

# Deciphering the Microbiome of Biodynamic preparations with insights into their potential effects on Apple rhizosphere Microbiome

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## INTRODUCTION

### Samples and Experimental Design

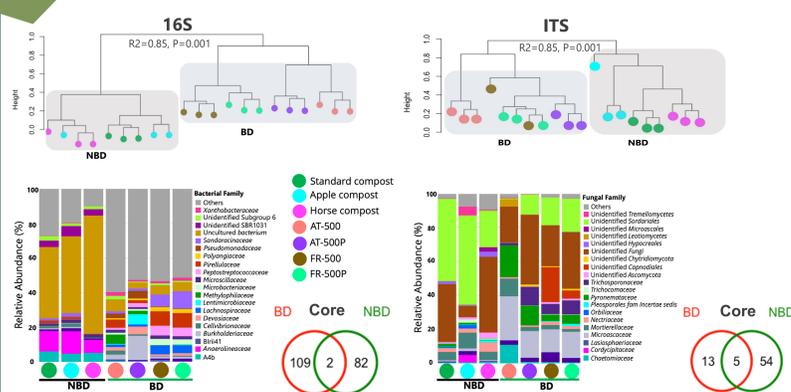


Research on the microbiome of biodynamic (BD) formulations (plant preparations and horn-manures) and their stability across regions post-storage has received less attention; nearly a century after Rudolf Steiner pioneered BD farming. Moreover, the potential impact of extracts from formulations on the plant rhizosphere microbiome is least studied. We applied high-throughput sequencing of bacterial and fungal community, and real-time qPCR to answer the following questions:

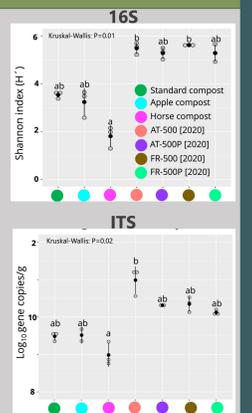
- Do non-biodynamic (NBD) composts and BD preparations have a similar microbiome?
- Do BD plant preparations have any impact on the microbiome of horn manures?
- Is the microbiome of BD manures independent of region and year of production?
- How does the microbiome of BD/NBD extracts differ from the precursor materials?
- What features, if any, do extracts impart to the plant rhizosphere microbiome?

**Objective:** To provide the basis for adoption of BD formulations in frame of other farm management systems (Integrated, or organic).

## RESULTS : BD manures & NBD composts were distinct in microbiome structures and composition

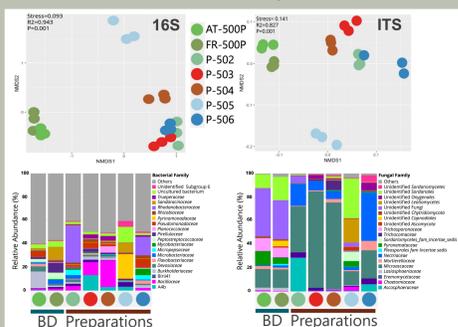


- Anaerolineaceae* (NBD), *Pseudomonadaceae*, *Lachnospiraceae*, and *Burkholderiaceae* (BD) were dominant.
- Paenibacillus*, *Mycobacterium*, *Cellulomonas*, and *Clostridium* (core bacterial microbiome).
- 16S diversity:  $P < 0.05$  for BD manures compared to Horse compost.
- ITS abundance:  $P < 0.05$  in BD manure (AT-500) compared to horse compost.

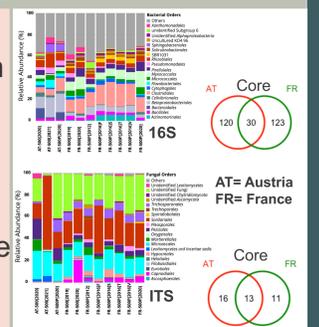


### BD manures and BD plant preparations hosted a distinct microbiome, with core microbiome

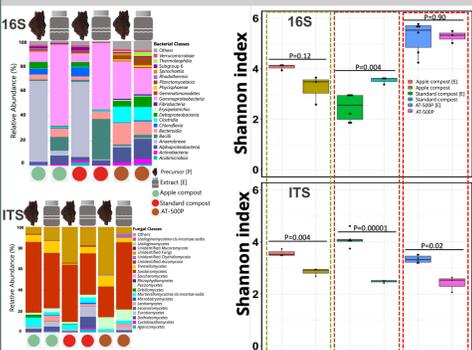
- BD plant preparations varied from BD manures.
- Bacterial and fungal families *Bacillaceae* & *Ascosphaeraceae* were seen in plant preparations.
- Shared core microbiome between BD manures & plant preparations were; *Romboutsia*, *Azotobacter*, & *Pedomicrobium* [16S], & *Fusarium*, *Arthrographis* [ITS].



- BD manures varied in structure & composition by country of origin, while no differences were seen between years.
- Countries shared a core microbiome in BD manures.



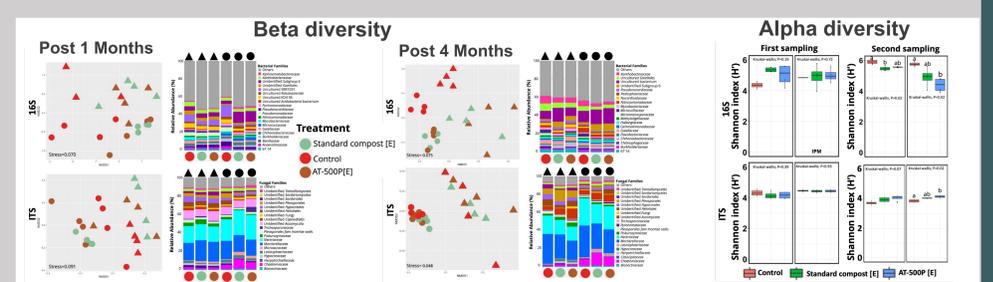
### Extracts and precursors of BD manure and NBD composts contained distinct microbiome and a core microbiome



- Extract [E] and precursor [P] were distinct in composition.
- [E] were generally higher in diversity as compared to [P].

	Precursor	Extract	16S	ITS
Apple compost			397	92
Standard compost			196	111
AT-500P			228	110

### A time-dependent impact of extracts on apple rhizosphere microbiome under different management was observed



### More from the EXCALIBUR project ([www.excaliburproject.eu](http://www.excaliburproject.eu))

Olini, E., Kusstatscher, P., Wicaksono, W. A., Abdelfattah, A., Cernava, T., and Berg, G. (2022). Insights into the microbiome assembly during different growth stages and storage of strawberry plants. *Environ. Microbiome* 2022 17(1), 1–15. doi:10.1186/S40793-022-00415-3.

Berg, G., Kusstatscher, P., Abdelfattah, A., Cernava, T., & Smalla, K. (2021). Microbiome Modulation—Toward a Better Understanding of Plant Microbiome Response to Microbial Inoculants. *Frontiers in Microbiology*, 12, 803.

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