Metabolic Dynamics in Chronic Gastritis: Examining Urinary Profiles Post H. Pylori Eradication

Musharaf I, Nashwan Aj. Metabolic Dynamics in Chronic Gastritis: Examining Urinary Profiles Post H. Pylori Eradication

Imshaal Musharaf, Abdulqadir J Nashwan

Abstract
Chronic gastritis is the persistent and insidious inflammation of the gastric lining. H. Pylori has been identified as the most common culprit behind it and consequently elimination of H. Pylori can lead towards its cure. The letter explores the use of urinary metabolic profile before and after eradication to identify biomarkers that can aid in prognosis and treatment. Despite providing promising insights, there are limitations such as small sample size (17 patients), a narrow treatment period of 2 wk and treatment heterogeneity, which raise concerns. Nevertheless, the findings have opened a gateway to enhancing the treatment and prognosis of chronic gastritis through urinary metabolomics.

Key Words: Gastritis; Helicobacter Pylori; Chronic Gastritis; Urine Metabolomics; Quadruple Therapy; Precancerous Lesions

Core Tip: The study explores the metabolic changes associated with the eradication of H. Pylori in H. pylori-positive chronic gastritis and accentuate the potential use of urinary metabolites as biomarkers for early prognosis and treatment potency. However, certain limitations such as a restricted sample size, short treatment duration and treatment homogeneity reduce the potency of the study. It calls for a more extensive and standardized investigation.

INTRODUCTION

Gastritis is characterized by inflammation of the stomach lining, which usually follows mucosal damage [1]. When it persists over a long period, it may become chronic. Chronic gastritis is one of the most common and persistent ailments in humans. It is a critical condition that progresses gradually but harmfully. Chronic gastritis can manifest in either nonatrophic or atrophic forms [2]. Chronic atrophic gastritis serves as a precursor condition in the progression towards gastric cancer [3], making it the second most prevalent cause of cancer-related death around the globe [4].

Helicobacter pylori (H. pylori) is a spiral-shaped Gram-negative bacterium equipped with flagella, which allows it to establish itself in the low oxygen conditions of the human gastrointestinal tract. It has advanced in its ability to thrive in the acidic environment of the stomach and to initiate infections [1]. H. pylori infections are the culprit behind many serious gastrointestinal problems, forming precancerous lesions. These include chronic atrophic gastritis, gastric intestinal metaplasia, peptic ulcer, and cancer. It has been identified as the most common cause of gastritis and after an acute H. Pylori infection, most acute gastritis turns into chronic gastritis [1]. It has been observed that eradication of H. pylori can resolve chronic gastritis [2].

Urine metabolomics is a way of extensively measuring all metabolites and low-molecular-weight molecules within a urine sample, representing an evolving field. It characterizes a substantial amount of metabolites than any other clinical laboratory technique and provides a peek into extensive biological processes and metabolic pathways [5]. It is an essential technique for discerning the relationship between drug
efficacy, pharmacological effects, and metabolic pathways through the evaluation of distinct biomarkers during the disease and its treatment. It can serve as an important tool in assessing the treatment and prognosis of $H.\ pylori$-positive chronic gastritis patients, however there are currently studies done on it.

A Wen-Ting et al propose an observational study that probes into the metabolic changes associated with $H.\ pylori$-positive chronic gastritis before and after $H.\ Pylori$ eradication. The study incorporated 17 H. pylori-positive chronic gastritis patients who were diagnosed through the 14C/13C urea breath test (UBT). These patients were subjected to conventional quadruple therapy. Urinary samples were collected from these patients before and after the treatment, which was then analyzed using LC-MS/MS to perform metabolomics and network pharmacology. Metabolomics analysis unveiled those urinary metabolic profiles changed significantly after $H.\ pylori$ eradication. The study established that metabolites, cis-aconitic acid, isocitric acid, citric acid, L-tyrosine, L-phenylalanine, L-tryptophan, and hippuric acid, that participated in four major metabolic pathways: phenylalanine metabolism, phenylalanine and tryptophan biosynthesis, citrate cycle, and glyoxylate and dicarboxylate metabolism, were the most affected by $H.\ pylori$ eradication therapy. Interestingly, it was also notable that changes in the levels of hippuric acid, isocitric acid, L-tryptophan, and L-phenylalanine are key indicators of efficacy and prognosis of $H.\ pylori$-positive chronic gastritis treatment. The study concludes by foregrounding the analysis of urinary metabolites in the treatment and prognosis of the affected patients.

While the study exhibits remarkable findings, shedding light on potential biomarkers and therapeutic insights, certain elements limit the cogency of the study. The study initially encompassed approximately 180 patients, which laid a robust foundation. However, the sample size substantially narrowed down to only 17 individuals because only these patients meeting the inclusion criteria and were willing to be reexamined post-treatment. The small sample size does not adequately represent the diverse patient population affected by $H.\ pylori$-positive chronic gastritis hence increasing susceptibility to random variation which can potentially induce unreliable results. The limited sample
size compromises the statistical power of the findings and makes it prone to sampling bias. There is heterogeneity in *H. pylori*-positive chronic gastritis which may manifest as severity, comorbidities and response to eradication therapy and a small sample size may not be able to account for it. A larger and more diverse sample would not only boost the reliability of the test but also consider the homogeneity among patients.

The treatment duration in the study is only 2 wk, which might not be enough to capture the full spectrum of metabolic changes associated with *H. pylori* eradication. *H. pylori*-positive chronic gastritis is a multifaceted condition, which triggers a series of complex metabolic changes. It is important to comprehend whether these changes persist or evolve over a long post-treatment period, which is not possible to detect in a limited duration. A prolonged duration of treatment or follow-up over an extended period could offer a more thorough understanding.

Another consideration is the treatment heterogeneity. The study employs various alternatives of the quadruple therapy strategies for *H. pylori* eradication. While this approach reflects actual clinical scenarios, it gives birth to treatment heterogeneity. Different therapeutic regimens can potentially invoke different responses in patients while making it perplexing to determine whether an observed effect is the result of the eradication therapy or due to specific components of the treatment regimen compromising the validity of the result. A standardized treatment protocol would increase the validity. Finally, the study has set the "Fifth National Consensus Report on the Treatment of *H. pylori* Infection" as the sole diagnostic criteria. This may not consider the progressing standards or the regional variations in *H. pylori* detection techniques. Furthermore, diagnostic criteria can impact the sensitivity and specificity of tests used to detect *H. pylori* infection. Depending solely on a single criteria may not take into account variations in diagnostic accuracy among different methods or tests. Incorporating the latest diagnostic guidelines or considering the regional variations would enhance the diagnostic accuracy of the study.

CONCLUSION
The study on urinary metabolomics during *H. pylori* eradication in chronic gastritis offers a comprehensive insight into the changes brought about by the treatment. The identification of the metabolic biomarkers in the study lays the foundation for revolutionary prognostic and therapeutic strategies. However, there are some limitations such as a restricted sample size, small treatment duration, non-standardized treatment protocol and a single diagnostic criterion, that need to be addressed in future studies to enhance the robustness and reliability of the findings and contribute to the medical world.
4% SIMILARITY INDEX

PRIMARY SOURCES

<table>
<thead>
<tr>
<th>#</th>
<th>Source</th>
<th>Internet</th>
<th>57 words — 4%</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td><a href="http://www.ncbi.nlm.nih.gov">www.ncbi.nlm.nih.gov</a></td>
<td>Internet</td>
<td></td>
</tr>
</tbody>
</table>

**EXCLUDE QUOTES** ON  
**EXCLUDE SOURCES** < 12 WORDS  
**EXCLUDE BIBLIOGRAPHY** ON  
**EXCLUDE MATCHES** < 12 WORDS