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Development of reduced-HiSeq genotyping-by-sequencing weedy rice

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Single Nucleotide Polymorphisms (SNPs) are the most common type of genetic variation among living organisms. With the advent of the Next-Generation Sequencing (NGS) technology, rapid advance in high throughput SNP genotyping such as Genotyping-By-Sequencing (GBS) have significantly increased efficiency in simultaneous discovery and genotyping of SNPs in complex plant species. However, the current Illumina HiSeq-based GBS protocols have their own limitations in terms of complex, high capacity bioinformatics analyses prohibiting the use of GBS among small laboratories and small-scale users. This study aims to produce a smaller scale, bioinformatically simplified and more convenient reduced-HiSeq GBS method, which possesses advantages of GBS over other SNP genotyping methods, including the high reproducibility of markers and reduced representation of genome. Weedy rice (*Oryza Sativa*) was used as the model species. Rice samples from selected paddy fields in Malaysia were collected and genomic DNA was extracted, used for library construction and subjected to sequencing using Illumina HiSeq platform. Reduced-HiSeq GBS datasets were generated and subjected to various population genetic tests. Comparative analysis between reduced-HiSeq and full HiSeq-GBS datasets revealed that the former is potentially useful and sufficient for genetics analyses in rice.

Biography

Jayasyaliny Jayaraj is currently pursuing her Master's degree at Monash University, Malaysia. She has completed her Bachelor of Science with Honors (Resource Biotechnology) at Universiti Malaysia Sarawak. She is also a Correspondent with Malaysia's first science newspaper, The Petri Dish.

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