



Study on the Characteristics of Intestinal Flora in Patients with Newly Diagnosed Small Cell Lung Cancer with Liver Metastasis

Yan Liu¹, Dan Zang², Jun Chen²
¹The Second Hospital of Dalian Medical University, Dalian, China ,²The second hospital of Dalian Medical University,Dalian, China



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INTRODUCTION

SCLC is a highly aggressive thoracic malignancy with extremely poor prognosis. Liver metastasis is a well-documented poor prognostic factor for SCLC patients. Gut microbiota plays a key regulatory role in tumorigenesis, metastatic progression and treatment response across multiple cancers. The composition and structural features of gut microbiota in SCLC patients with liver metastasis remain unclear.

METHODS

- Study cohort: 34 treatment-naïve SCLC patients were enrolled, including 12 patients with liver metastasis (SLM group) and 22 patients without liver metastasis (SN group).
- Sequencing: Fecal samples were collected and analyzed by 16S rRNA gene sequencing for gut microbiota profiling.
- Analysis: α -diversity, β -diversity, taxonomic composition analysis and LEfSe differential analysis (LDA threshold > 2) were performed.

DISCUSSION AND CONCLUSION

Newly diagnosed SCLC patients with liver metastasis present significant gut microbiota dysbiosis, manifested as reduced bacterial diversity, enrichment of opportunistic pathogens and depletion of beneficial symbiotic bacteria. This study firstly identified specific gut microbiota signatures associated with SCLC liver metastasis, which can provide novel non-invasive biomarkers for SCLC liver metastasis risk prediction, and offer new insights into the role of gut microbiota in SCLC progression.

REFERENCES & ACKNOWLEDGEMENTS

References
[1] T. Hakozaki et al., "The gut microbiome associates with immune checkpoint inhibition outcomes in patients with advanced non-small cell lung cancer," *Cancer Immunol. Res.*, vol. 8, no. 10, pp. 1243–1250, Oct. 2020, doi: 10.1158/2326-6066.CIR-20-0196.
[2] C. Li, C. Cai, C. Wang, X. Chen, B. Zhang, and Z. Huang, "Gut microbiota-mediated gut-liver axis: a breakthrough point for understanding and treating liver cancer," *Clin. Mol. Hepatol.*, vol. 31, no. 2, pp. 350–381, Apr. 2025, doi: 10.3350/cmh.2024.0857.
[3] Z. Deng et al., "Dysregulation of gut microbiota stimulates NETs-driven HCC intrahepatic metastasis: therapeutic implications of healthy faecal microbiota transplantation," *Gut Microbes*, vol. 17, no. 1, p. 2476561, Dec. 2025, doi: 10.1080/19490976.2025.2476561.

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RESULTS

- Microbial diversity
The SLM group had significantly reduced α -diversity (ACE index, $p = 0.028$) and distinct overall microbial community structure (PCoA, $R^2 = 0.04$, $P = 0.039$) versus the SN group.
- Taxonomic composition
Bacteroides was enriched in the SLM group, while Prevotella was more abundant in the SN group.
- LEfSe differential taxa
Beneficial Firmicutes were enriched in the SN group, whereas pro-inflammatory opportunistic pathogens were overrepresented in the SLM group.

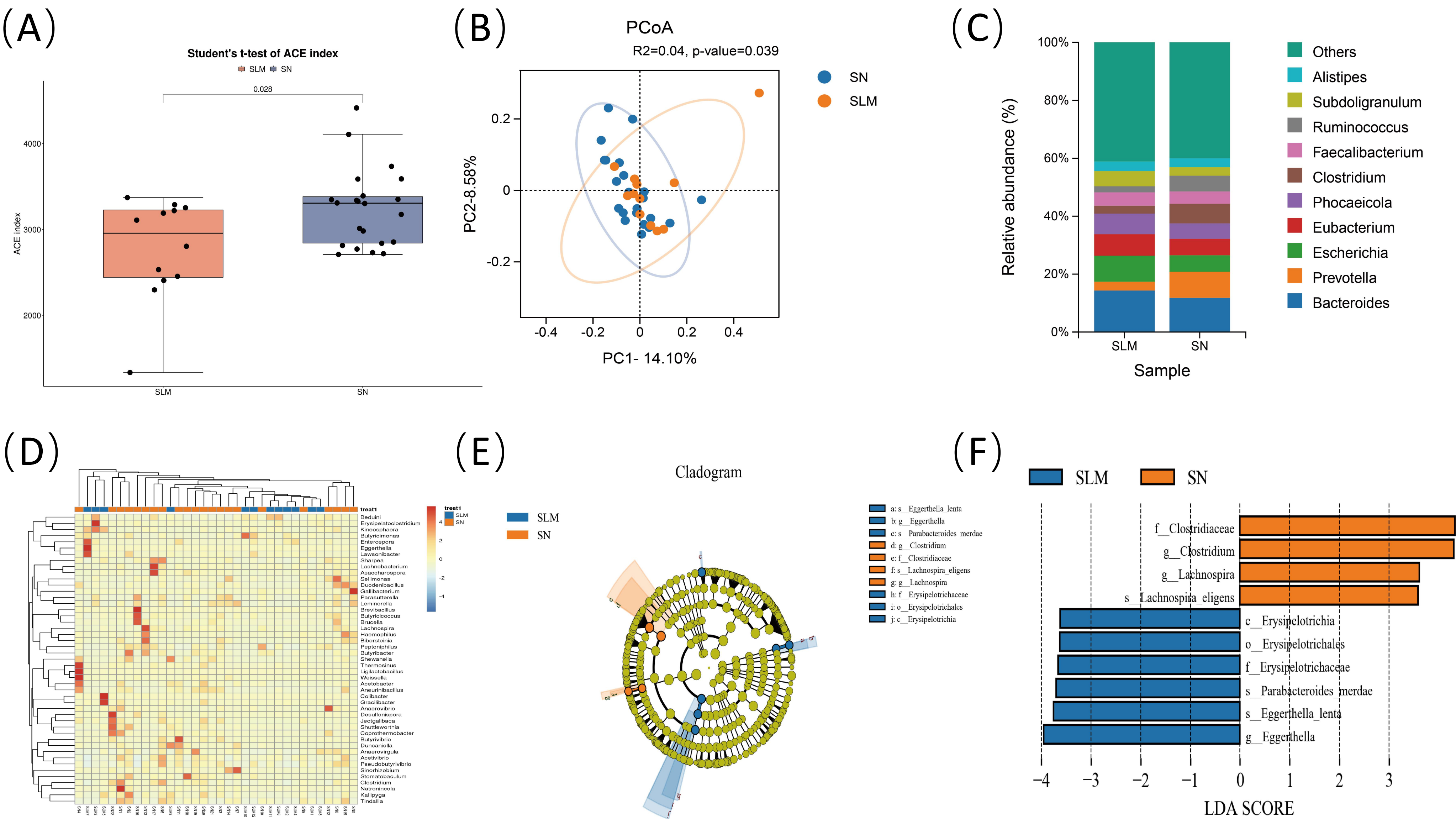


Figure 1. Gut microbiota characteristics in SCLC patients with or without liver metastasis. (A) ACE index for α -diversity. (B) PCoA plot for β -diversity. (C) Relative abundance of dominant genera. (D) Species abundance heatmap. (E) LEfSe cladogram. (F) LDA scores of differential taxa.