POSTER - DNA AND GENOMICS

GENOMIC ANALYSIS OF PETROLEUM HYDROCARBON DEGRADING BACTERIA AND THEIR POTENTIAL PERFORMANCE IN CONSORTIUM ON PRIORITY ENVIRONMENTAL HYDROCARBON POLLUTANTS

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Contamination of soils and marine ecosystems with petroleum hydrocarbons, as a result of oil spills or industrial waste, presents a major environmental risk. To reduce the environmental effects associated with such spills, traditional physical-chemical methods can be replaced with bioremediation via bioaugmentation, which employs microorganisms that have the ability to degrade petroleum compounds. Regulatory agencies have recognized the need for the remediation of 733 priority compounds due to their mutagenic role and toxicity. Researchers from the Laboratory of Molecular Biology and Genomics have established a bank of bacterial isolates obtained from oil-polluted environments, and the genomes of promising isolates for bioremediation are currently being sequenced to determine their taxonomy and metabolic profile. Twenty-three isolates from different oil samples were subjected to whole genome sequencing and analysis. Read quality was checked with FastQC (v0.11.9) software. Sequencing reads were trimmed with Trimmomatic (v0.36) and assembled using SPAdes (v3.15.3). Assembly quality was checked using Quast (v4.4), completeness was ascertained using CheckM (v1.0.18), and EggNOG (v.2.1.6) was used for functional annotation. The growth of the isolates was tested with 1% crude oil. Genomic data were analyzed using the R

programming language (v.4.1.1). We extracted data from the KEGG database (Organism, Orthology, Pathway, Genome, Compound, and Reaction) using the KEGG API, and the package KEGGREST (v.1.34.0) to study the potential of the isolates to act on the reported compounds and conducted a genomic analysis of the isolates to determine their composition with respect to priority compounds. This analysis aimed to identify the optimal bacterial combination that can effectively act on the highest number of compounds. As a result, four bacteria (Acinetobacter sp., Acinetobacter sp., Klebsiella sp., and Ochrobactrum sp.) were selected from the 23 bacteria to compose a consortium called CP1, for showing potential to act on 70 compounds. The isolates were found to have a higher count of genes related to hydrocarbon degradation when compared with reference strains. Together the four isolates contain 225 genes related to priority compounds, ranging from 166 to 119 in isolates. Benzoate degradation and aromatic compound degradation appeared as the most enriched pathways. According to in silico analysis, our results suggest the best combination to optimize isolates selection to set up a bacterial consortium that offers promising biotechnological application in bioremediation approaches.