Natalia Zielonka

Biodegradation of phosphonic acid compounds by fungi

Abstract:

Phosphonic acids and their derivatives constitute a steadily increasing percentage of industrially produced chemicals. This is mainly due to their mass scale use as phosphonic herbicides. These compounds are characterised by the presence of a covalent bond between a carbon atom and a phosphorus atom, which gives them an extremely stable structure and resistance to degradation. The ability of bacteria to mineralise these compounds has been well documented. In contrast, data on the biochemical characteristics of the metabolism of P-C compounds in eukaryotic or extremophilic organisms are still scarce.

The present study investigated the mechanisms of degradation of model phosphonic acids by fungi of the genus *Penicillium* and the newly isolated psychrotolerant yeast strain - *Solicoccozyma terricola* M 3.1.4.

As part of the research conducted in cooperation with the scientific team of Mr Hubert Cieslinski, Ph.D. D.Sc., Associate Professor of the Gdansk University of Science and Technology, the kinetics of decomposition of the *N*-phosphonomethylglycine (PMG) by the psychrotolerant yeast strain *Solicoccozyma terricola* M 3.1.4 and the enzymatic activity of the cell-free extract toward the compound mentioned above was studied. This strain used the tested phosphonic acid as a source of nitrogen and phosphorus for cellular purposes, in a phosphate independent manner. On the basis of this study, the degradation of PMG by *S. terricola* M 3.1.4 was proposed, indicating the involvement of the glyphosate oxidoreductase (GOX) pathway in the degradation of the PMG.

Additionally, a metabolomic analysis of selected fungi capable of degrading phosphonoacetic acid (PA) was carried out to obtain the metabolic profiles of two environmental isolates: *Penicillium crustosum* S2 and *Penicillium funiculosum* S4, which were collated and compared with the metabolic profile of the *Penicillium commune* strain. This research is a continuation of the studies carried out by our Research Team on phosphonoacetate hydrolase and was performed to understand the differences in the metabolism of the studied fungi.

An important objective of the research was to characterise the two-step biodegradation process of 2-aminoethylphosphonic acid (2-AEP) in a *Penicillium commune* strain. The kinetics of 2-AEP decomposition by the studied fungal strain was investigated and it was confirmed that

the use of the phosphonic substrate is dependent on the phosphate status of the cell. The characterisation of the first step of substrate decomposition - the ciliatine transamination process - was carried out. The most effective acceptor of the amine group in the reaction catalysed by transaminase 2-AEP was determined. For the first time, an eukaryotic phosphonatase was isolated and partially purified, catalysing the second step of this reaction - the enzymatic cleavage of the stable C-P bond in the phosphonoacetaldehyde moiety. The enzyme was characterised and compared with analogous bacterial enzymes described in the literature. The partially purified fungal phosphonatase probably belongs to the enzymes of the HAD superfamily and, like its bacterial counterparts, requires the presence of magnesium ions (Mg^{2+}) for its activity.

The mode of transformation of structurally different phosphonate compounds in the environment can only be known approximately. The more we know about the activity of individual microorganisms and their ability to degrade a given group of organic compounds, the more the picture of what happens in the environment will reflect reality.