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Understanding the genetic and physiological basis of arsenic responses and exclusion in rice (*Oryza sativa* L.)

AMBIKA PANDEY^{1,2}, LIN-BO WU¹, VARUNSEELAN MURUGAIYAN^{2,3}, GABRIEL SCHAAF³, JAUHAR ALI², MICHAEL FREI¹

¹*Justus Liebig University Giessen, Dept. of Agronomy and Crop Physiology, Inst. for Agronomy and Plant Breeding, Germany*

²*International Rice Research Institute (IRRI), Rice Breeding Platform, Philippines*

³*University of Bonn, Inst. Crop Sci. and Res. Conserv. (INRES) - Plant Nutrition, Germany*

Abstract

Arsenic(As) is a toxic metalloid ubiquitously present in the environment that threatens the major rice-growing regions in the world. However, rapid industrialisation and excessive use of arsenic-rich groundwater further fuel the increased As concentration in the agricultural topsoil. Contamination of paddy soils with As cause phytotoxicity in rice which enters the food chain, posing a risk to human health. Arsenic contamination in rice is well documented, but its interaction and accumulation in rice are poorly understood. So far, no candidate genes or QTLs associated with As interaction is utilised in breeding programmes to develop low-arsenic accumulating rice varieties. Therefore, this project strives to characterise loci and genes involved in As exclusion in rice by a series of experiments that include extensive screening, genome-wide association study, development of bi-parental populations, fine mapping of genes and loci, and analysis of candidate genes and physiological mechanisms underlying As exclusion which helps in potential exploitation of alleles for breeding rice varieties with better nutritional quality. The uptake and accumulation of As in rice depend on the different As species in the soil. Plants detoxify As by conjugating and sequestering xenobiotic compounds into vacuoles using various enzymes; glutathione S-transferase enzymes are one. In one of our studies, we investigated the effects of chronic or acute exposure to arsenite [As(III)] and arsenate [As(V)] on rice plants at the vegetative growth stage using the overexpression lines of glutathione S-transferase gene (OsGSTU40). As(III) was more detrimental to plant growth than As(V) in plant growth, biomass, and lipid peroxidation in chronic and acute exposure. Overexpression of OsGSTU40 led to better plant growth even though uptake of As(V), but not As(III), into shoots was enhanced in transgenic plants. In acute As(III) stress, transgenic plants exhibited a lower level of lipid peroxidation than wild-type plants. The element composition of plants was dominated by the different As stress treatments rather than by the genotype, while the As concentration was negatively correlated with phosphorus and silicon. Overall, our findings suggest that As(III) is more toxic to plants than As(V) and that OsGSTU40 differentially affects plant reactions and tolerance to different species of arsenic.

Keywords: Arsenic toxicity, candidate genes, quantitative trait loci