

Background and objectives

Soil microorganisms play critical roles in crop health and yield. Organic farming has been increasingly adopted as a sustainable alternative to conventional methods, and previous studies have shown differences in the soil microbiota between these farming systems^{1,2}. In this study, we focus on the root-associated microenvironment. Our aim is to assess **the influence of organic farming on rhizosphere microbial diversity and root gene expression in common bean** (*Phaseolus vulgaris* L.) compared to conventional.

Materials and methods

Ten samples of roots and their associated rhizosphere soil were collected at the beginning of flowering from bean plants (genotype A25) grown in two different soils: organic (N = 5) and conventional (N = 5). Rhizosphere soil was used for DNA extraction and 16S/ITS amplicon sequencing (DADA2/QIIME-2; SILVA v138, UNITE v8)^{3,4}, followed by α and β -diversity and differential abundance analyses (metagenomeSeq⁵). Root tissues were used for RNA extraction, sequencing, differential gene expression analyses with DESeq2⁶ ($|\log_2FC| \geq 2$, $\text{padj} < 0.05$), and functional enrichment with clusterProfiler⁷. Spearman correlation matrices were used to investigate the significant interactions between differentially abundant microorganisms (DAMs) and root differentially expressed genes (DEGs).

Results

1 Rhizosphere microenvironment: diversity and abundance

Organic farming promotes fungal diversity and enriches taxa associated with beneficial ecological functions in bean rhizosphere

- Organic farming favored higher fungal diversity, whereas conventional farming increased prokaryotic richness (Fig. 1).
- DAMs enriched in the organic rhizosphere (Fig. 2) were linked to plant-beneficial functions, such as symbiosis (*Rhizobium*, *Funneliformis*), chitin degradation (*Chitinophaga*), and biocontrol potential (*Metarhizium marquandii*).

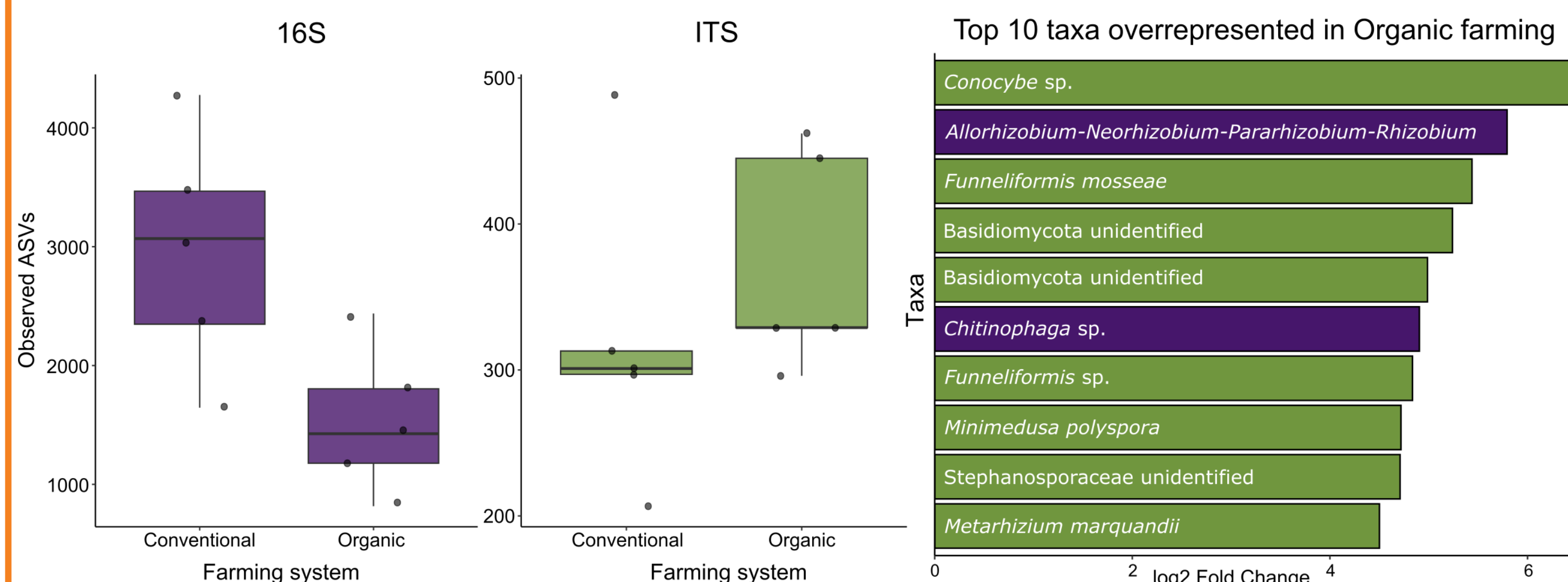


Figure 1. Alpha diversity was measured using the observed amplicon sequence variants (ASVs) of prokaryotic (16S, $p = 0.00232$, negative binomial) and fungal (ITS, $p = 0.315$, nb) communities across organic and conventional systems.

Figure 2. Top 10 taxa significantly abundant in organic rhizosphere ($\text{padj} < 0.05$) compared to conventional using metagenomeSeq. Purple bars represent prokaryotes (16S), and green bars indicate fungi (ITS).

2 Root gene expression and enriched biological functions

Organic bean roots exhibit enhanced metabolic activity linked to development and regulatory processes

- Organic farming revealed 917 upregulated and 168 downregulated genes (Fig. 3).
- Development and metabolic regulation processes were enhanced in organic farming (Fig. 4).

