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Diagnosis of dengue infection using metabolome analysis (biomarker profiles)

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Dengue is a major health and pressing threat to Malaysia with increasing atypical manifestations. In this study, metabolomics approach was used to identify metabolite candidates by means of ¹H NMR- spectrometry as a diagnostic tool for dengue disease. The mid-stream urine collected from 52 patients diagnosed with dengue fever at Penang General Hospital and 43 healthy individuals was analyzed with ¹H NMR spectroscopy, followed by chemometric multivariate analysis. NMR signals which highlighted in the OPLS-DA S-plot were selected and identified using Human Metabolome Database (HMDB) and Chenomx Profiler. A highly predictive model was constructed from urine profile of dengue infected patients versus healthy individuals with the total R²Y (cum) value is 0.935, and the total Q²Y (cum) value is 0.832. The differences between infected patients versus healthy individuals were found to be related to amino acid metabolism, tricarboxylic acid intermediates cycle and β -oxidation of fatty acids. Distinct variations in certain metabolites were recorded including amino acids, various organic acids, betaine, valerylglycine, myo-inositol and glycine. The results open up a possibility of rapid, non-invasive analysis and diagnosis of dengue disease using urine metabolic profile.

Biography

Abdel-Hamid Zaki is Deputy of Pharmaceutical and Drug Industries Division (NRC). He was appointed as a Head of Therapeutic Chemistry Department, National Research Centre, (2006, 2012)). He is working as Professor of Applied Biochemistry at the same department. His major field of interest is metabolomics in pharmaceutical research. He was awarded many scientific mission and grants from DANIDA (Denmark – 1994), TWAS (Italy-1997, 2001, 2003), FAPESP (Brazil, 2001), and UNESCO (2002). He obtained and held PI for 5 international research projects from ISESCO- (1990-1993), TWAS- (1995-1996), TWAS (1998-1999), TWNSO- (2004-2006) and STDF (2014-2016).

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