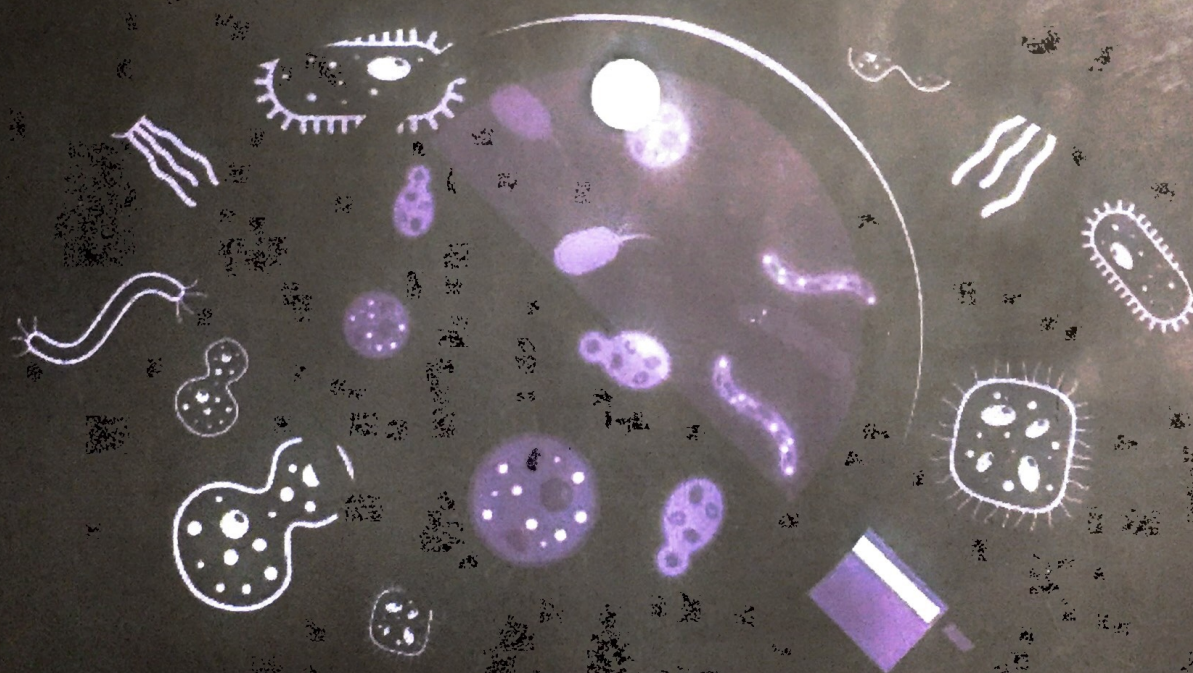# SRI LANKAN SOCIETY FOR MICROBIOLOGY (SSM)

8TH ANNUAL CONFERENCE & SCIENTIFIC SESSIONS
OF
THE SRI LANKAN SOCIETY FOR MICROBIOLOGY (SSM)

ABSTRACT AND DELEGATE INFORMATION 2019

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Characterization of lung bacterial microbiota of lung cancer and bronchiectasis patients: a 16S metagenomic approach

Ekanayake A[1], Madegedara D[2], Chandrasekharan V[3] and Magana-Arachchi D[1*]

[1]National Institute of Fundamental Studies, Kandy
[2]Teaching Hospital, Kandy
[3]Department of Chemistry, Faculty of Science, University of Colombo

*Email: dhammika.ma@nifs.ac.lk

Bacterial microbiota on the human body are assumed to play a role in causing and mediating various diseases. The respiratory tract is one of the main portal through which bacteria have access to the human body. Lung cancer and bronchiectasis are two chronic respiratory diseases that contribute to the global respiratory disease burden. In Sri Lanka, lung cancer is the most common malignancy among males while bronchiectasis is common in females. In this study, bacteria in the lungs of the cancer and bronchiectasis patients were characterized using 16S metagenomics analysis.

Ethical clearance was obtained from the Ethical Review Committee of Teaching Hospital, Kandy. Bronchoalveolar lavage (BAL) specimens were collected from the patient groups and due to ethical restrictions, sputum samples were collected from the healthy volunteers. Bacterial genomic DNA was extracted from the clinical samples and 16S rRNA metagenomic sequencing was performed commercially (lung cancer (n=4), bronchiectasis (n=3) and healthy volunteers (n=3). The V3–V4 region of the 16S rRNA gene amplification was done according to the Illumina 16S Metagenomic Sequencing Library preparation guide. Operational taxonomy units (OUT) analysis was carried out with a cut-off similarity of 97%. The sequenced data were deposited under NCBI BioProject PRJNA477678.

Healthy volunteers had 140 bacterial species and lung cancer and bronchiectasis had 255 and 236 bacterial species respectively. *Corynebacterium tuberculostearicum* and *Keratinibaculum paraultunense* were only observed in the patients with lung cancer while those with bronchiectasis did not have specific bacteria. *Achromocabacter xylosoxidans*, *Streptococcus sinensis* and *Staphylococcus sciuri* were the most abundant in lung cancer patients whereas *Pseudomonas aeruginosa*, *Burkholderia lata* and *Streptococcus dentisani* were abundant in the bronchiectasis group. *S. dentisani*, *Rothia mucilaginosa* and *S. salivarius* were the most abundant in healthy volunteers.

We observed increased bacterial diversity in the diseased compared to the healthy population. The results confirm the available literature on bacterial abundance in these groups. The study provides an insight to bacterial microbiota in these diseases. Future studies in larger sample will help to get conclusive answers about specific bacteria mediating these diseases.

Keywords: Lung cancer, bronchiectasis, bacterial microbiota, 16S metagenomics