

Understanding the Aral Sea microbiome and resistome for restoration

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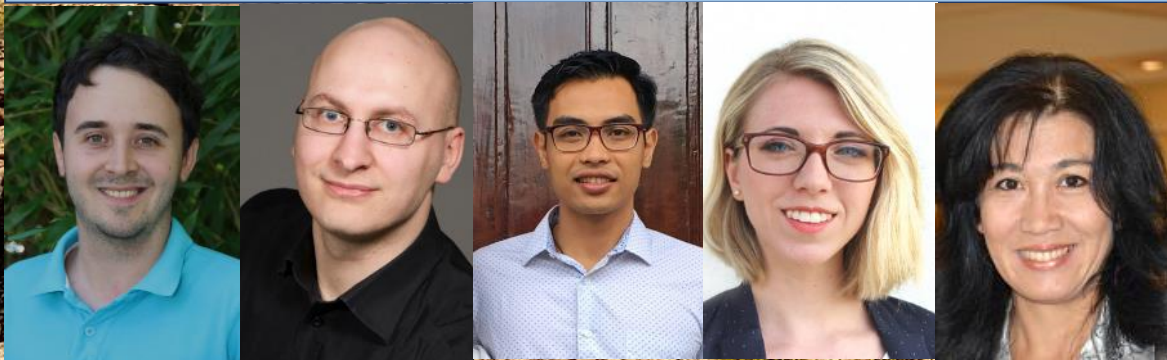
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INTRODUCTION: The Aral Sea Expedition



The Aral Sea Expedition
August 22-24. 2019

Our Team:

Dr. Dilfuza Egemberdiyeva
(National University of
Taschkent, Usbekistan)

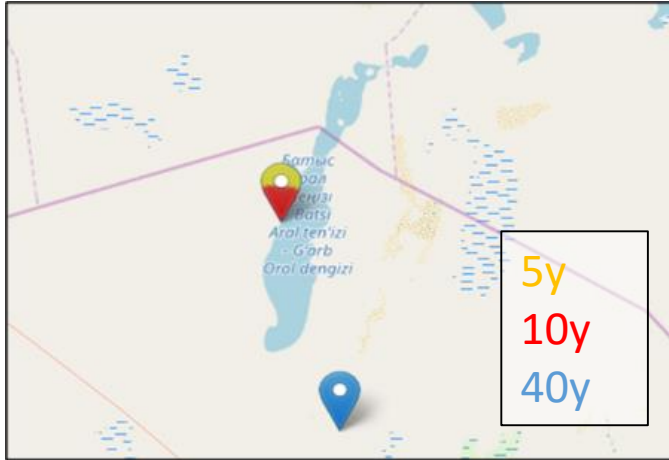
Dr. Maged Saad (KAUST Saudi
Arabia)

Dr. Tomislav Cernava (TU Graz)
Prof. Dr. Gabriele Berg (TU Graz)

Objective:

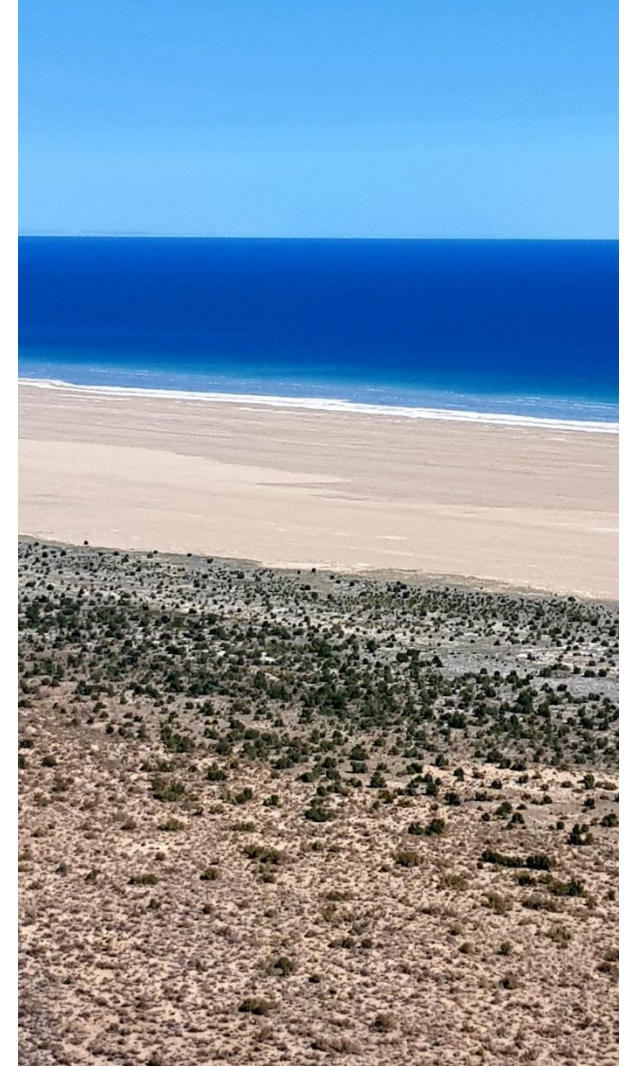
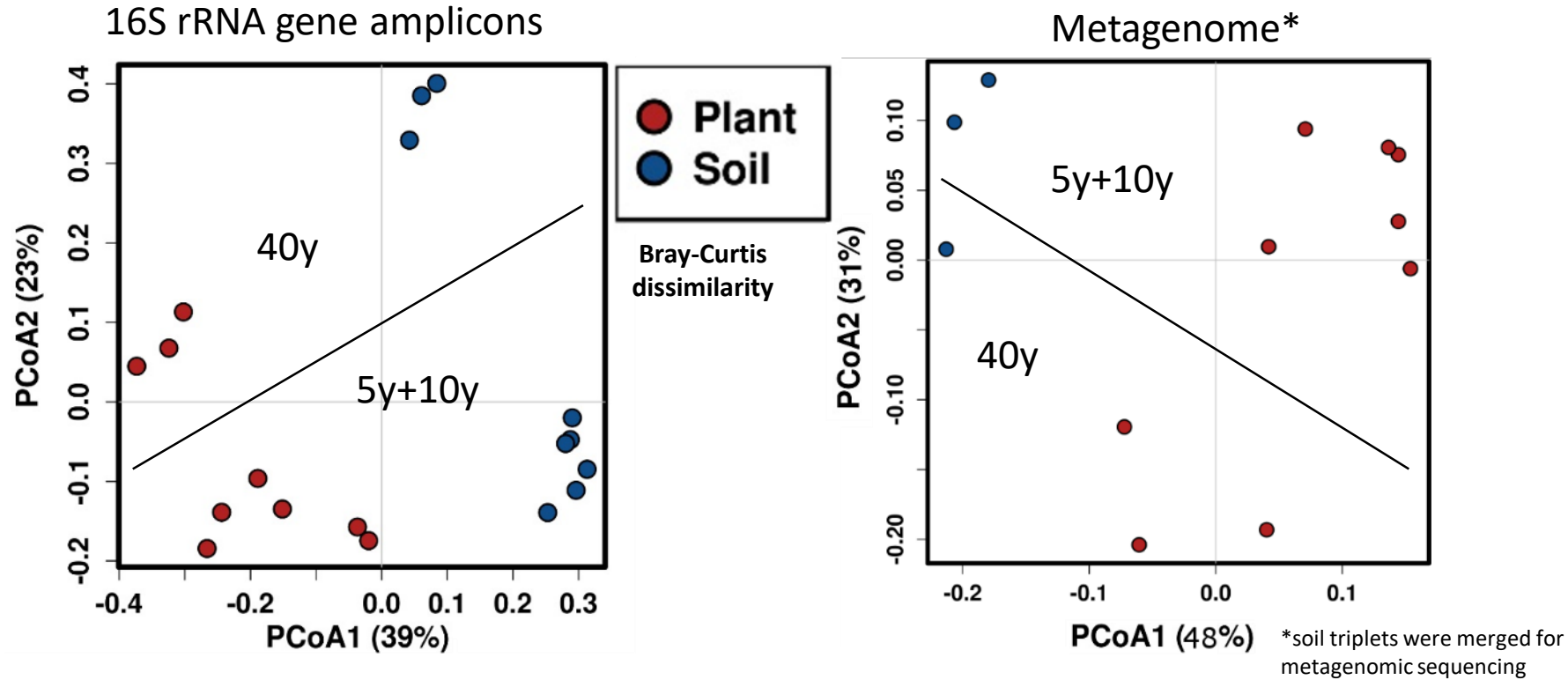
- I) to understand the microbiome and resistome in a highly disturbed ecosystem
- II) to find solutions for restauration

INTRODUCTION: The Sampling and method design



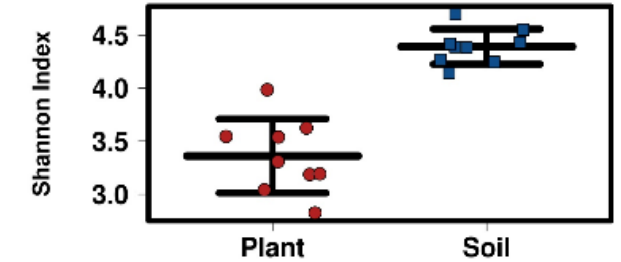
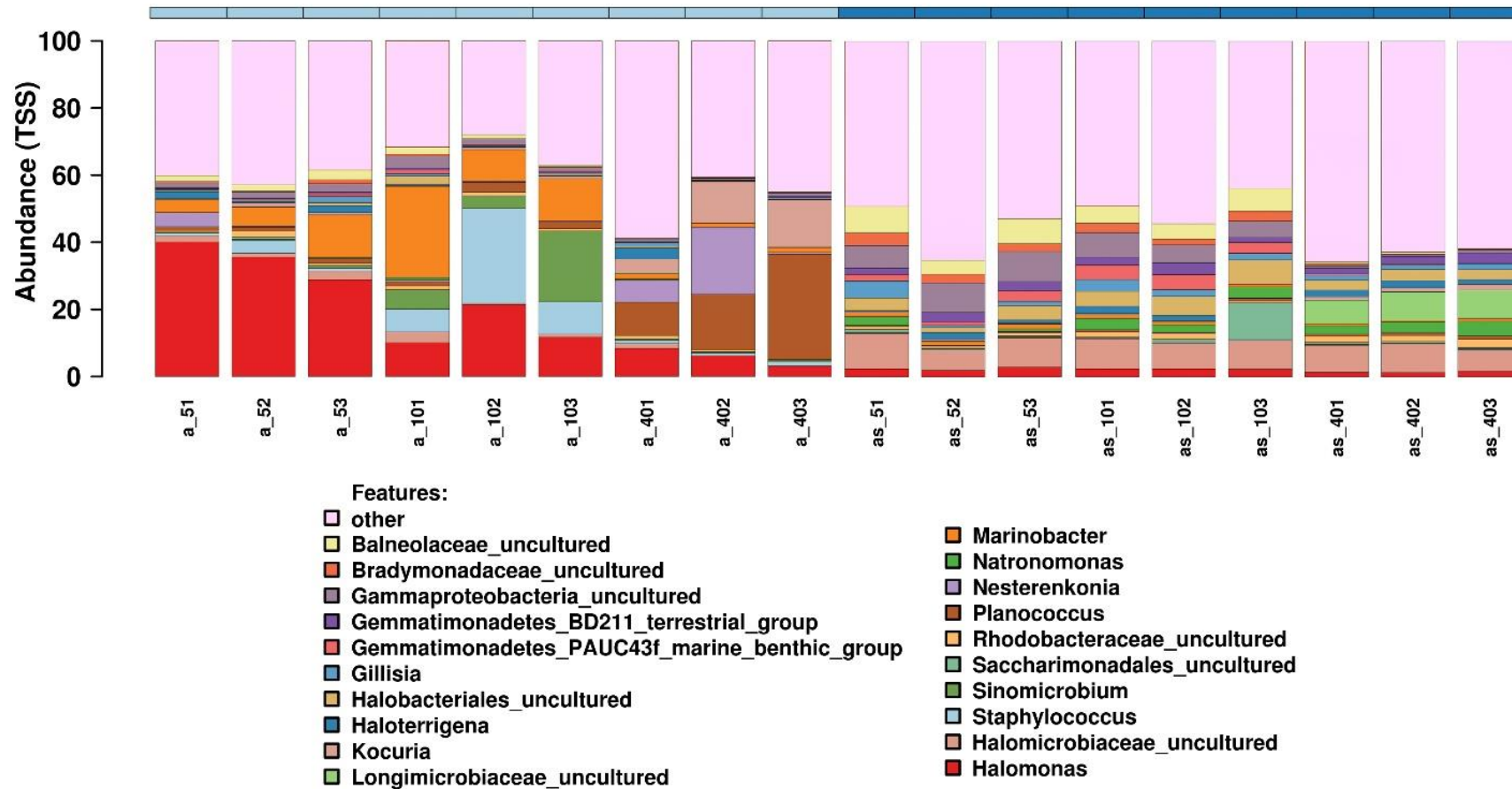
- Suaeda acuminata*** (C.A.Mey.) Moq.
rhizosphere and bulk soil samples
- at the Aral Sea shores where water receded 5years, 10years and 40 years ago
 - 16S rRNA gene and metagenomic sequencing

RESULTS: Microbiome: Very distinct microbial communities



Age and microhabitat were the most important drivers

RESULTS: Community composition and alpha diversity

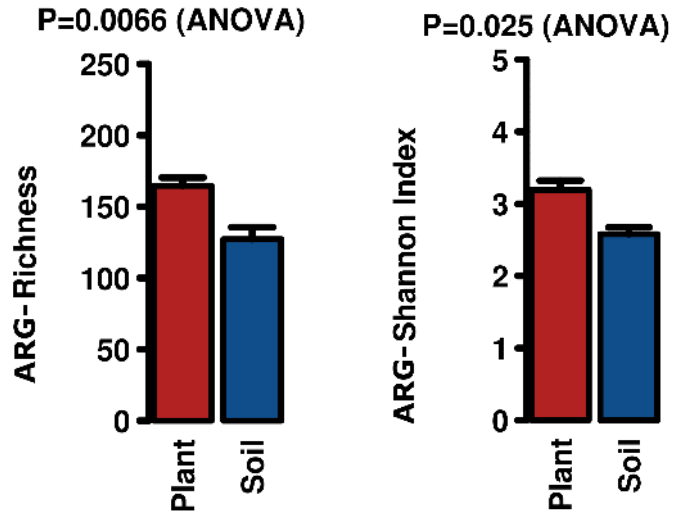


➤ Statistically significant difference in alpha diversity between plant and soil samples but not over time

↓ *Halomonas* and ↑ *Planococcus* over time without water

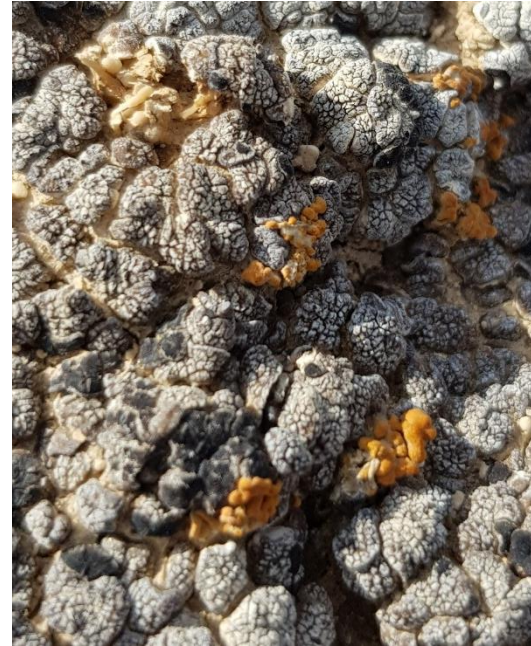
RESULTS: Resistome diversity versus Bacterial diversity

Antibiotic Resistance Genes (ARGs)

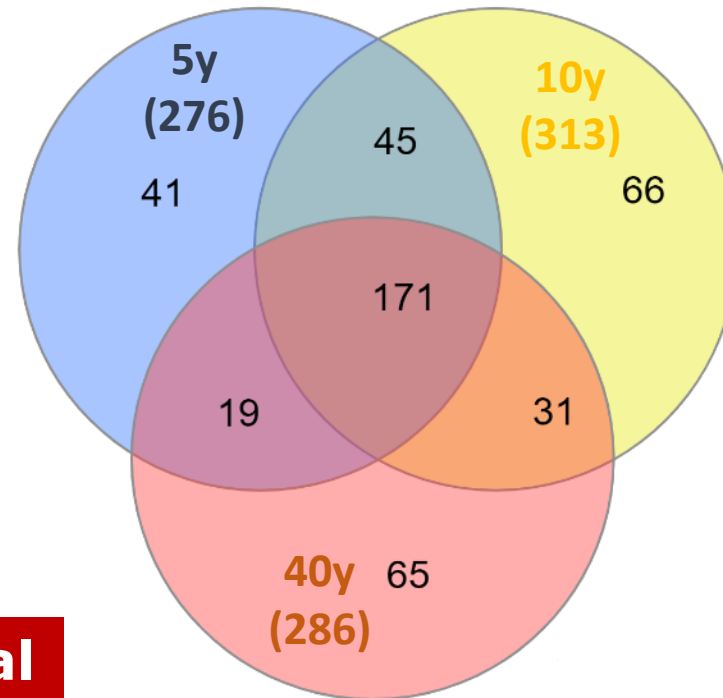
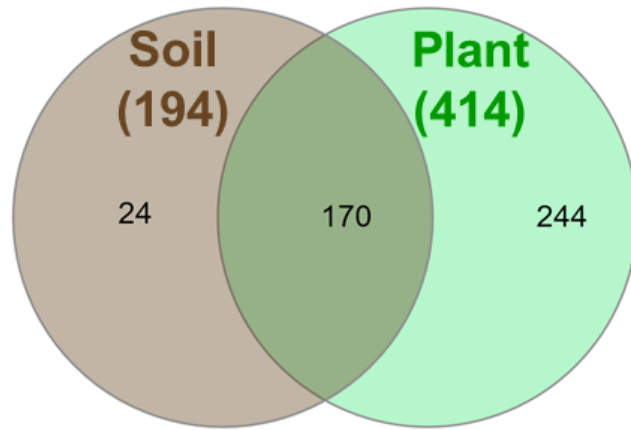


Soil:
High bacterial diversity,
low diversity of ARGs

Rhizosphere:
Lower bacterial diversity,
higher diversity of ARGs



RESULTS: Resistome diversity versus Bacterial diversity

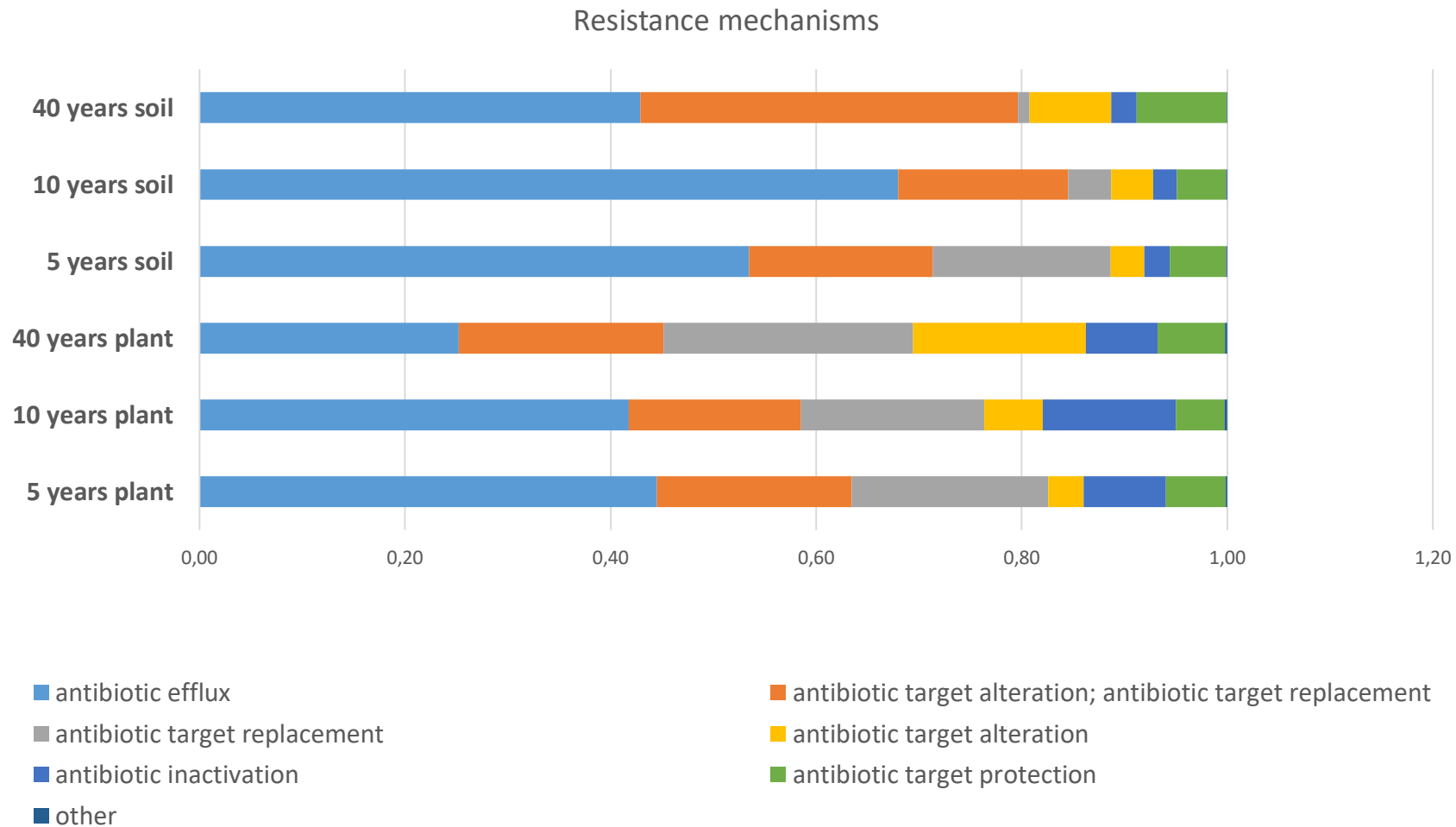


438 different ARGs in total

Habitat and Age-specific resistome



RESULTS: Resistance mechanisms

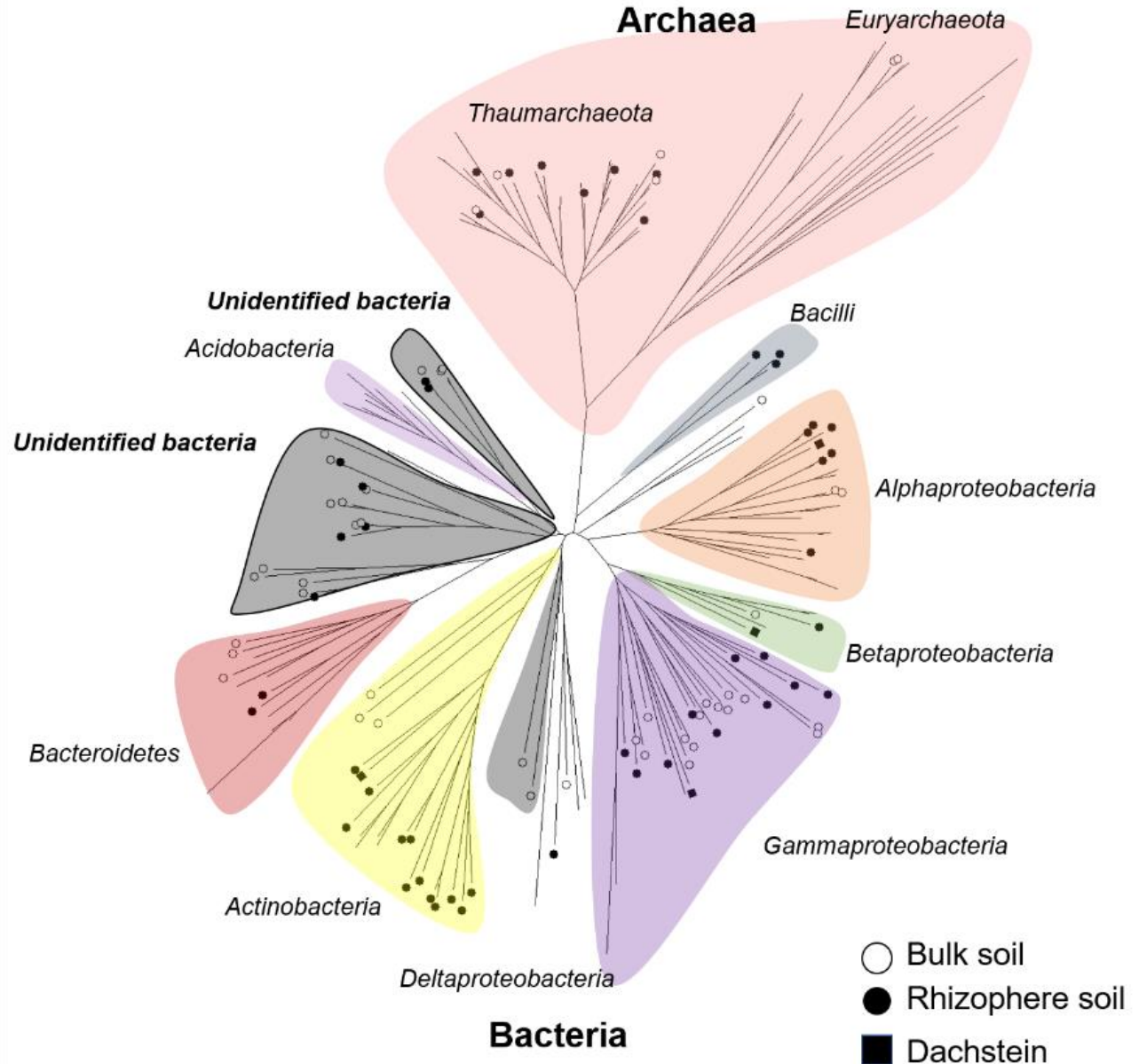


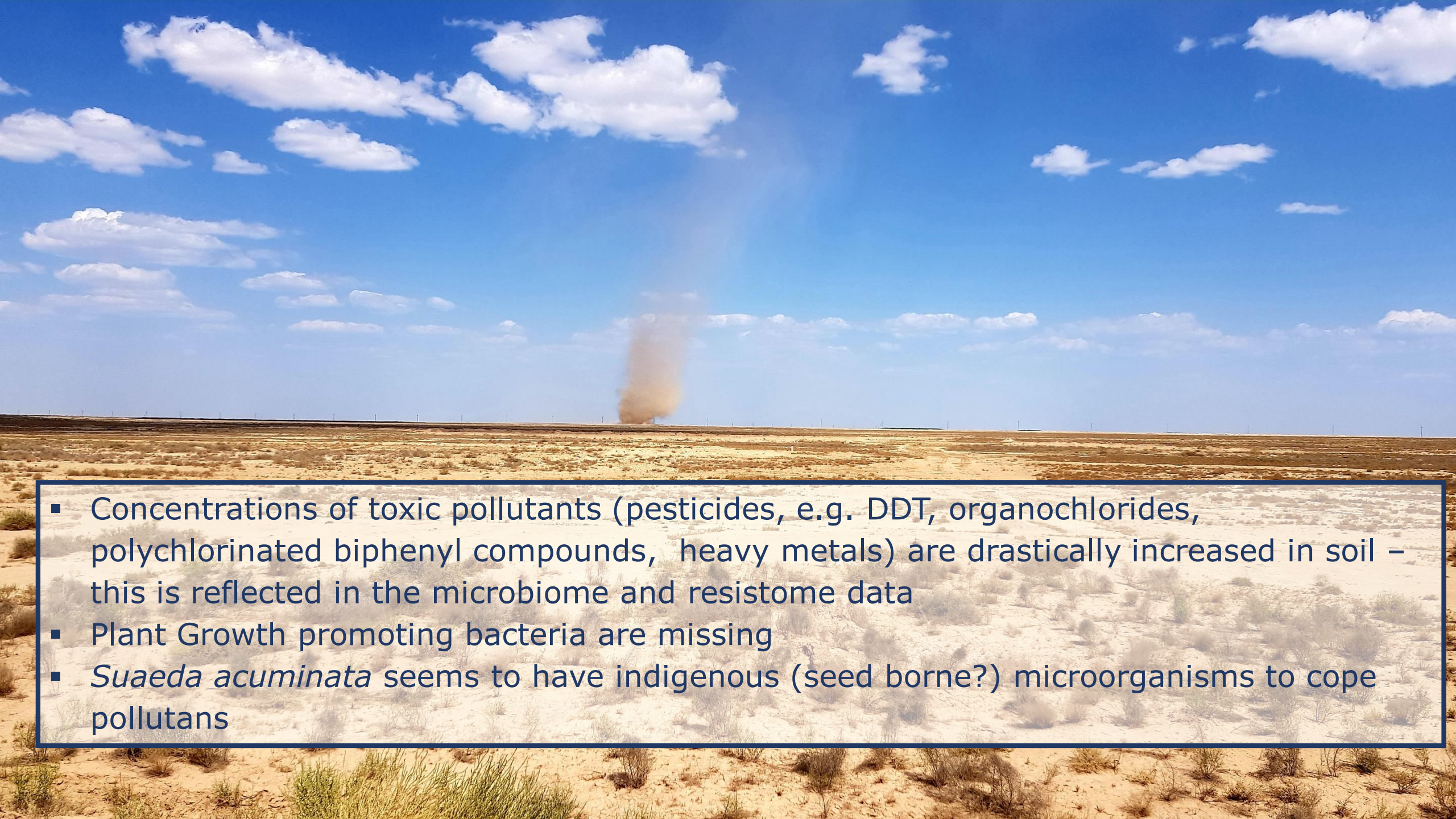
Dominance of (general) efflux mechanisms which is decreasing over time without water

Metagenome assembled genomes (MAGs)

97 MAGs from Aral Sea samples (Bacteria & Archaea)

Comparison to MAGs from environments with low anthropological input (here Dachstein Glacier, Austria, 7 MAGs)





- Concentrations of toxic pollutants (pesticides, e.g. DDT, organochlorides, polychlorinated biphenyl compounds, heavy metals) are drastically increased in soil – this is reflected in the microbiome and resistome data
- Plant Growth promoting bacteria are missing
- *Suaeda acuminata* seems to have indigenous (seed borne?) microorganisms to cope pollutants

What can we do for restoration?



- **Microbial inoculants** with plant growth promoting and stress protecting bacteria are necessary for plant growth
- **Plant rhizospheres** have a high activity, which can help to restore soil quality and recycle pollutants