UNIVERSITI TEKNOLOGI MARA

PROFILING THE METABOLITE CHANGES OF *KLEBSIELLA PNEUMONIAE* INFECTED LUNG ORGAN

NURNAZURAH BINTI FAISAL

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ABSTRACT

Metabolomics is the scientific study of the unique chemical fingerprint that a specific cellular processes leave behind. The focus of this study is to identify the metabolite changes between the control (noninfected) group and the *Klebsiella pneumoniae* infected group. The mixture of water: methanol: chloroform (1:2:2) was used as the extraction solvent. After that, the extracted metabolites were analysed by LC/MS-QTOF and then further analysed by the MassHunter Qualitative Analysis and Mass Profiler Professional software for the significant metabolites associated with the *Klebsiella pneumoniae* infection. The numbers of extracted metabolites are 164 metabolites. After filtration by the Mass Profiler Professional, the number was decreased to 24 metabolites. Next, the metabolomics data were analysed by the web-paged tool, MetPA for the significant metabolic pathways. Based on the MetPA analysis, the most expressed and significant pathways involved in the *Klebsiella pneumoniae* infection are retinol metabolism, arachidonic acid metabolism and D-glutamine and D-glutamate metabolism. These metabolic pathways involve directly and indirectly in activation of the immune system. Though, further study need to be conducted for further verification of specific biomarker(s) involved.

CHAPTER 1

INTRODUCTION

1.1 Background of study

Metabolomics study reflects the metabolite condition of cells and provides information on the biological regulations that are active during the specified growth condition. As the gene expression data and analysis of proteomic information may not be sufficient to understand the biological pathways occurring inside the cell, the metabolic profiling provides an instantaneous and comprehensive snapshot of the physiology of the cell. Hence, metabolomics study gives a better overview of cell phenotype than transcriptomics and proteomics (Dietmair, Timmins, Gray, Nielsen, & Krömer, 2010).

1.2 Problem statement

Rudan, Boschi-Pinto, Biloglav, Mulholland, and Campbell (2008) reported 2 million of death occurred each year in children aged below than 5 years due to pneumonia. The organisms that usually causes severe cases of pneumonia are *Staphylococcus aureus* and *Klebsiella pneumoniae* bacteria. This is shown that the bacteria acquired a mutation in its mechanisms of virulence as it can easily affect the human host.