

Novel polyethylene terephthalate (PET) plastic degrading enzymes from the environmental metagenome

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Abstract

Several plastic degrading enzymes have been described in the literature, most notably PETases that are capable of hydrolyzing polyethylene terephthalate (PET) plastic. One of them, the PETase from *Ideonella sakaiensis*, a bacterium isolated from environmental samples within a PET bottle recycling site, was the subject of extensive studies. To test how widespread PETase functionality is in other bacterial communities, we used a cascade of BLAST searches in the JGI metagenomic datasets and showed that PETases can also be found in other metagenomic environmental samples from both human affected and relatively pristine sites. To confirm their classification as PETases, we verified that the newly identified proteins have the PETase sequence signatures common to all PETases and that phylogenetic analyses group them with the experimentally characterized PETases. Additionally, docking analysis was performed in order to further confirm the functional assignment of the putative environmental PETases.

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