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16s rRNA Based Metagenomic Analysis of Palm Sap Samples From Bangladesh

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Abstract : Collecting palm sap as a food source is an everyday practice in some parts of the world. However, the consumption of palm juice has been associated with regular infections and epidemics in parts of Bangladesh. This is attributed to fruit-eating bats and other vertebrates or invertebrates native to the area, contaminating the food with their body secretions during the collection process. The frequent intake of palm juice, whether as a processed food product or in its unprocessed form, is a common phenomenon in large areas. The range of pathogens suitable for human infection resulting from this practice is not yet fully understood. Additionally, the high sugar content of the liquid makes it an ideal culture medium for certain bacteria, which can easily propagate and potentially harm consumers. Rapid diagnostics, especially in remote locations, could mitigate health risks associated with palm juice consumption. The primary objective of this research is the rapid genomic detection and risk assessment of bacteria that may cause infections in humans through the consumption of palm juice. Utilizing state-of-the-art third-generation Nanopore metagenomic sequencing technology based on 16S rRNA, and identified bacteria primarily involved in fermenting processes. The swift metagenomic analysis, coupled with the widespread availability and portability of Nanopore products (including real-time analysis options), proves advantageous for detecting harmful pathogens in food sources without relying on extensive industry resources and testing.

Keywords : raw date palm sap, NGS, metabarcoding, food safety

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