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ALTITUDE-DRIVEN VARIATIONS IN AIRBORNE BACTERIAL COMMUNITIES: A COMPARATIVE STUDY FROM PIDURUTHALAGALA AND COLOMBO, SRI LANKA

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Understanding the diversity and distribution of airborne bacteria is a critical concern. This study examined the differences in airborne bacteria at two varying altitudes in Sri Lanka: Piduruthalagala Mountain (PT) and Lotus Tower (LT). Eight samples were collected on filter papers from each location using an Envirotech APM 550 fine particulate air sampler. After 30 minutes of sample collection, the filter papers were cut into fine pieces and shaken in 8 mL of distilled water at 100 rpm for 2 h. After centrifugation, the filtrate was cultured on Luria-Bertani (LB) culture media. Bacterial DNA was extracted using Boom's method. Sample preparation was conducted, followed by 16S Metagenomic Sequencing Library Preparation targeting the 16S V3-V4 region. The DNA of 45 culturable isolates were extracted, comprising 25 from PT and 20 from LT. The PCR amplicons and metagenomic samples were sequenced per the manufacturer's instructions at Macrogen Inc., South Korea. The isolates exhibited taxonomic diversity, comprising 46 species from the Gammaproteobacteria, Betaproteobacteria, and Firmicutes phyla. 16S rRNA amplicon metagenome sequencing identified 80 bacterial species, including 21 phyla, 20 classes, 17 orders, 12 families, and 22 genera. Pseudomonadota was the most dominant phylum, followed by Firmicutes. Cyanobacteria were present at all sites; LT showed a higher abundance (0.48%) than PT (0.16%), likely due to its proximity to Beira Lake and the sea. The genera *Brevundimonas*, *Fenollaria*, *Prevotella*, *Peptoni*, *Enterococcus*, and *Corynebacterium* were exclusively found at high-elevation sites. The average Simpson index for the LT site was 0.6645 for bottom samples and 0.7733 for top samples. At the PB site, it was 0.8333 for the top, and 0.7307 for the bottom samples. Overall, the samples collected from higher altitudes exhibited greater alpha diversity. The viable microbes originating from high altitudes shape microbial dynamics in lower elevations. This research offers a framework for analyzing airborne microbial communities on both local and regional scales.

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Keywords: Airborne microorganism, Air samples, High altitudes, 16S rRNA amplicon sequencing, Microbial diversity