



S17. IDENTIFYING BIOMARKERS OF ARSENIC EXPOSURE AND METABOLISM IN HUMAN URINE THROUGH SPECTROSCOPIC TECHNIQUES

Parvez I. HARIS

De Montfort University, The Gateway, Leicester, LE1 9BH, UK

Our understanding of molecular changes associated with exposure to arsenic is poorly understood despite the fact hundreds of millions of people are exposed to this toxic element. Spectroscopic analysis of human biofluids from people exposed to arsenic can help identify biomarkers of arsenic exposure which can be valuable for diagnostic purposes and also for understanding biochemical changes induced by arsenic. Our methodology involves collecting and analysing urine samples from populations that are exposed to arsenic through their diet and drinking polluted water. The volunteers providing the urine samples are asked to complete a questionnaire on demographic characteristics, diet and life-style factors. Subsequently, the urine samples are analysed using different spectroscopic methods including ICP-MS, MALDI-TOF, FTIR and NMR spectroscopy. The talk will present data on urinary arsenic and its metabolites (determined using ICP-MS), associated with arsenic exposure from water and foods, and their relationship with other metabolites and macromolecules determined using MALDI-TOF (proteins), FTIR (proteins and other macromolecules) and NMR (metabolites) spectroscopy. For example, our NMR study revealed that urinary arsenic was significantly correlated to %dimethylamine ($r = 0.169$, $P = 0.044$) in a Bangladeshi population that is exposed to high concentration of arsenic through drinking contaminated water. The lecture will also present data which demonstrates human exposure to arsenic from consumption of rice in people from the United Kingdom and Bangladesh. For the population in Bangladesh, an increase in skin lesion prevalence ($P\text{-trend} = 0.007$) and skin lesion incidence ($P\text{-trend} = 0.07$) was associated with increased intake of steamed rice.