MOLECULAR DETECTION AND GENETIC DIVERSITY OF ENTERIC VIRUSES: A YEARLONG MONITORING OF SEWAGE THROUGHOUT ITALY

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Background: Urban sewage virological analysis may produce important information about the pathogens that cause clinical and subclinical infections in the population, thus supporting epidemiological studies. In this study we conducted a large-scale molecular-epidemiological investigation, a yearlong monitoring of 11 wastewater treatment plants throughout Italy, with the aim of studying the circulation of different enteric viruses (adenoviruses, noroviruses, enteroviruses, astroviruses, Hepatitis E viruses), as well as their genetic diversity.

Methods: Samples (110 inflows and 110 treated effluents) were collected on a monthly basis from April 2008 to March 2009 at 11 WTPs located in the following regions throughout Italy: Campania, Umbria, Tuscany, Piedmont, Friuli-Venezia Giulia, Basilicata, Lombardy, Emilia Romagna, Veneto, Latium, and Sardinia. RNA was extracted from 10 ml of sewage using the NucliSens miniMAG isolation kit. Nucleic acid amplification techniques (nested-PCR, Real-Time PCR) were applied for viral nucleic acid detection. Positive samples were confirmed by sequencing and phylogenetic analysis.

Results: all groups of viruses were detected with percentages ranging from 16% (Hepatitis E virus) to 96% (adenovirus). Noroviruses, astroviruses, enteroviruses were detected, at 75%, 74%, and 58% respectively. Of all tested viruses, adenoviruses had the highest concentrations measured by quantitative PCR in both raw and treated waters.

Conclusions: This work confirms the frequent occurrence of enteric viral genomes in sewage effluents, suggesting that treated sewage may represent a source of environmental contamination. Of all tested viruses, AdVs had the highest concentrations in both raw and treated waters, confirming the relevance of evaluating these viruses as possible indicators of viral contamination of water.