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Identification of bacteria in patients with bronchiectasis and suspected lung cancer: A Preliminary Study

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Respiratory diseases are a group of diseases, which affect and burden humans throughout the world. A diseased lung may present altered diversity of commensal bacteria as well as pathogenic bacteria, depending on the disease type and severity. According to scientific research carried out, lung cancer and bronchiectasis are two diseases where microbial dysbiosis is observed. As a tropical country, Sri Lanka accounts for many lung cancer and bronchiectasis patients, and it is timely to address the effect of bacterial microbiome. Theaim of the study was to identify culturable bacterial microbiome of respective patients. The ethical clearance for the study was obtained by Teaching Hospital, Kandy. The study population consisted oflung cancer suspects (according to symptoms) (n=20), and bronchiectasis patients(n=20). Oropharyngeal (OP) swabs and bronchoalveolar lavage (BAL) samples were collected from all patients as per the representation of upper and lower respiratory tract, respectively. Samples were collected and processed for culturing on Luria Bertani (LB) medium and on Lowenstein Jensen (LJ) medium. The obtained cultures were Gram stained. Following DNA extraction by the standard CTAB (N-Cetyl-N,N,N-trimethylammonium bromide) method, 16S rDNA gene amplification was carried out. The amplified DNA was sequenced to identify the bacterial species present by standard nucleotide BLAST. No cultures were obtained on the LJ medium, and the LB medium yielded 60 isolates. Gram's staining resulted in Gram positive rods (n=5), Gram negative rods (n=41), Gram positive cocci (n=3), and Gram negative cocci (n=11). Bacterial sequences belonging to six families, *viz.*, Enterobacteriaceae, Bacillaceae, Enterococcaceae, Neisseriaceae, Pseudomonadaceae, and Paenibacillacea were identified. Further analysis to genus level revealed seven genera,*viz.*, Enterobacter, Klebsiella, Bacillus, Enterococcus, Nesisseria, Pseudomonas and Paenibacillus. Therefore, the organisms belong to the two phyla, Proteobacteria and Firmicutes. **The commonest were genera Enterobacter and Pseudomonas in both Lung cancer (27.3% each) and bronchiectasis (28.5% each).** An important observation made was that OP swabs failed to produce cultures compared to BAL. The results further confirm that chronically diseased airways tend to become the habitat of many bacteria belonging to phylum Proteobacteria. A limited but supportive impression can be gained from identifying culturable bacteria, yet molecular methods might provide a specific insight.

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