

# 3<sup>rd</sup> THÜNEN SYMPOSIUM ON SOIL METAGENOMICS

FROM GENE PREDICTIONS  
TO SYSTEMS ECOLOGY

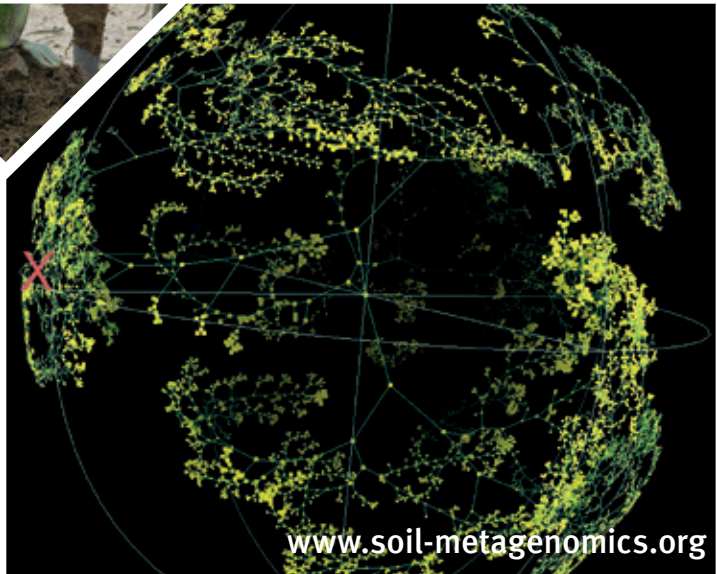
plus Workshop on Bioinformatic Tools

14–16 December 2016

Braunschweig, Germany



PROGRAM





## Conclusion

Soil microbiota could be a limiting factor of rice pests' growth and reproduction, and ultimately decide their life and death.

Figure 1

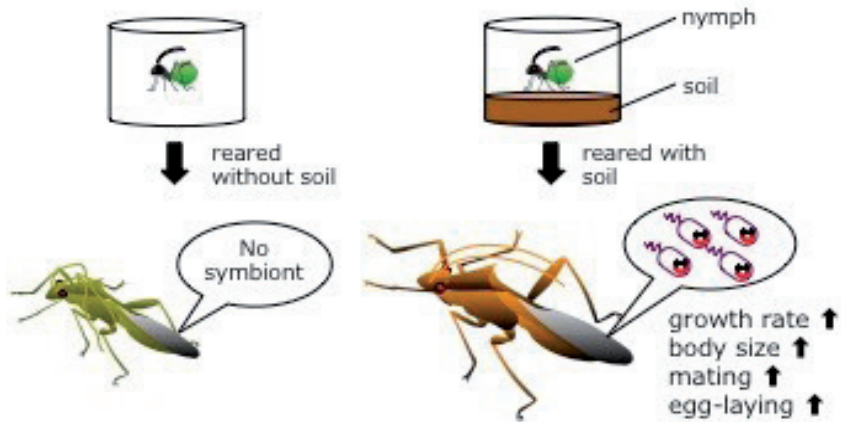


Figure 1. Fitness effects of soil-derived symbiotic bacteria on insects.

## P111

### Rhizosphere microbiome and disease resistance - Project presentation

P. Hohmann<sup>1</sup>, L. Wille<sup>1,2</sup>, B. Studer<sup>2</sup>, M. Messmer<sup>1</sup>

<sup>1</sup>Research Institute of Organic Agriculture (FiBL), Crop Sciences, Frick, Switzerland

<sup>2</sup>ETH, Environmental Systems Science, Zurich, Switzerland

Disease resistance is not a mere plant but a system trait involving the complex plant-associated microbial community (Berendsen et al. 2012). As with pathogens, past research often focussed on single, culturable symbiotic microbes. More recently, microbial shifts on the community level have been linked to disease resistance. However, simplistic statements such as "high microbial diversity equals healthier plants" were not confirmed in most recent microbiome analyses (Hartmann et al. 2014, Yu et al. 2012). Plants have the ability to influence the microbial structure in the rhizosphere. Besides soil type, it has been demonstrated that not only different plant species, but also different genotypes within the same species can modify the rhizosphere microbiome (e.g. Berg et al. 2006, Peiffer et al. 2013).



The overall goal of our project is to understand the complex genotype x microbiome interactions and to make use of this knowledge in resistance breeding programmes. For this, we will investigate a phenomenon called soil fatigue of pea, caused by a complex of soil-borne pathogens, and determine rhizosphere microbiome profiles of pea lines with contrasting levels of disease resistance in different agricultural soils using NGS and qPCR. The objective is to identify microbial hubs, diversity indices and key pathogens and beneficials involved in microbe-mediated disease resistance. This information will be linked with root exudate profiles in order to elucidate the plant's capacity to influence the microbiome composition leading to disease susceptibility or resistance. In the long-term, current and future research activities of our group aim to make use of plant-microbe interactions in plant breeding for an improved expression and stability of important plant traits.

Berendsen RL, Pieterse CMJ and Bakker PAHM (2012). *Trends in Plant Science* 17(8): 478-86.

Berg G, Opelt K, Zachow C, Lottmann J, Götz M, Costa R and Smalla K (2006). *FEMS Microbiology Ecology* 56(2): 250-61.

Hartmann M, Frey B, Mayer J, Mäder P and Widmer F (2014). *The ISME Journal* 9: 1177-94.

Peiffer JA, Spor A, Koren O, Jin Z, Green S and Dangl JL (2013). *PNAS* 110(16): 6548-53.

Yu L, Nicolaisen M, Larsen J and Ravnkov S (2012). *Plant and Soil* 357(1): 395-405.

This project is supported by the Mercator Foundation Switzerland and the Swiss Federal Office of Agriculture.

## **P112**

### **Fungal and bacterial diversity and community composition in the rhizosphere microbiome of grassland ecosystems along land use gradients.**

R. Schöps<sup>1,2</sup>, T. Wubet<sup>1,3</sup>, H. Bruelheide<sup>4,3</sup>, F. Buscot<sup>1,3</sup>

<sup>1</sup>UFZ-Helmholtz-Centre for Environmental Research, Department of Soil Ecology, Halle (Saale), Germany

<sup>2</sup>University of Leipzig, Department of Biology II, Leipzig, Germany

<sup>3</sup>German Centre for Integrative Biodiversity Research (iDiv), Leipzig, Germany

<sup>4</sup>University of Halle-Wittenberg, Department of Biology and Geobotany, Halle (Saale), Germany

The rhizosphere encompasses the soil along the plant root surface and represents a hotspot of microbial activity and diversity. The microbial abundance and activity is highly influenced by plants via the release of root exudates. Bacteria and fungi, in turn, have a substantial impact in the growth and fitness of their plant host. This plant-microbe relationship is a driver of different essential ecosystem processes e.g. nutrient cycling. However, it is not well known to which extent plant traits,