Research on fungal enzymatic system active toward organophosphorus compounds

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Organophosphonates are a group of compounds, both synthetic and biogenic, characterized by the presence of a stable carbon to phosphorus bond (C-P bond), which makes them very resistant to degradation [1]. Such compounds are believed to play a particularly important role in the biogeochemical circulation of phosphorus. Phosphonates enrich the global pool of phosphorus compounds, as synthetic compounds are widely used in industry and enter the environment in large quantities as xenobiotics [1, 2], but on the other hand, they are ubiquitous in biological systems

Phosphorus is a limiting nutrient in many environments and hence organisms have evolved metabolic pathways that can release phosphate from phosphonates of various origin. Several strategies have been discovered, including hydrolytic, oxidative, and reductive processes [3, 4] but the hydrolases activities towards phosphonate molecules are thought to contribute significantly to global P-cycling [2]. The most predominant biogenic P-C compound is ciliatine (2-AEP), which is very often found as a membrane lipid head-group analogues to phosphatidylethanolamine [4]. The amount of 2-AEP in phosphonic resources is dominant [5], so the degradation of this molecule containing P-C bond by microorganisms appears to be critical for the phosphorus cycle in various types of ecosystems. It is worth to stress, that since the phosphonates metabolism is, in most described cases, dependent on the presence of inorganic phosphate in the environment, data on the capability of microorganisms to mineralize P-C compound regardless of the phosphate status of the cell are relevant, but still incomplete, particularly for eukaryotic microorganisms.

The research presented here concerns the characterization of the two-step process of 2-AEP biodegradation by *Penicillium commune* strain. It was confirmed that the fungal decomposition process is independent of the phosphate status of the cell. For the first time, an eukaryotic phosphonatase catalyzing the enzymatic cleavage of the stable C-P bond in the phosphonoacetaldehyde moiety was isolated and partially purified. The enzyme was characterized 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.

References

[1] A. Furtak, A. Szafranek-Nakonieczna, K. Furtak, A. Pytlak, *Journal of Environmental Management, 355 (2024), 120453*; DOI: 10.1016/j.jenvman.2024.120453
[2] J.P. Chin, J.W. McGrath, J.P. Quinn, *Current Opinion In Chemical Biology, 31 (2016), 50-57*; DOI: 10.1016/j.cbpa.2016.01.010

[3] X. Yu, J.R. Doroghazi, S.C. Janga, J.K. Zhang, B. Circello, B.M. Griffin, D.P. Labeda, W.M. Metcalf, *PNAS, 110:51 (2013), 20759-20764*; DOI: 10.1073/pnas.1315107110
[4] D.M. Karl*, Annual Review of Marine Science*, *6 (2014), 279-337;* DOI: 10.1146/annurev-marine-010213-135046
[5] H. Studnik, S. Liebsch, G. Forlani, D. Wieczorek, P. Kafarski, J. Lipok, *New Biotechnology 32 (2015), 1-6*; DOI: 10.1016/j.nbt.2014.06.007