

Engineering rice root system architecture and exudate composition to optimize rhizosphere interactions.

Maria Florencia Ercoli¹, Subah Soni¹, Tracy Satomi Weitz¹, Artur Teixeira de Araujo Junior¹, Alexandra M. Shigenaga¹, Katerina Estera-Molina^{2,3}, Jack Kim³, Ling-Dong Shi³, Jill Banfield³, Jennifer Pett-Ridge^{2,3}, and Pamela C. Ronald^{1,3,4}.

¹Department of Plant Pathology and the Genome Center, University of California, Davis, CA 95616, USA.

²Physical and Life Sciences Directorate, Lawrence Livermore National Laboratory, Livermore, California, USA

³Innovative Genomics Institute, University of California, Berkeley, CA, USA.

⁴Grass Genetics, Joint BioEnergy Institute, Lawrence Berkeley National Laboratory, Berkeley, California 94720

Approximately 12% of anthropogenic methane emissions are attributed to rice paddy cultivation. We are exploring genetic strategies to reduce methane emissions. This study shows that OsPSY1, a member of the PLANT PEPTIDE SULFATED IN TYROSINE (PSYs) family, regulates root system architecture (RSA) in rice. OsPSY1 ectopic expression increases root length in rice. Root RNA-seq analysis showed that OsPSY1 modifies the expression of genes involved in primary and secondary metabolite biosynthesis. These metabolites are secreted into soil as part of root exudates. These results suggest that ectopic expression of OsPSY1 affects exudate composition and may alter rhizosphere dynamics. To test this hypothesis, we grew wild type and *Ubi:OsPSY1* rice transgenic lines in agricultural soil. We coupled the collection of rhizosphere samples with methane flux measurements throughout rice development. We observed that *Ubi:OsPSY1* transgenic rice lines exhibited a 30% reduction in methane emissions compared to controls at heading stage. Ongoing analysis of rhizosphere samples aims to elucidate the connection between modified RSA, root exudates, and microbial interactions, highlighting their collective impact on carbon cycling and greenhouse gas emissions.