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Mapping Quantitative Trait Loci Associated with Arsenic Tolerance in a Double Haploid Population of Rice (*Oryza sativa* L.)

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[Introduction]

Rice (*Oryza sativa* L.) is a staple meal consumed by more than half of the world population. Arsenic (As) is a toxic metalloid that affects the major rice-growing regions of the world and considered as class (1) carcinogen. Rice paddy fields in South Asia are mostly dependent on arsenic-contaminated water sources due to which rice takes up the arsenic from the soil through roots and accumulates it in plant different parts. Here, we present a quantitative trait locus (QTL) mapping study to find out candidate genes conferring As toxicity tolerance in rice (*Oryza sativa* L.) at the seedling stage.

[Materials and Methods]

Three weeks old, 120 double haploid CNDH lines derived from a cross between the Indica variety Cheongcheong and the Japonica variety Nagdong and their parental lines were used by treating with 25 μM As. After 2 weeks of As stress, 5 traits such as; shoot length (SL), root length (RL), shoot fresh weight (SFW), root fresh weight (RFW), and chlorophyll contents (CHC) were measured. A linkage map of 12 rice chromosomes was constructed from genotypic data DH lines using 778 SSR markers. The linkage map covered a total genetic distance of 2121.7 cM of the rice genome with an average interval of 10.6 cM between markers.

[Results and Discussion]

A total of seventeen QTLs (LOD >2) were mapped on chromosomes 1,2,3,6,7,8,9,11, and 12 using composite interval mapping with trait-increasing alleles coming from both parents. Five QTLs for SL, two QTLs for RL, five QTLs for SHL, three QTLs for RFW, and two QTLs for CHC were detected. The QTL *qCHC-3* having an LOD score of 4.13 and phenotypic variance of 27% within the interval RM6931-RM6266 on chromosome 3 was screened for candidate genes related to arsenic tolerance in rice. A total of 11 genes were screened in this interval based on gene ontology.

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