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MOLECULAR IDENTIFICATION OF BACTERIA ISOLATED FROM LUNG CANCER AND BRONCHIECTASIS PATIENTS' SAMPLES THROUGH 16S PCR

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Lung cancer is the most prevailing cancer in the world and it's responsible for 1.7 million deaths annually. Bronchiectasis is a significant cause of respiratory morbidity. In this study a total number of 25 (Bronchiectasis-09, suspected Lung cancer-16) patients' samples (Bronchoalveolar Lavage and Oropharyngeal swab) were collected from January-May 2018 from the patients who attended Teaching Hospital, Kandy, Sri Lanka. The specimens were divided into two portions. One portion was treated according to the modified Petroff's method and inoculated on Lowenstein-Jensen (LJ) media whereas the untreated portion was inoculated on Luria-Bertani (LB) media. Bacterial isolates were tentatively identified according to their morphology, Gram staining, available keys and standardized methods. As a result, the samples cultured under LJ media did not yield any positive isolates and the samples cultured under LB media produced 35 positive cultures, out of which 23 were Gram negative cocci, one was Gram positive cocci and 11 were Gram negative bacilli. Eight positive isolates were used to extract the DNA and that was subjected to 16S PCR. Among the positive cultures, *Nisseria* sp., *Enterobacter* sp., *Klebsiella sp.* and *Pseudomonas* sp. were tentatively identified. The 16S PCR produced a distinct band at 1500 bp for three samples that were obtained from suspected patients of lung cancer and one for the bronchiectasis patients. The study confirmed that suspected lung cancer and bronchiectasis patients harbour bacterial species in their lungs. Within that Gram-negative species were the most frequently identified bacteria. Sequencing and molecular characterizations of 16S PCR product are necessary for further identification of bacteria associated with lung cancer and bronchiectasis.

Keywords*: Molecular identification, Bacteria, Lung cancer, Bronchiectasis patients, 16S PCR.*

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