

[P4] Crop Genetics and Physiology

Thu. Sep 9, 2021 12:15 PM - 2:00 PM Room 4 (Poster) (Crop Genetics and Physiology)

1:15 PM - 2:00 PM

[P4-02] Genetic Diversities of Traits Associated with Culm Strength Using a *Temperate Japonica* Rice Varieties

*Nominated for Presentation Awards

○Koki Chigira¹, Natsuko Kojima¹, Masanori Yamasaki², Shunsuke Adachi³, Taiichiro Ookawa¹ (1. Graduate School of Agriculture, Tokyo University of Agriculture and Technology, Japan, 2. Food Resources Education and Research Center, Graduate School of Agricultural Science, Kobe University, Japan, 3. College of Agriculture, Ibaraki University, Japan)

Lodging is a serious problem in rice production, leading to yield loss and low grain quality. Having lodging resistance, modern varieties with semi-dwarfism have contributed to increasing rice productivity. However, their low biomass production and lodging under extreme weather (e.x. super typhoon hitting) have been still challenging for developing high yielding varieties. For next generation rice, the breeding of new type varieties with strong culms is a promising strategy. In this research, we cultivated a *temperate japonica* population composed of 135 varieties and evaluated the traits associated with culm strength over two years. We also detected the region associated with these traits by genome-wide association studies (GWAS). Large variances were observed in the traits for culm strength among the varieties, indicating that there were causal genes responsible for culm strength. The two remarkable landraces named 'Kameji' and 'Omachi' had superior traits for culm strength, and have been rarely used in modern breeding programs. The GWAS revealed 55 candidate regions associated with the traits, and the most likely association with culm thickness was detected on chromosome 5. From gene-based GWAS, some candidate genes which might be involved in cell division were detected in this region. Several landraces could have beneficial alleles for increasing culm diameter and culm strength. We need to identify causal genes and elucidate their physiological functions. The information obtained from this study will be useful for breeding new varieties with strong culms.