

A One-health impact of MPs: microbiological characterization and potential risks

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The widespread presence of plastic materials in the environment and their potential adverse effects on human health and ecosystems are currently a growing concern. Plastic pollution is commonly linked Anthropocene showing that microplastics (MPs) are detected in remote, low-impact areas, highlighting the need for further research in less contaminated ecosystems. In aquatic environments, microorganisms can rapidly colonise MPs, forming complex microbial communities known as “Plastisphere”. They differ from natural microbial communities and often include a higher abundance of pathogenic and antibiotic-resistant bacteria. The Plastisphere may facilitate the survival, persistence and spread of these microorganisms, posing potential ecological and health risks. Nevertheless, the role of MPs in the environmental persistence of pathogens remains unclear and warrants deeper investigation. The BioPlast4Safe project's research lines included a comparison of the environmental and adherent microbiota of two types of plastics (compostable PLA and non-biodegradable PP) in low-impacted river, using NGS sequencing. Antibiotic resistance genes (ARGs) of different classes were subsequently analysed, and microbiological and molecular analyses were performed to identify culturable pathogens, with SEM observations being made to visualise biofilms. Plastic materials were exposed in a riverine environment for four months and analyses were performed monthly. The two types of plastics were colonized in a similar way over time, with a slight increase in bacterial biofilm on PLA at the end of the experiment. Numerous culturable species, many of them associated with antibiotic resistance genes, were identified by Sanger sequencing. NGS analyses showed a complex interaction between the plastic and the environment, while SEM observations confirmed strong colonization, with a high abundance of diatoms and algae, especially on PP. Optimisation of qPCR protocols on individual colonies isolated from plastic surfaces is underway for the identification and quantification of resistance genes to different classes of antibiotics. Furthermore, in view of the presence of diatoms and algae, Next Generation Sequencing analyses are planned for the identification of 18S and ITS genes.

Research conducted in the framework of the Project – Biomonitoraggio di micro e nanoplastiche biodegradabili: dall’ambiente all’uomo in una prospettiva one health (BioPlast4Safe) - with the technical and economic support of the Italian Ministry of Health – PNC.