

ANTIMICROBIAL RESISTANCE IN AOTEAROA: OCCURRENCE AND TRANSPORT THROUGH WASTEWATER

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ABSTRACT (500 WORDS MAXIMUM)

Globally antimicrobial resistance (AMR) has been declared one of the top ten threats to public health. One source of AMR is through wastewater, inputs of antimicrobials, AMR bacteria within the treatment plant, and AMR genes that can lead to the transfer of resistance to other pathogenic bacteria that may be present. Specific antimicrobial resistance can lead to serious health outcomes e.g. Extended-spectrum beta-lactamases (ESBL-), AmpC beta-lactamases (AmpC-), and carbapenemase-producing bacteria. These bacteria cannot be killed by many of the antimicrobials prescribed and there is evidence that these AMR bacteria can transfer genetic material that can pass this resistance onto other pathogens which would otherwise be susceptible to antimicrobials.

In the late spring/early summer of 2019, we investigated the presence and fate of AMR bacteria and AMR genes in a municipal wastewater treatment plant (WWTP). We collated the data with known prescription rates of antimicrobials and the microbial resistome communities in the WWTP and changes in abundance and diversity of AMR genes throughout the wastewater treatment process.

The study took place over three consecutive days at Christchurch's Bromley WWTP. 24-hour composite samples were taken from influent (post screens), secondary effluent, and oxidation ponds final effluent. We used autosamplers and staggered sampling times to take the time of travel through the WWTP into account. A metagenomic approach to determine the resistome and the bacterial community composition in raw sewage and at different stages throughout the wastewater treatment was complemented by the isolation and characterisation of Extended-spectrum beta-lactamases (ESBL-), AmpC-and carbapenemase-producing Gram-negative bacteria.

The total detected bacteria and abundance of putative ESBL/AmpC-and carbapenemase-producing Gram-negative bacteria decreased through the wastewater treatment process. Likewise, the relative abundance of resistance genes and the total number of detected AMR genes decreased throughout the treatment (Figure 1). The microbial communities in the different sample types (influent, effluent, pond water, and pond sediment) were significantly different with a clear separation in principal coordinate analysis (Figure 2). AMR genes conferring resistance against β -lactam antimicrobials showed the highest relative abundance in all sample types and AMR genes encoding resistance against macrolides, tetracyclines, aminoglycosides, and fluoroquinolones were also present in high relative abundance. ESBL production and carbapenemase production was detected in isolates belonging to seven and six different species, respectively, with isolates displaying a wide range of resistance phenotypes against the tested antimicrobials, including resistance against meropenem, imipenem, ceftazidime, sulfamethoxazole/trimethoprim, aztreonam, and piperacillin/tazobactam.

Using a metagenomic approach as well as culture enabled us to identify AMR presence in the population serviced by the WWTP, the changes in microbial resistome in the WWTP through the treatment train, and the removal capacity of AMR bacteria and genes into the receiving environment. Metagenomic surveillance of wastewater provides useful information on the presence of AMR genes in a population and has the potential to complement clinical surveillance. This is the first study to investigate the presence and fate of AMR determinants in a WWTP in Aotearoa.

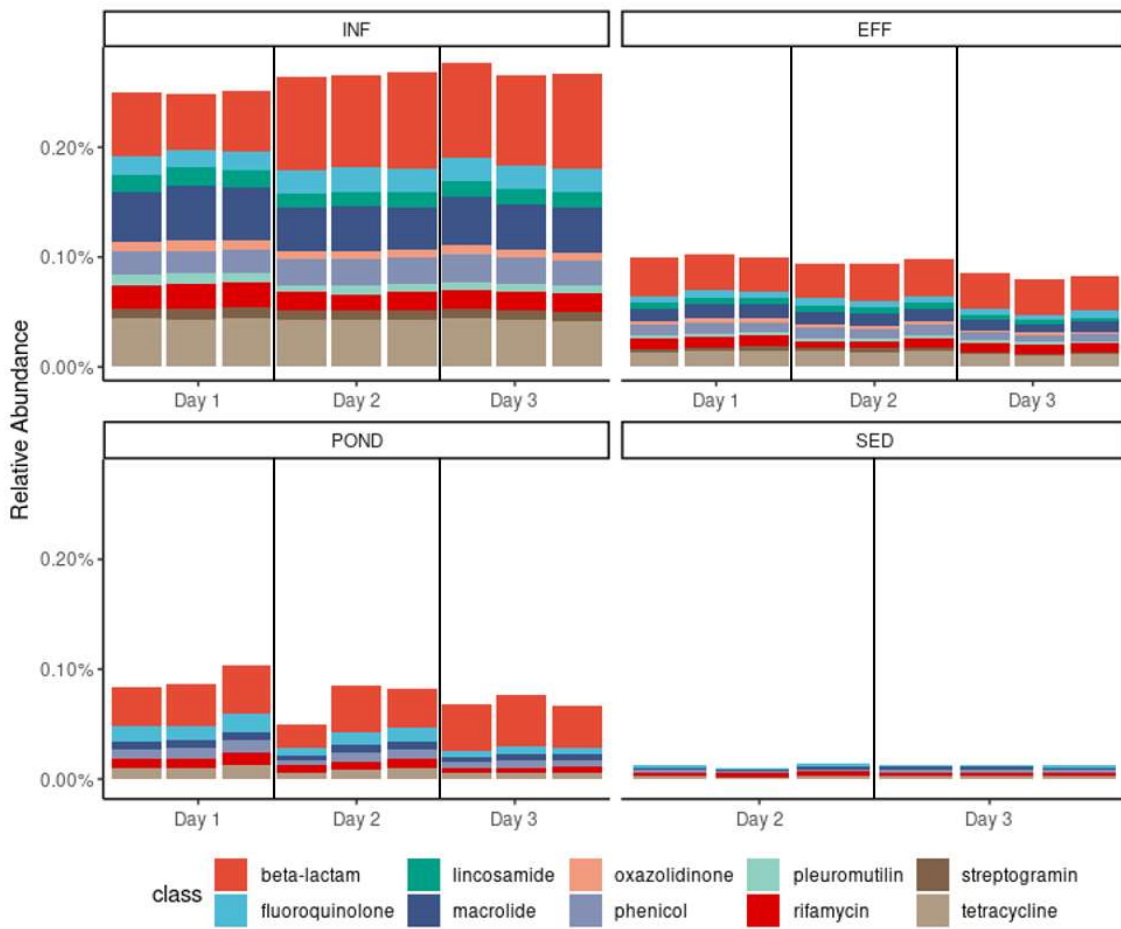


Figure 1 Relative abundance of the ten most abundance microbial classes found through the WWTP.

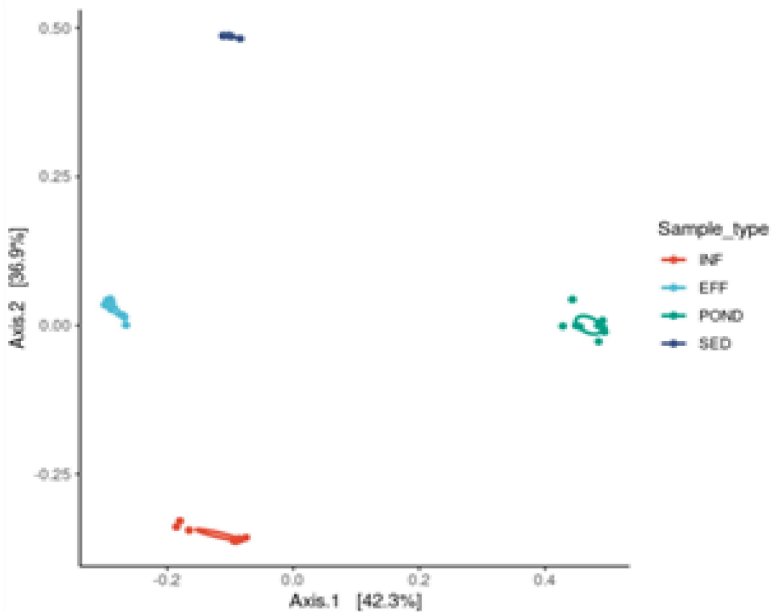


Figure 2 Taxonomic beta-diversity analysis, by principal coordinate analysis (PCoA), showing separation of the microbial communities through the WWTP.

KEYWORDS

Wastewater, AMR, antimicrobial, pathogens