

**Mapping of QTLs associated with to AG tolerance at seedling stage in rice (*Oryza sativa* L.)**

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**[Introduction]**

Stable germination and seedling establishment is an important factors for the success of direct seeding cultivation. In order to develop rice cultivar adaptable to wet direct seeding, it requires the ability to germinate at low oxygen condition. This study was conducted to get a genetic basis of tolerance of anaerobic conditions during germination.

**[Materials and Methods]**

QTL study was conducted using a population derived from a cross between Nampyeong, a Korean japonica variety, and WD3, an AG tolerant weedy rice from Korea. Phenotypic data was collected based on the survival rates of the seedlings at 30 days after sowing of dry seeds under 10 cm of water in field condition. QTL mapping was conducted using composite interval mapping (CIM) method.

**[Results and Discussions]**

AG of RILs ranged from 0.0 to 82.0% in Phytotron and 0.0 to 50.0% in Field condition. Linkage map was constructed using 917 SNP markers. The map covered 1,186cM, with a mean inter-marker distance of 1.3cM. Four putative QTLs for AG were detected, one on each of chromosomes 1, 3, 7 and 8. The WD3 alleles in three QTLs on chromosome 3, 7 and 8 act to increase LTG and Nampyeong allele in one QTL on chromosome 1 act to increase LTG. We propose that WD3 could make a major contribution to improving AG in rice breeding programs.

**[Acknowledgements]**

This research was supported by a grant from "Cooperative Research Program for Agriculture Science & Technology Development (PJ0110202018)" Rural Development Administration, Republic of Korea.

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