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Exploitation of rice genome sequence and genetic diversity in Vietnamese rice landraces for research and breeding programs to cope with climate change

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Rice (*Oryza sativa* L.) is a principle crop in Vietnam and plays an important role in economic activity in this country. However, rice growing areas and rice productivity are significantly reduced due to increasing adverse impacts from climate changes as emerging pathogens, drought and rising sea levels. Our attempts have made collaboration with The Genome Analysis Center-TGAC (Earlham Institute), the John Innes Centre (JIC) in UK to launch the collaborative projects which focused on re-sequencing some Vietnamese rice landraces. Some successful works have been made in investigation, data collection, building of native rice landraces of Vietnam (focus on good quality rice varieties with tolerance to biotic and biotic stresses); analyzing genetic diversity of native varieties in Vietnam at the molecular level, selected 36 elite rice varieties with high diversity for genome sequencing; coordinating full genome sequencing, building genotype databases; adding supplementary assessments of major morphological agronomy traits, establishing phenotype databases of the genome sequenced rice landraces; mapping SNPs; design to CAPS markers for research and breeding; launching the project website to manage and sharing genotype and phenotype database of rice; training researchers and staff in the field of genome sequence and genome-data mining of rice; published some research articles on the National and International Journals. In the second phase of collaboration, we have re-sequenced the genomes of more 600 Vietnamese native rice varieties and exploited their databases by applying bioinformatics pipelines to identify association of alleles with specific agronomic phenotypes traits of interest. The rapid identification of rice landraces those are tolerant and resilient to adverse conditions which will work towards alleviating the current challenges the country agriculture industry face and contribute to food security. Currently, a number of promising rice lines carrying specific/multiple genes, candidate genes of abiotic and biotic tolerances from rice genome sequence (salt tolerance, bacterial leaf blight, and plant brown hopper resistances) have been developed by molecular breeding programs and were sent for National Test and will be released to the farmers soon time.

Biography

Huu Trung is a Senior Researcher, working at Agricultural Genetics Insitute (AGI), Hanoi, Vietnam. He has expertise in field of genetics and crop breeding, molecular breeding as well as bioinformatic analysis. He is currently Deputy Director General of AGI

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