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Identification of QTLs for Improvement of Plant Type in Rice (*Oryza sativa* L.) Using Koshihikari / Kasalath Chromosome Segment Substitution Lines and Backcross Progeny F$_2$ Population

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Abstract: Thirty-nine chromosome segment substitution lines (CSSLs) population derived from a Koshihikari/Kasalath cross was used for quantitative trait locus (QTL) analysis of plant type in rice (*Oryza sativa* L.). Putative rough QTLs (26.2—60.3cM of Kasalath chromosomal segments) for culm length, plant height, panicle number, chlorophyll content of flag leaf blade at heading and specific leaf weight, were mapped on the several chromosomal segments based on the comparison of CSSLs with Koshihikari in the field experiment for 3 years. In order to verify and narrow QTLs detected in CSSLs, we conducted QTL analyses using F$_2$ populations derived from a cross between Koshihikari and target CSSL holding a putative rough QTL. The *qPN-2*, QTL for panicle number was mapped on chromosome 2. In traits of flag leaf, the *qCHL-4-1* and *qCHL-4-2* for chlorophyll content was mapped on chromosome 4, and the *qSLW-7* for specific leaf weight on chromosome 7. All QTLs were detected in narrow marker intervals, compared with rough QTLs in CSSLs. The *qPN-2*, *qCHL-4-1* and *qCHL-4-2* had only additive effect. On the other hand, the *qSLW-7* showed over-dominance. It could be emphasized

that QTL analysis in the present study with the combination of CSSLs and backcross progeny F_2 population can not only verify the rough QTLs detected in CSSLs but also estimate allelic effects on the QTL.

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