
	Type	SC_R (g/100 g)	FT_R	GC_R	MT_R	TCC_R (mg/100 g)	TAC_R (g/kg)	TFC_R	TPC_R
	BL	9.41 ± 1.71	1.87 ± 0.66 b	1.40 ± 0.67 b	0.69 ± 0.18 a	1.72 ± 4.06	0.36 ± 0.79 a	8.72 ± 5.98 b	4.99 ± 4.06 b
	IA	9.65 ± 1.54	2.17 ± 0.86 ab	1.68 ± 0.91 ab	0.68 ± 0.21 a	0.95 ± 2.17	0.15 ± 0.43 a	7.60 ± 5.25 b	3.95 ± 3.01 b
	LR	9.37 ± 1.71	2.80 ± 1.39 a	2.43 ± 1.44 a	0.62 ± 0.22 a	0.61 ± 1.14	0.01 ± 0.03 b	6.70 ± 5.72 b	3.38 ± 2.75 b
	RV	9.45 ± 1.87	2.55 ± 1.11 ab	2.24 ± 1.14 a	0.65 ± 0.25 a	2.23 ± 4.89	0.16 ± 0.46 ab	7.22 ± 5.61 b	3.88 ± 3.05 b
	WR	8.45 ± 1.68	2.15 ± 1.35 ab	1.72 ± 1.29 ab	0.45 ± 0.22 b	0.31 ± 0.42	0.00 ± 0.00 b	20.53 ± 9.21 a	9.28 ± 3.74 a

Five types of germplasm: breeding lines (BL), introduced accessions (IA), landraces (LR), released varieties (RV), and wild relatives (WR). The subscript S and R represents the trait of the stem tips and roots, respectively. DM: dry matter; CL: cellulose; CP: crude protein; SS: soluble sugar; CGA: chlorogenic acid; TAC: total anthocyanin content; TFC: total flavonoid content; TPC: total phenol content; TS: total starch; AL: amylose; AP: amylopectin; RAA: ratio of amylose to amylopectin; RS: reducing sugar; SC: sucrose; FT: fructose; GC: glucose; MT: maltose; TCC: total carotenoid content.

contributors to the sweet taste of sweetpotato roots (Wang et al., 2016), while phenols and flavonoids provide antioxidant properties (Milenković et al., 2024). These findings suggest that utilizing specific germplasm types, such as landraces and wild relatives, could facilitate the breeding of new sweetpotato varieties with enhanced sugar content (sweet taste) and higher phenolic compounds levels (health function).

Significant differences in quality traits were also observed among sweetpotatoes with different flesh colors, consistent with previous reports (de Albuquerque et al., 2019; Ji et al., 2015). Red-orange-fleshed accessions had higher dry matter (11.60 g/100 g) and cellulose (13.53 g/100 g) in stem tips, as well as a higher ratio of amylose to amylopectin (37.34 %), soluble sugar (16.19 g/100 g), reducing sugar (3.15 g/100 g), fructose (3.01 g/100 g), glucose (2.72 g/100 g), and total carotenoid content (6.51 mg/100 g) in roots (Fig. 5). In contrast, purple-fleshed accessions had higher total flavonoid content (21.74 g/kg) in stem tips, and higher dry matter (30.52 g/100 g), amylopectin (39.29 g/100 g), total starch (51.15 g/100 g), total anthocyanin (1.01 g/kg), total flavonoid (15.75 g/kg), and total phenol (9.12 g/kg) contents in roots. These results corroborate previous findings that anthocyanins, flavonoids, and phenols are concentrated in purple sweetpotatoes, while carotenoids are more abundant in orange-fleshed varieties (Grace et al., 2014; Ji et al., 2015; Park et al., 2016). In addition, sweetpotatoes with cream flesh also exhibited higher total starch content (51.12 g/100 g) in roots.

3.4. Comprehensive quality evaluation of germplasm resources

Sweetpotato quality is a multifaceted concept that reflects not only individual quality traits but also the interactions between them. To better understand relationships among the 24 quality traits evaluated across 296 germplasm resources, hierarchical cluster analysis and PCA were conducted. The germplasms were categorized into three clusters (Fig. 6a): cluster 1 (defined as high sugars and total carotenoids group) with high soluble sugar, reducing sugar, fructose, glucose, and total carotenoid contents, cluster 2 (high phenolic compound group) with high total flavonoid and phenol contents, and cluster 3 (high starch group) with high total starch and amylopectin contents (Table S3). Germplasms from cluster 1, particularly those with red-orange or yellow flesh, holds potential for developing varieties with attractive color, enhanced nutritional value, and functional properties (de Albuquerque et al., 2019; Tanaka, Ishiguro, Oki, & Okuno, 2017). Conversely, germplasms in cluster 2 are valuable for breeding antioxidant-rich varieties with elevated phenolic and flavonoid contents, particularly purple-fleshed sweetpotatoes (Laurie et al., 2020; Tomar et al., 2021). According to the correlation matrix of the 24 quality traits, the PC1 and PC2 explained 37 % of the total variability (Fig. 6b). The relatively low explained variance due to the large number of germplasm resources and indicators included in this study, which increased the noise and diversity in the data, making it difficult for the principal components to effectively capture the correlations among all variables. The PCA loadings revealed that sugars such as soluble sugar, reducing sugar, fructose, and glucose were positively correlated with PC1, whereas dry matter exhibited a negative correlation. Meanwhile, PC2 was primarily influenced by the positive correlations with total flavonoid and total phenol contents in roots.

Further, a MCDM process was employed to comprehensively evaluate the quality of the 296 sweetpotato germplasm. The EW-PCA-TOPSIS models were developed for the three dimensions, and the weight of each index and the comprehensive quality score of each germplasm are shown in Table S2 and Fig. 6c. Based on the overall quality assessment, accessions SP192, SP188, and SP116 were identified as top-performing germplasms. SP286, SP140, and SP153 were highlighted as ideal candidates for superior quality in stem tips, while SP192, SP188, and SP116 stood out for root quality. Detailed quality data for six elite germplasm resources are provided in Table S4. These accessions, noted for their superior quality traits, have great potential to be used as elite parental material for breeding programs aimed at improving the nutritional quality of sweetpotato. Moreover, the comprehensive quality scores for both stem tips and roots of the 296 germplasm accessions followed a normal distributed (Fig. 6d). The top 5 % of germplasms, based on their comprehensive quality scores, were classified as superior (list in Table S5), while the remaining 95 % were categorized as mediocre.

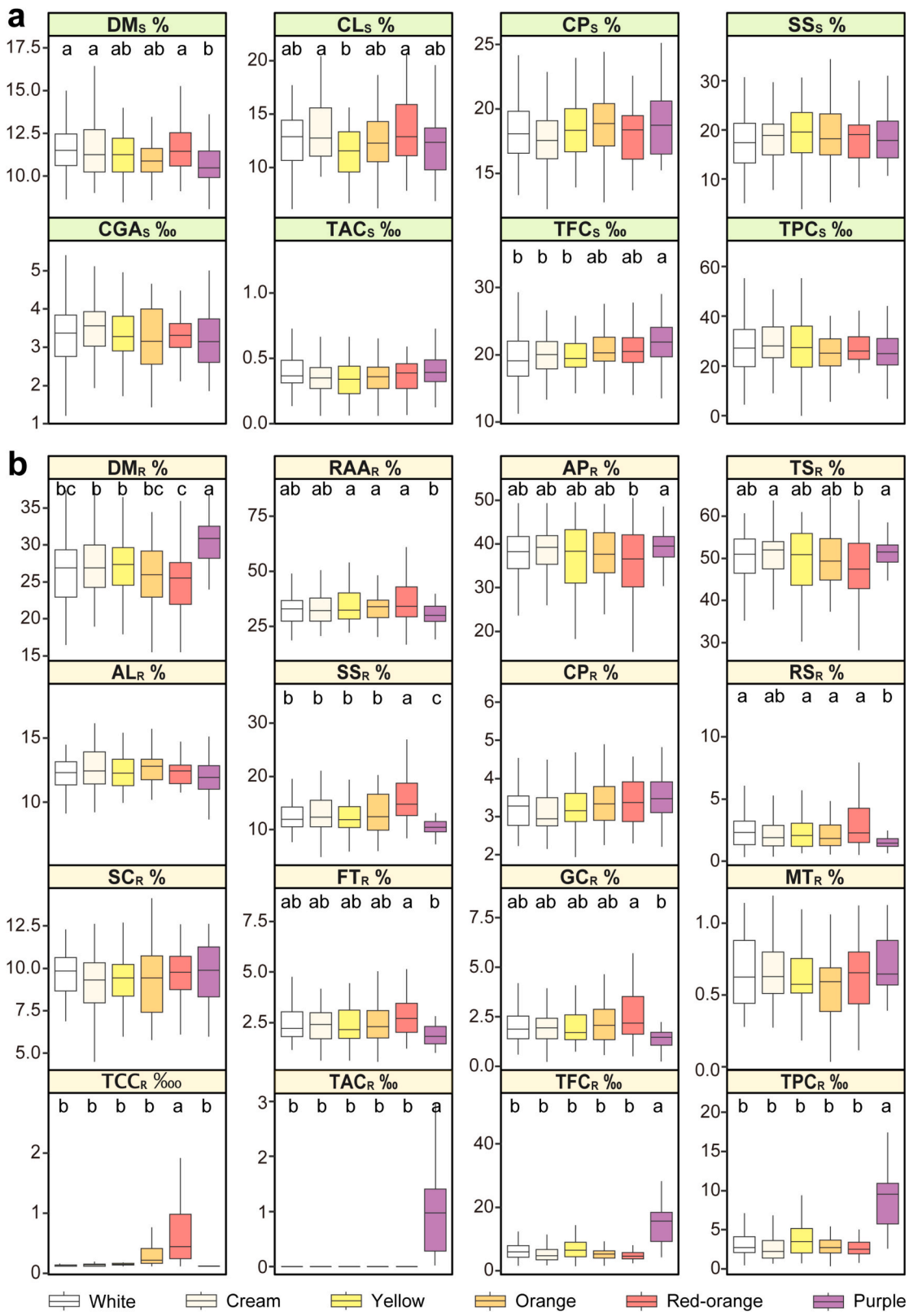

Fig. 5. Comparative analysis of 24 quality components of six different sweetpotato flesh colors. (a) 8 stem tip quality traits. **(b)** 16 root quality traits. Note: The subscript S and R represents the trait of the stem tips and roots, respectively. DM: dry matter; CL: cellulose; CP: crude protein; SS: soluble sugar; CGA: chlorogenic acid; TAC: total anthocyanin content; TFC: total flavonoid content; TPC: total phenol content; TS: total starch; AL: amylose; AP: amylopectin; RAA: ratio of amylose to amylopectin; RS: reducing sugar; SC: sucrose; FT: fructose; GC: glucose; MT: maltose; TCC: total carotenoid content.

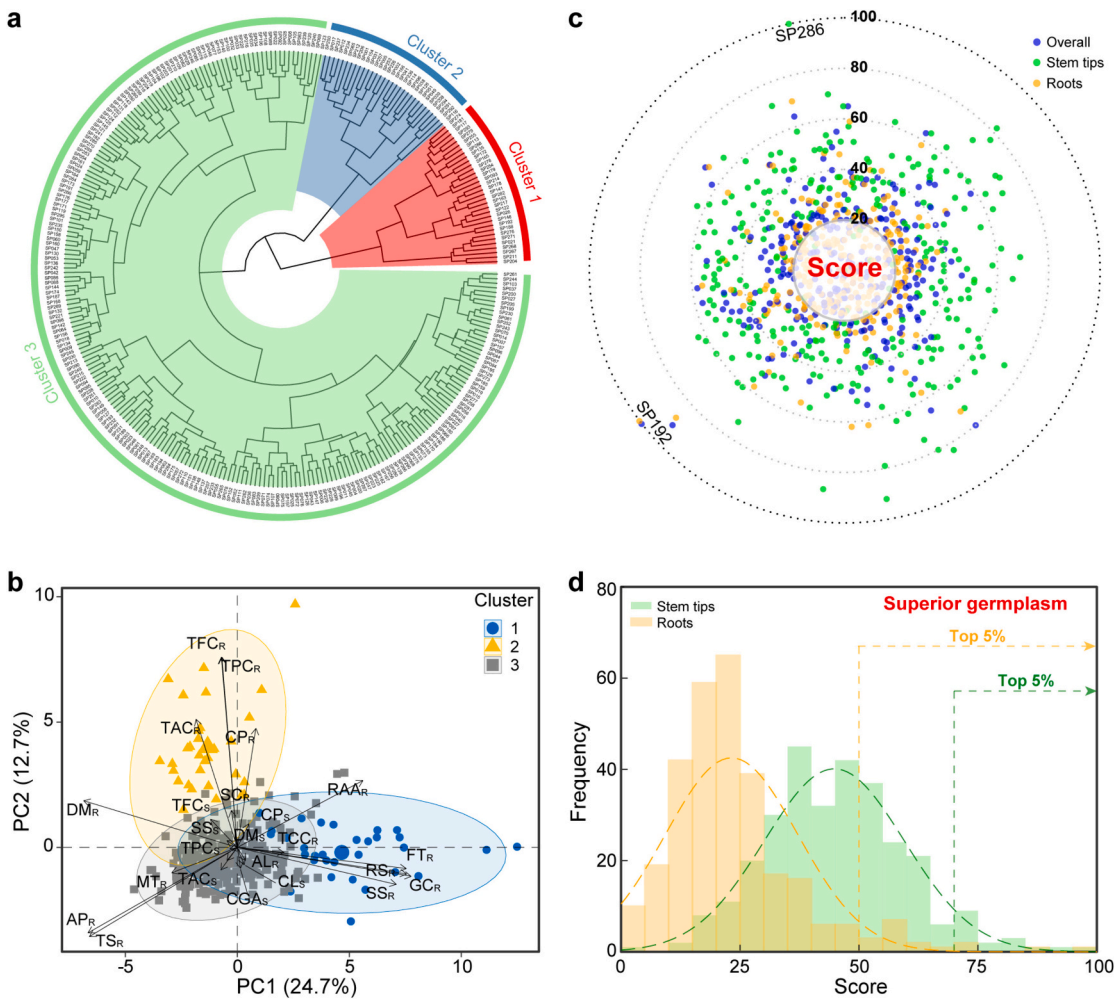

Fig. 6. Comprehensive quality analysis of 296 sweetpotato core germplasm resources. (a) Hierarchical clustering analysis. **(b)** Biplot from principal component analysis of the 24 quality characteristics of 296 sweetpotato accessions. **(c)** Comprehensive quality scores of 296 sweetpotato accessions across three dimensions. **(d)** Frequency distribution of comprehensive quality scores for stem tips and roots. Note: The subscript S and R represents the trait of the stem tips and roots, respectively. DM: dry matter; CL: cellulose; CP: crude protein; SS: soluble sugar; CGA: chlorogenic acid; TAC: total anthocyanin content; TFC: total flavonoid content; TPC: total phenol content; TS: total starch; AL: amylose; AP: amylopectin; RAA: ratio of amylose to amylopectin; RS: reducing sugar; SC: sucrose; FT: fructose; GC: glucose; MT: maltose; TCC: total carotenoid content.

3.5. NIRS modeling for rapid screening superior germplasm

The absorption band peaks were mainly located between 4000 and 7000 cm^{-1}, a range typical of both freeze-dried and hot-air-dried stem tip and root samples (Fig. 7a and b). Specifically, major peaks were observed at approximately 4328, 4560, 4744, 5168, 5776, and 6808–6816 cm^{-1} for stem tips, and at 4312–4376, 4752–4760, 5168–5176, 5632–5656, 6376–6384, and 6784–6848 cm^{-1} for roots. From a set of 751 spectral variables, we successfully identified between 44 and 76 feature variables across both freeze-dried and hot-air-dried stem tip and root samples. This outcome is consistent with previous findings, which have demonstrated the Random Frog algorithm's superior performance in variable selection (Li et al., 2012; Tang et al., 2023). The PCA scores for stem tip and root NIRS data from the calibration and prediction sets showed well-mixed, regardless of the were drying method (Fig. 7c and d). This even distribution indicates effective partitioning of the sample subsets, a crucial factor for selecting representative samples for calibration (Tang et al., 2024).

As one of the most robust ensembles learning algorithms, RF was employed to develop a rapid screening qualitative model for superior germplasm. In the calibration set, 224 germplasms were classified as mediocre and 12 as superior, while the prediction set included 57 mediocre and 3 superior germplasms. The classification performance of the established RF models was consistent across both freeze-dried and hot-air-dried stem tips and roots. As shown in Fig. 7e and f, all 236 calibration samples of stem tips and roots were correctly classified, achieving a recognition rate of 100 %. For the 60 predicted samples, the recognition rates for stem tips and roots were 97 % and 98 %, respectively. Overall, the RF models demonstrated satisfactory predictive accuracy, making them a reliable tool for the rapid screening of superior sweetpotato germplasm, whether for leaf-vegetable or root-based utilization purposes.

3.6. Research limitations and future prospects

The study is among the few that provides a comprehensive quality dataset for a large number of sweetpotato accessions from various regions worldwide, offering valuable insights for sweetpotato breeding programs. The quality information presented here can aid geneticists in developing sweetpotato varieties with enhanced nutritional value. Additionally, it can support growers and consumers in selecting superior germplasm resources for table use and processing, ultimately contributing to improved quality and health benefits (Song et al., 2022). We advocate that sweetpotato stem tips and roots be regarded as healthy

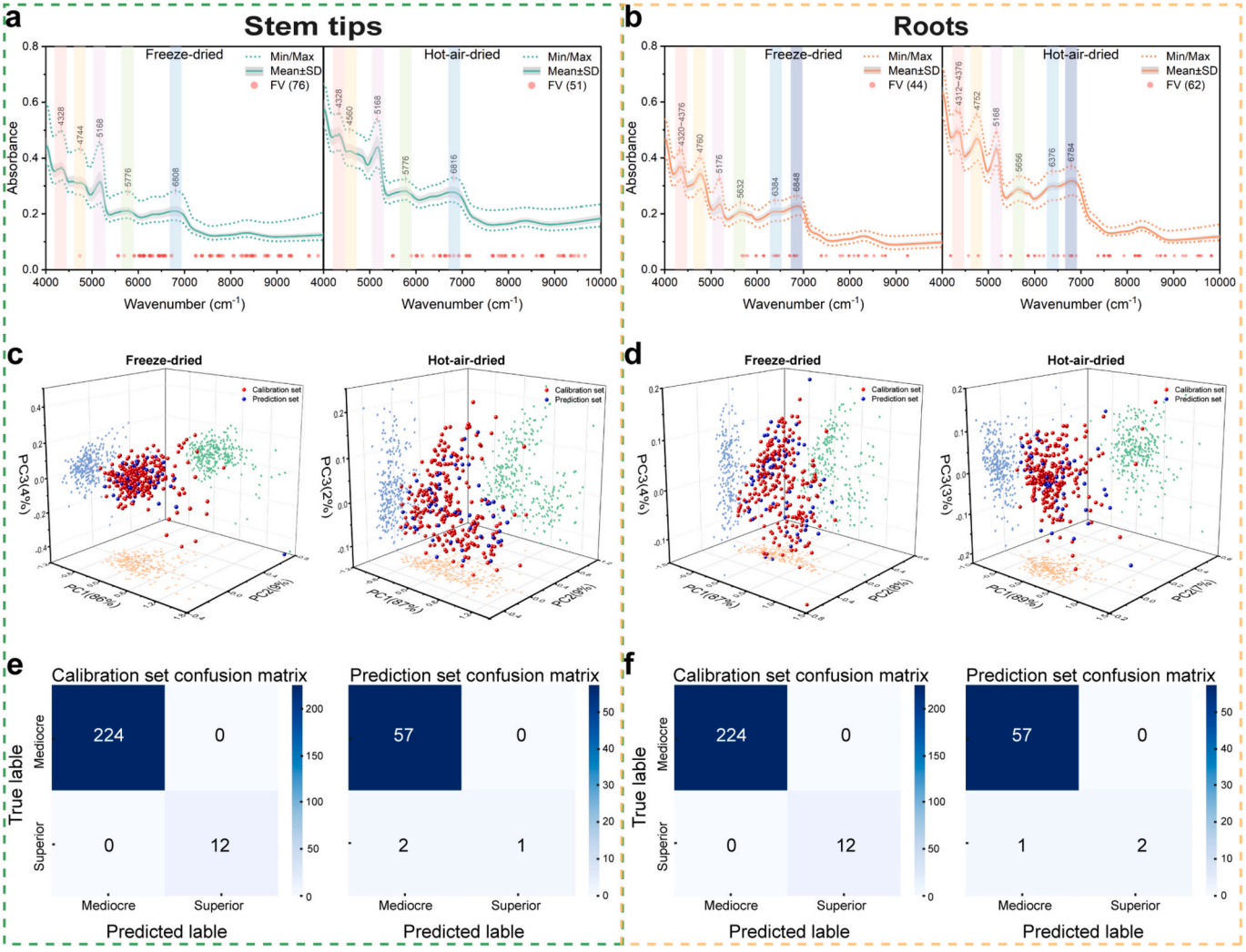

Fig. 7. Near infrared spectra of stem tips and roots and their rapid screening qualitative models. (a-b) Original spectra of freeze-dried and hot-air-dried for stem tips and roots. **(c-d)** PCA scores of freeze-dried and hot-air-dried for stem tips and roots. **(e-f)** Classification model performance of screening superior germplasm for stem tips and roots utilization. Min: minimum; Max: maximum; SD: standard deviation; FV: feature variable.

food options, suitable for direct use in home cooking and as ingredients in the food industry for creating value-added functional products (de Albuquerque et al., 2019).

Notably, this study is pioneering in its integration of a comprehensive quality scoring model with NIRS technology for the rapid screening of superior germplasm. This innovative approach offers breeders and researchers a systematic and efficient platform for qualitative evaluation, especially in the context of nutritional food development. However, it is important to acknowledge several limitations of this study, which highlight the need for further investigation. First, additional nutritional components, such as mineral elements and anti-nutritional components, as well as quality indicators related to taste and aroma, should be incorporated into the comprehensive quality scoring model. This will provide a more holistic evaluation of sweetpotato germplasm. Second, while this study objectively assigned weight coefficients to various quality traits, future research should consider incorporating subjective input from breeders and food scientists to adjust these coefficients based on the specific requirements of different end-use products. Such an approach would make the scoring model more applicable to practical production scenarios.

4. Conclusions

This study conducted a comprehensive quality assessment of 296 sweetpotato germplasm accessions, revealing significant phenotypic diversity. Landraces were found to be particularly rich in sugars, while wild relatives exhibited elevated levels of flavonoids and phenols. Accessions with red-orange flesh demonstrated high contents of sugars and carotenoids, whereas those with purple flesh were characterized by higher levels of dry matter, starch, and total flavonoids and phenols. Through our comprehensive quality scoring model, the top 5 % of accessions were identified as superior, with SP286, SP140, and SP153 and SP192, SP188, and SP116 standing out as ideal candidates for stem tips and roots, respectively. The integration of NIRS with the RF algorithm enabled the development of rapid and accurate screening models, achieving prediction accuracies of 97 % for stem tips and 98 % for roots. These advancements offer valuable tools for breeders and the food industry to enhance the nutritional quality of sweetpotatoes, contributing to improved food security and better nutritional outcomes.

CRediT authorship contribution statement

Chaochen Tang: Conceptualization, Data curation, Funding acquisition, Investigation, Methodology, Software, Visualization, Writing –

original draft. **Yi Xu:** Formal analysis, Methodology, Validation. **Rong Zhang:** Data curation, Investigation. **Xueying Mo:** Data curation, Investigation. **Bingzhi Jiang:** Data curation, Formal analysis, Investigation, Resources. **Zhangying Wang:** Conceptualization, Data curation, Funding acquisition, Investigation, Project administration, Resources, Supervision.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.fochx.2024.102009.

Data availability

Data will be made available on request.

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