The Surveillance of SARS-CoV-2 in Wastewaters

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The COVID-19 pandemic disease is caused by severe acute respiratory syndrome 2 (SARS-CoV-2). Sewage testing has been successfully used for the detection of viruses causing human diseases, such as polio. Individuals with both symptomatic and asymptomatic COVID-19 disease may shed the SARS-CoV-2 virus through feces into the wastewater system. Next-generation sequencing (NGS) techniques are excellent tools to monitor and identify viral pathogens circulating in the population in complex matrices. The purpose of this experiment was to investigate the possibility of conducting next-generation sequencing of RNA extracted from wastewater that will allow to detect the presence of the SARS-CoV-2 virus and coronavirus variants in the local community. Next-generation sequencing data from the wastewater samples collected in Adams Field (AF), Fourche Creek (FC), Little Maumelle (LM), and Pine Bluff (PB) wastewater treatment facility were analyzed with the Illumina DRAGEN COVID Lineage application and Explify Respiratory Pathogen ID/AMR Panel (RPIP) software. The highest titer of SARS-CoV-2 RNA was observed in FC and LM samples. Mutations were detected in different SARS-CoV-2 genes including S gene encoding spike protein. The D614G mutation, one of the first SARS-CoV-2 mutations detected at the beginning of the pandemic in early 2020, was present in FC and LM samples. Interestingly, no other respiratory viruses were detected in the wastewater samples. The SARS-CoV-2 RNA could be successfully detected and sequenced using targeted next-generation sequencing, enabling wastewater surveillance to capture the presence of SARS-CoV-2 shed by people with and without symptoms. Importantly, no sampling from the individual person is needed.

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