

CURRENT TRENDS IN MASS SPECTROMETRY AND CHROMATOGRAPHY

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The challenge of identifying tuberculosis proteins in ancient biological samples

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Introduction: Tuberculosis (TB) disease can be traced back to 9,000 years ago in human history. It is a chronic disease, which is caused by *Mycobacterium tuberculosis* complex (MTBC) bacteria, has infected one-third of the world's population nowadays.

Statement of the Problem: Skeletal TB is estimated only account for 3-5% of untreated cases, hence osteological analysis cannot provide a comprehensive study of TB infection on ancient human population. Ancient DNA (aDNA) analysis has been used in a number of studies for identification of ancient TB. However, contamination issue and reproducibility of the results are common problems of aDNA analysis. aDNA analysis can be used to confirm the presence of pathogens, but it cannot positively infer disease because pathogens could be present without causing infection. Difference from DNA, protein analysis does not rely on amplification; hence this analysis has less susceptible to contamination. The purpose of this study is to use proteomics approach to detect TB disease in ancient human remains.

Methodology: Mummified lung tissue proteins were extracted and digested using filter-aided sample preparation (FASP) modified for ancient samples and peptides were analyzed using maXis 3G(UHR-Q-TOF) mass spectrometer.

Findings: Shotgun proteomics analysis of mummified lung tissues has identified mycobacterial proteins, lung proteomes and other bacteria proteins. These included a number of proteins derived from the human immune system such as eosinophil peroxidase, eosinophil cationic protein, neutrophil elastase, alpha-1-antitrypsin, myeloperoxidase etc. These immune system proteins may provide important clue of tuberculosis infection in ancient remains. For example, eosinophil peroxidase has been shown to display bactericidal activity against *M. tuberculosis*.

Conclusion & Significance: Proteomics analysis covers a broad spectrum of proteins and can provide more resolved picture of tuberculosis infection in the past human population.

Biography

Kai Yik Teoh is currently conducting his PhD research at the Macquarie University, Australia. He is a Member of the Macquarie University Marine Research Centre and Palaeo, Research Centre of Human Palaeoecology and Evolutionary Origins in the University of York, UK. His previous research work on dental calculus has been named in top 100 scientific discoveries of 2014 in Discover magazine. He works on broad range of biological samples which included ancient biological samples, marine species and prokaryotes. His works focus on protein biomarkers detection in ancient biological samples and protein-protein interactions study in prokaryotes using mass spectrometry.

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