UNIVERSITI TEKNOLOGI MARA

THE EVALUATION OF METABOLITES PROFILING IN GENETICALLY MODIDFIED SOYBEAN WITH STACKED EVENT

SITI AISYA BINTI ASWANI

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ABSTRACT

Malaysia is a major importer of commodity crops such as maize and soybean. Importationof genetically-modified (GM) crops for the purpose of planting or food, feed and processing (FFP) requires approval from the National Biosafety Board (NBB). Most of the imported maize and soybean are GM varieties, and some of these are modified using multiple transgene inserts ('stacked events'). The risk assessment process for these cropsis complicated, as the presence of two or several transgenes in one organism can lead to interactions and unintended effects, which may not be immediately evident. To overcomethis problem, metabolomics profiling was proposed for immediate analysis on risk assessment of GM crops. These 'fingerprinting' techniques are data-rich and allow for the comparison of differences in the entire metabolite profiles and may provide useful insights in the evaluation of stacked events GM crops. This study aims to evaluate if metabolomics can detect differences between a GM plant and its non-GM near isogenic counterpart, and if this analysis can detect unintended effects of GM soybean with stacked events under controlled environments. GM soybeans with single *Pat* and *Cry1Ab* transgenes and stacked *Pat-Cry1Ab* transgenes were constructed in the same genetic background and grown under controlled conditions in the laboratory, and metabolomics analysis were then performed using leaf samples. The data from principle component analysis (PCA) by Metaboanalyst software indicate that levels of certain metabolites are significantly different between the non-GM and all GM samples, and data analysis can differentiate the metabolome profiles. The first two components in PCA analysis could differentiate about 50% of the variation between the GM and non-GM soybeans, while the best separation is at 80% or more. The analysis between single events and stacked events GM soybeans however did not result in clear differentiation between these samples,and the first two PCA components could at most account for 36.5 % of the difference. It is likely that intrinsic biological variations among the samples are large and obscured any differences due to GM. Thus, metabolomics data is not expected to add value to the risk assessment process for evaluation of GM crops with stacked events.

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