

Molecular detection of human astrovirus in an urban sewage treatment plant in Rio de Janeiro, Brazil

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The objective of this study was to evaluate the prevalence and dissemination of human astroviruses (HAstV) in the environment by analyzing urban sewage samples from a wastewater treatment plant in the city of Rio de Janeiro, Brazil. A one-year study was performed with a total of 48 raw and treated sewage composite samples, which were collected biweekly from an activated sludge plant. Virus particles were concentrated by the adsorption-elution method using negatively charged membranes associated to a Centriprep Concentrator[®] 50 (Nihon Millipore). HAstV were detected in 16.7% of the samples in raw and treated sewage by using both qualitative and quantitative reverse transcriptase-polymerase chain reactions (RT-PCR and qPCR, respectively). Positive untreated sewage sample exhibited mean values of 1.1×10^4 gEq/mL. The qPCR sensitivity was 18 gEq/reaction. Through utilization of qPCR, a HAstV recovery efficiency of 4.2% and 4.3% was demonstrated for raw and treated sewage samples, respectively. The presence of HAstV in both the raw and treated sewage samples demonstrated the dissemination of these viruses in the environment as well as viral permanence after sewage treatment. There was a reduction in the total and faecal coliform levels, indicating efficiency of the wastewater treatment plant.

Key words: astroviruses - wastewater - RT-PCR - qPCR

Recent developments in improved surveillance, routine screening and the application of sensitive molecular assays have increased recognition of enteric viruses as environmental contaminants. Furthermore, the burden of human astroviruses (HAstV) infections has been well reported and recognized as important secondary etiologic agents of viral gastroenteritis (Wilhelmi et al. 2003).

Due to the growing importance of HAstV in cases of acute gastroenteritis among children, studies in Europe, USA, South America and Africa have investigated these viruses in the environment and demonstrated HAstV presence in rivers, reservoirs, residual waters and sludge (Gofti-Laroche et al. 2003, Le Cann et al. 2004, Meleg et al. 2006, Miagostovich et al. 2008).

HAstV are non-enveloped viruses with icosahedral symmetry of 28 nm in diameter, which belong to the *Astroviridae* family. The viral genome consists of a single-stranded, positive sense RNA molecule that is polyadenylated and comprised of approximately 6.8-7.2 kilobases, with three open reading frames (ORFs), designated ORF1a, ORF1b and ORF2 (Jonassen et al. 2003). HAstV are classified into eight genotypes (HAstV-1-HAstV-8), based on the phylogenetic analysis of ORF2. HAstV-1 has

been described as the most prevalent genotype worldwide (Noel et al. 1995, Guix et al. 2002, Silva et al. 2006).

The objective of this study was to evaluate the prevalence and dissemination of HAstV in environmental samples using an adsorption-elution method for viral detection by using a negatively charged membrane technique, which was previously described for recovery of enteric viruses from seawater (Katayama et al. 2002). For this purpose, a one-year study was performed in an urban wastewater treatment plant in the city of Rio de Janeiro, since residual waters are the main source of pathogenic microorganisms. Therefore, such environments provide information regarding the different strains infecting human populations. Total and faecal coliforms were also investigated to characterize faecal contamination in the samples. To our knowledge, this is the first study demonstrating the circulation of HAstV in sewage samples of Brazil.

MATERIAL AND METHODS

Sewage samples - From January-December of 2005, 48 raw and treated sewage composite samples were collected biweekly from an activated sludge plant in the city of Rio de Janeiro, Brazil. Eight 250 mL aliquots were collected for each sample and a total of 2 L samples were stored in glass bottles. The samples were taken to the laboratory and immediately analysed for bacterial parameters. The samples were processed for viral concentration in the following 24 h and stored at -80°C, until utilized for virus detection assays. Samples from influent and effluent were collected as positive and negative control.

Bacterial parameters - Total coliform (TC) and faecal coliform (FC) were measured using the Colilert[®]-18

Financial support: Vice-Presidência de Serviços de Referência e Ambiente (Fiocruz), CNPq (472112/2004-0/303539/2004-6), CAPES.

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Received 15 August 2008

Accepted 19 November 2008

Quanti-Tray[®]/2000 method (IDEXX Laboratories, Westbrook, USA).

Viral particle concentration method - HAsV were concentrated using an adsorption-elution method with negatively charged membranes, which included the insertion of an acid rinse step for removal of cations, as previously described (Katayama et al. 2002). Prior to process filtration, 1.2 MgCl₂ was added in 2 L of water. The system was soaked briefly in a 10% bleach solution and rinsed in distilled water prior to each use. The eluate (10 mL) was re-concentrated to a final volume of 2 mL using a Centriprep Concentrator[®] 50 (Nihon Millipore).

Recovery efficiency of the method for HAsV concentration - In order to evaluate the recovery efficiency of HAsV from raw and untreated sewage, 100 µL of the 10% fecal suspension of HAsV genotype 1 strain (GenBank accession number DQ381498), prepared in Tris/HCl/Ca⁺⁺ 0.01M pH 7.2 buffer, was spiked with HAsV. The negative control, without HAsV spiking, was also tested in order to certify the absence of a natural contamination. All assays for viral concentration were performed in triplicate (independent experiments) for both treated and untreated wastewater.

Extraction of viral RNA - Prior to extraction, 70 µL of Vertrel[®] (Sigma-Aldrich Corporation, St. Louis, Missouri, USA) was added to 140 µL of the sample and then centrifuged at 800 g for 10 min. Nucleic acid extraction from the supernatant was performed using a QIAmp Viral RNA Mini Kit[®] (Qiagen, Inc, Valencia, California, USA), following the manufacturer's protocol.

Reverse transcription reaction (RT) - The synthesis of cDNA was performed with RT using a random primer (PdN6, 50 A260 units, Amersham Biosciences, Chalfont St Giles, Buckinghamshire, UK) as previously described (Ferreira et al. 2008).

Enzymatic amplification - (i) Reverse transcription-Polymerase chain reaction (RT-PCR). Amplification was performed using 10-µL aliquots of the cDNA, as described in a previous study (Noel et al 1995). HAsV type 2 strain, obtained from faecal suspension at the Regional Reference Centre of Rotaviruses, was used as positive control. To exclude the possibility of cross-contamination, all reagents used for PCR were prepared in a laminar flow cabinet. A positive and a negative control were included in all PCR reactions. (ii) Quantitative Real-time PCR (qPCR). For specific detection and quantification of the HAsV genome, 5 µL of cDNA was also assayed. Amplification was performed in a 25 µL reaction mixture with the PCR Master Mix[®] (Applied Biosystems, Branchburg, New Jersey, USA). The reaction contained 5 µL of a cDNA sample or 10 µL of a quantified plasmid DNA, 1X TaqMan master mix, and the corresponding primers and TaqMan probes at the appropriate concentrations. HAsV genomes were quantified with 0.1 µM of the primers AV1 and AV2 and 0.15 µM of the fluorogenic probe AVS, as described by LeCann et al. (2004). Then, the uracil N-glycosylase in the core mix was activated (2 min at 50°C), followed by activation of

the AmpliTaq Gold for 10 min at 95°C and 45 cycles (15 s at 94°C and 1 min at 55°C), performed with an ABI 7500[®] (Applied Biosystem, California, USA). All samples were performed in duplicate. Positive and negative controls were included. The amount of DNA was defined as the average of the duplicate data obtained. The RT-PCR/qPCR reactions were performed in separate rooms from those used for viral isolation and processing of water samples. Table I shows the sequences of the primers used in both enzymatic amplification reactions.

TABLE I

Primers and probe used for amplification and detection of human astrovirus

Name	Nucleotide sequence (5' -3')
Mon 269 (+) ^a	⁴⁵²⁶ CAA CTC AGG AAA CAG GGT GT ⁴⁵⁴⁵
Mon 270 (-) ^a	⁴⁹⁵⁵ TCA GAT GCA TTG TCA TTG GT ⁴⁹⁷⁴
AV1 (+) ^b	⁶⁷⁷⁵ CCG AGT AGG ATC GAG GGT ⁶⁷⁹⁷
AV2 (-) ^b	⁶⁷⁰⁸ GCT TCT GAT TAA ATC AAT TTT AA ⁶⁷²⁵
AVS (Probe) ^b	⁶⁷³⁹ Fam-CTT TTC TGT CTC TGT TTA GAT TA T TTT AAT CAC C ^{-Tama} ⁶⁷⁷²

a: primers used for qualitative amplification (Noel et al. 1995);
b: primers and probe used for quantitative polymerase chain reaction (Le Cann et al. 2004).

RESULTS

Detection and quantification of HAsV - The RT-PCR and qPCR protocol were both applied to 48 sewage samples: 24 from inflow and 24 from outflow. A total of seven HAsV strains (14.6%) were detectable by using qualitative RT-PCR, while qPCR detected one positive sample (2.1%) in a raw sewage with a titre of 1.1 x 10⁴ G eq/mL. By using both methodologies, the total number of positive samples was determined to be 16.7% (8/48) of HAsV detected. The detection limit of the qPCR was 18 gEq/reaction. The standard curve demonstrated a correlation coefficient (R²) from 0.995-0.999 and slope varying from -3.64-4.0. The HAsV recovery efficiency was 4.2% and 4.3% for raw and treated sewage samples, respectively, as demonstrated by qPCR.

After sedimentation and biological secondary treatment (activated sludge), 99.9% of TC and 99.9% of FC were removed (Table II). The efficiency of HAsV removal could not be calculated, since positive samples could not be quantified from the raw sewage. HAsV were detected in both outflow and inflow water samples collected on the same day (Table II).

DISCUSSION

In Brazil, studies have been developed in order to evaluate the microbiological quality of water, with an emphasis on bacterial contamination (Alves et al. 2002, Nogueira et al. 2003). However, few studies have investigated the presence of human enteric viruses in water samples (Mehnert & Stewien 1993, Mehnert et al. 1997, Villar et al. 2006, Miagostovich et al. 2008). The ab-

TABLE II
Microbiological results obtained from water samples collected at sewage treatment plant in Rio de Janeiro, 2005

Samples		Raw sewage			Treated sewage		Removal efficiency		
Month	Sampling collection	Total coliform	Faecal coliform	HAsTV detection	Total coliform	Faecal coliform	HAsTV detection	Total coliform %	Faecal coliform %
Jan	1	1,90E+06	6,20E+05	-	5,45E+04	4,10E+03	+	97.13	99.99
	2	5,30E+06	1,10E+06	-	6,60E+04	1,00E+04	-	98.75	99.99
Feb	3	ND	ND	-	ND	ND	+	ND	ND
	4	2,31E+07	7,40E+06	-	3,69E+05	1,34E+05	-	98.40	99.99
Mar	5	5,94E+07	8,60E+06	-	3,73E+05	5,20E+04	-	99.37	99.99
	6	2,31E+07	7,40E+06	-	6,97E+04	1,10E+04	-	99.99	99.99
Apr	7	6,80E+07	7,10E+06	-	1,90E+05	2,40E+04	-	99.72	99.99
	8	7,91E+09	2,43E+08	-	1,19E+05	2,00E+04	-	99.99	99.99
May	9	5,25E+08	3,05E+07	-	3,93E+04	2,00E+03	-	99.99	99.99
	10	ND	ND	-	ND	ND	-	ND	ND
Jun	11	ND	ND	-	ND	ND	-	ND	ND
	12	1,00E+08	1,33E+07	-	5,73E+05	7,40E+04	-	99.43	99.99
Jul	13	1,18E+08	4,86E+07	-	1,03E+05	1,43E+04	-	99.91	99.99
	14	1,78E+09	5,20E+07	+	1,66E+06	1,20E+05	+	99.91	99.99
Aug	15	1,45E+09	1,00E+07	-	6,60E+05	2,70E+04	-	99.95	99.99
	16	5,24E+08	7,40E+06	-	3,28E+05	8,50E+03	-	99.94	99.99
Sep	17	8,29E+09	3,10E+07	+	9,30E+06	ND	-	99.88	ND
	18	3,13E+09	3,00E+07	+	1,90E+06	2,00E+04	-	99.94	99.93
Oct	19	7,27E+09	1,34E+08	-	1,12E+07	8,60E+04	-	99.85	99.99
	20	1,39E+09	5,30E+07	+	1,20E+06	4,10E+04	+	99.91	99.99
Nov	21	1,57E+08	2,28E+07	-	3,13E+05	1,00E+04	-	99.80	99.99
	22	6,21E+08	1,65E+08	-	2,39E+05	9,10E+04	-	99.96	99.99
Dec	23	4,65E+08	4,00E+07	-	2,22E+04	1,00E+04	-	99.99	99.99
	24	2,28E+08	1,00E+07	-	6,24E+04	9,70E+04	-	99.97	99.99

a: HAsTV detection by qPCR; ND: not done.

sence of viral concentration methods of high recuperation efficiency and detection methods of low cost have been indicated as the primary reason for the low number of studies in the area of environmental virology. There is a growing demand for studies that establish fast and sensitive methods for the detection of viruses in environmental samples.

The recovery efficiency of the virus concentration method based on electrostatic interactions among viruses and an electronegative filter was previously evaluated for poliovirus (Katayama et al. 2002). Recently, the recovery of noroviruses and sapoviruses from sewage treatment plant also demonstrated the efficiency of this method for concentration and detection of viruses in water samples (Haramoto et al. 2006, 2008). In this study, the recovery of HAsTV in both influent and effluent of the wastewater treatment plant was demonstrated using this methodology. However, the prevalence of HAsTV (16.7%) was low when compared with other studies, with high indexes ranging from 43-100% and 82.3% from inflow and outflow wastewater samples, respectively (Nadan et al. 2003, Le Cann et al. 2004, Meleg et al. 2006). The high percentage of HAsTV detected in sewage samples are usually explained due to the high seroprevalence (80-90%) of HAsTV in the studied population, the high

stability of these viruses in the environment, and the efficiency of the ultracentrifugation method that is traditionally used to concentrate and recover viral particles from wastewater (Le Cann et al. 2004). The low recovery of HAsTV could be due to the low efficiency of the method used in this study and/or the low organic load supplied to the sewage treatment plant.

The prevalence of gastroenteritis associated with HAsTV infection ranges from 2-11% and 2-26% in the developed and developing countries, respectively (Chikhin-Brachet et al. 2002, Cunliffe et al. 2002, Dalton et al. 2002, Ratcliff et al. 2002). In Brazil, the prevalence of HAsTV in the paediatric population ranged from 2-28% (Cardoso et al. 2002, Gabbay et al. 2005, Silva et al. 2006, Resque et al. 2007, Victoria et al. 2007, Soares et al. 2008). The Regional Reference Centre of Rotaviruses demonstrated a 7.8% prevalence of HAsTV infection in the city of Rio de Janeiro in 2005 (unpublished data), which was lower than the prevalence detected from environmental samples in this study. According to studies based on HAsTV detection in environmental samples, asymptomatic and/or mild digestive morbidity HAsTV infections could create an underestimation of the real prevalence of infection by this virus in the population (Meleg et al. 2006). Studies with environmental

samples have been suggested to replace those with clinical samples in order better determine the circulation of HAsTV, since there is a higher prevalence of this virus in the environment than in clinical samples.

The presence of HAsTV in both raw and treated samples demonstrates the resistance of these viruses to wastewater treatment and corroborates previous studies that also detected HAsTV in inflow and outflow waters (Nadan et al. 2003, Le Cann et al. 2004, Meleg et al. 2006). This data suggest that HAsTV resist sewage treatment at the activated sludge plant, remaining in the environment after being discharged into water body and is not related to the observed high removal efficiency of the total and faecal coliforms. Data obtained with these samples were previously published and demonstrated that the removal index of hepatitis A virus HAV (42.3%) was less than that for TC and FC (Villar et al. 2006). Molecular methods used for detecting HAsTV cannot distinguish between infectious and non-infectious virions, although they provide a rapid and sensitive method to detect viruses as an alternative to overcome the limitations of conventional techniques, such as cell cultures, since HAsTV are considered fastidious viruses. The detection of a single strand RNA genome in the environment has suggested the presence of infective viruses, since this molecule is not very stable in the environment (Meleg et al. 2006).

Although described as a more sensitive method that is recommended for investigation of environmental samples with low viral concentrations (Laverick et al. 2004), utilization of qPCR (Le Cann et al. 2004) did not present satisfactory results. Previous investigations have indicated lower sensitivity of the qPCR technique in comparison to traditional PCR (Noble et al. 2003, Grimm et al. 2004, Bastien et al. 2008).

To our knowledge, this is the first study demonstrating the detection of HAsTV in a sewage treatment plant in Brazil. In a previous study, this methodology demonstrated the recovery of many human enteric viruses in the Amazon basin, with a 15.4% prevalence of HAsTV in river waters (Miagostovich et al. 2008). This methodology, designed to both concentrate and detect HAsTV in environmental samples, offers a new perspective for evaluation of viral circulation amongst the population via environmental dissemination.

ACKNOWLEDGEMENT

To Márcia Terezinha de Moraes e Souza, for supporting the cloning methodology, and Constança Britto, for helping with qPCR.

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