
Monitoring antibiotic resistant pathogens in hospitals by metagenomic characterization of sink and hospital wastewater biofilms in comparison with conventional culturing methods

Résumé

Introduction

Transmission of antibiotic resistant bacteria (ARB) and opportunistic pathogens to patients or health care workers can occur by hospital environmental sources such as colonized surfaces or bacterial biofilms present in sink and shower drains. Hospital wastewater (WW), which collects feces from patients could be an indicator of ARB and pathogens contained in the patient's gut microbiota. Monitoring of the hospital environment is generally carried out by sampling surfaces, followed by routine culturing methods, and usually does not include WW or biofilms collected from sink drains. Here we implemented culture and culture-independent approaches to assess hospital sink biofilms and WW biofilms as potential sources of ARB accumulation and transmission.

Methods

Biofilms were recovered from the siphons of 26 patient rooms in the neonatal ward of the Grenoble University Hospital. Hospital WW and WW biofilms from this ward were also collected. Samples were cultured on selective and non-selective media. The isolated species were identified by MALDI-TOF mass spectrometry. The resistome was studied using high-throughput qPCR targeting clinically relevant antibiotic resistance genes (ARGs) and associated mobile genetic elements (MGEs). To achieve identification of the microbiota on species level resolution, a full-length 16S rRNA sequencing approach using nanopore sequencing was implemented.

Results

No ARBs were identified by culture. The bacterial diversity was low, with an average of 3 (2 - 6) different bacterial species identified per sink, and 11 and 9 different bacterial species in the hospital WW and WW biofilm, respectively. Preliminary analysis of the full-length 16S rRNA sequencing data of 11 sink biofilm samples identified more than 100 different species across the samples. A high diversity of ARGs and MGEs in all biofilm samples was detected, amongst them carbapenemases and ESBL genes.

Conclusions and perspectives

We showed that hospital sink biofilms present a potential source of nosocomial pathogens and act as a reservoir for ARGs and MGEs, that is impossible to assess by routine culturing approaches. Correlation of these findings with the infection incidence, antibiotic treatment and hygiene protocols of this ward will reveal whether this translates to an actual transmission risk for ARB or rather "just" an accumulation of the latter.

Mots-Clés: One health, metagenomics, culturomics, AMR surveillance