**In search of PET-degrading enzymes: metagenomes reveal hidden homologues**

D. Khaleneva 1,5, P. Dzhelali l,5, V. Pirogov 1,2, G. Buckley 1,3, R. Shanin 1,4, L. Danilov 1,5, M. Raiko 1,6

*1. Bioinformatics Institute, Kantemirovskaya str. 2A, 197342, Saint Petersburg, Russia*

*2. Alferov University, Khlopina 8/3, 194021, St. Petersburg, Russia*

*3. National Research University Higher School of Economics, Pokrovskij bul'var, 11, 109028, Moscow, Russia*

*4. MIREA - Russian Technological University, Vernadskogo av., 78, 119454, Moscow, Russia*

*5. Saint Petersburg State University, Universitetskaya nab. , 7/9, 199034, St. Petersburg, Russia*

*6.* [*Center for Algorithmic Biotechnology*](https://cab.spbu.ru/)*, Saint Petersburg State University, Universitetskaya nab. , 7/9, 199034, St. Petersburg, Russia*

Polyethylene terephthalate (PET) is widely used all over the world in plastic products and its accumulation in the environment has become a global problem. Recently, various studies have been carried out to develop an efficient system for PET recycling.

*Ideonella sakaiensis* is a bacteria which, when grown on PET, produces two enzymes, PETase and MHETase, capable of hydrolyzing PET to produce terephthalic acid and ethylene glycol.

Our goal was to find enzymes that could potentially participate in PET processing. We reproduced the phylogenetic analysis of sequences homologous to PETase and MHETase, and then expanded it by adding information on metagenomic data.

We performed phylogenetic analysis using MEGA X software (Kumar, S., 2018) and it is consistent with the earlier studies of the phylogenetic position of PETase and MHETase (Yoshida, 2016; Knott, B., 2020). Our studies have shown that PETase and MHETase homologs exist independently of each other in some classes of bacteria (Actinobacteria, Cytophagales - PETase homologues, MHETase homologues). This may indicate different evolutionary pathways for both enzymes.

Metagenomic analysis revealed a number of metagenomes with high similarity to the *Ideonella sakaiensis* enzymes, which were collected mainly as oceanic samples or compost samples. Oceanic samples of metagenomic data were collected during the expeditions of the Craig Venter Institute, and are of great interest because they contain many previously undescribed species, which may include organisms capable of processing polycarbonate chains. Similar data were independently obtained recently (Danso, D., 2018), and can be combined with our results to increase further known amounts of potential PET-degrading bacteria.

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