



606/E2

Selection of an efficient n-hexadecane degrading fungal-bacterial community

S M D Perera¹, S D M Chinthaka², G Seneviratne³, W S SWijesundera¹,
C D Wijayarathna⁴ and S M T Jayasena^{1*}

^{1*}Department of Biochemistry and Molecular Biology, Faculty of Medicine, University of Colombo, Colombo 08

²Department of Chemistry, Faculty of Applied Sciences, University of Sri Jayewardenepura, Nugegoda

³National Institute of Fundamental Studies, Hantana Road, Kandy

⁴Department of Chemistry, Faculty of Science, University of Colombo, Colombo

Recalcitrant organic substances are a major environmental pollutant. Microbes such as *Pseudomonas*, *Acinetobacter*, *Rhodococcus*, *Bacillus*, *Aspergillus*, and *Penicillium* have been identified as agents that have the ability to degrade these organic pollutants. In nature, synergism plays an important role where it leads to the persistence of organisms in various habitats. Bacteria capable of growth on hexadecane were isolated from Meethotamulla garbage dump, Western province. During subsequent culture in hexadecane-containing medium, three isolates were observed to form a fungal-bacterial community. Visual disintegration of the hexadecane layer was observed to be more efficient in the fungal-bacterial communities compared to the single bacterial isolates. Therefore, these three communities were selected for further analysis. The three communities were grown on Bushnell and Haas medium supplemented with 1% (v/v) hexadecane as the sole source of carbon, at 40°C for 14 days. Residual hexadecane was extracted into hexane and the extract was analyzed by gas chromatography/mass spectrometry. All assays were conducted in duplicate. Hexadecane biodegradation by the three fungal-bacterial communities, FBC1, FBC2, FBC3 were found to be 99%, 74% and 98%, respectively. FBC1 was selected for further analysis. It was grown on both nutrient agar and Sabouraud dextrose agar in order to isolate the bacteria and fungi respectively. The community comprised of a single bacterium and a fungus. Identification of microbes was performed by microscopic, biochemical and molecular techniques. Gram's staining and biochemical tests based on Bergay's manual indicated the bacterium was *Bacillus* sp. 16s rRNA gene sequencing identified the bacterium as *Bacillus cereus* / *B. thuringiensis*. Microscopic observations via slide culture technique indicated the fungus to be *Aspergillus* sp. These results suggest that FBC1 is a potential bioremediation agent to remediate hydrocarbon contaminations.