ANTIBIOTIC RESISTANCE GENE RESERVOIRS IN A SEWAGE-IMPACTED COASTAL ENVIRONMENT

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Recent finding shows that due to coastal pollution, swimmers are 3 times more likely to carry resistant Escherichia coli in their gastrointestinal tract. Our laboratory has investigated the influence of stormwater input on the abundance of antibiotic resistance genes in estuaries and beaches in Sydney. Genes conferring resistance to a variety of antibiotics were found to increase by up to 102-fold above normal levels following major rainfall events that result in raw sewage overflow into the stormwater system. Resistance genes to last resort antibiotics, carbapenems and vancomycin were detected. These contaminated environments represent an exposure risk to humans and a transmission pathway for (re)introduction of circulating or, newly captured antibiotic resistance genes from environmental bacteria into the community.

MERCURY DRIVEN ANTIBIOTIC RESISTANCE GENES IN CONTAMINATED SOILS AND THEIR REMOVAL

Dr Khandaker Rayhan Mahbub

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Antibiotic resistance genes are commonly found in environments contaminated with human and animal waste. Microorganisms can interchange genetic traits through lateral gene transfer processes allowing for spread of antibiotic resistance genes across bacterial communities. Metal contaminated soils can serve as reservoir of antibiotic resistance genes. Our laboratory is investigating the chemistry between mercury and soil particles that potentially influence the increased abundance of antibiotic resistance genes. We are also developing a method for the removal of soil bound mercury that will subsequently decrease antibiotic resistance gene abundance in different soil environments.

Date: Wednesday 22nd August 2018
Time: 1 - 2 PM
Location: Auditorium, Research & Education Centre, St George Hospital
Ground Floor, 4 – 10 South St, Kogarah
Light refreshments will be provided
www.stgcs.med.unsw.edu.au/ripm

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