Enteric viruses are mainly associated with waterborne viral gastroenteritis. Adenoviruses (AdV, Adenoviridae family, double-stranded DNA), enteroviruses (EV, Picornaviridae family, single-stranded RNA) and rotaviruses from the genogroup A (GARV, Reoviridae family, segmented double-stranded RNA) could be candidates as indicator organisms of fecal pollution for different water sources. The aim of this study was to verify the presence of AdV, EV and GARV in groundwater samples collected in the municipality of Ivoti, RS. Twenty-three (23) samples were collected from artesian and dug wells in sterilized glass bottles and submitted to virological analysis. Putative present viral particles were concentrated through adsorption-elution process, using a negative polarity membrane. After, the extraction of viral DNA and/or RNA. For EV and GARV, it was performed the synthesis complementary DNA (cDNA) by reverse transcription. Conventional Polymerase Chain Reaction (PCR) was applied aiming the detection of the specific genomes. Oligonucleotides with potential alignment in conserved regions of the genome of each virus were used, corresponding to the hexon protein gene of AdV, the region 5′untranslated (5′UTR) of ENT and the VP6 GARV gene. The reaction products were marked with SYBR-Safe®, submitted to electrophoresis on 2% agarose gel and visualized under ultraviolet light. From the 23 samples analyzed, 34.7% were positive for ADV, 30.4% positive for GARV and all samples were negative for EV. These results indicate contamination by AdV and GARV in the region in study and demonstrate that the isolated analysis of a single virus (EV, for this study) may be not enough to reveal fecal contamination. From the knowledge of the authors, it was the first assessment of groundwater contamination within the Caí watershed, one of the most populated river basins in the south of Brazil. Financial Support: CNPq, Fapergs, FEEVALE, CAPES.

EV122 - MOLECULAR DETECTION OF HEPATITIS A VIRUS (HAV) IN MAIN WELLSPRING OF WATER SUPPLY OF THE CITY OF BELEM, PARA, BRAZIL.


HAV is the main causative agent of hepatitis in Amazon region. In the North of Brazil, infection by this virus is highly endemic, varying by location depending on the socioeconomic and sanitary conditions. HAV needs an extremely low infectious dose and can remain viable in water for several months resisting the processes of water and sewage treatment, such as chlorination. Studies show that the concentration of coliforms, current microbiologic
indicator, isn’t correlated with the presence of viral waterborne pathogens. This study aims the detection of HAV in samples collected monthly, from 08/2010 to 07/2011, at Utinga Wellspring: Bolonha Lake (PT 01), Água Preta Channel (PT 02), and the Bolonha water treatment plant (ETA). Two liters of each sample were concentrated by the adsorption–elution method using a negatively charged membrane followed by centrifugation using an Amicon Ultra (Millipore) with a final volume of 2 mL. Sterilized water was used as a negative control. Bacteriological tests were performed using the Colilert kit. Viral RNA was extracted by the QIAGEN kit. After reverse transcription, the region of HAV VP1/2A was amplified by Nested-PCR method. Of the 48 tests, 36 are samples and 12 controls. One sample from the PT 01, collected in June 2011, was positive for HAV (2.8%). The bacteriological analyses showed that the samples located in PT 01 and PT 02 exceeded the values established by the CONAMA Nº 357/05 for class 2 waters. Samples collected in the ETA were in accordance to the values established by Ordinance Nº 518/04 MS for drinking water. The result of this study demonstrated a possible evaluation of disease risk associated with water resources in Belém. Although the bacteriological analysis showed no correlation with the presence of HAV, the significant amounts of fecal coliforms present on PT 01 and PT02 indicate a potential risk in water use.

Financial support: FAPESPA, IEC/SVS/MS, PIBIC/CNPq/FAPESPA/IEC.