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**Genetic dissection of arsenic tolerance in rice (*Oryza sativa* L.) by a
genome - wide association study**

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Abstract

Rice (*Oryza sativa* L.) is the staple food for more than half of the world's population, especially in low income countries. Thus, it plays a major role in ensuring food security. Arsenic (As) is a carcinogen I heavy metal. It impairs the plant's growth and development and negatively impacts human health. In anerobic soil conditions that are prevalent in paddy rice fields, As is reduced from arsenate (As (V)) to arsenite (As (III)). The latter is more efficiently taken up by the plant and therefore more harmful. A genome - wide association study was conducted in order to reveal candidate loci that regulate As tolerance during germination. A newly composed panel of 267 rice genotypes covering all subgroups of Asian rice were used for phenotypic evaluation. Population structure analysis distinguished the panel in two clusters, an *indica* and *japonica* subgroup. Seeds were germinated under normal conditions and in a toxic 10 ppm As solution for 14 days. The germination rate after one week was inhibited by 72.6 % and after 14 days by 87 % on average. Plumule length decreased by 55.9 % compared to the control. Radical length was even more inhibited by 74.2 %. The seedling vigor index (SVI) was lowered to 92.8 % compared to the control. Association mapping correlated the relative phenotypic values and an average of 211,284 single nucleotide polymorphism (SNP) by using a mixed linear model. It detected 8 significant markers ($-\log_{10}(\text{P-value}) = 4$) on chromosome 2 and 4 for the relative germination rate 7 and 14 days after sowing (DAS) and 6 significant markers ($-\log_{10}(\text{P-value}) = 3.5$) on chromosome 3, 6, 8, 11 and 12 for the relative plumule length and relative SVI. Haplotype analysis demonstrated that As tolerance was not specific to any subgroup. Linkage block (LD) analysis revealed that 12 markers were located in different linkage blocks, where only 7 blocks harbored genes. LD blocks were small, therefore only two gene loci in two different LD blocks were completely located in their respective area. They were found for the relative germination rate 14 DAS. Both genes were located on chromosome 2. They encoded for an ubiquitin-conjugating enzyme and a GEM. Furthermore, two genes encoding for two enzymes belonging to the serine protease family, a serine carboxypeptidase (*OsSCP8*) and a Clp (*OsClp3*), were identified. This study showed the adverse effect of arsenite on germinating seeds and the opportunity of using GWAS for revealing insights into the genetic dissection of arsenic tolerance.