

Spatial distribution of selected water borne viruses in a slum environment in Kampala, Uganda

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Aims: To determine the spatial distribution of genomic copy concentrations of pathogenic adenoviruses 40 and 41, rotavirus, hepatitis A virus, hepatitis E virus and adenoviruses subgenus A,C,D,E,F in Bwaise III, a typical slum in Sub-Saharan Africa.

Methods and Results: To detect pathogenic viruses, samples were collected from a slum area in Kampala (Uganda). The virus particles were recovered by glass wool adsorption, elution and centrifugation. The presence of DNA and RNA viruses was tested using real time quantitative polymerase chain reaction (qPCR) and reverse transcriptase-qPCR (RT-qPCR) respectively.

Pathogenic adenoviruses 40 and 41 were detected in 70.7% of the samples with concentrations up to 8166 genomic copies per ml. Rotavirus and hepatitis A viruses were detected in 60.9% and 17.1% of the samples respectively with maximum genomic copy concentrations of 25030 ml⁻¹ and 131330 ml⁻¹, respectively. In addition, 78 % of the samples tested positive for the general adenoviruses subgenera A, C, D, E, F but all samples tested negative for hepatitis E virus. Surprisingly, adenoviruses 40 and 41 were detected in a groundwater spring used for domestic water supply. Moreover, rotavirus was also detected in ground water beneath pit latrines.

Conclusions: The results show that the slum environment is polluted and the wide spread of Pathogenic viruses pose a potential public health risk. In addition, the presence of these Pathogenic viruses in drinking water requires urgent attention by the relevant authorities.

Significance and impact of the study: The findings underline the need for identifying sources of public health hazards, carrying out public awareness campaigns, and the need for sanitation improvements in slums. These new data are essential for assessing the risk of infections caused by viruses, and for understanding the effects of environmental pollution in slums.

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