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BOOK OF ABSTRACTS

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I1. Environmental Microbiology and Biotechnology

P8. Monitoring antibiotic resistance genes by qPCR or metagenomics analyses: high sensitivity versus broad coverage?

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Antibiotic resistance is a major global human-health threat, with important connections to the environmental and veterinary domains. Detection and quantification of antibiotic resistance genes (ARGs) are therefore key players in any control measure. Two commonly used culture-independent approaches are quantitative PCR (qPCR) and metagenomics. While the first is a targeted method that screens a set of predefined ARGs, the second is non-targeted overview of ARGs/resistomes using sequence mapping to ARG database. It has been admitted that qPCR may be more sensitive compared to metagenomics, yet limited to the targeted ARGs coverage. Here, we compared the sensitivity of ARGs detection and quantification using qPCR and metagenomics in the same samples from two wastewater treatment plants (WWTP) at different treatment stages, surface water samples from rivers neighbouring the WWTP discharge points and a hospital effluent discharging into one of the WWTP, in addition to series of step-wise gradual increased volumes of pig and chicken faeces.
DNA was collected in duplicate and split into two groups; each was used for qPCR analyses and Illumina-sequencing metagenomics. The metagenomes were mapped against ResFinder and an in- house second ARG database, and the qPCR analysis targeted the 16S rRNA, *IntI1*, *uidA*, *incF* and 15 ARGs. Carbapenems, 3rd generation cephalosporins, aminoglycosides, sulfonamides, quinolones and glycopeptides ARGs were selected.
The resistome profiles identified 1099 ARGs with metagenomics, and the entire selected 15 ARGs for qPCR analyses. Animal faeces resistomes were markedly different in abundance and composition from the water samples. Genes with expected low abundance, e.g., carbapenem resistance gene, were detected with $bla_{\text{OXA-58}}$ being more abundant than $bla_{\text{OXA-48}}$ and bla_{KPC}, respectively, in raw influent. However, they were below the limit of quantification or in low abundance in animal faeces using either method. The ARGs bla_{CTX}, bla_{OXA} and bla_{SHV} were more dominant in wastewater, yet either absent or low in abundances in the animal faeces using either method. Finally, both methods were able to detect comparable dissimilarities in the resistome compositional profiles from wastewater and faeces. The metagenomics analyses were also able to gradually detect step-wise ARG differences in abundance and composition (10 folds) in complex matrices as animal faeces.