

Tracking a novel human adenovirus in untreated sewage waters of Córdoba city, Argentina

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Recent studies highlight the utility of analyzing untreated sewage waters to monitor shedding of viral pathogens and provide genetic information of newly species identified.

In recent years, several types of human adenoviruses (HAdV) have been discovered, and its epidemiology is poorly understood. One newly discovered type, HAdV-58, was first isolated from a stool sample of a chronic excretory HIV-infected patient in Córdoba city, Argentina [1]. The genome of HAdV-58 was completely sequenced and extensive genetic analyzes were made for understanding its genomic organization and evolutionary origin [2]. However, because there are no others reports of its isolation or detection, the possible circulation in the human population is completely unknown. Recently, a novel HAdV-65 was isolated from feces of children with acute gastroenteritis in Bangladesh [3]. Corresponding genes of HAdV-65 were related to a hexon gene of HAdV-10, penton base gene of HAdV-37 and HAdV-58, and a fiber gene of HAdV-9. This indicates that HAdV-58 could be circulating in Bangladesh and that HAdV-65 could be the consequence of a co-infection with different HAdVs strains, including HAdV-58.

The finding of the novel HAdV-58 in untreated sewage samples could reflect in part ongoing enteric infections in the sampled human population. In this way a thirty-months survey was conducted to investigate the presence of HAdV-58 in urban sewage samples of Córdoba city, Argentina.

Raw sewage samples were collected at the rate of one per month from February 2009 until July 2011 from Municipal Sewage Treatment Plant of Córdoba city. Viral particles concentration in the collected samples was performed using the PEG precipitation method. Then, DNA was extracted from 0.5 ml of concentrated samples using the phenol–chloroform protocol followed by isopropanol precipitation. Extracted DNAs were assayed for human adenoviruses by nested- PCR. Samples which resulted positives were then assayed for HAdV-58 DNA by a PCR which used specific primers designed to amplify a region of 512 bp of the hexon gene.

HAdVs DNA were detected in 86.7 % (26/30) of the sewage samples tested (95% bootstrap confidence interval 72-96). None of the HAdVs detected was characterized as the novel HAdV-58.

Although human adenoviruses were detected in high frequency in the raw sewage samples of Córdoba city, no evidence of HAdV-58 circulation was observed. This result could strongly indicate that this virus has no endemic circulation pattern in the region. The analysis of untreated sewage is an useful approach to foretell the potential impact of new and emerging viruses in the human population.

Keywords: New virus, Adenovirus 58; sewage surveillance

References

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