Monitoring antibiotic resistance in aquatic environments

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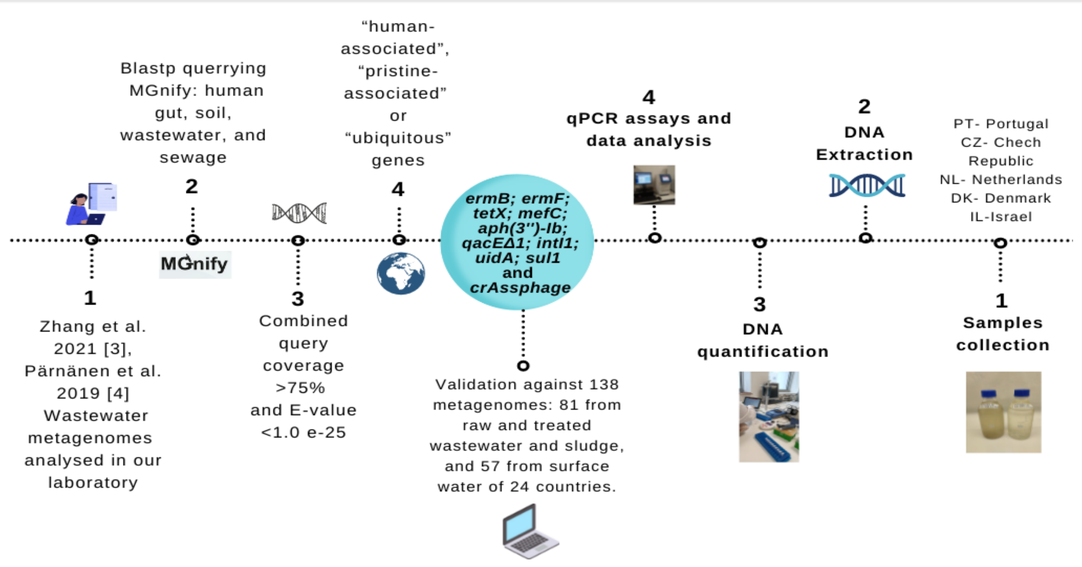
Introduction

Human sewage is a major source of antibiotic resistant bacteria and antibiotic resistance genes. Whereas in most world regions these effluents are treated before returning to the environment, it is estimated that half of the world population does not have access to adequate sanitation systems [1]. Even in regions where urban wastewater treatment plants are implemented and operating properly, it is demonstrated that antibiotic resistance emissions may have noticeable impacts on the receiving environment [2]. Simplified and low-cost monitoring systems might contribute to map the distribution of antibiotic resistance genes, measure its removal during wastewater treatment, and assess potential impacts on the receiving environment.

Objectives

- Identify suitable biomarkers, whose detection and quantification might indicate anthropogenic sources of contamination;
- Track antibiotic resistance dissemination in (waste)water.

Methods



Results

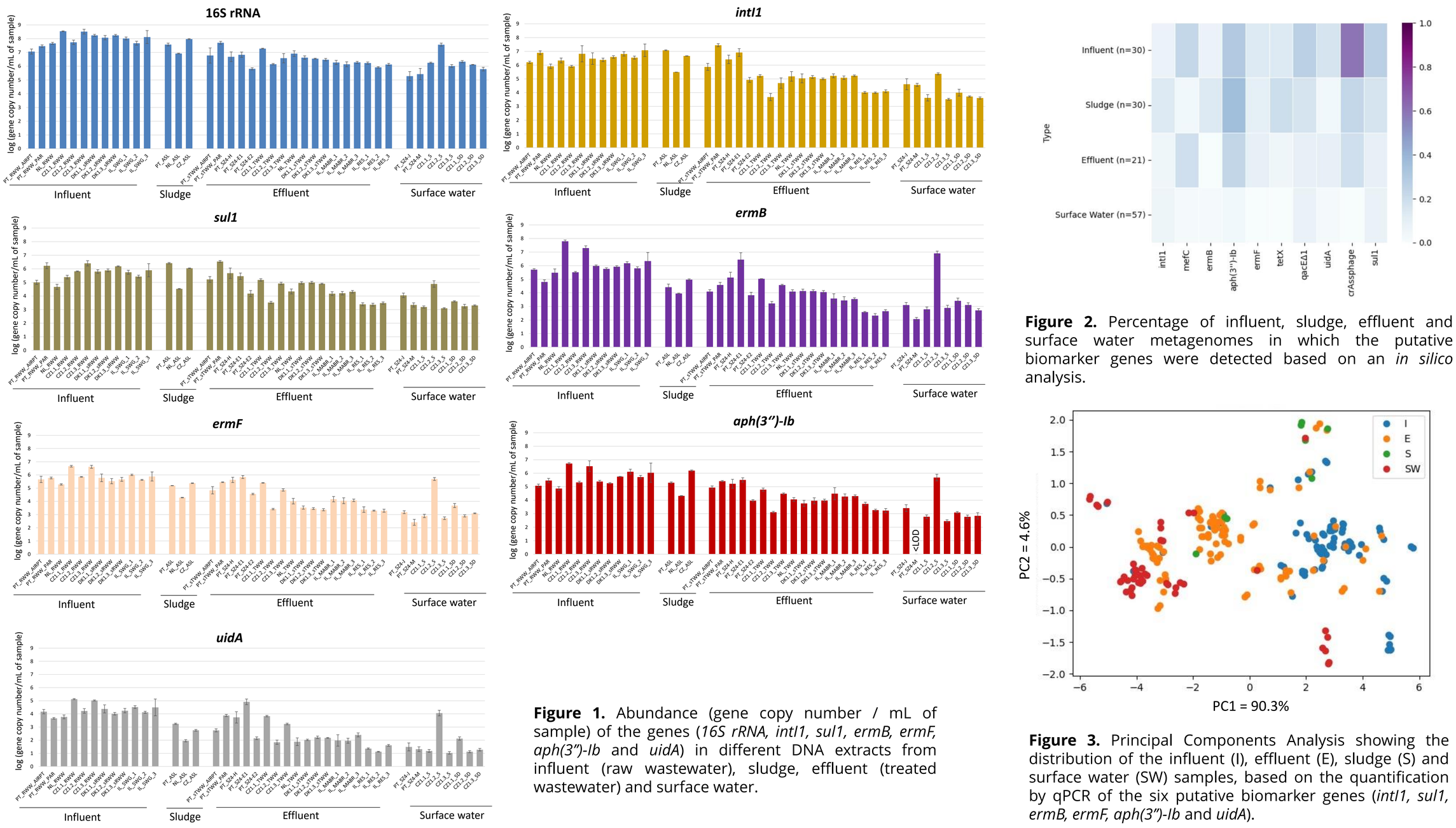


Figure 1. Abundance (gene copy number / mL of sample) of the genes (*16S rRNA, intI1, sul1, ermB, ermF, aph(3")-Ib* and *uidA*) in different DNA extracts from influent (raw wastewater), sludge, effluent (treated wastewater) and surface water.

Figure 2. Percentage of influent, sludge, effluent and surface water metagenomes in which the putative biomarker genes were detected based on an *in silico* analysis.

Figure 3. Principal Components Analysis showing the distribution of the influent (I), effluent (E), sludge (S) and surface water (SW) samples, based on the quantification by qPCR of the six putative biomarker genes (*intI1, sul1, ermB, ermF, aph(3")-Ib* and *uidA*).

Final remarks

The six putative biomarker genes had an expected variation from raw wastewater to surface water. Based on the qPCR analysis, the *uidA* and *aph(3")-Ib* may be the best biomarker candidates, as presented the highest variations between raw wastewater and surface water.
The *in silico* analysis suggested *crAssphage* and *aph(3")-Ib* genes as the best biomarker candidates since they were not detected in surface water metagenomes, being frequent in wastewater metagenomes.
The selected biomarker candidates *crAssphage, tetX, mefC* and *qacEΔ1* are currently being assessed based on qPCR analysis of the same samples.

References

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