Stockholm, 2020-10-05

## Summary of preliminary results from wastewater analysis for tracing SARS-CoV-2 in Stockholm region

### Background and method
Sampling of wastewater has been done since mid-April at Bromma, Henriksdal, and Käppala wastewater treatment plants (WWTP). These treatment plants receive wastewater from a population of approximately 290,000; 790,000 and 500,000, respectively.

The sampling at Henriksdal and Bromma started in week no. 16 (13 April) and the Käppala sampling started in week no. 18, following a sampling protocol developed by KTH. The flow-proportional pooled samples were taken bi-weekly until end of July. From week no.35 the sampling was done every week. After concentration, filtering and preparation, the samples have been analysed using qPCR technique for genetic material (RNA) belonging to the virus SARS-CoV-2, known to cause the COVID-19 pandemic.

During June and July, KTH researchers have compared four different concentration methods, two of them are commonly used internationally and the other two methods were adapted by the KTH team. The sensitivity of two ultrafiltration-based methods and two adsorption and extraction-based methods were compared for the SARS-CoV-2 as well as for two reference viruses. Our investigation concluded that the double ultra-filtration method adapted by KTH has a significantly higher efficiency compared to single filtration and adsorption methods. These findings will be published in an internationally leading scientific journal shortly.

### Preliminary Results
Currently we can report only on the relative changes in genomic level of the wastewater. The RNA signal from the wastewater analysis reflects the amount of virus excreted from infected persons within the catchment area, and may thus be used as an indicator when assessing the trend of the COVID-19 pandemic among the population.

The relative genomic level in the catchment area is calculated as a mean value for the three sampling sites, and are presented in figure 1.
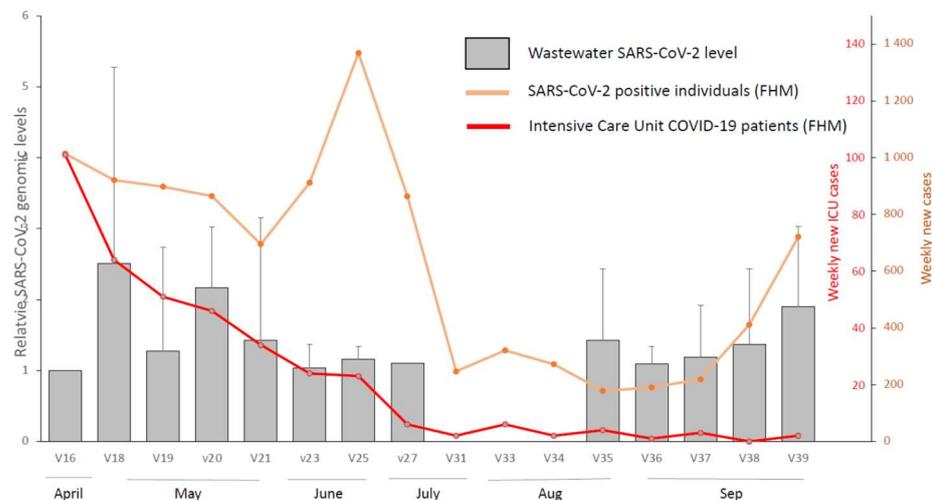
*Figure 1. Relative genomic level of RNA from SARS-CoV-2 in Stockholm wastewater between mid-April to end of September. Confirmed cases and ICU cases from Folkhälsomyndigheten, for the studied catchment area of the three wastewater treatment plants.*

**The highest genomic level in the wastewater was detected between end of April and middle of May.** From July 6th to August 24 we were not been able to detect the RNA from SARS-CoV-2 in any of the samples. **From August 24 (week 35) and to 27 September (week 39) the relative genomic level has increased steadily. In the most recent analysis period (week 39) the relative genomic level has reached a level similar to that detected in May.**

According to data from Folkhälsomyndigheten (FHM, Swedish Public Health Agency) the number of confirmed new COVID-19 cases in Stockholm region reached a peak in mid-June (week no. 25) while the highest number of intensive care unit cases was recorded in April. The total numbers of confirmed cases depend on individual testing, the frequency of which has varied significantly during the pandemic. According to FHM data, the number of confirmed cases has increased during the last weeks of September within the studied area of Stockholm (pop. 1.7 million). This is supported by our findings, which clearly show an increase of RNA from the new Coronavirus in the wastewater.

The results are still associated with uncertainties since we are yet to normalise the calculations against variation in flowrate and population. Nevertheless, we are confident about the observed trend of increasing genomic levels of the SARS-CoV-2 in the wastewater of Stockholm.

The ambition of KTH and partners is to continue the sampling and analysis throughout 2020 after which a new decision will be made, depending on resources available and demand from relevant public health authorities. We also welcome the continued collaboration with SciLifeLab,

Uppsala University and SLU, and international partners, in developing knowledge and methods for waste-water based epidemiology.

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