Bacterial Load in Respiratory Specimens in Lung Cancer and Bronchiectasis Suspected Patients; a Molecular Approach

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Anuradha Ekanayake[1], Dushantha Madegedara[2], Vishvanath Chandrasekharan[3], Dhammika Magana-Arachchi[1(*)]

[1]*National Institute of Fundemantal Studies, Kandy, Sri Lanka,* [2]*Respiratory Treatment Unit, Teaching Hospital, Kandy, Sri Lanka ,* [3]*University of Colombo, Sri Lanka*

(*) E.mail:dhammika.ma@nifs.ac.lk

Many bacteria are associated with human diseases as the causative agent. Some bacteria might play a different role in disease progression. Lung cancer and bronchiectasis patients' are immunologically suppressed. We aimed to quantify bacteria in lungs of the patients suspected of the two diseases. The ethical clearance was obtained by Teaching Hospital, Kandy. Lung cancer suspects (LCS) (n=20), bronchiectasis suspects (BRS) (n=20) along with a healthy population (HP) (n=20) were recruited for the study. Bronchoalveolar lavage and oropharyngeal swabs were collected from patients representing upper and lower respiratory tract (URT and LRT) whereas sputum was collected from healthy population. Bacterial DNA was extracted and forward primer-5'TCCTACGGGAGGCAGCAGT3', reverse primer 5'GGACTACCAGGGTATCTAATCCTGTT3' and probe (6-FAM)-5-CGTATTACCGCGGCTGCTGGCAC3-(TAMRA) was used to amplify and detect 16S rRNA gene. Bacterial load was calculated compared to a standard curve using Escherichia coli. Total bacterial load was observed as means of 8.14x104, 1.4x104 and 6.06x104 cells/mL, respectively in lung cancer and bronchiectasis suspects, and the healthy group. In URT samples, highest cell concentration was observed in LCS with 1.93x104 cells/mL whereas BRS exhibited lowest among the three groups being 1.49x104 cells/mL. In LRT samples, the highest bacterial cell number was seen in healthy individuals accounting 8.4x104 cells/mL, the lowest being 1.32x104 cells/mL in BRS. The three groups involved in this study has shown variations of bacterial load. The highest respiratory bacterial load was observed with LCS, whereas bronchiectasis showed the lowest bacterial load. This concluded that the lung bacterial microbiota numerically does not necessarily depend with these two chronic respiratory conditions.

Keywords: bacteria, lung microbiome, real-time PCR