EXPRESSION PROFILING OF GENES ENCODING AQUAPORINS AND UNIVERSAL STRESS PROTEINS IN RICE EXPOSED TO ARSENIC

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Abstract: Dietary exposure of humans to arsenic from rice consumption is emerging as a global health concern. Significantly higher concentrations of arsenic have been found in the roots of rice plants, especially in India, Bangladesh, Nepal and certain other rice producing regions in the world. Arsenic is transported into rice plants from ground water via transport proteins called aquaporins present in both plant and mammalian cells. Aquaporins (AQPs) are trans-membrane (TM) protein channels that provide selective and rapid transport of water across the cell membrane. The genome sequence of rice (\textit{Oryza sativa}) has revealed at least 33 proteins divided into four subfamilies (the nodulin 26-like intrinsic proteins (NIPs), plasma membrane intrinsic proteins (PIPs), tonoplast intrinsic proteins (TIPs), and small and basic intrinsic proteins (SIPs). Aquaporins typically share common structural features composed of six TM domains interconnected via five loops (labeled A-E) and can be regulated by environmental stresses. Genes encoding proteins that contain the universal stress protein domain (Usp) are known to provide plants with the ability to respond to environmental stresses such as nutrient starvation, drought, high salinity, extreme temperatures and exposure to toxic chemicals. At least 20 genes encoding USPs have been identified in the rice genome. It is our hypothesis that certain members of these two gene families that share expression profiles during exposure of rice plants to arsenic. The objective of this study was to determine the expression profiles of rice genes encoding aquaporins and universal stress proteins in response to arsenic accumulation. We have identified for analyses a collection of gene expression and literature datasets including a whole transcriptome dataset obtained from response of rice seedlings from varieties that are arsenate-tolerant (Bala) and -sensitive (Azucena) to 13.3 microM sodium arsenate (AsV) in hydroponic solution. Preliminary results from the analyses will be presented. Additionally, we plan to analyze gene expression in human gastrointestinal epithelial cell upon exposure to arsenic with or without processing through rice. These studies could unravel novel functional relationships between water transport and stress tolerance in rice varieties as well as the significance of molecular alteration of gastrointestinal cells relating to the mechanisms of arsenic caused pathological developments. Furthermore, it will provide the basis for computational-based modeling of ligands designed to prevent entry of arsenic into rice plants.

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