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Variations of bacterial load in respiratory specimens in lung cancer and bronchiectasis suspected patients

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The study of the human microbiome is paving its way to establishing relations between microorganisms in the human body with disease conditions. Bacteria in the human body have been linked to diseases such as asthma, cystic fibrosis and gastric cancer. In Lung cancer, patients are immunocompromised and in bronchiectasis, patient's respiratory defences are compromised thus, the bacteria assumed to play a significant role. We aimed to quantify bacteria in lungs of patients suspected of the two diseases. Ethical clearance was obtained from Teaching Hospital, Kandy. Two patient groups- suspected lung cancer (n=20), bronchiectasis suspect (n=20) along with a healthy population (n=20) were recruited. Bronchoalveolar lavage (BAL) and oropharyngeal (OP) swabs were collected from patients representing the upper and lower respiratory tracts (URT and LRT) and sputum was collected from the healthy population instead of BAL. Bacterial genomic DNA was extracted from the samples and real-time PCR was used to detect total bacterial load using standard primers and fluorescent probes with a standard curve generated by *Escherichia coli*. Total bacterial cells varied with lung cancer suspects, bronchiectasis suspects and the healthy group with respective means of 8.14×10^4, 1.4×10^4 and 6.06×10^4 cells/mL. In URT samples, highest concentration of cells was observed in lung cancer suspects with 1.93×10^4 cells/mL whereas bronchiectasis suspects exhibited lowest among the three groups being 1.49×10^4 cells/mL. In LRT samples, the highest bacterial cell number was seen in healthy group accounting 8.4×10^4 cells/mL, the lowest being 1.32×10^4 cells/mL in bronchiectasis suspects. A variation of total bacterial load among the respiratory samples were observed. Lung cancer suspects appear to be having the highest respiratory bacterial load. Bronchiectasis showed lower bacterial load even less than healthy population. Accordingly, lung bacterial microbiota numerically does not necessarily depend with these two chronic respiratory conditions.

Keywords: *bacteria, lung microbiome, respiratory diseases, real-time PC*