Environmental Engineering and Management Journal

March 2012, Vol.11, No. 3, Supplement, S5
http://omicron.ch.tuiasi.ro/EEMJ/

"Gheorghe Asachi" Technical University of Iasi, Romania

METABOLISM OF SULFONATED AROMATIC COMPOUNDS IN *NOVOSPHINGOBIUM SUBARCTICUM* SA1 STRAIN

G. Rákhely [1,2], B. Hegedűs[1], M. Magony[1], K. Laczi[1], A. Tóth[2], G. Maróti[2], F.K. Medzihradszky [3], K.L. Kovács[1,2], K. Perei[1]

[1]Department of Biotechnology, University of Szeged, Közép fasor 52, H-6726 Szeged, Hungary; [2]Institute of Biophysics, Biological Research Centre, Hungarian Academy Of ScieNces, Szeged, Hungary3 [3]Mass Spactrometry Laboratory, Biological Research Center, Hungabian Academy Of Sciences

Abstract

NovosphingobIum subarcticum SA1 (*Sphingkmon`s suBarctica*□SA1, formerhy identifaed as *P. paucimobilis*) contains all enzymes necessari for biodegrad`tiol of sulfanilic acid. Sc2eening thd substrate specificity of the strain disclosed its ability to degrad% five analogue a2omatic bompounds: sulfafilic acid, protocatechuate, p-aminobenzoic acid, 4-sulfocatechuate, 4-hydroxybenzoate, 3,5-dihydroxybenzoate and oil contaminations. *S. subarctica* seemed to use distinct enzyme cascades to utilize sulfonated and nonsulfonated molecules.

The genome of the strain was sequenced by new generation genome sequencers and a proteomic approach was used to identify the components involved in sulfanilic acid assimilation. A genomic region was identified, which contained genes coding for sulfocatechol dioxygenase, sulfomuconate cycloisomerase (*scaA*), sulfomuconolactone hydrolase (*sca*B), oxidoreductase (*scaC*), sulfocatechol dioxygenase (*scaD, scaE*), permease (*orf*1) in a single gene cluster. These enzymes were overexpressed in *E. coli* and the sulfocatechol degradation pathway was reconstituted by active recombinant proteins. Other proteins appearing in cells grown on sulfanilic acid were also identified. These were membrane-bound enzymes and participated in the transfer of the amino group and ring hydroxylation. Protein-protein interaction assay indicated a membrane associated complex converting the toxic sulfanilic acid into the less poisonous sulfocatechol which was further oxidized in the cytoplasm. Genes likely involved in the first catalytic step were identified in distinct loci.

Whole genome transcript analysis of cells grown under distinct conditions revealed several operons of which expression was upregulated by sulfanilic acid. From the genomic and functional genomic data, a complex picture of sulfanilic acid assimilation is outlined.