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Basic Study

Protective effect and mechanisms of action of Mongolian medicine Sulongga-4 on pyloric ligation-induced gastroduodenal ulcer in rats

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Abstract

BACKGROUND

Sulongga-4 (SL-4) is a herbal formula used in traditional Mongolian medical clinics for the treatment of peptic ulcers and gastroenteritis, even though its pharmacological mechanism has not been well characterized.

AIM

To evaluate the protective effect and identify the mechanisms of action of SL-4 on gastroduodenal ulcer induced by pyloric ligation (PL) in rats.

METHODS

PL was performed to induce gastric and duodenal ulcers in rats, which were then treated with oral SL-4 (1.3, 2.6, or 3.9 g/kg per day) for 15 d. PL-induced gastroduodenal ulceration. Therapeutic effects were characterized by pathological and histological evaluations and inflammatory indicators were analyzed by enzyme-linked immunosorbent assay. Microarray analyses were conducted to identify gene expression profiles of gastroduodenal tissue in PL rats with or without SL-4 treatment. The candidate target genes were selected and verified by quantitative reverse transcription polymerase chain reaction (qRT-PCR).

RESULTS

SL-4 decreased histopathological features in the PL-induced ulcerated rats. SL-4
Peptic ulcer disease is the most prevalent chronic disease of the digestive system, with complications resulting in high morbidity and mortality\(^1\). Many factors can lead to the formation of peptic ulcers, and one of the basic mechanisms is impairment of gastric mucosal barrier function by acidic gastric secretion\(^1\). Inflammation or injury of the digestive system cause visceral hypersensitivity that can drive the development of chronic pain and patient discomfort\(^2\), while inflammation is a key driver of gastric ulcer formation\(^3\). For protection against inflammation, cells respond with attenuated production of proinflammatory cytokines such as interleukin (IL)-1β, IL-6, endotoxin, platelet-activating factor, and increased prostaglandin E2 and epidermal growth factor in ulcer tissue. Microarray analysis was used to identify a panel of candidate target genes for SL-4 acting on PL-induced ulceration. Genes included some complement and coagulation cascade and retinol metabolism pathways that are closely associated with inflammatory responses and gastric mucosal protective mechanisms. qRT-PCR showed that altered expression of the selected genes, such as CYP2b2, UGT2b1, A2m, and MASPI was consistent with the microarray results.

**CONCLUSION**

SL-4 exerts protective effects against PL-induced gastroduodenal ulcers via reducing inflammatory cytokines and elevating expression of gastric acid inhibitory factors. Downregulation of CYP2b2 and UGT2b1 genes in retinol metabolism and upregulation of A2m and MASPI genes in the complement and coagulation cascades pathways are possibly involved in SL-4-mediated protection against gastroduodenal ulcer.

**Key Words:** Sulongga-4; Peptic ulcer; Pyloric ligation; Microarray analysis; Inflammatory reaction; Retinol metabolism

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**INTRODUCTION**

Peptic ulcer disease is the most prevalent chronic disease of the digestive system, with multifunctional effects reported such as immunostimulatory, anti-inflammatory, antiviral, anticancer, and radioprotective effects\(^9\). Plant or herbal extracts are also recognized as a source of therapeutics for gastric ulcers\(^9\). Traditional Mongolian
Materiales y métodos

**Etica del estudio**

Los ratones machos Sprague-Dawley (200 ± 20 g, 6 semanas de edad, SPF grado, lote no. SCXK 2015-0001) se adquirieron de Liaoning Chang-Sheng Biotechnology Co. Los procedimientos experimentales fueron aprobados por el Comité de Ética de Animal Experiments of Inner Mongolia University for Nationalities (approval no. NM-LL-2016-12-15-01), de acuerdo con los requisitos y lineamientos generales de la Administración de los Animales Experimentales de China. Todas las cirugías se realizaron bajo anestesia con pentobarbital sodico, y se hizo todo el esfuerzo por minimizar el sufrimiento.

**Tratamiento animal**

Se dividieron de forma aleatoria en cinco grupos (n = 12) que fueron tratados con una operación simuladora, cirugía de ligadura (PL) y 1.3, 2.6, o 3.9 g/kg de SL-4. Los ratones en los grupos operación simuladora y PL fueron tratados con 0.5% carboximetilcelulosa sódica (CMC-Na, Sigma). Los ratones en los tres grupos de SL-4 fueron tratados con 1.3, 2.6, o 3.9 g/kg de SL-4 en 0.5% CMC-Na suspendido por lavado gástrico una vez al día. Los ratones en todos los grupos fueron tratados durante 15 días consecutivos.

**Modelo de úlcera inducido por PL**

Una hora después de la última administración de medicamento, todos los ratones fueron privados de combustible y agua durante 24 h para evitar la penetración de la comida y el agua en la ulceración. Cada ratón fue anestesiado por inyección intraperitoneal de pentobarbital para inducir la ulceración gástrica PL como se describió previamente. El abdomen se abrió y la válvula se ligó, evitando dañar las arterias adyacentes. El estómago se reemplazó suavemente y se suturó. Después de ser privados de comida y agua durante 18 h, los animales fueron sacrificados y la estómago y duodeno fueron desgajados para el análisis subsecuente.

**Examen patológico y histológico**

Los ratones fueron anestesiados intraperitonealmente con pentobarbital y sacrificados. Las secciones gástricas y duodenales se conservaron para examen patológico. Para el examen histológico, la sección gástrica y duodenal se fijó con formaldehído al 4% durante 48 h; decalcificado en una solución acuosa de EDTA 10% (Sigma-Aldrich, St. Louis, MO, United States) a temperatura ambiente y agitación constante, procesado y embebido en parafina. Las secciones se cortaron en 4 μm serial y se dejaron en xileno a 37 °C por 15 min; rehidratadas a través de concentraciones decrecientes de etanol, y lavadas en agua destilada a temperatura de 5 min. Las secciones fueron teñidas con hematoxilina y eosina (H&E, Nanjing Jiancheng Bioengineering Institute, Nanjing, China).
Measurement of tissue cytokine expression
Gastroduodenal tissues were homogenized in Tris buffer on ice and centrifuged at 12000 g at 4 °C for 10 min. The supernatants were used to determine the activities of endotoxin (ET), IL-6, and platelet-activating factor (PAF) in the duodenal tissue and TNF-α, prostaglandin E2 (PGE2), epidermal growth factor (EGF) and IL-1β in the gastric tissue. Enzyme activity was determined with commercial assay kits (Nanjing Jiancheng Bioengineering Institute).

Total RNA extraction
Total RNA was extracted for microarray and qRT-PCR assay from gastric and duodenal tissue with TRIzol reagent (Invitrogen, Gaithersburg, MD, United States) and purified with mirVana miRNA Isolation Kits (Ambion, Austin, TX, United States). RNA was quantified with a Qubit fluorometer (Thermo Fisher Scientific, United States), and RNA integrity was assessed with a Bioanalyzer 2100 (Agilent, CA, United States). Only RNA extracts with an RNA integrity of > 6 were used in subsequent analyses.

Microarray analysis
Microarray hybridization, scanning, and analysis were performed by the Capital Biotechnology Corporation (Beijing, China). Using 100 ng total RNA, double-stranded cDNA containing the T7 RNA polymerase promoter sequence was prepared with CbcScript reverse transcriptase using a cDNA synthesis system (Capitalbio, Beijing, China) with the T7 Oligo(dT). cDNA labeled with a fluorescent dye (Cy5 or Cy3-dCTP) was produced by Eberwine’s linear RNA amplification method and subsequent enzymatic reactions. The procedure was improved by using CapitalBio cRNA Amplification and Labeling Kits to produce higher yields of labeled cDNA. The microarray slides were read with an Agilent G2565CA Microarray Scanner to obtain the microarray hybridization images. The array data were analyzed for data summation, normalization, and quality control with GeneSpring V13 (Agilent).

Differentially expressed genes and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis
Chip signal intensities ≥ 400 were included for comparison. A two-class unpaired algorithm in the CapitalBio expression microarray analyzer software (CBC analyzer) was applied to identify differentially expressed genes in the sham operation and PL groups, and the PL and SL-4 groups in both gastric and duodenal tissues. Differentially expressed genes with fold-change ≥ 2.0 or ≤ 2 and P values ≤ 0.05 were evaluated. KEGG pathways were analyzed with a CaptitalBio Molecule Annotation System integrated with the KEGG database as previously described.

qRT-PCR validation
To validate the microarray results, qRT-PCR was used to validate the expression of the selected genes in the SL-4 (3.9 g/kg), PL and sham groups. The RNA samples used for qRT-PCR were the same samples from individual rats that made up the pools. One microgram of total RNA and an oligo(dT) primer were used for cDNA synthesis following the manufacturer’s protocol for SuperScript III reverse transcriptase (Invitrogen, Carlsbad, CA, United States). Primers for the four genes chosen for verification were designed based on sequences published in GeneBank (Table 1). The validated genes were CYP2b2, UGT2b1, MASP1, and A2m. qRT-PCR was performed with an ABI PRISM 7900 sequence detection system (PE Applied Biosystems, Foster City, CA, United States) under the following conditions: 50 °C for 10 min, 40 cycles of 95 °C for 1 min, and 60 °C for 1 min. The program was ended with a melting curve from 72 °C to 95 °C and cooling to 40 °C. The GAPDH gene was used as a housekeeping control. Relative gene expression (ΔΔct) was calculated and graphed as a fold-change.

Statistical analysis
Pharmacological data were analyzed using SPSS 17.0 and reported as means ± SD. Intergroup comparisons was conducted with t-tests, and P < 0.05 was taken to indicate a significant difference. Regarding the microarray, a CBC analyzer (expression profile analysis procedures based on R Bioconductor and PERL) was used for the analysis. To select the DEGs, the threshold values were ≥ 2 and ≤ 2 fold-change and a t-test P value of 0.05. The data were Log, transformed and median centered by genes using the adjust data function of CLUSTER 3.0 software and further analyzed by hierarchical
Table 1 Primers used for quantitative reverse transcription polymerase chain reaction analysis of gene expression in gastric and duodenal tissue

<table>
<thead>
<tr>
<th>Gene</th>
<th>Accession No.</th>
<th>Forward primer</th>
<th>Reverse primer</th>
</tr>
</thead>
<tbody>
<tr>
<td>MASP1</td>
<td>NM_022257.1</td>
<td>CAACTACATCGCCGGCTACTACTG</td>
<td>GCTGGTGATTGTGCCTGTCCTC</td>
</tr>
<tr>
<td>A2m</td>
<td>NM_012488.2</td>
<td>TCACTCAAGTCCTGCTCTTCCTC</td>
<td>CCAGAACATATACGGCTGT</td>
</tr>
<tr>
<td>CYP2b2</td>
<td>NM_001198676.1</td>
<td>GGAAGAACGGATTCAGGAGGAAGG</td>
<td>CTGTGATGCACTGGAAGAGGAAGG</td>
</tr>
<tr>
<td>UGT2b1</td>
<td>NM_173295.1</td>
<td>ATGTCAATTCTCGCAGATGCTGTGG</td>
<td>ATAGGAAGGAGCCAGTGAAGTCC</td>
</tr>
</tbody>
</table>

Results

SL-4 decreased histopathological features in ulcerated rats
In the PL group, rats showed severe injury and inflammation of the gastroduodenal epithelium and edema of the submucosa. SL-4 improved these alterations dose-dependently, and showed less mucosal damage and milder inflammation than the PL group (Figure 1). H&E staining confirmed the pathological alterations of gastroduodenal tissues. The SL-4-treated groups showed a recovery trend toward normal histology and only superficial lesions. More precisely, the mucosal structure and the epithelium were intact, with normal glandular size, morphology, and distribution in the SL-4 3.9 g/kg group compared with PL untreated rats, which was essentially the same as the control sham group.

SL-4 modulated cytokine expression in the damaged gastroduodenal tissue
The levels of enzymes present in tissue homogenates were determined by enzyme-linked immunosorbent assays. SL-4 pretreatment significantly ameliorated elevation of the inflammatory factors TNF-α and IL-1β in rat gastric tissue and increased the expression of prostaglandin E_2 (PGE2) and EGF hormones that inhibit gastric acid secretion compared with the PL group (Figure 2). In comparison, SL-4 treatment attenuated the expression of IL-6, ET and PAF in ulcerated duodenal tissue compared with the PL group in (Figure 3).

SL-4 altered gene expression in rats with PL-induced gastroduodenal ulcers
DEGs were identified in the ulcerated gastroduodenal tissues by an mRNA fold-change between two experimental groups of ≥ 2 and a P value ≤ 0.05. Volcano plot analysis showed that 1415 genes (731 upregulated and 784 downregulated) and 1460 genes (792 upregulated and 668 downregulated) were differentially expressed in gastric tissue from sham and PL, and PL and SL-4 groups (Figure 4A and B), and 2610 (1344 upregulated and 1266 downregulated) and 209 (100 upregulated and 109 downregulated) DEGs were identified in sham vs PL and PL vs SL-4 in the duodenal tissue (Figure 4C and D).

KEGG pathways analysis
To define the biological pathways associated with PL and SL-4 treatment in rat gastroduodenal ulceration, we analyzed the microarray data using R software, which was based on the KEGG database. The top ten DEG-enriched pathways in the sham vs PL and PL vs SL-4 groups in gastric and duodenal tissue are summarized in Tables 2 and 3. In gastric tissue, four pathways were engaged in the crosstalk of sham vs PL and PL vs SL-4, including Staphylococcus aureus infection, retinol metabolism, cytokine-cytokine receptor interaction, and the hematopoietic cell lineage pathway. In duodenal tissue, among the top 10 KEGG pathways in the sham vs PL and PL vs SL-4, two were the same in both groups, which were the complement and coagulation cascade pathways and S. aureus infection pathway.

According to the rat phenotype, retinol metabolism in the gastric tissue and complement and coagulation cascade pathways in the duodenal tissue were both closely associated with inflammatory responses and gastric mucosal protection mechanisms. Twelve genes were found to have > 2-fold expression and P values ≤ 0.05 in the two pathways. Gene expression pattern variations had the same trends in the PL and SL-4 groups. More precisely, when gene expression associated with retinol.
metabolism was upregulated in the PL group, SL-4 downregulated the same genes relative to the PL group. In contrast, the pathways for certain genes in the complement and coagulation cascade were downregulated in the PL group and upregulated in the SL-4 group (Table 4).

**qRT-PCR validation**

The SL-4-mediated increase or decrease in CYP2b2 and UGT2b1 in the retinol metabolism pathway, and A2m and MASP1 in the complement and coagulation cascades pathway were verified by qRT-PCR. Changes in the expression patterns of the four selected genes were consistent with the microarray results (Figure 5). Expression of CYP2b2 and UGT2b1 mRNA were increased in the PL group and decreased by SL-4 treatment. In contrast, expression of A2m and MASP1 were decreased in the PL group and increased in the SL-4 group.

**DISCUSSION**

In Mongolian folk medicine, SL-4 is traditionally used to treat peptic ulcers and gastroenteritis. Previous studies have shown that SL-4 has therapeutic effects against infantile diarrhea and improves intestinal health[13-15]. However, the anti-ulcerogenic effect of SL-4 and its pharmacological mechanism have not been well investigated. Thus, we aimed to study whether SL-4 had a protective effect on PL-induced gastroduodenal ulcers in a rat model and examined its molecular mechanism by microarray analysis.

PL is a well-established methodology to develop gastric ulceration in rats[16]. PL induces accumulation of gastric acid and pepsin, resulting in breakdown of the gastric
Table 3 Top 10 Kyoto Encyclopedia of Genes and Genomes pathways enriched with differentially expressed mRNAs in duodenal tissue from rats the study groups

<table>
<thead>
<tr>
<th>Treatment</th>
<th>KEGG pathway</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Shame vs PL</td>
<td>Complement and coagulation cascades</td>
<td>3.93 × 10^{-9}</td>
</tr>
<tr>
<td></td>
<td><em>Staphylococcus aureus</em> infection</td>
<td>4.53 × 10^{-9}</td>
</tr>
<tr>
<td></td>
<td>Cytokine-cytokine receptor interaction</td>
<td>6.48 × 10^{-7}</td>
</tr>
<tr>
<td></td>
<td>Hematopoietic cell lineage</td>
<td>9.84 × 10^{-6}</td>
</tr>
<tr>
<td></td>
<td>Rheumatoid arthritis</td>
<td>2.78 × 10^{-5}</td>
</tr>
<tr>
<td></td>
<td>Osteoclast differentiation</td>
<td>4.40 × 10^{-5}</td>
</tr>
<tr>
<td></td>
<td>PI3K-Akt signalling pathway</td>
<td>2.13 × 10^{-4}</td>
</tr>
<tr>
<td></td>
<td>Tuberculosis</td>
<td>2.89 × 10^{-4}</td>
</tr>
<tr>
<td></td>
<td>ECM-receptor interaction</td>
<td>3.02 × 10^{-4}</td>
</tr>
<tr>
<td></td>
<td>Amoebiasis</td>
<td>3.37 × 10^{-4}</td>
</tr>
<tr>
<td>PL vs SL-4</td>
<td>Maturity onset diabetes of the young</td>
<td>2.10 × 10^{-7}</td>
</tr>
<tr>
<td></td>
<td>Complement and coagulation cascades</td>
<td>7.39 × 10^{-6}</td>
</tr>
<tr>
<td></td>
<td><em>Staphylococcus aureus</em> infection</td>
<td>7.99 × 10^{-5}</td>
</tr>
<tr>
<td></td>
<td>Regulation of autophagy</td>
<td>2.26 × 10^{-5}</td>
</tr>
<tr>
<td></td>
<td>Type II diabetes mellitus</td>
<td>8.47 × 10^{-5}</td>
</tr>
<tr>
<td></td>
<td>Longevity regulating pathway – multiple species</td>
<td>1.51 × 10^{-2}</td>
</tr>
<tr>
<td></td>
<td>Phototransduction</td>
<td>2.05 × 10^{-2}</td>
</tr>
<tr>
<td></td>
<td>Mucin type O-Glycan biosynthesis</td>
<td>2.35 × 10^{-2}</td>
</tr>
<tr>
<td></td>
<td>Porphyrin and chlorophyll metabolism</td>
<td>3.51 × 10^{-2}</td>
</tr>
<tr>
<td></td>
<td>Longevity regulating pathway</td>
<td>4.01 × 10^{-2}</td>
</tr>
</tbody>
</table>

KEGG: Kyoto Encyclopedia of Genes and Genomes; Sham: PL: Pyloric ligation; Sham operation; SL-4: Sulongga-4 decoction.

mucosal barrier and causes inflammatory injury, which are key drivers of gastric ulcer formation\(^{(14)}\). To protect against inflammation, the cells respond with attenuated production of proinflammatory cytokines such as IL-12, TNF-\(\alpha\), IL-1, IL-6, and IFN\(^{(18)}\). Our findings show that SL-4 significantly improved the protective effects against gastroduodenal mucosal hemorrhage and inflammation, as confirmed by histopathology. Additionally, inflammatory factors such as IL-6, TNF-\(\alpha\) and IL-1\(\beta\) were significantly reduced by SL-4 in contrast to the PL group, which indicates that the antiulcer effects of SL-4 can be attributed to anti-inflammatory activity. PAF, a potent phospholipid mediator of leukocyte activation, is a potent mediator of endogenous ulcer formation\(^{(19)}\). ET is a hormone secreted by the endothelial cells of blood vessels that can also promote ulceration\(^{(18)}\). Our data showed that SL-4 suppressed expression of PAF and ET in the gastroduodenal tissues in PL model mice in a dose-dependent manner, suggesting an inhibitory role for SL-4 in the activation of endothelial cells during ulcer maintenance. Additionally, SL-4 increased expression of PGE2 and EGF in gastroduodenal tissue, which indicates that it may effectively inhibit the secretion of gastric acid, enhance the gastric mucosal defensive function, promote the repair of gastric mucosal injury, and reduce recurrence rate of gastric ulcer\(^{(29)}\). A previous study reported that PGE2 was responsible for the production and maintenance of the cellular integrity of the gastric mucosa, and that depletion of PGE2 could cause gastric ulcers\(^{(31)}\). Histological evaluation showed that SL-4 reduced mean ulcer size and minimized ulcer formation, congestion, inflammation, hemorrhage, and necrosis of the gastric mucosa. Together, these findings demonstrated the antiulcer effect of SL-4 in PL rats.

*Forsythia suspensa* is a major herbal component of SL-4. It has been reported that its active ingredients forsythiaside and forsythin exert potent anti-inflammatory and antibacterial activities, which may have possible use as antiulcer agents\(^{(22)}\). A number of medicinal plants have been reported useful for the treatment of gastrointestinal
Table 4 Sequence of major genes involved in two main Kyoto Encyclopedia of Genes and Genomes pathways in gastric and duodenal tissue

<table>
<thead>
<tr>
<th>Tissue pathway</th>
<th>Gene symbol</th>
<th>Gene name</th>
<th>Sham vs PL</th>
<th>PL vs SL-4</th>
<th>GeneBank accession No.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gastric (retinol metabolism)</td>
<td>UGT2B1</td>
<td>UDP glucuronosyl transferase 2 family, polypeptide B1</td>
<td>+13.71</td>
<td>-30.56</td>
<td>NM_173295</td>
</tr>
<tr>
<td></td>
<td>SDR16c5</td>
<td>Short chain dehydrogenase/reductase family 36C, member 5</td>
<td>+7.16</td>
<td>+3.12</td>
<td>NM_001106634</td>
</tr>
<tr>
<td></td>
<td>RDH7</td>
<td>Retinol dehydrogenase 7</td>
<td>+5.89</td>
<td>-45.38</td>
<td>NM_133543</td>
</tr>
<tr>
<td></td>
<td>CYP2b2</td>
<td>Cytochrome P450, family 2, subfamily b, polypeptide 2</td>
<td>+5.57</td>
<td>-12.51</td>
<td>NM_001198676</td>
</tr>
<tr>
<td></td>
<td>CYP4a1</td>
<td>Cytochrome P450, family 4, subfamily a, polypeptide 1</td>
<td>+3.93</td>
<td>-83.27</td>
<td>NM_175837</td>
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<tr>
<td>Duodenal (complement and coagulation cascades)</td>
<td>CYP1a1</td>
<td>Cytochrome P450, family 1, subfamily a, polypeptide 1</td>
<td>-3.47</td>
<td>+1.86</td>
<td>NM_012540</td>
</tr>
<tr>
<td></td>
<td>A2m</td>
<td>Alpha-2-macroglobulin</td>
<td>-20.37</td>
<td>+33.00</td>
<td>NM_012488</td>
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<tr>
<td></td>
<td>FGG</td>
<td>Fibrinogen gamma chain</td>
<td>-41.01</td>
<td>+15.50</td>
<td>NM_012559</td>
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<td>FGA</td>
<td>Fibrinogen alpha chain</td>
<td>-23.51</td>
<td>+6.49</td>
<td>NM_001008724</td>
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<td>MASP1</td>
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<td>-11.09</td>
<td>+3.19</td>
<td>AY149996</td>
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<tr>
<td></td>
<td>VSIG4</td>
<td>V-set and immunoglobulin domain containing 4</td>
<td>-6.37</td>
<td>+3.26</td>
<td>NM_001025004</td>
</tr>
<tr>
<td></td>
<td>CF8</td>
<td>Complement factor B</td>
<td>+3.08</td>
<td>-5.43</td>
<td>NM_212466</td>
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Genes involved in the retinol metabolism pathway in gastric tissue and in the complement and coagulation cascade pathways in duodenal tissue with > 2-fold change associated with different experimental treatments were determined by microarray analysis. Fold-induction was calculated as the normalized intensity in the study groups. Positive and negative numbers represent up- and downregulated gene expression. PL: Pyloric ligation; Sham: Sham operation; SL-4: Sulongga-4 decoction.

disorders. Wu et al[23] reported that a Chinese medicinal herb, Pogostemon cablin, and its main active compound β-patchouliene profoundly inhibited ulcer formation by reducing the inflammatory response and improving angiogenesis. Kumar et al[24] studied the antiulcer activity of an Indian medicine Cedrus deodara and found that its volatile oil had a potent gastroprotective effect on ulceration and inflammation in PL- and ethanol-treated rats. Al-Wajeeth et al[25] reported that a Malaysian medicine Cibotium barometz hair protected against ethanol-induced ulceration through regulation of antioxidant enzymes and gastric secretory actions. Consistent with those findings, our data confirmed that the gastroprotective effects of SL-4 components primarily work through modulation of inflammatory and gastric secretory mechanisms.

Microarray techniques are crucial for understanding and interpreting the activity of traditional medicines, particularly in revealing their mechanisms of action and drug targets[26]. To investigate the underlying molecular mechanisms of SL-4, we determined the gene expression profiles of gastric and duodenal tissues obtained from rats with PL-induced ulcers with or without SL-4 treatment. Retinol metabolism was one of the most significantly modified pathways in gastric tissue after SL-4 treatment. Retinoic acid (RA) intake and metabolism change dramatically during the acute-phase response (APR) to inflammation[25]. The APR is a metabolic system responding to infection, trauma, or tissue injury, and the PL method used in this study may have caused a strong APR in the intestinal tract. Inflammation drives decreased retinol usage by a reduction of retinol-binding protein synthesis[26]. RA increases the synthesis of inflammatory cytokines including transforming growth factor (TGF)-β, IL-10, IL-4, IL-5, and IL-6, and enhances white blood cell production[25]. Microarray analysis found that SL-4 decreased the expression of key transcriptomes associated with retinol metabolism. RA concentration is controlled by glucuronosyltransferases, including UGT2B1, and P450 cytochromes including CYP26A1, CYP26B1, and CYP26C1. These subfamilies catalyze RA oxidation to forms including 5,8-epoxy RA, 4-oxo RA, 4-hydroxy RA, and 18-hydroxy RA[25,26]. Thus, decreased enzyme activation blocks RA accumulation in the other areas and maintains a suitable physiological RA concentra-
The current results also suggest that SL-4 accelerates the anti-inflammatory effects of retinol metabolism. This further indicates the therapeutic effect of SL-4 on inflammatory bowel disease and other clinical inflammatory symptoms.

Additionally, KEGG analysis found significant differences in the complement and coagulation cascade pathways that could have been caused by an inflammatory response. Damage of the intestinal tract activates the coagulation cascade. Fibrin formation provides a physical barrier that can be a potential shield from inflammation. Our microarray results indicated that SL-4 elevated the transcriptome expression of A2m, which acts as a carrier protein to bind numerous growth factors and cytokines, such as platelet-derived growth factor, basic fibroblast growth factor, TGF-β and IL-1β, thus inhibiting inflammation. MASP1 is a serine protease that functions as a component of the lectin pathway of complement systems, which plays a pivotal role in the defense against infection. Elevation of MASP1 expression by SL-4 may be responsible for improving the immune activity and defense against gastric infections. The above results suggest that SL-4 may have several active substances that promote anti-inflammatory responses that prevent peptic ulcer formation via retinol metabolism and the complement and coagulation systems.

*S. aureus* infection was found in both gastric and duodenal tissues, which indicated that PL activated the immune system against *S. aureus* infection. Although our KEGG analysis did not find a direct protective effect, antimicrobial activity for SL-4 has been reported. The intestinal immune system plays a vital role in the prevention of and defense against inflammation caused by harmful pathogens. In our study, PL induced an increase in IL-1β secretion in gastric tissues. Although the IL-1β-mediated immune response to *S. aureus* has not been confirmed, IL-1β is a key cytokine in orchestrating host defenses against the organism. Therefore, the effect of SL-4 on bacterial infection of the intestinal tract should be investigated in a future study.

**CONCLUSION**

Our data demonstrate that SL-4 protected against PL-induced gastroduodenal ulceration by reducing inflammatory cytokines and increasing the expression of gastric acid inhibitory factors. We propose that regulation of CYP2b2 and UGT2b1 gene
Figure 2 Expression of interleukin-6, endotoxin, and platelet-activating factor in duodenal tissue obtained from rats in different groups, and determined by enzyme-linked immunosorbent assay. Data are reported as means ± standard error (n = 10-12). A: Interleukin-6; B: Endotoxin; C: Platelet-activating factor. *P < 0.05 vs the sham group; †P < 0.05 vs the pyloric ligation (PL) group. Sham: Sham surgery; SL-4: Sulongga-4 decoction.

expression in the retinol metabolism pathway and A2m and MASP1 genes in the complement and coagulation cascade pathways are may be involved in mechanism by which SL-4 protects against gastroduodenal ulcers. Most notable are the effects of SL-4 on the transcriptome involved in retinol metabolism, which has not been described previously. The Mongolian folk medicine SL-4 is a promising gastroprotective agent with potential use for treating gastric ulcers in clinical practice.
Figure 3 Expression of tumor necrosis factor-α, interleukin-1β, prostaglandin E2 and epidermal growth factor in the gastric tissue from rats in different groups, and determined by enzyme-linked immunosorbent assay. Data are means ± standard error (n = 10-12). A: Tumor necrosis factor-α; B: Interleukin-1β; C: Prostaglandin E2; D: Epidermal growth factor. aP < 0.05 vs the sham group; bP < 0.05 and cP < 0.01 vs the pyloric ligation (PL) group, respectively. Sham: Sham surgery; SL-4: Sulongga-4 decoction.
Figure 4 Volcano plots of microarray data on differentially expressed mRNA in gastric and duodenal tissue. A and B: There were 1415 and 1460 differentially expressed genes in the sham operation vs pyloric ligation (PL) (A) and PL vs SL-4 groups (B), respectively in gastric tissue; C and D: There were 2610 and 209 differentially expressed genes in the sham operation vs PL (C) and PL vs SL-4 groups (D), respectively in duodenal tissue. Vertical lines correspond to 2-fold up- and downregulation. The horizontal line represents a P value of 0.05. Significantly up- and downregulated genes are shown in red and green, respectively. Statistical significance was defined as a fold-change of 2.0 and P value of 0.05 between groups. Sham: Sham operation, SL-4: Sulongga-4 decoction.
Figure 5 Relative expression of CYP2b2 and UGT2b1 mRNA in gastric tissue and A2m and MASP1 mRNA in duodenal tissue by reverse transcription polymerase chain reaction assay. A: CYP2b2; B: UGT2b1; C: A2m; D: MASP1. GAPDH was used as the reference gene. Values are means ± standard error (n = 6). *P < 0.05 vs sham operation; †P < 0.05 vs pyloric ligation (PL). Sham: Sham operation; SL-4: Sulongga-4 decoction.

ARTICLE HIGHLIGHTS

Research background
Sulongga-4 (SL-4) is a classic herbal formula used in traditional Mongolian medical clinics for the treatment of peptic ulcers and gastroenteritis, even though its pharmacological mechanism has not been well characterized.

Research motivation
The study objective was to identify the protective effect and mechanism of SL-4 against peptic ulcer disease.

Research objectives
To evaluate the protective effect and identify the mechanisms of action of SL-4 on gastroduodenal ulcer induced by pyloric ligation (PL) in rats.

Research methods
PL was performed to induce gastric and duodenal ulcers in rats that were then treated with oral SL-4 (1.3, 2.6, or 3.9 g/kg per day) for 15 d. PL-induced gastroduodenal ulceration. Therapeutic effects were evaluated by pathological and histological evaluation. Inflammatory indicators were analyzed by enzyme-linked immunosorbent assay. Microarray analyses were conducted to determine the gene expression profiles of gastroduodenal tissue in PL rats with or without SL-4 treatment. The candidate target genes were selected and verified by quantitative reverse transcription polymerase chain reaction (qRT-PCR).

Research results
SL-4 improved the histopathology of the PL-induced ulcers. SL-4 significantly (*P < 0.05) decreased the expression of tumor necrosis factor-α, interleukin (IL)-1β, IL-6, endotoxin, PAF, and increased prostaglandin E2 and EGF in ulcer tissue. Microarray
analysis was used to identify a list of candidate target genes for SL-4 acting on PL-induced ulceration. The genes included some that modulate complement and coagulation cascade pathways, and retinol metabolism pathways that are closely associated with inflammatory responses and gastric mucosal protective mechanisms. qRT-PCR showed that altered expression of the selected genes, such as CYP2b2, UGT2b1, A2m, and MASPI, was consistent with the microarray results.

Research conclusions
SL-4 exerted protective effects against PL-induced gastroduodenal ulcers via reducing inflammatory cytokines and elevating the expression of gastric acid inhibitory factors. Downregulation of the CYP2b2 and UGT2b1 genes in retinol metabolism and upregulation of the A2m and MASPI genes in the complement and coagulation cascade pathways may have been involved in the protection against gastroduodenal ulcers.

Research perspectives
SL-4, a Mongolian folk medicine, is a promising gastroprotective agent with potential clinical use as a treatment of gastric ulcers.

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