



One Health EJP Annual Scientific Meeting 2021

9-11 June in Copenhagen, Denmark and online



Abstract Book

of the 3rd Annual Scientific Meeting
of the One Health EJP



Hosted by Statens Serum Institut and
National Food Institute at the Technical University of Denmark

[O13] COMPARATIVE ANALYSIS OF THE RESISTOME AND THE MOBILOME OF ESTUARINE AQUACULTURES AND OTHER AQUATIC ENVIRONMENTS

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Aim: Rivers and estuaries are generally considered to be a natural reservoir of antibiotic resistance genes (ARGs) that can be transmitted to terrestrial animals and to the environment. Furthermore, human activities such as aquaculture industry in those regions contribute to the increase of ARGs. In this scenario, we aimed at performing a comparative analysis of the ARGs metagenomic profiling of sediments of intensive aquaculture farms with other aquatic environments

Methods: High-throughput sequencing-based metagenomics was used to characterize the wide-spectrum profile of ARGs in sediments from bivalve and sea bass aquacultures, and compare with other aquatic environments. Analysis of sequences was performed using the MG-RAST pipeline. We searched for ARGs orthologues, classified into antibiotic resistance families, and also for relaxases, transposases and integrases, indicative of mobile genetic elements (MGEs), using the Resfams and MUSTAD databases.

Results: We characterize both the diversity of antibiotic resistance genes and estimate the number of mobile genetic elements in all microbiomes of our dataset. Our preliminary results show that the microbiomes of natural environments are very rich in ARG and MGE. Yet, the ratio of MGE/ARG is higher in estuarine aquacultures, suggesting that the capability of resistance determinants transfer is higher in these regions subjected to anthropogenic activities.

Conclusions: Although samples of environmental microbiomes from untouched environments like Antarctica share a very rich and diverse repertoire of ARGs and high number of horizontal gene transfer elements, microbiomes belonging to sediments from river aquaculture, close to an urban location show a greater epidemic potential of ARGs spreading.



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