

The response of soil and root microbial communities to faba bean-wheat intercropping



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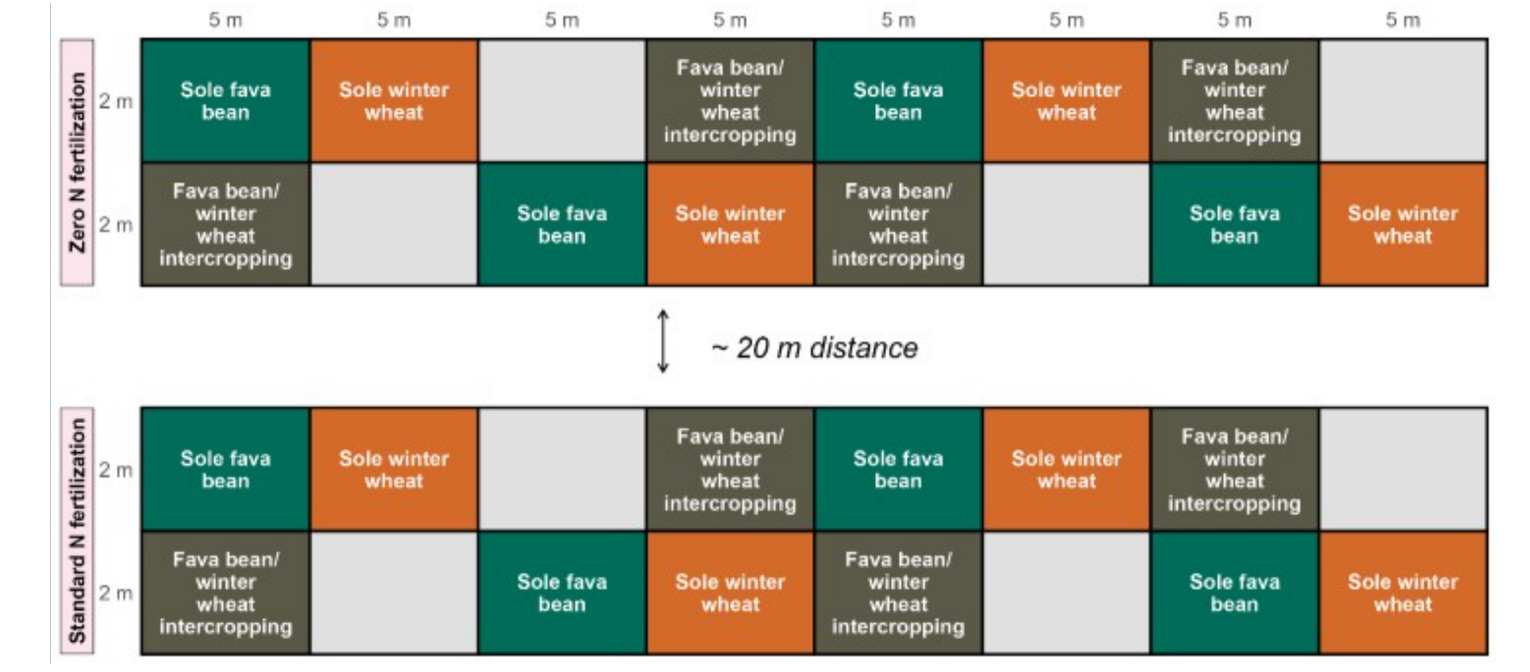
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INTRODUCTION

- More **sustainable** crop production requires a **yield intensification** coupled to an enhanced **agroecosystem multifunctionality**
- **Legume-cereal intercropping** is a valid solution for a more **sustainable intensification** (up to **50% increase** in yield)
- How the intercropping shapes the **root** and **soil microbial community** structure and functionality is still not fully elucidated
- We hypothesized that the intercropping could favor an **increase** of the **microbial functional potential** resulting in more closed **nutrient** cycles, while the community **structure** would substantially **differ** from the relative sole crops

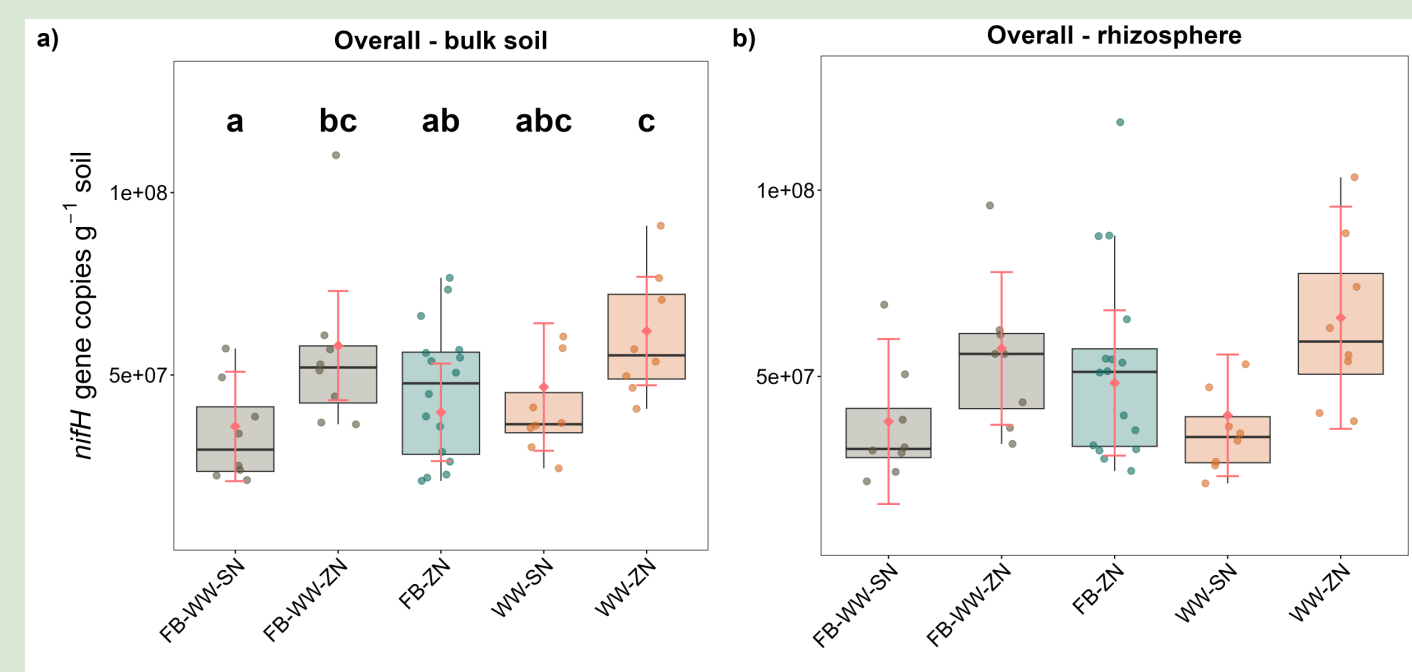
METHODS

- **Rhizosphere** and **bulk soil** as well as **plant root** samples were collected during the plant reproductive stages
- **Total DNA** extraction
- **qPCR** of the **phylogenetic** and **functional** markers
- **Bacterial 16S** and **fungal ITS** **metabarcoding**

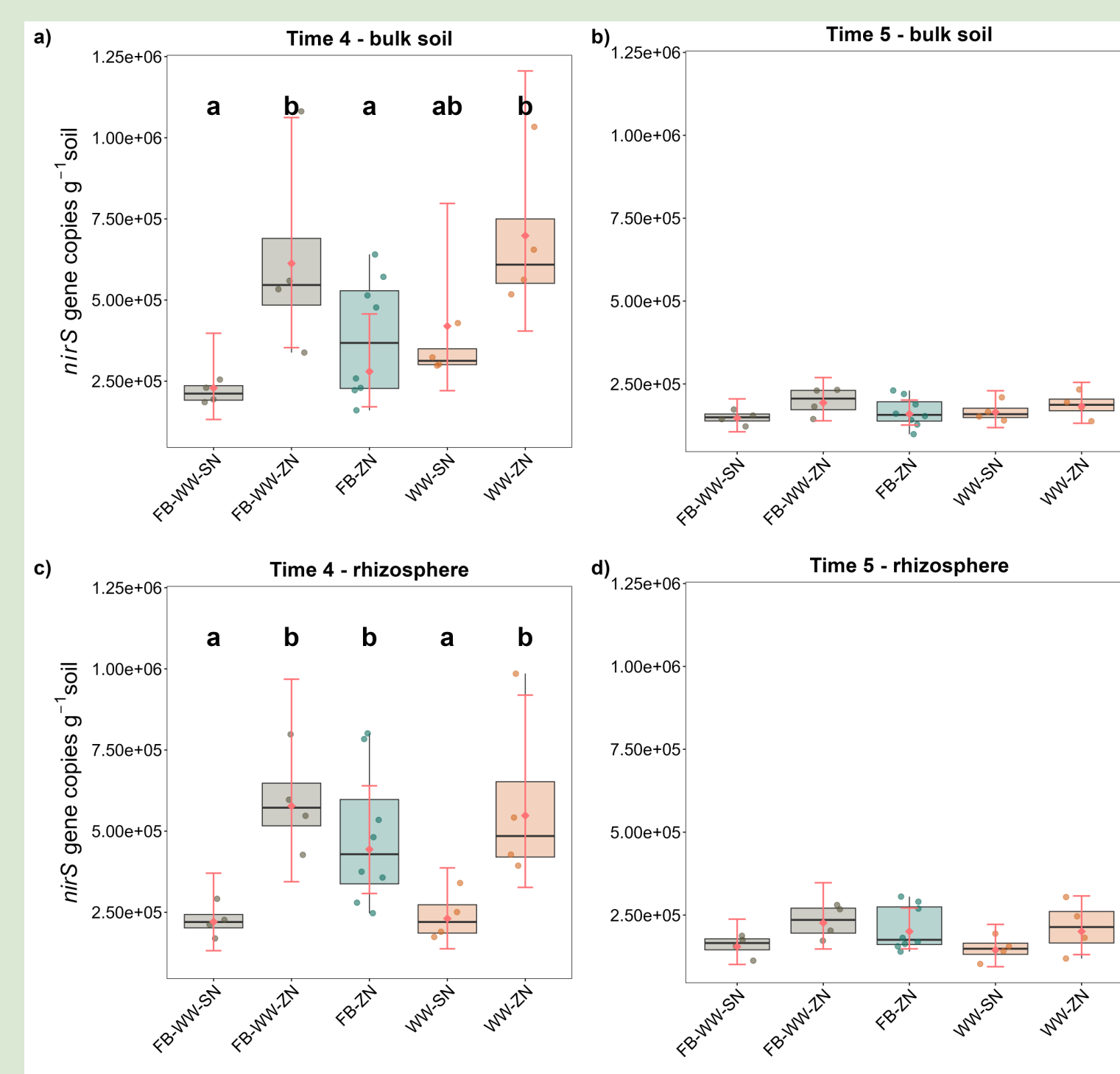


RESULTS

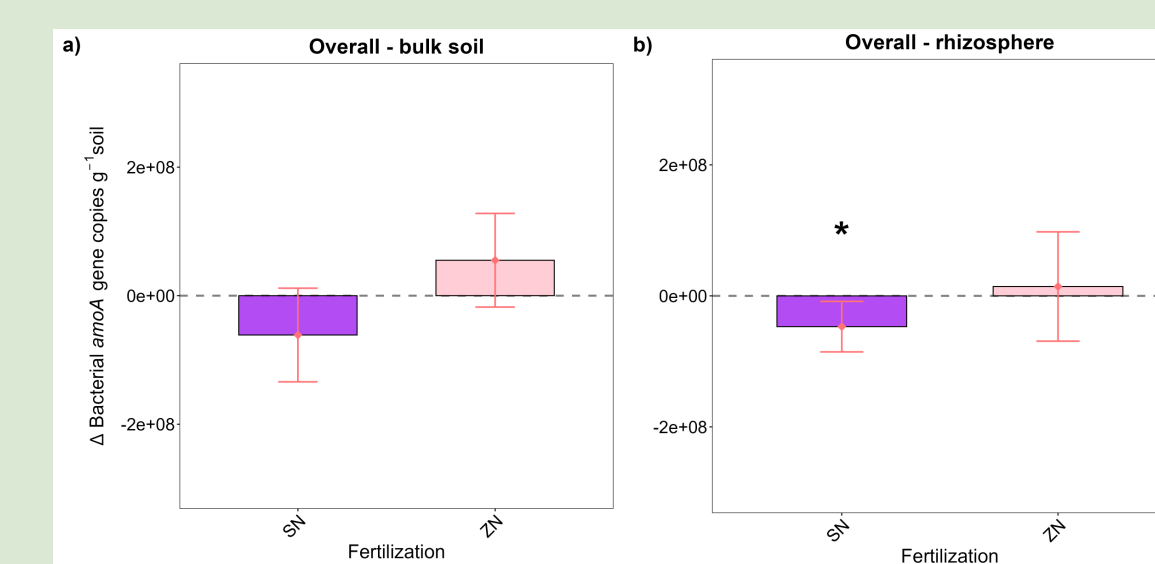
- The **intercropping** favors the proliferation of **rhizosphere fungi**
- The ***nosZ*** gene abundance is only affected by the **N fertilization** under the **sole wheat**



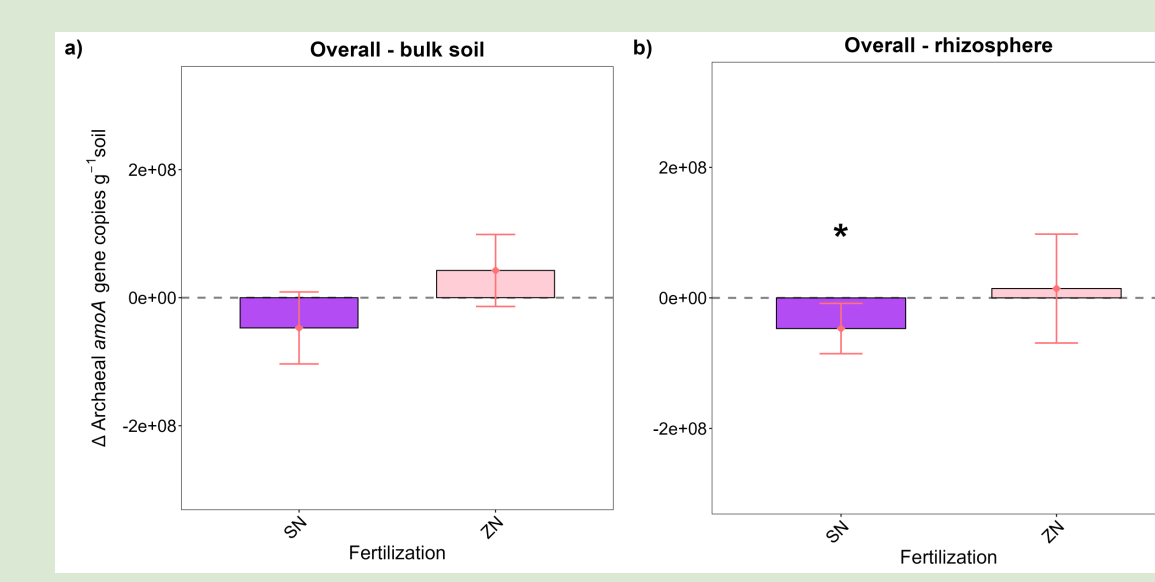
***nifH* gene abundance**
 Different letters only indicate significant differences among the treatments ($p < 0.05$). FB = faba bean; WW = winter wheat; ZN = zero N; SN = standard N



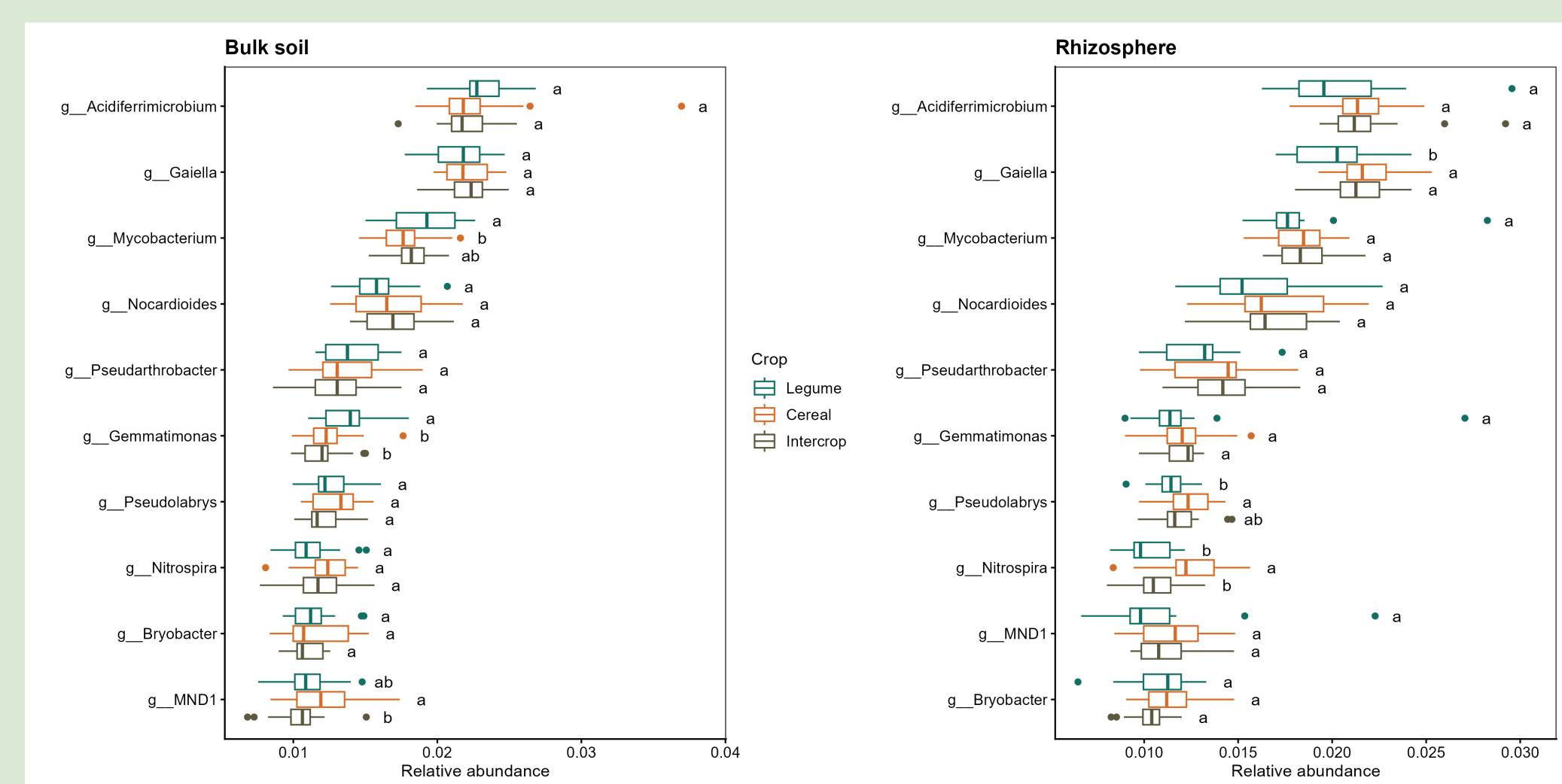
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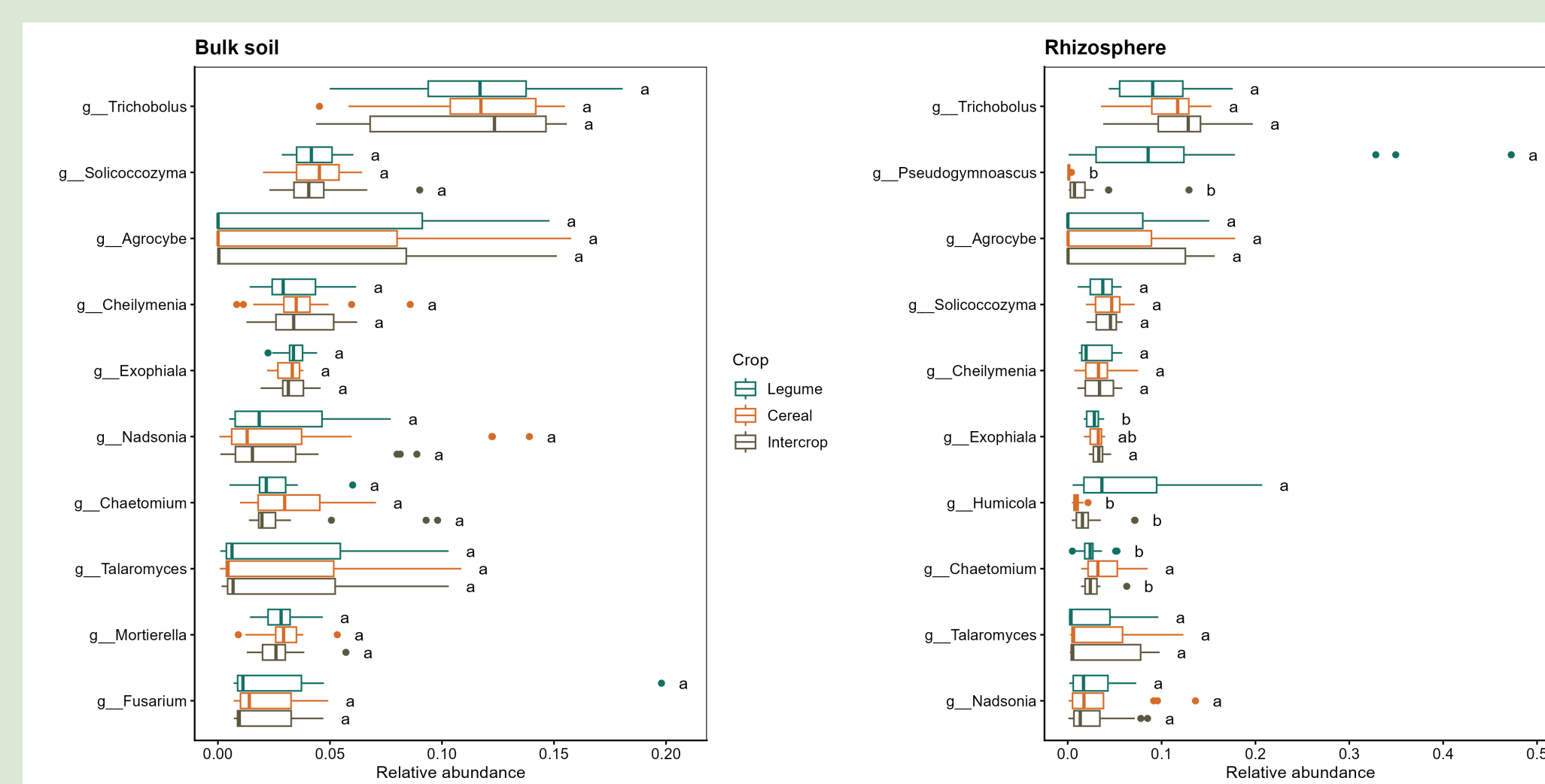
Delta bacterial *amoA* (real vs expected)
 The asterisks indicate values significantly different from zero ($p < 0.05$). ZN = zero N; SN = standard N



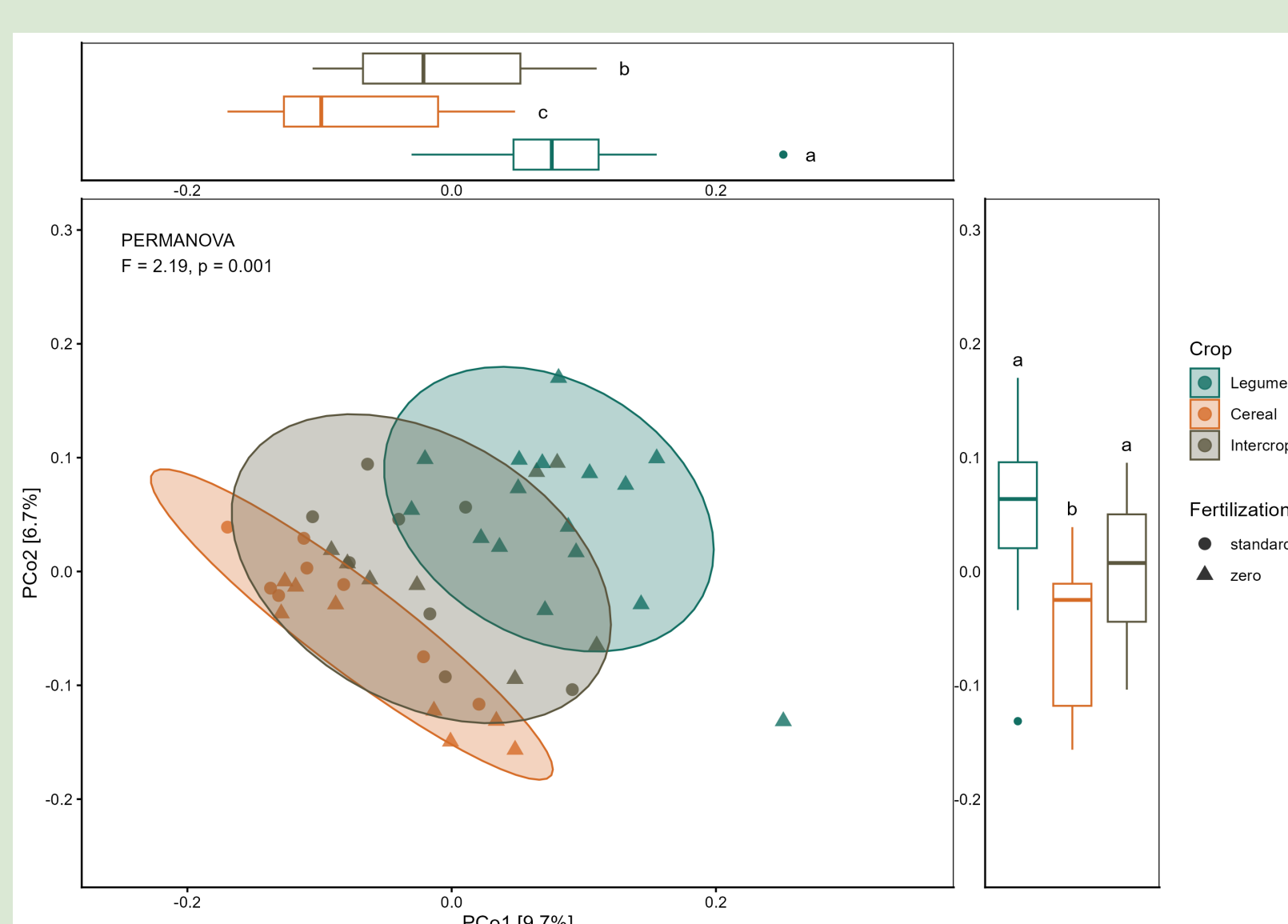
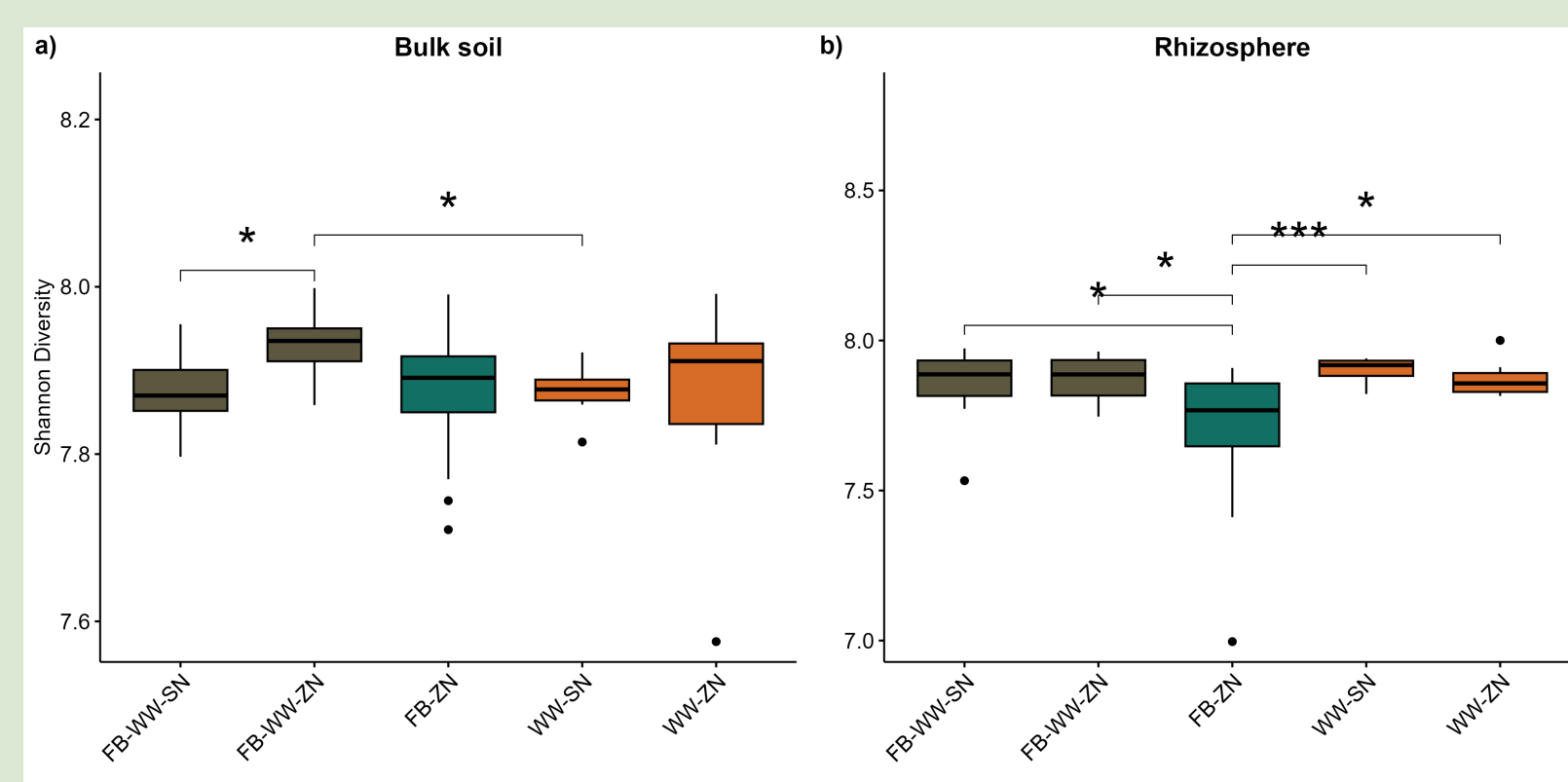
Delta archaeal *amoA* (real vs expected)
 The asterisks indicate values significantly different from zero ($p < 0.05$). ZN = zero N; SN = standard N



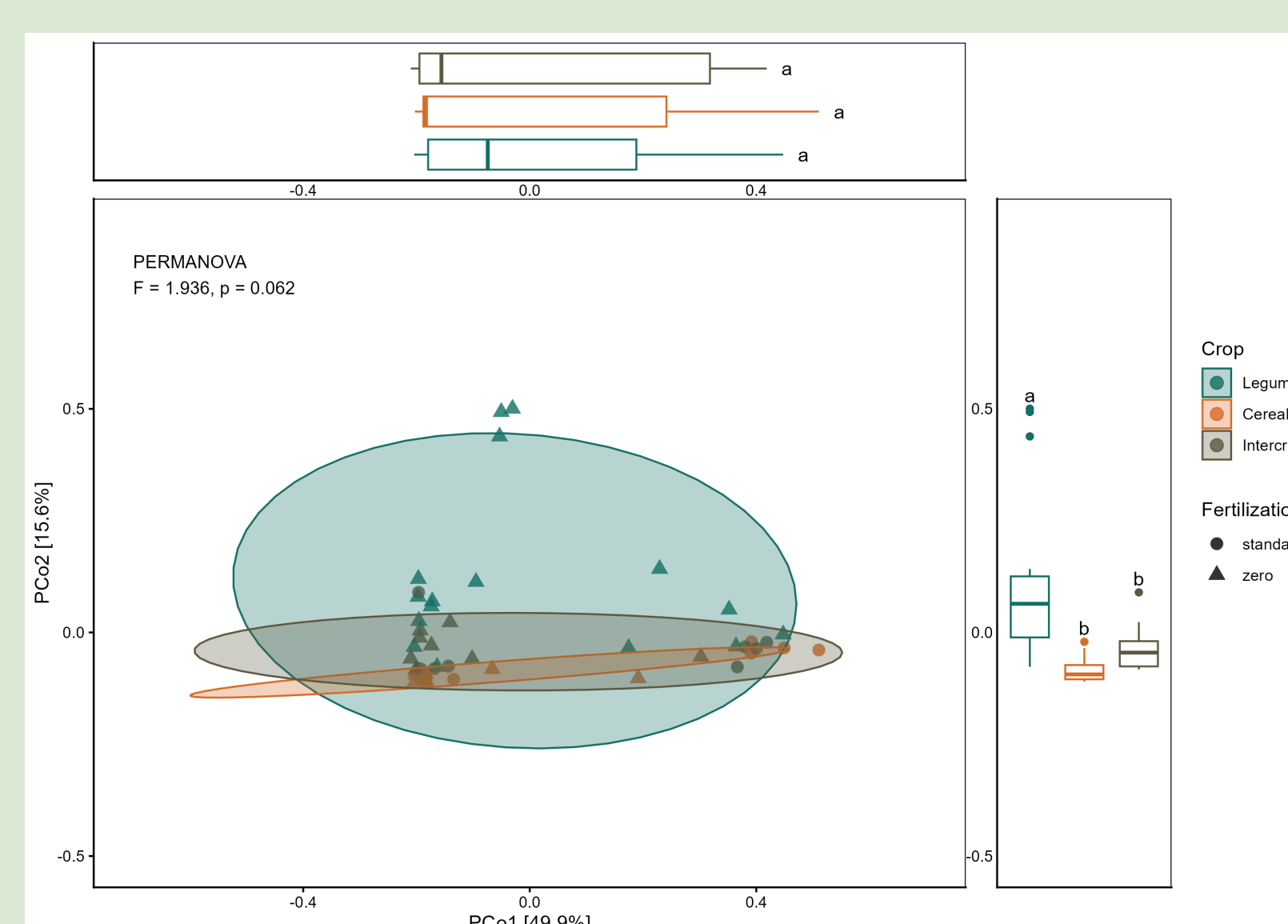
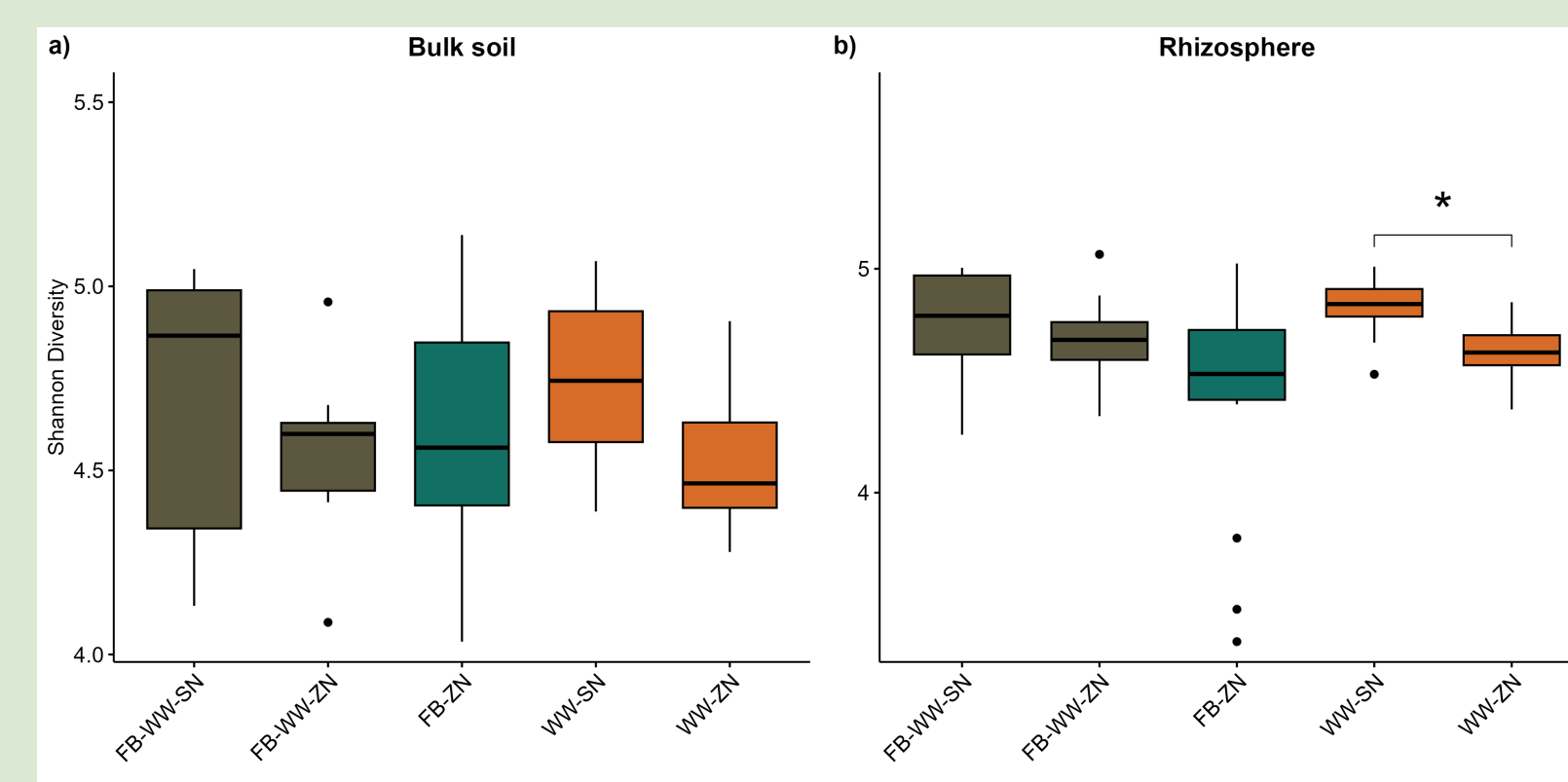
Differences in the bacterial genera abundance
 Different letters only indicate significant differences among the treatments ($p < 0.05$)



Differences in the fungal genera abundance
 Different letters only indicate significant differences among the treatments ($p < 0.05$)



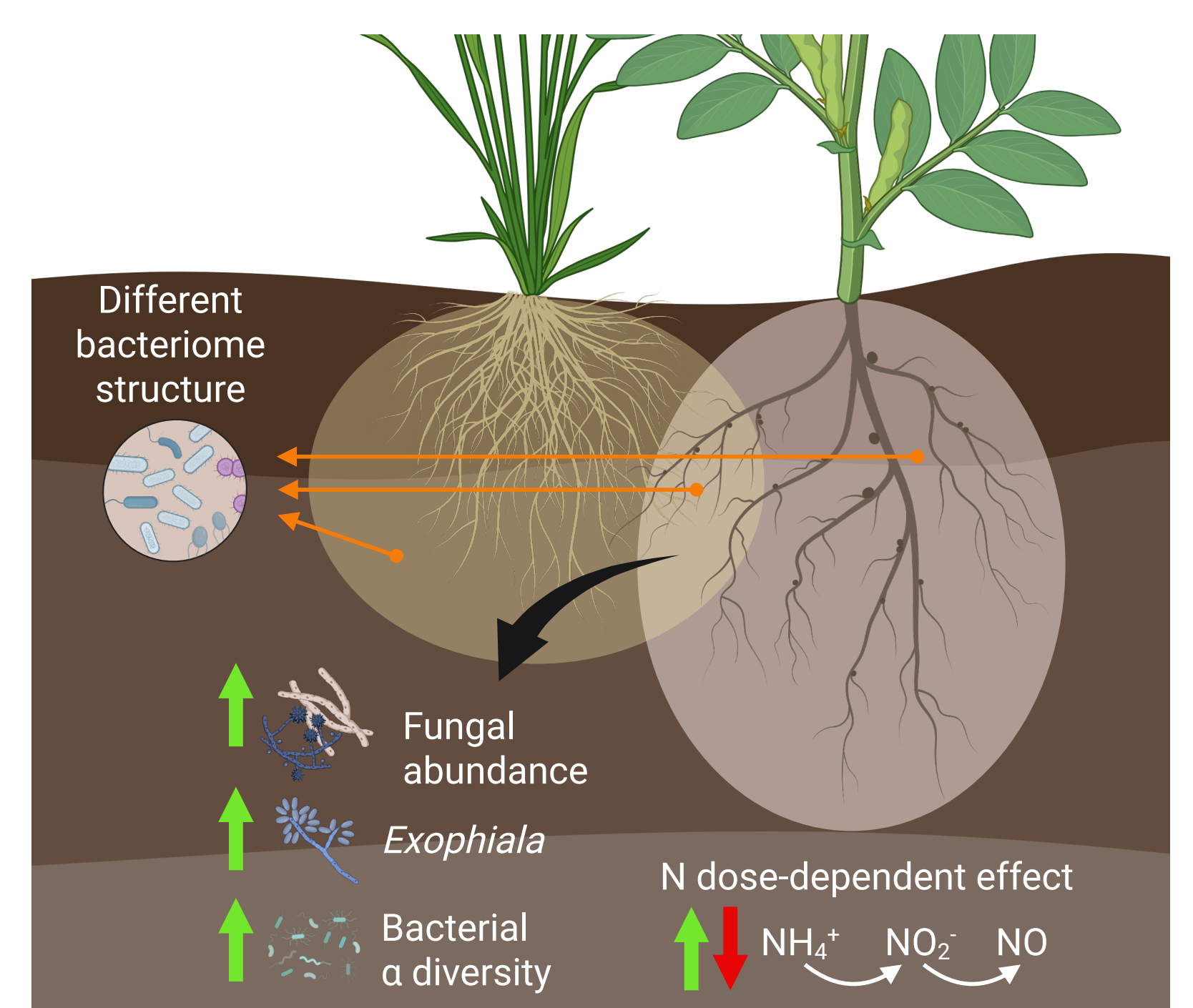
Bacterial α and β diversity
 Different letters only indicate significant differences among the treatments ($p < 0.05$). FB = faba bean; WW = winter wheat; ZN = zero N; SN = standard N



Fungal α and β diversity
 Different letters only indicate significant differences among the treatments ($p < 0.05$). FB = faba bean; WW = winter wheat; ZN = zero N; SN = standard N

CONCLUSIONS

- The **intercropping** favors the proliferation of **fungi** in the **rhizosphere**
- The **N_2 -fixation potential** depends on the **N dose** under the co-culture
- The intercropping **restricts** the **nitrification** under the **SN** but **favors** the **denitrification** under the **ZN**
- The **abundance** of some **bacterial** and **fungal genera** is driven by **one** of the two crops
- In the **shared rhizosphere**, the **bacteriome α diversity** is higher, and its **structure** changes



Created in <https://BioRender.com>

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