PROGRAM BOOK

FEMS 2011

4th Congress of European Microbiologists

FEDERATION OF EUROPEAN MICROBIOLOGICAL SOCIETIES

FEMS

Geneva, Switzerland
June 26-30, 2011

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Wednesday, June 29, 2011

08:00-18:00 **Poster Area**

POSTER SESSION 3: ENVIRONMENTAL MICROBIOLOGY (contd.)

Poster No

122 **SELECTION OF BIOINDICATORS FOR LEAD POLLUTION IN MICROBIAL MATS USING HIGH-RESOLUTION MICROSCOPIC TECHNIQUES**
J. Maldonado, A. Solé, I. Esteve, *Spain*

123 **A STUDY ON FUMARATE REDUCTASE ACTIVITY OF MICROORGANISMS ISOLATED FROM KOREAN BLACK GOAT**
L.L. Mamuad, M.J. Alam, S.H. Kim, K.K. Cho, C.O. Jeon, S.S. Lee, *Republic of Korea*

124 **DETECTION OF VIRULENCE FACTORS OF *AEROMONAS HYDROPHILA* ISOLATED FROM TREATED WASTEWATER AND TREATED SLUDGE**
D.E. Oliveira, L.C. Balsalobre, M. Dropa, E.M. Hachich, M.I.Z. Sato, G.R. Matté, **M.H. Matté**, *Brazil*

125 **IDENTIFICATION OF NEW ENZYMATIC ACTIVITIES FROM GRAM-POSITIVE BACTERIA ISOLATED FROM TERMITE GUT (*RETICULITERMES SANTONENSIS*)**
C. Mattéotti, P. Thonart, F. Francis, E. Haubruge, J. Destain, C. Brasseur, J. Bauwens, E. De Pauw, D. Portetelle, M. Vandenbol, *Belgium*

126 **DETECTION OF ENVIRONMENTAL MYCOBACTERIA IN WATER BY REAL TIME QUANTITATIVE PCR**
G. Meheut, S. Lamart, S. Billard, K. Delabre, N. Charni Ben Tabassi, *France*

127 **A BACTERIAL REPORTERS PANEL FOR THE DETECTION OF ANTIBIOTICS**
S. Melamed, C. Lalush, S. Yagur-Kroll, T. Elad, N. Kessler, R. Pedahzur, S. Belkin, *Israel*

128 **SCREENING FOR ANTIVIRAL ACTIVITY OF MARINE ACTINOMYCETES COLLECTED ON THE NORTH COAST OF SÃO PAULO STATE, BRAZIL**
C.B.A. Menezes, C.K. Mantovani, G.K. Kimura, L.K. Kohn, C.W. Arns, F. Fantinatti-Garboggini, *Brazil*

129 **BIOLOGICAL COBALT REMOVAL FROM WASTEWATER OF D.M.T. COMPANY, ISFAHAN**
S.M. Meybodi, F. Amiri, J. Nekoui, A. Nasrollahi, *Iran*

130 **DEFINING CONSORTIUM OF HYDROCARBON-DEGRADING BACTERIA AND DETERMINATION OF THEIR BIODEGRADATION POTENTIAL**
J. Milic, G. Gojgic-Cvijovic, V. Beskoski, M. Ilic, T. Narancic, B. Vasiljevic, M.M. Vrvic, *Serbia*

131 **DYNAMICS OF CYPRINID HERPESVIRUS-3 IN NATURAL ENVIRONMENTS IN JAPAN**
T. Minamoto, M.N. Honjo, Z. Kawabata, *Japan*

DEFINING CONSORTIUM OF HYDROCARBON-DEGRADING BACTERIA AND DETERMINATION OF THEIR BIODEGRADATION POTENTIAL

J. Milic[1], G. Gojgic-Cvijovic[1], V. Beskoski[1], M. Ilic[1], T. Narancic[2], B. Vasiljevic[2], M.M. Vrvic[3]

[1]Department of Chemistry, Institute of Chemistry, Technology and Metallurgy, University of Belgrade, [2]Institute of Molecular Genetics and Genetic Engineering, University of Belgrade, [3]Faculty of Chemistry, University of Belgrade, Belgrade, Serbia

Background: Oil contaminated soil is a widespread problem that often requires clean-up of the contaminated site. It has been suggested that the addition of hydrocarbon-degrading microbes to polluted site is less effective in hydrocarbons removal than stimulating the growth of the indigenious microorganisms with potential in biodegradation.

Objectives: The aim of this study was to examine biodegradation potential of four hydrocarbon-degrading bacteria both individually and as consortium, primarily on PAHs and BTEX.

Methods: Bacteria were isolated from Oil rafinery Pancevo (Serbia) and identified based on 16S RNA sequences.Cell respiration was determined by measuring dehydrogenase activity. Biofilm formation was investigated in stationary conditions [1].Biodegradation potential of isolated bacteria individually and in consortium was tested by degradation of PAH (phenantrene, pyrene, dibenzothiophene) and BTEX, at 28°C and rotation of 120 rpm for one month. Criteria for microbial growth.were weakly measurements of optical density (620 nm)

Conslusions: Isolated bacteria were identified as *Rhodococcus spp*, *Staphylococcus pasteuri*, *Planomicrobium sp* and *Micrococcus sp*, based on 16S RNA sequence.Results showed that *Rhodococcus spp* is the most efficient in degradation of all hydrocarbons used, while *Planomicrobium sp* is slowest hydrocarbon-degrader. However, this bacterium has strong ability for biofilm formation, and probably plays an important role in the consortium, in terms of the substrate initial degradation, thus making it more available to other constituents of the consortium.Experiments with defined consortium showed that community is more efficient in later stages of hydrocarbon degradation.

References:

[1] H. Mehdi, E. Giti, Int. Biodeter. Biodegr. Vol. 62 (2008) 170.

DEFINING CONSORTIUM OF HYDROCARBON-DEGRADING BACTERIA AND DETERMINATION OF THEIR BIODEGRADATION POTENTIAL

J. Milic[1*], G. Gojgic Cvijovic[1], V. Beskoski[1], M. Ilic[1], T. Narancic[2], B. Vasiljevic[2], M. M. Vrvic[1,3]

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BACKROUND

Oil contaminated soil is a widespread problem that often requires clean-up of the contaminated site. It has been suggested that the addition of hydrocarbon-degrading microbes to polluted site is less effective in hydrocarbons removal than stimulating the growth of the indigenious microorganisms with potential in biodegradation.

The aim of this study was to examine biodegradation potential of four hydrocarbon-degrading bacteria both individually and as consortium primarily on PAHs and BTEX.

METHODS

Bacteria were isolated from Oil rafinery Pancevo (Serbia) and identified based on 16S RNA sequences.

Cell respiration was determined by measuring dehydrogenase activity. Biofilm formation was investigated in stationary conditions [1].

Biodegradation potential of isolated bacteria individually and in consortium was tested by degradation of PAH (phenantrene, pyrene, dibenzothiophene) and BTEX, at 28°C and rotation of 120 rpm for one month. Criteria for microbial growth were weakly measurements of optical density (620 nm).

RESULTS

Isolated bacteria were identified as *Rhodococcus sp., Staphylococcus pasteuri, Planomicrobium sp.* and *Micrococcus sp.,* based on 16S RNA sequence.

Results showed that all bacteria has higher affinity to degrade PAH than BTEX. *Rhodococcus sp.* is the most efficient in degradation of all hydrocarbons used, while *Micrococcus sp.* is slowest hydrocarbon-degrader (Fig. 1.). However, *Micrococcus sp.* has strong ability for biofilm formation, and probably plays an important role in the consortium, in terms of the substrate initial degradation, thus making it more available to other constituents of the consortium (Fig .2.). *Staphylococcus pasteuri* and *Planomicrobium sp.* have highest dehydrogenase activity, indicating these bacteria as important parts of microbial consortium. (Fig. 3)

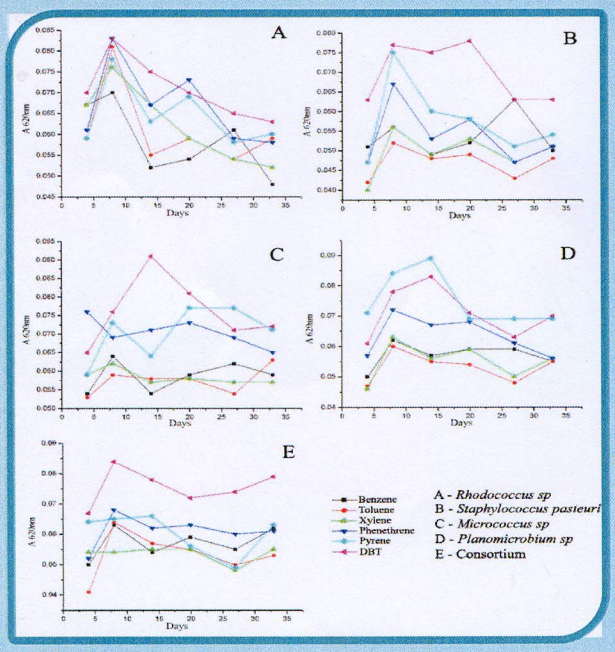

Fig. 1. Time course of the hydrocarbon concentration during the biodegradation process

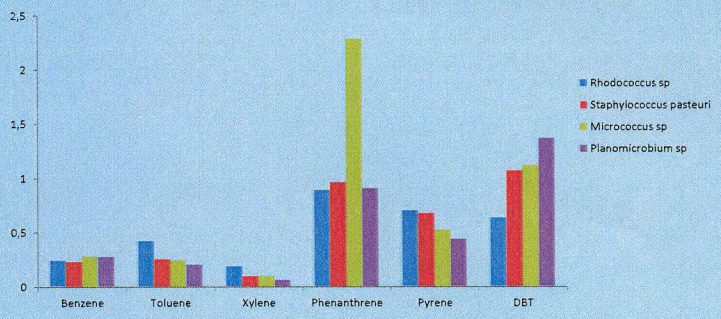

Fig. 2. Biofilm formation (A 620nm)

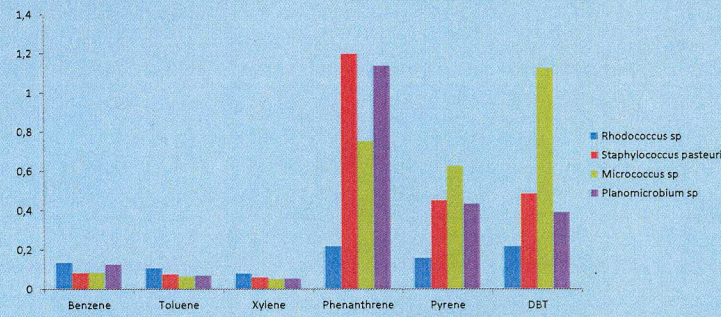

Fig. 3. Dehydrogenase activity (A 492nm)

CONCLUSIONS

Experiments with defined consortium showed that community is more efficient in later stages ofhydrocarbon degradation.

REFERENCE

[1] H. Mehdi, E. Giti, *Int. Biodeter. Biodegr. Vol. 62 (2008) 170.*