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**Contact 9th Meeting of the Swiss Microbial Ecology from tcastaneda@ethz.ch**

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**From** tcastaneda@ethz.ch <nicht-beantworten@sme2025.ch>

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**To** Merlin Unternährer <merlin.unt@limnol.uzh.ch>

**Name (Presenter):**

Tania Galindo

**E-Mail address:**

tcastaneda@ethz.ch

**Type of presentation:**

Oral presentation

**Title:**

Interactions of root architecture and anatomy with root microbial communities under abiotic stress in maize

**Authors:**

Tania Galindo-Castañeda, Elena Kost, Elias Barmettler, Elena Giuliano, Rafaela Feola Conz, Johan Six, Martin Hartmann

**Institution(s):**

ETH Zurich

**Abstract (300 words maximum): :**

The associations between root architecture and anatomy and soil microorganisms are important, but rarely considered in selecting plant cultivars with enhanced soil resource uptake. Including this aspect in breeding programs targeting roots could lead to the discovery of genetic determinants of microbial recruitment associated with specific root architectures or anatomies. We hypothesized that maize plants with contrasting root architecture and anatomy maintain unique microhabitats that promote the associations with different microorganisms. We studied the composition of rhizosphere and endosphere prokaryotes in greenhouse-grown maize under low nitrogen (N) by using 1.5m-tall mesocosms containing 27 L of a sandy mixture with 5 and 15% soil. We measured the intra- and inter-genotype variability in root traits and their associations with root microbiomes in two experiments. First, we assessed the microbial distribution along the root systems of a single genotype. Second, we studied four inbred genotypes with contrasting root architecture and anatomy, and associated prokaryotes. Different prokaryotic communities were found in the seminal vs nodal root systems, as well as in nodal roots at 0-40 vs 40-150 cm depth. Prokaryotic communities showed the most contrasting differences in the endosphere, and under low N compared to the rhizosphere and high N conditions. Among 5 architectural and anatomical traits measured, significant effects of root diameter, lateral root branching density, and lateral root length on the prokaryotic beta diversity of both endosphere and rhizosphere were observed within

a single genotype. Lateral root length was the only root trait significantly associated to either rhizosphere or endosphere prokaryotic diversity across the four evaluated genotypes, regardless of the fertilization regime. The selection of maize genotypes using lateral root branching density and length might involve the selection of root prokaryotic communities adapted to the different levels of this root phenotype. Lateral root length, therefore, is a trait that may present synergism with microbial associations under low nitrogen.

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