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Insights on the Biomarker Identification for Chronic Gastritis with TCM Damp Phlegm Pattern [Letter]

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Dear editor

We appreciate the You et al's efforts in exploring the metabolomic changes in tongue coatings to identify biomarkers for chronic gastritis (CG) with the Damp Phlegm (DP) pattern.[1] However, several critical issues warrant further consideration and clarification.

Firstly, the authors have emphasized the pivotal role of lipids and lipid-like compounds as the primary differential metabolites in patients with the DP pattern of CG. Although this discovery is noteworthy, they have not provided a thorough mechanistic elucidation of how these metabolic perturbations contribute to the etiology of DP-pattern. Specifically, the precise pathways or interactions that precipitate these lipid alterations remain to be delineated. A deeper understanding of these mechanisms is indispensable for comprehending the disease progression and devising targeted therapeutic strategies.

Secondly, the diagnostic model, formulated using phenol, 2,6-diaminoheptanedioic acid, and N-hexadecanoyl pyrrolidine, has exhibited high levels of accuracy, specificity, and sensitivity. Nonetheless, the authors acknowledge the constraints imposed by the sample size and population distribution. With a cohort of only 300 patients, the generalizability of these findings to a wider population remains uncertain. Moreover, while the external validation set comprising 50 patients shows promise, it is still relatively limited in size. To validate the robustness and applicability of these biomarkers, larger, multicenter studies encompassing diverse ethnic and geographic populations are imperative.

Although this study focuses on the DP pattern in CG, the diagnostic criteria for DP pattern were derived from textbooks, and while the authors reported diagnostic items, they did not disclose the specific process for diagnosing DP pattern. Was the diagnosis made by consensus among two senior Chinese medicine experts with advanced professional titles? The readers are left uninformed. Consequently, the clinical validity of criteria constructed without diagnostic trials is questionable. Furthermore, the authors have underscored the significance of sphingolipid metabolism in the pathophysiology of DP-pattern. Nevertheless, the precise functional implications of the identified sphingolipid metabolites, notably sphinganine 1-phosphate and sphingomyelin, remain speculative at present. Recent findings suggest that these sphingolipid metabolites may be associated with CG beyond being specific to the DP phenotype.[2,3]

Lastly, the article focuses solely on tongue coating metabolomics without considering other potential biomarkers or diagnostic modalities. While tongue coating analysis is a non-invasive and convenient method, integrating it with other omics approaches (eg, genomics, proteomics, and metagenomics) may provide a more holistic understanding of CG.[4] By integrating these omics techniques, the identification of extremely early-stage cancer can be facilitated, thus promoting the discovery of early diagnostic markers and overcoming the challenge of diagnosing cases where traditional symptoms are absent or indistinct. Indeed, tongue-coating proteins[5] have already showcased their potential as a promising indicator for identifying high-risk groups for gastric cancer, further highlighting the significance of this multidisciplinary approach.

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Future research should address these concerns by conducting larger, multicenter studies, exploring the underlying mechanisms of metabolic alterations, and integrating multiple omics approaches for a holistic understanding of CG with the DP pattern.

Disclosure

The authors report no conflicts of interest in this communication.

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