

MICROBIAL AND ANTIMICROBIAL RESISTANCE GENE DIVERSITY IN EXTRACELLULAR AND TOTAL DNA ACROSS RURAL ECOSYSTEM BARRIERS IN EUROPE

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Aim: To determine the microbial community composition and antimicrobial resistance genes (ARGs) diversity in total and extracellular DNA in agricultural ecological compartments in Europe. This work is part of the OHEJP FED-AMR consortium, which aims to investigate the role of free extracellular DNA (exDNA) in the spread of AMR genes across ecosystem barriers via bacterial transformation.

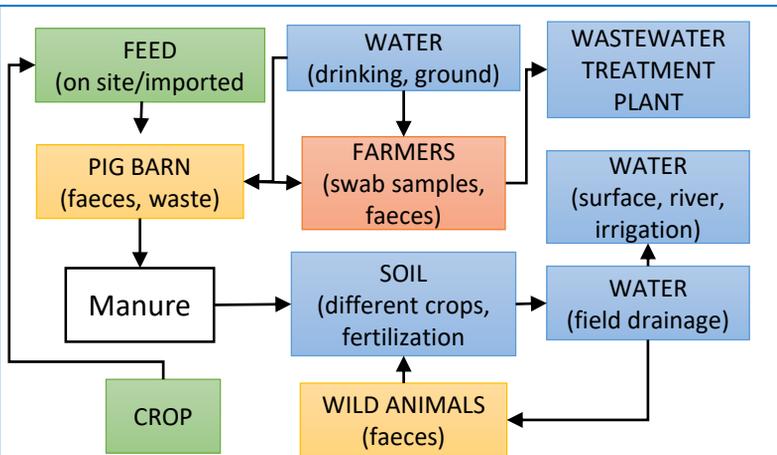


Figure 1. Possible routes of ARG spread across ecosystem barriers and targeted ecological compartments in FED-AMR

Results: The 16S and ARGs sequencing results were obtained for 511 samples, including 258 exDNA samples. Naturally-transformable bacteria, capable of incorporating exDNA into their cells, were present in the samples.

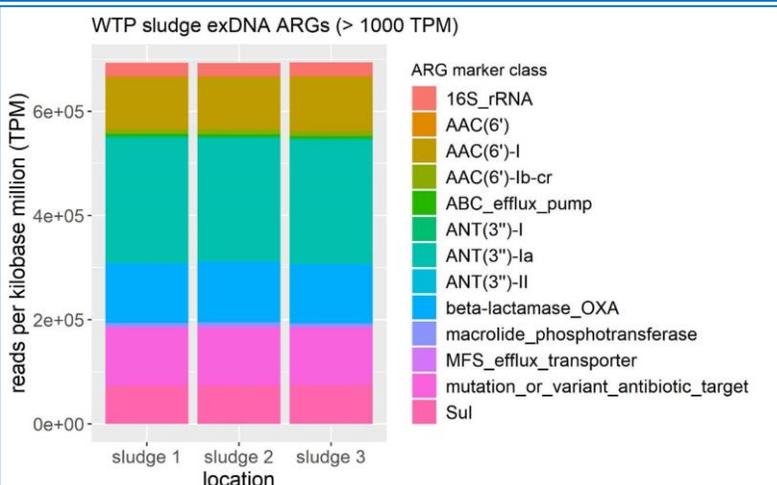


Figure 3. ARG composition of exDNA of wastewater sludge from Ireland. Sludge exDNA had a large number of ARGs, showing their potential for ARG spread in the environment

Methods: Sampling was carried out in Austria, Portugal Czech Republic, Estonia, UK and Ireland. Both total (tDNA) and extracellular DNA (exDNA) were extracted along one crop-growing season, and sequencing of the 16S rRNA genes and ARG-capture coupled with metagenomic sequencing were performed.

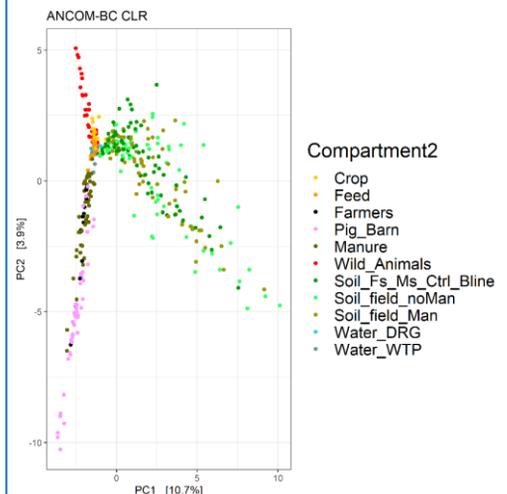


Figure 2. Ordination plot of microbial diversity. Ecological compartment influenced microbiome and ARG diversity.

Conclusions: Further analyses will link microbiome and ARGs with contaminants, antibiotics, heavy metals and trace elements to better understand the importance of exDNA as a vector for AMR spread in agricultural ecosystems.

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