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BOOK OF ABSTRACTS

POSTR PRESENTATIONS I

PP 16

Rapid molecular technique for the detection of bacteria in lung cancer and bronchiectasis patients

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Human lung microbiota comprises of commensal, symbiotic and pathogenic microorganisms. Bacteria are assumed to have a positive relationship with lung cancer and bronchiectasis.

The objective was to identify lung bacteria in the patients of above diseases and to develop a rapid diagnostic method to identify the most influential pathogens inhabiting the human respiratory tract.

Ethical clearance was obtained from Teaching Hospital, Kandy. Patients visiting the respiratory ward of Teaching Hospital, Kandy, who were suspected as lung cancer (n= 20) and bronchiectasis (n=20) and a volunteer control group were recruited. Bronchoalveolar lavage and sputum were collected and cultured for the isolation of bacteria using Luria-Bertani media and Lowenstein- Jensen media for *Mycobacterium* species. The isolates were sequenced for 16S rRNA gene. Simultaneously, real-time PCR using specific primers was performed to identify *Escherichia* sp., *Pseudomonas aeruginosa*, *Staphylococcus aureus* and *Mycobacterium* sp.

Real-time PCR identified *P. aeruginosa* in lung cancer (n=3) and in bronchiectasis (n=7) which was also confirmed by DNA sequencing. *Mycobacterium* sp. was also identified in bronchiectasis by real-time PCR although no isolates were found. *S. aureus* was only seen in the healthy group while *Escherichia* sp. was present in both bronchiectasis and the healthy groups. DNA sequencing identified a total of 14 bacterial species.

The results suggested that most bacterial populations inhabiting the human lung belonged to the phyla Proteobacteria and Firmicutes. Real-time PCR is a conclusive method for rapid bacterial detection and 16S metagenomics is being currently performed for the confirmative analysis with respect to the identification of total bacterial population.