Environmental Engineering and Management Journal March 2012, Vol.11, No. 3, Supplement, S20
http://omicron.ch.tuiasi.ro/EEMJ/

"Gheorghe Asachi" Technical University of Iasi, Romania

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METABOLIC AND PROTEIN-PROTEIN INTERACTIONS OF SULFANILIC ACID CATABOLISM IN *Novosphingobium subarcticum* SA1

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

[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, Hungary

Abstract

Novosphingobium subarcticum SA1 (*Sphingomonas subarctica* SA1, formerly identified as *P. paucimobilis*) alone is able to degrade sulfanilic acid. It was shown that the strain could catabolize five analogue aromatic compounds including protocatechuate, p-aminobenzoic acid, 4-hydroxybenzoate. The protein patterns of the strains grown on sulfonated and nonsulfonated molecules were distinct indicating alternative routes for the assimilation of these compounds.

The genome of the strain was sequenced by new generation genome sequencers and revealed numerous genes of enzymes potentially catalyzing the oxidation of aromatic compounds.

A genomic region containing the genes coding for sulfocatechol and protocatechuate dioxygenase were identified in distinct gene clusters. The analysis of enzymatic activity of cells grown on sulfo- or protocatechuate revealed, that the protocatechol and sulfocatechol pathways overlapped at the ring cleaving reaction, but the next step required different specific cycloisomerase enzymes.

Investigation of the proteins appearing upon sulfanilic acid induction disclosed proteins likely involved in the sulfanilic acid transport, conversion as well as the iron transport. The oxidation of sulfanilic acid requires iron containing enzymes, therefore this would be reasonable that the increased iron demand of the dioxygenase enzymes would be provided by the induction of an iron transport pathway.

A localization study of the proteins likely involved in the transport of amino group and ring hydroxylation pointed out that these enzymes were membrane associated and they appeared simultaneously. Recombinant enzymes were produced in homologous host and the proteins copurifying with either of these proteins were identified. The results suggest a membrane associated complex which is responsible for coupled uptake and conversion of sulfanilic acid.