
Oral sessions | Crop Genetics and Physiology | O42: Assimilate Partitioning for Crop Productivity and Quality

[O42] Assimilate Partitioning for Crop Productivity and Quality

Chair: Naohiro Aoki (The University of Tokyo, Japan)

Chair: Tatsuro Hirose (Takasaki University of Health and Welfare, Japan)

Chair: Yong-Ling Ruan (The University of Newcastle, Australia)

Thu. Sep 9, 2021 2:30 PM - 4:30 PM Room 4 (Oral) (Crop Genetics and Physiology)

3:25 PM - 3:40 PM

[O42-04] What Factor Affects Genotypic Difference in Endophytic Nitrogen-fixing Ability in Rice?

*Nominated for Presentation Awards

○Takanori Okamoto¹, Rina Shinjo¹, Arisa Nishihara², Kazuma Uesaka³, Aiko Tanaka¹, Daisuke Sugiura¹, Motohiko Kondo¹ (1. Graduate School of Bioagricultural Sciences, Nagoya University, Japan, 2. Bioproduction Research Institute, National Institute of Advanced Industrial Science and Technology, Japan, 3. The Center for Gene Research, Nagoya University, Japan)

Enhancement of nitrogen (N) fixing ability by endophytic bacteria in rice could lead to improving N utilization under low available N conditions. Endophytic N-fixing bacteria need a lot of energy to fix atmospheric N. However, it is unknown what carbon source and bacteria would affect N-fixing activity in rice. This study aimed to explore the effects of non-structural carbohydrates (NSC) on the N-fixing activity and the endophytic bacterial flora in field-grown rice.

Field experiments were conducted at the Togo field of Nagoya University in 2017 & 2018. Six varieties were grown in 2017, and eight varieties and two mutant lines of Nipponbare (*agp1* and *lse1*, each with different compositions of NSC) were grown in 2018. Acetylene reduction activity (ARA; the N-fixing activity) and NSC (glucose, sucrose and starch) concentrations in rice stems were determined at the heading stage. For the bacterial flora analysis, total DNA were extracted from the stems of three varieties and one mutant grown in 2018. Two genes were amplified by a primer set of 16S rRNA gene and nitrogenase (*nifH*) gene-specific primers (PoIF/PoIR) using Illumina MiSeq.

CG14 and *agp1* mutant with higher sugar concentration showed higher ARA than Leafstar with higher starch concentration. These results suggest that stem ARA was influenced by the levels of soluble sugars. Bacterial flora analysis suggested the presence of variety and line-specific bacterial flora in both 16S rRNA and *nifH* genes. We will further discuss a new strategy for enhancing N-fixing ability in rice.