Development of a metabolic pathway-based genome analytical tool for identifying unique environmental bacteria

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Abstract

Bacteria inhabit diverse environments, adapting unique functions suited to their surroundings. Recognized as valuable genetic resources, bacteria have been widely isolated and utilized in various industries. Advances in second-generation sequencing have made bacterial genome data more accessible, unveiling new species and genetic diversity. Numerous bioinformatics tools now enable the identification of unique and potentially useful bacteria from environmental samples. However, many rely on complex algorithms, making rapid identification challenging. Here, we introduce a genome analysis tool designed to efficiently identify unique and beneficial bacteria based on metabolic pathway profiling. To validate its accuracy, we first tested model bacterial strains, using their genome-derived metabolic pathways to characterize distinctive traits. The tool determines bacterial uniqueness by performing a global comparison of metabolic pathway profiles among different genomes. We then applied the tool to environmental bacterial isolates, assembling draft genomes using nanopore sequencing. Upon validation, it successfully identified unique metabolic pathways in each bacterium, highlighting functional differences between strains. The simplified output system allows for comparative analysis of annotated pathways, providing insights into bacterial roles within their respective populations. This study demonstrates the potential of our genome analysis tool in characterizing environmental bacteria efficiently. By facilitating the discovery of novel metabolic traits, it offers a valuable approach for microbial ecology, biotechnology, and industrial applications.

Keywords: unique traits, environmental bacteria, genome analytical tool, metabolic pathways

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