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Abstract Title:

Comparison of Bacterial Microbiome of Suspected Lung Cancer and Bronchiectasis Patients with Healthy Traffic Policemen

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Abstract Body:

Background The association of the lung cancer with bacterial infections is addressed widely but the role of lung microbiome in lung cancer is yet to be confirmed. Many pathogens including *S. pneumoniae* and *H. influenzae* have been observed in lung microbiome of bronchiectasis patients. Therefore, lung microbiome studies may lead to potential biomarkers for these diseases. This study aimed to compare the lung microbiome of suspected lung cancer and bronchiectasis patients with a selected healthy population. **Method** The ethical clearance was obtained from Teaching Hospital, Kandy, Sri Lanka. The bronchoalveolar lavage (BAL) was collected from suspected lung cancer (20), bronchiectasis patients (20) and sputum was collected from healthy (5). The samples were treated with modified Petroff method and were cultured on Luria Bertani and Lowenstein Jensen media. Genomic DNA extracted from culture isolates with standard CTAB method were amplified for 16S rDNA gene followed by DNA sequencing. Genomic DNA extracted by Boom's method from original samples were subjected to Real time PCR with SYBR green using specific primers for the identification of *Escherichia* sp., *Mycobacterium* sp., *Pseudomonas* sp., and *Staphylococcus aureus*. **Results** Nine bacterial genera were identified among the study groups and the sequences were deposited into NCBI Genbank (Table 1.). Real time PCR identified *Escherichia* sp. and *Pseudomonas* sp. in both bronchiectasis and healthy, whereas *Staphylococcus aureus* was present only in healthy controls, which produced respective melt curves at 82.5-83.2 °C, 93.5- 94.5 °C, and 75.3-75.8 °C. Confirmative data was obtained from agarose gel electrophoresis as 90 bp, 179 bp and 80 bp fragments respective. **Conclusion** Significantly, viable organisms of genera *Paenibacillus* and *Delftia* were obtained only in bronchiectasis suspected samples whereas *Neisseria* and *Morganella* were limited to lung cancer suspects. Also, *Staphylococcus aureus* was only seen in healthy controls. The mutual among the three groups were the genera *Bacillus* and *Klebsiella*. 16S metagenomics and real time PCR are being performed for identification and quantitation of total bacterial population to determine the potential bacterial biomarkers for the respective diseases.

Table1. Comparison of viable bacterial diversity within study groups by sequencing

Organism (Genera)	Lung Cancer suspects (Patients n=20)	Bronchiectasis suspects (Patients n=20)	Healthy (n=5)	NCBI Genbank accession number
<i>Pseudomonas</i>	✓	✓		MG733166.1
<i>Klebsiella</i>	✓	✓	✓	MG733165.1
<i>Enterobacter</i>	✓	✓		MG738354.1
<i>Enterococcus</i>	✓	✓		MF498499.1
<i>Bacillus</i>	✓	✓	✓	MG733159.1
<i>Paenibacillus</i>		✓		MF498508.1
<i>Neisseria</i>	✓			MF498500.1
<i>Delftia</i>		✓		MG733163.1
<i>Morganella</i>	✓			MG733162.1