

**P GCEH 4****Plastic debris: a distinct niche in the marine environment**

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Living the plastic age has major implications on the marine environment, from entanglement of birds, fish and mammals to ingestion of plastic debris.

Recent research shows that marine plastic litter (MPL) is colonised by micro-organisms, especially bacteria (Zettler et al., 2013). These bacteria can be alien or invasive, using the plastic as a transport vector. Some of these bacteria could be pathogenic for man and animals, while other could be beneficial and for instance biodegrade the plastic particles.

In this research we aim at identifying the major bacterial taxa present on MPL. To investigate the source of bacteria living on marine plastics, we conduct a comparative analysis against bacterial communities of the nearby environment (sediment, seawater). Parameters influencing the plastic bacterial composition were investigated as well.

Samples were taken at multiple locations along the Belgian part of the North Sea during several seasons. 16S (V3-V4) amplicon sequencing was used to study their bacterial communities.

Differences in bacterial community structure and diversity showed that plastic represent a distinct microbial niche compared to sediment and seawater. Most of the bacterial families on plastic were identified in sediment and/or seawater. However some bacterial families identified on plastics, e.g. Vibrionaceae and Pseudoalteromonadaceae, are rarely found in sediment and seawater. The bacterial diversity of plastic was higher compared to seawater and in the same range as sediment. In addition, a high diversity was observed between bacterial communities of the plastic samples, which could not always be related to differences in sampling location or date. Apart from environmental parameters like salinity, pollution and sampling depth, that may influence the plastic bacterial communities, less obvious factors such as chemical adsorption, additives of the plastic and biofilm formation stage might contribute to bacterial colonisation patterns on marine plastics.

Based on these observations MPL was defined as a distinct microbial niche in the marine environment, influenced by environmental and plastic-related factors.

(1) Zettler, E.R.; Mincer, T.J. and Amaral-Zettler, L.A. Life in the "Plastisphere": microbial communities on plastic marine debris. *Environ. Sci. Technol.* 2013, 47(13)

**P GCEH 5****Microbial community structure and function vertical distribution in snowpack over sea ice from Greenlandic fjord**

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Seasonal snowpack can extend over 14% of the total Earth surface at times, covering up to 46 million km<sup>2</sup> of land and 25 million km<sup>2</sup> of sea ice. Far from sterile, snow has recently been shown to have an unexpected abundance and diversity of microorganisms with average of 10<sup>3</sup> and up to 10<sup>5</sup> cells per mL of melted snow and with representatives of numerous microbial taxa among Bacteria, Archaea and Eukarya. Although these microorganisms have been detected, the ecology of the snowpack microbial habitat remains largely unknown, especial the selection of specific microbial communities by variable environmental conditions and the resulting functional signature reflecting the snowpack environment. In this study, we focused on snow over sea ice with samples collected in the vicinity of Nuuk in South West Greenland in a fjord with snow covered sea ice. A vertical gradient: seawater, sea-ice, snow and atmosphere, was sampled. Within the snow, four layers identified by visual structure, a first thin hard top layer in direct contact with the atmosphere, one basal saline snow wetted by brine ascendant flow and two intermediate layers, were sampled. We addressed how the microbial communities are influenced by their different seeding sources, atmosphere and sea-ice, and what were the specific functions involved in response to abiotic characteristic of the snowpack (e.g. UV-light exposure and salinity). We applied a combined metagenomic and metatranscriptomic approach to each component of this vertical gradient sea water, sea-ice, snow and atmosphere. Comparison of distribution of sequences in taxonomical and functional groups among all samples helped identify common and specific patterns of microbial communities in this complex habitat. The expression pattern induced in part from the RNA sequencing could lead to a better understanding of which microorganisms are the most active, what their dominant metabolic processes are, and how rapidly they respond to this highly fluctuating environment.