Abstract

Title: Establishing a high-throughput phenotyping method for quantifying traits of interest using NAM rice population

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I. Abstract Body

Beside its economical importance, rice has long served as a model system in monocotyledon not only for research on plant development, but also a model crop for research on cereal's genomics, pathology and physiology. It's small genome size, complete genome sequencing and the availability of tools for functional genomics made the identification of new genes of agronomical interest easier. With the emergence of the Next Generation Sequencing (NGS) technologies, the isolation of new rice genes became more easy and rapid, revolutionizing the world of genomics. However, while genotyping protocols have advanced as a result of the technological progress achieved in Whole Genome Sequencing (WGS), establishing high-throughput phenotyping methods for quantifying traits of interest has remain challenging.

Our research group at the Food Resources Education and Research Center, Kobe University has generated two populations for genome-wide association studies (GWAS): (1) Japanese rice population composed of 112 diverse cultivars and (2) nested association mapping (NAM) population composed of 3567 lines, using the most popular Japanese cultivar Koshihikari as a common parent. For accurate and complete phenotyping of these large populations, our group is also developing efficient and economical strategies to collect phenotypic data quickly and accurately using data capture tools.

II. Image:

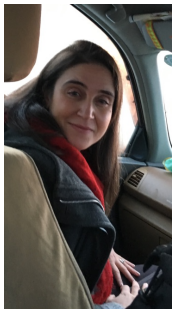


JNAM population in the paddy field of Kobe University, Hyogo, Kasai city.

III. Biography:

Fekih Rym has completed her PhD in 2009 from the University of Tsukuba, Japan and moved to Iwate prefecture to join the research group of Rice Genetics and Genomics at the Iwate Biotechnology research Center (IBRC), Kitakami, Japan for a postdoctoral position followed by JSPS fellow for 4 years. During her research term in IBRC, one of her major achievement was done, by taking advantages of next generation sequencing technology to develop new methods for rapid isolation of novel genes in Rice (Fekih et al., 2013). Recently, she moved to Kobe University to further investigate on rice genomics and apply novel technology for efficient rice breeding.

IV. Presenting author details



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