

Identification of the multiple bioactive derivatives and their endogenous molecular targets that may mediate the laxative effect of rhubarb in rats

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Abstract— The goal of this study is to use a bioinformatics and in vivo method to figure out how rhubarb (*Rheum tanguticum* Maxim. ex Balf.) causes rats to go to the toilet more often. **Methods:** Using high-performance liquid chromatography in conjunction with linear ion-trap quadrupole Orbitrap high-resolution mass spectrometry, substances originating from rhubarb that were found in the colorectum were identified. Using databases and the literature, we identified targets with the potential to have laxative effects. Then, we employed compounds derived from rhubarb in molecular docking modelling. Then, using western blotting, we assessed the expression of potential endogenous target molecules that bind specific rhubarb components in rats that were either given or not given rhubarb for constipation. In the end, the components of compounds that showed promise as bioactive were identified. We found 17 anthraquinones and 21 anthrones in the rat colorectum, which is a good indicator of the plant's medicinal value. Based on G-scoring, three proteins—c-kit, 5-hydroxytryptamine receptor 4 (5-HT4), and aquaporin-3 (AQP3)—may mediate the laxative action. Furthermore, ten components derived from rhubarb—aloe-emodin, emodin, rhein, chrysophanol, physcion, sennoside A, sennoside C, physcionanthrone, aloe-emodinanthrone, and rheinanthrone—were chosen as compounds with high probability of activity due to their strong binding affinity for multiple potential targets. It is possible that the laxative action of rhubarb extract is mediated by the fact that it enhanced the expression of c-kit and 5-HT4 while decreasing the expression of AQP3 in the colon of rats that were constipated. Additionally, we discovered that a single prototype component may undergo metabolism into many active metabolites, and that different molecules from the prototype can be combined to form a single active ingredient. The current research concludes that rhubarb's anthraquinones and anthrones may be metabolised into bioactive chemicals that enhance defecation via c-kit, 5-HT4, and/or AQP3.

Keywords: Al7075 alloy composite, E-glass, MMCs, and short E-glass fibres

Introduction

The Chinese herbal remedy rhubarb, scientifically known as *Rheum tanguticum* Maxim. ex Balf., is a

popular choice for relieving constipation.1, 2 Sennoside A, the main laxative component of rhubarb, is metabolised to rheinanthrone by gut

But recent research has found that rhubarb only contains around 0.08% sennoside A,^{7,8} which is much too little to explain the plant's strong laxative effects. In addition, we found that rhubarb extract had a much stronger laxative effect than the same amount of sennoside A in our early trial. According to their research, the exact process by which rhubarb produces its laxative effects is still up for debate. Thus, we set out to better understand how rhubarb's laxative action works so that its therapeutic usage may be based on good theoretical grounding.

For clinically-approved laxatives, the two main ways they work are by increasing the rate of intestinal motility and the stimulation of electrolyte and water secretion. One popular medicine, prucalopride, increases colonic motility by stimulating neuronal 5-hydroxytryptamine receptor 4 (5-HT₄), which in turn increases the contraction of the muscles lining the intestines.¹¹ As an example, osmotic laxatives like magnesium sulphate control the expression of aquaporin-3 (AQP3) in colonic epithelial cells, which leads to water buildup in the intestinal lumen and promotes defecation.^{12, 13} Since these laxatives act on specific molecular targets in the colon, it is vital to identify these targets and the specific rhubarb components involved in order to deduce how rhubarb exerts its laxative effects.

Applying the notion of induced FIT and the lock-and-key principle,¹⁴ One efficient method for identifying therapeutic targets and quickly screening possible active molecules is molecular docking modelling. The sole applications for this are the screening of bioactive compounds and potential targets. We wanted to conduct molecular docking analysis utilising active, biotransformed rhubarb derivatives and endogenous molecules that could mediate the laxative action to discover the active compounds in the col-orectum. Our goal was to increase the data's biological relevance. We used the *in vivo* metabolic understanding of the chemicals in rhubarb to discover the appropriate bioactive derivatives in the prototype by tracing the biotransformation products back to the original plant.¹⁵ Establishing suitable quality control procedures and providing a reference for the use of rhubarb derivatives in the clinic would be greatly aided by the identification of bioactive components in rhubarb. Our goal here was to find endogenous molecular

targets that might modulate the actions of rhubarb derivatives that could have cumulative or synergistic effects to stimulate defecation. The first step was to use high-performance liquid chromatography in conjunction with linear ion-trap quadrupole Orbitrap high-resolution mass spectrometry to identify the rhubarb derivatives that were found in the colorectum. The next step was to find possible molecular targets by searching the literature, the Drug Bank Database (DBD), and the Therapeutic Target Database (TTD). As a further step, we ran molecular docking simulations with all of the rhubarb derivatives and all of the possible molecular targets to find binding partners. Next, we performed protein analysis of treated rats' colonic lysates to find out whether the molecular targets that were identified *in silico* were controlled *in vivo*. Lastly, the active elements in colorectum were identified by tracing them back to components of rhubarb, utilising knowledge of the metabolism of related chemicals. This study technique has greatly contributed to our understanding of the laxative mechanism of rhubarb by identifying essential components responsible for its therapeutic actions and their prospective molecular targets. Because herbal medicines include several bioactive components with various potential mammalian molecular targets, this technique might be valuable in future mechanistic investigations of these treatments.

Materials and methods

Ethical approval

The study protocols were approved by the Ethics Committee of Beijing University of Chinese Medicine (BUCM-4-2017102601- 1026; Beijing, China).

Chemicals and reagents

Rhubarb was provided by the Modern Research Center of Traditional Chinese Medicine, Peking University (Beijing, China).

Loperamide was purchased from Xian Janssen Pharmaceutical (Xi'an, China). Standard substances, including emodin (lot code: 110756-201512, 98.7%), rhein (lot code: 110757-201607, 99.3%), physcion (lot code: 110758-201616, 99.0%), aloe-emodin (lot code: 110795-201710, 98.3%), chrysophanol (lot code: 110796-201721, 99.2%), sennoside A (lot code: 110824-201702, 95.2%), and senno-side B (lot code: 110825-201603, 95.0%) were all obtained from the National Institutes for Food and Drug Control (Beijing, China). Standard substances, including emodin-8-*O*- β -D-glucopyranoside (lot code: 23313-21-5, >95%), aloe-emodin-8-*O*- β -D-glucopyrano-side (lot code: 33037-46-6, >95%), and sennoside C (lot code: 37271-16-2,

>95%) were purchased from Chengdu Biopurify Phytochemicals (Sichuan, China). Mass spectrometry grade acetoni-trile, methanol, and formic acid were obtained from Thermo Fisher Scientific (Fair Lawn, NJ). Ultrapure water was obtained using a Synergy UV water purification system (Millipore, Billerica, MA).

Preparation of references and rhubarb extracts

We weighed and dissolved compounds in suitable volumes of 0.5% sodium carboxymethylcellulose to prepare reference samples (Supplemental Table 1).

The rhubarb herbal medicine (31.0 g) powder was weighed,

300 mL ultra-pure water was added, then the suspension was boiled for 20 min at 100 °C. The extracted solution was evaporated to 100 mL.

Rhubarb should be used at a dose of 0.05e0.25 g/kg/day in humans, according to the *Pharmacopoeia of the People's Republic of China* (2015).¹⁶ According to the dose conversion relationship between human and rat, the dose for rats was 0.31e1.54 g/kg/day. In our previous study, we showed that the administration of 1.54 g/kg/day of a rhubarb extract for 3 days exerted an effective laxative in rats.

Rat model of constipation and rhubarb administration

Thirty rats were acclimatized for 7 days, then allocated to three groups: control, model, and treatment. The control group was administered saline solution, and the model and treatment groups were administered loperamide at a dose of 1.5 mg/kg/day twice daily for 7 days by gavage to induce constipation. During the first 6 days, the wet and dry masses of the fecal pellets produced by the rats were measured each day.¹⁷

After the model of constipation had been successfully established, the treatment group was fed with rhubarb extract at a dose of 1.54 g/kg/day for 3 days, during which the other groups were administered substances as above. The evacuation index (EI) was used to evaluate the laxative effect of rhubarb.¹⁸ In addition, the feces of rats in the treatment group were collected for analysis. All the rats were sacrificed on the 10th day, their mid-colons were collected, snap-frozen in liquid nitrogen, and stored at 80 °C until western blot analysis.

Animals

Specific pathogen-free male Sprague-Dawley rats weighing 200 ± 20 g were obtained from Beijing Vital River Laboratory Animal Technology (Beijing, China) and maintained at a constant temperature (23 ± 2 °C) and humidity (60 ± 5%).

Identification of rhubarb derivatives in feces

Preparation of samples

Fecal samples were collected over a 24-h period from another 20 Sprague-Dawley rats that had been administered solutions of 10 reference substances. These feces were dried in a ventilator, crushed, and then placed in a centrifuge tube. Fecal samples weighing 20 mg were extracted using 200 mL 80% methanol and vortex-mixed for 30 min. Then, the samples were centrifuged at 13 522×g at 4 °C for 15 min and

the supernatant was evaporated to dryness under nitrogen. The residue was reconstituted with 200 mL of 50% methanol, vortex-mixed for 3 min, then centrifuged at 13 522×g at 4 °C for 10 min.

Chromatography and MS conditions

We used previously optimized chromatographic and MS conditions.¹⁹

Data processing

The raw mass data generated by the HPLC-LTQ-Orbitrap MS analysis were processed using Qual Browser of Xcalibur 2.1 (Thermo Fisher Scientific, San Jose, CA). Online chemical databases (<http://www.chemspider.com/> and <https://www.ncbi.nlm.nih.gov/>) were used to identify the compounds obtained. The identification of potentially novel compounds was accomplished using the Sci-Finder database (<https://sso.cas.org/>).

Creation of a laxative target database

First, we used the TTD (<https://db.idrblab.org/ttd/>) to identify molecular targets for the treatment of constipation and the Drug Bank Database (<https://www.drugbank.ca/>) to summarize the targets of existing laxatives. Then, we searched the literature to further screen for molecular targets with a possible laxative effect.

Homology modeling

The target sequences of 5-HT₄ and AQP3 were acquired from Uniprot (<http://www.uniprot.org/>; Uniprot IDs Q13639 [5-HT₄] and Q92482 [AQP3]). Template crystal structures for these target sequences were identified using BLAST and downloaded from the Research Collaboratory for Structural Bioinformatics Protein Data Bank (RCSB PDB, <http://www.rcsb.org/>), using the PDB IDs of 6H7J for 5-HT₄ and 6F7H for AQP3.²⁰ MOE v2014.0901 software (Molecular Operating Environment (MOE); Montreal, Canada) was used for homology modeling. The QuickPrep module in MOE was used to determine the likely sites of protonation of the proteins and the orientation of hydrogen atoms in pHs up to 7 and temperatures up to 300 K. First, the target sequence was aligned with the template sequence, and 10 independent intermediate models were established. These models, with differing homologies, were the result of permutational selection of different loop candidates and side-chain rotamers. Then, we selected the intermediate model with the highest generalized born/volume integral score as the final model, which was subjected to further energy minimization using AMBER10: EHT force field (MOE).

Molecular docking between rhubarb derivatives in the colorectum and molecules mediating a laxative effect

The 2D structures of the rhubarb derivatives were drawn in ChemBioDraw 2014 and chemically standardized, which consisted of the addition of hydrogens, ionization at pHs from 5.1 to 9.1, and the formation of stereoisomers and effective single 3D conformations using the LigPrep module in Maestro (version 9.4, Schrödinger).

The 3D structures of the proteins were downloaded from RCSB PDB. In addition, homology modeling was conducted for protein structures that were not found in the database. The

3D structure of c-kit was downloaded from the RCSB PDB (PDB ID: 6GQK),²¹ and those of 5-HT₄ and AQP3 were obtained by homology modeling.

The Glide module in Schrödinger v2015.09 was used for molecular docking modeling and to predict the binding affinity of ligands for target proteins. The structures of the proteins were manipulated using the "Protein Preparation Wizard" workflow in Maestro. The main operations were exclusion of water molecules, protonation, and optimization via OPLS_2005 force field. The Glide module was used to generate a grid file for each protein receptor, to determine the location of the active site of the protein, in order to model the binding of ligands and proteins. The grid enclosed a box centered on the binding site with dimensions of 10 × 10 × 10 Å. A scaling factor of 0.8 was used for the van der Waals radii of receptor atoms with a partial atomic charge of <0.15.

An extra-precise Glide docking procedure (Glide-XP) was employed to model the docking of the compounds to the binding sites of the proteins and the optimal orientation of the compound, determined using the Glide scoring function (G-score), was recorded. The more negative the G-score is, the stronger is the expected binding affinity of the compound and receptor. Molecular graphics were generated using PyMOL (<https://www.pymol.org/>).

Western blotting

Protein lysates of colonic tissue were prepared using RIPA Lysis Buffer (Solarbio, Beijing, China) containing protease inhibitors. The protein content of each was quantified using the bicinchoninic acid method (Beyotime, Shanghai, China), then the samples were separated by sodium dodecyl sulfate-polyacrylamide gel electrophoresis on 10% polyacrylamide gels, and transferred to polyvinylidene fluoride membranes (Millipore, Billerica, MA). The membranes were then blocked with 5% skimmed milk powder (BioRuler, Danbury, CT) in tris-buffered saline

for 2 h, and incubated overnight with primary antibodies targeting c-kit (sc-365504, 1:100; Santa Cruz, San Francisco, CA), 5-HT₄ (TA323344, 1:200; Origene, Rockville, MD), AQP3 (ab125219, 1:1000; Abcam, Cambridge, UK), or glyceraldehyde 3-phosphate dehydrogenase (GAPDH; 1:2000; Proteintech, Chicago, IL) at 4 °C. The membranes were then incubated with a secondary antibody, after three washes. Specific protein bands were detected using Enhanced chemiluminescence solution (Proteintech) and imaged using a ChemiDoc MP Imaging System (Bio-Rad, Hercules, CA).

Statistical analysis

Data are shown as means (SEMs). Student's *t*-test was used to compare data between the two groups. *P* < .05 was accepted as indicating statistical significance. Data analysis was performed using GraphPad Prism 8.0 software (www.graphpad.com).

Results

Laxative effect of rhubarb extract in constipated rats

To confirm the laxative effect of rhubarb, we administered rhubarb extract to Sprague-Dawley rats in which constipation had been induced by loperamide gavage for 7 days. Loperamide is commonly used to increase mucosal contact time, which has the effect of inducing additional absorption of electrolytes and water, thereby reducing fecal mass and the number of bowel movements. Twenty-four-hour fecal water content was monitored for the first 6 days of loperamide administration, and a reduction was identified in the model group from the second day (Fig. 1A), which confirmed that constipation had been successfully induced. Then, rhubarb

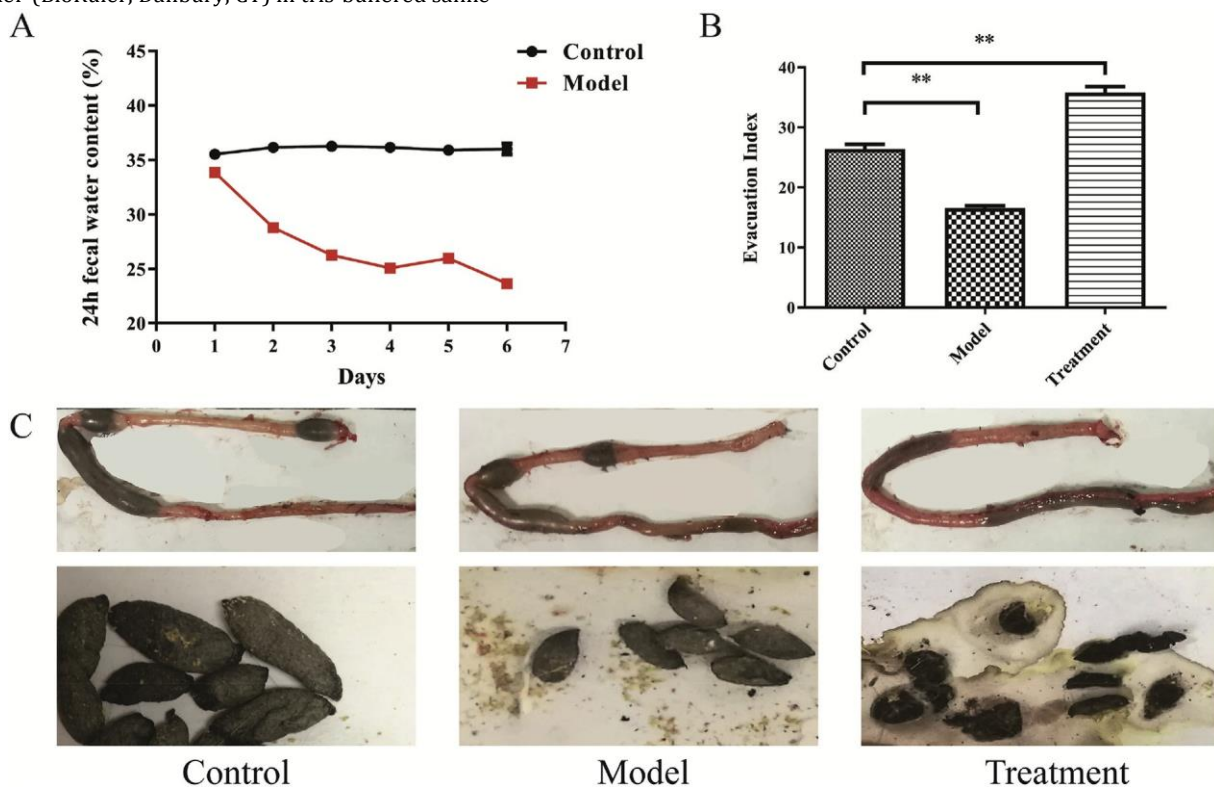


Fig. 1. Laxative effect of rhubarb extract in constipated rats (A) The 24-h fecal water content of the control and model groups (B) The evacuation indices of the three groups (C)

The contents of the colorectum and the shape of the feces.

Note: Data are presented as the mean (SEM), $n = 10$, $**P < .01$ vs. the control group. Extract was administered to the treatment group for 3 days. A significant increase in EI occurred in this group (Fig. 1B), which confirmed that rhubarb extract has a laxative effect in constipated rats. We then compared the water content of the colorectal contents of the control, model, and treatment groups (Fig. 1C) and found that the rhubarb extract increased this. These results imply that rhubarb may have its laxative effect by increasing the retention of water in the colorectum.

Identification of rhubarb derivatives in rat feces

We used HPLC-LTQ-Orbitrap MS to identify the derivatives of rhubarb in the colorectum that might contribute to its laxative effect. Using the established strategy of characteristic fragment filtration for the detection of rhubarb derivatives,^{19,22} a series of anthraquinones and anthrones were identified. The identification process can be illustrated using the example of the metabolite emodin-*O*-glucuronide (Fig. 2). The full ion chromatogram of a fecal sample is shown in Fig. 2A and the extract ion chromatogram for emodin-*O*-glucuronide is shown in Fig. 2B. In negative mode, the diagnostic ion fragments of m/z 269.0451 and 225.0552 were detected, which suggested that the skeleton of the target compound was the same as that of emodin (Fig. 2C). In addition, the detection of a quasi-molecular ion of m/z 445.0765 [M-H], which differs from the expected m/z 269.0451 for emodin by 176.0814 Da, implied that the compound was emodin-*O*-glucuronide (Fig. 2D). Overall, 38 derivatives of known rhubarb components, including 17 anthraquinones and 21 anthrones, were identified in colorectal samples, including prototypes and various metabolites (Fig. 3), and the compound identification data are presented in Supplemental

Tables 2–4.

Construction of a target protein database

To determine the mechanism of the laxative effect of rhubarb, the molecular targets of clinically-approved laxatives were identified using the TTD, Drug Bank Database, and published literature. As shown in Supplemental Table 5, there are 17 types of molecular target for laxatives. All of these, which include channel proteins and receptors, have been identified to mediate effective treatments for constipation. For instance, magnesium sulfate, which is classified as an osmotic laxative, increases AQP3 expression in the epithelial cells, which has the effect of retaining water in the intestinal lumen and promoting defecation.²³ In addition, linaclotide is a secretagogue that activates the guanylate cyclase-C receptor on intestinal epithelial cells to increase fluid secretion into the intestinal lumen.^{24,25} Some previous studies have shown that the number of interstitial cells of Cajal (ICCs) is lower in the colons of patients with slow-transport constipation,^{26,27} and c-kit is a specific marker of ICCs, which have been shown to be intestinal pacemaker cells.²⁸ Finally, prucalopride, a highly selective 5-HT₄ receptor agonist, directly activates afferent neurons and improves intestinal motility.^{29,30} The creation of a molecular target database for laxatives provided a tool for us to identify potential targets and bioactive derivatives of rhubarb compounds for the treatment of constipation.

Candidate colorectal molecular targets and potentially bioactive compounds

To screen the candidate targets and bioactive rhubarb derivatives, molecular docking modeling was performed using 38 rhubarb derivatives from the colorectum and 17 endogenous

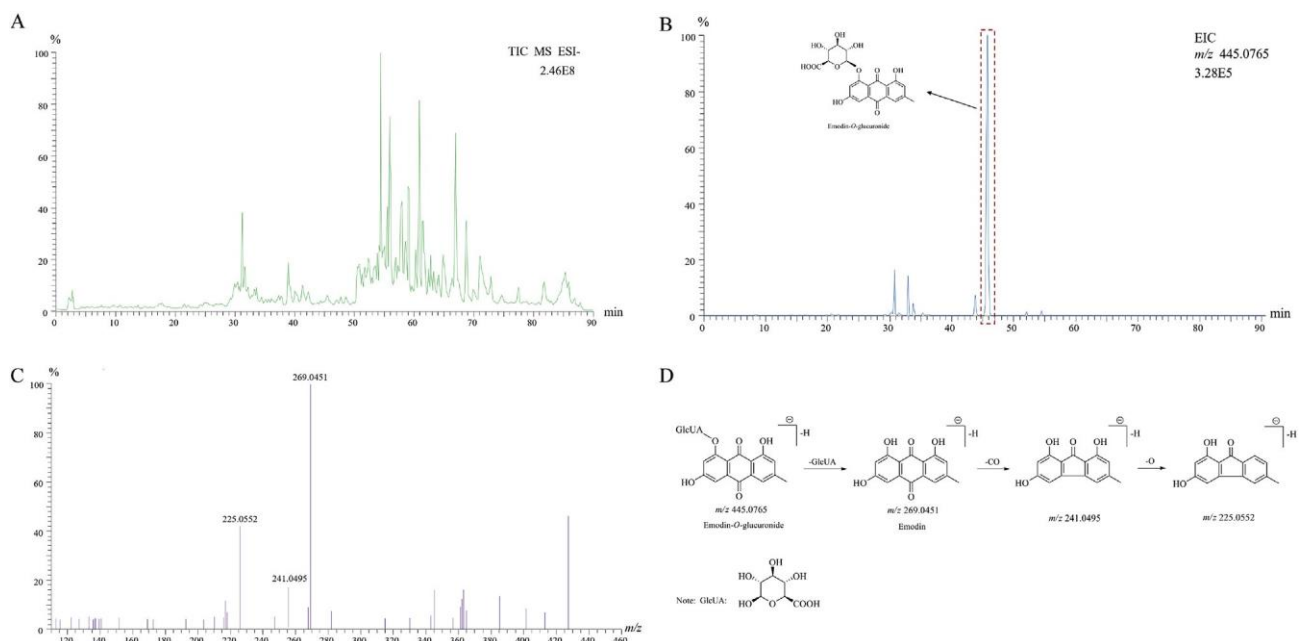


Fig. 2. The identification process for emodin-*O*-glucuronide (A) The total ion chromatogram of a fecal sample (B) The extract ion chromatogram (C) Mass spectrometry (MS)/MS spectrum (D) The identification of an ion with m/z 445.0765 in the fecal sample.

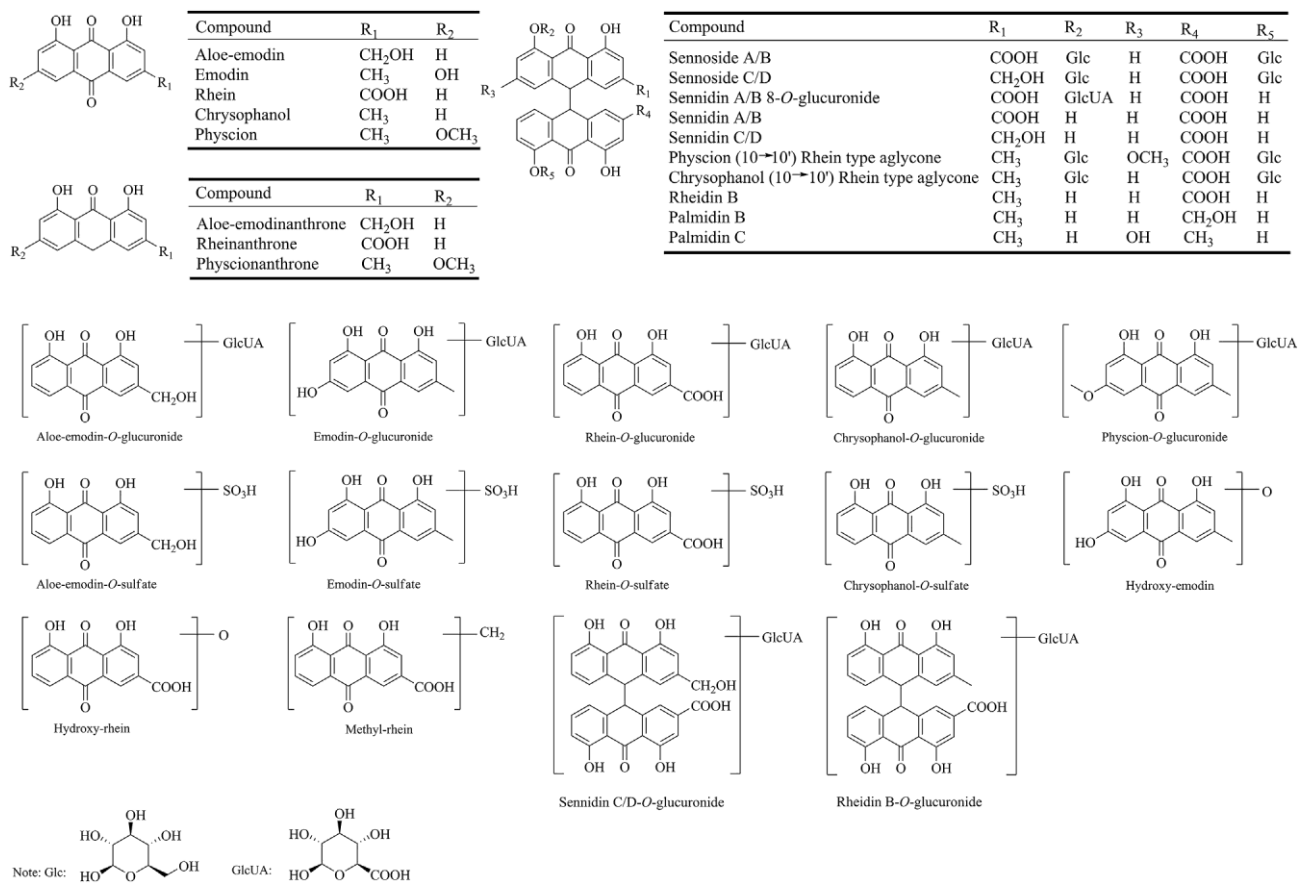
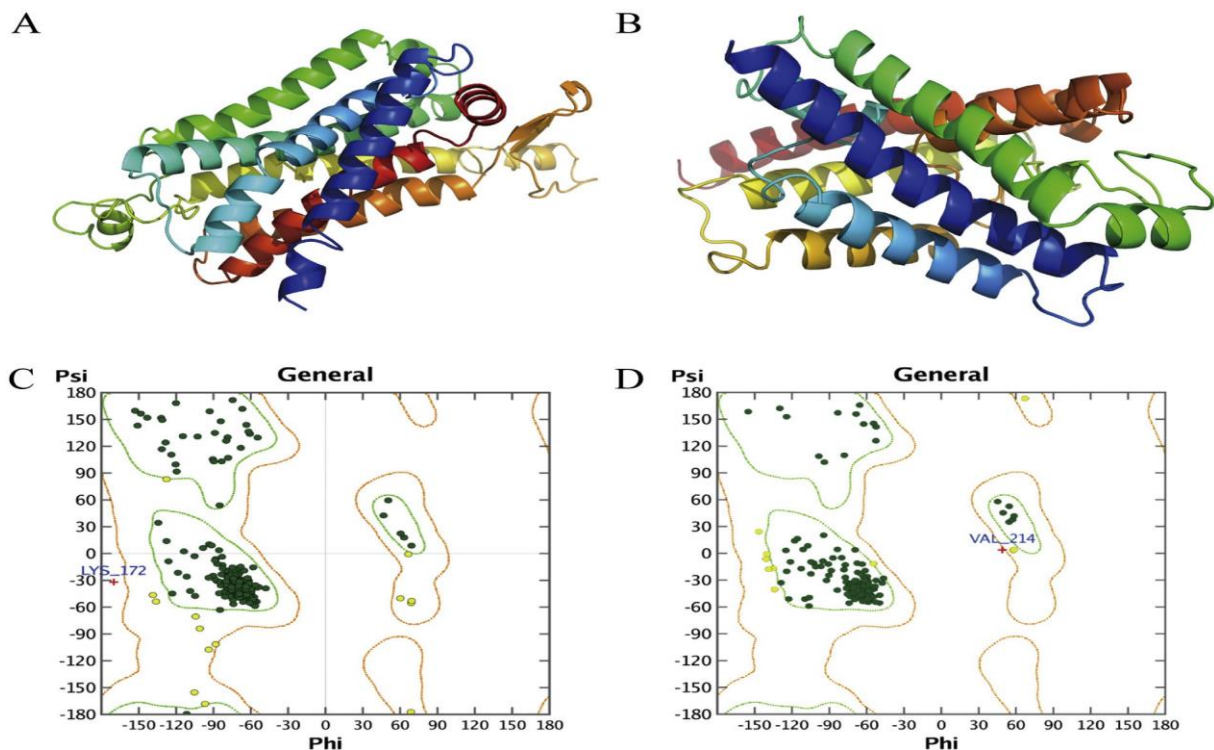


Fig. 3. Structures of the 38 rhabarb derivatives identified in fecal amples.

molecules that mediate laxative effects. First, homology modeling was conducted to predict the structures of proteins that were not found in the database, such as 5-HT₄ and AQP3. The models generated for 5-HT



depicted in Fig. 4A and B,

4 and AQP3 are

Fig. 4. Structural modeling of molecules mediating laxative effects (A) Homology model of 5-HT4 (B) Homology model of AQP3 (C) Ramachandran plot for 5-HT4 and AQP3. Darkgreen dots represent the residues in favored regions, yellow dots represent the residues in permitted regions, and red crosses represent the residues in irrational regions. Abbreviations: 5-HT4: 5-hydroxytryptamine receptor 4; AQP3: aquaporin-3.

respectively. Ramachandran plots for 5-HT4 and AQP3 showed that more than 99% of their amino acid residues were in permitted regions, which indicates that the predicted 3D structures were reasonable (Fig. 4C and D). Then, on the basis that the more negative the G-score is, the stronger is the binding affinity between

Table 1
G-scores for the binding of the top-ranked rhubarb derivatives with their potential molecular targets.

No.	Ligand	Receptor (kcal/mol)		
		c-kit	5-HT4	AQP3
1	Aloe-emodin	-8.476	/	-5.289
2	Emodin	-9.378	-5.541	-5.743
3	Rhein	-8.453	-5.963	-5.270
4	Chrysophanol	-8.530	-6.221	-5.514
5	Physcion	-8.275	-5.241	-5.987
6	Sennoside A	-6.854	-8.891	/
7	Sennoside C	-9.019	-8.810	/
8	Physcionanthrone	-9.069	-5.246	-6.809
9	Aloe-emodinanthrone	-9.278	-5.163	-6.165
10	Rheinanthrone	-9.747	-5.914	-5.763

Abbreviations: 5-HT4: 5-hydroxytryptamine receptor 4; AQP3: aquaporin-3.

the compound and receptor, we selected candidate targets and rhubarb derivatives. The G-scores are listed in Table 1, and show that three molecules, c-kit, 5-HT4, and AQP3, represented candidate targets. Furthermore, 10 rhubarb derivatives (aloe-emodin, emodin, rhein, chrysophanol, physcion, sennoside A, sennoside C, physcionanthrone, aloe-emodinanthrone, and rheinanthrone), were found to have strong binding affinities for the three targets, and were therefore selected as potentially bioactive rhubarb derivatives.

To gain insight into the binding affinity of rhubarb derivatives for the binding sites of the three candidate molecular targets, the ligand-receptor interactions were analyzed *in silico*, and we found that all 10 of the derivatives are likely to bind strongly to c-kit. Multiple oxygen atoms in hydroxyl and carbonyl groups in the basic skeleton of the anthraquinones and anthrones were shown to be located in the binding site and to form hydrogen bonds with the Cys673, Lys623, Glu671, and Leu595 residues of c-kit. The compound with the strongest predicted binding affinity for c-kit was rheinanthrone (-9.747 kcal/mol). The predicted interaction is shown in Fig. 5A, which involves three hydrogen bonds and one H- π conjugation: the oxygen atoms at the 9- and 3-sites of the carbonyl group, and the oxygen atom at the 1-site of the hydroxyl

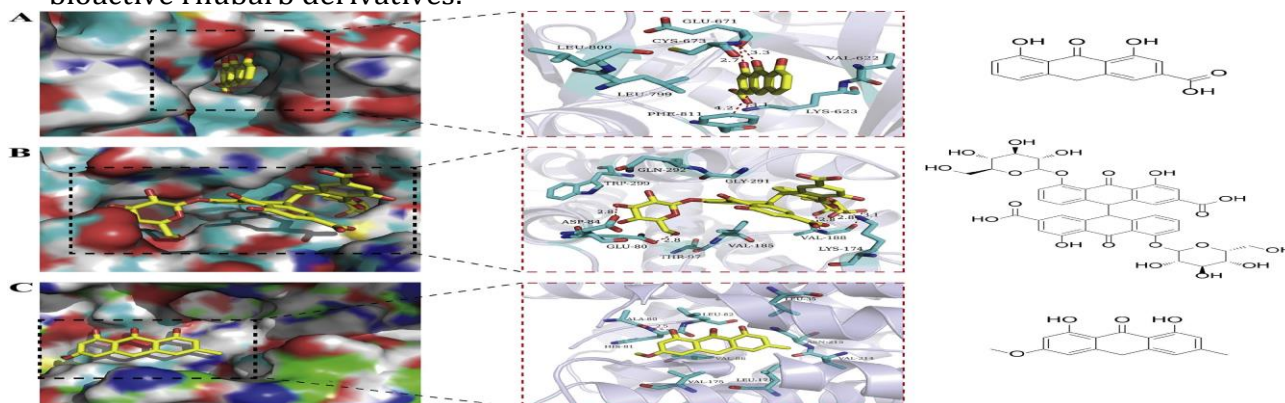


Fig. 5. Interaction models for the three candidate molecular mediators of the laxative effect of rhubarb. The interaction model for rheinanthrone and c-kit (A), sennoside A and 5-hydroxytryptamine receptor 4 (B), and physcionanthrone and aquaporin-3 (C). The ligands are yellow and the surrounding residues in the binding pockets are cyan. The backbone of the receptor is depicted as a light blue ribbon.

group in rheinanthrone formed hydrogen bonds with the Cys673, Lys623, and Glu671 residues of c-kit, respectively. In addition, the carbon atom at the 4-site in rheinanthrone formed an H-p conjugation with the Phe811 residue of c-kit.

Sennoside A and sennoside C were shown to have the strongest binding affinities with 5-HT4 of the bioactive derivatives. They were predicted to bind via hydrogen bonds to the Asp84, Val188, Lys174, Glu80, and Asn279 residues of 5-HT4. The strongest predicted binding affinity for 5-HT4 — was that of sennoside A (8.891 kcal/mol). The five hydrogen bonds are shown in Fig. 5B: the oxygen atom at the 8-site of the hydroxyl group in the glucose group of sennoside A formed a hydrogen bond with the Glu80 and Asp84 residues of 5-HT4, separately. In addition, two oxygen atoms of at the 8⁰ site of the hydroxyl group in the glucose group connected with the backbone and side-chain of Val188, and the oxygen atom at the 9⁰ site of the carbonyl group of sennoside A interacted with the Lys174 residue of 5-HT4.

However, in contrast to the situation with c-kit and 5-HT4, in which the bioactive compounds interacted with amino acid residues via numerous hydrogen bonds, AQP3 was predicted to have few, weak interactions with the rhubarb derivatives.

The strongest binding affinity with AQP3 was shown by physcionanthrone (6.809 kcal/mol): the oxygen atom at the 1-site of the hydroxyl group in physcionanthrone formed a hydrogen bond with the Ala80 residue of AQP3 (Fig. 5C). Taken together, the results of the molecular docking modeling showed that various oxygen atoms of basic skeletons and glucose groups of the 10 bioactive compounds derived from rhubarb can form hydrogen bonds with the three molecules that mediate laxative effects.

Effects of rhubarb extract on the expression of c-kit, AQP3, and 5-HT4 in the colons of rats

In order to increase the biological relevance of the molecular docking data, the effects of rhubarb extract on c-kit, 5-HT4, and AQP3 expression were evaluated by western blot analysis. Colonic lysates prepared from rats in the control, model, and treatment groups were prepared and immunoblotted for each of the proteins. As shown in Fig. 6, the expression of c-kit and 5-HT4 was much lower, and that of AQP3 was higher in model rats than in the control group. When constipated rats were treated with rhubarb extract, these changes in expression were all reversed. The increase in c-kit expression in the colon would tend to maintain the phenotype of ICCs, thereby promoting intestinal motility.^{31,32} In addition, the

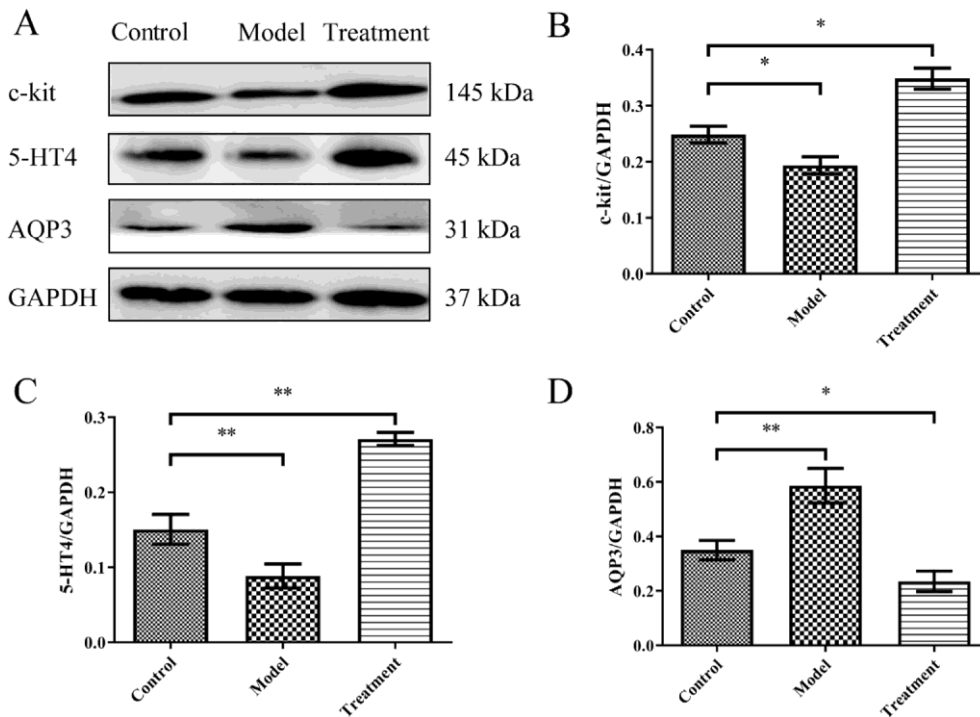


Fig. 6. The effects of rhubarb extract on the expression of c-kit, 5-HT4, and AQP3 in the colons of rats (A) c-kit, 5-HT4, and AQP3 protein expression in the colon, measured using western blotting (B&D): c-kit, 5-HT4, and AQP3 protein expression, normalized to that of GAPDH, respectively.

Note: 5-HT4: 5-hydroxytryptamine receptor 4; AQP3: aquaporin-3; GAPDH: glyceraldehyde 3-phosphate dehydrogenase. Data are expressed as mean (SEM). n = 3. *P < .05,

**P < .01 vs. the control group.

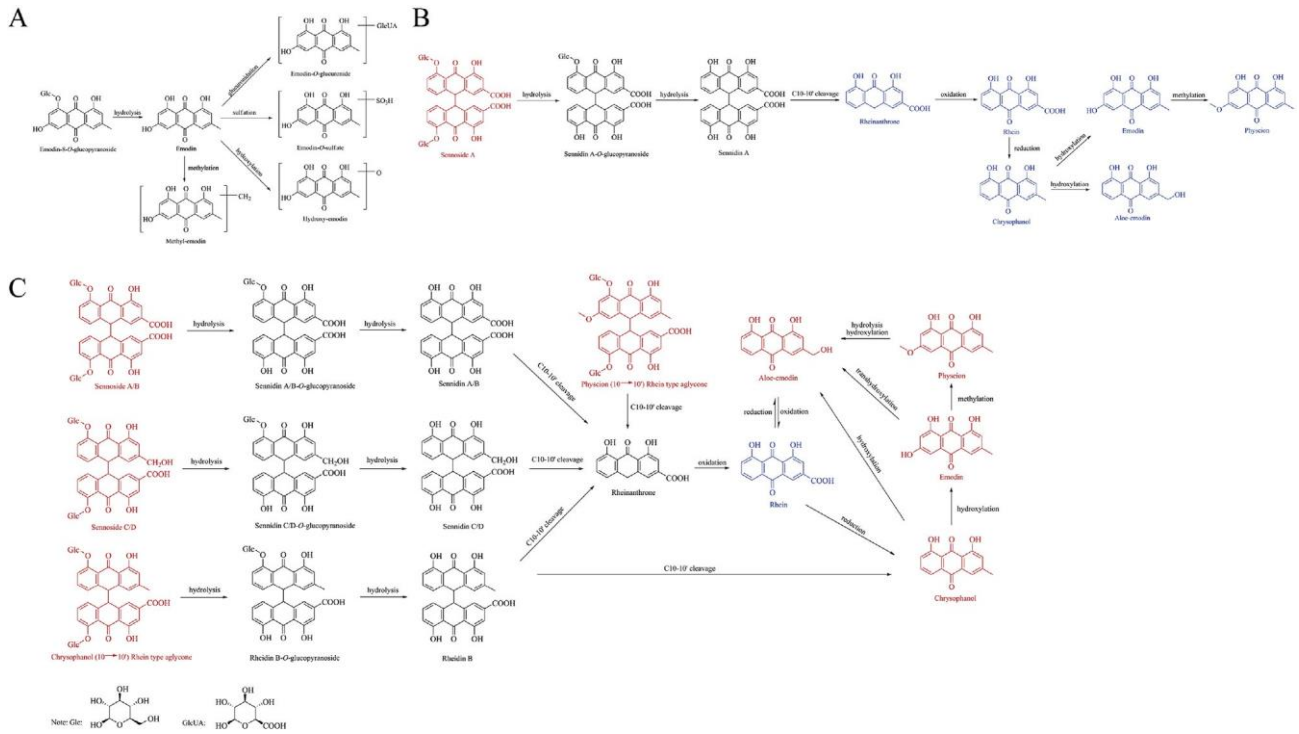


Fig. 7. Potential metabolic pathways for the anthraquinones and anthrones (AeC) Biotransformation of emodin, sennoside A, and rhein as a product of the metabolism of various prototype compounds. The prototype components are shown in red and the active metabolites are shown in blue.

increase in 5-HT4 expression in the colon would be expected to increase intestinal transport.^{11,33,34} Finally, and as expected, lower expression of AQP3 was shown in the colon of treated rats, which would be expected to inhibit water absorption, which would also have a laxative effect.³⁵⁻³⁷ Thus, rhubarb extract regulates the expression of the identified potential mediators of a laxative effect.

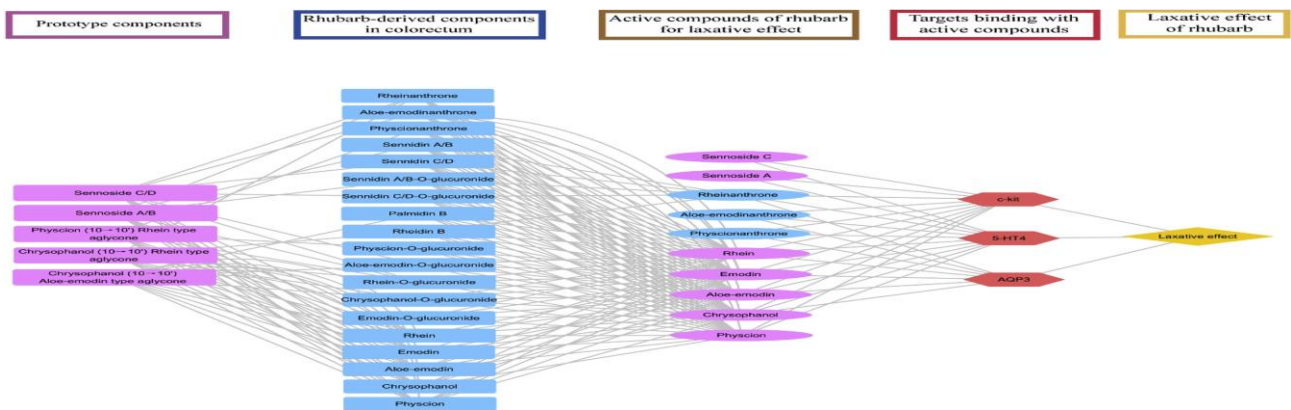


Fig. 8. Network describing the prototype components of rhubarb, their colonic derivatives, and the endogenous molecular targets potentially mediating a laxative effect. The prototype components are shown in pink and the rhubarb-derived components present in the colorectum are shown in blue.

Tracing of the candidate bioactive derivatives back to the components of rhubarb

To trace the biotransformation products to its prototype, we explored the *in vivo* metabolic transformation of the compounds in rhubarb. We studied the metabolism of 10 representative compounds, including both anthraquinones (emodin, rhein, physcion, aloe-emodin, chrysophanol, emodin-8-*O*- β -D-glucopyranoside, aloe-emodin-8-*O*- β -D-glucopyranoside) and anthrones (sennoside A, sennoside B, and sennoside C). As shown in Fig. 7A, anthraquinone-type components are metabolized to glycosides *in vivo*, and the principal metabolic pathways involved are hydroxylation, methylation, glucuronidation, and sulfonation. For anthrone-type compounds (Fig. 7B), the glucose group is typically lost as a result of hydrolysis. In addition, it was predicted that anthrone-type compounds would principally undergo C10eC10' bond cleavage *in vivo* and be further metabolized to anthraquinone-type metabolites. Overall, similar metabolic patterns were predicted for the 10 representative compounds. We found that a prototype component, for instance sennoside A (Fig. 7B), may be metabolized to form several active metabolites (rheinanthrone, emodin, chrysophanol, aloe-emodin, rhein, and physcion), and a single bioactive molecule, such as rhein (Fig. 7C), can also be generated from various prototype compounds (sennoside A, sennoside B, sennoside C, physcion [10 \nearrow 10⁰] rhein type aglycone, chrysophanol [10 \nearrow 10⁰] rhein type aglycone, aloe-emodin, emodin, physcion, and chrysophanol).

Finally, using this information regarding the likely metabolic

pathways involved, the active compounds identified in colorectal contents were traced back to the prototype components of rhubarb. As shown in Fig. 8, anthraquinone derivatives, anthrone derivatives, and their glucosides in rhubarb can all be metabolized to generate the 10 potentially bioactive compounds identified, which have the potential to provide three complementary molecular mechanisms for the laxative effect.

Discussion

In the present study, we have used an MS-based approach and molecular modeling to determine the mechanisms involved in the laxative effect of rhubarb. We have shown that anthraquinone and anthrone derivatives in rhubarb can be metabolized in the rat intestine to generate various bioactive compounds, which are all capable of regulating molecular targets in the colon that mediate the laxative effects of known drug substances (Fig. 9). Thus, derivatives of rhubarb may have additive or synergistic effects to promote defecation.

This strategy represents a valid approach to ensure quality control and to provide a reference for the rational medicinal use of rhubarb in the clinic. Because of the complexity of potential medicinal compound-target interactions, the identification of interaction domains is still in its infancy. However, high-affinity ligand-receptor interactions can be validated using surface plasmon resonance studies,^{38,39} and this method may be used to

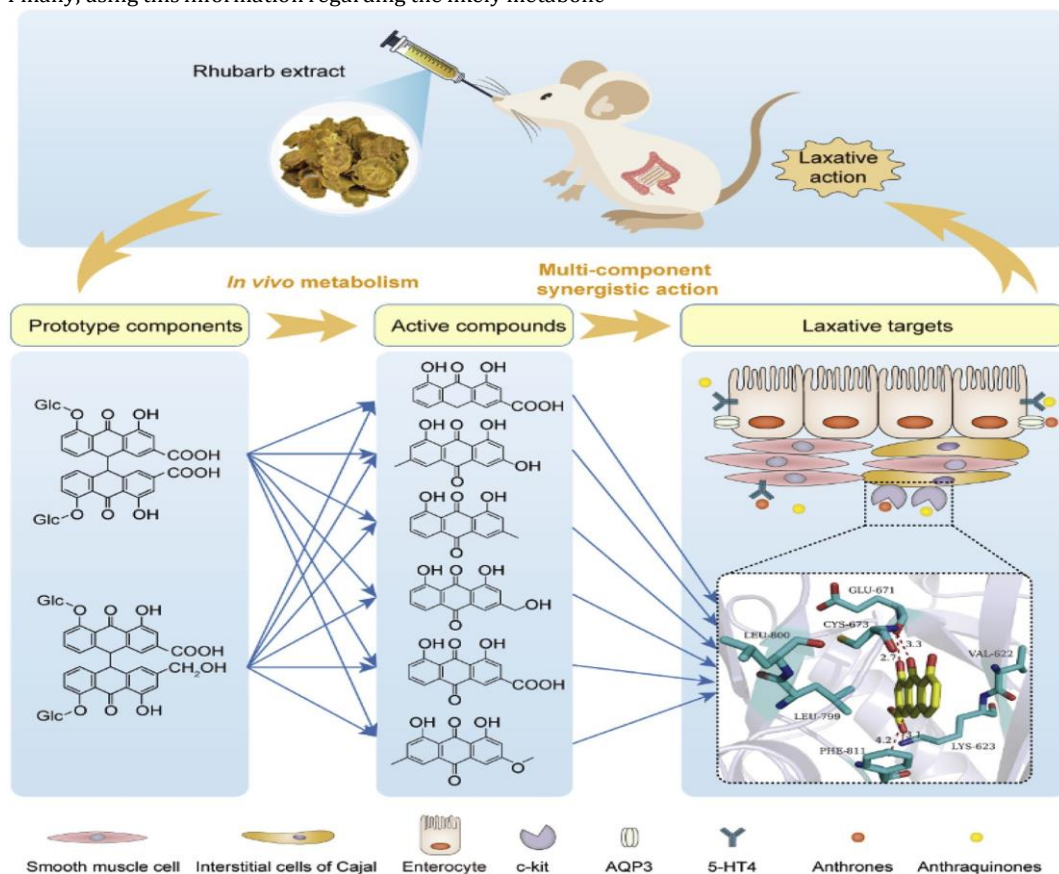


Fig. 9. Summary of the study findings.

Abbreviations: 5-HT4: 5-hydroxytryptamine receptor 4; AQP3: aquaporin-3.

further characterize the molecular mechanisms involved in the laxative effect of rhubarb and to identify lead compounds for further investigation.

Most herbal medicines contain numerous components that may be bioactive or metabolized to form bioactive derivatives, such as flavonoids, alkaloids, and organic acids. Rhubarb is a common Chinese medicine that also contains several components of this type, including anthraquinone derivatives, anthrone derivatives, glucosides, tannins, and organic acids. In the present study, rhubarb was used as an example to illustrate an approach to the determination of the mechanisms of a medicinal effect of a plant product. In it, we identified bioactive compounds, determined their origin in the plant, and identified potential binding partners that are known mediators of the medicinal effect. This strategy can provide insights into the mechanisms whereby multiple components of herbal medicines may have additive or synergistic effects, exerted via multiple molecular targets, to achieve a therapeutic endpoint.

Conclusion

By binding to c-kit, 5-HT₄, and/or AQP3, the current research showed that bioactive chemicals with a laxative action might be generated by metabolism of anthraquinones and anthrones in rhubarb. It was indicated using molecular docking modelling that five anthraquinones (aloe-emodin, emodin, rhein, chrysophanol, and physcion) and five anthrones (sennoside A, sennoside C, physcionanthrone, aloe-emodinanthrone, and rheinanthrone) interact with c-kit, 5-HT₄, and AQP3. Importantly, we have shown that rhubarb extract, which is believed to mediate the laxative action of the plant, raised the expression of c-kit and 5-HT₄, while reducing that of AQP3 in the rat colon. Additionally, we discovered that a single proto-type component in rhubarb, like sennoside A, can be metabolised into multiple active metabolites (rheinanthrone, emodin, chrysophanol, aloe-emodin, rhein, and physcion), as well as one active ingredient,

compounds including physcion, emodin, chrysophanol, aloe-emodin, sennoside C, and sennoside A are potentially potential building blocks for compounds like rhein. Our results suggest that rhubarb's laxative action could be due to the interaction of several derivative chemicals with various molecular targets in the colon, which might lead to cumulative or synergistic effects.

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