



Bridging the Gap Between Culture-based and Genomic Characterization of Tropical Marine Heterotrophic Bacteria from the Coastal Interface of the Dikkowita Fisheries Harbor, Sri Lanka

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Anthropogenic maritime activities have led to increased petroleum pollution along the coastal zones of Sri Lanka, yet the diversity and functional roles of tropical marine heterotrophic bacteria remain understudied. While metagenomic approaches provide insights into total microbial communities, they often lack the physiological resolution provided by culture-dependent studies. This study employs a polyphasic approach to bridge the gap between culture-dependent observations and experimental validation by isolating and molecular characterizing of marine heterotrophic bacteria, particularly hydrocarbon-degrading marine isolates from the Dikkowita fisheries harbor. Using selective enrichment in the Artificial Sea Water (ASW) supplemented with 0.1% (w/v) hydrocarbon (i.e. n-C20) substrates as the sole source of carbon, native hydrocarbon-degrading bacterial strains were isolated by plating on Marine Agar. Controls were maintained without a hydrocarbon supplementation. Bacterial genomic DNA was extracted from overnight grown marine agar broth using the QIAamp DNA mini kit (Qiagen, Germany). The isolates were taxonomically identified via bidirectional metagenome 16S rRNA amplicon sequencing, targeting 16S (V3-V4) region with Macrogen's (South Korea) default primers: Bakt_341F and Bakt_805R. The sequence analysis using EPI2ME Metagenome workflow and further validation with the Galaxy Europe tool revealed that the microbial community in the selected environment is naturally dominated by *Oceanobacter* sp., *Salinimonas* sp., *Alteromonas* sp., etc. whereas the treatment conditions were dominated by *Alteromonas* sp. Therefore, the study confirmed that *Alteromonas* sp. outpaced *Oceanobacter* sp. under the selective pressure of hydrocarbon supplementation. By integrating cellular morphological and genomic data, this study provides a more comprehensive view of the culturable fraction of marine microbial diversity. Further, these sequence data contribute to enhance the representation of tropical taxa within the global marine microbiome databases while uncovering the ecological significance of local heterotrophic bacteria and offering a foundation for developing indigenous bioremediation strategies for marine oil spill management in Sri Lanka.

Keywords: *Marine metagenomics, Marine heterotrophic bacteria, Alteromonas* sp., *Oceanobacter* sp., *Marine bioremediation*