

Genome-wide association study to understand the genetics of manganese toxicity tolerance in rice

Shrestha, A.¹, A. K. Dziwornu¹ and M. Frei¹

1: University of Bonn

Corresponding author: m.frei@uni-bonn.de

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 characterized by high levels of manganese in soil solution, which can become toxic when taken up into the plants. To test genotypic differences in response to excess Mn at different concentrations, seven genotypes of rice were grown in hydroponics with concentrations of manganese ranging from 0.5 (optimum concentration for growing rice in hydroponics) to 50 ppm. A toxic effect of manganese was observed already at 1 ppm, which led to almost 12% reduction in root weight and 0.2% reduction in shoot weight when averaged over all genotypes. There was 17% reduction in shoot weight at 2 ppm and 40% at 50 ppm concentration. Likewise, root dry weight was reduced by 12% (1ppm) to 53% (50 ppm). As a measure of visible leaf damage, average leaf bronzing score (LBS) at 50 ppm concentration was 3.3, 2.3 and 1.8 times higher than LBS at 1 ppm, 2ppm and 10 ppm respectively. For further experiments, 5ppm manganese concentration was selected for the induction of toxicity as substantial genotypic variation in stress response was observed at that level. Currently, a genome-wide association study (GWAS) is ongoing to identify candidate loci conferring manganese toxicity tolerance in rice. A diversity panel of 300 rice genotypes representing indica and japonica sub-populations is being screened. Phenotypic variation in leaf bronzing, dry weight and manganese content of shoots is determined for association mapping. Association mapping will be performed to link the observed phenotypes with more than 40,000 readily available SNP markers. This study will contribute to the understanding of genetic background of variable responses of rice genotypes to toxic levels of manganese.

Keywords: GWAS, manganese, rice