Genetic and network analysis of wild rice introgression lines with improved production under low nitrogen/nutrient conditions

[1]Adu B. G., [1,2]Ohmori Y., [1]Fujiwara T.

[1]Laboratory of Plant Nutrition, Grad Sch. Agric. Life Sci., The University of Tokyo.
[2]Agricultural Bioinformatics Research Unit, The University of Tokyo.
Email: adubright1992@gmail.com

Abstract

To reduce fertilizer demand and ensure sustainable rice production, the development of high yielding cultivars under low nitrogen (N) conditions has become a center stage of most breeding research. Studies have shown that wild rice species serve as useful genetic resources for improving cultivated species responses to abiotic stresses. Several QTLs/genes related to low N tolerance have been identified with the pyramiding of these loci or genes from wild rices suggested to improve grain yield under limited nitrogen conditions. Two wild rice introgression lines (KR8, KR37) that carries a small region of the *Oryza rufipogon* genome in the *O. sativa* L. cv Koshihikari background was found to produce higher panicle yield than the recurrent cultivar parents under deficient nutrient conditions over several years. Candidate regions (QTLs) for panicle weight have been identified for KR8 (*qGY1*) and KR37 (*qGY6*) using NGS and QTLseq data analysis. F_3 pyramiding lines harboring two QTLs from KR8 x KR37 showed over 40% increase in panicle weight over the best parent under nutrient deficient paddy conditions suggesting positive QTL interaction effects. In addition, we also focused on molecular insights into low N tolerance through gene co-expression analysis and identified gene modules (networks) related to cell wall biogenesis, cellulose metabolism and auxin signaling which could coordinates cell wall modification, nutrient signaling for improved root organ growth in the introgression lines. Detailed results will be presented.