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UHPLC Q-Orbitrap Mass Spectrometry-Based Molecular Networking for Identification of Chemical Constituents in the Multi-Herb Formula Runyan Mixture

Huihui Zhang, Yingzhi Zhang, Jiahao Li, Chuanjiang Fan, Junjie Gu, Yinzhi Jin,* and Yingpeng Tong*

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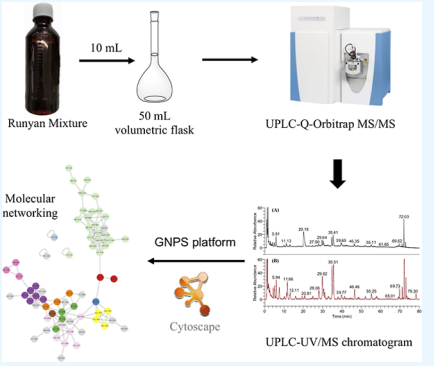
ABSTRACT: Traditional Chinese medicine (TCM) in-hospital preparations are approved for use only in the hospital where they are prepared. They are widely used in China because of their efficacy and affordable price. However, few researchers focused on their quality controls and treatment mechanisms, for which a key consideration is the elucidation of their chemical composition. Runyan mixture (RY) is a typical in-hospital TCM preparation comprising a formula of eight herbal drugs used for adjuvant therapy of upper respiratory tract infections. The chemical constituents of formulated RY have not yet been elucidated. In the present work, RY was analyzed by a ultrahigh-performance liquid chromatography system equipped with high-resolution orbitrap mass spectrometry (MS). The acquired MS data were processed by MZmine and a feature-based molecular networking was constructed to identify the metabolites of RY. 165 compounds including 41 flavonoid *O*-glycosides, 11 flavonoid C-glycosides, 18 quinic acids, 54 coumaric acids, 11 iridoids, and 30 others were identified. This study demonstrates an efficient method to identify compounds in complex herbal drug mixtures using high-resolution MS and molecular networking tools which will support future research into quality controls and treatment mechanisms of in-hospital TCM preparations.



1. INTRODUCTION

The practice of traditional Chinese medicine (TCM) and the clinical application of its herbal pharmacopoeia date back thousands of years.[1] The chemical components of TCM prescriptions are complex mixtures, especially those composed of several herbs.[2] The elucidation of the chemical composition of TCM herbal formulae is required as a basis for research into a prescription's efficacy and safety.[3]

Ultrahigh-performance liquid chromatography combined with high-resolution mass spectrometry (UHPLC−HRMS) has proven to be an excellent chemical analysis method for complex systems due to its high sensitivity and specificity.[4,5] UHPLC−HRMS has been widely used in the detection of small molecules from plants,[6] animals,[7] and human samples.[8] Despite abundant available MS data, unequivocal identification of compounds in complex mixtures remains a challenge. A variety of commercial software sets for chemical identification have been developed, including Waters UNIFI[9] and Thermo Fisher Compound Discoverer.[10] These were developed primarily for the identification of chemicals through targeted screening using known databases. Recently, a new and open method, named Global Natural Products Social molecular networking (GNPS, https://gnps.ucsd.edu/), has been established by the Center for Computational Mass Spectrometry of the University of California San Diego.[11] This platform and its molecular networking (MN) application identify compounds by comparing their MS/MS spectral similarity. A development of MN, feature-based MN (FBMN), supports MS data processing tools such as MZmine in feature detection and alignment, with the additional capacity to differentiate positional and stereoisomers in complex systems.[6]

In China, some TCM formulations, so-called in-hospital preparations, are approved for use only in the hospitals in which they are prepared. Clinical trials have demonstrated the efficacy of same in-hospital preparations in disease treatment.[12] Widely used in China, especially in county or municipal hospitals, nearly 4000 in-hospital preparations are used in 253 hospitals in nine provinces.[13] Due to the lack of research funding and multidisciplinary interest, little research has focused on in-hospital preparations and, in particular, their quality control and treatment mechanisms. The identification of the active chemical components in in-hospital preparations is a key factor in this regard, for which UHPLC−HRMS is an effective, rapid, and affordable tool.[14]

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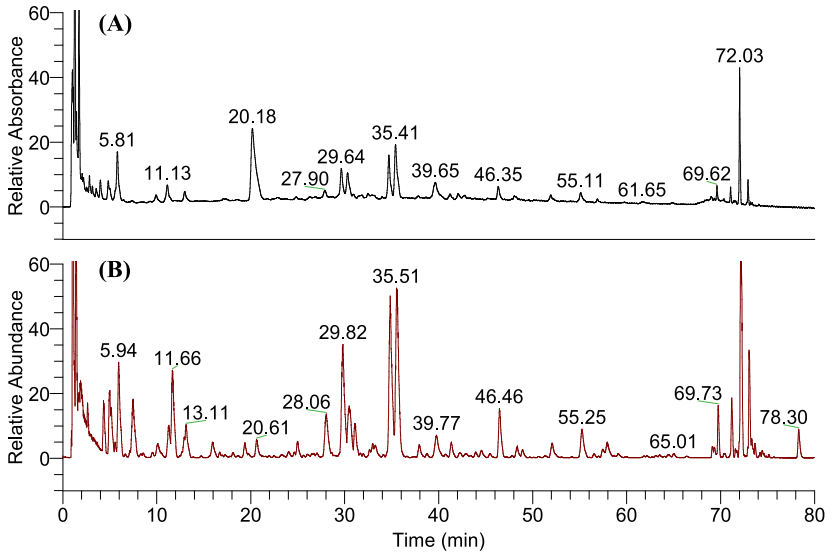

Figure 1. UPLC-UV chromatogram at 280 nm (A) and base peak ion chromatograms (BPC) in negative model (B) of RY.

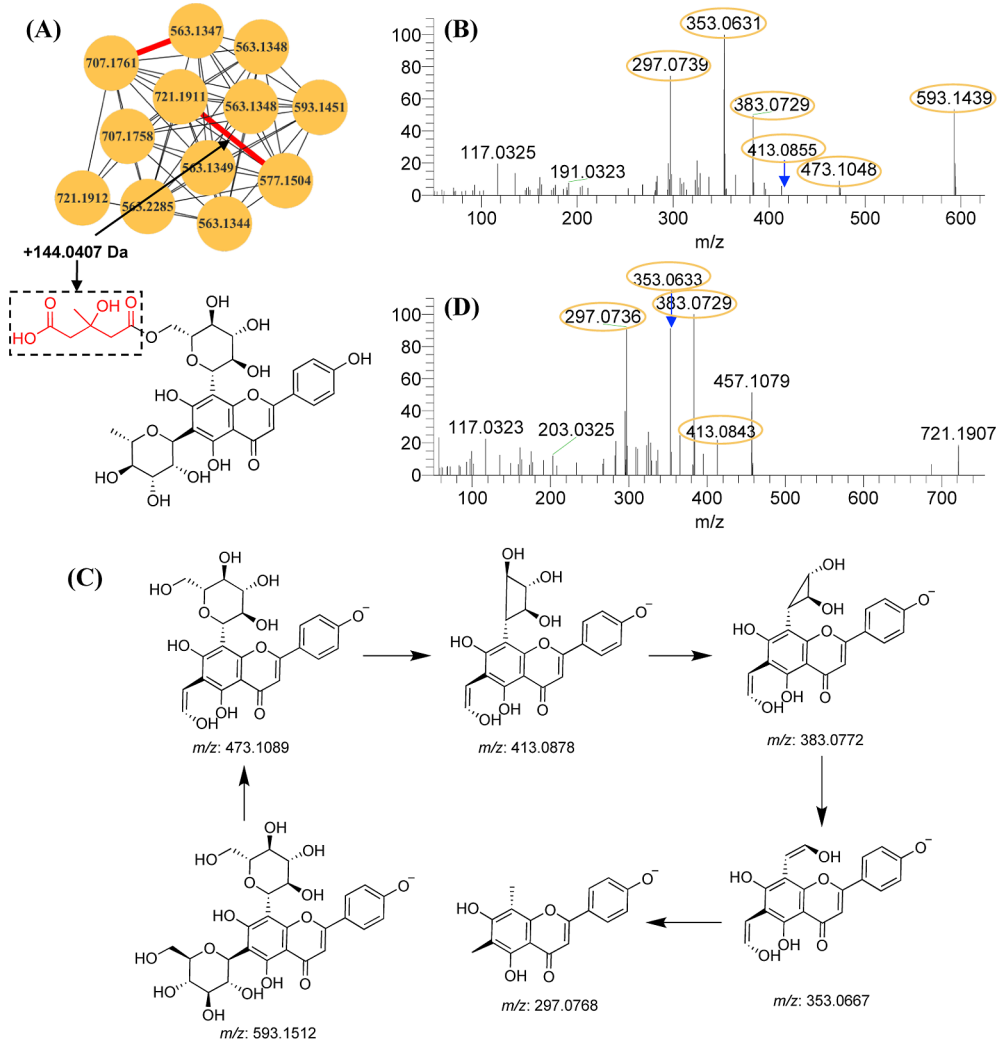

Figure 2. MN and annotation of flavonoid C-glycosides in RY. (A) MN of flavonoid C-glycosides in RY. (B) The MS/MS spectrum of vicenin 2. (C) The proposed fragmentation pathway of vicenin 2. (D) The MS/MS spectrum of FC10 of proposed structure 6‴-(3-hydroxy-3-methylglutaryl) violanthin.

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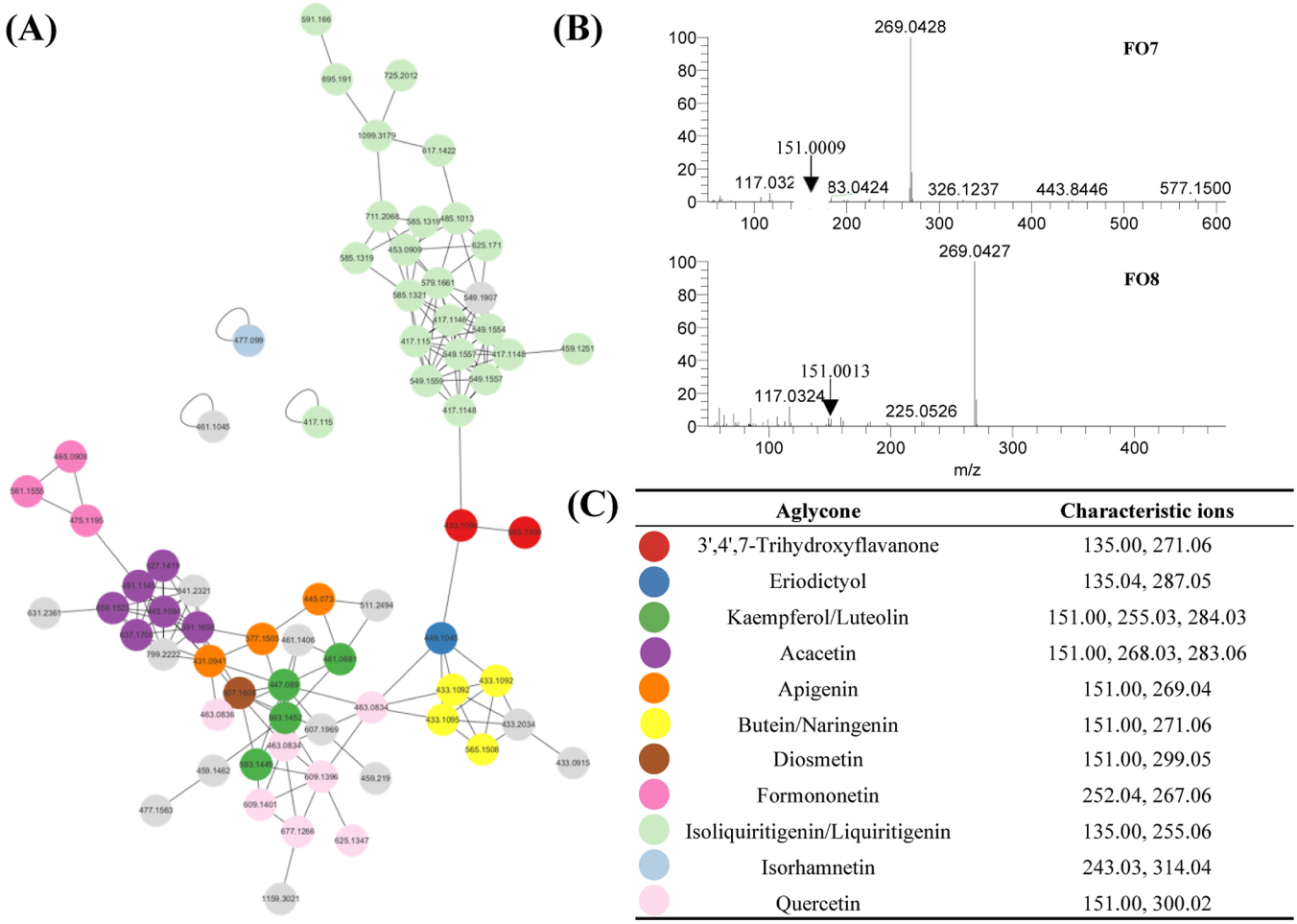

Aglycone	Characteristic ions
3',4',7-Trihydroxyflavanone	135.00, 271.06
Eriodictyol	135.04, 287.05
Kaempferol/Luteolin	151.00, 255.03, 284.03
Acacetin	151.00, 268.03, 283.06
Apigenin	151.00, 269.04
Butein/Naringenin	151.00, 271.06
Diosmetin	151.00, 299.05
Formononetin	252.04, 267.06
Isoliquiritigenin/Liquiritigenin	135.00, 255.06
Isorhamnetin	243.03, 314.04
Quercetin	151.00, 300.02

Figure 3. MN and annotation of flavonoid *O*-glycosides in RY. (A) MN of flavonoid *O*-glycosides in RY. (B) The MS/MS spectrum of FO7 and FO8. (C) The flavonoid aglycones tentatively identified in RY.

Runyan mixture (RY) is a typical and effective in-hospital TCM preparation approved by a county municipal hospital for adjuvant therapy in upper respiratory tract infections. It contains eight TCM herbal drugs including *Solidaginis herba*, *Asparagi radix*, *Scrophulariae radix*, *Ophiopogonis radix*, *Rehmanniae radix*, *Chrysanthemi indici Flos*, *Forsythiae fructus*, and *Glycyrrhizae radix et rhizome*. The chemical composition of formulated RY remains unclarified. In the present work, UHPLC−HRMS was applied to separate and analyze RY and its complex composition was elucidated by FBMN. This study provides an efficient method to support further research into quality control and treatment mechanisms of in-hospital TCM preparations.

2. RESULTS AND DISCUSSION

2.1. Total Ion Chromatograms and RY Molecular Networking. Although MS does not require prior complete chromatographic separation, it is beneficial for compound structure identification. In this work, the run time was extended to 80 min for good baseline separation of most of the main RY constituents (Figure 1).

On this basis, a molecular network was constructed by MS, Figure S1, comprising 1546 nodes and 158 clusters (nodes > 1). The chemical classes of 17 clusters were assigned by MolNetEnhancer, including flavonoids, coumaric acids, quinic acids, and oligosaccharides. The different chemical classes of 17 clusters are indicated by different colors.

2.2. Identification of RY Flavonoids. Flavonoids, compounds with a C6−C3−C6 structure, are one of the largest groups of chemical constituents of TCM herbal drugs. In the herbs of RY, many flavonoids from *G. radix et rhizome*, *Ophiopogonis radix*, and *Chrysanthemi indici Flos* have been isolated and characterized on the basis of their MS and NMR spectra.[15−17] Little research on the chemical constituents of *Solidaginis herba* has been conducted, but the flavonoid content was expected to be high based on other plants of the *Solidago* genus.[18] In herbs, flavonoids mostly exist as *O*-glycosides or C-glycosides. In the present work, 12 nodes in cluster 26 (MN 26) were considered to be flavonoid C-glycosides by MolNetEnhancer (Figure 2A). Compound FC1, for example, has a $[M-H]^-$ ion at m/z 593.1451 and molecular formula $C_{27}H_{30}O_{15}$. In the MS/MS spectra (Figure 2B), the diagnostic ions at m/z 473.1048, 413.0855, 383.0729, and 353.0631 were produced by neutral losses of 30, 60, 90, and 120 Da, indicative of a flavonoid C-glycoside. Comparing with the MS/MS spectra with literature data, FC1 was tentatively identified as vicenin 2, its proposed fragmentation pathway shown in Figure 2C.[19] Compounds FC2-7 produced the same diagnostic ions at m/z 413.0855, 383.0729, 353.0631, and 297.0736 (Table S1), indicating that they were flavonoid C-glycosides of the same aglycone, tentatively identified as

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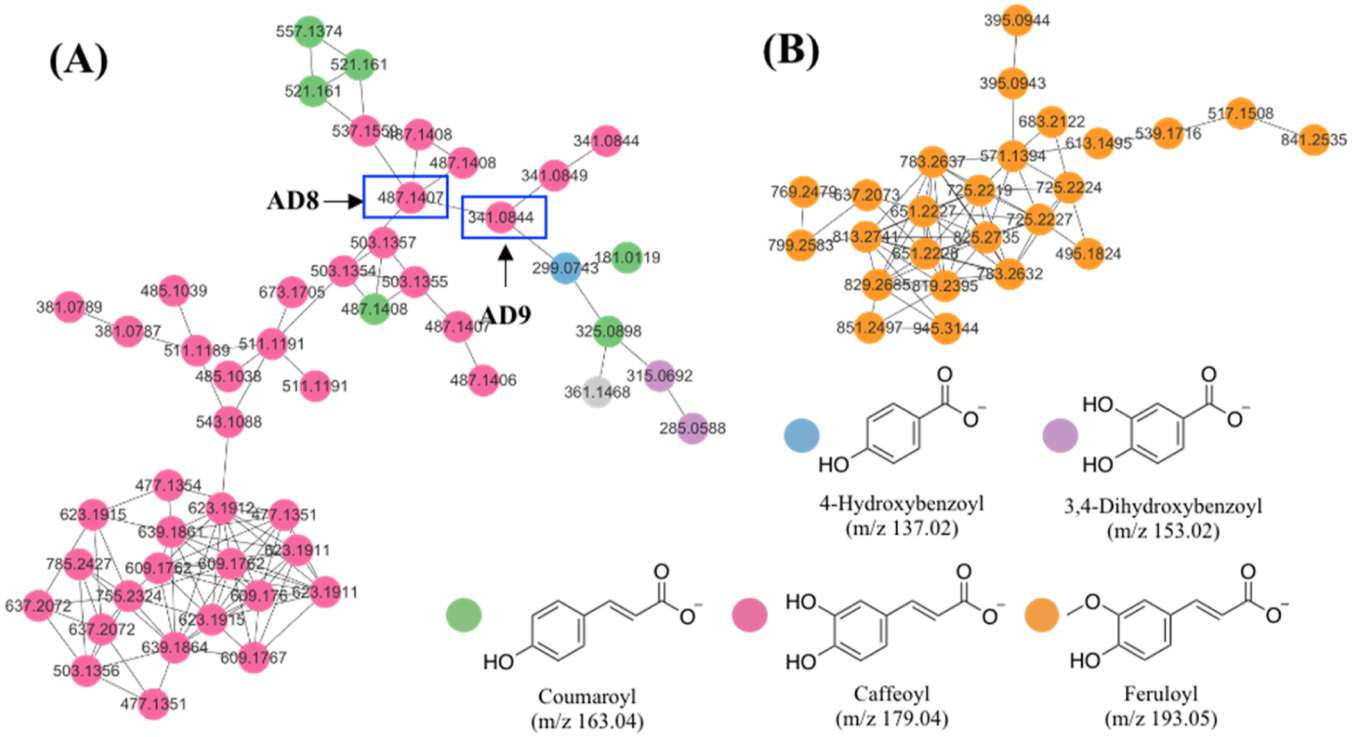

Figure 4. MN of coumaric acids. Five kinds of coumaric acids are indicated with different colors. (A) Sub-MN consisting of 4-hydroxybenzoyl, 3,4-dihydrobenzoyl, coumaroyl, and caffeoyl compounds. (B) Sub-MN consisting of feruloyl compounds.

vicenin 1, isoschaftoside, schaftoside, neoschaftoside, vicenin 3, and violanthin by comparing with previous reports.[20] Compound FC10 with $[M-H]^-$ ion at m/z 721.1911 and molecular formula $C_{33}H_{38}O_{18}$ gave diagnostic ions at m/z 413.0855, 383.0729, 353.0631, and 297.0736 (Figure 2D). Having the same aglycone as violanthin (m/z 577.1504), a neutral loss of 144.0407 and being directly connected with violanthin in the MN (Figure 2A), FC10 may bear a chemical group linked to the sugar unit of violanthin. Retrieved from the PubChem database, the MS/MS spectra of 6‴-(3-hydroxy-3-methylglutaryl) violanthin were consistent with those of compound FC10.

Cluster MN27 and three single nodes were considered to be flavonoid *O*-glycosides by MolNetEnhancer (Figure 3A). The characteristic ions of flavonoid *O*-glycosides were the aglycone ions ($[aglycone]^-$ and/or $[aglycone-H]^-$) resulting from loss of one or more sugar moieties. Neutral losses of 132, 146, 162, and 176 Da indicated the presence of sugar moieties of apiose/xylose/arabinose, rhamnose, glucose/galactose, and glucuronic acid, respectively. The process of qualitative analysis for selected nodes in MN27 is as follows. Compound FO8 gave the $[M-H]^-$ ion at m/z 445.073 with molecular formula $C_{21}H_{18}O_{11}$. The in-house RY database identified apigenin 7-*O*-glucuronide and baicalin and isolated *Chrysanthemi indici Flos* and *Forsythiae fructus*, with molecular formula $C_{21}H_{18}O_{11}$. The characteristic ions at m/z 269.0427, 151.0013, and 117.0324 indicated apigenin to be the FO8 aglycone whose structure was tentatively assigned apigenin 7-*O*-glucuronide. In the molecular network of flavonoid *O*-glycosides, the node of compound FO7 was directly connected with that of FO8 (Figure 3A) with the same characteristic ions at m/z 269.04, 151.00, indicating that it was also an apigenin *O*-glycoside (Figure 3B). By comparison with literature MS data, FO7 was tentatively identified as apigenin-7-*O*-rutinoside, isolated from *Chrysanthemi indici Flos*.[18] Similarly, at least 11 flavonoid aglycones were tentatively identified according to the characteristic ions listed in Figure 3C, including 3′,4′,7-trihydroxyflavanone, eriodictyol, kaempferol/luteolin, acacetin, apigenin, butein/naringenin, diosmetin, formononetin, isoliquiritigenin/liquiritigenin, isorhamnetin, and quercetin. MN27 nodes with different aglycones were given different colors (Figure 3A), indicating that nodes with the same aglycones are clustered together and confirming MN to be an effective tool for chemical identification.

More than 75 prenylated flavonoids, with one or more prenyl groups attached to a flavonoid aglycone by a C−C bond, have been isolated from *G. radix* et *rhizome*.[21] Neutral losses of 55 and/or 68 Da are observed in prenylated flavonoids.[22] In the present work, the precursor ions of MN nodes were first compared with theoretical $[M-H]^-$ ions of compounds from the in-house database. Of six potential compounds (<10 ppm), none were confirmed to be prenylated flavonoids by MS/MS. Because RY is an aqueous extract, the absence of prenylated flavonoids may be due to their poor water solubility.[23]

2.3. Identification of RY Quinic Acids. MolNetEnhancer identified cluster MN28 as quinic acid derivatives, further confirmed by the diagnostic fragmentation ions in MS/MS spectra at m/z 191.05, 173.04, 137.02, 129.05, and 127.04 (Table S1). In addition to the diagnostic fragmentation ions, other diagnostic ions of acylated units were also detected, including caffeoyl and coumaroyl. Compounds QA3, QA5, QA6, QA8, and QA9 showed the same $[M-H]^-$ ions at m/z 353 with a molecular formula of C16H18O9. In the MS/MS spectra, the diagnostic ions at m/z 179.03, 161.02, and 135.04 suggested the caffeoyl unit, so these compounds were tentatively assigned as mono-caffeoyl quinic acids. Three kinds of mono-caffeoyl quinic acids have been isolated from

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Chrysanthemum indicum L.[17] and *Solidago decurrens* Lour,[24] including 3-*O*-caffeoylquinic acid (chlorogenic acid), 4-*O*-caffeoylquinic acid, and 5-*O*-caffeoylquinic acid (neochlorogenic acid), while at least five mono-caffeoyl quinic acids were detected in our work, suggesting the presence of compounds such as 1-caffeoylquinic acid or *cis*-chlorogenic acid. These two mono-caffeoyl quinic acids have been detected in other members of the *Chrysanthemum* genus, including *Chrysanthemum morifolium* Ramat.[25,26] Chlorogenic acid, *cis*-chlorogenic acid, and neochlorogenic acid have the same *C* log *P* value at −1.879 which is smaller than that of 4-*O*-caffeoylquinic acid (*C* log *P* = −1.400) and 1-*O*-caffeoylquinic acid (*C* log *P* = −1.332), indicating a similar retention time for the former three, while the latter two would be eluted later.[27] Therefore, compounds QA3, QA5, QA6, QA8, and QA9 were tentatively identified as chlorogenic acid, *cis*-chlorogenic acid, neochlorogenic acid, 4-*O*-caffeoylquinic acid, and 1-*O*-caffeoylquinic acid, the elution order of these mono-caffeoyl quinic acids being consistent with previous reports.[28] Compounds QA12 and QA15-18 gave the same $[M-H]^-$ ion at *m*/*z* 515 with the diagnostic ions of the caffeoyl unit and ions at *m*/*z* 353 $[M-H-176]^-$, suggesting the presence of two caffeoyl moieties. Thus, these compounds were tentatively identified as di-*O*-caffeoylquinic acid, also isolated from *C. indicum* L,[17] and *S. decurrens* Lour.[24] According to the difference in *C* log *P* values, compounds QA12 and QA15-18 were tentatively identified as 3,4-di-*O*-caffeoylquinic acid (Rt = 20.61 min), 4,5-di-*O*-caffeoylquinic acid (Rt = 34.25 min), 1,3-di-*O*-caffeoylquinic acid (Rt = 35.88 min), 1,5-di-*O*-caffeoylquinic acid (Rt = 36.60 min), and 3,5-di-*O*-caffeoylquinic acid (Rt = 41.35 min). The precursor ions of compounds QA1 and QA2 were 18 Da larger than those of mono-caffeoyl quinic acids and, although they had similar diagnostic ions, QA1 and QA2 eluted earlier than these. According to a recent report, chlorogenic acids may exist as water complexes in aqueous solution,[29] so these two compounds were tentatively identified as isomers of chlorogenic acid hydrate.

Compounds QA11 and QA12 gave the same $[M-H]^-$ ions at *m*/*z* 337 with a molecular formula of $C_{16}H_{18}O_8$. In the high-resolution orbitrap MS/MS spectra, the diagnostic ions at *m*/*z* 163.04, 145.03, and 119.05 together with the typical loss of 146.04 Da indicated the presence of a coumaroyl moiety. By comparison with compounds from the in-house RY database and from their *C* log *P* values, compounds QA11 and QA12 were tentatively identified as 5-*O*-coumaroyl quinic acid and 4-*O*-*p*-coumaroyl quinic acid.

2.4. Identification of RY Coumaric Acids. Diagnostic ions of acylated units were commonly observed in the coumaric acid compounds. Clusters MN5 (Figure 4A) and MN33 (Figure 4B) were assigned as coumaric acids. The diagnostic ions of feruloyl (*m*/*z* at 193.05, 178.02, 175.04, 160.01), caffeoyl (*m*/*z* at 179.03, 161.02, 135.04), coumaroyl (*m*/*z* at 163.04, 135.04, 119.05, 93.03), 3,4-dihydroxybenzoyl (*m*/*z* at 153.02, 109.03), and 4-hydroxybenzoyl (*m*/*z* at 137.02, 93.03) were observed in these two clusters. As shown in Figure 4, most components in cluster MN5 were caffeoyl derivatives and all nodes in cluster MN33 were feruloyl derivatives.

Compounds AD6, AD7, and AD9 gave the same $[M-H]^-$ ions at *m*/*z* 341.08, molecular formulae of $C_{15}H_{18}O_9$, and diagnostic losses of 162 Da ($C_6H_{10}O_5$) in their MS/MS spectra, indicating that these compounds were mono-caffeoyl glucosides. Such compounds have not been isolated from the herbs of RY, so they were tentatively assigned as 6-*O*-caffeoyl-glucose (Rt = 6.34 min, *C* log *P* = −1.0609), 1-*O*-caffeoyl-glucose (Rt = 7.67 min, *C* log *P* = −0.7240), and 3-*O*-caffeoyl-glucose (Rt = 10.02 min, *C* log *P* = −0.6021) by comparison with the compounds in PubChem and their *C* log *P* values. Compounds AD5, AD8, AD10, AD15, and AD16 gave the same $[M-H]^-$ ions at *m*/*z* 487.14 and molecular formulae of $C_{21}H_{28}O_{13}$. In the MN, compounds AD8 and AD9 were directly connected and the mass difference between them was 146 Da ($C_6H_{10}O_5$), suggesting these compounds were mono-caffeoyl-di-glucosides. Only one compound from the in-house database, cistanoside F, matched with the MS/MS spectra of compounds AD5, AD8, AD10, AD15, and AD16, the others were identified from PubChem. According to their *C* log *P* values, AD5, AD8, AD10, AD15, and AD16 were tentatively identified as cistanoside F (Rt = 6.00 min, *C* log *P* = −2.9169), caffeoylsophorose (Rt = 9.77 min, *C* log *P* = −2.3250), 6-deoxy-*α*-D-manno-hexopyranosyl-(1->3)-4-*O*-(3-hydroxycoumaroyl)-*β*-D-*gluco*-hexopyranose (Rt = 11.06 min, *C* log *P* = −2.2107), swertiamacroside (Rt = 14.89 min, *C* log *P* = −1.7492), and [(2S,3R,4S,5R,6R)-3,5-dihydroxy-6-(hydroxymethyl)-4-[(2S,3R,4R,5R,6S)-3,4,5-trihydroxy-6-methyloxan-2-yl]oxyoxan-2-yl] (*E*)-3-(3,4-dihydroxyphenyl)prop-2-enoate (Rt = 16.53 min, *C* log *P* = −1.041).

In addition to the caffeoyl moiety, the diagnostic ion at *m*/*z* 153.05 indicated a C6−C2 hydroxytyrosol moiety (Table S1) in the components of the MN5 cluster.[30] Compound AD26, for example, displayed an obvious peak at *m*/*z* 609.1762($[M-H]^-$) of $C_{28}H_{34}O_{15}$, producing $[M-H-C_6H_{10}O_5]^-$ at *m*/*z* 447.1432 by neutral loss of a glucose. The diagnostic ions at *m*/*z* 179, 161, 135, and 153 indicate that two substituents including caffeoyl and hydroxytyrosol are linked with a glucose. The C6−C2 glucoside conjugates have been isolated from *Forsythiae fructus*.[31] Therefore, compounds AD21 and AD25-27 were tentatively assigned as forsythoside J (Rt = 28.03 min, *C* log *P* = −0.8258), calceolarioside C (Rt = 31.71 min, *C* log *P* = −1.2192), calceolarioside E (Rt = 32.64 min, *C* log *P* = −1.4614), and lianqiaoxinoside C (Rt = 32.98 min, *C* log *P* = −1.4716).

2.5. Other Compounds. MN compounds could also be tentatively identified by comparison of the experimental MS/MS spectra with GNPS spectral libraries. Chemical similarity was evaluated by MQScore. Ranging from 0 to 1, a score closer to 1 indicates greater chemical similarity. 73 compounds were identified with MQScore >0.9. Among these, 41 compounds were flavonoids, quinic acids, coumaric acids, or benzoic acids, tentatively identified above. Four compounds, including piscidic acid, *N*-acetylphenylalanine, guanosine, and calceolarioside A, related to single MN nodes, and the remaining 28 compounds in the clusters were tentatively identified by comparison of the mass spectra of other nodes in the same clusters. The chemical class of nodes in cluster MN64 (Figure S2) was not identified by MolNetEnhancer, while two nodes were identified by matching GNPS spectral libraries with MQScore >0.9. The IR10 node gave a precursor ion at *m*/*z* 493.1661, assigned as harpagoside by the GNPS library by comparison with the characteristic ions at 103.0528, 121.0275, 147.0427, and 165.0531. The node directly connected with compound IR10 gave a precursor ion at *m*/*z* 539.171, 46 Da greater than that of IR10 with the same RT. This node at *m*/*z* 539.171 represents an adduct ion ($[M + HCOO]^-$) of compound IR10. Another compound CC1 assigned by GNPS library comparison was forsythoside E, isolated from *Forsythiae*

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ACS Omega 2023, 8, 6515−6522

fructus, with characteristic ions at 113.0222, 135.043, 153.0537, 315.1054, and 461.1627. The node directly connected with CC1 gave a precursor ion at m/z 475.1772, 14 Da greater than CC1, indicating that it was a methylated derivative of forsythoside E. After comparison with the in-house database, this node was tentatively assigned as darendroside B, detected in both *Scrophulariae radix* and *Rehmanniae radix*. Similarly, another 49 nodes were tentatively assigned and listed in Table S1.

3. CONCLUSIONS

In the present investigation, 165 compounds associated with 193 nodes in the molecular network of RY were systematically characterized by combining UHPLC−HRMS and FBMN data processing. The component clusters represent flavonoid-*O*-glycosides, flavonoid-C-glycosides, quinic acids, coumaric acids, and iridoids. This is the first study to provide comprehensive chemical information on the multi-herb formula RY.

By providing compositional information, the quality control and understanding of therapeutic mechanisms will be facilitated, allowing effective and safe prescriptions of RY to be developed. Furthermore, the analytical methods described can be applied to efficiently assign and identify the chemical components of other complex herbal formulae. In the future, the elucidation of potential chemical differences between single herb and multi-herbal formulations should support quality control efforts and preparation method development. RY is a case in point, in which new chemical components have been identified in the combination of eight herbs.

4. MATERIALS AND METHODS

4.1. Materials and Reagents. RY was prepared by Dongyang People's Hospital. HPLC grade acetonitrile was bought from the Tedia Company Inc. and formic acid was purchased from Sinopharm Chemical Reagent Co., Ltd.

4.2. Instruments and Equipment. An UltiMate 3000 high-performance liquid chromatography system (Thermo Fisher Scientific, Waltham, MA, USA) equipped with Eclipse SB-C_{18} Rapid Resolution column and coupled with a Q-Exactive high-resolution benchtop quadrupole orbitrap mass spectrometer (QE, Thermo Fisher Scientific) was used for sample analysis. The equipment was controlled by Xcalibur 3.0 software (Thermo Fisher Scientific).

4.3. Sample Preparation. RY solution (10 mL) was accurately diluted with water into to a 50 mL volumetric flask. After thorough shaking, the test solution was passed through a 0.22 μm filter before analysis.

4.4. LC−MS/MS Analysis. Samples were eluted with the following gradient where the mobile phases were 0.5% formic acid in water (A) and acetonitrile (B): 0−5 min, 3% B; 5−65 min, 3−25% B; 65−90 min, 25−100% B. The flow rate was 0.3 mL min^{-1}. Peaks were detected in the negative mode and the ESI source conditions were set as follows: sheath gas flow rate 40 arb; aux. gas flow rate 10 arb; capillary temperature 320 °C; full mass resolution 70,000; MS/MS resolution 17,500; collision energy 20/40/60 eV (NCE model); spray voltage −3 kV.

4.5. Construction of MS/MS-Based Molecular Networking. To convert the raw LC−MS/MS mass data into *mzXML* file format, a complete package was downloaded from the GNPS platform (https://ccms-ucsd.github.io/GNPSDocumentation/fileconversion/). The converted MS data were processed by MZmine 2.53. An MS/MS-based MN of RY was constructed by uploading the processed MS/MS data to the GNPS platform following the FBMN workflow.[32] The mass tolerances of precursor ions and fragment ions were both set as 0.0075 Da. To generate the MN, the cosine score >0.6 and the number of matched fragment ions was >5. Cytoscape 3.9.1 was used for network visualization.

4.6. Workflow of Chemical Constituent Identification. First, an in-house database of chemical constituents was compiled from literature reported chemical compositions of RY herbal drugs, collected from the following databases: web of science, CNKI, and SciFinder. Second, the constructed molecular network was further processed by MolNetEnhancer, a useful tool to assign chemical classes in the molecular network, combining GNPS tools including Network Annotation Propagation, DEREPLICATOR, and ClassyFire.[32] Third, from MN results, RY constituents were tentatively identified by comparing their diagnostic fragmentation ions with literature data. If no compounds from the in-house database matched the fragmentation ions from our work, compounds were retrieved from GNPS library, PubChem, or ChemSpider databases. Some nodes in the molecular network were tentatively assigned by comparison of the previously identified differences between connected nodes.

■ ASSOCIATED CONTENT

Supporting Information

The Supporting Information is available free of charge at https://pubs.acs.org/doi/10.1021/acsomega.2c06885.

MN of RY; MN of cluster MN64; and tentatively identified compounds from RY (PDF)

■ AUTHOR INFORMATION

Corresponding Authors

Yinzhi Jin − *Traditional Chinese Medicine Pharmacy, Affiliated Dongyang Hospital of Wenzhou Medical University, Jinhua 322100, China*; Email: 397235191@qq.com

Yingpeng Tong − *Institute of Natural Medicine and Health Products, School of Pharmaceutical Sciences, Taizhou University, Zhejiang 318000, PR China*; orcid.org/0000-0002-6643-1132; Email: fish166@126.com

Authors

Huihui Zhang − *Traditional Chinese Medicine Pharmacy, Affiliated Dongyang Hospital of Wenzhou Medical University, Jinhua 322100, China*

Yingzhi Zhang − *Institute of Natural Medicine and Health Products, School of Pharmaceutical Sciences, Taizhou University, Zhejiang 318000, PR China*

Jiahao Li − *Institute of Natural Medicine and Health Products, School of Pharmaceutical Sciences, Taizhou University, Zhejiang 318000, PR China*

Chuanjiang Fan − *Institute of Natural Medicine and Health Products, School of Pharmaceutical Sciences, Taizhou University, Zhejiang 318000, PR China*

Junjie Gu − *Institute of Natural Medicine and Health Products, School of Pharmaceutical Sciences, Taizhou University, Zhejiang 318000, PR China*

Complete contact information is available at:

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Notes

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