

Marine copepods and diversity of their microbiome

Agnese Fumanti^{1,2*}, Iole Di Capua^{2,3}, Cinzia Corinaldesi^{3,4}

¹ Department of Life and Environmental Sciences, Polytechnic University of Marche, Breccie Bianche, 60131, Ancona, Italy;

² Marine Organism Taxonomy Core Facility (MOTax), Research Infrastructures for Marine Biological Resources Department, Stazione Zoologica Anton Dohrn, Villa Comunale, Naples, Italy;

³ NBFC, National Biodiversity Future Center, Palermo 90133, Italy;

⁴ Department of Science and Engineering of Matter, Environment and Urban Planning, Polytechnic University of Marche, Breccie Bianche, 60131 Ancona, Italy

*E-mail: a.fumanti@pm.univpm.it

The associations between marine invertebrates and microbes are widespread throughout the oceans. Microbiota can indeed play crucial roles in the digestion, nutrient uptake, reproduction, immune response, and defense mechanisms of almost all marine animals, thus influencing their health and well-being^[1,2]. So far, information about the copepod microbiome is limited, although copepods represent key components in the functioning of marine ecosystems. Therefore, a better understanding of the diversity of the copepod microbiome also throughout their lifetime is needed. This is even more important in the context of ongoing global change scenarios, where unraveling the copepod-microbe associations contributes to a broader comprehension of marine ecosystem changes.

In the current study, we investigated the diversity and origin of the microbiome of planktonic calanoid copepods (i.e., *Temora stylifera*, *Clausocalanus lividus*, *Centropages typicus*, and *Acartia clausi*) and their contextual seawater, in two sectors of the Mediterranean Sea. We used a molecular method based on metabarcoding, which involves amplicon sequencing of the 16S rRNA gene.

Preliminary results of our research suggest that copepod-associated microbiota is species-specific and independent of the copepod sex as well as their life stage (e.g., juveniles vs adults). In particular, each copepod species exhibited a distinct core microbiome. Despite this, we also found that several bacterial families were shared among different hosts leading to hypothesize their key role in the copepod's functions. These results expand the understanding of the relationships between copepods and their associated microbiota opening new research perspectives on the crucial role of symbiosis in the oceans.

References

1. Bass, et al. "Parasites, pathogens, and other symbionts of copepods." *Trends in Parasitology* 37.10 (2021)
2. Datta, et al. "Inter-individual variability in copepod microbiomes reveals bacterial networks linked to host physiology." *The ISME journal* (2018)