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Eawag Seminar Invitation

Open Questions on the Viral Contamination of Water: Next Generation Sequencing and Water Quality Control

Speaker **Prof. Rosina Girones,**
University of Barcelona, Dept. of Microbiology, Spain

When **September 28, 11.00 – 12.00 a.m.**

Where **Forum Chriesbach, room C20, Eawag Dübendorf**

Abstract In recent years, water scarcity and the application of more sustainable water reuse practices has favoured the utilisation of treated sewage for several purposes, including irrigation and river catchment replenishment. Sewage treatment plants (STP) are known to be less efficient for virus removal compared to faecal indicator bacteria. This higher viral survival in STP treated water can represent a threat to consumers because STP effluents containing viral pathogens can contaminate water and food. The application of next-generation sequencing (NGS) techniques for the identification of the viral pathogens and indicators present in water has not been yet fully explored. The virome of urban sewage and different types of irrigation water will be described using different protocols including metagenomics and targeted metagenomics. Urban raw sewage consists of the excreta of thousands of inhabitants; therefore, it is a representative sample, producing a lot of information on the circulating viruses useful for public health metagenomics surveillance programs.

The control of the microbiological quality of irrigation water has been the main objective of the METAWATER project: i. to evaluate the viruses present in irrigation water (tertiary effluents, river water and groundwater) and wastewater. ii. Evaluate the efficiency of WTPs and the reduction required for achieving acceptable risks for water reuse in irrigation of fresh vegetables. During one-year period, 72 irrigation water samples were analyzed and human viral pathogens and indicators and animal viruses used as MST tools were quantified by q(RT)PCR. To study the virome of irrigation water we developed a metagenomics protocol using Nextera XT and Illumina MiSeq 2x300bp. The results will be discussed considering limitations of the available quantification methods and QMRA studies.