

Category	: Other
Select Theme	: Climate change and environmental sustainability
Endorsement email	:
Keyword 1	: Mitigation of climate change
Keyword 2	: Adaptation to climate change
Keyword 3	: Environmental sustainability
Title of Entry	: PROFILES OF RHIZOSPHERE SOIL MICROBIAL COMPOSITION AFFECTING METHANE EMISSIONS
Presenting author	: Jinyoung Barnaby
Presenting author email	: jinyoung.barnaby@ars.usda.gov
Co author 1	: 1 Woojae Kim / 2 Adam Rivers
Co author 2	: 3 Anna McClung / 4 Jude Maul
Affiliation presenting author	: U.S. Department of Agriculture, Agricultural Research Service, Dale Bumpers National Rice Research Center
Affiliation 1	: 1 Rural Development Administration, National Institute of Crop Science, South Korea / 2 U.S. Department of Agriculture, Agricultural Research Service, Genomics and Bioinformatics Research Unit
Affiliation 2	: 3 U.S. Department of Agriculture, Agricultural Research Service, Dale Bumpers National Rice Research Center / 4 U.S. Department of Agriculture, Agricultural Research Service, Sustainable Agricultural Systems Laboratory
Select only one type of presentation	: 15 minute oral presentation
Abstract	: Agriculture is recognized as a significant contributor to greenhouse gas emissions (GHGE) globally. Methane (CH ₄) is an important GHG and is 25 times more potent than CO ₂ and is the primary GHGE from flooded rice fields, which have ideal conditions for methanogens, the anaerobic bacteria that produce methane. Because of the extensive global rice acreage, reducing CH ₄ emissions due to rice production would have a significant impact on global warming. Research has shown that the amount of methane emitted from paddy rice can vary by cultivar indicating that genetics has the potential for mitigating the effects of GHGE. In this study, we sought to investigate whether genetic variation in methane emissions exists and further to understand the mechanism of soil-rice-methane producing bacteria interactions. Five rice cultivars were examined to relate seasonal methane profiles with anatomical and/or physiological characteristics i.e. root and shoot biomass, tiller number, aerenchyma density, plant height, developmental stage, etc. The results showed that root biomass was a major driver that affected total methane emissions. This was verified in a subsequent study with nine recombinant inbred line (RILs) and their parents, Francis and Rondo, segregating for methane emissions and root biomass.

Moreover, next-generation sequencing was performed to characterize the predominant microbes present in the soil microbiome among those nine RILs and their parents. The profiles of seasonal CH₄ emissions and root biomass were associated with the temporal profiles of rhizosphere soil microbial composition to understand the mechanisms of rice-soil-microorganisms interactions that produce methane. This study provided the fundamental information to identify/develop low CH₄ emitter lines with high yield potential that will have sustainable grain production in response to changing environments.

[Read Less»](#)

Uploaded Files »

No files found.