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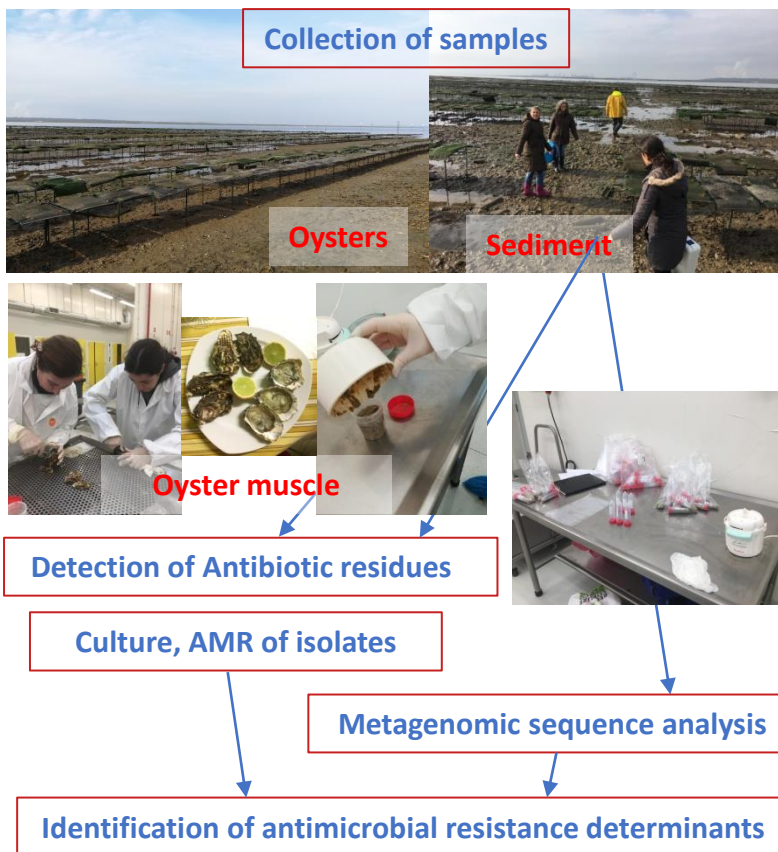
Metagenomic Analysis Of Antimicrobial Resistance Profiles In Aquatic Environments

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Presently, antimicrobial resistance (AMR) threatens some of the greatest medical advances. Current AMR and pathogen detection are primarily reliant on classical culturing techniques. Metagenomic sequencing technology can detect the composition of microbial communities for the assessment of potential pathogens and AMR or virulence genes. The rapid growth in aquaculture is likely to be accompanied by a rapid increase in the therapeutic and prophylactic use of antimicrobials, including those that are important in human therapy. In this scenario, the AquaRAM (Antimicrobial Resistance Determinants in Aquaculture Environments) project aims at characterizing resistant bacteria and genomic and mobile genetic elements (MGE) determinants of antimicrobial resistance, in intensive aquaculture farms.

METHODS



To get a broad picture of aquaculture resistomes and as proof of concept, in silico comparison of resistome profiles, based on worldwide published metagenomes of aquaculture and sediments, we performed studies using Blast alignments against antibiotic resistance Resfams database.

REFERENCES

- Wilke A, Bischof J, Harrison T, Brettin T, et al. 'A RESTful API for Accessing Microbial Community Data for MG-RAST'. PLoS Computational Biology. 2015 11(1): e1004008
- Gibson MK, Forsberg KJ, Dantas G. Improved annotation of antibiotic resistance functions reveals microbial resistomes cluster by ecology. ISME J. 2014 Jan;9(1):207-16

RESULTS

This preliminary analysis revealed that the majority of antibiotic resistance traits found in oyster and mussel samples from the UK and USA, correspond to proteins belonging to the cell envelop, and in particular to efflux pumps. Efflux pumps are responsible for antibiotic extrusion from the cell and for a non-specific detoxifying process. It can be thus an intrinsic and ubiquitous trait

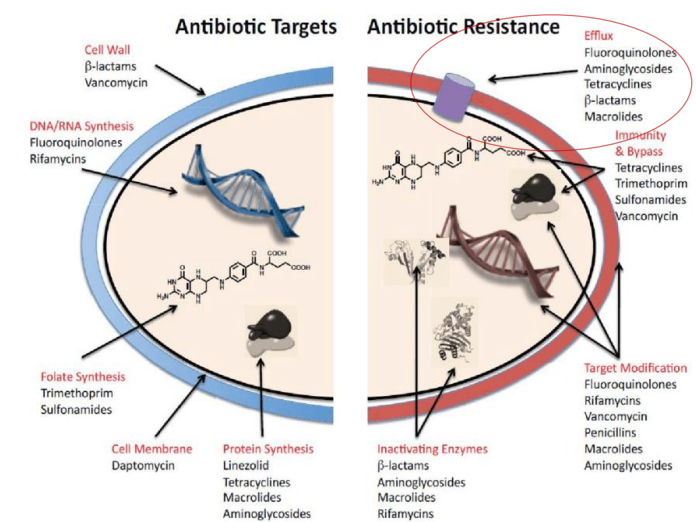


Fig 1 Antibiotic target sites and mechanism of resistance (Wright, 2005)

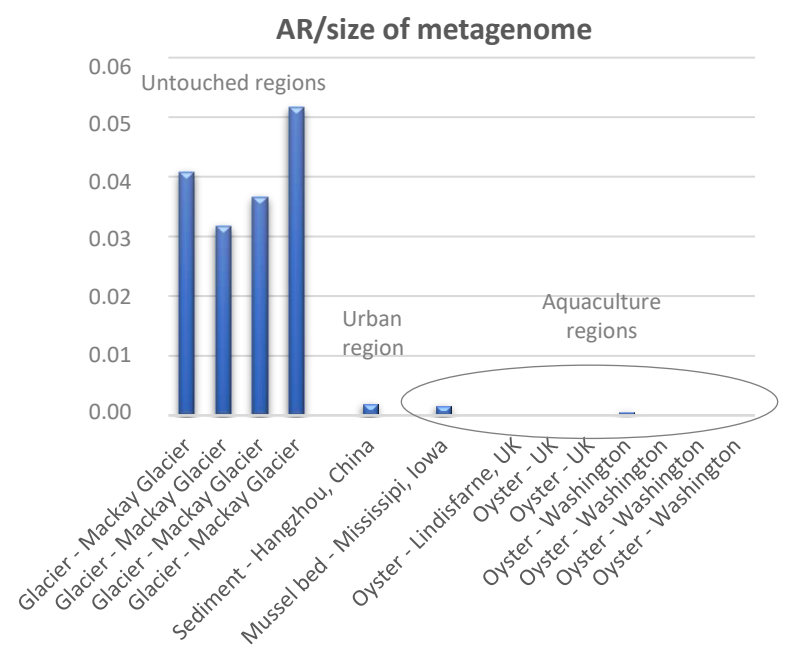


Figure 2 - Ratio the between the number of antimicrobial resistance determinant homologues and the size of the metagenome

Y axis: relative frequency of antibiotic resistance homologues per metagenome; X axis: Region where metagenomic samples were collected. The higher the ratio, the higher the number of antimicrobial resistance determinants in that metagenome