

CORONASTEP Report 26 (Week 47) SARS-CoV-2 Sewage Surveillance in Luxembourg

Summary

This report 26 presents the results of SARS-CoV-2 contamination of wastewater at the inlet of all wastewater treatment plants (WWTPs) for week 47. Two separate sampling days, Tuesday and Thursday, were analysed during this week, with eleven and thirteen wastewater samples respectively. Most of the WWTPs were therefore analysed twice, with the exception of Hespérance and Boevange-sur-Attert.

During week 47, **the SARS-CoV-2 RNA flows in the treatment plants were very comparable to those observed during from weeks 44 to 46. The level of contamination remains in the thirteen treatment plants analysed at high values of SARS-CoV-2 fluxes, indicating a still very high prevalence of the virus in wastewater** (Figures 1a and 1b). For the second time, the data collected this week seem to indicate a slight downward trend, although it remains very low. This trend will have to be confirmed in the coming days or weeks.

At the scale of WWTPs, the SARS-CoV-2 RNA fluxes show sawtooth variations at high levels, giving no clear signs of decrease or increase.

Table 1 – National level of SARS-CoV-2 contamination of wastewaters in Luxembourg.

 *Dark green: negative samples for SARS-CoV-2 gene E (-), Green to red: positive samples for SARS-CoV-2 gene E. The intensity of the color is related to the national SARS-CoV-2 flux (RNA copies / day / 100 000 equivalent inhabitants).*

| Week | First Wave | | | | | | | | | | | | | | | |
|------------------------------|------------|--------|--------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|
| | Week 3 | Week 7 | Week 9 | Week 11 | Week 14 | Week 15 | Week 16 | Week 17 | Week 18 | Week 19 | Week 20 | Week 21 | Week 22 | Week 23 | Week 24 | Week 25 |
| National Contamination Level | | | | | | | | | | | | | | | | |

| Week | Second wave | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|------------------------------|-------------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|--|
| | Week 26 | Week 27 | Week 28 | Week 29 | Week 30 | Week 31 | Week 32 | Week 33 | Week 34 | Week 35 | Week 36 | Week 37 | Week 38 | Week 39 | Week 40 | Week 41 | Week 42 | Week 43 | Week 44-1 | Week 44-2 | Week 45-1 | Week 45-2 | Week 45-3 | Week 46-1 | Week 46-2 | Week 46-3 | Week 47-1 | Week 47-2 | |
| National Contamination Level | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Figure 1a – RT-qPCR quantification time-course monitoring of SARS-CoV-2 (E gene) in Luxembourgish wastewater samples from December 2019 to November 2020. Grey squares: daily-confirmed cases for Luxembourgish residents (<https://data.public.lu/fr/datasets/donnees-covid19/>), dots: cumulative SARS-CoV-2 flux (RNA copies / day / 100 000 equivalent inhabitants). Blue line: Loess regression of the cumulative SARS-CoV-2 flux (RNA copies / day / 100 000 equivalent inhabitants).

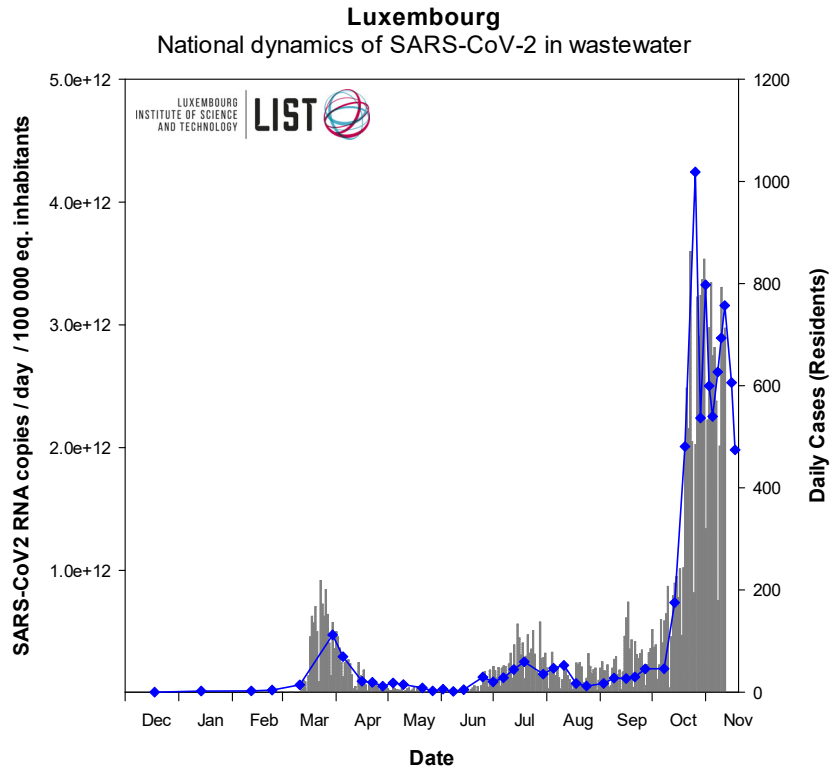


Figure 2b – Close-up of Figure 1a showing results from September 1st on.

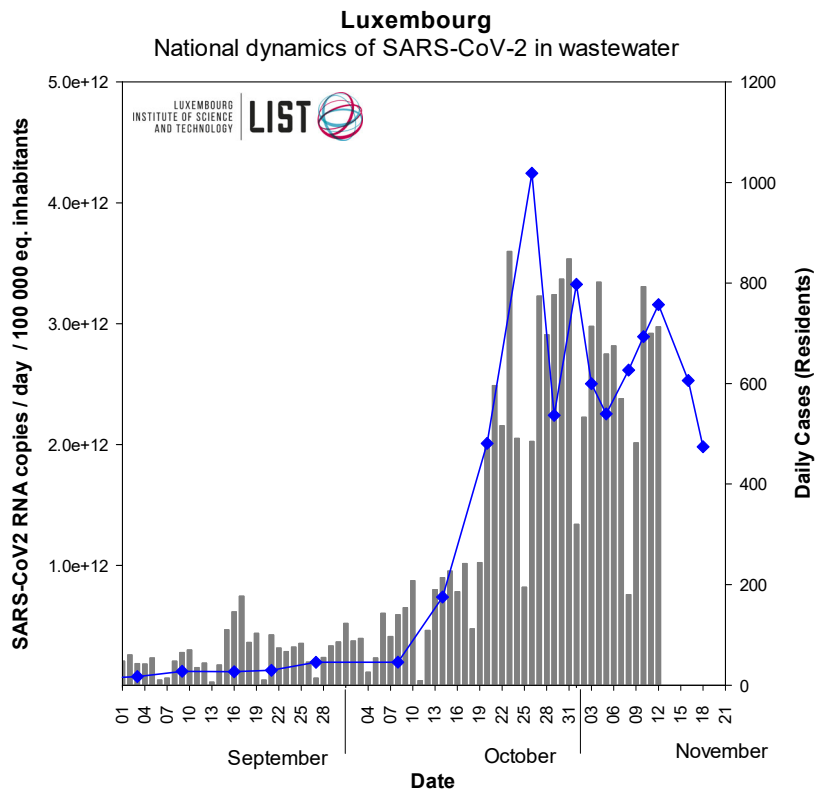


Figure 3a – RT-qPCR quantification time-course monitoring of SARS-CoV-2 (E gene) in the four most impacted wastewater treatment plants from March to November 2020. Grey squares: daily-confirmed cases for the contributory area of each wastewater treatment plant, dots: SARS-CoV-2 flux (RNA copies / day / 10 000 equivalent inhabitants).

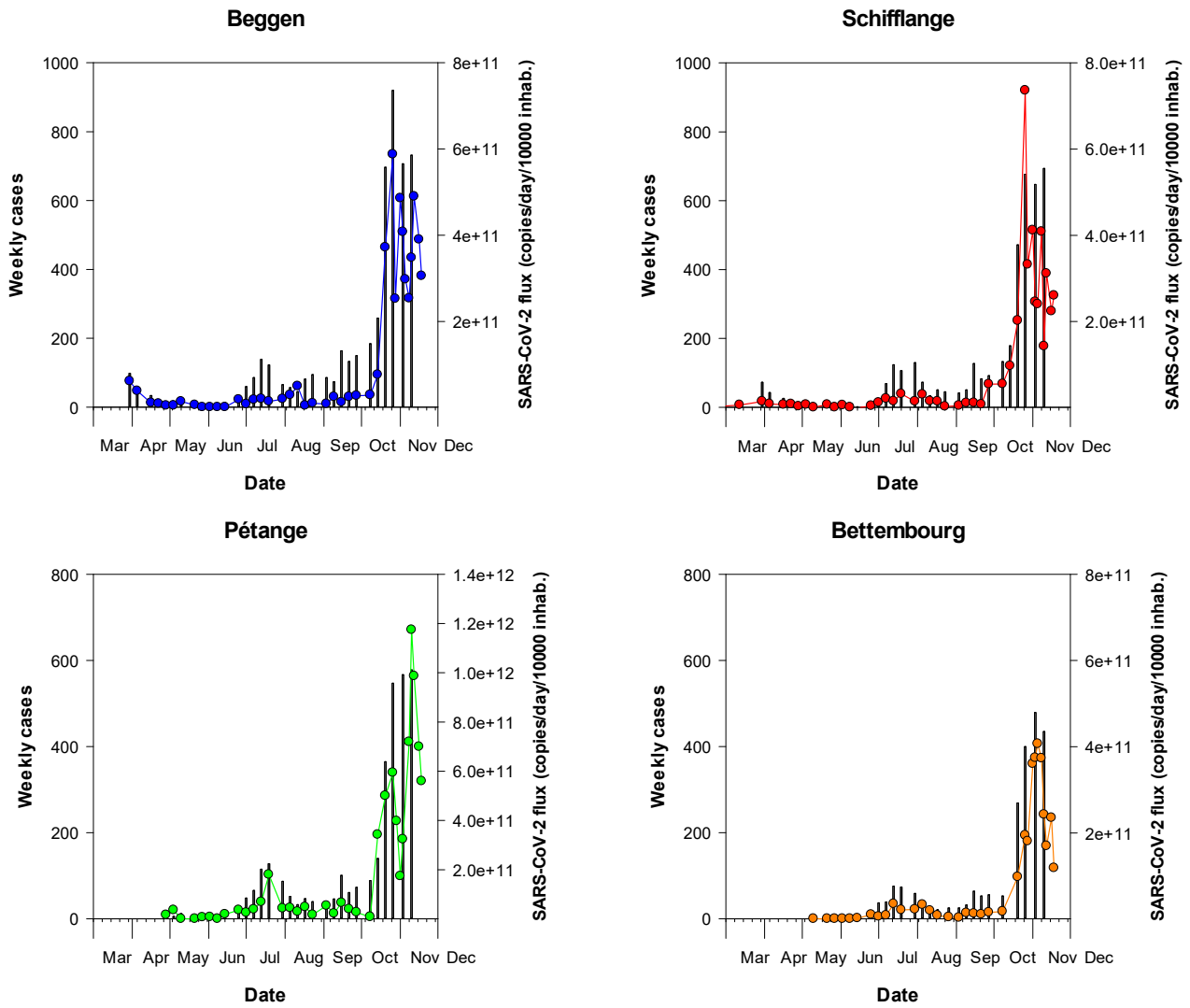


Figure 4b – Close-up of Figure 2a showing results from September 1st on.

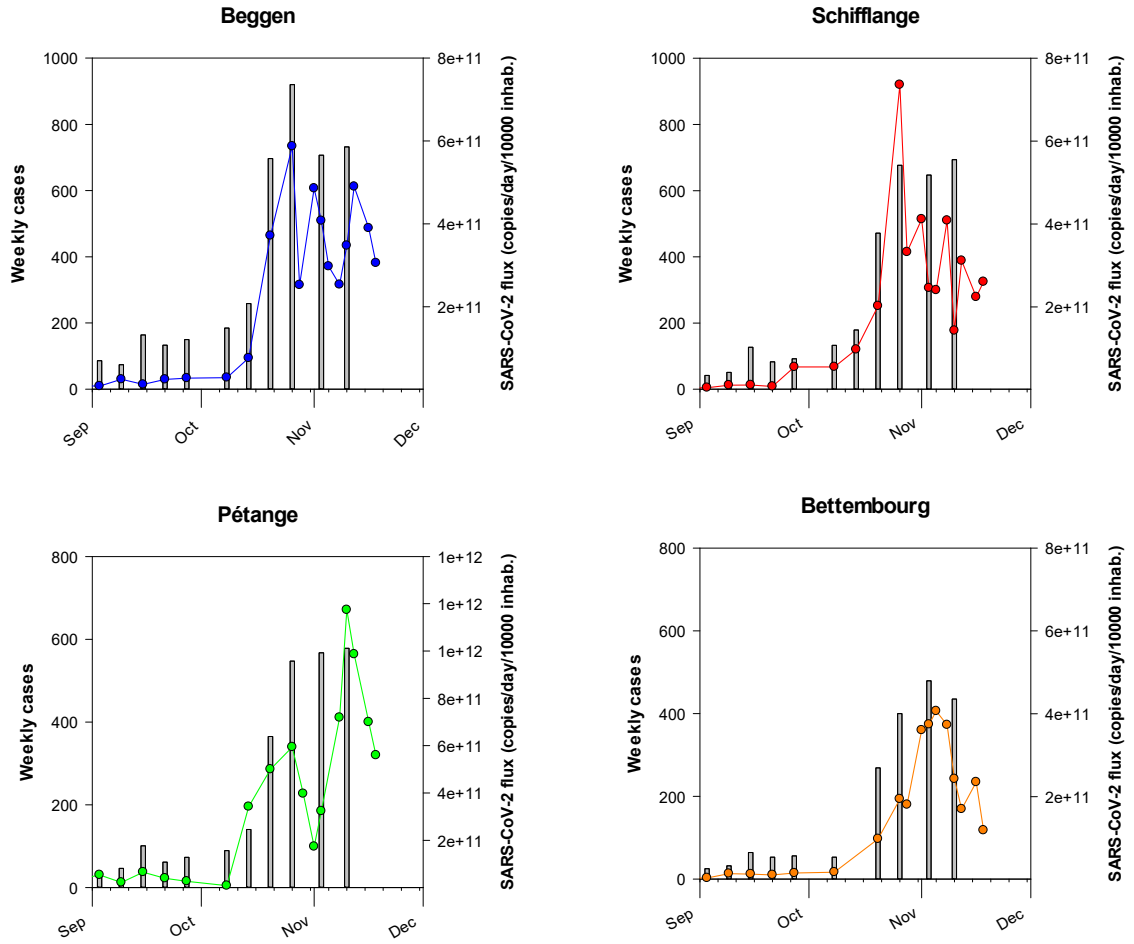


Figure 5a – RT-qPCR quantification time-course monitoring of SARS-CoV-2 (E gene) in Hespérange, Mersch and Boevange-sur-Attert wastewater treatment plants from March to November 2020. Grey squares: daily-confirmed cases for the contributory area of each wastewater treatment plant, dots: SARS-CoV-2 flux (RNA copies / day / 10 000 equivalent inhabitants).

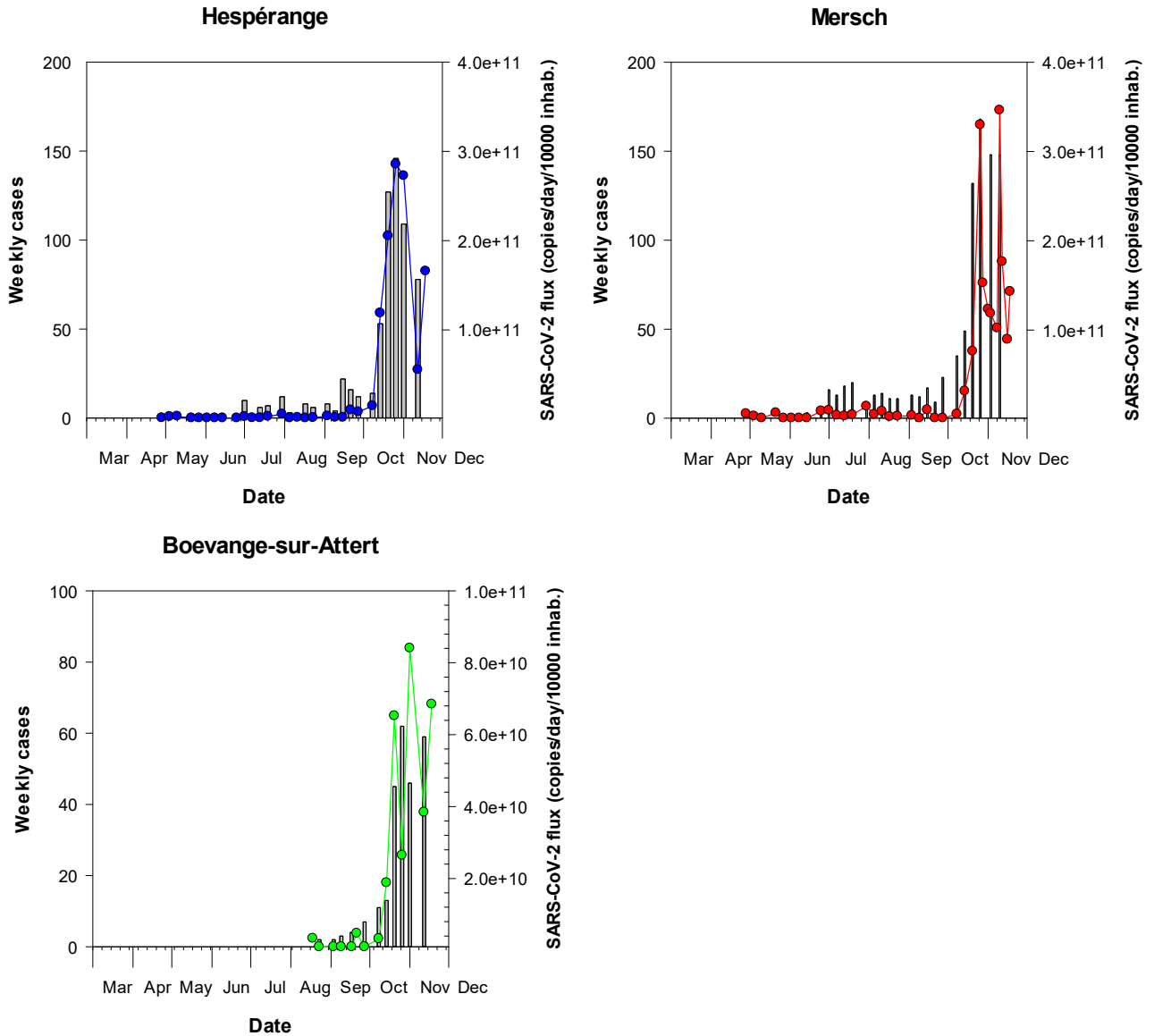


Figure 3b – Close-up of Figure 3a showing results from September 1st on.

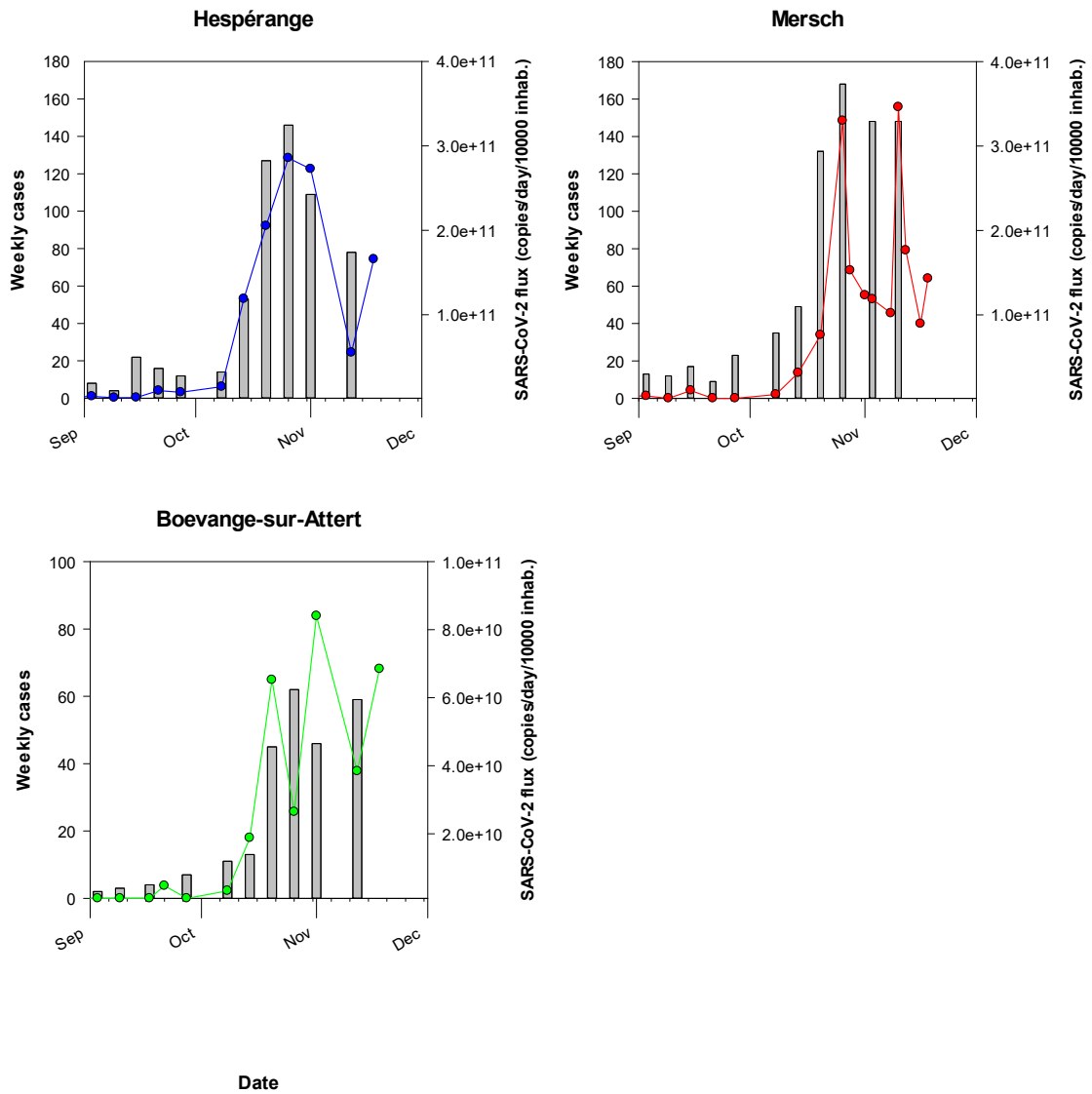


Figure 6a – RT-qPCR quantification time-course monitoring of SARS-CoV-2 (E gene) in SIDEST wastewater treatment plants from March to November 2020. Grey squares: daily-confirmed cases for the contributory area of each wastewater treatment plant, dots: SARS-CoV-2 flux (RNA copies / day / 10 000 equivalent inhabitants).

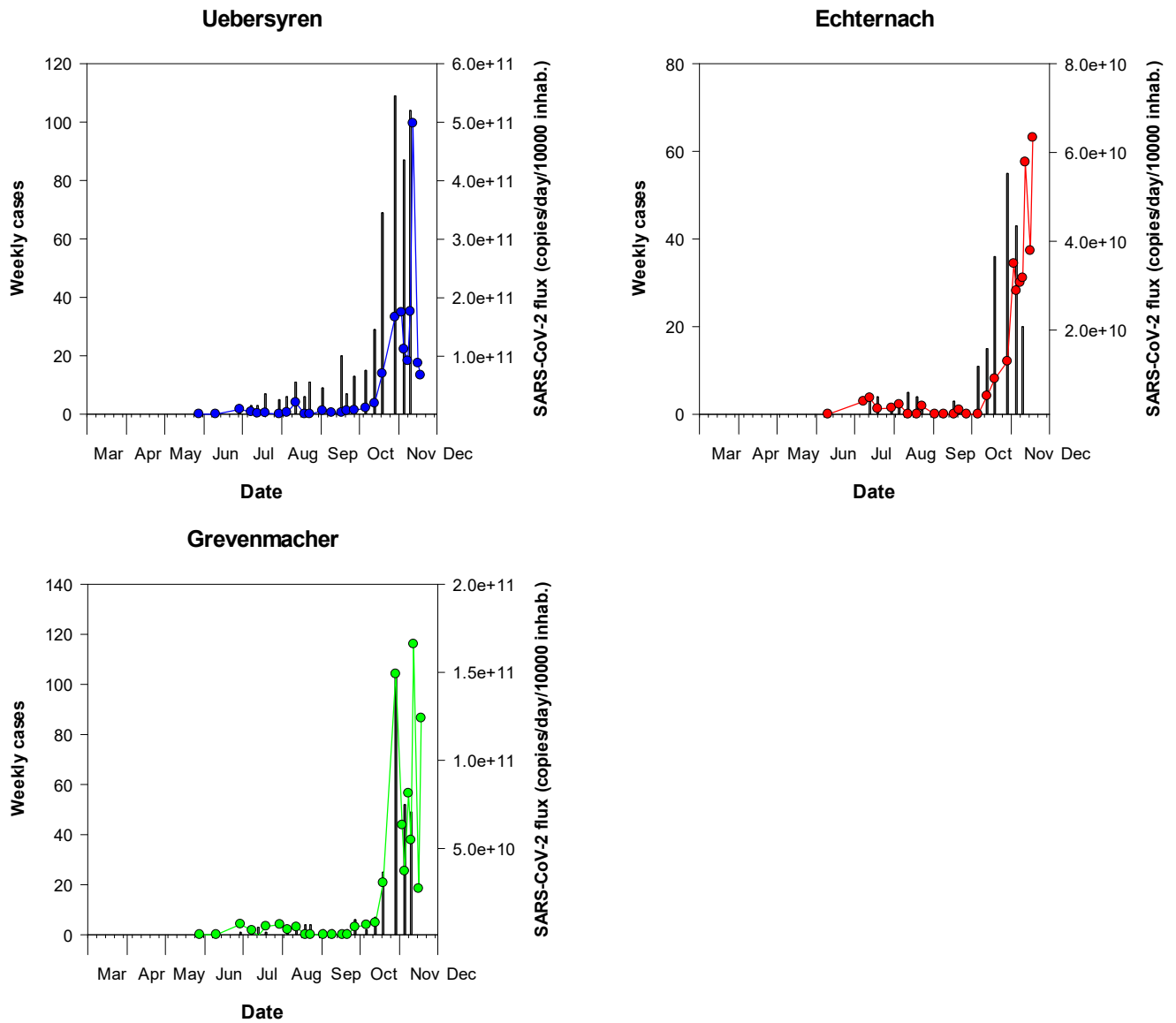


Figure 4b – Close-up of Figure 4a showing results from September 1st on.

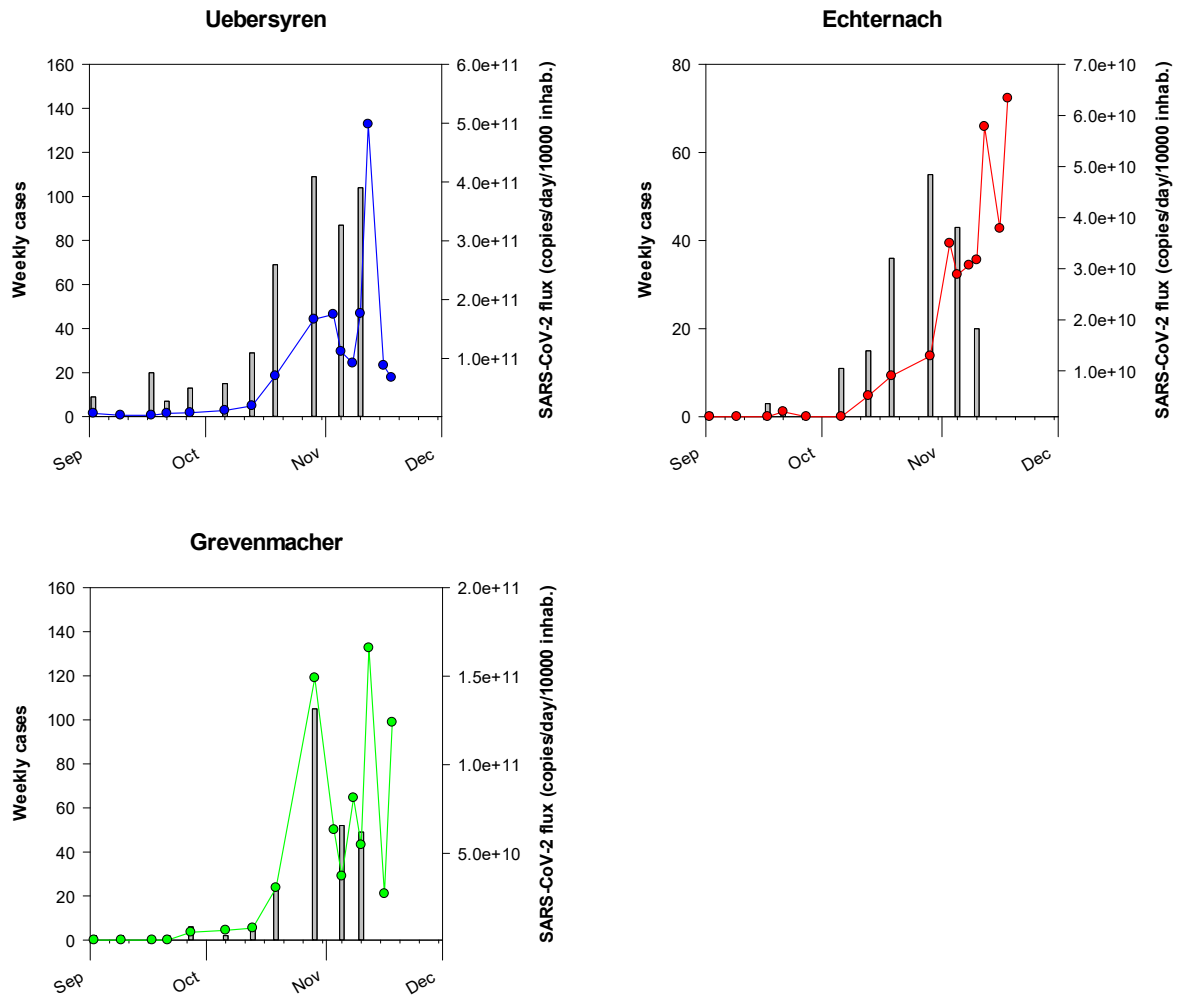


Figure 7a – RT-qPCR quantification time-course monitoring of SARS-CoV-2 (E gene) in SIDEN wastewater treatment plants from March to November 2020. Grey squares: daily-confirmed cases for the contributory area of each wastewater treatment plant, dots: SARS-CoV-2 flux (RNA copies / day / 10 000 equivalent inhabitants).

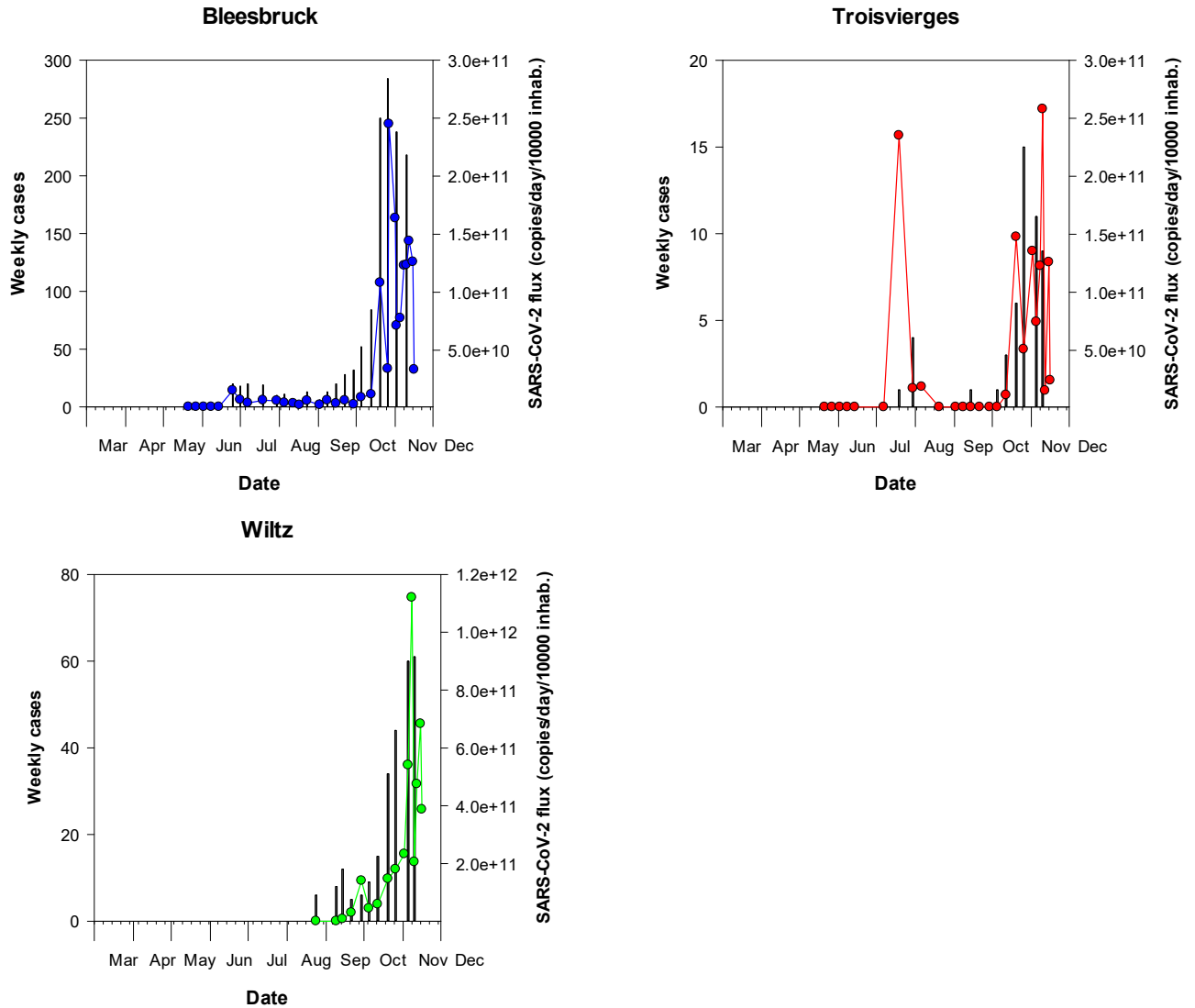
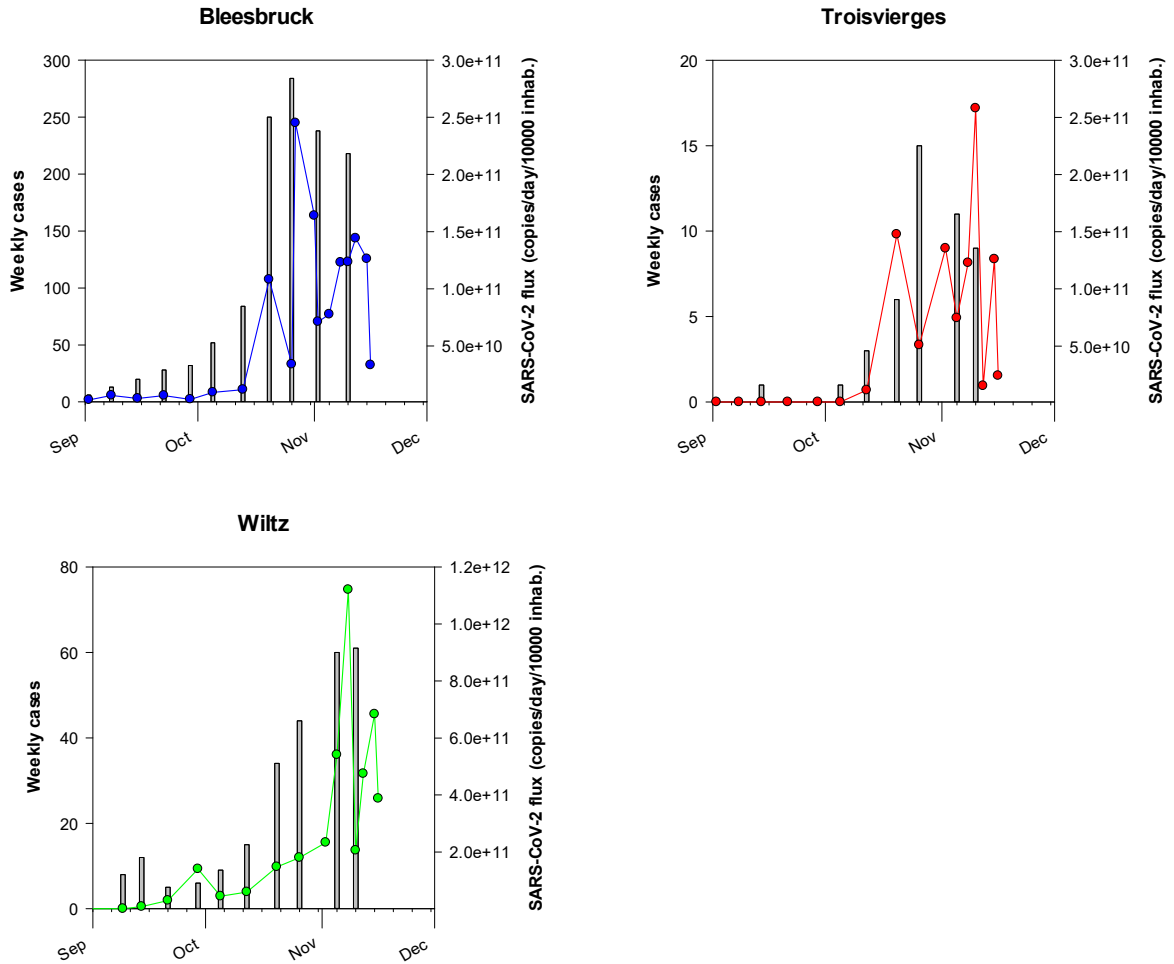


Figure 5b – Close-up of Figure 5a showing results from September 1st on.



Materials and Methods

Sewage samples

From March to November 2020, up to thirteen WWTPs were sampled at the inlet of the plant according to the planning presented in Table 2. The operators of the WWTPs sampled a 24-h composite sample of 96 samples according to your own sampling procedure. Composite sample was stored at 4°C until sample processing.

Sample processing

The samples were transported to the laboratory at 4°C and viral RNA was isolated on the day of sampling. Larger particles (debris, bacteria) were removed from the samples by pelleting using centrifugation at 2,400 x g for 20 min at 4°C. A volume of 120 mL of supernatant was filtered through Amicon® Plus-15 centrifugal ultrafilter with a cut-off of 10 kDa (Millipore) by centrifugation at 3,220 x g for 25 min at 4°C. The resulting concentrate was collected and 140 µL of each concentrate was then processed to extract viral RNA using the QIAamp Viral RNA mini kit (Qiagen) according to the manufacturer's protocol. Elution of RNA was done in 60 µL of elution buffer.

Real-time One-Step RT-PCR

Samples are screened for the presence of *Sarbecovirus* (*Coronaviridae*, *Betacoronaviruses*) and/or SARS-CoV-2 virus RNA by two distinct real-time one-step RT-PCR, one on the E gene (Envelope small membrane protein) and the second on the N gene (nucleoprotein). The E gene real-time RT-PCR can detect *Sarbecoviruses*, i.e. SARS-CoV, SARS-CoV-2 and closely related bat viruses. In the context of the COVID19 pandemic, it can be assumed that only SARS-CoV-2 strains will be detected by this assay given that SARS-CoV virus has been eradicated and other bat viruses do not commonly circulate in the human population. The E gene assay is adapted from Corman et al. [17]. The N gene real-time RT-PCR assay (N1 assay) specifically detects SARS-CoV-2 virus. It is adapted from the CDC protocol¹. The two primers/probe sets are presented in Table 3. The RT-qPCR protocols and reagents were all provided by the LIH.

Table 4 – RT-qPCR primer-probe sets

| Target | Primer name | Primer sequence (5' to 3') | References |
|--------|--------------------|------------------------------------------------|---------------------|
| E gene | E_Sarbeco_F1 | 5-ACAGGTACGTTAATAGTTAATAGCGT-3 | Corman et al., 2020 |
| | E_Sarbeco_R2 | 5-ATATTGCAGCAGTACGCACACA-3 | |
| | E_Sarbeco_P1 | 5'-FAM-ACACTAGCCATCCTTACTGCGCTTCG-BHQ1 | |
| N gene | 2019-nCoV_N1_Fw | 5'-GAC CCC AAA ATC AGC GAA AT-3' | CDC |
| | 2019-nCoV_N1_Rv | 5'-TCT GGT TAC TGC CAG TTG AAT CTG-3' | |
| | 2019-nCoV_N1 Probe | 5'-FAM-ACC CCG CAT TAC GTT TGG TGG ACC-BHQ1-3' | |

Each reaction contained 5 µL of RNA template, 5 µL of TaqPath 1-step RT-qPCR MasterMix (A15299, Life Technologies), 0.5 µL of each primer (20 µM) and probe (5 µM) and the reaction volume was adjusted to a final volume of 20 µL with molecular biology grade water. Thermal cycling reactions were carried out at 50 °C for 15 min, followed by 95 °C for 2 min and 45 cycles of 95 °C for 3 sec and 58°C (E gene) or 55°C (N gene) for 30 sec using a Viiia7 Real-Time PCR Detection System (Life Technologies). Reactions were considered positive (limit of detection – LOD) if the cycle threshold (Ct value) was below 40 cycles.

¹ <https://www.cdc.gov/coronavirus/2019-ncov/downloads/rt-pcr-panel-primer-probes.pdf>

Controls

A non-target RNA fragment commercially available (VetMAX™ Xeno™ IPC and VetMAX™ Xeno™ IPC Assay, ThermoFischer Scientific) was added to the viral RNA extract from sewage concentrates as an internal positive control (IPC). This IPC-RNA is used to control the performance of the RT-qPCR (E gene) and to detect the presence of RT-qPCR inhibitors.

Viral RNA copies quantification of both targeting genes in wastewater samples was performed using RT-qPCR standard curves generated using EDX SARS-CoV-2 Standard (Biorad). This standard is manufactured with synthetic RNA transcripts containing 5 targets (E, N, S, ORF1a, and RdRP genes of SARS-CoV-2, 200,000 copies/mL each). Using such a standard, the limits of quantification (LOQ) of both RT-qPCR assays were estimated to 1 RNA copy per reaction (Figure 6).

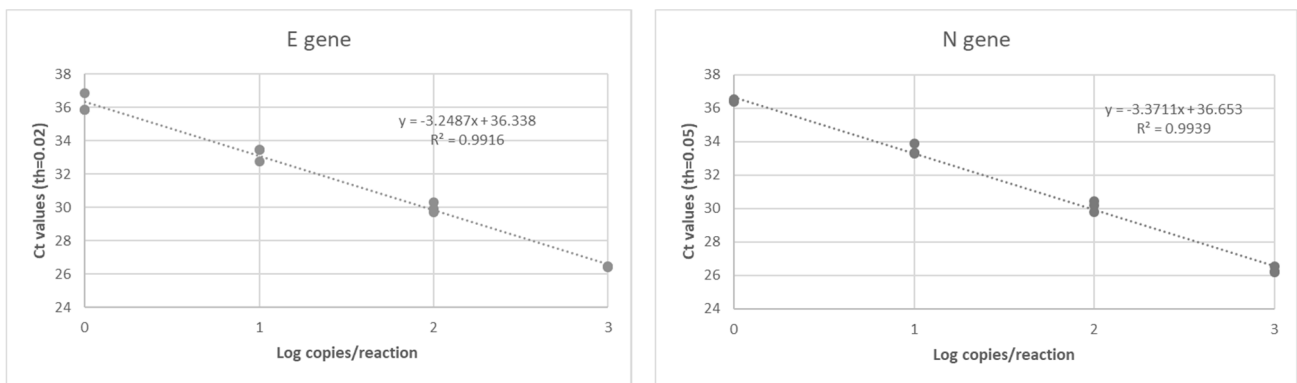


Figure 8 – RT-qPCR standard curves established for both targeting genes (E gene and N gene) of SARS-CoV-2 using a commercially available standard (Biorad).

Data interpretation

A sample is declared positive for the presence of SARS-CoV-2 if both targets (E and N gene) are detected with Ct values less than or equal to the LOQ. If only one target is detected or if target genes are detected with Ct values between the LOD and the LOQ, samples are reported as presumptive positive (+/-). A sample is declared negative when no target genes are detected (Ct values superior to the LOD).

In case of presumptive positive, sample is tested again using another RT-qPCR detection assay (Allplex 2019-nCoV Assay, Seegene). This commercially available detection kit is a multiplex real-time RT-PCR assay for simultaneous detection of three target genes of SARS-CoV-2 in a single tube. The assay is designed to detect RdRP and N genes specific for SARS-CoV-2, and E gene specific for all *Sarbecovirus* including SARS-CoV-2.

As shown in Figure 7, a good linear relationship (R^2 : 0.92) was obtained between the SARS-CoV-2 RNA concentrations estimated using the E gene and the N gene, respectively. Therefore, only the E gene results were presented in this report.

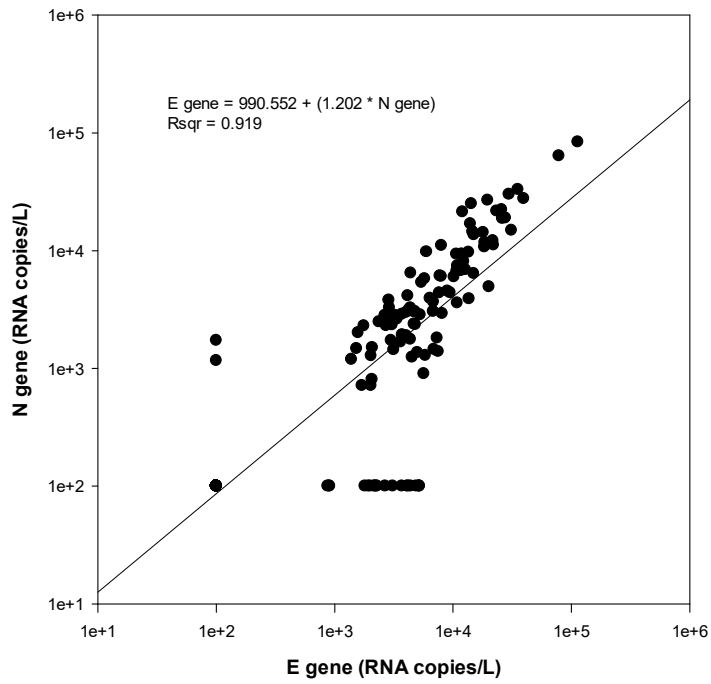


Figure 9 - Relationship between the SARS-CoV-2 RNA concentration (RNA copies / L of wastewater) estimated by the both distinct RT-qPCR systems targeting the E and N gene, respectively