

EGU2020-7975

<https://doi.org/10.5194/egusphere-egu2020-7975>

EGU General Assembly 2020

© Author(s) 2021. This work is distributed under the Creative Commons Attribution 4.0 License.



Differential microbial colonization on microplastic in the Mediterranean Sea coastal zone

Annika Vaksmaa¹, Katrin Knittel², Alejandro Abdala Asbun¹, Maaïke Goudriaan¹, Andreas Ellrott², Harry Witte¹, and Helge Niemann^{1,3,4}

¹Royal Netherlands Institute for Sea Research, Department of Marine Microbiology and Biogeochemistry, and Utrecht University, Texel, the Netherlands (annika.vaksmaa@nioz.nl)

²Max Planck Institute for Marine Microbiology, Department of Molecular Ecology, Bremen, Germany

³University of Utrecht, Faculty of Geosciences, Department of Earth Sciences, Utrecht, the Netherlands

⁴University of Tromsø, Centre for Arctic Gas Hydrate, Environment and Climate, Tromsø, Norway

Ocean plastic debris poses a large threat to the marine environment. Millions of tons of plastic end up in the ocean each year and the Mediterranean Sea is one of the most plastic polluted sea. Ocean plastic particles are typically covered with microbial biofilms, but it remains unclear if different polymer types are colonized by different communities. Knowledge in this aspect strengthens our understanding if microbes purely use plastic debris as attachment surface or if they may even contribute to the degradation of plastic. To gain a better understanding of the composition and structure of biofilms on microplastic particles (MP) in the Mediterranean Sea, we analyzed microbial community covering floating MP in a bay/marina (Marina di Campo) on the island of Elba. MPs were collected with a plankton net (mesh size 50µm), fixed for fluorescence microscopy and stored for subsequent DNA extraction, and identification of the polymer with Raman spectroscopy. The particles were mainly comprised of polyethylene (PE), polypropylene (PP) and polystyrene (PS) and were often brittle and with cracks (PE, PP) and showed visual signs of biofouling (PE, PP, PS). Fluorescence in situ hybridization and imaging by high resolution confocal laser scanning microscopy of single MPs revealed high densities of colonization by microbes. 16S rRNA gene amplicon sequencing (Illumina Miseq) revealed higher abundance of archaeal sequences on PS (up to 29% of the reads) in comparison to PE or PP (up to 3% of the reads). The bacterial community in the biofilms on each of the three plastic types consisted mainly of the orders Flavobacteriales, Rickettsiales, Alteromonadales, Cytophagales, Rhodobacterales and Oceanospirillales. Furthermore, we found significant difference in the community composition of biofilms on PE compared to PP and PS but not between PP and PS. The indicator species on PE were Calditrichales, detected at 10 times higher sequence abundance on PE than on PP and PS, as well as several uncultured orders. This study sheds light on preferential microbial attachment and biofilm formation on microplastic particles, yet it remains to be revealed, whether and which of these may contribute to plastic degradation.