**Poster Presentation**

**MS29.P40**

## *Structural characterization of Polycyclic Aromatic Hydrocarbon degrading enzymes*

J. Coitinho[1], D. Costa[1], S. Guimaraes[1], C. Neves[1], S. Araujo[1], M. Costa[1], R. Nagem[1]

[1]*Universidade Federal de Minas Gerais, Departamento de Bioquimica e Imunologia, Belo Horizonte, Brazil*

Polycyclic aromatic hydrocarbons (PAHs) are a group of aromatic hydrocarbons composed of two or more fused rings and include naphthalene, phenanthrene, pyrene and benzo[a]pyrene amongst others. Exposure to naphthalene has been associated with several toxic manifestations in humans and laboratory animals, with the lens of the eye and the lungs being most sensitive [1]. Additionally, this compound has been reclassified as a possible human carcinogen by the US Environmental Protection Agency and the International Agency for Research on Cancer. It has recently been suggested that naphthalene undergoes metabolic activation to 1,2-naphthoquinone, which reacts with DNA, leading to the formation of apurinic sites on DNA and depurinating DNA adducts [2]. Moreover, a number of studies have attested to the carcinogenic and mutagenic properties of more complex PAHs, suggesting the need for further work on the elimination of these compounds from the environment. The Gram-negative bacterium P. putida G7 is among the best studied naphthalene-degrading species. The genes associated with naphthalene metabolism are localized on NAH7, an 83 kilobase plasmid. In P. putida G7 the naphthalene-oxidation genes are organized into two operons under salicylate control. The first operon (upper naphthalene-degradation pathway) includes the genes nahAaAbAcAdBCDEF, which code for the conversion of naphthalene to salicylate, while the second operon (lower pathway) includes the genes nahGTHINLOMKJ responsible for the oxidation of salicylate via the catechol meta-cleavage pathway [3]. In the last years, our group focused on the structure elucidation and the kinetic characterization of the P. putida G7 enzymes involved in the naphthalene degradation pathway. We intend to present these results which basically describe the 3D structures of NahB, NahF, NahG, NahI, NahK and NahK/NahL complex and some kinetic data of these enzymes and their mutants. This work was supported by FAPEMIG, CNPq and VALE S.A.

***[1]*** *Stohs, S. J., Ohia, S. & Bagchi, D. (2002). Toxicology, 180, 97–105.,* ***[2]*** *Saeed, M., Higginbotham, S., Gaikwad, N., Chakravarti, D., Rogan, E. & Cavalieri, E. (2009). Free Radic. Biol. Med. 47, 1075–1081.,* ***[3]*** *Yen, K.-M. & Gunsalus, I. C. (1985). J. Bacteriol. 162, 1008–1013.*

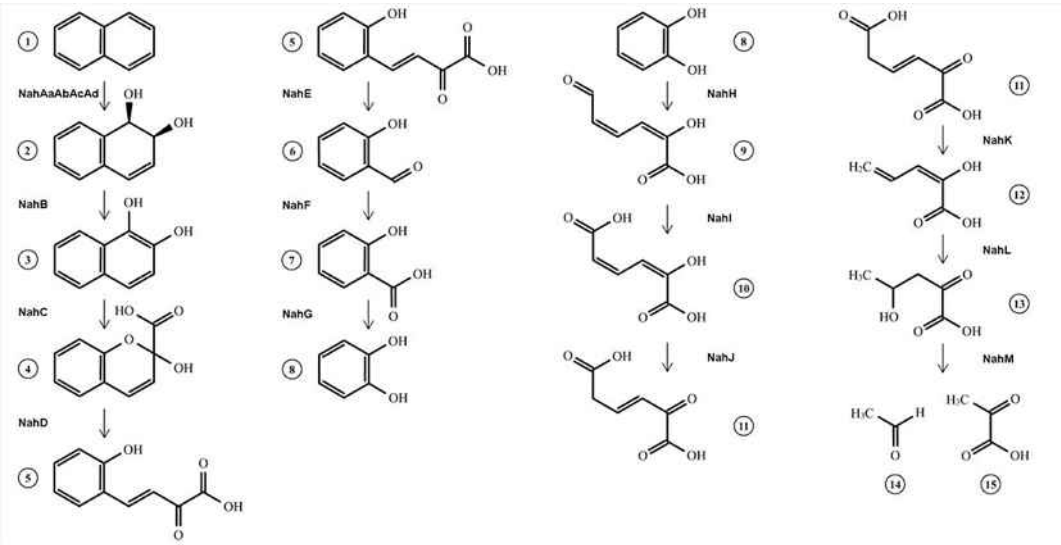


Figure 1 – Enzymes, substrates and products involved in the naphtalene degrading pathway in *Pseudomonas putida* G7. NahAaAbAcAd – naphthalene dioxygenase complex, NahB – cis-naphthalene dihydrodiol dehydrogenase, NahC – 1,2-dihydro naphthalene dioxygenase, NahD – 2-hydroxy-2H-chromen-2-carboxylate isomerase, NahE – hydroxy benzo pyruvate hydratase-aldolase, NahF – salicylaldehyde dehydrogenase, NahG – salicylic acid hydroxylase, NahH – catechol 2,3-dioxygenase, NahI – aminomuconate-semialdehyde dehydrogenase, NahJ – 4-oxalocrotonate tautomerase, NahK – 4-oxalocrotonate decarboxylase, NahL – 2-oxopent-4-enoate hydratase e NahM – 2-oxo-4-hydroxy pentanoate aldolase, (1) naphthalene, (2) cis-1,2-dihydronaphthalene-1,2-diol, (3) 1,2-dihydronaphthalene, (4) 2-hydroxy-2H-chromene-2-carboxylic acid, (5) trans-o-hydroxyphenyl pyruvate acid, (6) salicylaldehyde, (7) salicylic acid, (8) catechol, (9) 2-hydroxy muconate semialdehyde, (10) 2-hydroxy muconate, (11) 4-oxalocrotonate, (12) 2-oxopent-4-enoate, (13) 4-hydroxy-2-oxopentanoate, (14) acetaldehyde (15) pyruvate.

**Keywords:** polycyclic aromatic hydrocarbons, degrading enzymes