Speaker
Ts. Dr. Mohd Hafis Yuswan

Ts. Dr. Mohd Hafis Yuswan is a Research Officer with a Ph.D. in Halal Products Science, possessing extensive knowledge and expertise in advanced analytical techniques for halal analysis.His research journey began at the Agro-biotechnology Institute (ABI) in Malaysia, where he spent 5 years conducting proteomics studies on mushrooms using LC-QToF-MS. He then joined Biocon Sdn. Bhd. as an Analyst for 3 years, focusing on insulin characterization using LC-IonTrap-MS to ensure the quality and effectiveness of insulin products.

Currently, he serves as a Research Officer at the Halal Products Research Institute, UPM. Since 2017, he has been at the forefront of halal analysis, utilizing advanced techniques such as chemometrics-assisted shotgun proteomics and multiple reaction monitoring by LC-QToF-MS and LC-QTrap-MS, respectively. His research focuses on establishing peptide markers for halal meat, ensuring the integrity and compliance of halal products. Additionally, he conducts research on peptide markers for halal meat-glue, addressing emerging concerns in the industry.

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INTRODUCTION

In the issue of halal food purity studies, scientific equipment such as liquid chromatography mass spectrometry (LC-MS-QTOF) is essential for studies based on proteins and small molecules such as metabolites. Liquid chromatography - mass spectrometry (LC-MS) is an analytical chemistry technique that combines the physical separation capabilities of liquid chromatography (or HPLC) with the mass analysis capabilities of mass spectrometry (MS). Paired chromatography - MS systems are popular in chemical analysis because the individual capabilities of each technique are synergistically enhanced. While liquid chromatography separates mixtures with several components, mass spectrometry provides the structural identity of individual components with high molecular specificity and detection sensitivity.

The LC-MS technique requires specific post-analysis methods in analyzing the data generated by LC-MS. Some of the required methods for the LC-MS technique include converting raw data to open data, searching through a database, and validating database results. All of these techniques will be carried out using the open-source software known as Trans-Proteomics Pipeline (TPP).

OBJECTIVES

- ✓ To expose the participants on the usage of LC-MS in protein analysis.
- ✓ To demonstrate the fundamental method of using LC-MS QTOF correctly in protein analysis.
- ✓ To demonstrate the appropriate post-analysis method for LC-MS QTOF data for protein samples.

PARTICIPANT

Student, researcher and individual who have interest on conduct research and development using LCMS QToF

VENUE

Seminar Room
Halal Products Research Institute
Universiti Putra Malaysia
43400 UPM Serdang, Selangor

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TENTATIVE PROGRAM

Day 1
25.10.23

8.30 am – 09.00 am	Registration
09.00 am – 09.30 am	Opening ceremony & briefing
09.30 am – 11.15 am	Lecture 1 : QToF Theory & Hardware Overview
11.15 am – 11.30 am	Refreshment
11.30 am – 01.00 pm	Practical 1 : Tuning & Calibration
01.00 pm – 02.00 pm	Break / Lunch
02.00 pm – 05.00 pm	Practical 2 : QToF Acquisition
05.00 pm	Tea break

Day 2
26.10.23

08.30 am – 09.00 am	Registration
09.00 am – 10.30 am	Practical 3 : Running Samples
10.30 am – 11.00 am	Refreshment
11.00 am – 12.30 pm	Practical 4 : Qualitative Analysis
12.00 pm – 02.00 pm	Break / Lunch
02.00 pm – 04.30 pm	Practical 5 : Quantitative Analysis
04.30 pm – 05.00 pm	Reporting
05.00 pm	Tea break

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