

Specialized Microbiome of a Halophyte and its Role in Helping Non-Host Plants Withstand Salinity

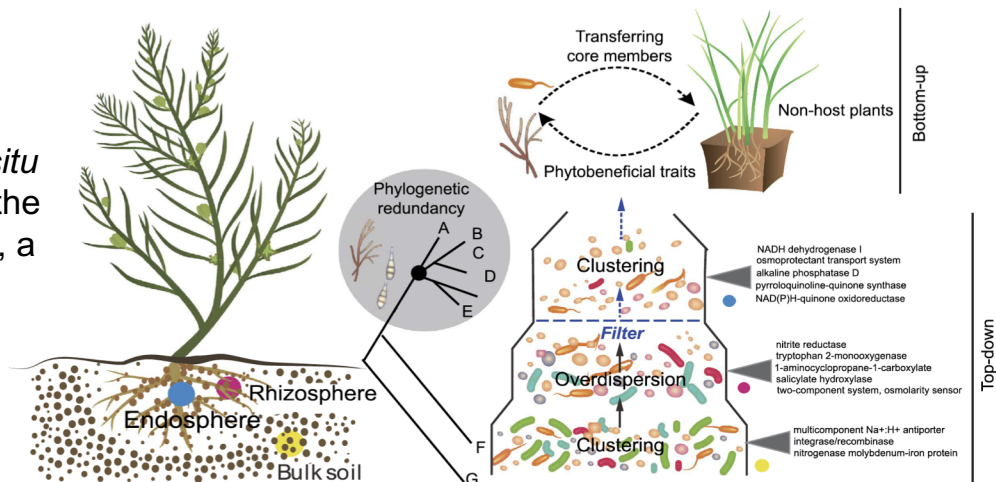


Contact: Jessy Labbé (labbejj@ornl.gov); 865.576.3478

Funding Source: Non-Profit Sector Special Research Fund of the Chinese Academy of Forestry; The National Foundation of China; DOE Office of Biological and Environmental Research, Genomic Science Program

Background

- Root microbiota is a crucial determinant of plant productivity and stress tolerance.
- We investigated the assembly and structure of *in situ* bacterial and fungal microbiomes associated with the root endosphere and rhizosphere of *Suaeda salsa*, a halo-tolerant coastal plant, to demonstrate the phytobeneficial effects of the core culturable microorganisms on stress tolerance in agricultural crops.



Conceptual illustration of the microbial community assembly and functional traits in the bulk soil (BS), rhizosphere soil (RS) and root endosphere (R).

Science

- α - and γ -proteobacteria represent the primary members of the microbiome, the root endosphere shows a lower level of phylogenetic diversity when compared to the bulk and rhizosphere soil.
- At least 14 diverse halotolerant bacterial groups were identified across all samples and fell within 4 phyla: α - and δ - proteobacteria, *Bacteroidetes* and *Verrucomicrobia*, while fungal genera *Beauveria* and *Monosporascus* were more abundant in the soil and root endosphere while *Leptosphaeria* and *Retroconis* dominate the rhizosphere.
- The genomes of rhizospheric and endophytic bacteria associated with *S. salsa* are enriched in genes contributing to salt stress acclimatization, nutrient solubilization and competitive root colonization. Both rhizospheric and endophytic *Pseudomonas* spp. were observed to be responsible for strengthening plant growth and salt stress responses, while a melanized fungus, *Montagnulaceae* sp. showed it behaved as a plant growth promoter and also increased salt tolerance.

Significance

- This study provides novel insights into the structure and functional profiling in a halophyte rhizosphere microbiome.