

3rd THÜNEN SYMPOSIUM ON SOIL METAGENOMICS

FROM GENE PREDICTIONS
TO SYSTEMS ECOLOGY

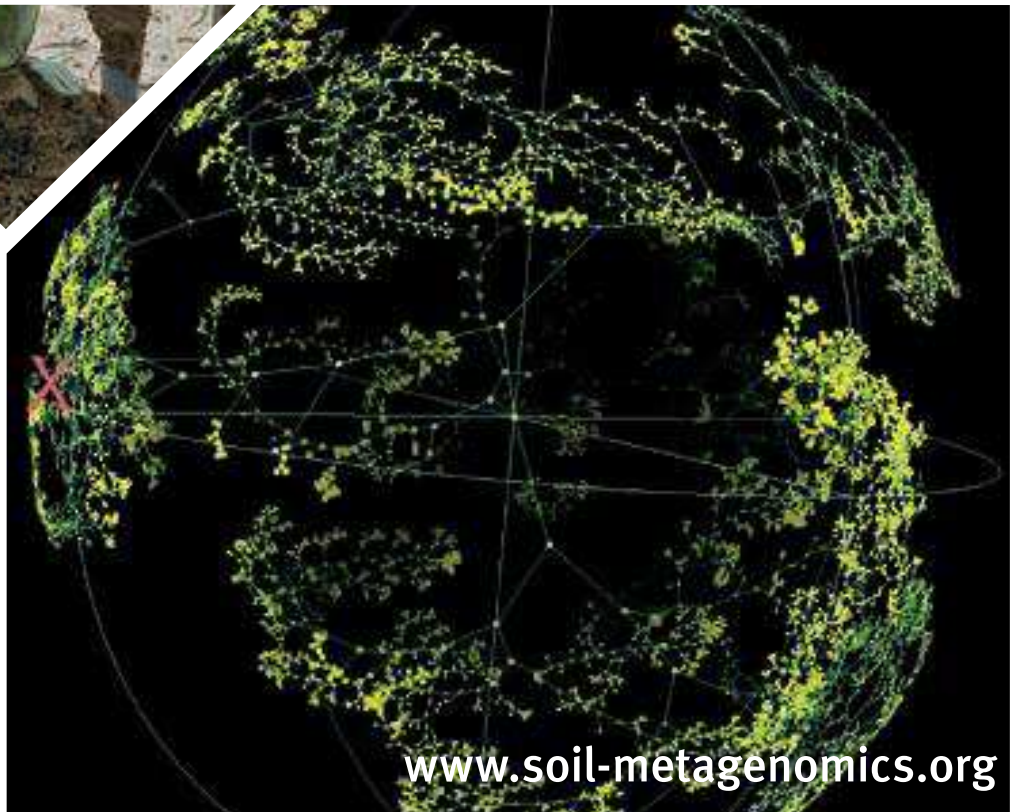
plus Workshop on Bioinformatic Tools

14–16 December 2016

Braunschweig, Germany



PROGRAM







www.soil-metagenomics.org



SCIENTIFIC PROGRAM OVERVIEW

Wednesday, 14 December	Thursday, 15 December	Friday, 16 December
08:30–10:20		
Workshop I – Analyses of Metagenomes I p. 17	09:00–10:45 Spatial Ecology & Functional Diversity I p. 19	09:00–10:45 Climate Change & Other Stressors I p. 22
Coffee break		
10:40–12:20	Industrial exhibition & coffee break	Industrial exhibition & coffee break
Workshop I – Analyses of Metagenomes II p. 17	11:10–13:10 Spatial Ecology & Functional Diversity II p. 19	11:05–11:50 Climate Change & Other Stressors II p. 22
Industrial exhibition & lunch break <i>for workshop participants only</i>		11:50–12:50 From Systems Ecology to Biotechnology p. 22
13:00–13:45		
Opening of the Symposium p. 17	Industrial exhibition & lunch break	12:50–13:45 What's Next? Soil Biology & Omics Technologies p. 23
13:45–15:15		
Dealing with Huge Datasets p. 17	14:00–15:45 Plant Microbiomes p. 20	Industrial exhibition & lunch break
Industrial exhibition & coffee break		14:15–15:30 Workshop II – Beyond Metagenomes I p. 23
15:35–17:20	Industrial exhibition & coffee break	Coffee break
From Omics to Systems Ecology: Integrative Approaches p. 18	16:05–17:20 Forest Microbiomes p. 21	15:45–18:00 Workshop II – Beyond Metagenomes II p. 23
17:20–19:20	17:20–19:20	
Posters and drinks p. 25	Posters and drinks p. 33	
	20:00–00:00 Conference dinner p. 16	

Key

Workshop	
Scientific Session	
Social Program	
Poster Session	



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Venue and Date

Thünen Institute, Forum
Bundesallee 50 • 38116 Braunschweig (Germany)
14–16 December 2016

Conference Website

www.soil-metagenomics.org



Conference Chair

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Conference Organization

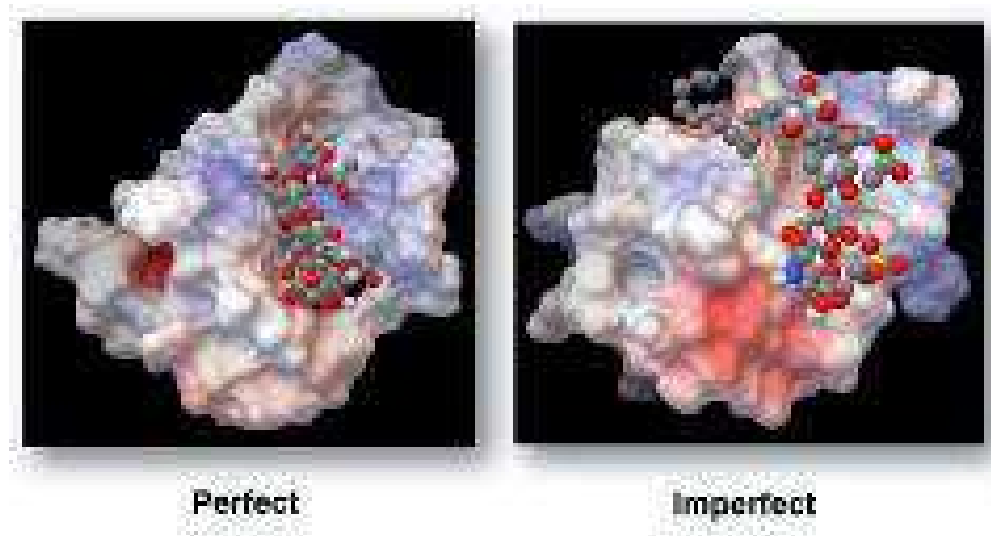
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Figure 2



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Meta-analysis of microbiomes in soils affected by Apple Replant Disease

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Introduction

Apple replant disease (ARD) is a complex syndrome that causes reduced growth in apple trees that are replanted in the same soil. A precise etiology of this disease has not been described yet, although it is thought to have a microbiological origin. In the last years, thanks to NGS, some light was cast on the microbiome of ARD-affected soils, however, such single case studies often do not deliver results that may be considered generalizable.

Objectives

The aim of this study was to estimate the main microbiological drivers in ARD-affected soils by using a meta-analytical approach.

Materials and Methods

A literature search was performed, looking for all the deep-sequencing studies and datasets on ARD-affected soil microbiomes. From these studies, metadata on both environmental variables of soil sampling sites and molecular techniques used were extracted, together with the raw sequencing data from NCBI SRA database. The sequencing datasets of bacteria (n=5) and fungi (n=3) were analyzed using a taxonomic approach in mothur, using SILVA and UNITE databases, respectively.



Results

Both bacterial and fungal communities in ARD-affected soils had a significantly different structure and were genetically different from those in healthy soils. Thanks to the broader meta-analysis approach, a pool of co-occurring fungal and bacterial OTUs was also identified in ARD-affected soils. For bacteria, it was possible to explain most genetic variability with the environmental and molecular meta-data collected; however, the different molecular methods used accounted for 25% of the variability. For fungi, instead, the meta-data collected explained 40% of the observed variability, which seemed not influenced by the difference in molecular methods among the studies. The variables that affected most the microbial communities were the presence of ARD, the soil treatments and the plant rootstock.

Conclusion

Our meta-analysis showed that healthy and ARD-affected soils exhibited significantly different soil microbiomes and shared differentially abundant microbial groups. However, an important fraction of the signal was obscured by diverse analytical approaches.

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Interplay between plant-beneficial and plant pathogenic microorganisms in agricultural soils cropped with winter wheat

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The rhizosphere and soil microbiomes are determinants for plant health, and their importance has been compared to the importance of the gut microbiome for animals and humans. Various plant beneficial organisms have been identified in the rhizosphere, providing functions such as protection from fungal pathogens, solubilisation of nutrients from soil and induction of resistance to abiotic and biotic stress. Pathogenic microorganisms include various saprophytic fungi and bacteria causing root rots and wilts. While single beneficial or detrimental organisms have been extensively studied, the links between different groups of beneficial or detri-