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An untargeted metabolomics approach to determine component differences and variation in their *in vivo* distribution between Kuqin and Ziqin, two commercial specifications of Scutellaria Radix†

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Kuqin (KQ) and Ziqin (ZQ), derived from the roots of *Scutellaria baicalensis* Georgi, are two important commercial specifications of Scutellariae Radix (SR, termed *Huang qin* in Chinese). According to traditional Chinese medicine, KQ is used for the treatment of upper energizer lung heat syndrome while ZQ is used to clear lower energizer large intestine heat syndrome. The chemical basis for differences in efficacy between KQ and ZQ is currently unknown. Here, we present an untargeted metabolomics approach to rapidly screen and identify chemical and *in vivo* distribution differences between KQ and ZQ. We identified 114 constituent differences between KQ and ZQ, of which 35 were identified in SR for the first time. Furthermore, 19 prototype constituents and 16 metabolites were tentatively identified in rat colon and lungs after oral administration of SR, of which six prototype constituents and 12 metabolites were reported for the first time. Distribution differences of baicalin, wogonoside, wogonin and oroxylin A between colon and lungs were observed. To interpret such differences, their metabolic pathways were proposed. The peak area ratio of baicalin to eriodictyol calculated from the extracted ion chromatogram was proposed as a differentiation index for the classification and quality control of KQ and ZQ. These results may partially explain the efficacy differences between KQ and ZQ, and provide references for clinical treatment of related diseases.

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Introduction

Scutellariae Radix (SR) is one of the most widely used traditional Chinese medicines and is used to treat infection of the respiratory and gastrointestinal tracts.[1,2] Kuqin (KQ) and Ziqin (ZQ) are two important specifications of SR. Perennial and hollow roots with dark cores are defined as KQ and solid new roots are designated as ZQ. According to the theories of traditional Chinese medicine, KQ is used to treat upper energizer lung heat syndrome while ZQ is used for lower energizer large intestine heat syndrome. It has been reported that baicalein,[3] baicalin,[4] wogonin,[5] wogonoside[6] and SR extracts[7] can protect against lipopolysaccharide (LPS)-induced acute lung injury (ALI) in rats. Baicalein,[8,9] baicalin,[9] wogonoside,[9] wogonin,[9] and SR extracts[2,10–12] can all ameliorate the inflammatory symptoms of induced colitis. The above mentioned compounds are found in KQ and ZQ. These results suggest that the target organs of KQ and ZQ might be lungs and colon.

We have previously reported that KQ is more potent than ZQ at inhibiting NO production by blocking inducible nitric oxide synthase (iNOS) expression in NR8383 cells (a rat alveolar macrophage cell line), indicating that the effects of KQ and ZQ on lung inflammation are different.[13] Also, the ratios of baicalein to baicalin, wogonin to wogonoside, and oroxylin A to oroxylin A 7-*O*-glucuronide are significantly higher in KQ compared with ZQ.[14] However, differences in the levels of six constituents between KQ and ZQ are not sufficient to explain the observed efficacy differences, and the *in vivo* chemical and distribution differences between them are not clear. Therefore, the chemical basis for the difference in efficacy between KQ and ZQ is not known.

We, therefore, used Q Exactive mass spectrometry-based untargeted metabolomics to investigate systemic chemical differences between KQ and ZQ. We then compared the distribution differences of prototype constituents and metabolites between lungs and colon. Finally, we proposed a differentiation

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index for the classification and quality control of KQ and ZQ. The study workflow is shown in Fig. 1.

Experimental

Chemicals and materials

Baicalein (≥98%, Lot no. 140115), baicalin (≥98%, Lot no. 131219), wogonin (≥98%, Lot no. 140203), wogonoside (≥98%, Lot no. 140403), scutellarein (≥98%, Lot no. 140215), scutellarin (≥98%, Lot no. 130615), oroxylin A (≥98%, Lot no. 131207), oroxylin A 7-*O*-glucuroside (≥98%, Lot no. 140116), acteoside (≥98%, Lot no. 140322), apigenin (≥98%, Lot no. 130312) and chrysin (≥98%, Lot no. 130402) were purchased from Beijing Tetra Biological Technology Co., Ltd (Beijing, China). Chrysin 6-*C*-glucoside 8-*C*-arabinoside (purity 98%, Lot no. CFS201601) and chrysin 6-*C*-arabinoside 8-*C*-glucoside (purity 98%, Lot no. CFS201601) were purchased from Wuhan Chemfaces Biochemical Co., Ltd (Wuhan, China). Viscidulin III (purity 98%, no. BBP00429) and 4′-hydroxywogonin (purity 98%, no. BBP00586) were obtained from BioBioPha Co., Ltd (Yunnan, China). HPLC grade methanol and acetonitrile, and LC/MS grade formic acid (Lot no. 136037) were supplied by Fisher Scientific (Fairlawn, NJ, USA). Ammonium acetate (AR. Lot no. F20091117a) was obtained from Sinopharm Chemical Reagent Co., Ltd (Shanghai, China). Ultrapure water was purified using a Milli-Q Water Purification System (Merck Millipore, Germany). All other reagents were of analytical grade or higher. Fifty-one different KQ and ZQ samples were purchased from Chinese druggists in corresponding producing areas (Table S1†). All samples were authenticated by Professor Shao-Qing Cai (School of Pharmaceutical Sciences, Peking University). The voucher specimens were deposited at the Herbarium of Pharmacognosy, School of Pharmaceutical Sciences, Peking University.

Instruments and liquid chromatography-tandem mass spectrometry (LC/MS-MS) conditions

LC conditions. Chromatographic separation was performed in 30 min gradients over a Waters ACUQITY UPLC BEH C18 (100 × 2.1 mm, 1.7 μm) column. A flow rate of 0.3 mL min^{-1} and a column temperature of 35 °C were set for separation of SR and biological samples. The mobile phase consisted of (A) 0.1% formic acid solution containing 5 mM ammonium acetate and (B) acetonitrile. The step gradient was as follows: 15–20% (v/v) B during 0–2 min, 20–22% B during 2–6 min, 22–38% B during 6–10 min, 38–80% B during 10–19 min, 80–98% B during 19–20 min and held at 98% B for 5 min, decreasing to 15% B during 25–26 min and re-equilibration time of gradient elution was 4 min. The injection volume was 5 μL.

MS conditions. LC/MS analysis was performed using a Q Exactive mass spectrometer (Thermo Fisher Scientific, USA). A heated electrospray ion source (HESI) was used for ionization. The HESI parameters were optimized as follows: sheath gas flow

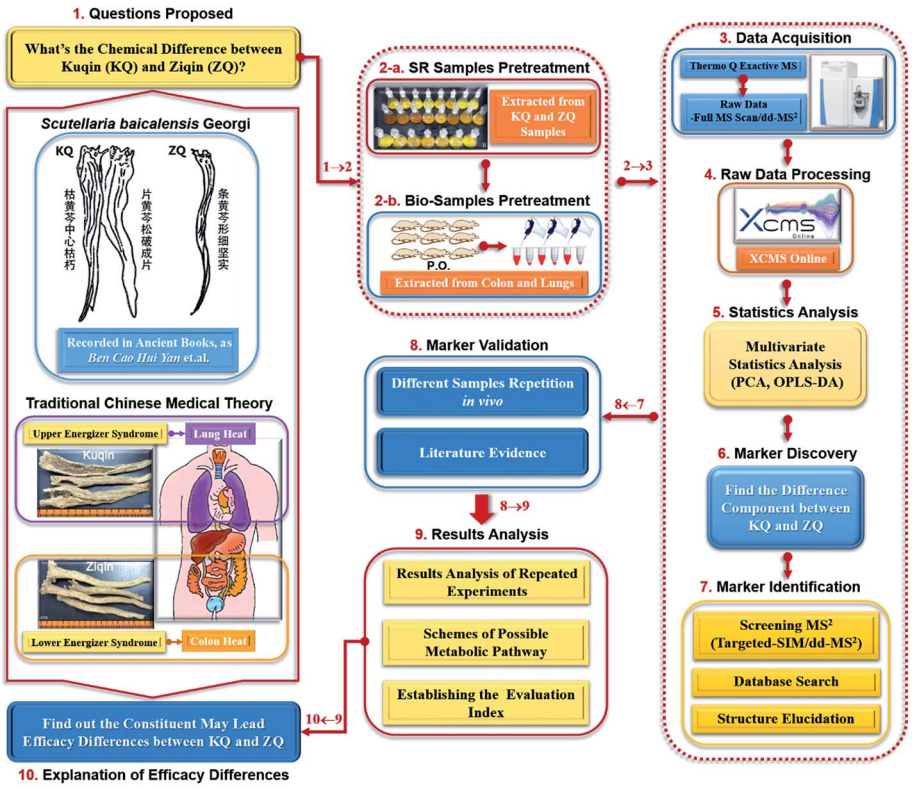

Fig. 1 Workflow for Q Exactive MS data analysis, quality marker discovery, identification, validation and samples evaluation. This figure illustrates the key steps in a typical workflow, which comprises preparation of *S. baicalensis* extract and biological samples, data acquisition, raw data processing, multivariate statistical analysis, marker discovery and structure identification.

rate 35 units; auxiliary (aux.) gas flow rate 10 units; capillary temperature 320 °C; aux. gas heater temperature 350 °C; spray voltage 2.8 kV for (−)-ESI and 3.5 kV for (+)-ESI; and S lens RF level 50.

MS data were acquired using full scan/data dependent (dd)-MS^2 and targeted-selected ion monitoring/data dependence (SIM/dd)-MS^2 methods dynamically choosing the top five most abundant precursor ions from the survey scan for higher-energy collisional dissociation (HCD) fragmentation. Full scan data in both positive and negative ion modes were acquired over the range m/z 100–1000 with a mass resolution of 75 000 (at m/z 200), and the automatic gain control (AGC) was set at 3×10^6 and maximum injection time (IT) was set to 100 ms. Data dependent MS/MS (dd-MS^2) scans were acquired in negative ion mode at a resolving power of 17 500 (at m/z 200), and AGC was set at 1×10^5 and maximum IT was set to 50 ms. The precursor ions were filtered by the quadrupole which operated in an isolation window of 2 Da, and collision energy was set to 35% normalized collision energy (NCE). The dynamic exclusion time was set to 10 s. Targeted-SIM was performed on selected m/z values at a resolution of 70 000 (at m/z 200), with AGC of 5×10^4, maximum IT of 100 ms and a detection window of 2 Da. Data dependent-MS/MS was performed using HCD and the detection was set at a resolution of 35 000 (at m/z 200), with AGC of 2×10^5 and maximum IT of 100 ms. NCE was set to 35%, and dynamic exclusion time was 10 s.

Preparation of SR extracts

For LC/MS-MS analysis. Each SR (KQ and ZQ) sample was pulverized to a powder and passed through a 40-mesh sieve. The powder was placed in a weighing bottle and dried at 55 °C for 4 h, then allowed to cool to ambient temperature in a desiccator. One gram of powder sample was added to 50 mL 70% methanol in a capped 100 mL conical flask, and was ultrasonically extracted for 45 min in a water bath. About 1.0 mL of supernatant was filtered through a 0.22 μm polypropylene membrane filter (GH Polypro, Pall) for LC/MS/MS analysis.

For animal experiments. A 20 g SR powder sample (passed through a 40-mesh sieve) was extracted by decocting with boiling water (1 : 100, w/v) for 30 min with intermittent mixing. The extract was passed through 16 layers of medical gauze and filtered again through filter paper under vacuum. The filtrate was then concentrated using a rotary vacuum evaporator (BÜCHI Rotavapor R-200, Switzerland) in a 60 °C water bath to obtain an SR extract (0.1 g crude drug per mL). Six batches of KQ (no. 7591-1, 7591-2, 6616, 6620, 70002, and 7486) and ZQ (no. 7593-1, 7593-2, 6619, 6614, 70002, and 7487) extracts were prepared using the above procedure. The HPLC peak areas of baicalin, wogonoside, oroxylin A 7-*O*-glucuronide, chrysin 6-*C*-arabinoside 8-*C*-glucoside, chrysin 6-*C*-glucoside 8-*C*-arabinoside, baicalein, wogonin, oroxylin A and chrysin in these extracts are shown in Table S2.†

Animal treatment

Animal experiments were conducted in accordance with the Guide for the Care and Use of Laboratory Animals published by the US National Institutes of Health and were approved by the Biomedical Ethical Committee of Peking University (no. SYXK2012-0024). Efforts were made to minimize the number of animals used and their suffering. Male Sprague-Dawley rats (220 ± 20 g) were provided by the Department of Laboratory Animal Science, Peking University Health Science Center (Beijing, China), and they had free access to pellet food and tap water. The rats were maintained in an environmentally controlled breeding room (temperature at 20–25 °C, relative humidity of 50–60%) in a 12 h light–dark cycle throughout the experiments. Each rat was housed in a metabolic cage for 5 days to adapt to the environment before the formal experiment.

Rats were randomly divided into KQ, ZQ and blank control groups, with six rats in each group. Rats in the KQ and ZQ groups were orally administrated 10 mL kg^{-1} KQ and ZQ extract, respectively, and the blank control group was orally administrated purified water. All rats were dosed twice daily for 5 days. Four hours after the last oral administration, the rats were sacrificed. Their lungs and colon were quickly removed, rinsed three times with precooled (4 °C) 0.9% saline solution, drained on filter paper, placed in 5 mL tubes in an ice bath, and then stored at −80 °C.

The animal experiment was repeated six times (E1–E6). In E1–E6, KQ and ZQ group rats were treated with six batches of KQ (no. 7591-1, 7591-2, 6616, 6620, 70002, and 7486) and ZQ (no. 7593-1, 7593-2, 6619, 6614, 70002, and 7487) extracts, respectively.

Pretreatment of lungs and colon samples

All samples were weighed on an electronic balance (AL204, Mettler Toledo), and homogenized in two volumes of cold purified water using an electric homogenizer (IKA T10, Germany) in an ice bath. Five hundred microliters of homogenate were placed in an Eppendorf tube and 1500 μL of 50% methanol and 50% acetonitrile (v/v = 1 : 1) solution containing 0.1% formic acid was added and vortexed for 3 min. The precipitate and the supernatant were then separated by centrifugation at 20 200 (×*g*) for 20 min at 4 °C. The supernatant (1.5 mL) was evaporated to dryness under a stream of nitrogen gas at 37 °C and re-suspended in 200 μL of methanol. The mixture was vortexed well and centrifuged at 20 200 (×*g*) for 10 min at 4 °C. One hundred and fifty microliters of the supernatant was transferred to an autosampler vial (2 mL, Agilent) with a vial insert (250 μL insert, polypropylene, Agilent) and a 5 μL aliquot was injected into the LC/MS-MS system for analysis.

Multivariate data processing approaches

XCMS online processing approach. Data were analyzed using interactive XCMS Online, which is freely available at https://xcmsonline.scripps.edu/.[15] All raw data were exported into netCDF files, and the converted files were uploaded to XCMS Online for nonlinear alignment of peak intensities.[16] Parameter settings for XCMS processing were as follows: centWave for feature detection ($\Delta m/z = 5$, minimum peak width = 5 s, and maximum peak width = 20 s); obiwarp settings for retention time correction (profStep = 1); parameters for chromatogram

alignment included mzwid = 0.025, minfrac = 0.5, and bw = 5. An unpaired parametric *t*-test (Welch *t*-test) was used for statistical testing. The values of other parameters were set to default values based on UPLC/Q-Exactive system parameters.

Multivariate statistical analysis. The data matrix (derived from XCMS Online) was imported into Simca-P software (version 13.0, Umetrics, Umeå, Sweden). Model parameter settings were tested with unit variance (UV), pareto (Par) and centre (Ctr) scaled models. The quality of the models was assessed by cumulative (cum) modeled variation in the X matrix R^2X (cum) and Y matrix R^2Y (cum). R^2Y (cum) is described as the proportion of variance in the data explained by models and indicates goodness of fit. A high Q^2 (cum) value [Q^2 (cum) ≥ 0.5] indicated good predictivity.[17] The data of colon and lung samples and SR extracts were first evaluated using unsupervised principal component analysis (PCA) to identify outliers and trends, and was considered to be well discriminated (Fig. S1, S2A and D†). Supervised orthogonal partial least squares-discriminant analysis (OPLS-DA) was then used to refine the model fit. Colon samples [scaling type: Par, negative: R^2Y (cum) = 1, Q^2 (cum) = 0.674; scaling type: Ctr, positive: R^2Y (cum) = 1, Q^2 (cum) = 0.943] and lung samples [scaling type: Ctr, negative: R^2Y (cum) = 0.999, Q^2 (cum) = 0.949; scaling type: Ctr, positive: R^2Y (cum) = 1, Q^2 (cum) = 0.974] established good models (Fig. 2). For SR samples, in the negative ion mode, when scaling type was Par, a good model fit [R^2Y (cum) = 0.985, Q^2 (cum) = 0.872] was obtained (Fig. S1, S2B and C†). Model fit and predictive power were reliable [R^2Y (cum) = 0.965, Q^2 (cum) = 0.845] using Par scaling type in positive ion mode (Fig. S2E and F†). As can be seen from Fig. 2, S1 and S2,† KQ and ZQ samples were divided into two parts, and variable importance on projection (VIP) values lists (VIP > 1) were exported as the different chemical constituents between KQ and ZQ groups. Screened data lists were regarded as a targeted mass list for further analysis and confirmation by MS/MS experiments.

Results and discussion

Strategy for structural elucidation

MS analysis and fragmentation mechanisms of various aglycones (such as flavone, flavonol, and flavanone) have been studied.[18,19] Nomenclature and the fragmentation behavior of flavonoids are illustrated for flavone *C*, *O*-glycosides and flavones (Fig. 3). The $^{1,3}A_0$, $^{1,4}A_0$, $^{1,3}B_0$, and $^{0,4}B_0$ fragments were

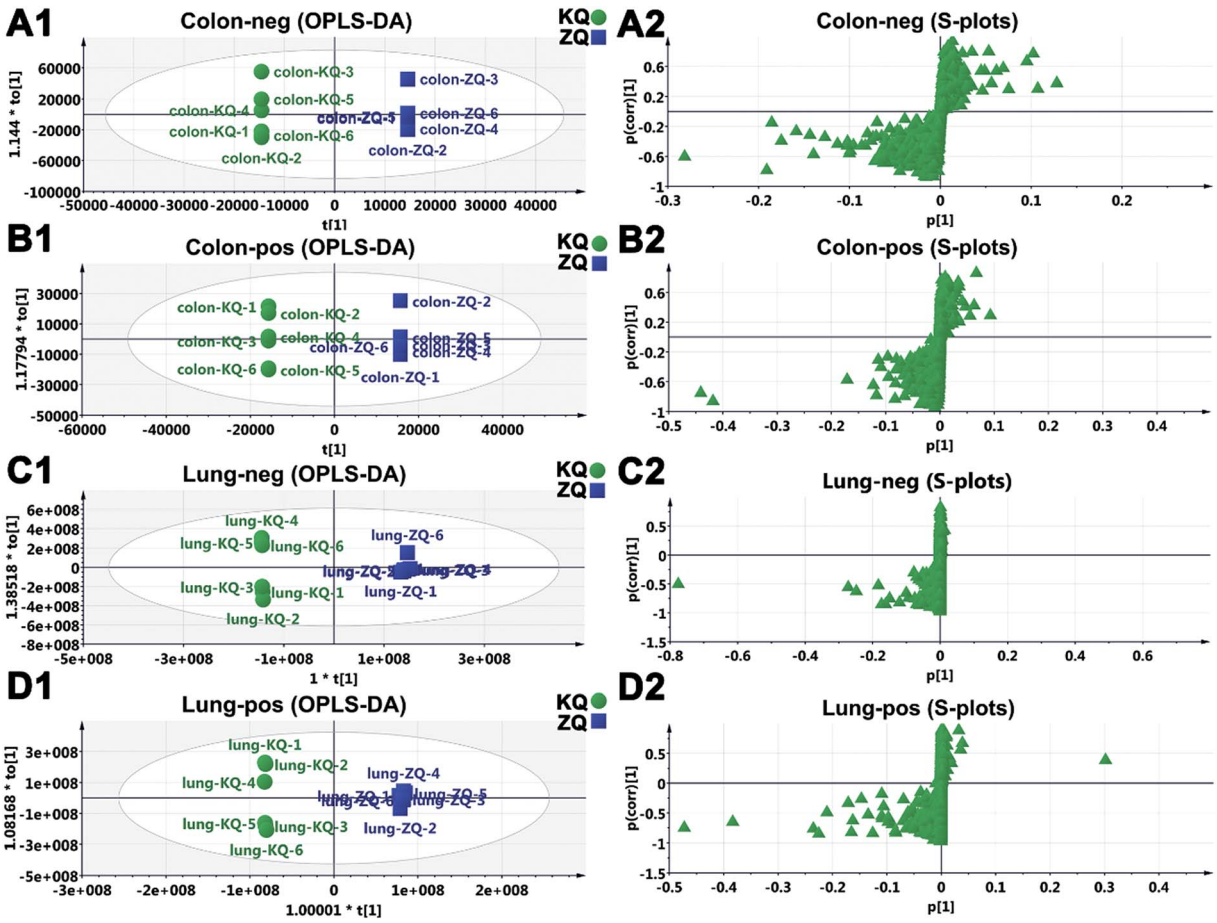

Fig. 2 Pattern analysis and scores scatter plots between Kuqin (KQ) and Ziqin (ZQ) groups after oral administration of SR extracts. OPLS-DA in negative (A1) and positive (B1) ion modes in colon; OPLS-DA in negative (C1) and positive (D1) ion modes in lungs; S-plot of the OPLS-DA model in negative (A2) and positive (B2) ion modes in colon; S-plot of the OPLS-DA model in negative (C2) and positive (D2) ion modes in lungs.

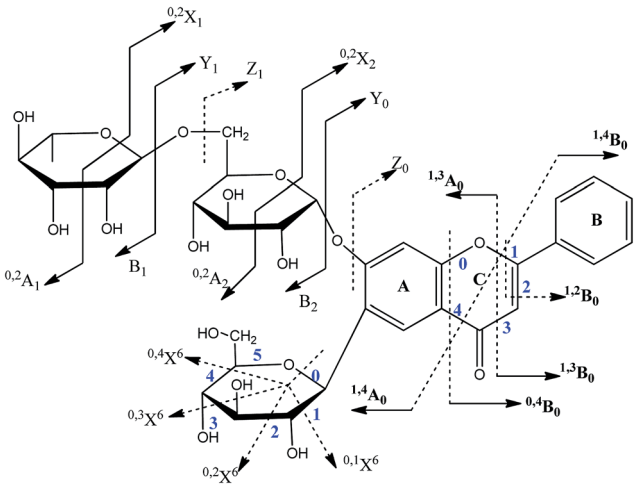

Fig. 3 Nomenclature and diagnostic fragmentations of flavonoids.

often the major fragment ions of flavones, while the $^{0,3}B_0$ ion was the major peak and characteristic ion for isoflavones.[20] The first fragmentation of 6-/8-methoxyflavone involved loss of a $CH_3^{\bullet}$ free radical to form a strong peak, which in turn lost CO.[21] Information on the glycosylation position and the glycosidic linkage position could be obtained from the Target-SIM/dd-MS^2 method. All flavonoid *O*-glycosides were characterized by the loss of 162 Da (hexosyl), 146 Da (deoxyhexosyl), and 176 Da (uronyl), owing to cleavage at the glycosidic *O*-linkages.[22] In flavonoid *C*-glycosides, the sugar was directly linked to the aglycone *via* a *C*–*C* bond. The MS^2 analysis allows the characterization of *C*-glycosides in both negative and positive ion mode. As far as we know, there are two types of flavonoid *C*-glycoside: 6-*C*-glycoside and 8-*C*-glycoside. 6-*C*-glycosyl flavonoids lost water molecules more easily than 8-*C*-glycosyl flavonoids. For flavonoid *C*-glycosides, the characteristic neutral losses of 90 Da, 120 Da, 134 Da or 60 Da, 90 Da, and 104 Da formed by cross-ring cleavages indicate a hexose or pentose residue.[22] Phenylethanoid glycosides were composed of saccharide and phenylethanoid aglycone. Some substituents, such as feruloyl or caffeoyl groups, usually replaced the hydroxyl groups at the 4- or 6-carbon of the central saccharide. The neutral losses of 162 Da, 152 Da, or 146 Da were related to caffeic acid/glucose, phenethanol aglycon, and rhamnose.[23]

Identification of prototype SR constituents by comparison with reference compounds

Baicalein (**S59**), wogonin (**S60**), oroxylin A (**S62**), scutellarein (**S58**), apigenin (**S67**), chrysin (**S78**), viscidulin III (**S57**), 4′-hydroxywogonin (**S76**), baicalin (**S39**), wogonoside (**S25**), oroxylin A 7-*O*-glucuronide (**S21**), scutellarin (**S22**), chrysin 6-*C*-arabinoside 8-*C*-glucoside (**S40**) and chrysin 6-*C*-glucoside 8-*C*-arabinoside (**S46**) were identified in KQ and ZQ using their reference compounds (Table S3†), and their extracted ion chromatograms (EICs) are shown in Fig. S3.†

Identification of prototype SR constituents by comparison with the literature

Phenylethanoid glycosides. The fragmentation patterns of **S1–S5** were very simple, with $[M - H]^-$ ions at *m/z* 623.19869 (**S1**), *m/z* 637.21439 (**S2**), *m/z* 651.23014 (**S3**), *m/z* 651.23018 (**S4**), and 475.18188 (**S5**), and molecular formulae of $C_{29}H_{36}O_{15}$, $C_{30}H_{38}O_{15}$, $C_{31}H_{40}O_{15}$, $C_{31}H_{40}O_{15}$, and $C_{21}H_{32}O_{12}$, respectively. The characteristic product ions of **S1** at *m/z* 179.04, *m/z* 161.02, and *m/z* 135.05 indicate caffeoyl, anhydroglucose and anhydrophenethanol, respectively. In MS^2 spectra of **S2**, **S3** and **S4**, fragment ions at *m/z* 193.05, *m/z* 175.04, and *m/z* 149.06 were observed, indicating that caffeoyl, anhydroglucose and anhydrophenethanol were methylated. Therefore, **S1**, **S2**, **S4**, and **S5** were tentatively identified as acteoside, leucosceptoside A, martynoside, and darendoside A, respectively, which were previously isolated from SR.[24] **S3** was identified as isomartynoside and this is the first report of its presence in SR.[25]

Flavonoid *O*-glycosides. In total, 48 flavonoid *O*-glycosides were found and tentatively identified in KQ and ZQ extracts (Fig. S3 and Table S3†). **S7**, **S13**, **S17**, **S20** and **S29** exhibited $[M - H]^-$ ions at *m/z* 445.07798, *m/z* 445.07796, *m/z* 445.07793, *m/z* 445.07795, and *m/z* 445.07795, respectively, and their molecular formulae were predicted to be $C_{21}H_{18}O_{11}$. In their MS^2 spectra, sequential losses of 176.0321 Da ($C_6H_8O_6$, glucuronyl) and 18.0106 Da (H_2O) were detected. They were tentatively identified as baicalein 6-*O*-glucuronide (**S13**), norwogonin 7-*O*-glucuronide (**S17**), norwogonin 8-*O*-glucuronide (**S29**) and isomers of **S13** (**S7** and **S20**).[26]

S19 was identified as chrysin 7-*O*-glucuronide with an $[M + H]^+$ ion at *m/z* 431.09677 ($C_{21}H_{19}O_{10}$) and a fragment ion at $[M + H - 176]^+$.[26] **S24** showed an $[M - H]^-$ ion at *m/z* 477.10424 ($C_{22}H_{21}O_{12}$) with an MS^2 base peak at *m/z* 286.04889 ($[M - H - 176 - CH_3^{\bullet}]^{\bullet-}$)^{1,3} and A^- at *m/z* 181.01442. It was, therefore, identified as 5,7,2′-trihydroxy-6-methoxyflavanone 7-*O*-glucuronide.[26]

Based on $[M - H]^-$ ions at *m/z* 475.08834, *m/z* 475.08809, *m/z* 475.08836, and *m/z* 475.08832, the molecular formulae of **S26**, **S27**, **S36**, and **S37** were determined to be $C_{22}H_{20}O_{12}$. The MS^2 spectra of *m/z* 475.09 showed $[aglycone - H]^-$ at *m/z* 299.06 and $[aglycone-H-CH_3^{\bullet}]^{\bullet-}$ at *m/z* 284.03, identifying **S37** as 5,7,2′-trihydroxy-6-methoxyflavone 7-*O*-glucuronide[26] and **S26**, **S27**, and **S36** as its isomers.

Apart from the glycosylation position, the glycan sequence (link type: 1 → 2 or 1 → 6) also has a significant effect on the relative abundances of Y_0^- (or Y_0^+), $[Y_0 - H]^-$ (or $[Y_0 + H]^+$), and Y_1^- (or Y_1^+) ions.[27] The Y_0^-/Y_1^- ratio is always larger for a 1 → 2 linkage compared with a 1 → 6 linkage, where Y_1^- corresponds to loss of 162 Da or 176 Da, indicating that the terminal monosaccharide was glucose or glucuronic acid.[28] The Y_0^-/Y_1^- ratio of **S12** and **S32** was larger than that of **S30**. They were, therefore, tentatively identified as trihydroxyflavone *O*-glucoside-(1 → 2)-*O*-glucuronide (**S12**), trihydroxyflavone *O*-glucuronide-(1 → 2)-*O*-glucoside (**S32**), and dihydroxy-methoxyflavone *O*-glucuronide-(1 → 6)-*O*-glucoside (**S30**), and they are reported in SR for the first time.

S99, **S100**, **S103**, **S106** and **S110** possessed a malonyl hexose group and formed their aglycone ions by losing a characteristic neutral unit of 248 Da in MS^2 spectra, and were tentatively identified as dimethoxyflavone *O*-6″-malonyl glucoside (**S99**), trihydroxy-methoxyflavone *O*-6″-malonyl glucoside (**S100**), apigenin 7-6″-malonyl glucoside or its isomer (**S103** and **S106**), and dihydroxy-methoxyflavone *O*-6″-malonyl glucoside (**S110**),[29] and they are reported in SR for the first time. On the basis of a literature survey,[21,24,26,30–35] all of the other flavonoid *O*-glycosides were putatively identified.

Flavonoid C-glycosides. A total of 10 constituents were putatively identified (Fig. S3 and Table S3†), according to literature reports.[21,24,26,30–35] **S44** showed $[M - H]^-$ ions at *m/z* 415.10373; **S48** and **S101** showed $[M + H]^+$ ions at *m/z* 417.11762 and *m/z* 417.11739, which indicated that their molecular formulae were $C_{21}H_{20}O_9$. **S44**, **S48**, and **S101** yielded $^{0,3}X_6^-$ and $^{0,2}X_6^-$ fragment ions at *m/z* 325.07 ($[M - H - 90]^-$) and *m/z* 295.06 ($[M - H - 120]^-$), and yielded fragment ions at *m/z* 307.06 ($[M - H - 90 - H_2O]^-$), suggesting that they were 6-*C*-glycosyl flavonoids with a hydroxyl group at the 2″-position of the sugar residue and a hydroxyl group at the 5- or 7-position of the aglycone.[22] Thus, they were tentatively identified as chrysin 6-*C*-glucoside (**S48**) and its isomer (**S44**), and chrysin 8-*C*-glucoside (**S101**).[26]

The MS^2 characteristics of **S40** and **S46** were a series of fragment ions of $[M - H - (60/90/120)]^-$ formed by cross-ring cleavages of the glycosyl moiety and higher abundance of $^{0,2}X_{6\text{ or }8}$. **S40** showed a higher abundance of $[M - H - 90]^-$ ions at *m/z* 457.11 ($^{0,2}X_6$, 22%) compared with $[M - H - 120]^-$ ions at *m/z* 427.10 ($^{0,2}X_8$, 15%), indicating that a 6-*C*-pentosyl unit was present. For **S46**, the $[M - H - 120]^-$ ion at *m/z* 427.10 ($^{0,2}X_6$, 66%) showed higher abundance compared with the $[M - H - 90]^-$ ion at *m/z* 457.11 ($^{0,2}X_8$, 40%), indicating the presence of a 6-*C*-hexosyl unit.[36] Therefore, **S40** and **S46** were characterized as chrysin 6-*C*-arabinoside 8-*C*-glycoside and chrysin 6-*C*-glycoside 8-*C*-arabinoside, respectively.

Flavonoid aglycones. A total of 30 flavones (Table S3†) were identified in KQ and ZQ extracts based on negative and positive ion mode mass spectra, and their EICs are shown in Fig. S3.† **S51**, **S53**, **S54**, and **S82** exhibited $[M - H]^-$ ions at *m/z* 329.06682, *m/z* 329.06680, *m/z* 329.06679, and *m/z* 329.06678, respectively, and their molecular formulae were predicted to be $C_{17}H_{14}O_7$. In MS^2 spectra of **S53**, $[M - H - 2 \times CH_3^{\bullet}]^{\bullet -}$ at *m/z* 299.01953, $[M - H - 2 \times CH_3^{\bullet} - CO_2]^{\bullet -}$ at *m/z* 255.02936, and $[M - H - 2 \times CH_3^{\bullet} - CO_2 - CO]^{\bullet -}$ at *m/z* 227.0462 were observed. In addition, the $[M - H - CH_3^{\bullet}]^{\bullet -}$ ion of **S53** fragmented into *m/z* 180.00636 ($^{0,3}A_0$) due to Retro-Diels–Alder (RDA) fragmentation of the C ring, indicating the presence of two hydroxyls and two methoxyls on the A ring. According to the literature,[26] **S53** was tentatively identified as 5,8,2′-trihydroxy-6,7-dimethoxyflavone. Similarly, there are two hydroxyl groups and one methoxyl group on the A ring of **S54**, and characteristic ions at *m/z* 180.00696 ($^{1,3}A_0$, $C_8H_4O_5^{\bullet -}$), *m/z* 165.99080 ($C_7H_2O_5^{\bullet -}$) and *m/z* 137.99586 ($C_6H_2O_4^{\bullet -}$) were observed in MS^2. Accordingly, **S54** was identified as 5,7,6′-trihydroxy-8,2′-dimethoxyflavone.[25] Using the same method, **S51** and **S82** were tentatively identified as trihydroxy-dimethoxyflavone (an isomer of **S54**).

S68, **S74**, **S79**, and **S81** showed $[M - H]^-$ ions at *m/z* 283.06122, *m/z* 283.06137, *m/z* 283.06165, and *m/z* 283.06149, and their molecular formulae were $C_{16}H_{12}O_5$. In their MS^2 spectra, $[M - CH_3^{\bullet}]^{\bullet -}$ could be observed. They were tentatively identified to be dihydroxy-methoxyflavone (an isomer of **S60**).

S65 and **S73** presented $[M - H]^-$ ions at *m/z* 299.05618 and *m/z* 299.05616, which indicated that their molecular formulae were $C_{16}H_{12}O_6$. $[M - H - CH_3^{\bullet}]^{\bullet -}$ ions at *m/z* 284.0329 were observed in the MS^2 spectra of **S73** and **S65**. The $[M - H]^-$ ion of **S73** fragmented to *m/z* 151.00368 due to RDA fragmentation of the C ring, which indicated the presence of three hydroxyls and one methoxyl on the A ring. Hence, **S73** was identified as trihydroxy-methoxyflavone, with trihydroxyl and methoxyl groups on the A ring. **S65** was identified as an isomer of 4′-hydroxy wogonin.

S52, **S55**, **S61**, **S63**, and **S69** showed $[M - H]^-$ ions at *m/z* 313.07190, *m/z* 313.07188, *m/z* 313.07224, *m/z* 313.07211, and *m/z* 313.07190, respectively, which indicated that their molecular formulae were $C_{17}H_{14}O_6$. In their MS^2 spectra, $[M - H - 2 \times CH_3^{\bullet}]^{\bullet -}$ ions could be observed. **S61** displayed characteristic fragmentation ions at *m/z* 195.0301 and *m/z* 117.03396 formed by cleavage of the C ring. Therefore, **S61** was tentatively identified as 5,8-dihydroxy-6,7-dimethoxyflavone.[24,26] **S63** was identified as skullcapflavone I.[26] **S52**, **S55**, and **S69** were tentatively identified as isomers of 6-methoxywogonin (dihydroxy-dimethoxyflavone).

S50 and **S72** had $[M - H]^-$ ions at *m/z* 409.02370 and *m/z* 349.00236 and their molecular formulae were predicted to be $C_{17}H_{14}O_{10}S$ and $C_{15}H_{10}O_8S$, respectively. **S50** and **S72** produced a neutral loss of 79.9563 Da which was predicted to be SO_3. In MS^2 spectra, $[M - H - 80 - 2 \times CH_3^{\bullet}]^-$ at *m/z* 299.01993 was observed for **S50** but not for **S72**. The $[M - H]^-$ of **S50** and **S72** fragmented into *m/z* 195.03003 ($C_9H_7O_5$) and *m/z* 139.00328 ($C_6H_3O_4$) due to RDA fragmentation of the C ring, indicating the presence of two hydroxyls and two methoxyls on the A ring and three hydroxyls on the A ring, respectively. Thus, **S50** and **S72** was tentatively identified as 2′,5,6-trihydroxy-7,8-dimethoxyflavone 6-*O*-sulfate and baicalein 6-*O*-sulfate, respectively.[30]

According to $[M - H]^-$ ions at *m/z* 287.05625 and *m/z* 287.05622, the molecular formulae of **S64** and **S71** were determined to be $C_{15}H_{12}O_6$. In their MS^2 spectra, $[M - H - H_2O]^-$ at *m/z* 269.05 was observed, which indicated that they might have adjacent hydroxyl groups. In addition, the characteristic fragmentation ions of **S71** at *m/z* 243.06630 ($[M - H - CO_2]^-$), *m/z* 225.05594 ($[M - H - CO_2 - H_2O]^-$), and *m/z* 179.0350, *m/z* 125.02432, and *m/z* 135.04514, generated from RDA fragmentation of the C ring, were detected. Thus, **S71** was tentatively identified as eriodictyol,[24,37] and **S64** was identified as an isomer of eriodictyol. According to the literature,[21,24,26,30–35] all of the other aglycones were putatively identified.

Other constituents. In total, 13 other constituents were tentatively identified. **S83** and **S84** showed $[M - H]^-$ ions at *m/z* 191.01970 and *m/z* 191.01969, respectively, which indicated that their molecular formulae were $C_6H_8O_7$. Both of them showed $[M - H - H_2O - CO_2]^-$ and $[M - H - H_2O - CO_2 - 2 \times H_2O]^-$ ions at *m/z* 147.03 and *m/z* 111.01. Thus, **S83** and **S84** were tentatively

identified as galactaric acid 1,5-lactone or its isomer,[38] and they are reported in SR for the first time. **S85** exhibited $[M-H]^-$ ions at *m/z* 503.14106 ($C_{21}H_{27}O_{14}$), and fragment ions at *m/z* 323.07770 ($[M-H-162-H_2O]^-$), *m/z* 179.03532 ($[M-H-2\times162]^-$), and *m/z* 161.02457 ($[M-H-2\times162-H_2O]^-$). Thus, **S85** was identified as 1-caffeyllaminaribiose.[39] **S86** presented $[M-H]^-$ ions at *m/z* 417.11947 ($C_{21}H_{21}O_9$) with a base peak at *m/z* 211.07681 ($[M-H-162-CO_2]^-$), and was tentatively identified to be gaylussacin. Other constituents were also putatively identified based on the literature and public databases (Fig. S3 and Table S3†).

Based on the untargeted metabolomics approach, 114 constituents were detected in different amounts between KQ and ZQ. They were tentatively identified, and 35 constituents were identified for the first time in SR. **S30** was identified as a new compound named dihydroxy-methoxyflavone *O*-glucoside-(1 → 6)-*O*-glucuronide.

As an example (SR samples no. 7591-1 and no. 7593-1), the peak areas of 49 constituents were larger in KQ than in ZQ, and 26 of them in KQ were 2.0–18.2 times as large as those in ZQ. The peak areas of 65 constituents in ZQ were larger than those in KQ, and 39 of them in ZQ were 2.0–18.2 times larger than those in KQ (Fig. S4 and S5†). We also found the peak areas of 68.4% of aglycones were larger in KQ than those in ZQ. In contrast, the peak areas of 72.4% of glycosides in ZQ were larger than those in KQ. Such differences in flavonoid aglycones and glycosides between KQ and ZQ may be responsible for the difference in their efficacy.

The bioactivities of the 114 constituents with differential content between KQ and ZQ were summarized by literature review. Twenty-eight constituents (**S1–S5**, **S17**, **S19**, **S21**, **S22**, **S24**, **S25**, **S39**, **S40**, **S45**, **S46**, **S56–S60**, **S62**, **S63**, **S66**, **S67**, **S71**, **S77**, **S78**, and **S114**) have anti-inflammatory activity *in vitro* and *in vivo*. Among these, the peak areas of 13 constituents (**S2–S5**, **S24**, **S62**, **S63**, **S66**, **S67**, **S71**, **S77**, **S78**, and **S114**) in the KQ group were higher than those in the ZQ group. Eleven constituents (**S1**, **S22**, **S25**, **S39**, **S58–S60**, **S62**, **S67**, **S77**, and **S78**) can protect against ALI in rodents, and the peak areas of **S62**, **S67**, **S77**, and **S78** in the KQ group were higher than those in the ZQ group. Eight constituents (**S1**, **S25**, **S39**, **S59**, **S60**, **S62**, **S67**, and **S78**) are able to alleviate colitis in rodents, and the peak areas of **S1**, **S25**, **S39**, **S59**, and **S60** in the ZQ group were higher than those in the KQ group (Table S4†). These literature-based results indicate that flavonoids in KQ and ZQ are bioactive (30 of 114 constituents are bioactive, 25 of which are flavonoids) and might provide an essential link between KQ, ZQ and inflammatory diseases and might play important beneficial roles in clearing lungs and colon heat symptoms.

Establishment of a differentiation index for KQ and ZQ crude drug samples

According to multivariate statistical analysis (OPLS-DA), the above-identified constituents (VIP ≥ 3) in SR were used to evaluate SR. A differentiation index was established using the ratio of peak areas and applied to 23 ZQ and 28 KQ samples. For known samples, the EIC peak area ratio (PAR) of **S40** plus **S46** to **S78** was above 1.60 in all ZQ samples, but in 75.0% (21/28) of KQ samples the PAR was below 1.60. Similarly, the PAR of **S25** to **S60** was not more than 0.90 in 89.3% (25/28) of KQ samples, but in only 69.6% (16/23) of ZQ samples was the PAR above 0.90. The PAR of **S39** to **S71** was the best for distinguishing KQ and ZQ samples (Table S5†). The PAR of **S39** to **S71** (<9.0) can be used as a differentiation index of 28 KQ samples with prediction accuracy of 96.4%, and a PAR ≥ 9.0 was a differentiation index for 23 ZQ samples with prediction accuracy of 95.7% (Fig. 4). For unknown SR samples, it must be ensured that the degree of difference between KQ and ZQ samples should be satisfactory. As a result, the PAR of **S39** (baicalin) to **S71** (eriodictyol) could be used as a differentiation index of KQ and ZQ samples with a low false negative rate (3.6%).

Identification of prototype constituents and metabolites in colon and lungs

Nineteen prototype SR constituents (**S13**, **S21**, **S25**, **S39**, **S40**, **S46**, **S57**, **S59–S62**, **S64–S67**, **S71**, **S76**, **S78**, and **S80**) and 16

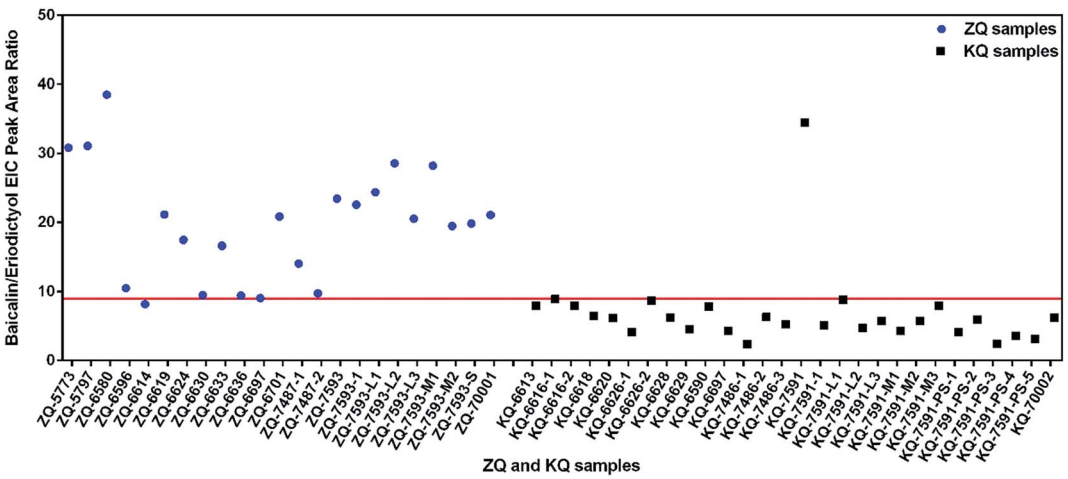

Fig. 4 Extracted ion chromatogram peak area ratios of baicalin (**S39**) to eriodictyol (**S71**) in KQ and ZQ.

metabolites (**M1–M16**) were tentatively identified in colon and lungs (Fig. 5). Among them, four prototype constituents (**S64, S65, S71**, and **S80**) and 12 metabolites (**M5–M16**) were identified *in vivo* for the first time after oral administration of SR extracts. **M12** was identified in colon as a new compound named 5,7-dihydroxy-flavonone 6-*C*-arabinoside. The LC/MS data of KQ and ZQ prototype constituents and metabolites detected in lungs and colon are shown in Tables 1 and 2.

M1 exhibited $[M - H]^-$ ions at *m/z* 333.00798, which indicated that its molecular formula was $C_{15}H_{10}O_7S$. In MS^2 spectra, a base peak $[M - H - 80]^-$ ion at *m/z* 253.05118 was observed, tentatively identifying **M1** as chrysin *O*-sulfate. **M2** and **M3** showed $[M - H]^-$ ions at *m/z* 349.00, which indicated that their molecular formulae were $C_{15}H_{10}O_8S$. In their MS^2 spectra, $[M - H - 80]^-$ ions at *m/z* 269.05 were observed, and $[M - H - 80 - H_2O]^-$ ions could only be observed in **M3**. These data indicate that **M3** contains adjacent hydroxyl groups. Thus, **M3** was identified as baicalein *O*-sulfate, and **M2** was identified as apigenin *O*-sulfate. **M4** presented $[M - H]^-$ ions at *m/z* 363.01881 ($C_{16}H_{12}O_8S$) with MS^2 peaks at *m/z* 283.06204 ($[M - H - 80]^-$) and *m/z* 268.03584 ($[M - H - 80 - CH_3^{\bullet}]^{\bullet -}$); therefore, **M4** was identified as wogonin *O*-sulfate. **M5** showed $[M - H]^-$ ions at *m/z* 267.03054 ($C_{15}H_7O_5$) with MS^2 peaks at *m/z* 239.03534 ($[M - H - CO]^-$) and *m/z* 211.04114 ($[M - H - 2 \times CO]^-$), and it was identified as 6,7-dehydrobaicalein. **M6** and **M7** showed $[M - H]^-$ ions at *m/z* 285.0412 ($C_{15}H_9O_6$), which was 16 Da larger than that of baicalein or scutellarein ($C_{15}H_9O_5$), thus they were hydroxylated baicalein or scutellarein. **M7** showed $^{0,3}A^-$ ions at *m/z* 151.00395 resulting from cross-ring cleavage of the *C*-ring. Thus, **M7** was tentatively identified as tetrahydroxyflavone. **M6** was tentatively identified as hydroxylated baicalein or its isomer. **M8** was identified as an isomer of kanzakiflavone I with $[M - H]^-$ ions at *m/z* 327.05179 ($C_{17}H_{11}O_7$). By the same method, **M9**, **M10**, **M11**, **M13**, **M15**, and **M16** were tentatively identified as trihydroxy-dimethoxyflavone, dihydroxy-trimethoxyflavone, trihydroxy-trimethoxyflavone, trihydroxy-tetramethoxyflavone, trihydroxyflavone *O*-glucuronide, and trihydroxy-tetramethoxyflavone *O*-sulfate, respectively.

M12 exhibited $[M - H]^-$ ions at *m/z* 387.10951, which suggested that its molecular formula was $C_{20}H_{20}O_8$. **M12** yielded $^{0,3}X_6^-$ and $^{0,2}X_6^-$ fragment ions at *m/z* 327.08862 ($[M - H - 60]^-$) and 297.07758 ($[M - H - 90]^-$), suggesting they were formed by cross-ring cleavages in a pentose residue. The $[M - H - H_2O]^-$ ion at *m/z* 369.09869 indicated that the eliminated water was produced from the 2″-hydroxyl of the sugar and the 5- or 7-hydroxyl of the aglycone,[22] and $[M - H - 2 \times H_2O]^-$ at *m/z* 351.08817 suggested that the 3-hydroxyl and 2-hydrogen of

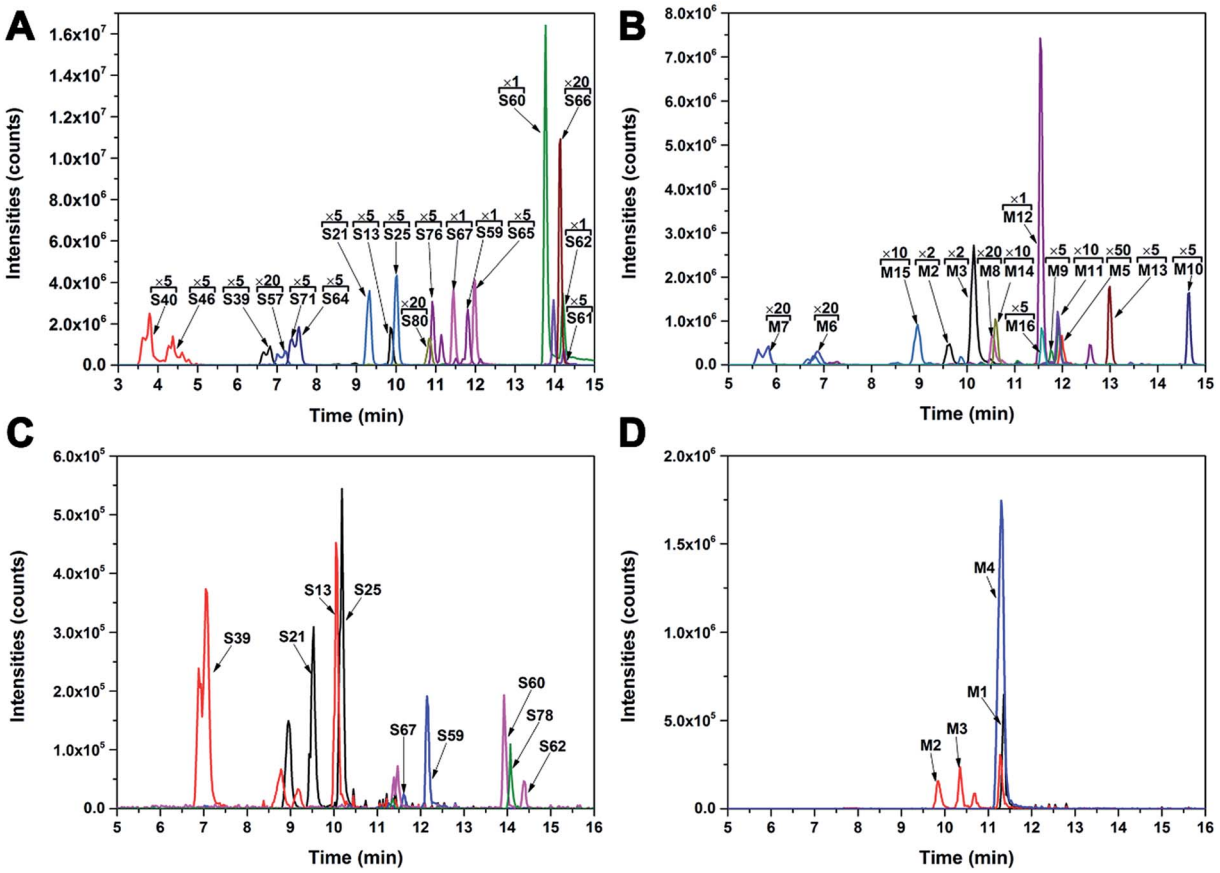

Fig. 5 Extracted ion chromatograms of prototype constituents and metabolites in colon and lungs in SR sample (batch no. 7591-1). (A) prototype constituents in colon; (B) metabolites in colon; (C) prototype constituents in lungs; (D) metabolites in lungs (×1, ×2, ×5, ×10, and ×20 denote amplification factor).

Table 1 Characterization of prototype constituents and metabolites in lungs with peak area differences between Kuqin and Ziqin[a]

ID	t_R (min)	$[M-H]^-$/ $[M-H]^+$ m/z	Ion mode	ESI-MS^2 m/z (% relative)	Predicted formula	Diff (ppm)	Identification	Structure type
S13	9.9	445.07672	−	269.04588 (100)	$C_{21}H_{18}O_{11}$	−2.055	Baicalein 6-*O*-glucuronide	Flavone *O*-glycoside
#**S21**	9.9	459.09278	−	283.06142 (31.05), 268.03806 (100)	$C_{22}H_{20}O_{11}$	−1.099	Oroxylin A 7-*O*-glucuronide	Flavone *O*-glycoside
#**S25**	10.0	461.10779	+	285.07513 (100), 270.05173 (12)	$C_{22}H_{20}O_{11}$	−0.104	Wogonoside	Flavone *O*-glycoside
#**S39**	6.6	445.07698	−	269.04602 (100)	$C_{21}H_{18}O_{11}$	−1.471	Baicalin	Flavone *O*-glycoside
#**S59**	11.9	269.04525	−	269.04612 (100), 251.03522 (3.93), 241.05328 (3.70), 223.04423 (1.16)	$C_{15}H_{10}O_5$	−1.103	Baicalein	Flavone
#**S60**	13.7	283.06062	−	269.04105 (20.10), 268.03806 (100), 221.19221 (4.80)	$C_{16}H_{12}O_5$	−2.037	Wogonin	Flavone
#**S62**	14.1	283.06063	−	269.04114 (17.87), 268.03809 (100)	$C_{16}H_{12}O_5$	−2.002	Oroxylin A	Flavone
#**S67**	11.3	283.06054	−	269.04580 (100), 225.0551 (3.73), 197.06120 (4.06)	$C_{15}H_{10}O_5$	−1.474	Apigenin	Flavone
#**S78**	13.8	253.05005	−	253.05109 (100), 209.15492 (2.53)	$C_{15}H_{10}O_4$	−2.300	Chrysin	Flavone
M1	11.1	333.00798	−	253.05118 (100)	$C_{15}H_{10}O_7S$	1.602	Chrysin *O*-sulfate	Flavone
M2	10.1	349.00292	−	269.04642 (100), 225.05632 (1)	$C_{15}H_{10}O_8S$	1.601	Apigenin *O*-sulfate	Flavone
M3	10.5	349.00290	−	269.04636 (100), 251.03532 (0.3), 197.06163 (0.1)	$C_{15}H_{10}O_8S$	1.544	Baicalein *O*-sulfate	Flavone
M4	11.1	363.01881	−	283.06204 (96), 268.03854 (100)	$C_{16}H_{12}O_8S$	2.200	Wogonin *O*-sulfate	Flavone

[a] #, Identification by comparing the retention time, UV spectra, and MS data with authentic standards.

flavanone were eliminated. Thus, **M12** was tentatively identified as a new compound, 2,5-dihydroxyflavonone 6-*C*-arabinoside.

M14 showed $[M-H]^-$ ions at m/z 419.13573, which suggested that its molecular formula was $C_{21}H_{24}O_9$. In MS^2 spectra, $^{0,3}X_6^-$ and $^{0,2}X_6^-$ fragment ions at m/z 329.10379 ($[M-H-90]^-$) and 299.09293 ($[M-H-120]^-$) were observed, which are characteristic of cross-ring cleavages in a hexose residue. Furthermore, from the fragment ions at m/z 197.04630 and m/z 167.03580, its aglycone should contain three hydroxyl groups. Thus, **M14** was tentatively identified to be phlorizin c and is reported as a metabolite of SR for the first time.

Exploring the basis of KQ and ZQ efficacy *in vivo*

To investigate the effect of KQ and ZQ samples from different places and batches on the distribution of chemical constituents in colon and lungs, the distribution experiment was repeated six times. The EIC peak areas of 13 prototype constituents (**S13**, **S21**, **S25**, **S39**, **S40**, **S46**, **S59–S62**, and **S65–S67**) and six metabolites (**M2**, **M3**, **M9**, **M10**, **M12**, **M14**) in the colon of KQ and ZQ groups are shown in Table S6.† Similarly, the EIC peak areas of nine prototype constituents (**S13**, **S21**, **S25**, **S39**, **S59**, **S60**, **S62**, **S67**, and **S78**) and four metabolites (**M1–M4**) in the lungs of KQ and ZQ groups are shown in Table S7.† From the results of these six separate experiments, we found that the peak areas of seven constituents (**S21**, **S25**, **S39**, **S59**, **S60**, **S62**, and **S67**) were larger in colon than in lungs. Furthermore, in colon, the peak areas of **S25**, **S39**, **S60**, and **S62** in the ZQ groups were larger than those in the KQ groups. In lungs, the peak areas of **S25**, **S39**, **S60**, and **S62** in the ZQ groups were smaller than those in the KQ groups.

The peak area of baicalin (**S39**) in KQ groups was 0.66 times as large as that in ZQ groups for SR samples. In colon, the baicalin peak area in KQ groups was 0.86-fold as large as that in ZQ groups, but in lungs its peak area in KQ groups was 1.13 times as large as that in ZQ groups. The peak area of wogonoside (**S25**) of KQ groups was 0.66 times as large as that in ZQ groups in SR samples. In colon, the wogonoside peak area in KQ groups was 0.91 times as large as that in ZQ groups, but in lungs its peak area in KQ groups was 1.13 times as large as that in ZQ groups. In SR samples, the peak areas of wogonin (**S60**) and oroxylin A (**S62**) of KQ groups were 1.27 and 1.68 times as large as those in ZQ groups. In colon, the peak areas of wogonin (**S60**) and oroxylin A (**S62**) in KQ groups were 0.80 and 0.70 times as large as those in ZQ groups. In lungs, their peak areas in KQ groups were 1.50 and 1.08 times as large as those in ZQ groups (Fig. 6). In SR and colon, the peak areas of baicalin (**S39**) and wogonoside (**S25**) in KQ groups were smaller than those in ZQ groups, but in lungs their peak areas in KQ groups were larger than those in ZQ groups. Similarly, in SR and lungs, the peak areas of wogonin (**S60**) and oroxylin A (**S62**) in KQ groups were larger than those in ZQ groups, but in colon their peak areas in KQ groups were smaller than those in ZQ groups. In addition, the peak areas of wogonoside, baicalin, wogonin, and oroxylin A in colon were larger than those in lungs (Fig. 6). Therefore, these results indicate that metabolic conversion might occur *in vivo*, and that these constituents were much more easily distributed in colon than in lungs.

These constituents had various biological activities. Baicalin (**S39**) and baicalein (**S59**) alleviate gut inflammation *via* the Cdx2/Pxr pathway in a mouse model of chemical colitis.[40] Wogonoside (**S25**)[41] and wogonin (**S60**)[42] can protect against dextran sulfate sodium (DSS)-induced experimental colitis in mice. Oroxylin A (**S62**) can also inhibit colitis-associated carcinogenesis.[43] In animal models of pulmonary inflammation, baicalin attenuates air embolism-induced ALI in rats.[44] Baicalein can protect against LPS-induced ALI in rats.[3] and wogonoside (**S25**) has a protective effect on LPS-induced ALI in mice.[6] ALI induced in mice by LPS was inhibited by wogonin (**S60**) *via*

Table 2 Characterization of prototype constituents and metabolites in colon with peak area differences between Kuqin and Ziqin[a]

ID	t_R (min)	$[M-H]^-/[M-H]^+$ m/z	Ion mode	ESI-MS^2 m/z (% relative)	Formula	Diff (ppm)	Identification	Structure type
S13	9.9	445.07796	−	269.04630 (100), 251.03685 (0.6)	$C_{21}H_{18}O_{11}$	0.731	Baicalein 6-*O*-glucuronide	Flavone *O*-glycoside
#**S21**	9.1	459.09374	−	283.06137 (47), 268.03900 (100)	$C_{22}H_{20}O_{11}$	0.992	Oroxylin A 7-*O*-glucuronide	Flavone *O*-glycoside
#**S25**	9.8	459.09363	−	283.06137 (75), 268.03836 (100), 85.02944 (28)	$C_{22}H_{20}O_{11}$	0.752	Wogonoside	Flavone *O*-glycoside
#**S39**	6.6	445.07788	−	269.04642 (100), 251.03580 (1), 241.05072 (1), 225.0602 (0.4)	$C_{21}H_{18}O_{11}$	0.552	Baicalin	Flavone *O*-glycoside
#**S40**	3.7	547.14611	−	547.14618 (30), 529.13562 (3), 487.12500 (2), 469.11435 (4), 457.11453 (40), 439.10385 (4), 427.10352 (66), 409.09323 (4), 397.09296 (9), 367.08307 (83), 349.07202 (7), 337.07214 (100)	$C_{26}H_{28}O_{13}$	0.724	Chrysin 6-*C*-arabinoside 8-*C*-glucoside	Flavone *C*-glycoside
#**S46**	4.3	547.14609	−	547.14642 (17), 529.13593 (3), 487.12570 (14), 457.11572 (40), 439.1 (4), 427.10434 (66), 409.09360 (10), 397.09317 (8), 367.08246 (64), 367.08258 (83), 337.07224 (100)	$C_{26}H_{28}O_{13}$	0.687	Chrysin 6-*C*-glucoside 8-*C*-arabinoside	Flavone *C*-glycoside
*,#**S57**	7.0	347.07574	+	347.07541 (63), 332.05203 (100), 314.04147 (35), 286.04645 (2), 183.02850 (3), 169.01292 (7), 142.02594 (3)	$C_{17}H_{14}O_8$	−1.164	Viscidulin III	Flavone
#**S59**	11.9	271.05975	+	271.06064 (100), 253.05013 (1)	$C_{15}H_{10}O_5$	−1.291	Baicalein	Flavone
#**S60**	13.7	283.06125	−	268.03845 (100), 283.06198 (3)	$C_{16}H_{12}O_5$	0.188	Wogonin	Flavone
***S61**	14.2	313.07193	−	313.07281 (13), 298.04904 (58), 283.02554 (100)	$C_{17}H_{14}O_6$	0.539	5,8-Dihydroxy-6,7-dimethoxyflavone	Flavone
		315.08590	+	315.08585 (100), 300.06247 (40), 285.03897 (5)	$C_{17}H_{14}O_6$	−1.316		
#**S62**	14.2	283.06129	−	268.03854 (100), 283.06201 (6)	$C_{16}H_{12}O_5$	0.330	Oroxylin A	Flavone
***S64**	7.7	287.05625	−	287.05680 (4), 269.04592 (3), 225.05589 (1), 215.03502 (9), 161.02478 (17), 125.02463 (100)	$C_{15}H_{12}O_6$	0.483	Isomer of **S71** (tetrahydroxyflavanone)	Flavanone
***S65**	12.1	299.05618	−	299.005698 (5), 284.03354 (100)	$C_{16}H_{12}O_6$	0.230	Trihydroxy-methoxyflavone	Flavone
S66	14.5	373.09289	−	358.07050 (22), 343.04675 (100), 328.02344 (23)	$C_{19}H_{18}O_8$	−0.002	Scullcapflavone II	Flavone
#**S67**	11.4	269.04552	−	269.04636 (100), 241.05702 (4), 225.05634 (8), 197.06136 (12)	$C_{15}H_{10}O_5$	−0.099	Apigenin	Flavone
***S71**	7.2	287.05622	−	161.02477 (25), 125.02464 (100)	$C_{15}H_{12}O_6$	0.379	Eriodictyol	Flavanone
***S76**	10.7	299.05611	−	299.05692 (13), 284.03333 (100)	$C_{16}H_{12}O_6$	−0.004	4′-Hydroxy wogonin	Flavone

Table 2 (*Contd.*)

ID	t_R (min)	$[M-H]^-/[M-H]^+$ m/z	Ion mode	ESI-MS^2 m/z (% relative)	Formula	Diff (ppm)	Identification	Structure type
***S80**	10.7	301.07175	−	301.07175 (10), 286.04865 (100), 283.02444 (4), 258.05128 (3), 255.23323 (10), 185.06107 (5), 181.01100 (8), 18000667 (16), 166.99010 (14), 165.99078 (45), 152.01132 (5), 137.99594 (9), 119.05031 (8), 110.00878 (8)	$C_{16}H_{14}O_6$	−0.038	Trihydroxy-methoxyflavanone	Flavanone
M2	9.5	349.00297	−	269.04642 (100), 225.05632 (1)	$C_{15}H_{10}O_8S$	1.744	Apigenin *O*-sulfate	Flavone
M3	10.1	349.00301	−	269.04636 (100), 251.03532 (0.3), 197.06163 (0.1)	$C_{15}H_{10}O_8S$	1.859	Baicalein *O*-sulfate	Flavone
***M5**	11.9	267.03054	−	239.03534 (100), 211.04114 (1.14), 136.98807 (13.85)	$C_{15}H_8O_5$	2.409	6,7-Dehydrobaicalein	Flavone
***M6**	6.9	285.04126	−	285.04123 (100), 151.08276 (1)	$C_{15}H_{10}O_6$	2.802	Isomer of hydroxylation of baicalin	Flavone
***M7**	5.8	285.04125	−	285.04132 (100), 241.05148 (20), 199.04099 (15), 151.00395 (66)	$C_{15}H_{10}O_6$	2.767	Hydroxylation of baicalin	Flavone
***M8**	10.5	327.05179	−	—	$C_{17}H_{12}O_7$	2.336	Isomer of kanzakiflavone I	Flavone
***M9**	11.8	329.06732	−	329.06747 (5), 314.04416 (97), 299.02051 (100), 271.02548 (4), 227.03551 (11), 199.04102 (4)	$C_{17}H_{14}O_7$	1.957	Trihydroxy-dimethoxyflavone	Flavone
***M10**	14.6	343.08295	−	328.05975 (27), 313.03641 (100), 298.01288 (14), 271.01740 (2), 209.00899 (0.5), 194.99405 (2)	$C_{18}H_{16}O_7$	1.819	Dihydroxy-trimethoxyflavone	Flavone
***M11**	11.8	359.07789	−	344.05469 (60), 329.03140 (100), 314.00830 (2), 311.02087 (2), 301.03745 (6), 297.00381 (2), 285.04218 (1), 242.02234 (1), 198.03300 (3), 154.99925 (2)	$C_{18}H_{16}O_8$	1.808	Trihydroxy-trimethoxyflavone	Flavone
***M12**	11.4	387.10951	−	369.09869 (0.4), 351.08817 (1), 327.08862 (4), 309.08862 (3), 297.07758 (100), 269.08313 (5), 255.06735 (2), 191.03568 (5)	$C_{20}H_{20}O_8$	2.504	2,5-Dihydroxyflavonone 6-*C*-arabinoside	Flavone *C*-glycoside
***M13**	12.9	389.08871	−	374.06497 (100), 359.04156 (84), 344.01788 (25), 316.02380 (4), 300.02774 (7), 285.00543 (1), 183.03052 (1)	$C_{19}H_{18}O_9$	2.325	Trihydroxy-tetramethoxyflavone	Flavone
***M14**	10.5	419.13573	−	329.10379 (17), 299.09293 (100), 257.08221 (32), 197.04630 (9), 195.77 (2), 167.03508 (55)	$C_{21}H_{24}O_9$	2.325	Phlorizin c	Flavone *C*-glycoside
***M15**	8.8	445.07863	−	269.04626 (100), 197.06091 (0.6), 171.04570 (0.7), 113.02453 (2)	$C_{21}H_{18}O_{11}$	2.237	Trihydroxyflavone *O*-glucuronide	Flavone *O*-glycoside
***M16**	11.5	469.04555	−	389.08881 (19), 374.06531 (100), 359.04163 (25)	$C_{19}H_{18}O_{12}S$	1.983	Trihydroxy-tetramethoxyflavone *O*-sulfate	Flavone

[a] #, Identification by comparing the retention time, UV spectra, and MS data with authentic standards. *, first report of compound after oral administration of SR extracts.

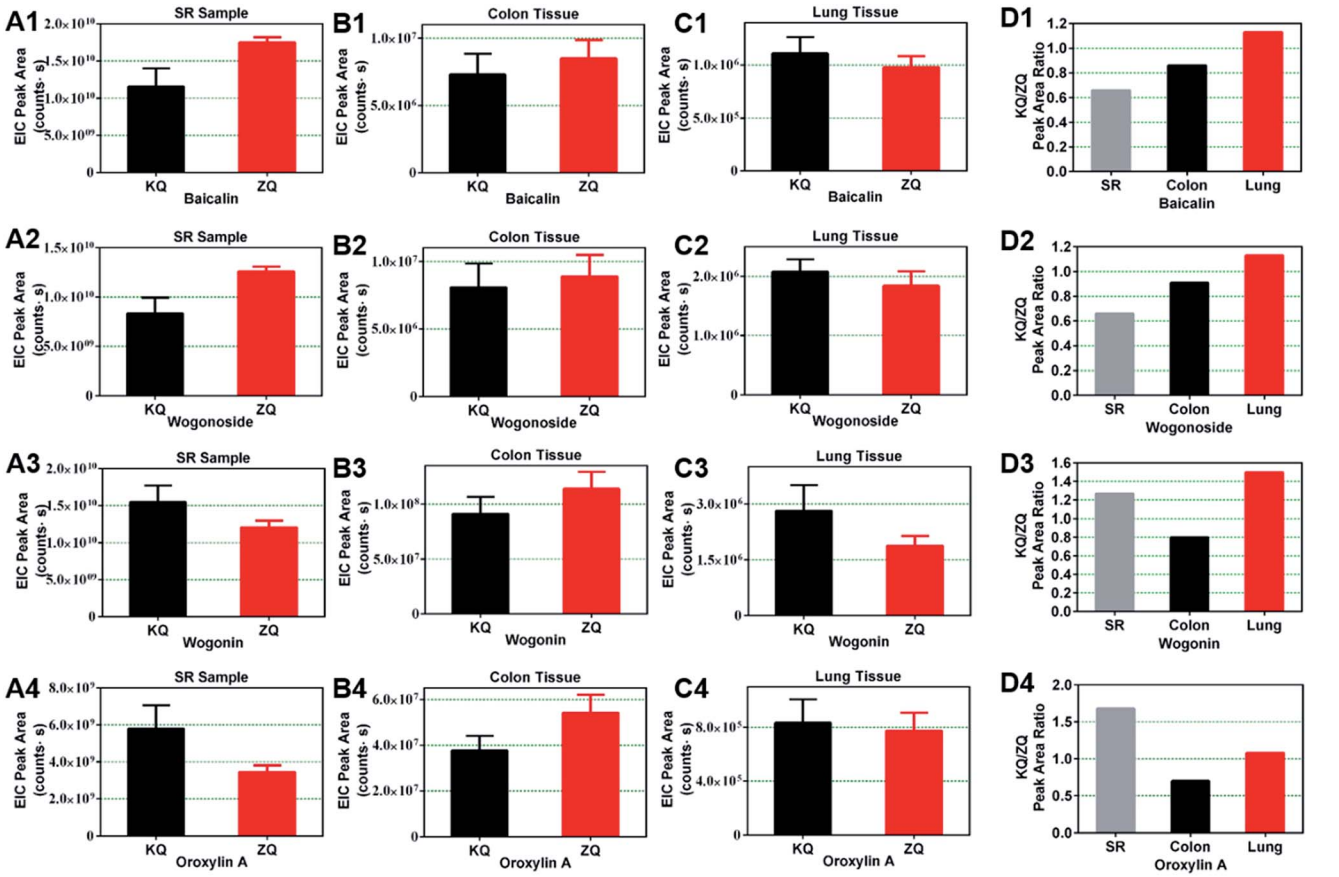

Fig. 6 The peak areas of baicalin, wogonoside, wogonin, and oroxylin A in crude drug, colon, and lungs samples. A1–A4, the peak areas in SR samples; B1–B4, the peak areas in colon; C1–C4, the peak areas in lungs; D1–D4, the peak area ratios of KQ group to ZQ group in SR samples, colon, and lungs samples for the four constituents. Values are expressed as the mean ± SEM. SR samples, $n = 6$ in each group; colon and lungs samples, $n = 36$ in each group containing six repeated experiments ($n = 6$ in each experiment).

duction of Akt phosphorylation and RhoA activation.[45] Oroxylin A (**S62**) can attenuate cigarette smoke-induced lung inflammation[46] and rescue LPS-induced ALI in rodents.[47]

The constituents, **S25, S39, S60,** and **S62,** might work together to produce differences in efficacy, such that ZQ is used to treat lower energizer colon heat symptoms and KQ is effective for clearing upper energizer lung heat syndrome. Furthermore, they may be the basis for KQ and ZQ acting on colon and lungs. The characteristic distribution of **S39** (baicalin), **S25** (wogonoside), **S60** (wogonin), and **S62** (oroxylin A) in colon and lungs might be the basis for the different efficacies of KQ and ZQ. All of the above may cause the differences in efficacy between KQ and ZQ.

The relationship among constituents after oral administration of KQ and ZQ extracts

After oral administration, multiple components in KQ and ZQ samples might undergo intestinal flora metabolism, extensive first-pass effect and enterohepatic circulation, which may significantly contribute to the differences in exposure of these components between colon and lungs. Therefore, clarifying KQ and ZQ component metabolic pathways could contribute significantly to our understanding of metabolism *in vivo* and help us to interpret the distribution differences of **S39, S25, S60,** and **S62** between colon and lungs. It will also provide a theoretical basis to explain efficacy differences between KQ and ZQ.

It is well known that the main reactions involved in the metabolism of xenobiotics are: (de)hydroxylation, (de)methylation, (de)glycosylation, glucuronidation, and sulfation. For example, *in vivo* metabolic reactions of **S39** include methylation, hydroxylation, glucuronidation, sulfation and their composite reactions.[48] Based on these processes, 22 constituents might be converted into the constituents **S21, S25, S39, S40, S46, S59, S60,** and **S62** *via* metabolic reactions.

As can be seen from Fig. 7, baicalin (**S39**) can be metabolized by intestinal microflora into baicalein (**S59**) and oroxylin A (**S62**).[1,49] Oroxylin A 7-*O*-glucuronide (**S21**) can also be converted into **S62** and **S39** by deglucuronidation and demethylation reactions.[50] Wogonoside (**S25**) can be metabolized to wogonin (**S60**) by fecal microflora.[51] **S25** can be metabolized to scutellarin (**S17**) by demethylation and then transformed into scutellarein (**S58**) by deglucuronidation. Dehydroxylation and hydroxylation reactions of flavonoids have also been reported.[52–54] **S60** might be converted into **S58** and chrysin (**S78**) *via* demethylation and dehydroxylation reactions. **S40** and **S46** were deglycosylated to **S48** and **S101**, and eventually converted into **S78.**[55] **S78** might be metabolized to **S67** and **S59** by hydroxylation.[54]

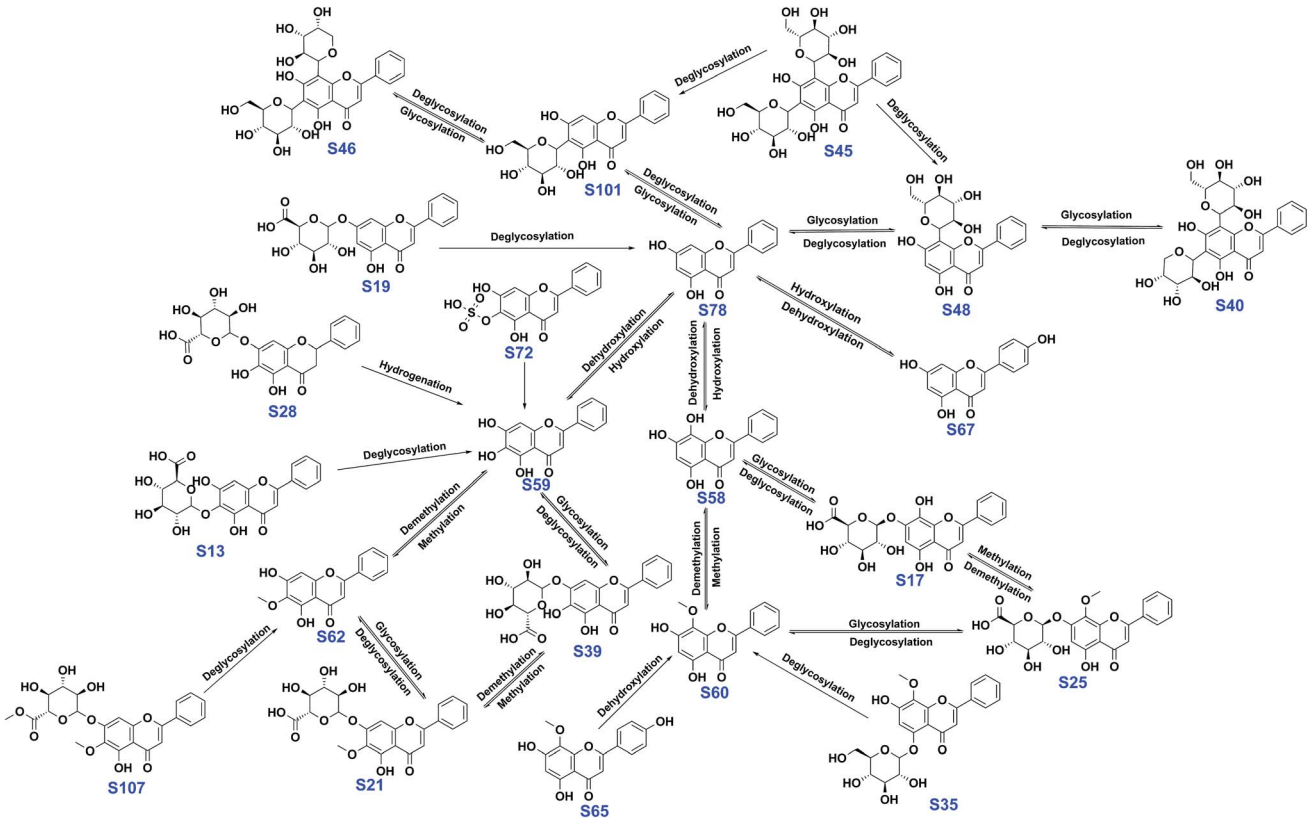

Fig. 7 Proposed metabolic pathways of the main active constituents after oral administration of SR extracts to rats.

Conclusions

To determine chemical differences and *in vivo* distribution differences between KQ and ZQ, we applied a metabolomics approach. A total of 114 constituents with peak area differences between KQ and ZQ crude drug samples were tentatively identified. Thirty-five of these constituents were identified in SR for the first time. Nineteen prototype constituents and 16 SR metabolites with peak area differences between KQ and ZQ were identified in colon and lungs. Among these, four constituents and 12 metabolites were reported for the first time after oral administration of SR extracts. According to the results of six repeated *in vivo* experiments, baicalin, wogonoside, oroxylin A 7-*O*-glucuroside, chrysin 6-*C*-arabinoside 8-*C*-glucoside, chrysin 6-*C*-glucoside 8-*C*-arabinoside, baicalein, wogonin, and oroxylin A were indicated to be the basis of KQ and ZQ efficacy. The differences in distribution among baicalin, wogonoside, wogonin and oroxylin A, which have anti-inflammation activities in colon and lungs, provides a theoretical foundation for explaining the differences in efficacy between KQ and ZQ. In addition, the PAR of baicalin/eriodictyol was proposed as a differentiation index for the quality control or classification of KQ (ratio <9.0 with 96.4% prediction accuracy) and ZQ (ratio ≥ 9.0 with 95.7% prediction accuracy) crude drug samples with good prediction accuracy. These results may provide a theoretical explanation for the differences in efficacy between KQ and ZQ.

Conflicts of interest

There are no conflicts to declare.

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