

Host Genetic Variation Drives the Differentiation in the Ecological Role of the Native *Miscanthus* Root-Associated Microbiome

Background/Objective

- The rhizosphere microbial community plays a vital role in plant health and development and can be influenced by a variety of factors including host plant genetic variation and soil conditions. However, the relative importance of these factors remains unclear.
- In this study, researchers examined prokaryotic and fungal communities present in the rhizosphere soil and root endophytic compartment of two *Miscanthus* species, *M. sinensis* and *M. floridulus*.

Approach

M. sinensis and *M. floridulus* rhizosphere soil and root endophytic samples were collected from 16 sites across their native range in Taiwan.

Microsatellites were used to characterize the genetic structure of individual *Miscanthus* populations. The 16S rRNA and fungal ITS loci were sequenced for prokaryotic and fungal communities, respectively, in both rhizosphere soil and the root endophytic compartment.

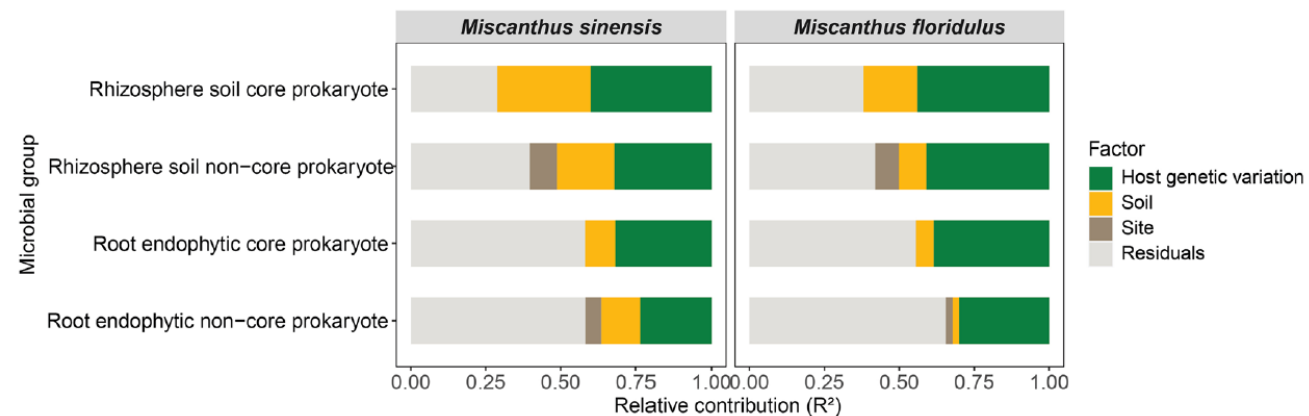
Results

Host plant genetic variation, soil characteristics, and site effects each influenced the endophytic and rhizosphere soil microbial communities of both *Miscanthus* species. Plant genetic variation had a greater impact on root endophytic communities than rhizosphere soil communities across both species. Plant genetic variation more strongly influenced the core prokaryotic community than the non-core prokaryotic community in both the rhizosphere and endophytic compartment of both species (see figure). Diazotrophs were present in the core prokaryotic microbiomes of both *Miscanthus* endophytic compartments, suggesting N-fixation capacity that could potentially enhance *Miscanthus* sustainability.

Significance/Impacts

This work demonstrates a relationship between host genetic variation and variation in the root-associated *Miscanthus* microbiome. Results from this study provide baseline data for future efforts to harness the miscanthus microbiome and its sustainability functions to enhance bioenergy crop management.

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Host genetic variation had a larger contribution than soil or site-related factors across core- and non-core-microbial communities across rhizosphere and root endophytic compartments in both species.