# Metabolomic Analysis of Flower Color Metabolites in Three Rose Cultivars: A Postprint

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## Abstract

Rosa rugosa possesses high ornamental and commercial value; however, its relatively limited flower color variation restricts its development, utilization, and application in landscape design. To investigate the color-producing compounds in three different rose varieties—'Kushui Rose', 'Mohong Rose', and 'Bulgarian White Rose'—this study employed ultra-high performance liquid chromatography-quadrupole-time-of-flight mass spectrometry (UPLC-Q-TOF-MS) to detect the types and contents of flavonoids in petals, conducted enrichment analysis of differential metabolites via the KEGG database, screened key metabolites, and analyzed their correlation with flower color phenotypic values. The results demonstrated: (1) A total of 58 metabolites were detected in the petals of the three different colored rose varieties, among which only one anthocyanin, cyanidin-3-O-glucoside, was identified, accounting for approximately 30.45%; (2) K-means clustering analysis indicated that 12 key metabolites were annotated to KEGG metabolic pathways, with pinocembrin and myricetin being the primary substances determining the red coloration of 'Kushui Rose' and 'Mohong Rose', while eriodictyol, luteolin, and kaempferol were the main substances determining the white coloration of 'Bulgarian White Rose'. These findings can provide a theoretical basis for breeding roses with specific colors and promote their application in landscape greening.

## Full Text

### Metabolomics Analysis of Flower Color Substances in Three Rosa rugosa Cultivars

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**Abstract**

Rosa rugosa is a deciduous shrub in the Rosaceae family with high ornamental and commercial value, but its relatively limited color range restricts its development and landscape applications. To investigate the color-forming substances in three distinct rose cultivars—'Kushui Rose' (Rosa rugosa × Rosa sertata), 'Crimson Glory' (Rosa Crimson Glory), and 'Bulgarian White Rose' (Rosa alba)—this study employed ultra-high performance liquid chromatography-quadrupole time-of-flight mass spectrometry (UPLC-Q-TOF-MS) to identify and quantify flavonoid compounds in petals. Differential metabolites were enriched and analyzed using the KEGG database to screen for key metabolites and examine their correlation with flower color phenotypic values. The results revealed: (1) A total of 58 metabolites were detected across the three cultivars, with only one anthocyanin—cyanidin-3-O-glucoside—accounting for approximately 30.45% of total flavonoids; (2) K-means clustering analysis identified 12 key metabolites annotated to KEGG metabolic pathways, among which pinocembrin and myricetin were the primary compounds determining the red coloration of 'Kushui Rose' and 'Crimson Glory', while eriodictyol, luteolin, and kaempferol were the main substances responsible for the white coloration of 'Bulgarian White Rose'. These findings provide a theoretical foundation for breeding roses with specific colors and promote their application in landscape greening.

**Keywords:** Rosa rugosa cultivars; flower color substances; metabolomics; UPLC-Q-TOF-MS; correlation

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## Introduction

Flower color represents a crucial characteristic of ornamental plants, determining both their aesthetic and commercial value [**?**]. Recent research has demonstrated that the primary factors influencing flower color formation are the types and contents of plant pigments, which mainly include three major categories: flavonoids, carotenoids, and alkaloids [**?**, **?**]. Among these, the accumulation of flavonoid secondary metabolites constitutes a key determinant of flower color. Anthocyanins, which appear as glycosylated anthocyanidins in plants, constitute the main components of red, blue, and purple pigments in petals, while chalcones represent important yellow colorants; however, flavones and flavonols are typically colorless or pale white [**?**, **?**]. Studies on Ericaceae species have revealed that flower color depends on flavonoid composition, with anthocyanins playing a critical role and flavonols serving auxiliary coloration functions [**?**, **?**]. With recent advances in plant metabolomics technology, the coloration mechanisms of numerous ornamental plants have been preliminarily investigated, including Camellia japonica, Prunus serrulata, and P. pseudocerasus [**?**], as well as Helianthus annuus [**?**]. Shi et al. [**?**] utilized metabolomics to elucidate how different metabolites and metabolic pathways regulate color differences between

Yunnan red and Crimson Glory roses. Collectively, current research indicates that pigment types, contents, and metabolic synthesis pathways represent important factors influencing floral color diversity [**?**, **?**].

Rosa rugosa, a deciduous shrub in the Rosaceae family native to China with a long cultivation history, is renowned as the "Queen of Flowers" and "Flower of Love." It possesses ornamental, economic, ecological, and edible value and has been designated as a second-class protected plant in China [**?**]. Chinese rose cultivars are extremely diverse, encompassing double-petaled, single-petaled, and multi-petaled varieties, including: 'Kushui Rose' (Rosa rugosa × Rosa sertata), a natural hybrid between traditional Chinese rose and Rosa sertata, characterized by numerous small magenta flowers with fragrance and high oil yield, serving as an important edible double-petaled variety [**?**]; 'Crimson Glory' (Rosa Crimson Glory), also known as 'Zhumo Shuanghui,' a hybrid between Hybrid Tea Rose and Hybrid Perpetual Rose, featuring deep red flowers with extended flowering period, intense fragrance, and high yield, widely cultivated as a primary edible rose variety in Yunnan [**?**]; and 'Bulgarian White Rose' (Rosa alba), also called 'Turkish Rose,' producing pale pink, pink, and white flowers with high yield, oil content, and quality, representing another premium edible rose variety for essential oil extraction and rose water processing [**?**]. However, as an important ornamental plant, roses predominantly exhibit red, pink, white, and purple colors, with few other color variations, significantly limiting their landscape applications [**?**]. Current research on roses primarily focuses on volatile oil extraction and utilization, resource development and conservation, genetic diversity analysis and molecular markers, food production, transgenic color regulation technology, and cultivation and propagation techniques [**?**]. Although several studies have reported on transgenic color regulation in roses with promising results, research on color formation mechanisms and pigment composition in edible roses remains incomplete, and systematic analysis of the material basis for rose coloration is lacking, hindering the development and utilization of rose pigments and their landscape applications [**?**, **?**].

This study investigated three edible double-petaled rose cultivars with different flower colors—'Kushui Rose,' 'Crimson Glory,' and 'Bulgarian White Rose'—using targeted metabolomics to explore key metabolites affecting color formation. The research addressed: (1) analysis of flavonoid compound types and content differences among the three cultivars; and (2) screening of differential metabolites and metabolic pathways to identify primary color-determining compounds. These findings provide theoretical foundations for breeding roses with specific colors and promote their application in landscape greening.

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## Materials and Methods

**1.1 Sample Collection and Processing** Experimental materials comprised three cultivated rose varieties: magenta 'Kushui Rose' (Rosa rugosa × Rosa ser-

tata, KSMG), red 'Crimson Glory' (Rosa Crimson Glory, MHMG), and white 'Bulgarian White Rose' (Rosa alba, BMG). Petal materials were collected from the rose germplasm resource base at the Yongdeng County Rose Research Institute in Gansu Province. For each variety, three healthy, uniformly managed plants free from disease were selected. Petal samples were collected at full bloom stage on May 20 and June 5, 2022 [Figure 1: see original paper]. During collection, petals were sampled from four directional orientations and mixed. Each variety underwent three biological replications. Samples were immediately placed in numbered sealed bags, stored in ice boxes to prevent wilting, and subsequently preserved at -80 °C for metabolomic analysis [**?**].

**1.2.1 Flower Color Phenotype Measurement** Flower color was measured using the CIE L*ab** color space system [**?**, **?**]. Fresh petals were analyzed with a WR18 precision colorimeter (Shenzhen Weifu Optoelectronics Technology Co., Ltd.) to determine brightness (L*), redness (a*), and yellowness (b*) values, from which chroma (C*) and hue angle (h°) were calculated. This approach enabled digital quantification of flower color [**?**]. Under C/2° illumination, the light collector was positioned at the central upper epidermis of petals, with three flowers measured per sample and average values calculated [**?**].

**1.2.2 Flavonoid Extraction** Fresh petals were freeze-dried at -80 °C and pulverized (60 Hz, 30 s). A 100 mg sample was placed in a 5 mL centrifuge tube with 3,000 L extraction solution (75% methanol containing 1% acetic acid), vortexed for 30 s, homogenized at 40 Hz for 4 min, and sonicated in an ice bath for 30 min. The mixture was centrifuged at 12,000 $r \cdot min^{-1}$ (13,800 × g, 8.6 cm radius) for 15 min at 4 °C. The supernatant (2,500 L) was dried under nitrogen and reconstituted with 1,500 L extraction solution B (50% methanol containing 0.1% formic acid with internal standard). After vortexing for 1 min and sonicating in an ice bath for 15 min, the solution was centrifuged again at 12,000 $r \cdot min^{-1}$ (13,800 × g) for 15 min at 4 °C. The final supernatant was filtered through a 0.22 m membrane and transferred to a 2 mL sample vial. Quality control (QC) samples were prepared by mixing equal aliquots from all samples for instrumental analysis [**?**, **?**, **?**].

**1.2.3 Qualitative and Quantitative Analysis of Flavonoids** Flavonoids in petals were analyzed qualitatively and quantitatively using UPLC-Q-TOF-MS. The system comprised an ACQUITY™ UPLC I-Class ultra-high performance liquid chromatograph (Waters Corporation, Milford, MA, USA), an Xevo G2-XS QTof MS mass spectrometer (Waters Corporation, Manchester, UK), and UNIFI 1.8 software. Chromatographic separation was performed on a Waters UPLC BEH C18 column (1.7 m, 2.1 mm × 150 mm) using 0.1% formic acid aqueous solution (A) and acetonitrile (B) as mobile phases at a flow rate of 0.3 $mL \cdot min^{-1}$. The gradient elution program was: 0–0.5 min, 10% B; 0.5–15 min, 10–60% B; 15–16.01 min, 60–98% B; 16.01–18.00 min, 98% B; 18.00–18.01 min, 98–10% B; 18.01–20 min, 10% B. The column oven temperature was set at 40

°C, the autosampler at 8 °C, and injection volume was 2 L. Mass spectrometry data were acquired in multiple reaction monitoring (MRM) mode [**?**].

**1.3 Data Analysis** Color parameters (L, *a*, b*) were used to calculate chroma (*C* = (a$^2$ + *b*$^2$)$^1$/$^2$)* and hue angle (h° = arctan(a/*b*)). SPSS 22.0 software was employed for correlation analysis between flower color and key metabolites. Flavonoid metabolites in different colored roses were determined using the UPLC-MS/MS detection platform of Shanghai Biotree Biomedical Technology Co., Ltd. MetaboAnalyst 5.0 software was used for qualitative and quantitative analysis of all target compounds. Multivariate statistical analysis of metabolites across sample groups was performed in unsupervised mode, with significantly differential metabolites selected based on $P < 0.05$ and VIP $\geq 1$. Pathway enrichment analysis was conducted using the KEGG database, MBROLE 2.0, and the Microbiome Analysis website.

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## Results

**2.1 Flower Color Characteristics of Three Rose Cultivars** In the CIE L*ab** color space, L* represents brightness variation, with higher values indicating greater petal luminosity. As shown in Table 1 , 'Bulgarian White Rose' exhibited the highest L* value (78.41), indicating a brighter, whiter appearance. The a* parameter ranges from positive (red) to negative (green) values; 'Crimson Glory' showed an a* value 106.46 units higher than 'Bulgarian White Rose', confirming its red coloration. The b* parameter transitions from positive (yellow) to negative (blue); 'Bulgarian White Rose' displayed intermediate b* values, corresponding to white petals with yellowish tints. Chroma (C*) indicates color vividness, with higher values representing more saturated colors. 'Crimson Glory' exhibited the maximum C* value (110.37), reflecting deep red coloration, followed by 'Kushui Rose' (C* = 71.60) with magenta hues. Hue angle (h°) describes color tones across the red, orange, yellow, green, cyan, blue, and purple spectrum, with red near 0°, yellow around 90°, and red reappearing between 270°–360° through the purple region. Both 'Crimson Glory' and 'Bulgarian White Rose' showed h° values between 0°–90° (red-yellow range), while 'Kushui Rose' fell within 270°–360°, passing through the purple region.

**2.2 Flavonoid Composition and Content in Petals of Three Rose Cultivars** As illustrated in Figure 2 [Figure 2: see original paper], a total of 58 flavonoid metabolites were detected across the three rose varieties, including 24 flavones (~18.85%), 9 flavonols (~31.89%), 1 anthocyanin (~30.45%), 8 flavanols (~14.49%), 6 dihydroflavones (~0.08%), 3 isoflavones, 2 chalcones (~0.09%), and 5 other polyphenolic compounds (~4.15%). Hierarchical cluster analysis of petal samples and metabolites revealed significant differences in flavonoid accumulation patterns among the three varieties. After normalization, color intensity

represented metabolite content, with red indicating high abundance and blue indicating low abundance.

**2.3 Screening Analysis of Differential Metabolites** Differential flavonoid metabolites between groups were screened using criteria of $P < 0.05$ and VIP $\geq 1$, with fold-change representing the ratio of metabolite expression between different colored petal samples. As shown in Figure 3 [Figure 3: see original paper]A–C, 45 differential flavonoid metabolites were identified between 'Crimson Glory' and 'Bulgarian White Rose', including 22 significantly upregulated and 10 downregulated metabolites. Between 'Bulgarian White Rose' and 'Kushui Rose', 41 differential metabolites were found (8 upregulated, 22 downregulated). Between 'Crimson Glory' and 'Kushui Rose', 41 differential metabolites were detected (11 upregulated, 14 downregulated).

To investigate variation trends of flavonoid metabolites across different colored roses, the average relative content of all differential metabolites was z-score standardized and subjected to K-means clustering analysis. During the color transition from white to magenta to deep red (Table 2 ), 33 metabolites showed increasing trends while 8 exhibited decreasing trends. Flavones and flavonols displayed mixed patterns, whereas the anthocyanin cyanidin-3-O-glucoside consistently increased, suggesting it serves as the primary pigment responsible for red coloration in rose petals.

**2.4 KEGG Functional Annotation and Enrichment Analysis of Differential Metabolites** Enrichment analysis was performed on flavonoid metabolites showing increasing and decreasing trends from K-means clustering. Twelve key metabolites were successfully annotated to KEGG metabolic pathways, with several participating in multiple pathways (Table 3 ). Among the 33 upregulated metabolites, nine were annotated, including: vitexin and pinocembrin involved in flavonoid biosynthesis; eriodictyol and (-)-epigallocatechin in flavonoid biosynthesis and secondary metabolite biosynthesis; myricetin in flavonoid biosynthesis, flavone and flavonol biosynthesis, and secondary metabolite biosynthesis; naringenin, cianidanol, and chalconaringenin in four pathways including flavonoid biosynthesis, secondary metabolite biosynthesis, phenylpropanoid biosynthesis, and metabolic pathways; and apigenin in five pathways. Among eight downregulated metabolites, three were annotated: quercetin, kaempferol, and luteolin, all participating in flavonoid biosynthesis, flavone and flavonol biosynthesis, secondary metabolite biosynthesis, and metabolic pathways.

**2.6 Relationship Between Petal Phenotype and Key Metabolite Content in Three Rose Cultivars** During the color transition from white to magenta to deep red, 12 metabolites showing increasing (9) and decreasing (3) trends were successfully annotated to flavonoid metabolic pathways. Correlation analysis between color phenotypic values and these 12 key metabolites revealed significant relationships (Table 4 ). Brightness (L*) was extremely significantly*

*negatively correlated with redness (a*) and chroma (C*) (P < 0.01), indicating that increased brightness shifts petals toward white. Pinocembrin and myricetin were significantly negatively correlated with L* ($P < 0.01$ and $P < 0.05$, respectively) and positively correlated with a* and C* ($P < 0.01$), demonstrating that their accumulation enhances color vividness while reducing brightness. Conversely, eriodictyol, luteolin, and kaempferol were significantly positively correlated with L* and negatively correlated with a* and C* ($P < 0.01$), indicating their accumulation increases brightness and shifts petals toward white. Luteolin showed positive correlation with b* and negative correlation with h°, suggesting its accumulation moves color toward yellow. Hue angle (h°) was significantly negatively correlated with a* and C* ($P < 0.01$), confirming that increased redness reduces hue angle, moving color toward red. These results indicate that pinocembrin and myricetin are primary determinants of red coloration, while eriodictyol, luteolin, and kaempferol are key factors for white coloration, with luteolin specifically contributing to yellow hues.

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## Discussion and Conclusion

Flavonoid compounds constitute primary pigments in flower color formation, with anthocyanins being essential components whose content directly affects flower color [**?**]. Previous studies have demonstrated that cyanidin and its derivatives widely contribute to red petals in various plants [**?**]. Li et al. [**?**] identified cyanidin-3-O-glucoside as the main anthocyanin in red Camellia petals, and research on 30 Rhododendron cultivars found cyanidin content highest in red varieties [**?**], confirming cyanidin as a primary red pigment—consistent with our findings. Earlier studies reported cyanidin as the major flavonoid in Crimson Glory roses, with significantly higher content than other compounds [**?**], and identified cyanidin-3-glucoside as the main component of Kushui Rose pigment [**?**, **?**]. Our analysis detected 58 flavonoid metabolites across the three cultivars, with cyanidin-3-O-glucoside as the sole anthocyanin (~30.45% of total flavonoids). In Crimson Glory and Kushui Rose, cyanidin-3-O-glucoside accounted for 47.75% and 15.55% of total flavonoids, respectively—far exceeding the 0.04% in Bulgarian White Rose—demonstrating its critical role in red coloration and establishing it as the primary pigment in these cultivars.

To further investigate differential metabolites underlying color variation, numerous studies have shown that flower color formation is influenced by pigment types and contents [**?**, **?**]. Research on 'Zizhi' roses found that white petals contained only flavonoids, while pink and purple petals contained both flavonoids and anthocyanins [**?**]. White Camellia cultivars 'Silver White Charles' and 'White Phoenix' showed highest levels of luteolin and quercetin-3-O-glucoside [**?**], while white rose and chrysanthemum flowers contained only pale yellow or colorless flavones and flavonols [**?**], consistent with our results. Our screening ($P < 0.05$, VIP $\geq 1$) identified 12 key metabolites: 6 flavones, 2 flavanols, 2 flavonols, 1 dihydroflavone, and 1 chalcone. Flavones pinocembrin and myricetin

accumulation affected L, *a*, and C* values, with higher content producing more vivid red coloration and reduced brightness. In contrast, flavone luteolin, dihydroflavone eriodictyol, and flavonol kaempferol accumulation increased brightness and shifted petals toward white. Luteolin's positive correlation with b* indicated its role in yellow coloration, making it the primary compound for yellow hues and significantly correlating with the yellowish tint in Bulgarian White Rose petals. Thus, pinocembrin, myricetin, luteolin, eriodictyol, and kaempferol are all key metabolites influencing rose coloration.

In summary, significant differences in flavonoid metabolite types and contents were detected among 'Kushui Rose,' 'Crimson Glory,' and 'Bulgarian White Rose,' substantially impacting flower color. The study identified 58 flavonoid metabolites across the three cultivars, with cyanidin-3-O-glucoside, pinocembrin, and myricetin serving as primary pigments for red coloration in Kushui and Crimson Glory roses, while eriodictyol, luteolin, and kaempferol were key determinants of white coloration in Bulgarian White Rose.

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*Note: Figure translations are in progress. See original paper for figures.*