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Genome-Wide Association Study to Understand the Genetics of Manganese Toxicity Tolerance in Rice

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Abstract

Manganese is a transition metal occurring in different oxidative states. Rice (*Oryza sativa* L.) is mostly cultivated in anaerobic soil conditions where micro-organisms use redox active metals such as manganese as final electron acceptors to complete their energy metabolism. In this process, Mn^{4+} ions are reduced to Mn^{2+} ions leading to high levels of plant available manganese. Therefore, flooded rice fields are often characterised by high levels of manganese in soil solution, which can become toxic when taken up by the plants. Here, we discuss a genome-wide association study (GWAS) to identify candidate loci conferring manganese toxicity tolerance in rice. A diversity panel of 288 rice genotypes representing indica and japonica sub-populations was screened. 12 days old rice seedlings were grown in hydroponics at 5ppm manganese concentration for three weeks to induce toxicity effects. Manganese toxicity significantly affected several biomass traits with reduction of 29% in root weight, 21% in shoot weight, 9% in root length, 4% in shoot length and 18% in tiller numbers when averaged over all genotypes. Association mapping based on more than 30,000 single nucleotide polymorphism (SNP) markers produced 11 significant markers throughout the genome (significance threshold of $p < 0.0001$). Linkage disequilibrium blocks associated with significant markers in chromosome 6 yielded 58 candidate genes. The candidate region comprises genes coding for proteins like receptor kinase, transposon protein, RING-H2-finger protein, retrotransposon protein, F-box domain and LRR containing protein, resistance LR10 protein and coffeoyl-CoA O-methyltransferase protein. Sequence variation in contrasting haplotypes will be determined to test the validity of candidate genes found on target locus on chromosome 6. This study indicates significant natural variation in rice to high level of manganese and possibility of using GWAS to unfold the genetic factors responsible for manganese toxicity tolerance.

Keywords: GWAS, manganese, rice