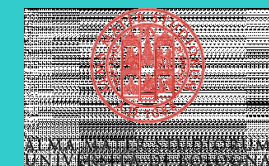


# Depth-dependent dietary influence on the gut microbiome of Norway lobster (*Nephrops norvegicus*) from the central Adriatic Sea (Mediterranean Sea)



Lorenzo ZACCHETTI<sup>1,2</sup>, Marco BASILI<sup>1,2</sup>, Filippo DOMENICHETTI<sup>1</sup>, Grazia Marina QUERO<sup>1,3</sup>, Elena MANINI<sup>1,3</sup>, Michela MARTINELLI<sup>1</sup>

<sup>1</sup>National Research Council (CNR), Institute for Biological Resources and Marine Biotechnologies (IRBIM), Largo Fiera della Pesca 2, 60125 Ancona, Italy

<sup>2</sup>Department of Biological, Geological and Environmental Sciences (BiGeA), Alma Mater Studiorum – University of Bologna, Bologna, Italy

<sup>3</sup>NBFC, National Biodiversity Future Center, Palermo 90133, Italy

\*lorenzo.zacchetti@irbim.cnr.it

## INTRODUCTION

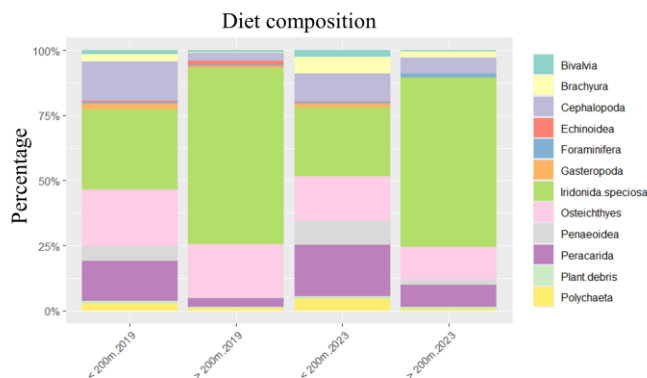
The Norway lobster, *Nephrops norvegicus*, has a considerable commercial value in the Mediterranean, especially in the Adriatic Sea. The gut microbiome plays a critical role in many key biological aspects. Diet significantly influences the composition of intestinal microbiota, underscoring the importance of its analysis (Silva et al. 2011). Given the high economic and ecological significance of the Pomo/Jabuka pits, assessing the ecological characteristics of key species over time and space is crucial.

## MATERIAL & METHODS

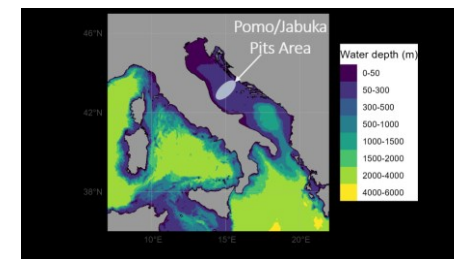
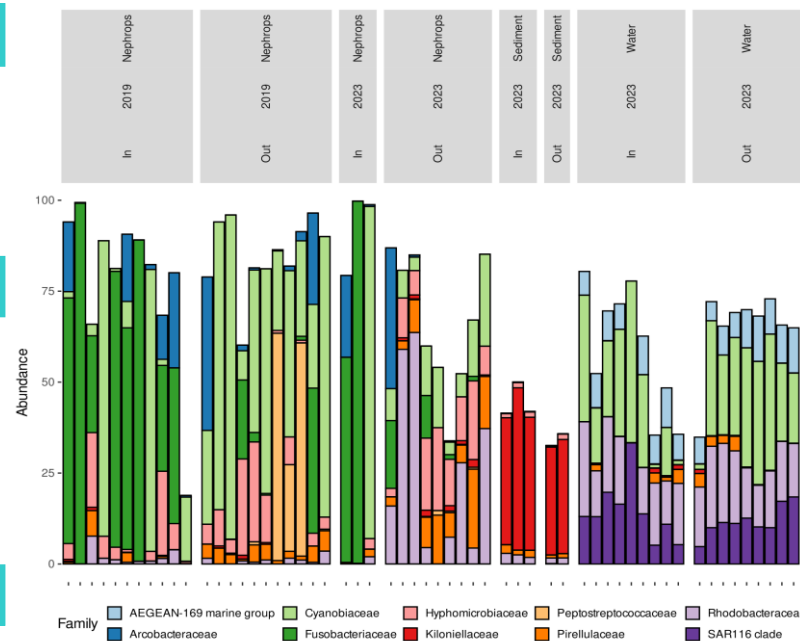
The Pomo/Jabuka Pits hosts a dense population of small Norway lobsters (Angelini et al. 2020). Over time, various management measures were implemented, culminating in the establishment of a Fishery Restricted Area (FRA) in 2017 by the GFCM. The microbiome of *N. norvegicus* and of the surrounding environment were assessed through 16S rRNA gene V3-V4 region high-throughput sequencing. The specimens were collected through scientific trawling surveys in 2019 and 2023. 80 samples, equally distributed over the years, were examined for the gut microbiome analysis, whereas 382 samples were involved for stomach content analyses (SCA) to assess the diet (229 in 2019 and 153 in 2023).

## RESULTS & DISCUSSION

Figure 1. Graph showing the different composition in terms of biomass (%W) of the prey that characterise the *N. norvegicus*'s diet over the years and between depths.



SCA showed that *N. norvegicus* consumes crustaceans, fish, and cephalopods. Significantly different dietary patterns were observed depending on depth. *Iridonida speciosa* dominates the diet at greater depths. At lower depths, a more diversified diet was observed. The significant differences found in the diet may have influenced the gut microbial communities.



Alpha diversity of gut microbiome varied significantly with depth and was distinct from environmental ones. Gut microbiome was less diverse, with 77% of Amplicon Sequence Variants (ASVs) being unique and not shared with the environment. Although community composition did not show significant differences considering the depth, gut microbiome at depths greater than 200m was primarily characterised by Fusobacteriota. In contrast, at shallower depths, the community more heterogeneous, dominated by Synechococcales and characterised by Rhodobacteriales and Hyphomicrobiales.

## CONCLUSIONS

The results obtained can be employed to improve fisheries management. Furthermore, important data on the eukaryotic and prokaryotic biodiversity of the study area are provided.

## REFERENCES

- Silva, F.C.P.; Nicoli, J.R.; Zambonino-Infante, J.L.; Kaushik, S.; Gatesoupe, F.J. Influence of the diet on the microbial diversity of faecal and gastrointestinal contents in gilthead sea bream (*Sparus aurata*) and intestinal contents in goldfish (*Carassius auratus*), FEMS Microbiology Ecology, Volume 78, Issue 2, November 2011, Pages 285–296.
- Angelini, S.; Martinelli, M.; Santojanni, A.; Colella, S. Biological Evidence of the Presence of Different Subpopulations of Norway Lobster (*Nephrops norvegicus*) in the Adriatic Sea (Central Mediterranean Sea). Fish. Res. 2020, 221, 105365.