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# Into the plastisphere, where only the generalists thrive: Early insights in plastisphere microbial community succession

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## Abstract

The ubiquity of plastic debris in marine environments raises the question, what impacts do plastics have on our marine microbiota? To investigate this, we applied bacterial 16S rRNA gene and fungal ITS2 region sequencing to identify changes in microbial biofilm community compositions on marine plastic, over time. We sampled biofilm on virgin linear low-density polyethylene (LLDPE), nylon-6 (PA) and glass after 2, 6 and 12 weeks of constant immersion in Te Whakaraupō-Lyttelton Harbour, Aotearoa-New Zealand. Of the prokaryotes, *Proteobacteria* and *Bacteroidetes* were predominant in all samples and *Verrucomicrobiota* were most abundant in mature biofilms. Microbial communities on the three substrate types were significantly distinct from those in the surrounding seawater, regardless of age, but not between attachment substrates. Bacterial communities occurring two weeks after immersion and fungal communities at six weeks were found to vary more among substrate types than at other times; however, no significant substrate-specific communities were identified overall. Taxa closely related to previously reported plastic-biodegrading species were found in very low abundance across all substrates, including on the glass slides. Our findings suggest that microorganisms do not selectively persist on the LLDPE or PA surfaces to gain significant direct metabolic benefit, instead using these plastics primarily as an attachment surface on which they form generalist biofilm communities.

**Keywords:** microbial community, 16S rRNA gene, ITS2 region, plastisphere, LLDPE (linear low density polyethylene), PA (nylon, 6), biofilm, metabarcoding

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