

Title: TRMS: From Ionome to Genome: Mapping the Gene Networks Controlling Nutrient Content in Rice Grain

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Summary of Scientific Objectives and Approaches: Rice provides the major source of nutrition for a large proportion of the world's population. Mineral nutrients such as Ca, Fe, and Zn play critical roles in human health, with over 3 billion people suffering from Fe and Zn deficiencies. Unfortunately for those who rely on rice for subsistence, rice grain is not a good source of these nutrients and can contain toxic elements such as As and Cd. As such, alterations in the mineral content of rice grain to either increase or decrease levels of various elements would impact human health. In this project, we will take advantage of reverse genetics and mine our existing ionic data sets on 4385 yeast, and 1054 Arabidopsis knockout lines to identify genes that potentially function to control the rice grain ionome. T-DNA, *tos17* and Ds insertional alleles in these candidate genes will then be identified. We also propose to use the tools of high-throughput elemental analysis, genetics and DNA microarray-based mapping to identify loci that regulate mineral nutrient accumulation in rice grain. A core set of rice accessions selected from the USDA National Small Grains Collection (NSGC) (1,790 accessions) will be screened using ICP-MS for variation in accumulation of B, Na, Mg, P, K, Ca, Mn, Fe, Co, Cu, Zn, As, Se, Mo, Cd and I. We will also screen rice grain from the genotyped Lemont x TeQing (F16) RIL population which our preliminary studies have already shown to be segregating QTLs for a number of important elements including Fe and Zn. The availability of TeQing-into-Lemont introgression lines (TILs) will be used for finer mapping of these QTLs. The integration of high-throughput phenotyping and genotyping will allow the rapid identification of genes and linked markers for application to breeding and transgenic improvements in the mineral nutrient content of rice grain.

Expected Broader Impacts of the Proposed Research: For most of the world, plants are the major source of essential minerals. Food-based solutions to "hidden hunger" offer sustainable solutions to problems of malnutrition. Therefore, this project will contribute to increasing bio-available minerals in plants and to solving important problems in human health. If we are successful, nutrient-rich seed should also lead to agronomic benefits such as increased seedling vigor, resistance to disease and other stresses, and increased crop yields. Furthermore, understanding the pathways by which toxic metals accumulate in plants will enable the development of crops to exclude toxic metals and create healthier food sources, or to extract toxic metals from the soil as a strategy to clean up polluted lands and water. Rice grain ionic data, DNA microarray genotyping, transcript profiling and mapping data, and QTL information will be made available via the web-based Purdue Ionomics Information Management System (PiiMS) (www.purdue.edu/dp/ionomics/). Educational outreach will include training of postdoctoral fellows, undergraduates and graduate students in the field of ionomics. Our efforts will also include contributions to science museums through our exhibit "The Genomics Revolution Uncloaked" which is currently under development.