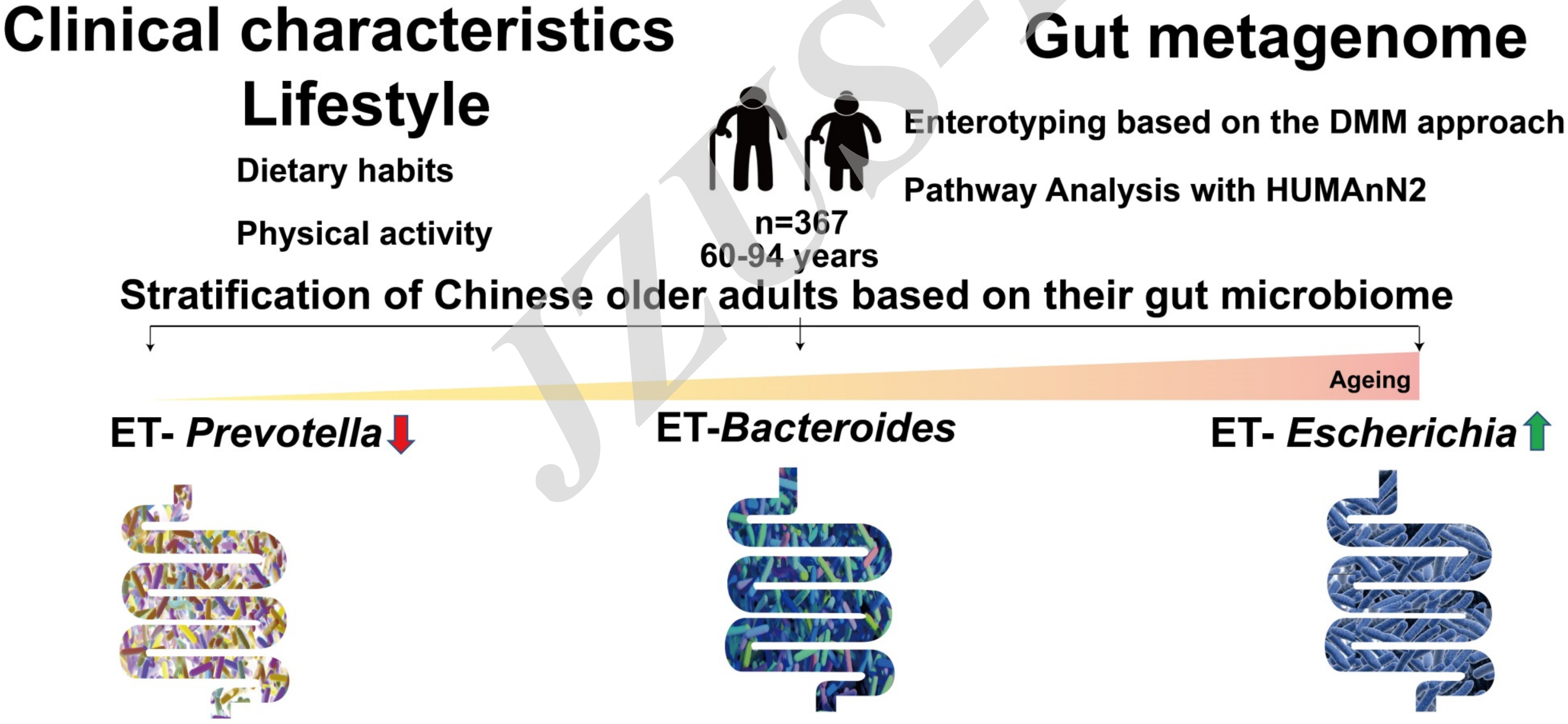
Cite this as: Jinyou LI, Yue WU, Yichen YANG, Lufang CHEN, Caihong HE, Shixian ZHOU, Shunmei HUANG, Xia ZHANG, Yuming WANG, Qifeng GUI, Haifeng LU, Qin ZHANG, Yunmei YANG, 2025. Metagenomics reveals an increased proportion of an *Escherichia coli*-dominated enterotype in elderly Chinese people. *J Zhejiang Univ-Sci B (Biomed & Biotechnol)*, 26(5):477-492. http://doi.org/10.1631/jzus.B2400341

Metagenomics reveals an increased proportion of an *Escherichia coli*-dominated enterotype in elderly Chinese people

Key words: Gut microbiome; Aging; Elderly population; *Escherichia*-dominated enterotype; Enterotype; *Escherichia coli*

Research Summary

This paper claims to identify a novel enterotype dominated by *E. coli*, that shows a strong association with older age in a geographically homogeneous cohort.



Clinical characteristics

Lifestyle

Dietary habits

Physical activity

n=367
60-94 years

Gut metagenome

Enterotyping based on the DMM approach

Pathway Analysis with HUMAnN2

Stratification of Chinese older adults based on their gut microbiome

Ageing

ET- *Prevotella*↓

ET-*Bacteroides*

ET- *Escherichia*↑

Innovation points

- Redundancy analyses to identify factors correlated to the enterotypes are reported to indicate that age explains more of the variance in enterotype than previously identified factors such as diet and lifestyle habits or inflammatory factors.

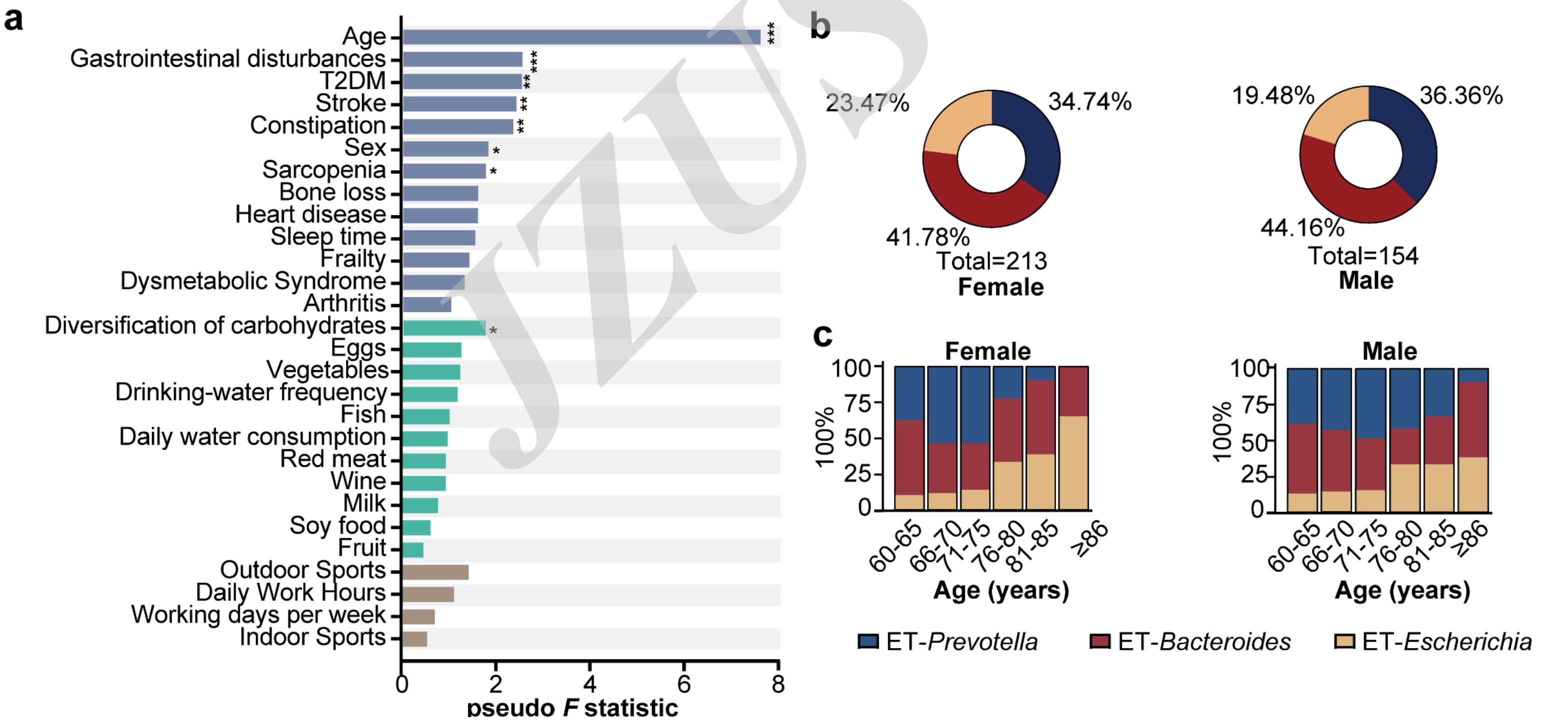


Figure 2

Innovation points

- Functional gene analyses are also performed to support this model. Functional variations across enterotypes are associated with age.

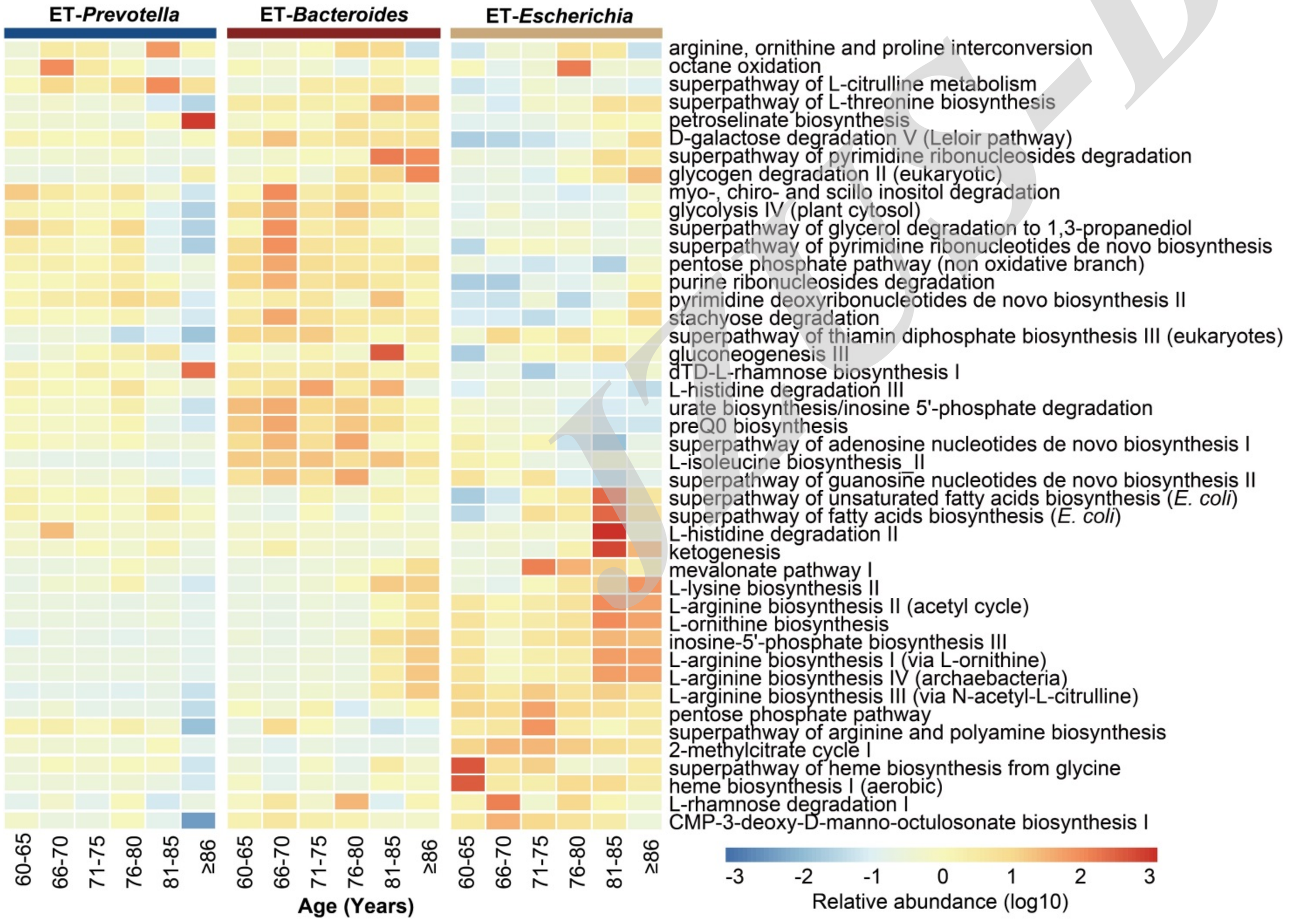


Figure 3