
Microbial community and functions of marine plastisphere in Hong Kong

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Abstract

Investigating the members of the plastisphere - the microbial community that forms specifically on plastic items - is key to understand how they contribute to the distribution and fragmentation of plastics in the ocean. My key objective is to identify the members of plastisphere in Hong Kong, and their potential functions. Plastic plates made of high-density polystyrene (HDPE), low-density polystyrene (LDPE), polypropylene (PP) and polystyrene (PS) were deployed at two coastal location with different levels of anthropogenic impact, and water sample was collected in the location with higher anthropogenic impact for comparison. After 1 month, 16S rRNA sequencing and metagenomic sequencing were conducted on DNA extracted from plastic biofilm to identify plastisphere members and their potential metabolic functions. Phylum of Proteobacteria dominates both water and plastisphere, while class of Gammaproteobacteria dominates water samples, Alphaproteobacteria and other phyla were more abundant in plastisphere samples. Significant differences between plastisphere and community in water were observed, sampling location and plastic type also exhibits effect on the plastisphere. From the plastisphere of LDPE and its corresponding surrounding water, we discovered the family of *Oleiphilaceae* was highly enriched on plastic, accounting for 14.3% of the plastisphere members. Metagenomic sequencing reveal the presence of genes related to hydrocarbon degradation in *Oleiphilaceae*, such as *alkB* and *AlmA*, which indicates potential degradation activity enriched on plastic surfaces. These results on plastisphere metabolic function may provide insight in understanding the biological aspects of microplastic formation and developing potential solution in responds to microplastic pollution.

Keywords: plastisphere, microbial community, biodegradation, marine plastics, metagenomic sequencing

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