

## **A GENOME-WIDE ASSOCIATION STUDY OF THE GRAIN IONOME TRAIT IN RICE *ORYZA SATIVA* SUBSP. *JAPONICA* UNDER TWO DIVERSE WATER MANAGEMENT SYSTEMS**

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Rice (*Oryza sativa* L.) is a major staple food, since it provides >40% of the daily calories for the world's population and is considered as an important source of minerals and vitamins, for those dependent on a rice-based diet. At the same time, some trace element such as heavy metals, particularly enriched in rice kernels, may pose a health risk to high consumer. The composition in terms of mineral and trace elements is defined as the plant ionome, and a pivotal task in plant ionomic research is to unravel the genetic basis underlying its variations across different accessions and crop cultivars. However, the plant ionome is a complex trait since it is affected by genetic, environmental (including water management, soil properties and conditions that affect mineral supply and availability), and developmental factors as well as their interaction. Here, we describe a comprehensive study of the rice ionome based on GWAS using 299 diverse rice accessions, mainly belonging to *O. sativa* ssp. *japonica*, each genotyped at 246,084 SNP loci. The rice diversity panel was grown under two different water management conditions (permanent flooding -

PF- and limited water -LW-) for two years. Rice grains were analyzed for 13 mineral elements (Na, Mg, K, Ca, Mn, Fe, Ni, Cu, Zn, As, Mo, Cd and P) using inductively coupled plasma mass spectrometry. GWAS were carried out to identify significant marker-trait association loci that were stably expressed. Subsequently, multiple potential causal candidate genes were identified. Favourable alleles and candidate genes for improved micronutrient nutrition, as well as for excluding toxic elements from grains, were identified that they could be used in rice biofortification programs.