



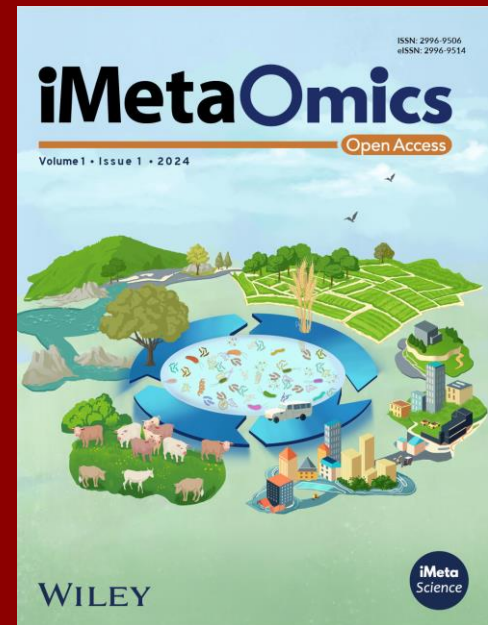
主要鞘翅目储粮害虫中微生物组的宿主特异性与确定性组装

Abrar Muhammad^{1#}, 沈晓强^{1#}, 陈立超¹, 郭恩惠¹,
张花瑞¹, 雷晓雨¹, 孙超², 吕建华³, 邵勇奇^{1*}

¹马普伙伴小组, 浙江大学动物科学学院

²浙江大学农生环测试中心

³河南工业大学粮油食品学院



Abrar Muhammad, Xiaoqiang Shen, Lichao Chen, Enhui Guo, Huarui Zhang, Xiaoyu Lei, Chao Sun, et al. 2026.

Host-specific and deterministic microbiome assembly in major coleopteran stored-grain pests.

iMetaOmics 3: e70109. <https://doi.org/10.1002/imo2.70109>



研究背景

Economic impact

Coleopteran stored-grain pests cause substantial post-harvest losses worldwide.



Role of microbiomes

Microbiomes contribute to host nutrition, digestion, detoxification, immunity and environmental adaptation.



Current knowledge gaps

- Most studies rely on DNA-based approaches that profile total microbiota only.
- The metabolically active fraction remains poorly understood.
- The ecological processes shaping microbiome assembly in stored-grain pests are largely unknown.

Why it matters

Answering these questions will deepen our understanding of insect-microbe interactions and support novel strategies for sustainable pest control.



1 Are microbiomes host-specific despite a common diet?

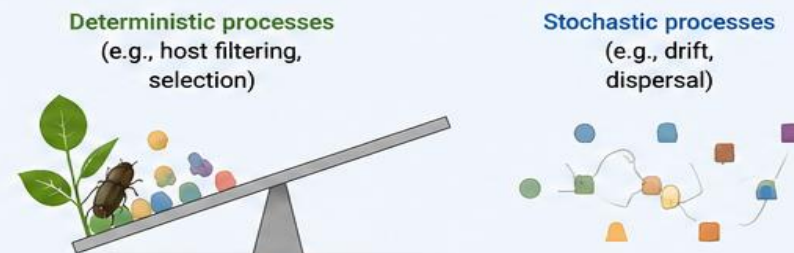


Shared wheat flour substrate

2 How do metabolically active communities differ from total communities?



3 Are communities shaped by deterministic or stochastic processes?



Study aim

To characterize and compare the total and metabolically active bacterial and fungal microbiomes of major stored-grain pests and their substrate, and to elucidate the ecological processes driving microbiome assembly.



Our approach

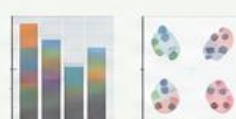
Five major coleopteran pests + substrate



DNA- and RNA-based amplicon sequencing



Diversity and community analyses



Core microbiota identification

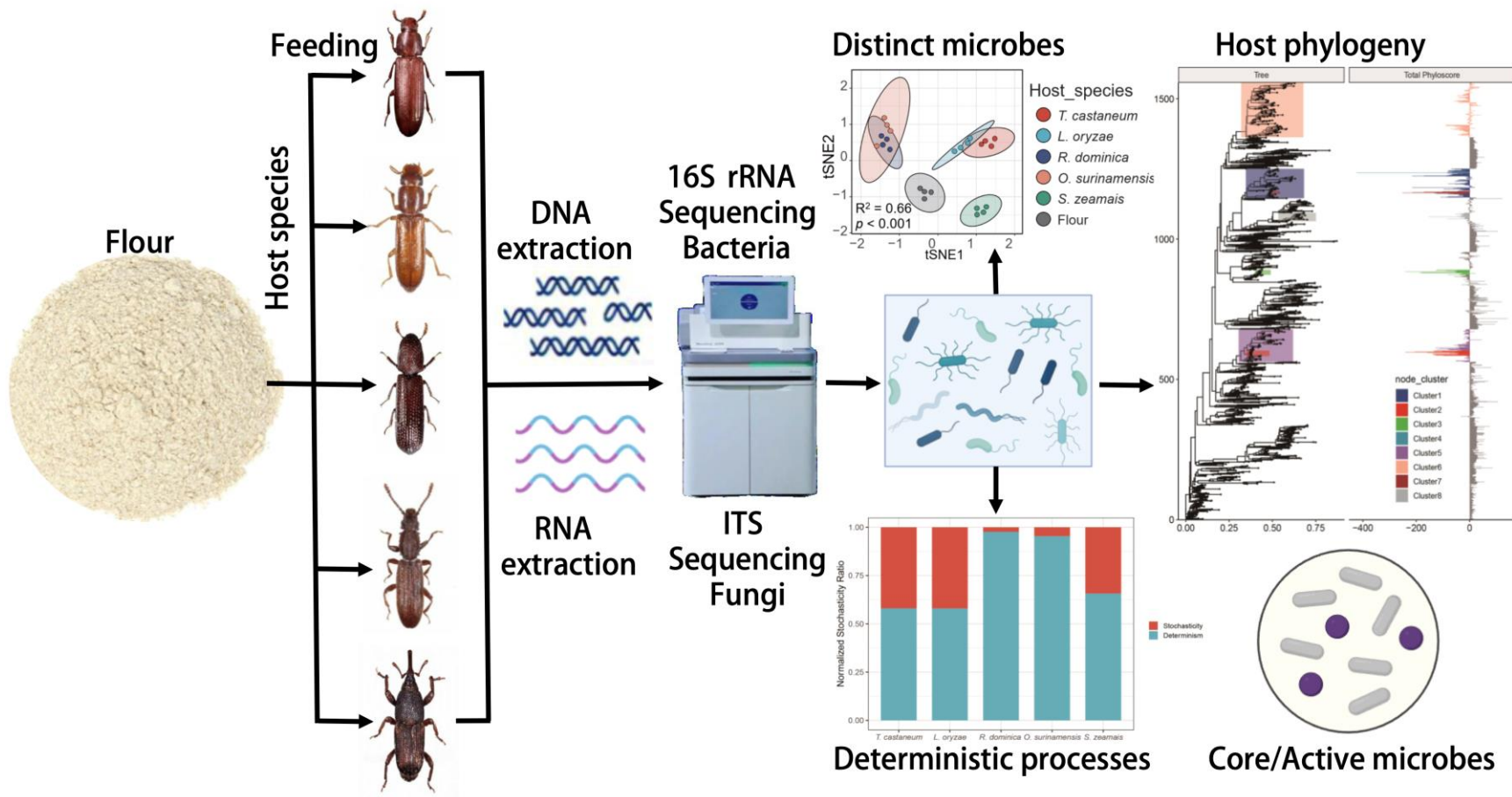


Ecological assembly frameworks





研究亮点

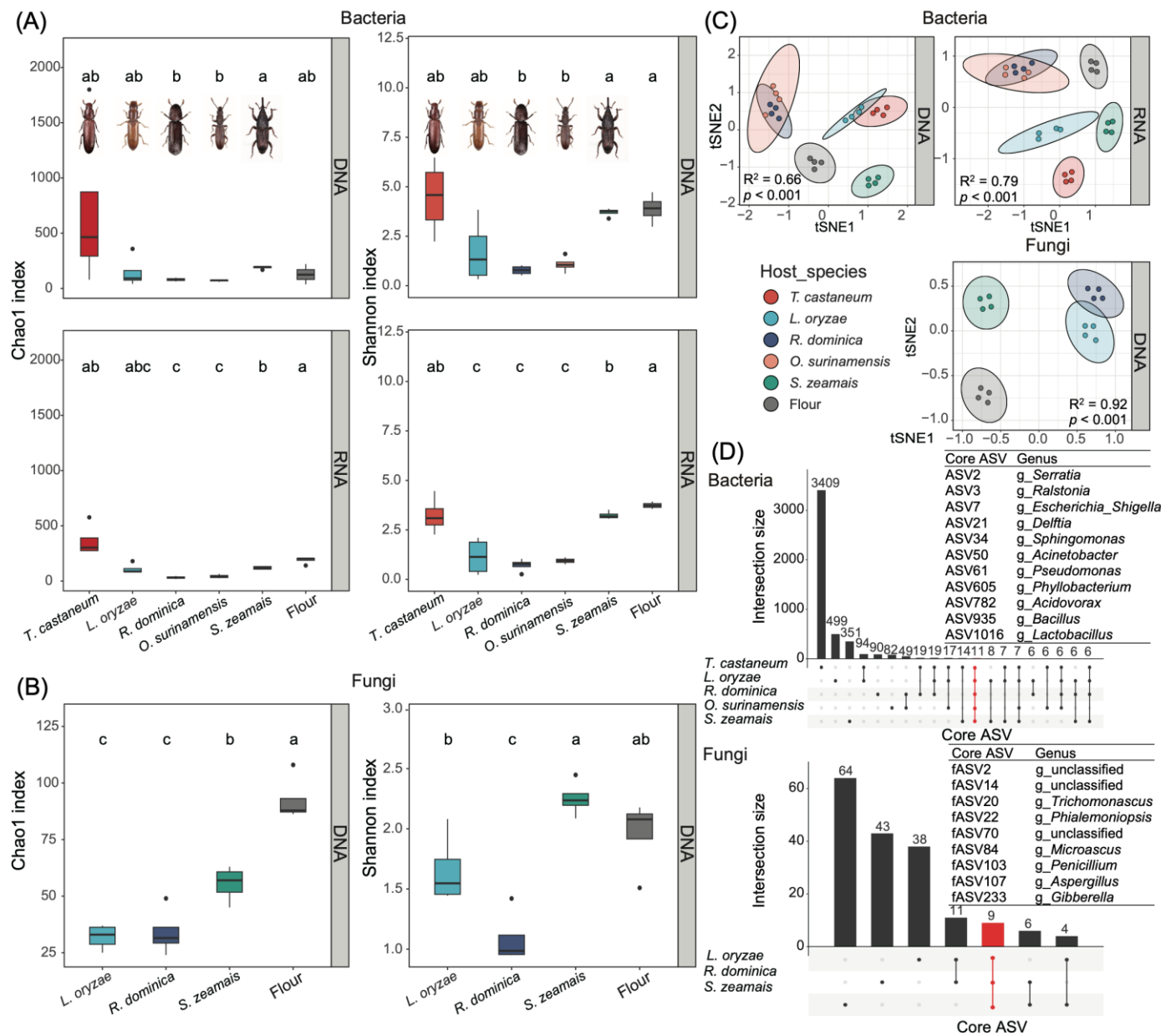


- 研究了五种鞘翅目储粮害虫
- DNA/RNA 分析：总体微生物组与活跃微生物组
- 宿主特异性微生物群落
- 保守的核心和活跃细菌类群
- 确定性过程主导微生物组组装
- 宿主系统发育不是主要驱动因素

DNA/RNA测序 | 活跃微生物类群 | 核心类群 | 宿主特异性 | 确定性组装



宿主特异的多样性与核心微生物联盟

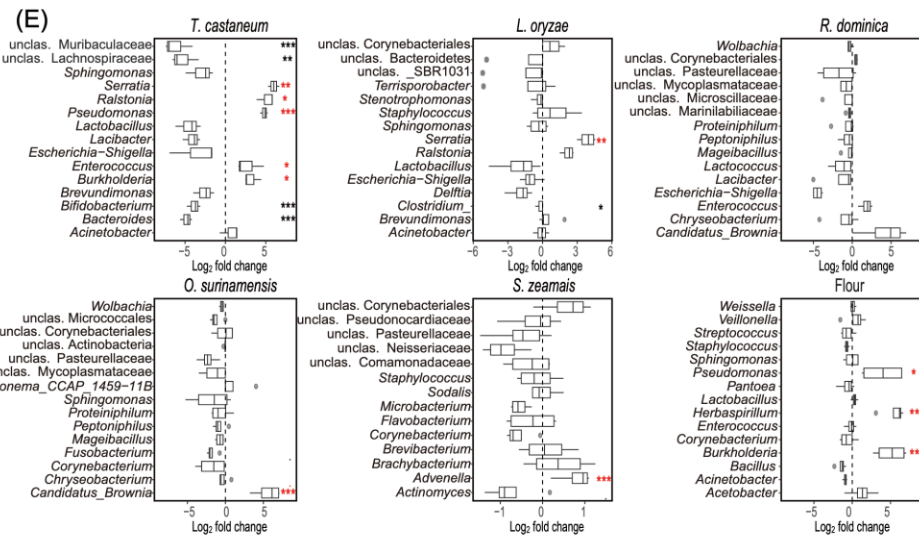
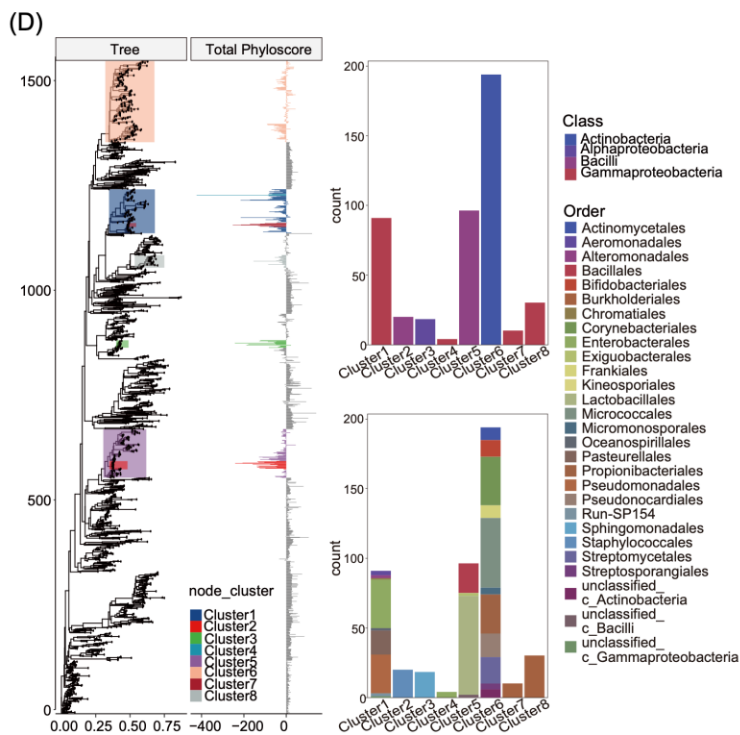
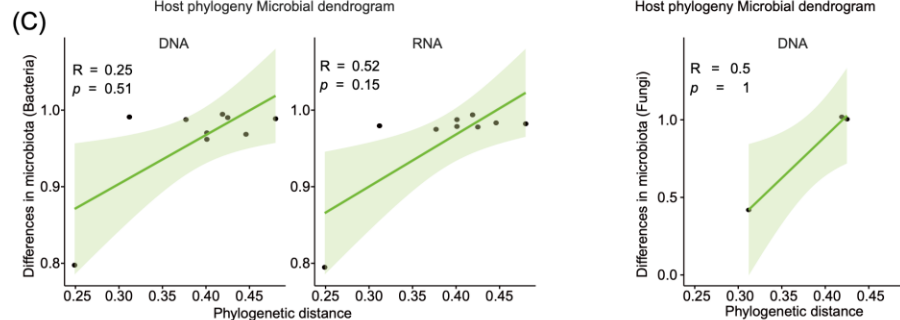
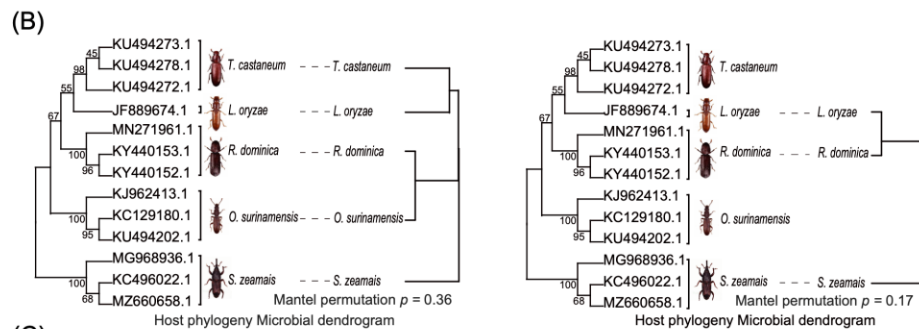
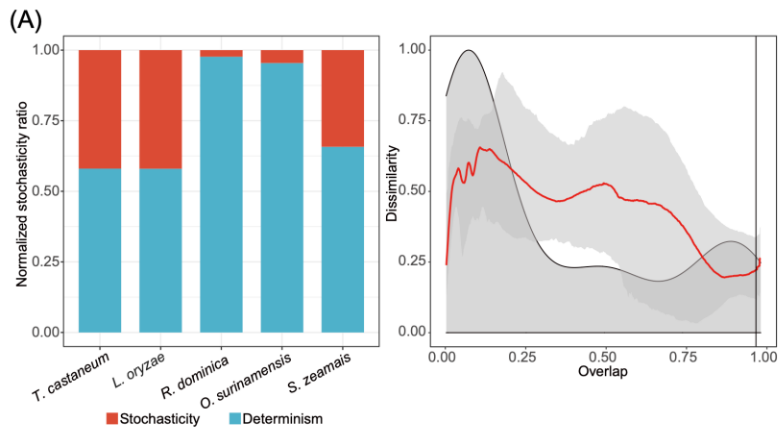


- ❑ 宿主特异的细菌和真菌多样性
- ❑ DNA/RNA分析揭示总体微生物群落与活跃微生物群落
- ❑ 面粉微生物组与害虫微生物组明显分离
- ❑ 保守核心类群：11个细菌ASV和9个真菌ASV
- ❑ 共同食物来源 ≠ 相同微生物组

❖ 尽管共享相同的面粉基质，储粮害虫仍维持宿主特异性微生物组



生态组装、宿主系统发育、保守分支与活跃细菌类群



- ❑ 确定性过程的作用强于随机性过程
- ❑ 谷蠹和锯谷盗中确定性组装作用最强
- ❑ 宿主系统发育与微生物组结构之间无显著相关性
- ❑ 鉴定出8个保守的细菌分支
- ❑ RNA分析揭示潜在的活跃细菌类群
- ❑ 保守且活跃的细菌类群可能有助于宿主适应

确定性生态过滤，而非单纯的宿主系统发育，驱动了储粮害虫微生物组的组装



总结

- 宿主特异性，而非共同食物来源，塑造了储粮害虫微生物组组成
- DNA/RNA测序区分了总体微生物群落和代谢活跃微生物群落
- 本研究鉴定到由11个细菌ASV和9个真菌ASV组成的保守核心微生物群
- 宿主系统发育与微生物组结构之间未检测到显著相关性
- 确定性过程在所有宿主物种的微生物组组装中都占主导地位
- 8个保守细菌分支与代谢活跃类群存在重叠
- 保守活跃微生物可能是未来可持续害虫管理的潜在靶标

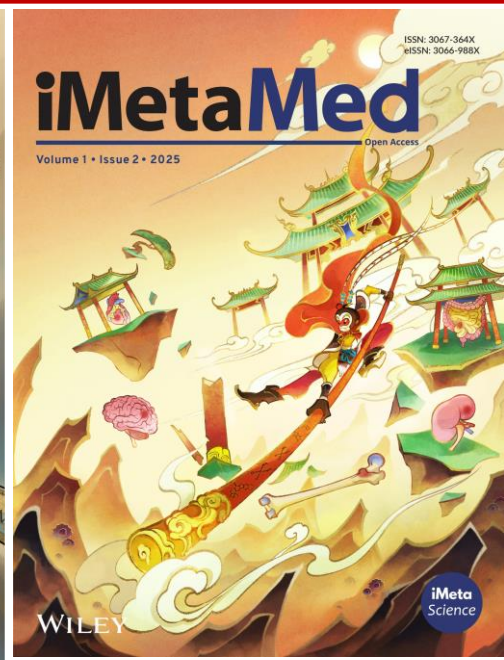
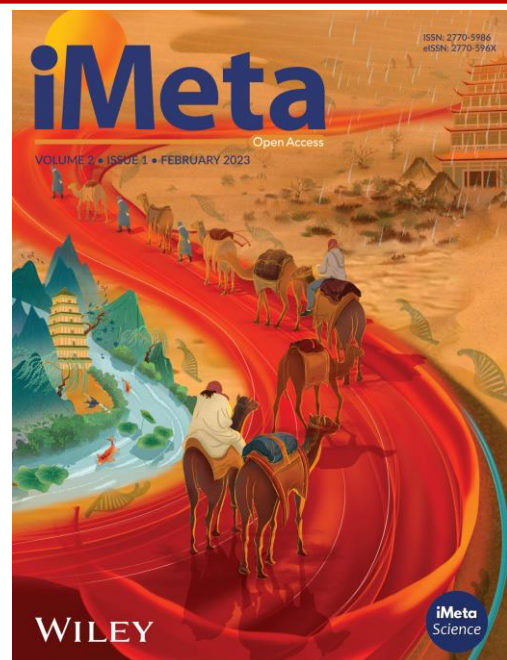
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