Elucidation of Musa acuminata cv. Berangan root infection by FOC (Tropical Race 4) by RNA sequencing and analysis

ABSTRACT

Musa acuminata cv. Berangan (AAA) is a type of banana locally grown in Malaysia. These bananas as well as Musa acuminata cv. Cavendish (AAA) are also facing a major threat from a typical soil borne fungus identified as Fusarium oxysporum f. sp. cubense race 4 (FocR4). Its characteristics as a complex pathogen manifesting as subtypes or races are the main reasons its infections are difficult to control. Genome sequence availability of the double haploid Musa acuminata originating from Pahang has become very useful to analyse RNA-seq reads and to identify the transcriptome profile of the host response between different groups was accomplished using RNA-Seq technology based on the Illumina HiSeqTm 2000 platform. Three sets of libraries derived from infected and mock infected plants (experimental groups) between different time points (0, 48, 96 h) shows over forty million reads were generated, each corresponding to coverage of >4,000,000,000 to <8,000,000,000 bases. About 0.10-66% reads were mapped to Musa acuminata DH Pahang genome sequence. This study provides the statistical analysis of the sequence reads. Based on this information, further analysis on gene expression patterns influenced by Foc race infection within the tested groups and time points will help in the understanding of the host pathogenic responses. In future discovery on many new genes for diagnosis of plant infection could be achieved through excessive transcriptomic data.

Keyword: Musa acuminata cv. Berangan; Root infection; FOC (Tropical Race 4); RNA sequencing