

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 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 to isolate for bacteria on Luria-Bertani medium and on Lowenstein- Jensen medium 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 along with identification of *Mycobacterium sp.* in bronchiectasis though no isolates were present. *S. aureus* were only seen in the healthy group and *Escherichia sp.* was present in both bronchiectasis and the healthy groups. DNA sequencing identified a total of 14 bacterial species.

The results suggested that the most bacterial populations inhabiting the human lung belonged to the phyla Proteobacteria and Firmicutes. The 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.