



Emerging virus communities in groundwater below slums in Sub Saharan Africa

Jan Willem Foppen (1), Jack van de Vossenbergh (1), Yvonne Hoiting (1), Alimamy Kolipha Kamara (1), Manuel Kofi Tetteh (1), George Lutterodt (2), Hans Komakech (3), Robinah Kulabako (4), and Philip Nyenje (4)

(1) IHE Delft, The Netherlands (j.foppen@un-ihe.org), (2) Central University College, Accra, Ghana, (3) Nelson Mandela African Institute of Science and Technology, Arusha, Tanzania, (4) Makerere University, Kampala, Uganda

We present the results of a mapping campaign of dsDNA virus communities in groundwater below slums in three pilot areas in Sub-Saharan Africa. Thereto, we carried out two separate Illumina Miseq runs (paired end, 300 bp per end) for 31 groundwater samples as-is, i.e. without prior amplification, from Dodowa (Ghana; 14 samples), Arusha (Tanzania; 8 samples), and Kampala (Uganda; 9 samples). Viruses were concentrated from 100 L samples, taken mostly from 2 m depth intervals in the upper 50 m of the top aquifer in wells drilled under our supervision. Furthermore, samples were taken from springs, dug wells and surface water (of which only 10 L was concentrated). Output sequence data were converted to fasta format and submitted to blastn and tblastx searches against the virus RefSeq database. The total number of read pairs in the DNA samples was 42,295,906, and the average length of the reads was 244 bases. The average percentage of identified virus or phage reads was 0.8% for blastn and 4.1% for tblastx, indicating that tblastx was more capable in detecting dissimilar viral sequences. The results indicated the presence of a number of dsDNA viruses (Adenoviridae, Ascoviridae, Asfarviridae, Baculoviridae, Herpesviridae, Iridoviridae, Nimaviridae, Nudiviridae, Papillomaviridae, Polyomaviridae, and Poxviridae) having a human, mammal, vertebrate, or other multi-cellular (e.g. insects, worms) host. These viruses must have come from or near the surface, and their presence in the samples indicated they can be transported to considerable depths into the aquifer. As such, they can be considered to be -previously unknown- new tracers of above-ground activity. Furthermore, in 100% of the sequenced samples we found Poxviridae, while in 33% of all samples human papillomavirus was present. These viruses are human pathogens, and both have not been detected before in groundwaters. Finally, some 70% of all DNA was not recognized, and will be stored for future generations.