



# Faculty of Engineering and Applied Science

## Chemical Engineering Seminar Series



### Dynamics of antimicrobial resistance and virulence genes in *E. coli* during wastewater treatment

Dr. Dominic Frigon/McGill University  
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#### **ABSTRACT**

The rise of antimicrobial resistance and its threats on the capacity of modern medicine to fight infectious diseases led to the definition of a new kind of emerging pollutants: horizontally mobile genes conferring health-threatening functions to microbes. In this category can be included antimicrobial resistance genes (ARGs) and virulence genes (VGs) of opportunistic pathogens. The increasingly recognized importance of environmental pathways in the dissemination of these genes requires an understanding of their ecology under different conditions. Although several studies focused simply on overall abundances, the gene ecology depends on how they cluster on mobile genetic elements such as integrons, transposons and pathogenicity islands. In the case of ARGs, clustering leads to co-selection; while for VGs, the expression of a several genes in the same opportunistic pathogenic strain is often necessary to cause the infection. Because they are under different selective pressures, comparing the dynamics of these two groups of genes may provide important insights on their respective ecologies.

In this study, the strain distribution of ARGs and VGs in the *E. coli* population found in wastewater was characterized by isolating strains and genotyping them by microarrays. The ARGs and VGs co-occurred at a significantly high level in the isolate collection, likely due to the exposure of pathogenic strains to antimicrobials through medical interventions. Interestingly, through activated sludge and physicochemical wastewater treatment plants, the relative abundances of pathogenic isolates were lowered in similar fashions; for ARGs, while the prevalence of ARGs also decreases through physicochemical plants, their prevalence increased through the activated sludge. Similarly, disinfection by UV and peracetic acid (PAA) equally reduced the prevalence of pathogenic strains, while only PAA prompted the reduction of ARGs. A timescale analysis of biological phenomena suggested that the interaction of the *E. coli* population with other populations carrying related genes could explain these observed results. In general, the results point out to the need of obtaining both population specific and community-wide gene dynamics observations to properly understand the forces allowing the control of the risks associated with various gene pools.