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QTLs analysis associated with a major agronomic traits in hanareum2×unkwang rice recombinant inbred line

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Abstract

This study was carried out to improve yield potential of Tongil type rice variety based on QTLs analysis associated with yield component using a total of 386 rice recombinant inbred lines (RILs) derived from a cross between Tongil type high yield variety “Hanareum2” and Japonica variety “Unkwang”. 384 SNP markers were used, and 241 of them (62.6%) were polymorphic between Hanareum2 and Unkwang. One hundred forty-four QTLs in 11 traits, such as heading days, were detected. Most of them were 21 QTLs associated with 1000 grain weight and the least was 8 QTLs associated with panicle number. The QTL, qDTH3-2 associated with days to heading was identified to delay heading date for 2.4～2.6 day. Eleven QTLs were associated with culm length. The QTL, qCL1-2 on chromosome 1, was identified to decrease culm length. A total of 16 QTLs were detected for panicle length. Three QTLs, qPL3, qPL6, and qPL7-1 were increased panicle length. Seven QTLs related to panicle number except qPN7 were increased the number of panicle. Four QTLs related to grain number per panicle, qGNP2-1, qGNP6, and qGNP7, were increased the number of grains. Three QTLs associated with grain filling rate, qGFR1, qGFR2-2, and qGFR7-1 were increased grain filling rate. Twelve QTLs associated with 1,000 grain weight. were increased the grain weight. Fourteen QTLs were identified associated with grain length. 10 QTLs, such as qGL1-1, were increasing grain. Fifteen QTLs associated with grain width were detected. The 8 QTLs, such as qGW1-1, were elongated grain width. Seventeen QTLs were associated with grain thickness, and ten QTLs of them were increased grain thickness. We need further study to develop introgression lines of each QTL to improve yield potential of Tongil type rice variety,

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