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Molecular detection and characterization of human adenoviruses in wastewater and air samples of aeration tanks, Tehran, Iran

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Human adenoviruses (HAdV) are worldwide distributed pathogens that cause a variety of illnesses, including gastrointestinal infections. These viruses are considered as important pathogens in wastewater, reclamation, and reused water. We aimed to investigate the molecular prevalence and characterization of HAdV in wastewater samples as well as air samples of aeration tanks of a wastewater treatment plant (WWTP) in Tehran, Iran. From November 2017 to April 2018, a total of 14 wastewater and 9 air samples were collected and analyzed for the presence of HAdV by an integrated cell culture/polymerase chain reaction (ICC/PCR) technique. The samples were collected from the Ekbatan WWTP in the west of Tehran. To capture bio-aerosols, a liquid impingement biosampler was used. Typing of HAdV was performed by sequencing analysis. Out of nine untreated wastewater samples, one sample (11.1%) was positive for the presence of HAdV cytopathic effect (CPE), while two (40.4%) of five treated wastewater samples were positive for the HAdV CPE. The results of PCR assay also showed that 44.4 % (four out of 9 samples) of the untreated wastewater and 60% (three out of 5 samples) of the treated wastewater samples were positive for HAdV genome. Regarding the air samples of aeration tanks, four (44.4%) of nine samples were positive for presence of the HAdV genome. HAdV in the wastewater samples were type B (40%), type C (40%), and type D (20%) and all four positive air samples for HAdV were type C.

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