

# Environmental Monitoring of Enteric Viruses in Wastewater

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## Introduction

Human enteric viruses respond to aquatic environment due to contamination with inadequately treated or untreated wastewater. Untreated sewage contains a very heavy load of different serotypes of viruses depending on the season, the population of the geographical area and the types of viruses circulating in the population. Also treated waste may contain several types of viruses depending on the type and the degree of virus removal during treatment [1]. The classic method for detection of enteric viruses in wastewater contains cell culture, which is costly and time-consuming. There is also a lack of effective cell lines to isolate some of the epidemiologically most important enteric viruses such as Enterovirus, Hepatitis A virus, Adenovirus and Norovirus. For these reasons, nucleic acid-based methods such as PCR, nested PCR and real time PCR have been used largely for the detection [2].

## Enterovirus

Enteroviruses are small viruses, made of single stranded RNA. Enteroviruses can be detected in the respiratory secretions, like saliva, spittle, rhinal mucus, and also through excrements of infected people. Humans acquired infection through direct contact with already infected or via polluted surfaces, for example telephones, glasses etc. An *enterovirus* is a virus belonging to the family of *Picornaviridae*, which also includes the polioviruses, coxsackieviruses, echoviruses, and other enteroviruses. In addition to the three different polioviruses, there are a variety of non-polio enteroviruses that can cause disease in humans, like coxsackie A viruses, coxsackie B viruses, echoviruses and other strains of enteroviruses. Enteroviruses have been associated with waterborne gastroenteritis of non bacterial origin, and are of significant concern for public health. A high number of viruses can be isolated from human feces, as well as from raw and polluted wastewater, respectively [3].

## Hepatitis A

Hepatitis A is the prototype of the *Hepatovirus* genus within the *Picornaviridae* family. Genetic range among HAV isolates from various regions of the world allowed the classification of HAV strains into 7 different genotypes, four of which (I, II, III and VII) are associated with human HAV infections and three were derived from simian HAV strains (IV, V and VI). HAV is the primary agent for acute hepatitis with a distribution around the world. It is primarily transmitted by person-to-person contact through fecal contamination. At least one other common source epidemic is the contaminated food and water. Two million cases every year, of symptomatic hepatitis A, occur worldwide. In developed countries, the incidence of illness is low; while in developing countries is significant higher [4].

## Adenovirus

Adenoviruses are human EVs that contain DNA and belong to the *Adenoviridae* family, *Mastadenovirus* genus. Researchers began to recognize these viruses as causative agents of gastroenteritis. Ads are pathogenic to humans and their presence in environmental samples like polluted waters may lead to infections. Their attendance in polluted water and their role as originators of gastroenteritis have probably

been underestimated. The detection of human adenoviruses by PCR has challenged attention in association to the evaluation of viral quality of environmental samples, because the adenovirus genome is well distinguished. Adenoviruses are more stable in various environments, like raw wastewater and more resistant to some disinfection treatments (UV, chlorine) than other EVs. They are the most prevalent human viruses detected by PCR in sewage and shellfish. The detection of human adenoviruses has been proposed as a molecular index of viral contamination of human origin by Pina et al. [5].

## Norovirus

*Norovirus* is the most common etiological agent for gastroenteritis outbreaks as well as a common cause of acute gastroenteritis in children and has a significant public health impact worldwide. Morphology and genome organization classified NV as a member of the family *Caliciviridae*, which now comprises the two human related genera *Norovirus* (previously, "Norwalk-like virus") and *Sapovirus* (previously, "Sapporo-like virus"). Genetically, noroviruses can be divided into five genogroups (GGI, GGII, GGIII, GGIV, and GGV), which consist of different genotypes. Noroviruses are the viruses most commonly associated with food- and waterborne outbreaks of gastroenteritis. Illness takes place in people of all ages, is characterized by nausea, vomiting and diarrhoea [6]. NV is transmitted mostly through the faecal oral route but may also be transmitted through person to person contact. There have been reported many outbreaks due to NVs-contaminated foods, like salads, oysters, fishes and to NVs-contamination of water. Low infectious dose, resistant to disinfection, multiple routes of transmission and strain diversity give reasons for the high prevalence and their persistence. Noroviruses have been detected in raw urban sewage and surface waters [7]. Rapid and secure methods have been developed to detect NV in contaminated food and water as long as NV can not be propagated in cell culture.

## Conclusions

Raw wastewater was found to be contaminated by many and several types of bacteria and EVs that mainly cause variety of diseases in humans such as gastroenteritis. Wastewater treatment usually applied in depuration plants, including physicochemical and biological processes, has significantly reduced the incidence of diseases among the population, especially those etiologically related to bacteria. Yet, viruses, protozoa and parasites are more resistant than bacteria to most treatments. Primary and secondary sewage treatment processes do not potentially decrease the virus concentration, in contrast with tertiary

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processes [8]. Therefore, depending on the applied processes, treated sewage discharged onto surface waters may significantly enhance the virus concentrations in the environment. Water quality may be affected by the presence of these pathogenic enteric viruses flow from sewage discharged to the aquatic environment. Waterborne disease may be transmitted by consumption of polluted drinking water [9]. Human Adenoviruses have been described as stable in the environment and highly resistant even to water treatments, particularly to UV disinfection [10].

In conclusion, the presence of high amount of pathogenic viruses in sewage and their possible survival after the sewage treatment is a possible problem for public health [11]. Epidemiological and environmental studies must specify the root of an outbreak. Detailed sequence data is required, following the molecular detection, in the search for links between causative agents from environment and the patients.

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