A Metabolomic Study to Identify Potential Tissue Biomarkers for Indomethacin-Induced Gastric Ulcer in Rats

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Abstract

Background: Gastric Ulcer (GU) is the most prevalent gastrointestinal disorder induced by various factors and Non-Steroid Anti-Inflammatory Drugs (NSAIDs) as one of the most common reasons. Due to the absence of appropriate molecular markers for GU, the aim of this study was to utilize a metabolomics approach in order to find potential metabolite markers for the disease.

Methods: Stomach tissue samples from indomethacin-treated rats and normal controls were used to perform a 1H-NMR metabolomics study. The altered metabolites were identified using random forest multivariate analysis.

Results: ROC curves showed that the random forest model had a good predictive performance with AUC of 1 for the test and 0.708 for the training sets. Seventeen differentially expressed metabolites were found between GU and normal tissue sample. These metabolites included trimethylamine, betaine, carnitine, methionine, acetylcholine, choline, N,N-Dimethylglycine, cis-aconitate, tryptophan, spermidine, acetylcar nitine, creatinine, pantothenate, taurine, isoleucine, glucose and kynurenine.

Conclusion: The results of the study demonstrated that metabolomics approach could serve as a viable method to find potential markers for GU. Surely, further studies are needed for the validation of the results.

Keywords: Gastric ulcer, Indomethacin, Metabolomics, Nuclear magnetic resonance

Introduction

Gastric ulceration is a benign lesion on the mucosal epithelium upon exposure of the stomach to excess acid and aggressive pepsin activity 1. Gastric Ulcer (GU) is a very common gastrointestinal disease which may lead to dangerous complications and even death. It is accounting for an estimated 15 mortality out of every 15,000 complications yearly in the world 2. GU affects approximately 10% of the population worldwide 3, so its prevention and management are considered very important challenges. As a multifactorial disease, it mainly occurs due to imbalance between acid secretion and cytoprotective factors such as bicarbonate secretion, prostaglandins, cell renewal and antioxidants 4. Main factors causing GU usually include *Helicobacter pylori* (H. pylori) infection, acid secretion, types of diet, alcohol consumption and Non-Steroid Anti-Inflammatory Drugs (NSAIDs) 5,6. Specifically, gastrointestinal toxicity of NSAID drugs origin may be as high as 4-8% per year and the complications are even higher for those with prior history of ulcer disease 7. NSAIDs are from the most commonly used drugs in the world 8 and NSAID-induced gastric damage is known to be the most common side-effect of these drugs in about 25% of the users 9. Indomethacin (INDO) as the main NSAID is an indole derivative, non-steroidal, inflammatory drug with anti-inflammatory, analgesic, and antipyretic effects 10. It has also been demonstrated to have a stronger effect to induce gastric injury than other currently used NSAIDs. Therefore, indomethacin became the first-choice drug to produce an experimental ulcer model as a result of having higher ulcerogenic potential than other NSAIDs 11. Inhibition of prostaglandin syn-
thesis is one of the mechanisms suggested for the GU caused by NSAIDs. It has been suggested that indomethacin induces gastric damage via inhibiting the release of protective factors like COX-1, PGE2, bicarbonate, and mucus; the aggressive factors like acid, and oxidant parameters increase while antioxidant parameters are decreasing. Currently, the NSAIDs side effects are only detectable by endoscopy, and no biomarkers have been yet presented. Furthermore, identifying novel biomarkers would likely improve the safety of NSAIDs use. According to the literature, the relation between peptic ulcer and stomach cancer has long been disputed and there is accumulating evidence that gastric ulcer disease is positively associated with the risk of developing stomach cancer. Therefore, identification of high-confidence diagnostic biomarkers is very important for GU. In recent years, many attempts have been made in order to find molecular markers for GU and some candidate biomarkers were also introduced. According to Takeuchi et al., hydroxyproline can be a new serum biomarker of gastric injury. The results of other studies on serum showed that the NSAIDs induced decrement of citrate, cis-aconitate, succinate, 3-hydroxy butanoic acid, o-acetyl carnitine, proline and hydroxyproline.

"Omics" approaches including genomics, proteomics, and metabolomics have gained much attention in recent years to find potential markers for GU using various biological samples such as tissues, biological fluids and cell cultures. By detection and quantification of all metabolites in a specific sample, metabolomics provides a "snapshot" of metabolic changes related to the disease. Due to more dynamical status of metabolomics rather than both of genomics and proteomics analyses, this approach can detect metabolic changes associated with different physiological states in a shorter time frame. Moreover, metabolomics has the ability to detect and introduce biomarkers in a broad range of samples including whole blood, serum, plasma, urine, saliva and tissues in various disease conditions. In recent years, a few studies on gastric ulcer biomarker detection were done by different metabolomics-based techniques in urine and serum samples. So, in the current study, a nuclear magnetic resonance-based metabolomics approach was investigated to find potential metabolite markers in stomach tissue samples of indomethacin-induced rat models of GU and also to better understand the underlying mechanisms of NSAIDs-induced gastric ulcer.

Materials and Methods

Experimental animals

A total of 24 male Wistar rats aging 6-8 weeks with the average weight of 180-220 g were used in the study. Rats were kept in temperature controlled houses with a 12 hr/12 hr dark/light cycles. They were also provided with sufficient water and food access. The rats were kept in houses with raised floors to avoid coprophagy. The rats were randomly divided into 3 groups: group 1=normal rats receiving water (n=8), group 2=indomethacin-induced ulcer rats (n=8), and group 3=rats receiving vehicle (n=8). The rats were fasted for 24 hr before the indomethacin administration with free access to water. After that, 45 mg/kg indomethacin was administered. The water, CMC, and indomethacin were administered by oral gavage to each rat. After 6 hr, the animals were anesthetized by 60 mg/kg ketamine and 20 mg/kg xylazine. The rats were then sacrificed and their stomachs were removed and photographed.

Ulcer index measurement

The number of ulcers in each stomach were counted and averaged to calculate the ulcer index number according to the following formulae: Ulcer Index= (U/N) ×100, where U is the number of ulcers in the stomachs of group 2 rats and N is the number of rats in this group. This study was carried out in accordance with the Guidance for the Care and Use of Laboratory Animals of the NIH. The experiment was approved by the clinical ethics committee of Shahid Beheshti University of Medical Sciences.

Histopathology analyses

The rats’ stomachs were opened along the greater curvature and were completely washed with normal saline to remove any contaminants. A part of the stomach samples was flash frozen with liquid nitrogen and stored at -80°C for metabolomics analysis. The other part of the stomach samples was fixed in 10% formalin and was paraffin embedded to pathologically confirm the gastric ulcer in rats. The paraffin embedded samples were cut into 5 μm thick sections and stained with Hematoxylin and Eosin (H&E) solution to microscopically determine the ulcer regions by pathologist.

Sample preparation for metabolomics study

For preparation of the stomach tissue extracts, 300 mg of the frozen tissues were grounded completely in liquid nitrogen and homogenized in 1 ml of 2:1 v/v Methanol/Chloroform solution. After that, 1 ml of 1:1 v/v Chloroform/H2O was added and the solution was centrifuged for 20 min at 15,000 g and 4°C. 600 μl of the upper phase was then collected and lyophilized. For Nuclear Magnetic Resonance (NMR) analysis, the lyophilized tissue extract was dissolved in 600 μl of phosphate buffer solution containing 80% D2O, 2% TSP (trimethylsilyl propionate), 4% KH2PO4 and 0.01% NaN3.

1H-NMR spectrometry

The 1H-NMR analysis was performed on a Bruker Avance 400 MHz instrument equipped with 5 mm probe at 298 K. The Carr-Purcell-Meiboom-Gill (CPMG) platform was used by a standard pulse sequence irradiating residual water peak, relaxation delay of 2 s and total T2 relaxation time of 60 ms. Other features of the spectrum collection included 150 total scans, spectral width of 8389.26 Hz, 90° pulse width and 0.5 Hz.
line broadening prior to Fourier transformation. The spectra were phased and base-line corrected and were referenced to the peak of TSP at 0 ppm. The NMR spectra were binned in the range of 0.3 and 9.5 as 0.01 ppm parts and were normalized and log-transformed. The region between 4.5 and 5.5 ppm was also omitted for water signal suppression. The NMR spectra were deconvoluted by ProMetab software in MATLAB.

**Statistical analyses**

The data matrix resulted from 1H-NMR analysis was used to perform multivariate statistical modeling to identify the most significant and relevant metabolites differentiating gastric ulcer from normal controls. The Random Forest (RF) algorithm was implemented using MATLAB software. Random Forest is a machine learning method based on the construction of multiple decision trees by bootstrapping the data 23. Each decision tree predicts an independent classification of the samples. The original dataset resulted from 1H-NMR analysis was divided into training and test sets. About one third of the samples did not participate in the construction of the model which are called Out Of Bag (OOB). After construction of the model, each OOB is entered to its relevant kth decision tree to estimate the classification ability of the RF model. The predictive performance of the RF model was measured based on the difference between the predicted and expected outcomes by counting the number of True Negatives and Positives (TN, TP) and False Negatives and Positives (FN, FP). The following formula were used to assess sensitivity, specificity, precision (positive predictive value), accuracy and overall error rate: sensitivity= TP/TP+FN, specificity= TN/TN+FP, precision (PPV)= TP/TP+FP, accuracy= TP+TN/P+N, overall error rate= (FP+FN/P+N)×100, where P and N indicate the total number of positive and negative values, respectively. The predictive power of the model was demonstrated by Receiver Operating Characteristic (ROC) Curves for both training and test datasets.

**Metabolites identification and pathway analysis**

The variables (NMR spectral bins) with the highest importance value resulted from the RF model which had p-values of less than 0.05 were considered significant. The metabolites were identified using relevant databases of NMR metabolomics including Biological Magnetic Resonance Bank (BMRB) 24 and Human Metabolome Database (HMDB) 25. The tolerance for searching spectral bins was ±0.01 ppm. The significantly altered metabolites were then used to find the most important pathways in the pathogenesis of gastric ulcer. The pathway enrichment analysis was performed using the MetaboAnalyst 4 26 online server.

**Results**

The stomach tissues of the rats in each group were utilized for a metabolomics investigation to find potential diagnostic tissue markers for gastric ulcer. In this study, an attempt was made to compare 3 groups including normal controls which only received drinking Table 1. The RF model predictive performance features

<table>
<thead>
<tr>
<th>Overall error rate</th>
<th>Sensitivity</th>
<th>Specificity</th>
<th>Accuracy</th>
<th>Precision</th>
</tr>
</thead>
<tbody>
<tr>
<td>Test set</td>
<td>0</td>
<td>100%</td>
<td>100%</td>
<td>100%</td>
</tr>
<tr>
<td>Train set</td>
<td>28.60%</td>
<td>66.70%</td>
<td>75%</td>
<td>71.42%</td>
</tr>
</tbody>
</table>

Table 2. The significantly altered metabolites between GU and normal control

<table>
<thead>
<tr>
<th>Metabolite</th>
<th>Chemical shifts (δ)</th>
<th>KEGG ID</th>
<th>RF model importance</th>
<th>p-value</th>
<th>Fold change (ulcer/control)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Choline</td>
<td>3.195, 3.505, 4.055, 3.515</td>
<td>C00114</td>
<td>0.0331</td>
<td>0.0172</td>
<td>3.28 ↓</td>
</tr>
<tr>
<td>Cis-aconitate</td>
<td>3.095, 3.105</td>
<td>C00417</td>
<td>0.0263</td>
<td>2.32E-05</td>
<td>2.05 ↓</td>
</tr>
<tr>
<td>Tryptophan</td>
<td>3.285, 3.295, 3.465, 3.475</td>
<td>C00078</td>
<td>0.0240</td>
<td>0.0066</td>
<td>3.79 ↓</td>
</tr>
<tr>
<td>Spermidine</td>
<td>3.155, 3.145</td>
<td>C00315</td>
<td>0.0194</td>
<td>0.0010</td>
<td>6.40 ↓</td>
</tr>
<tr>
<td>Trimethylamine</td>
<td>3.255</td>
<td>C00565</td>
<td>0.0190</td>
<td>0.0276</td>
<td>1.75 ↑</td>
</tr>
<tr>
<td>N,N-Dimethylglycine</td>
<td>2.915, 3.705</td>
<td>C01026</td>
<td>0.0190</td>
<td>0.0150</td>
<td>2.50 ↓</td>
</tr>
<tr>
<td>Acetylcarnitine</td>
<td>3.175, 3.605, 3.185, 3.595</td>
<td>C02571</td>
<td>0.0138</td>
<td>0.0184</td>
<td>1.90 ↓</td>
</tr>
<tr>
<td>Creatinine</td>
<td>4.045</td>
<td>C00791</td>
<td>0.0138</td>
<td>0.0157</td>
<td>6.60 ↓</td>
</tr>
<tr>
<td>Pantothenate</td>
<td>3.425</td>
<td>C00864</td>
<td>0.0135</td>
<td>0.0085</td>
<td>3.52 ↓</td>
</tr>
<tr>
<td>Betaine</td>
<td>3.265</td>
<td>C00719</td>
<td>0.0125</td>
<td>0.0490</td>
<td>1.60 ↓</td>
</tr>
<tr>
<td>Taurine</td>
<td>3.405, 3.415, 3.395, 3.385</td>
<td>C00245</td>
<td>0.0125</td>
<td>0.0010</td>
<td>7.90 ↓</td>
</tr>
<tr>
<td>Carnitine</td>
<td>3.205, 3.215</td>
<td>C00318</td>
<td>0.0123</td>
<td>0.0128</td>
<td>1.80 ↑</td>
</tr>
<tr>
<td>Isoleucine</td>
<td>3.655, 3.665</td>
<td>C00407</td>
<td>0.0121</td>
<td>0.0061</td>
<td>5.05 ↓</td>
</tr>
<tr>
<td>Glucose</td>
<td>3.455, 3.235, 3.525, 3.725, 3.825</td>
<td>C00031</td>
<td>0.0119</td>
<td>0.0010</td>
<td>3.88 ↓</td>
</tr>
<tr>
<td>Kynurenine</td>
<td>3.695</td>
<td>C00328</td>
<td>0.0114</td>
<td>0.0113</td>
<td>5.50 ↓</td>
</tr>
<tr>
<td>Methionine</td>
<td>2.115, 3.855</td>
<td>C00073</td>
<td>0.0110</td>
<td>0.0447</td>
<td>2.18 ↓</td>
</tr>
<tr>
<td>Acetylcholine</td>
<td>3.205</td>
<td>C01996</td>
<td>0.0057</td>
<td>0.0285</td>
<td>2.00 ↑</td>
</tr>
</tbody>
</table>
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Table 3. The significant biochemical pathways involved in the pathogenesis of gastric ulcer

<table>
<thead>
<tr>
<th>Pathway</th>
<th>Matched metabolites</th>
<th>p-value</th>
<th>FDR</th>
</tr>
</thead>
<tbody>
<tr>
<td>Betaine metabolism</td>
<td>Betaine, Dimethylglycine, Choline, Methionine</td>
<td>2.62E-4</td>
<td>0.0216</td>
</tr>
<tr>
<td>Methionine metabolism</td>
<td>Betaine, Dimethylglycine, Choline, Methionine, Spermidine</td>
<td>4.37E-4</td>
<td>0.0216</td>
</tr>
<tr>
<td>Beta-oxidation of very long chain fatty acids</td>
<td>Carnitine, Acetyl carnitine</td>
<td>0.0304</td>
<td>0.839</td>
</tr>
<tr>
<td>Spermidine and spermine biosynthesis</td>
<td>Methionine, Spermidine</td>
<td>0.0339</td>
<td>0.839</td>
</tr>
</tbody>
</table>

Discussion

Gastric ulcer is the upper gastrointestinal mucosa damage caused by helicobacter pylori and NSAIDs such as indomethacin as major reasons. 1H-NMR spectroscopy is a very powerful tool for profiling and co-

Figure 1. The macroscopic appearance of the stomach from (A, B) normal control, (C) control receiving CMC and (D-F) indomethacin-induced gastric ulcer rats. Arrows show linear and focal hemorrhagic areas.

Figure 2. The gastric mucosa appearance in (A) normal and (B, C) indomethacin-induced lesions stained with H&E (100x magnified). Normal stomachs have intact epithelium with distinct chief and parietal cells where ulcer areas show epithelium damage and infiltration of lymphocytes and monocytes.

Figure 3. The plot of the OOB error for the random forest model.
parison of tissue samples metabolic profiles with some advantages over other techniques such as easier sample preparation, the high reproducibility and lower costs. However, a few studies evaluated the stomach tissue metabolic alterations induced by indomethacin using metabolomics analysis to better understand disease mechanism, drug toxicity, drug response and to distinguish predictive biomarkers. In the current study, metabolite comparison in stomach tissue samples of control and indomethacin treated group was performed. According to the study results, betaine decreased in treated group. Betaine (trimethylglycine) is known as an antioxidant in previous reports. Based on Alirezaei et al, lipid peroxidation significantly decreased in betaine pretreated rats and significantly decreased ulcer occurrence. Alterations of betaine content was previously observed in rat models of gastric ulcer. Methionine and isoleucine amino acids decreased in our study. Methionine is an essential amino acid in humans which is a substrate of other amino acids such as taurine and also the important antioxidant, glutathione. Previous studies reported that some of amino acids including methionine and leucine inhibit indomethacin-induced gastric ulcers at a dose-dependent manner. According to the present study results, decreased levels of these amino acids in the stomach susceptible to the ulceration depleted their protective function.

In this study, taurine level was significantly decreased in rats treated with indomethacin. Taurine is an intracellular free thiol-containing β-amino acid that can be found in various mammalian tissues. It has been reported that taurine plays important biological roles including nutrition, antioxidation, anti-inflammatory function, membrane stabilization, modulation of intracellular free calcium concentration and protection against oxidant-mediated injury in several organs. Indeed, it protects against the drug-related gastric damage and colonic injury by its antioxidant properties. Antioxidant function of taurine in membrane organization is done by its protection against free radicals. In addition, the results of several studies have shown that taurine prevents gastric ulcer induced by indomethacin through lipid peroxidation inhibition and neutrophil activation. Furthermore, taurine changes might imply the oxidative stress-related gastric ulceration. Decreased taurine level was also reported in a metabonomic study by Um et al in indomethacin-induced gastric ulcer rat models. The result of our study indicates that glucose level decreased in the indomethacin-treated group, indicating excessive glucose was consumed to ameliorate gastric injury. Several investigations have found glucose metabolism is increased in cell transformations. According to our results, indomethacin administration increased kynurenate and decreased choline and tryptophan levels. Indomethacin stimulated the conversion of tryptophan into kynurenate, which inhibits fibroblast growth factor and delays ulcer healing. Fibroblast growth factors are major factors in ulcer healing in stomach mucosa by using embryogenesis and tissue regeneration function. NS-AIDs such as indomethacin inhibit COX-1 and COX-2 which lead to suppression of prostaglandins. FGFs accelerate healing rate through increasing microcircula-
tion around the ulcer and COX-2-derived prostaglandins. Our finding indicated that the lack of metabolism of choline to produce phosphatidylcholine caused the gastric mucosa damage. All of these findings suggested depleted protective compounds role in the gastric mucosa damage. Cis-aconitate is another metabolite that decreases in indomethacin-induced ulcer group which occurs as a result of inhibition of aconitase. Aconitase catalyzes citrate to isocitrate via cis-aconitate in the Tricarboxylic acid cycle (TCA). Because this compound is one of the intermediates in the TCA cycle, this alteration might suggest the disturbance of energy metabolism in GU. Alterations of serum cis-aconitate level was previously reported in a metabolomics study of Takeuchi et al. on gastric ulcer induced by nonsteroid anti-inflammatory drugs. Glycine is a glucogenic amino acid and provides glucose for energy metabolism. It was also reported that glycine is essential for defense system in cells and helps in digestion of fats by the bile acid regulation. Carnitine is an acetylated form of carnitine that is broken down to carnitine which is used by the body to transport fatty acids into the mitochondria for breakdown. Carnitine is a quaternary amine and an essential cofactor which plays important role in long chain fatty acid oxidation in mitochondria. Carnitine decreased in ulcerated model in comparison with indomethacin treatment. The metabolic differences between rats in control group and rats treated with indomethacin were classified based on the multivariate random forest model. Several putative biomarkers between control and NSAID-induced gastric ulcer group. The results of this study demonstrated that metabolomics-based investigations can be used to effectively identify biomarkers for GU caused by indomethacin treatment. The metabolic differences between rats in control group and rats treated with indomethacin were classified based on the multivariate random forest model. Several putative biomarkers were identified for diagnosis of NSAID-related gastric ulcer including alterations of pantotheinate, isoleucine, spermidine, methionine, acetylcarnitine, trimethylamine, creatinine, carnitine, cis-aconitate, choline, taurine, betaine, glucose, N,N-Dimethylglycine, acetylcholine, tryptophan, and kynurenine. In this study, all of the rats were treated with the same dose of indomethacin, but each of rats in a same group showed different ulcer degrees. This difference seems

Conclusion

In this study, 1H-NMR metabolomics analysis was performed on stomach tissue samples of indomethacin-induced gastric ulcer rats in order to find putative diagnostic biomarkers between control and NSAID-induced gastric ulcer group. The results of this study demonstrated that metabolomics-based investigations can be used to effectively identify biomarkers for GU caused by indomethacin treatment. The metabolic differences between rats in control group and rats treated with indomethacin were classified based on the multivariate random forest model. Several putative biomarkers were identified for diagnosis of NSAID-related gastric ulcer including alterations of pantotheinate, isoleucine, spermidine, methionine, acetylcarnitine, trimethylamine, creatinine, carnitine, cis-aconitate, choline, taurine, betaine, glucose, N,N-Dimethylglycine, acetylcholine, tryptophan, and kynurenine. In this study, all of the rats were treated with the same dose of indomethacin, but each of rats in a same group showed different ulcer degrees. This difference seems
to be justified by the difference in the response to the drug in each of the rats. Despite the identification of several potential metabolite biomarkers in this study, further investigations are needed to clarify identified metabolites and also on the potential role of these metabolites in the disease pathology and consequently in the development of new NSAID drugs. The present study demonstrated that metabolomics can be used as a new, simple and rapid approach to identify molecular biomarkers for NSAID drugs-induced gastric ulcers. Moreover, metabolomics is a powerful tool to determine drug toxicity and biological pathways involved in drug-related gastric damages.

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**Conflict of Interest**

The authors declared no conflict of interest.

**References**


