

Microplastic-associated bacterial assemblages in the intertidal zone of the Yangtze Estuary

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Plastic trash is common in oceans. Terrestrial and marine ecosystem interactions occur in the intertidal zone where accumulation of plastic frequently occurs. However, knowledge of the plastic-associated microbial community (the plastisphere) in the intertidal zone is scanty. We used high-throughput sequencing to profile the bacterial communities attached to microplastic samples from intertidal locations around the Yangtze estuary in China. The structure and composition of plastisphere communities varied significantly among the locations. We found the taxonomic composition on microplastic samples was related to their sedimentary and aquatic origins. Correlation network analysis was used to identify keystone bacterial genera (e.g. Rhodobacterales, Sphingomonadales and Rhizobiales), which represented important microbial associations within the plastisphere community. Other species (i.e. potential pathogens) were considered as hitchhikers in the plastic attached microbial communities. Metabolic pathway analysis suggested adaptations of these bacterial assemblages to the plastic surface-colonization lifestyle. These adaptations included reduced “Cell motility” and greater “Xenobiotics biodegradation and metabolism.” The findings illustrate the diverse microbial assemblages that occur on microplastic and increase our understanding of plastisphere ecology.