

Category	: 8th Rice Genetics Symposium
Select Theme	: Genetics of Biotic interactions: Stress tolerance, Mitigation and Microbiome
Endorsement email	:
Genetics of Biotic interactions Stress tolerance Mitigation and MicrobiomeKeyword 1	: microbiome
Genetics of Biotic interactions Stress tolerance Mitigation and Microbiome Keyword 2	: bacteria
Genetics of Biotic interactions Stress tolerance Mitigation and MicrobiomeKeyword 3	:
Title of Entry	: Community structural and predictive functional analyses show evidence of association between leaf microbiome and rice plant
Presenting author	: Dale Pinili
Presenting author email	: dspinili@up.edu.ph
Co author 1	: Ricardo Oliva
Co author 2	: Veronica Roman-Reyna
Co author 3	:
Co author 4	:
Co author 5	:
Co author 6	:
Co author 7	:
Co author 8	:
Co author 9	:
Co author 10	:
Co author 11	:
Co author 12	:
Co author 13	:
Co author 14	:

Affiliation presenting author : University of the Philippines Los Banos

Affiliation 1 : International Rice Research Institute

Affiliation 2 : International Rice Research Institute

Affiliation 3 :

Affiliation 4 :

Affiliation 5 :

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Affiliation 7 :

Affiliation 8 :

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Select only one type of presentation : 15 minute oral presentation

Abstract : In recent studies, phyllomicrobiomes (or leaf microbiomes) hold remarkable biological information on how they affect their plant hosts and vice versa, yet challenging to understand due to high variations in their community structures. We investigated the phyllomicrobiome of 3,204 rice varieties through read-based metagenomics and statistical approaches in order to provide further information about plant-microbiome interactions. In terms of microbial diversity, the dominating bacterial groups (including Proteobacteria, Actinobacteria, Firmicutes, Tenericutes, and methanotrophic members of Euryarchaeota) in rice leaves suggest that the phyllomicrobiome structure is a result of mixed influence of the surrounding soil, water, and other environmental factors. On the other hand, discriminative analyses on the phyllomicrobiome abundance patterns revealed significant difference ($P = 0.001$) between Indica and Japonica varieties, suggesting that phyllomicrobiome structure reflects the phylogenetic characteristics of its host despite the inherently high variations. Furthermore, we conducted genome-wide association study using predicted functional data of the phyllomicrobiome as phenotypic traits of the 3024 rice varieties. Results showed strong signals ($P < 1.09 \times 10^{-8}$) located at chromosomes 2 and 11 proximal to several genes involved in stress-related responses like nitrogen uptake and temperature changes. Our findings demonstrate a strong evidence of host-microbiome association in rice plant at the genetic level by looking into the metabolic aspect of the phyllomicrobiome, in addition to its structural characteristics.

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