



THE MICROBIOME OF FARMED MUSSEL *MYTILUS GALLOPROVINCIALIS* IN THE ESTUARY OF KRKA RIVER



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INTRODUCTION

Mytilus galloprovincialis, or Mediterranean mussel, is the most important shellfish species in Croatian marine aquaculture.

Microbiome: integral part of their physiology and a potential source of advanced functions but also disease.

➤ **GOAL:** investigate microbiome during rearing cycle

RESULTS

After data processing, removal of mitochondrial and chloroplast, as well as rare ASVs, 1399 ASVs were retained. Similar alpha diversity was recorded for both tissues without temporal changes.

According to the analysis of the main beta diversity components (PCA on CLR transformed data), hepatopancreas and gills do not form homogeneous groups and there is large interindividual variability. The difference between tissues is significant (PERMANOVA, $p < 0.05$)

In the microbiome, there is largest contribution of **Proteobacteria** (monthly average of 52.6% - 91.7% in the gills and 16.6% - 75.7% in the hepatopancreas), **Bacteroidota** (gills 8% - 45.1%, hepatopancreas 8% - 28.4%), while **Firmicutes** occurred only in fall and winter as a significant proportion of the hepatopancreatic microbiota (0.9% - 66.6%).

At the family level, most represented were **Comamonadaceae**, **Weeksellaceae** and **Xanthomonadaceae** in both tissues.

Vibrio, **Clostridium** and **Escherichia-Shigella** group were recorded foodborne pathogenic genera (they sporadically exceeded a monthly average relative proportion of > 1% in hepatopancreas).

CONCLUSION

The data provide an important basis for understanding mussel physiology and the development of tools for early warning systems, biomonitoring and the traceability of marine products.

METHODOLOGY

- Monthly sampling from October 2022 to September 2023
- Mussel farm near Šibenik, Krka river estuary
- DNA extracted from gills and hepatopancreas using Dneasy PowerSoil Pro Kit
- **16S rRNA V4-V5** region
- Illumina NovaSeq 2 x 250 bp PE
- QIIME2, ASVs obtained with DADA2
- Taxonomic classification: SILVA 138 database

