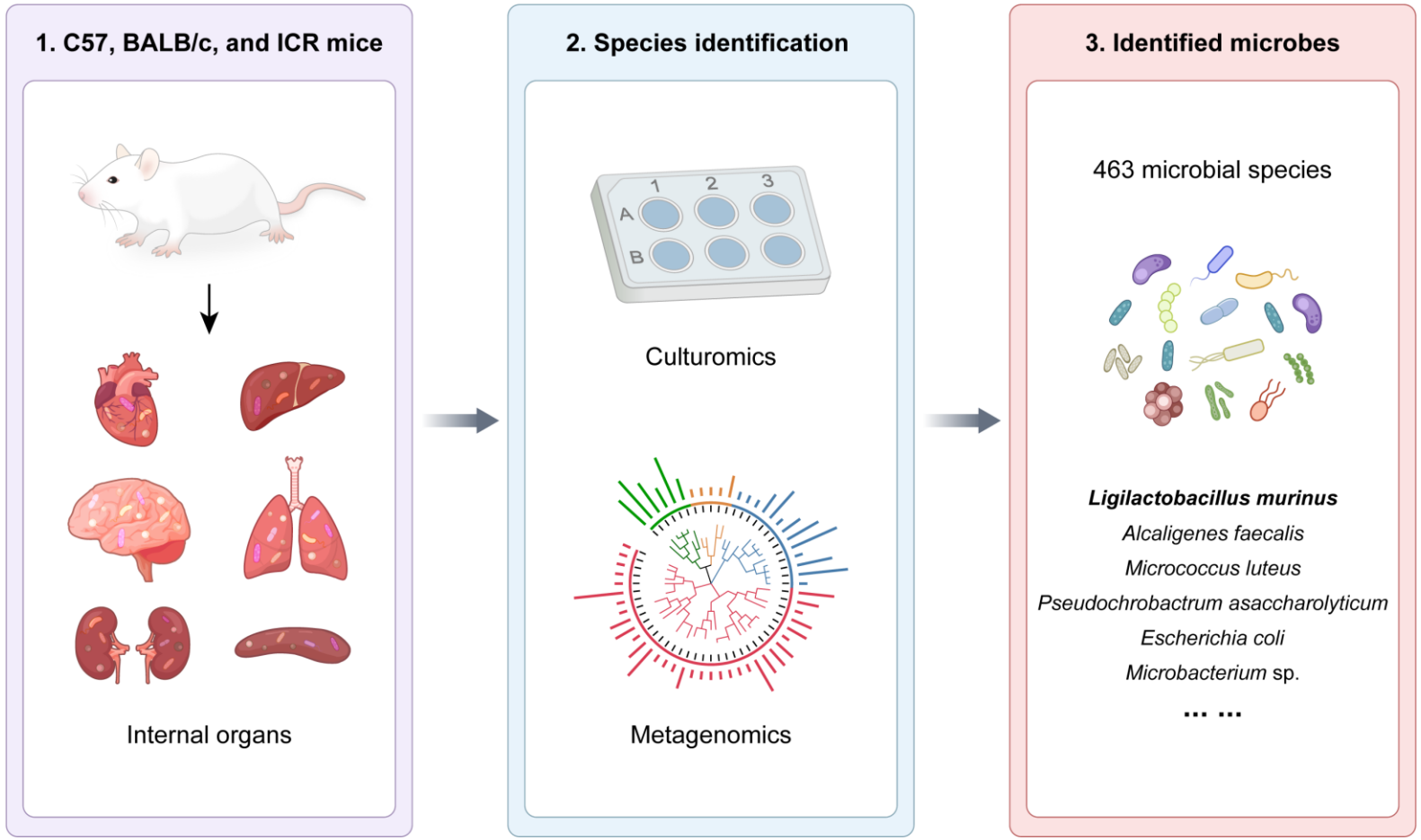
Characterizing the Microbiome of 'Sterile' Organs in Experimental Mice and Evidence of Translocation of Bacteria from the Gut to Other Internal Organs

Ming Xu[1], Shuyun Guan[1], Chaoran Zhong[1], Mingyang Ma[1], Li Tao[1], and Guanghua Huang[1,2]

[1]Shanghai Institute of Infectious Disease and Biosecurity, State Key Laboratory of Genetics and Development of Complex Phenotypes, School of Life Sciences, Department of Laboratory Medicine, Department of Infectious Diseases, Huashan Hospital, Fudan University, Shanghai, 200438, China
[2] College of Pharmaceutical Sciences, Southwest University, Chongqing 400716, China

Ming Xu, Shuyun Guan, Chaoran Zhong, Mingyang Ma, Li Tao, and Guanghua Huang. 2025. Characterizing the Microbiome of “Sterile” Organs in Experimental Mice and Evidence of Translocation of Bacteria from the Gut to Other Internal Organs. ***iMeta*** 4: e70081. https://doi.org/10.1002/imt2.70081.

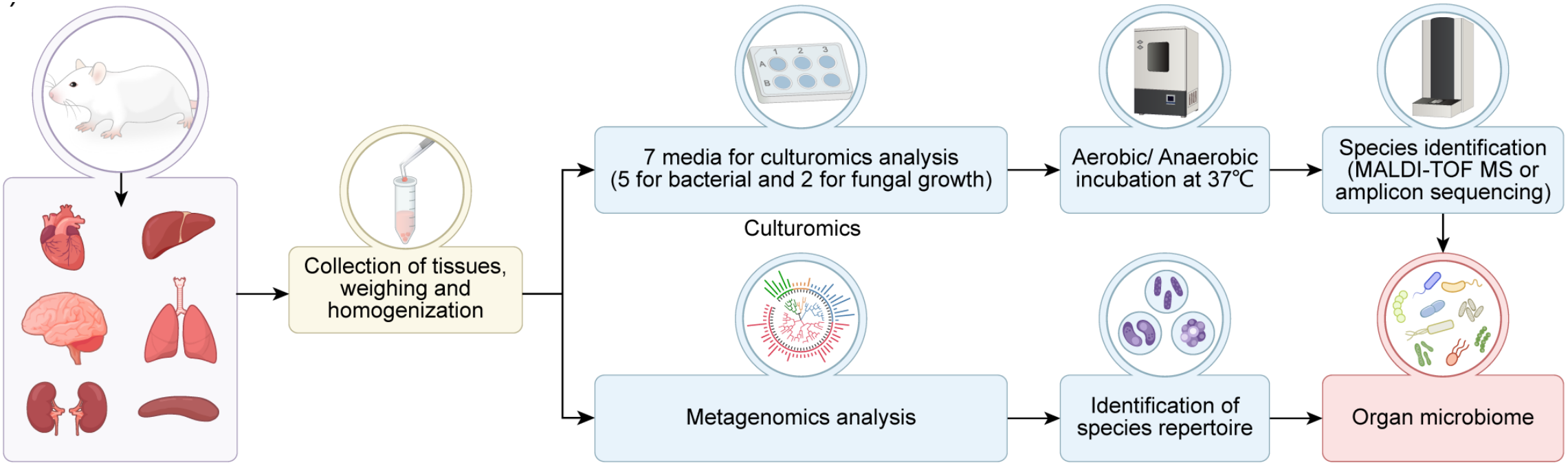
Highlights



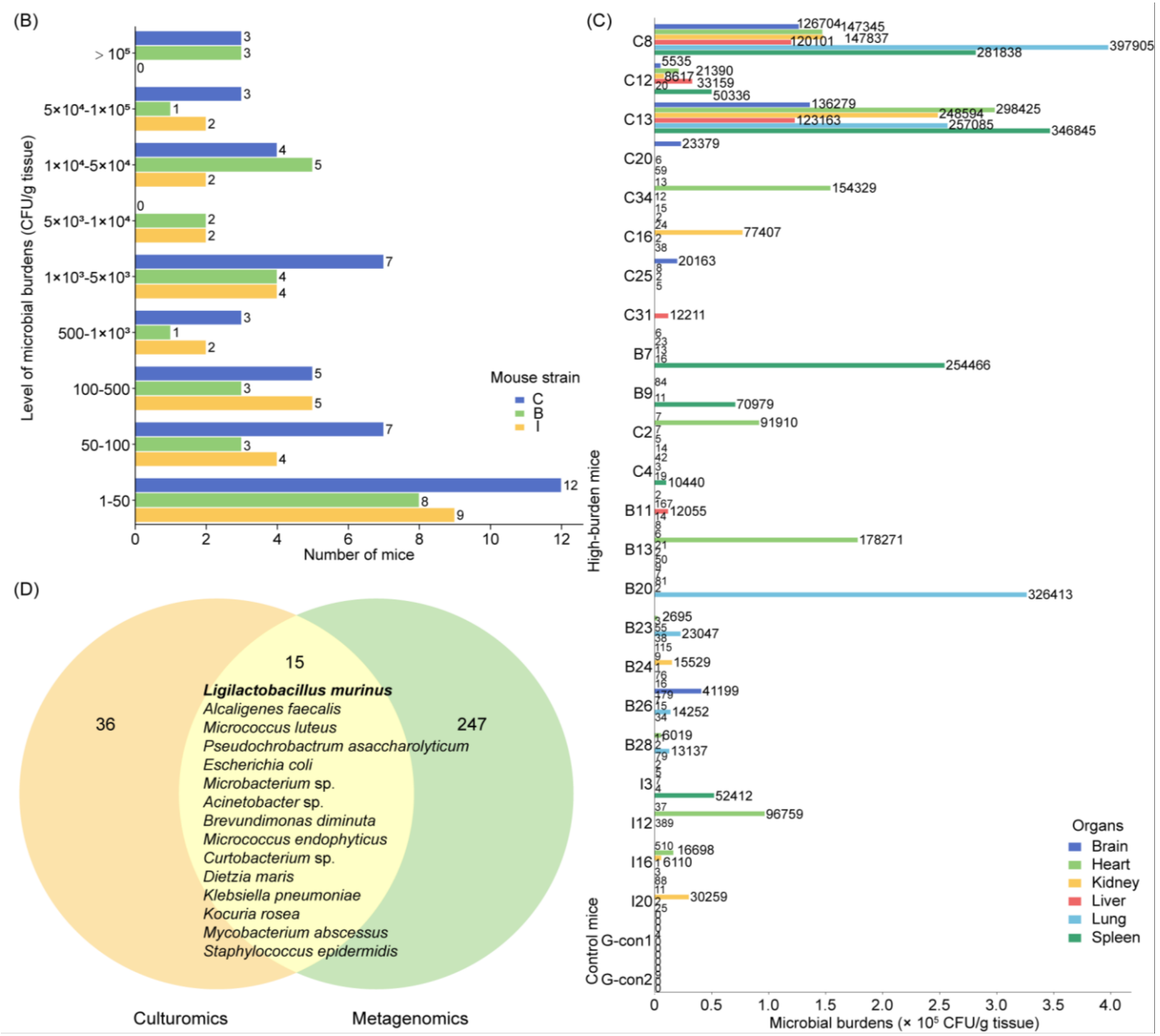
- More than 20% of the commercial lab mice tested exhibit a high microbial burden in the internal organs, contradicting traditional sterility assumptions.
- *Ligilactobacillus murinus* exhibited a high relative abundance in both culturomics and metagenomics analyses.
- Microorganisms found in the “sterile” tissues are associated with the gut microbiota.
- Non-pathogenic microbes in the "sterile" tissues would introduce uncontrolled variables in rodent-based research, impacting reproducibility.

Concept and research design

◆ **Concept and research design for microbiome analysis of experimental mouse organs.**



Results



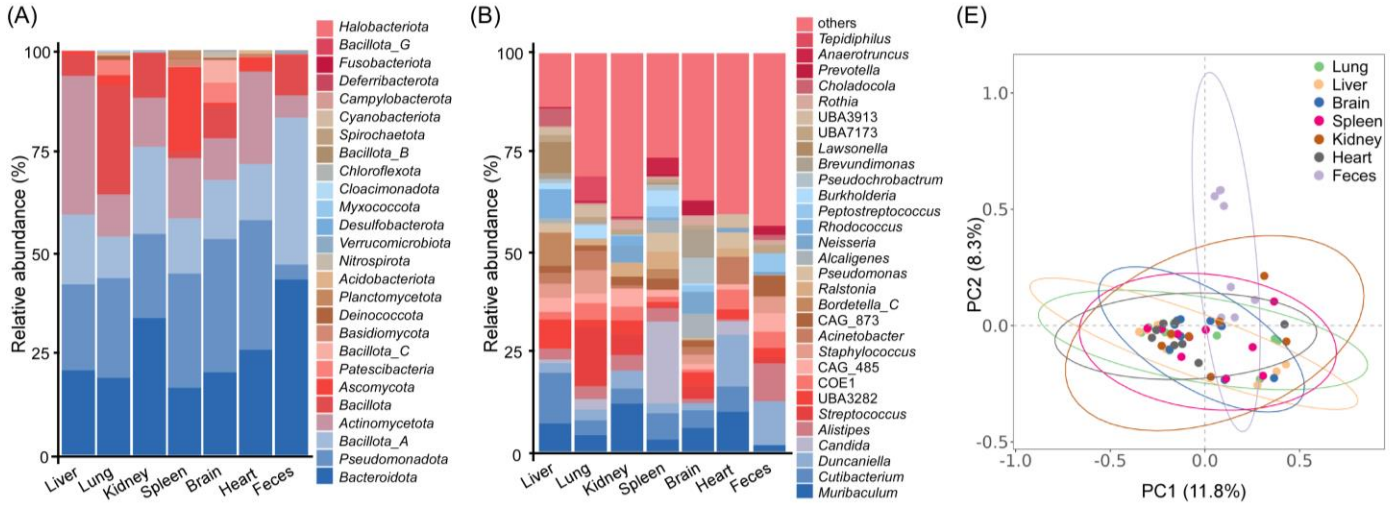
- **The presence of viable microbes in the organs traditionally considered "sterile" in experimental mice.**

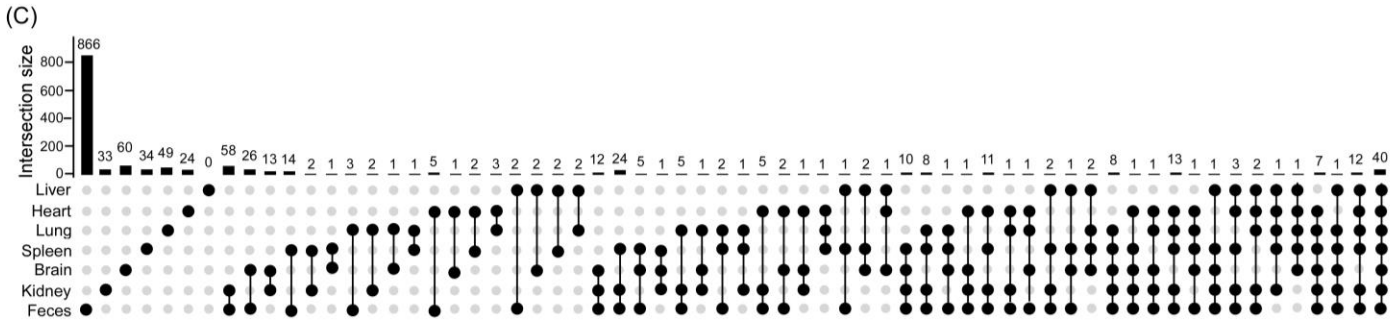
- Overall, 23 mice (22.1%) showed high microbial burden (> 1 × 10^4 CFU/g tissue) in at least one organ, while 42 mice (40.4%) exceeded 1 × 10^3 CFU/g tissue in at least one organ.

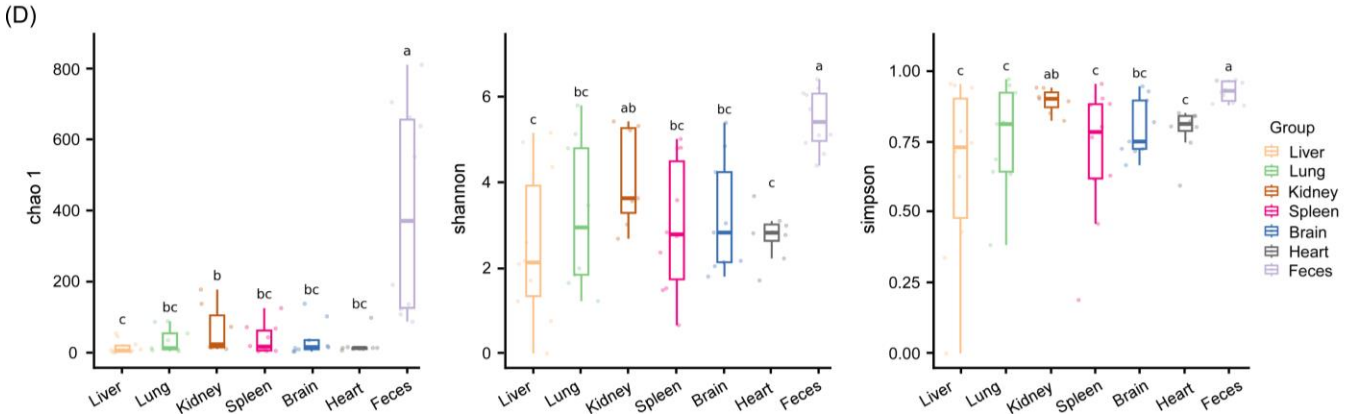
- Fifteen overlapping species were detected by both metagenomics and culturomics approaches.

- *L. murinus* exhibited a high relative abundance.

Results







◆ **A potential link between the fecal and organ microbiomes.**

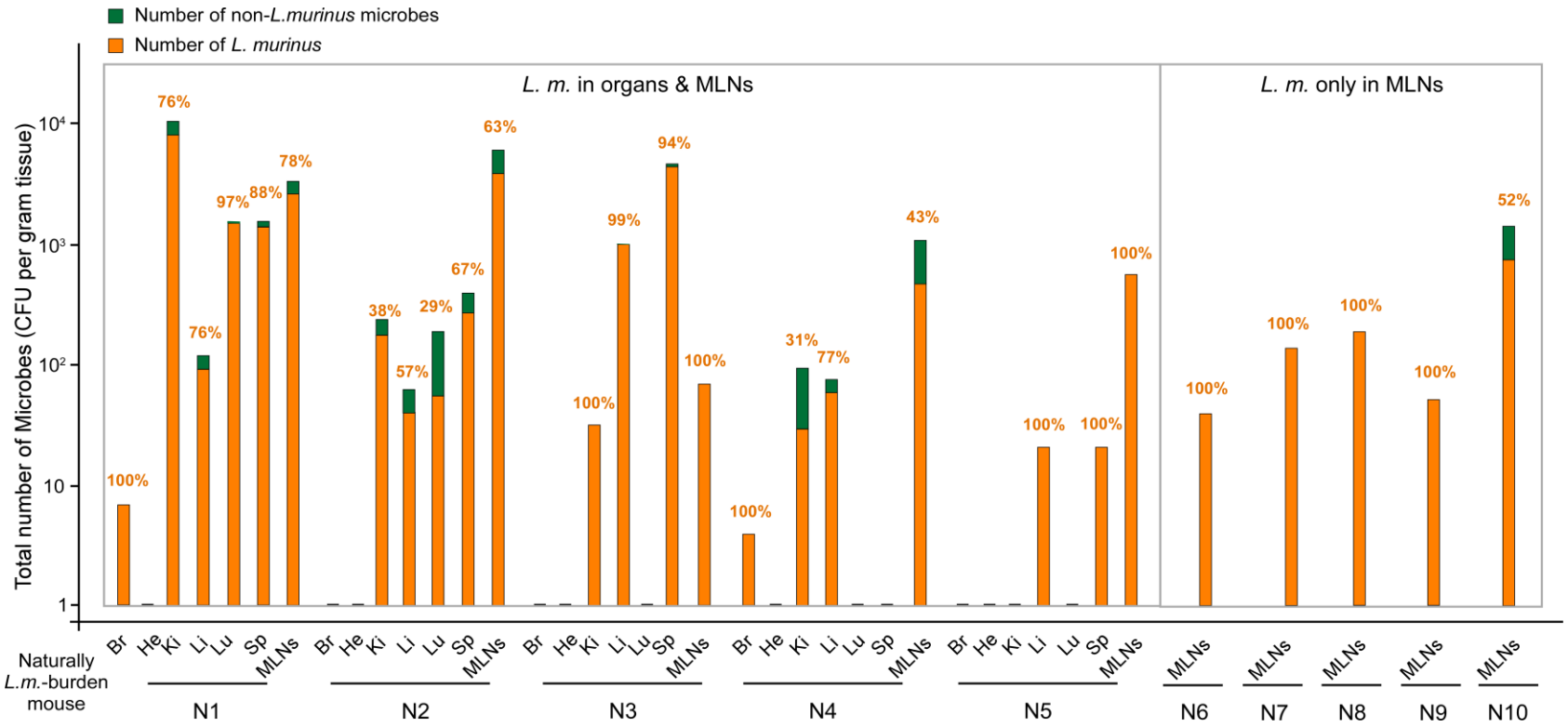
❑ Compared to the fecal microbiomes, the microbial profiles of the “sterile” organs exhibit more similarity.

❑ Most of the intratissue microbial species could also be found in the fecal microbiota, suggesting a potential link to the gut microbiota.

❑ *L. murinus* exhibited a high abundance in both organs and feces.

Results

◆ The distribution of *L. murinus* in the mouse organs and MLNs.

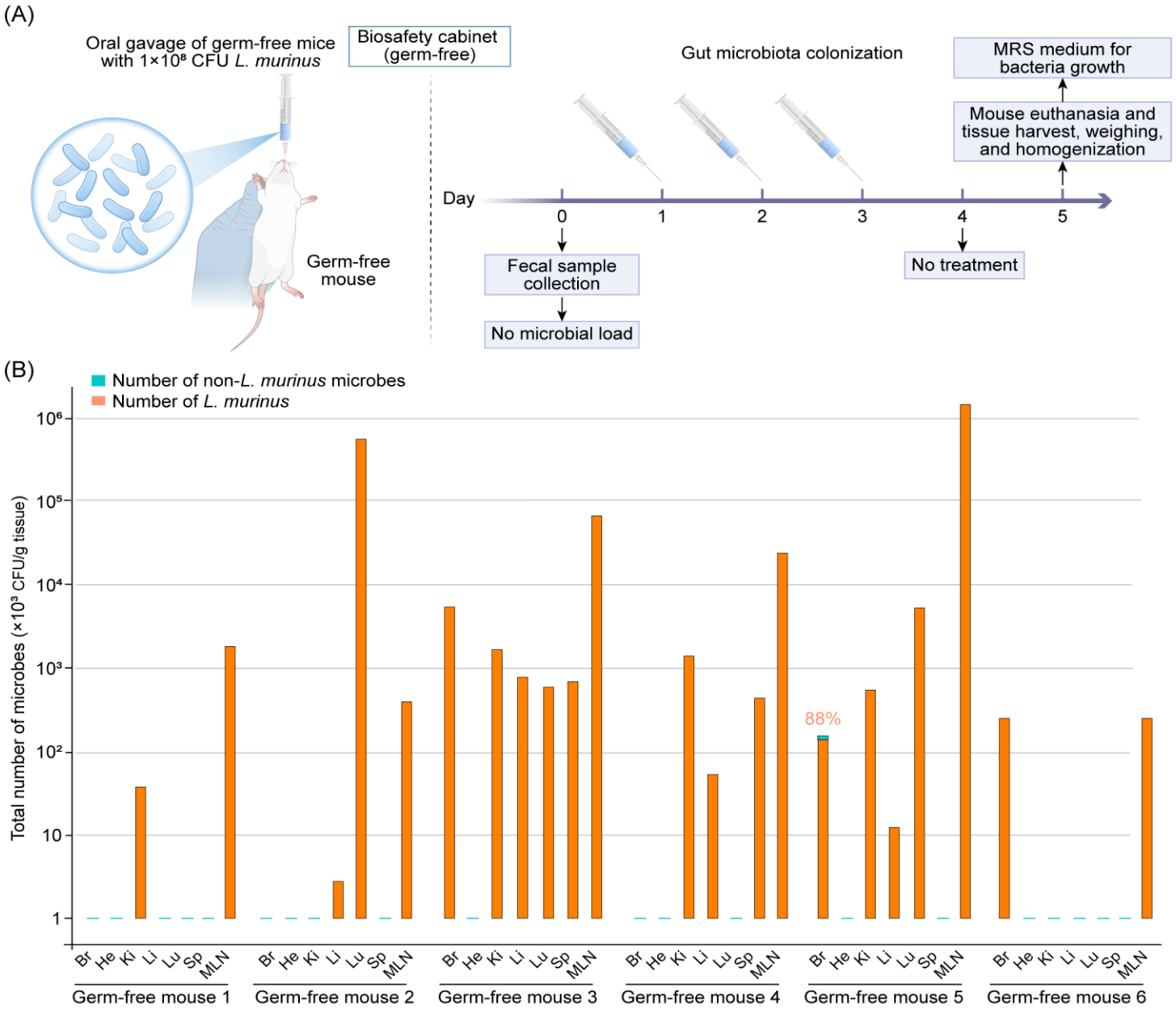


❑ *L. murinus* was detected in MLNs of all the ten mice, in the brain and lung tissues of two mice, in the kidney and spleen of four mice, and in the liver of five mice.

❑ In eight out of ten mice, the abundance of *L. murinus* in the MLNs was higher than that in the other organs.

❑ *L. murinus* could translocate from the gut microbiota to MLNs, with subsequent dissemination to historically “sterile” organs.

Results



◆ **Evidence of translocation of bacterium *L. murinus* cells from the gut to the "sterile" organs in a germ-free mouse model.**

❑ *L. murinus* was detected in at least two organs and in MLNs of all the tested mice.

❑ In five out of six mice, the abundance of *L. murinus* in the MLNs was higher than that in the other "sterile" organs.

❑ *L. murinus* was the sole bacterium identified in nearly all the organs.

Summary

- Our findings reveal the widespread presence of living microbiomes in the traditionally considered “sterile” organs of laboratory mice with different genetic backgrounds.

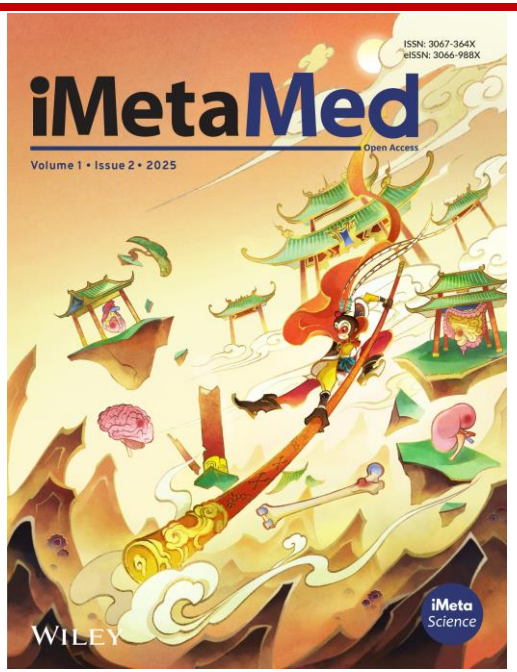
- Microorganisms found in the “sterile” tissues are associated with the gut microbiota.

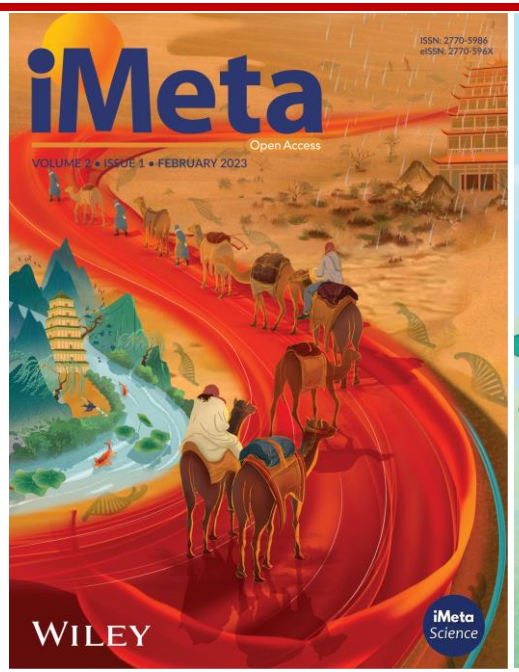
- The presence and variation of microbes in different mouse individuals may exert physiological effects and confound experimental outcomes, raising a caveat about the interpretation of results.

Ming Xu, Shuyun Guan, Chaoran Zhong, Mingyang Ma, Li Tao, and Guanghua Huang. 2025. Characterizing the Microbiome of “Sterile” Organs in Experimental Mice and Evidence of Translocation of Bacteria from the Gut to Other Internal Organs. ***iMeta*** 4: e70081. https://doi.org/10.1002/imt2.70081.

iMeta: To be top journals in biology and medicine

WILEY





"***iMeta***" launched in 2022 by iMeta Science Society, impact factor (IF) **33.2**, ranking top 65/22249 in world and 2/161 in the microbiology. It aims to publish innovative and high-quality papers with broad and diverse audiences. **Its scope is similar to *Cell*, *Nature Biotechnology/Methods/Microbiology/Medicine/Food***. Its unique features include video abstract, bilingual publication, and social media with 600,000 followers. Indexed by **SCIE/ESI**, **PubMed**, **Google Scholar** etc.

"***iMetaOmics***" launched in 2024, with a **target IF>10, and its scope is similar to *Nature Communications*, *Cell Reports***, *Microbiome, ISME J, Nucleic Acids Research, Briefings in Bioinformatics,* etc.

"***iMetaMed***" launched in 2025, with a **target IF>15, similar to *Med, Cell Reports Medicine*, *eBioMedicine, eClinicalMedicine*** etc.

Society: http://www.imeta.science
Publisher: https://wileyonlinelibrary.com/journal/imeta
iMeta: https://wiley.atyponrex.com/journal/IMT2
Submission: iMetaOmics: https://wiley.atyponrex.com/journal/IMO2
iMetaMed: https://wiley.atyponrex.com/journal/IMM3

iMetaScience
iMetaScience

office@imeta.science
imetaomics@imeta.science

Promotion Video

Update 2025/7/6