

Development of low arsenic accumulating rice variety for safer human consumption

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Arsenic (As) contamination of the environment has emerged as a serious problem. One of the findings was that partitioning of arsenic in rice grains showed major variation in diverse germplasm of rice. The molecular basis for phenotypic divergence in the different or contrasting genotypes is still unclear. Several QTLs for variations in the As accumulation in different rice tissues have been already mapped in rice genome. However, they are failed to elucidate the mechanism related to the variability in As accumulation among different rice genotypes and limiting molecular breeding program. Transgenic technology is being widely enforced for improving heavy metal tolerance in plants. We have also identified several candidate genes that are involved in arsenic metabolism in rice and generated several transgenic rice plants that accumulate less arsenic in their grains. Our study described the principal understanding on the molecular basis of arsenic toxicity

and accumulation in plant parts. And also covered the transgenic and bioremediation approaches to minimize As accumulation in rice which further reduces food chain contamination. The data suffice to mitigate the effects of As toxicity as much as possible by reducing the As accumulation in rice grain. We described the measures to decrease As accumulation in rice, and to understand the mechanism and transport of As uptake, its transport from root to shoot to rice grain, its metabolism, detoxification as well as the mechanisms lying behind its accumulation in rice grain. We proposed various checkpoints which can be targeted to reduce As accumulation in rice grain. Genes/protein involved in As detoxification like glutathione biosynthesis, Phytochelatin synthesis, and arsenic methyltransferase are also provided a great pool of pathways that can also be castellated for the same purposes.

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