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Marker-assisted breeding to Develop Salt Tolerant and Low Lignin-whole Crop Silage Rice for Versatile Use

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[Introduction]

Developing new rice varieties for feed, the main goals are to enhance biomass production and lodging resistance as well as to improve feed digestibility. It is also important to have salt tolerance to adapt to reclaimed land for expansion of cultivation through adaptation to harsh environment. And so salt tolerant *Saltol* QTL and lignin modification has been a breeding target for the improvements of salt tolerance, forage digestibility and fermentation in whole crop silage (WCS) rice. In rice, major QTL for salinity tolerance named *Saltol*, which responsible for seedling stage salinity tolerance was identified on the short arm of chromosome 1 and explain more than 40% of the phenotypic variation. Also, *gold hull and internode 2 (gh2)* was identified as a lignin-deficient mutant. *gh2* exhibits a reddish-brown pigmentation in the hull and the internode is located on the short arm of chromosome 2 and codes for cinnamyl-alcohol dehydrogenase (CAD). We are now marker-aided introgressing *Saltol* and CAD and selecting a high-biomass, salt tolerant and low-lignin WCS lines for developing WCS rice variety improved salt tolerance and digestibility.

[Materials and Methods]

A total of 19 primers for detecting the *Saltol* QTLs were applied to the parent varieties to select polymorphic primers for screening the breeding populations. The 443 'Yeongwoo/IR64-*Saltol*' F₆ lines were analyzed to evaluate the introgression of *Saltol* fragment into 'Yeongwoo' cultivar by 0.6% (12dSm⁻¹) salt treatment. The 55 Jungmo1038/J.collection lines (F₆) including parental cultivar were grown and harvested 5-internode at 20 days after heading. We measured lignin content and developed gene specific marker using J.collection cultivar CAD gene first intron region and applied it to the 55 promising lignin-deficient lines.

[Results and Discussion]

For target *Saltol* QTL selection, after 11 polymorphic markers were used for screening homozygote plants, the some promising lines were selected based on visual symptoms. Using IRR1's SES for rice, when the susceptible variety IR64 scored 9 and FL478 were used as highly tolerant scored 3, all the 'Yeongwoo/IR64-*Saltol*' selected plants have the same score as the tolerant checks. To identify lines harboring mutated CAD gene(*gh2*), we performed marker-assisted selection. As results, among total 55 'Jungmo1038/J.collection' lines(F₆) including parental cultivar, *gh2* were introgressed into 44 lines. Also, those lines had lignin content range from 0.82 to 6.61%, compared to 'Jungmo1038'(1.53), 'J.collection'(0.98), 'Yeongwoo'(2.22). Based on genotype and low-lignin phenotype, we finally selected 19 promising high biomass-low lignin elite lines. These studies will provide new strategies for improving salt tolerance, forage digestibility and fermentation in WCS rice.

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