

Abstract

# Anthropogenic Activities and Microbial Populations: War, Peace or Adaptation? †

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Aquaculture is one of the fastest-growing food sectors in Central, North, and Eastern Europe. Freshwater farming is changing the biodiversity of fishing ponds to fulfill industrial needs, and these changes can impact adjusting water bodies. Precautions should be taken to protect ecosystems and ensure that they are sustainable. The main objective of this research was to evaluate the influence of intensive fish farming on the condition of fishery ponds themselves and the surrounding water ecosystems, as well as to evaluate the possibility of transferring pollutants and antibiotic resistance genes to both environment and human hosts. Sediment samples and fish gut microbiome samples were collected during September 2019 and the Summer of 2020 in three locations in Lithuania: fishery ponds, Simnas Lake upstream from the fishery ponds, and Dusia Lake, which is downstream from the fishery ponds. Heavy metals and antibiotic residues were measured in the samples. Genomic DNA was isolated from the samples using the ZymoBIOMICSTM DNA Miniprep Kit according to the manufacturer’s recommendations. The composition of the bacterial community was determined using next-generation sequencing (NGS) by scanning the amplicons of the bacterial 16S rRNA gene. The V3–V4 16S rRNA regions were chosen for sequencing because they are capable of detecting both bacterial and archaea taxa with a high resolution [1,2]. NGS was performed by Novogene Bioinformatics Technology Co., Ltd. (Beijing, China) on an Illumina paired-end platform to generate 250 base pairs (bps) length paired-end raw reads. None of the tested sediment samples showed significantly elevated heavy metal concentrations or substantial veterinary antibiotic pollution. From the antibiotic resistance genes tested, the presence of aminoglycoside and b-lactam resistance determinants, as well as the presence of integrons, could be of concern for the possibility of being transferred to humans. The microbiome beta-diversity analysis results clearly indicated the differences between the microbiota composition of all pond sediments and the entrance point, treated as a clean area.



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**Informed Consent Statement:** Not applicable.

**Data Availability Statement:** The datasets presented in this study can be found in online repositories. The names of the repository/repositories and accession number(s) can be found at: NCBI Bioproject PRJNA715198.

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## References

1. Wear, E.K.; Wilbanks, E.G.; Nelson, C.E.; Carlson, C.A. Primer selection impacts specific population abundances but not community dynamics in a monthly time-series 16S rRNA gene amplicon analysis of coastal marine bacterioplankton. *Environ. Microbiol.* **2018**, *20*, 2709–2726. [[CrossRef](#)] [[PubMed](#)]
2. Bukin, Y.S.; Galachyants, Y.P.; Morozov, I.V.; Bukin, S.V.; Zakharenko, A.S.; Zenskaya, T.I. The effect of 16s rRNA region choice on bacterial community metabarcoding results. *Sci. Data* **2019**, *6*, 190007. [[CrossRef](#)] [[PubMed](#)]

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