## The Bioremediation Potential of Hydrocarbonoclastic Bacteria Isolated From a Mangrove Contaminated by Petroleum Hydrocarbons on the Cilacap Coast, Indonesia

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Abstract	The main purpose of the study was to isolate strains of bacteria capable of degrading hydrocarbons from contaminated mangroves and to investigate the ability of the isolated bacteria to degrade total petroleum hydrocarbons (TPH) in a microcosm model of an oily sludge. The potential use of these bacteria strains as environmental clean-up agents was tested by culturing them with six different polyaromatic hydrocarbon (PAH) compounds (phenothiazine, fluorene, fluoranthene, dibenzothiophene, phenanthrene, and pyrene). Six viable and culturable bacteria were isolated, and the 16S rDNA sequence for each was amplified using the primers 9F and 1510R. Sequence results were compared using the National Center for Biotechnology Information (NCBI) BLAST program and, combined with phenotypic and phylogenetic data, were used to identify three strains that belonged to the Bacillus genus and were most closely related (9899%) to Bacillus aquimaris, Bacillus megaterium, and Bacillus pumilus. The other three strains were closely related (98100%) to Flexibacteraceae bacterium, Halobacilus trueperi, and Rhodobacteraceae bacterium. Two isolates, BA-PZN and BM-PFFP, which were related to Bacillus aquimaris and Bacillus megaterium, respectively, were further characterized and showed great potential for the removal of more complex hydrocarbon compounds in the oily microcosm model.
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