

Evaluating the Effect of Mammal Compost Addition on Native Soil Microbiota

Location: Helmholtz Centre for Environmental Research (UFZ), Leipzig, Germany

Supervisor: Dr. Stephanie Jurburg

Project Start Date: ASAP

Human composting, also known as natural organic reduction, is gaining attention as an environmentally sustainable alternative to conventional burial and cremation. However, its ecological impact, particularly on native soil microbial communities, remains poorly understood. We will assess how microbial communities from pig-derived compost interact with native soil microbiota over time. This study will address the integration of compost and soil-derived microbial communities over time, and evaluate seasonal and temporal variations in microbial dynamics following human compost incorporation.

In October 2024, composted derived from three adult pigs were buried in the Leipzig botanical gardens, and have been sampled every two weeks to track microbial succession and integration. Each test site os sampled in two areas, the compost-amended and the control soil. This project will involve taking the final samples from this experiment, performing DNA extraction and sequencing, quantifying total carbon and nitrogen in the soil, and performing bioinformatics and statistical analyses of the resulting data.

Requirements: basic knowledge of R and basic molecular skills

Skills learned

- Field sampling
- DNA isolation and quantification
- PCR, qPCR, amplicon sequencing
- Total C and N quantification
- Bioinformatic analyses (in R)
- Multivariate statistics (in R)

PPP Project 1: Bacterial Responses to Reduced Water Management in Rice Fields in Argentina

Location: Helmholtz Centre for Environmental Research (UFZ), Leipzig, Germany

Supervisor: Dr. Stephanie Jurburg

Project Start Date: October 2025

This MSc project is part of an international collaboration investigating the effects of Reduced Water Management Technologies (RWMT) on microbial communities in rice fields.

Traditional rice farming relies on continuous flooding, which leads to significant greenhouse gas (GHG) emissions, particularly methane. RWMT offers a promising alternative for improving water efficiency and reducing environmental impact, yet its influence on the soil and root microbiome remains largely unknown.

The student will participate in field sampling and soil and root sample collection and DNA extraction in an ongoing RWMT experiment in Argentina, testing different watering schemes. In Germany, the student will perform quality checking, PCR, and sequencing of the 16S RNA gene to characterize the bacterial communities associated with rice roots under RWMT and traditional flooding systems. Statistical analyses in R will be used to examine microbial community structure, link microbial shifts to environmental variables, and investigate potential indicator species associated with methane and nitrous oxide emissions. A major focus of the project will be to assess how the bacterial community composition correlates with GHG emissions, management soil health, and nutrient cycling.

Requirements: basic knowledge of R and basic molecular skills, fluent in English, Spanish is a bonus

Skills learned

- Field sampling
- DNA isolation and quantification
- PCR, amplicon sequencing
- Bioinformatic analyses (in R)
- Multivariate statistics (in R)

PPP Project 2: Responses of Microeukaryotes to Reduced Water Management in Rice Fields in Argentina

Location: Helmholtz Centre for Environmental Research (UFZ), Leipzig, Germany

Supervisor: Dr. Stephanie Jurburg

Project Start Date: October 2025

This MSc project focuses on the role of microeukaryotic communities, including protists and fungi, in rice fields managed under Reduced Water Management Technologies (RWMT) in Argentina. Traditional rice farming relies on continuous flooding, which leads to significant greenhouse gas (GHG) emissions, particularly methane. While bacterial communities in agricultural soils are well studied, microeukaryotes play a key role in nutrient cycling, microbial interactions, and soil food web stability. However, their response to changing irrigation practices is still poorly understood. Investigating these communities will provide critical insights into the broader ecological impacts of RWMT on rice field microbiomes.

The student will participate in field sampling and soil and root sample collection and DNA extraction in an ongoing RWMT experiment in Argentina, testing different watering schemes. In Germany, the student will perform quality checking, PCR, and sequencing of the 18S RNA gene to characterize the bacterial communities associated with rice roots under RWMT and traditional flooding systems. Statistical analyses in R will be used to examine microbial community structure, link microbial shifts to environmental variables, and investigate potential indicator species associated with methane and nitrous oxide emissions. The project will specifically examine changes in the composition of protist communities under different irrigation regimes and how these shifts influence bacterial populations and soil microbial interactions.

Requirements: basic knowledge of R and basic molecular skills, fluent in English, Spanish is a bonus

Skills learned

- Field sampling
- DNA isolation and quantification
- PCR, amplicon sequencing
- Bioinformatic analyses (in R)
- Multivariate statistics (in R)