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Using environmental samples to study genomic diversity of human viruses

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Viruses infecting humans can not only be found in the human body, but in a range of environmental samples from our surroundings. This includes indoor surfaces such as handrails or door handles, air within closed spaces, or sewage. While quantitative detection of viral pathogens in such samples is established for decades, the comprehensive exploration of the genomic therein is a much more recent development, driven by the still dropping costs of high-throughput sequencing.

In our previous study, we analyzed total RNA sequencing over 17 months from a wastewater treatment plant in Germany along with published, comparable data from other continents. This approach allowed enabled the temporal and geographic tracking of viral variants down to individual genome positions. Currently, we are focusing on an in depth investigation of the genomic diversity within enteroviruses and noroviruses in samples from Germany and internationally. Here, we present open questions and directions for future research.

Keywords

Genomics, Sequencing, Environmental Samples, Wastewater, Norovirus, Enterovirus

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139

Professional Status of the Speaker

Senior Scientist

Junior Scientist Status

No, I am not a Junior Scientist.

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