How do host selection and microbial species pools influence diazotrophic community assembly?

Do specific diazotrophic taxa play key roles in microbial networks and crop production?

Research Question & Hypotheses

What are the N metabolism pathways in phylloplane microbiomes?

Site and compartment are primary drivers of community assembly.

Keystone taxa (Azospirillum, Methylobacterium) identified.

Phylloplane microbiomes possess diverse N metabolism pathways (nitrate reduction, denitrification, DNRA).

Complete denitrification pathway found in Pseudomonas mendocina MAG.

Raw sequencing data: SRA - PRJNA784384 (nifH) and PRJNA679917 (metagenomics)

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Data Availability

Key Findings

Raw data and scripts: Figshare 🔗

