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Selective introgression lines-based QTL mapping and QTL-designed breeding in rice

Advances in re-sequencing and fast phenotyping technologies greatly facilitate gene mapping and favorable allele mining of important agronomic traits from germplasms and mapping populations in crops. However, separation of QTL mapping studies from breeding practice results in difficult use of most mapping results in breeding program due to sensitivity of QTL to genetic background and environment. Here, we proposed a selective introgression line strategy to tightly connect QTL mapping and QTL-designed breeding together. Using three sets of trait-specific introgression lines (ILs) in a *Xian (indica)* variety Huanghuazhan (HHZ) background, we identified nine drought tolerance QTL (DT-QTL) and seven low nitrogen tolerance QTL (LNT-QTL) by a segregation distortion approach and a genome-wide association study, respectively. Based on performances of DT and LNT and genotypes at the detected QTL, two ILs M79 and M387 with DT and LNT were selected for cross-making to validate the identified QTL and to develop DT and LNT rice lines by pyramiding two DT-QTL (*qDT3.9* and *qDT6.3*) and two LNT-QTL (*qGY1* and *qSF8*). Using four pairs of kompetitive allele specific PCR (KASP) SNP markers, we selected 66 F₂ individuals with different combinations of the target DT- and LNT-QTL favorable alleles and they showed expected improvement in DT and/or LNT, which were further validated by the significant improvement in DT and/or LNT of their F₃ progeny testing. Based on evaluation of pyramiding lines in F₃ lines under drought, low nitrogen (LN) and normal conditions, four promising pyramiding lines having different QTL favorable alleles were selected, which showed significantly improved tolerances to drought and/or LN than HHZ and their IL parents. Our results demonstrated that trait-specific ILs could effectively connect QTL mapping and QTL pyramiding breeding, and designed QTL pyramiding (DQP) using ILs could be more effective in molecular rice breeding for complex quantitative traits.

Recent publication:

1. Ali J, Xu JL, Gao YM, et al (2017) Harnessing the hidden genetic diversity for improving multiple abiotic stress tolerance in rice (*Oryza sativa* L.). PLoS One 12: e0172515.
2. Cui Y, Zhang F, Xu J, et al (2015) Mapping quantitative trait loci in selected breeding populations: a segregation distortion approach. Heredity 115, 538–546.
3. Li ZK, Fu BY, Gao YM, X, et al (2005) Genome- wide introgression lines and their use in genetic and molecular dissection of complex phenotypes in rice (*Oryza sativa* L.). Plant Mol Biol 59, 33–52.

Biography

Jianlong Xu got PhD degree on Crop Genetics & Breeding in 2001 in Zhejiang University, China. After finishing postdoctoral career of molecular rice breeding for two years at IRRI, he joined the Institute of Crop Sciences, Chinese Academy Agricultural Sciences, focusing on gene mapping and favorable allele mining for molecular rice breeding in high yield, high grain quality, abiotic and biotic stress tolerance. So far, he has published 70 papers in international journals, obtained four provincial awards and 13 patents.

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