
A mechanistic understanding of polyethylene biodegradation by the marine bacterium *Alcanivorax*

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Abstract

To this date, the extent of microbial biodegradation of plastics is still an open question. The presence of hydrocarbon degraders as part of the plastisphere identified from marine plastic debris (MPD) samples has prompted different ideas about the role of such a group of microorganisms in the degradation of these synthetic polymers. In this investigation, we have tested the potential of the hydrocarbonoclastic bacteria *Alcanivorax* sp. 24 (bacterial isolate obtained from MPD) to degrade polyethelene (PE) –one of the most recalcitrant carbon-based synthetic materials produced and, currently, the most ubiquitous plastic pollutant found in nature. Evidence indicates that an array of abiotic and biotic processes eventually breaks down PE. However, the biological impact and mechanistic understanding of the process are unclear. Here, using high-throughput proteomics, we investigated the molecular processes that take place in the hydrocarbon-degrading marine bacterium *Alcanivorax* sp. 24 when grown in the presence of low-density PE (LDPE). As well as efficiently utilising and assimilating the leachate of weathered LDPE, the bacterium was able to reduce the molecular weight distribution and overall mass of pristine LDPE films (0.9 % after 34 days of incubation). Most interestingly, *Alcanivorax* acquired the isotopic signature of the pristine plastic and induced an extensive array of metabolic pathways for aliphatic compound degradation. Presumably, the primary biodegradation of LDPE by *Alcanivorax* sp. 24 is possible via the production of extracellular reactive oxygen species as observed both by the material's surface oxidation and the measurement of superoxide in the culture with LDPE. Our findings confirm that hydrocarbon-biodegrading bacteria within the plastisphere may in fact have a role in degrading PE.

Keywords: *Alcanivorax*, Biodegradation of polyethylene, Plastic marine pollution, High, through-put proteomics, Reactive oxygen species

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