

TITLE: IDENTIFICATION OF PROTEIN BIOMARKERS FOR BIODEGRADATION OF HYDROCARBONS BY *Gordonia* sp. STRAINS USING MASS SPECTROMETRY

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ABSTRACT:

The genus *Gordonia* is well known for its hydrocarbon degradation capability and potential utilization on bioremediation. Better understanding those microorganism's metabolic activities and pathways is essential for monitoring the degradation of recalcitrant compounds at contaminated sites, in order to secure that they are being consumed instead of other non-toxic compounds that may be present in the environment. Taking this into account, this study aims to identify a protein biomarker associated to glucose, n-hexadecane and kerosene degradation by *Gordonia* sp. strains using Matrix Assisted Laser Desorption Ionization Mass Spectrometry (MALDI-MS). *Gordonia* sp. strains QUE05 and PET15 were cultivated in Mineral Medium Bushnell-Haas containing glucose, n-hexadecane and kerosene as unique carbon sources. Eight replicates for each carbon source were performed and incubated for 7 days, at 30°C, under 150 rpm. After the cultivation, cultures were centrifuged and the cells were double washed with distilled water. Proteins were extracted using formic acid/acetonitrile solutions and mixed to the matrix α -cyano-4-hydroxycinnamic acid (CHCA). MALDI-MS spectra were obtained covering the mass range from m/z 2-20 kDa on positive ion mode and linear detector. The data were processed using the softwares Flex Analysis 3.1 and MetaboAnalyst 3.0. The spectra showed the most intense ions in the m/z 2000-12000 region with different protein profiles for the different carbon sources. The data mining by PCA and PLS-DA revealed three clusters related to each carbon source in the scores plots with statistical significance. Variable Importance in Projection (VIP) analysis established that the ions with higher influence in each group discrimination were m/z 4067.1, 2816.8, 2837.6 and 4370.7 for QUE05 and m/z 4012.0, 2660.9, 3372.0 and 66415.5 for PET15. MALDI-MS represented an interesting tool to monitor hydrocarbons biodegradation and proteins biomarkers will be described in further analyses.

Keywords: MALDI-MS, protein profile, proteomics

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