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

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Introduction

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.

Nutrition & digestion

Immunity

Detoxification

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

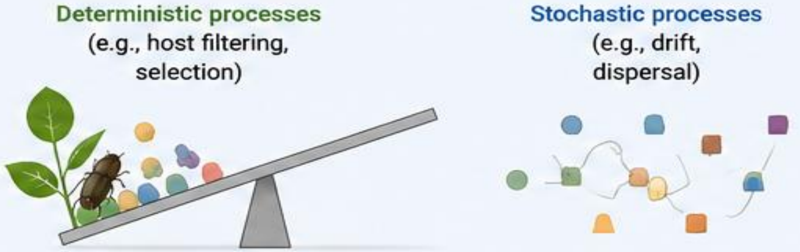
Answering these questions will deepen our understanding of insect–microbe interactions and support novel strategies for sustainable pest control.

1 Are microbiomes host-specific despite a common diet?

Shared wheat flour substrate

2 How do metabolically active communities differ from total communities?

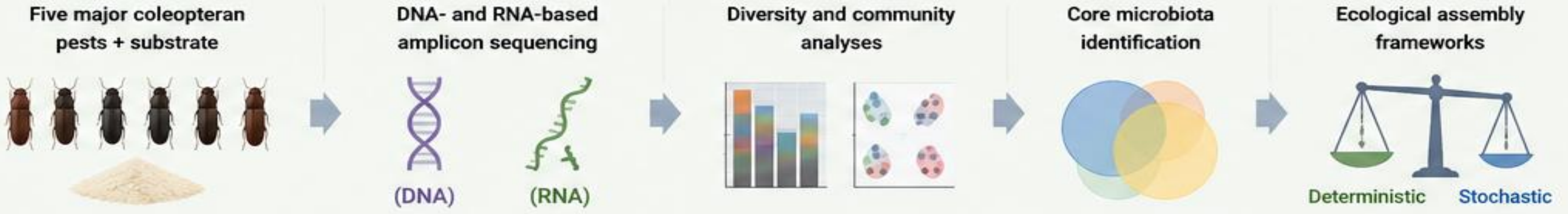
3 Are communities shaped by deterministic or stochastic processes?



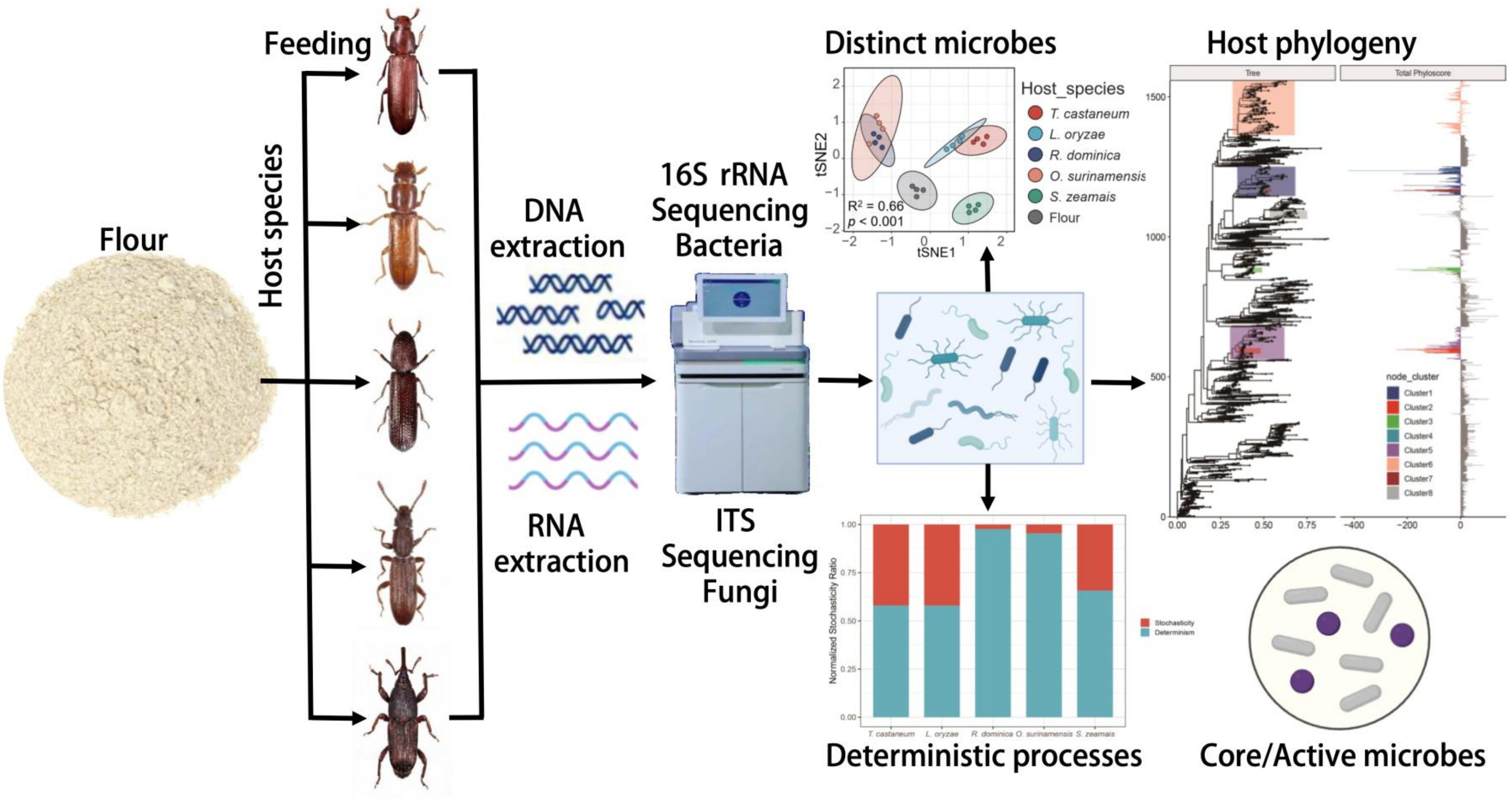
Study aim

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



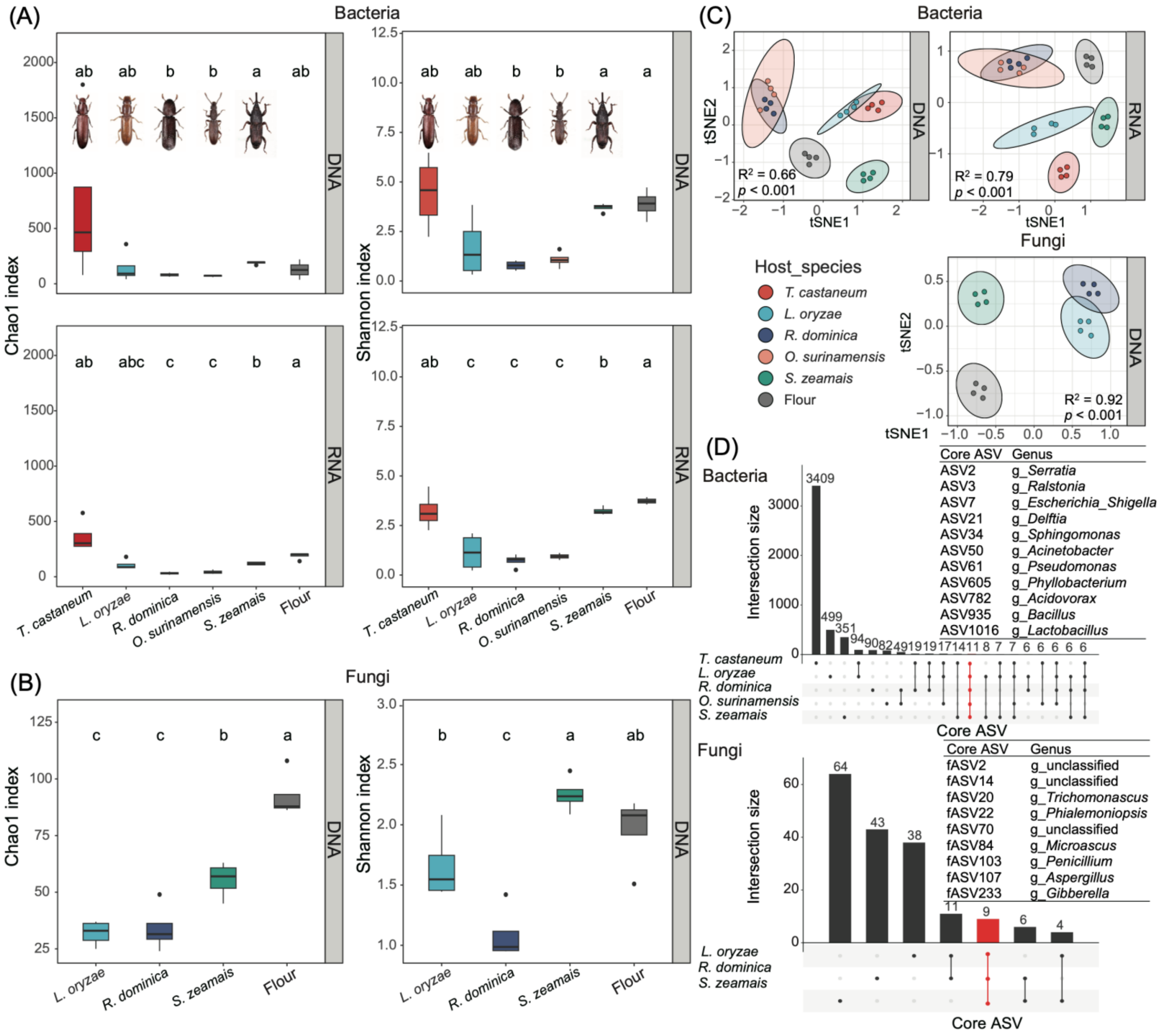
Highlights



- Five major stored-grain beetle pests
- DNA/RNA profiling: total vs. active microbiomes
- Host-specific microbial communities
- Conserved core and active bacterial taxa
- Deterministic processes dominate assembly
- Host phylogeny was not the main driver

DNA/RNA sequencing | Active microbiome | Core taxa | Host specificity | Deterministic assembly

Host-specific diversity and core consortia



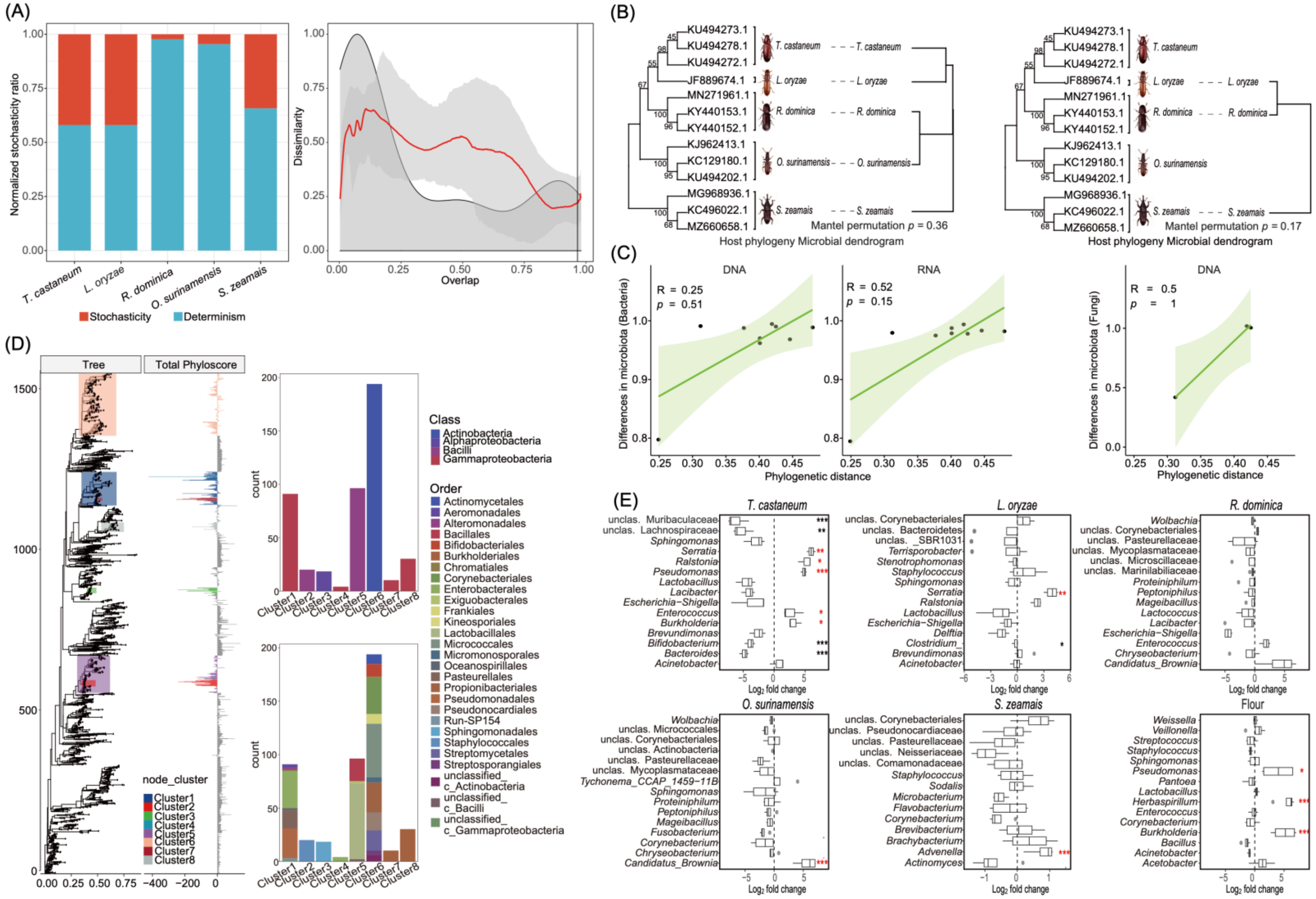
Core ASV	Genus
ASV2	g_*Serratia*
ASV3	g_*Ralstonia*
ASV7	g_*Escherichia_Shigella*
ASV21	g_*Delftia*
ASV34	g_*Sphingomonas*
ASV50	g_*Acinetobacter*
ASV61	g_*Pseudomonas*
ASV605	g_*Phyllobacterium*
ASV782	g_*Acidovorax*
ASV935	g_*Bacillus*
ASV1016	g_*Lactobacillus*

Core ASV	Genus
fASV2	g_unclassified
fASV14	g_unclassified
fASV20	g_*Trichomonascus*
fASV22	g_*Phialemoniopsis*
fASV70	g_unclassified
fASV84	g_*Microascus*
fASV103	g_*Penicillium*
fASV107	g_*Aspergillus*
fASV233	g_*Gibberella*

- ☐ Host-specific bacterial and fungal diversity
- ☐ DNA/RNA profiles reveal total and active communities
- ☐ Flour microbiome separated from pest-associated microbiomes
- ☐ Conserved core: 11 bacterial ASVs and 9 fungal ASVs
- ☐ Common diet ≠ common microbiome

❖ **Stored-grain pests maintain host-specific microbiomes despite sharing the same wheat flour substrate.**

Ecological assembly, host phylogeny, conserved clades, and active bacterial taxa



- ❑ Deterministic processes outweighed stochasticity
- ❑ Strongest deterministic assembly in *R. dominica* and *O. surinamensis*
- ❑ Host phylogeny showed no significant microbiome correlation
- ❑ Eight conserved bacterial clades identified
- ❑ RNA profiles revealed putatively active bacterial taxa
- ❑ Conserved and active taxa may support host adaptation

Deterministic ecological filtering, rather than host phylogeny alone, drives microbiome assembly in stored-grain pests.

Summary

☐ **Host species**, rather than a shared **diet**, strongly structured microbiome composition.

☐ **DNA/RNA** sequencing distinguished total and **metabolically active** microbial communities.

☐ A conserved core microbiota comprising **11 bacterial** and **9 fungal ASVs** was identified.

☐ **No significant** relationship was detected between host **phylogeny and microbiome structure**.

☐ **Deterministic** processes dominated **microbiome assembly** across all host species.

☐ **Eight conserved** bacterial clades overlapped with **metabolically active** taxa.

☐ **Conserved active microbes represent potential targets for sustainable pest management**.

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