Multi-omic analysis of the biological impacts of exposure to PTFE micro- and nanoplastics in *Drosophila melanogaster*

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The increasing environmental presence of micro and nanoplastics (MNPLs) raises growing concerns regarding their biological effects and underlying molecular mechanisms. Polytetrafluoroethylene (PTFE, Teflon®) is of particular relevance due to its extensive industrial and consumer applications, yet its impact on living organisms remains poorly understood. Its widespread use in household and cooking wares facilitates particle transfer into food, representing a potential route of direct exposure and a possible risk to human health.

In this study, we employed an integrated omic approach combining 16S rRNA gene amplicon sequencing and transcriptomics to evaluate the biological effects of PTFE micro- and nanoparticles using *Drosophila melanogaster* as an *in vivo* model. *D. melanogaster* is well suited for investigating the dynamics of gastrointestinal microbiota due to its advantages such as short life cycle, well-characterised genetic background, and intestinal structure and function similar to humans.

Drosophila was exposed to PTFE particles of micro- (MPLs) and nanoscale (NPLs) dimensions to identify size-dependent biological responses. Whole-organism RNA sequencing was conducted to characterise host transcriptional responses, while 16S rRNA gene sequencing was used to assess changes in gut microbial community composition. The analyses revealed pronounced size- and concentration-dependent alterations affecting both host gene expression and microbiota structure. Integrated multi-omic analyses evaluated potential interactions between host transcriptional regulation and microbiota dynamics, highlighting the role of the gut ecosystem in mediating nanoparticle-induced biological effects.

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