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Identification and Characterization of Quantitative Trait Loci in Nitrogen Utilization of Rice

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Nitrogen is quantitatively the most essential nutritient for plant growth and hence a major limiting factor in the productivity. The exogenous concentration of nitrogen directly influences the growth rates. For example, root elongation to spread its surface area is more active under nitrogen deficient condition. The use of natural variation of rice is one of the best way in identification of regulatory genes in nitrogen utilization. Thirty-eight chromosome segment substitution lines (CSSLs) developed between Koshihikari (japonica rice) and Kasalath (indica rice) were employed in this study to detect quantitative trait loci (QTLs) controlling nitrogen utilizations, demonstrating comparison of maximum root length as an indicator grown under various concentrations of NH_4^+.

Germinated seedlings were hydroponically grown in an outdoor-growth chamber supplied with 5, 50 or 500 μM NH_4^+ for a week, and then maximum length of roots were determined. A probability of less than 0.01 (t-test) was used as the threshold for the detection of QTL. The root of Kasalath was statically longer than that of Koshihikari under various NH_4^+ applications tested. Many QTLs were detected for root length under various concentrations of NH_4^+ on several chromosomes, indicating chromosomes 1, 2, 4 and 6-12. In particular, Kasalath allele on a QTL of chromosome 6 greatly promoted the root elongation under various NH_4^+ concentrations. A nearly-isogenic line, NIL-A, was grown in an outdoor-growth chamber supplied with 5, 50, 500 or 1000 μM NH_4^+ for 8 days. When grown under either 50 or 500 μM NH_4^+ concentration, total nitrogen in the NIL-A was about 20% higher than that in the Line-B which had Kasalath segment on chromosome 6 but the QTL region is replaced with a segment of Koshihikari. On the other hand, total nitrogen in the NIL-A was equal to that in the Line-B under either 5 or 1000 μM NH_4^+ concentration. These data suggest that the QTL gene plays an important role in the control of NH_4^+ utilization at a specific range of NH_4^+ concentration. Linkage analyses for maximum root length revealed that target QTL was delimited in a 135 kb region. High-resolution mapping is now in progress.