

**PROJECT TITLE**

Genetic basis of quality variation in grain of Vietnamese rice landraces: an ionomic approach

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## SUMMARY OF THE REPORT

Rice (*Oryza sativa*) is one of the most consumed staple foods worldwide. With improved living standards, consumer demand for rice grain quality is increasing. Meanwhile, grain cooking and nutritional behaviours are the most important components of rice quality. In developing countries, rice is the main source of carbohydrates. However, white rice contains limited amount of some essential mineral nutrients such as Fe, Zn to sustain a good health and development. Besides, rice may accumulate hazardous trace levels of toxic elements (As, Cd...).

To date, large number of QTLs associated with mineral content in grain have been reported (Lu et al, 2008; Garcia-Oliveira et al, 2009; Norton et al, 2010; Du et al, 2013; Zhang et al, 2014; Ohmori et al, 2016). However, most of these studies used biparental populations, which have limited allelic diversity and poor resolution in QTL positioning (Korte and Farlow, 2003). More recently developed, genome-wide association studies (GWAS) provide opportunities to explore the enormous allelic diversity existing in natural populations and to position QTLs more precisely. GWAS offers the opportunity to scan collections of local rice landraces that has actually exceptional cooking quality (flavor, aroma, texture...) and nutritional value that often carry genes and alleles absent in modern varieties. A GWAS for ionic variation on *Arabidopsis* accessions has led to the identifications of QTLs and genes related to mineral accumulation, such as *HKT1;1* for Na (Baxter et al, 2010; Segura et al, 2012), *MOT1* for Mo (Forsberg et al, 2015), *HMA3* for Cd (Chao et al, 2012) and *HAC1* for As (Chao et al, 2014).

In a previous study conducted in the joint Vietnam-France laboratory (LMI RICE) hosted at the Vietnam Agricultural Genetics Institute (AGI), we established a panel of 182 local rice varieties from various geographical origins of Vietnam and various watering regimes (upland, rainfed, irrigation). The panel was genotyped with ~ 22,000 polymorphic single-nucleotide polymorphism markers (SNPs) using Genotyping-by-Sequencing (Phung et al, 2014). Moreover, the entire sequencing of all the genomes have been obtained recently within the frame of AGI project entitled "Sequencing and exploiting of the genetic diversity in Vietnamese native rice lines served for rice research and breeding programs". A total of 500,000 SNPs had been called out.

In this project we used the high-throughput phenotyping platform (HTP Ionomics, Nottingham) to assess a core-collection of 182 Vietnamese rice landraces already genotyped with 500,000 SNPs, for their ionic compositions in grain and beside in AGI Vietnam for some other cooking quality traits (fragrance and amylose content). Using the determined phenotyping dataset, a genome-wide association study (GWAS) is now planned to identify loci associated with cooking quality, mineral nutrient fortification and toxic mineral element accumulation in rice grain. This will help to breed for improving quality of Vietnamese rice varieties.