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| Category   | : 8th Rice Genetics Symposium   |
| Select Theme   | : High through-put technologies: Genotyping, Phenotyping and Omics  |
| Endorsement email  | :   |
| High through put technologies Genotyping Phenotyping and Omics Keyword 1 | : SNPs  |
| High through put technologies Genotyping Phenotyping and Omics Keyword 2 | : Variants  |
| High through put technologies Genotyping Phenotyping and Omics Keyword 3 | :   |
| Title of Entry   | : Genome-wide SNP discovery in a diverse panel of Thai rice using genotyping-by-sequencing (GBS) approach   |
| Presenting author  | : Phanchita Vejchasarn  |
| Presenting author email  | : phanchitav@gmai.com   |
| Co author 1  | : Jirapong Jairin, Varapong Chamarek  |
| Co author 2  | : Sissades Tongsimma, Sithichoke Tangphatsornruang  |
| Affiliation presenting author  | : Rice Department, Ministry of Agriculture and Cooperatives, Bangkok, Thailand  |
| Affiliation 1  | : Rice Department, Ministry of Agriculture and Cooperatives, Bangkok, Thailand  |
| Affiliation 2  | : Genome Institute, National Center for Genetic Engineering and Biotechnology, Bangkok, Thailand  |
| Select only one type of presentation                                     | : 3-5 minute flash talk   |
| Abstract   | : The advent of next-generation sequencing (NGS) technology for genotyping by sequencing (GBS) has revolutionized the field of rice genomics, enabling an increasingly rapid, accurate, and cost-effective approach for de novo genome sequencing and large-scale discovery of single nucleotide polymorphism (SNPs). In the present study, we utilized a GBS assay for the genome-wide identification of SNPs and the assessment of genetic diversity in a collection of 354 rice accessions, preserved mostly at the National Rice Gene bank operated under the Rice Department of Thailand. This collection, which represents four geographically distinct regions, consists of wild ( <i>O. rufipogon</i> ) rice as well as elite and traditional landraces ( <i>O. sativa</i> ) accessions with economically and agronomically important characteristics such as yield, pest and disease resistance, abiotic stress tolerance, and nutraceutical properties. A total of approximately 70,000 high-quality SNP markers with read-depth $\geq 10$ , minor allele frequency (MAF) $\geq 0.01$ and SNP call rate $\geq 70\%$ were identified. Genetic distance was calculated as IBS values using TASSEL v5.0 and an unrooted neighbour joining (NJ)-based phylogenetic tree was constructed. An analysis of population structure revealed four distinct subpopulations among 297 rice accessions. Furthermore, genome-wide association (GWA) analyses of important agronomic traits were performed. Our findings reflect the effectiveness of the developed platform for high-throughput genotyping and GWA analysis in detecting genomic regions and potential candidate SNPs specifically regulating such relevant traits in rice and pave the way towards the implementation of genomic selection (GS) in rice breeding program. |

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