

# **METAGENOMIC EXPLORATION OF ESTUARINE MICROORGANISMS WITH FOCUS ON PET-DEGRADING ENZYMES**

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Anthropogenic plastic pollution severely impacts marine ecosystems and biodiversity. Biodegradation is one of the promising methods of plastics processing. Many microorganisms and fungi can produce enzymes associated with decomposition of polymers. Polyethylene terephthalate is widely used plastic polymer that can be degraded by enzymes from the class of PETases (polyethylene terephthalate hydrolases). In order to detect new plastic degrading enzymes, we analyzed 12 metatranscriptomes from the river estuaries of the North and South America. We found 133 candidate genes, from which 42 have no close analogues in the NCBI database. Based on 3 parameters: presence of the PETase-specific conservative domain, affinity to PETases (whether detected by BLAST or by phylogenetic tree) and percent identity of the gene matches in the NCBI database, we have chosen 3 candidate genes which products might be able to degrade polyethylene terephthalate. These are polyhydroxybutyrate depolymerase (Ga0129322\_10011272), phospholipase/carboxylesterase (Ga0393217\_000473\_3101\_3565), phosphatidylinositol phospholipase C beta (Ga0210357\_10010551). We assume that the product enzymes of these 3 genes might be of use by development of eco-friendly methods of plastic biodegradation.