UNIVERSITI TEKNOLOGI MARA

STUDY ON UNINTENDED METABOLIC INTERACTIONS IN GENETICALLY MODIFIED SOYBEAN WITH STACKED EVENTS

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AUTHOR'S DECLARATION

I declare that the work in this thesis was carried out in accordance with the regulations of Universiti Teknologi MARA. It is original and is the results of my own work, unless otherwise indicated or acknowledged as referenced work. This thesis has not been submitted to any other academic institution or non-academic institution for any degree or qualification.

I, hereby, acknowledge that I have been supplied with the Academic Rules and Regulations for Post Graduate, Universiti Teknologi MARA, regulating the conduct of my study and research.

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ABSTRACT

Malaysia imports a large amount of maize and soybean, included genetically-modified (GM) varieties approved by the National Biosafety Board (NBB) for the purpose of food, feed and processing (FFP). Continuous breeding by seed developers has led to a large variety of GM maize and soybean with multiple transgene inserts ('stacked events'). This pose a new challenge to the risk assessment of these GM crops – the presence of two or several transgenes in one organism can lead to unintended and unpredicted effects and interactions, which may not be captured by the current data requirements. Proponents of biosafety regulation has long requested for the inclusion of metabolomics profiling data, which can provide a snapshot of a large number of metabolites, in the risk assessment of stacked events. Such 'metabolic fingerprints' techniques can technically be used to compare non-GM and stacked events GM crops and to uncover irregularities in the metabolism. This study was proposed to investigate the suitability of using metabolomic profiling to detect unpredicted effects when transgenes are stacked together, and to evaluate if such data will add value to the risk assessment process. Experiments were designed to eliminate as many confounding factors as possible by constructing and maintaining the sample materials under similar laboratory environment. Using standard molecular biology and plant tissue culture techniques, GM corn and soybean were constructed carrying the *Pat* and *Cry*1Ab transgenes, singly and in stack. Despite the success in developing the transgenic maize calli, none of them were able to develop into full leaves and thus were terminated at this point. On the other hand, it was found that while the presence and levels of certain metabolites are changed in non-GM, single GM and stacked GM of soybean samples, the overall metabolomic analysis is not able to clearly differentiate the metabolome profiles. Principle component analysis (PCA) of the data indicate that the first two components could at most explain for 25% of the variation between the 4 categories. Observations indicate that the inherent biological variability within and between the samples are large and tend to eclipse any variations induced by the genetic modifications. Thus, metabolomics data do not add value to the risk assessment of GM stacked events at this stage of technology.

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TABLE OF CONTENTS