

New Zealand Wastewater Surveillance Programme COVID-19

Monthly Report April 2024

Weeks ending 07 April to 28 April 2024

Report prepared 09 May 2024

Key Trends & Insights

100%

Sites (44/44) where SARS-CoV-2 was detected.

65%

NZ population covered by wastewater testing

JN.1

Most prevalent variant detected (77%)

- In April 2024, 264 samples were collected across Aotearoa. SARS-CoV-2 RNA was detected in 262/264 (99%) of samples from 44/44 sites (100%).
- Following a brief upward trend in early 2024, the latest data shows a slight to moderate decline in SARS-CoV-2 RNA in wastewater nationally in April 2024.
- The variants KP.2 and KP.3, along with JN.1.16, were added to the tracked variants. While these represent relatively low percentages nationally, KP.3, first detected in early March in wastewater, reached 10% by week 16 (week ending 21 April 2024).

National Results

National SARS-CoV-2 levels in wastewater and reported cases

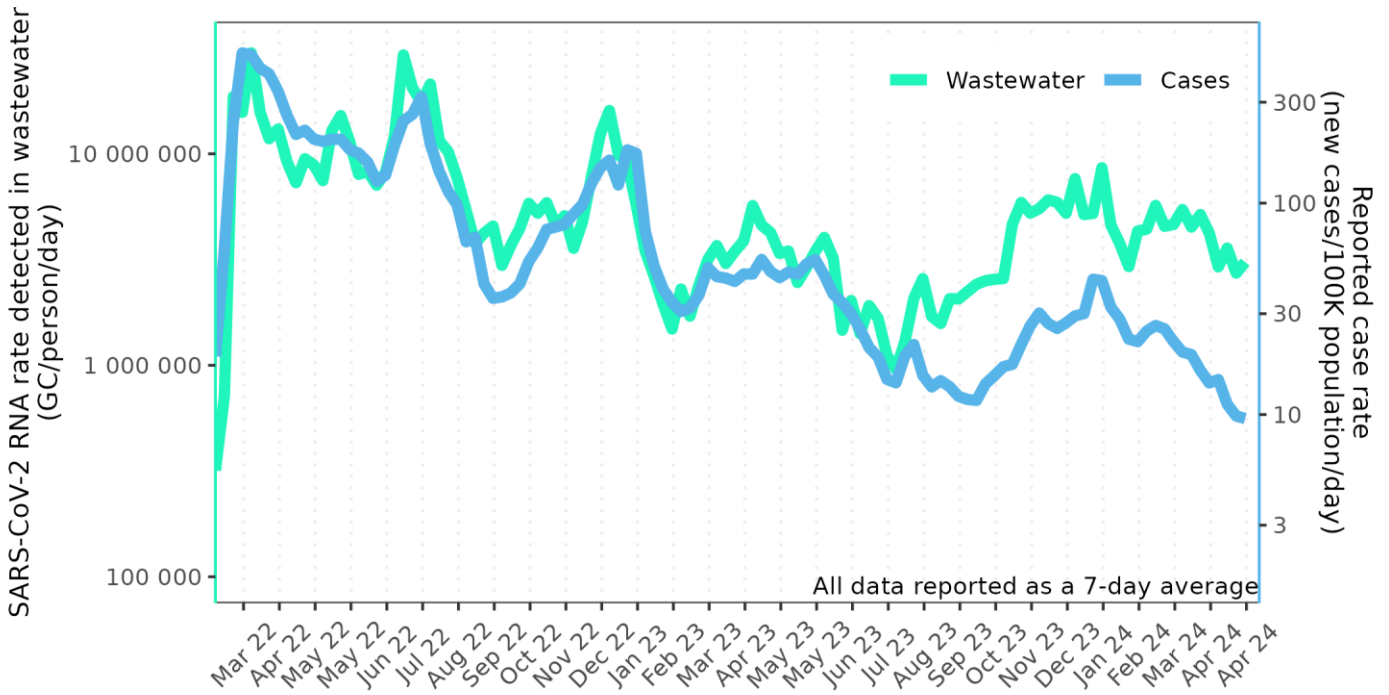


Figure 1. National timeseries of estimated SARS-CoV-2 wastewater rate (GC/person/day, green line) and reported case rate (new cases/100,000 population/day, blue line) on a log₁₀ scale.

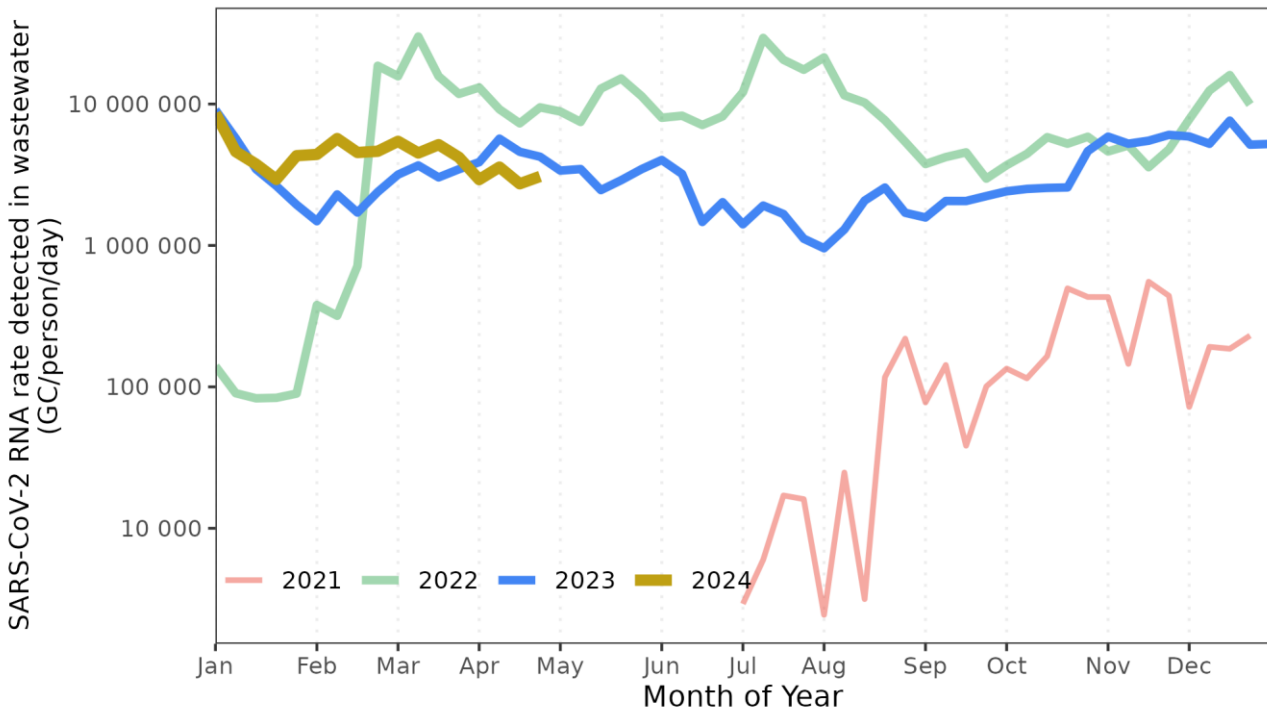


Figure 2. National timeseries of estimated SARS-CoV-2 wastewater rate (GC/person/day) on a log₁₀ scale.

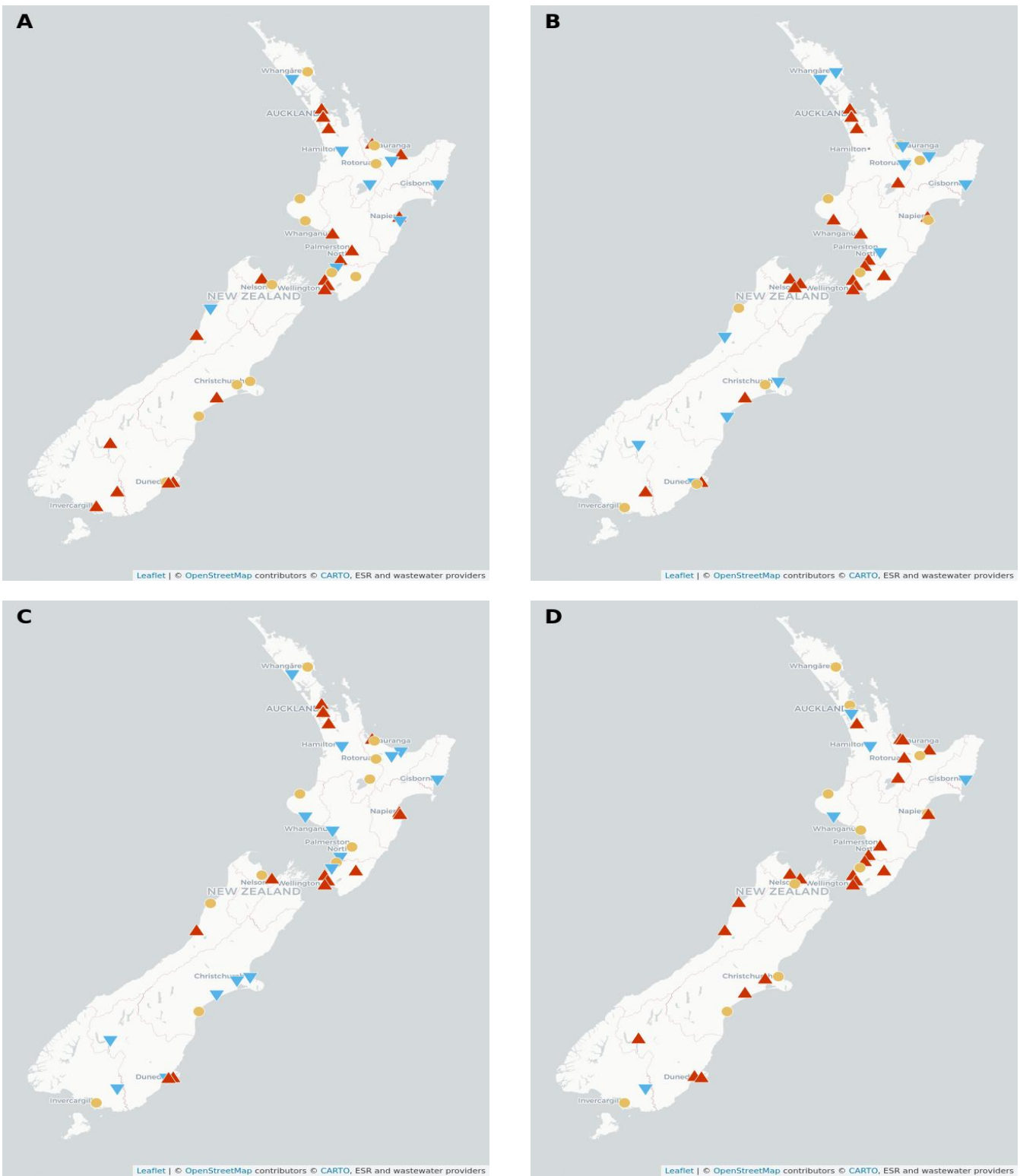


Figure 3. Comparison of SARS-CoV-2 levels for the week ending 28 April 2024, compared to levels measured: A) 1 week ago; B) 2 weeks ago; C) 4 weeks ago; D) 12 weeks ago. Only sites with results for both time points are included. When the viral quantity is 30% or more higher this is labelled as increased (red up arrow on map). When the viral quantity is 30% or more lower, this is labelled as decreased (blue down arrow on map). If viral levels have changed less than this in the compared weeks, this is labelled as no change (yellow circle on map). Interactive map of weekly results available publicly at <https://www.poops.nz/>

Variant Analysis

Results from the last four weeks of sampling up to week 16 (week ending 21 April 2024) from twenty sentinel wastewater sites) across New Zealand shows that the JN.1 family of lineages continues to dominate (Table 1, Figure 4, Figure 5).

In April, three descendant lineages of JN.1, designated JN.1.16, KP.2 and KP.3, were also specifically tracked and retrospective analysis of wastewater sequence data performed. KP.2 and KP.3 were first detected in municipal wastewater in February 2024 (week 8) and March 2024 (week 10) respectively. The earliest sample to have detectable JN.1.16 sequences was collected in November 2023, but has remained at relatively low levels to date in 2024. Percentages of JN.1.16 and KP.2 reached at least 1% nationally by week 9 (week ending 3 March), and KP.3 by week 12 (week ending 24 March). While detected in wastewater collected from several sites (Table 1), the percentages of these variants were still relatively low up to week 16. The national percentage of KP.3 was approx. 10% by week 16 (Figure 4).

The set of tracked lineages is continually reviewed and subject to change.

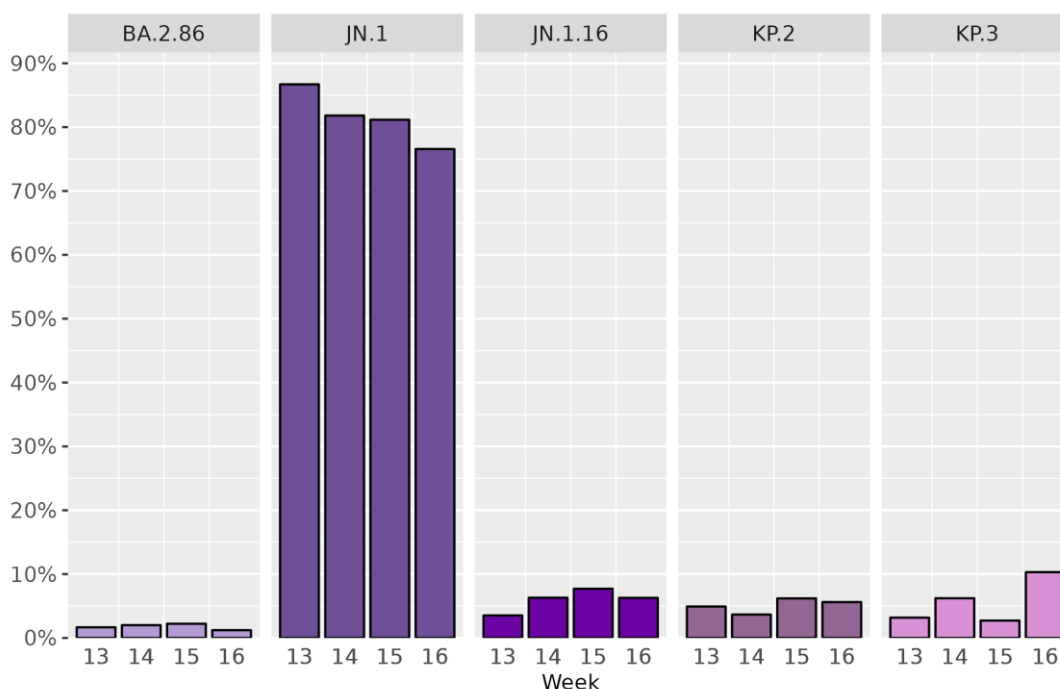


Figure 4. National percentage of each variant for week 13 (ending 31 March 2024) to week 16 (ending 21 April 2024).

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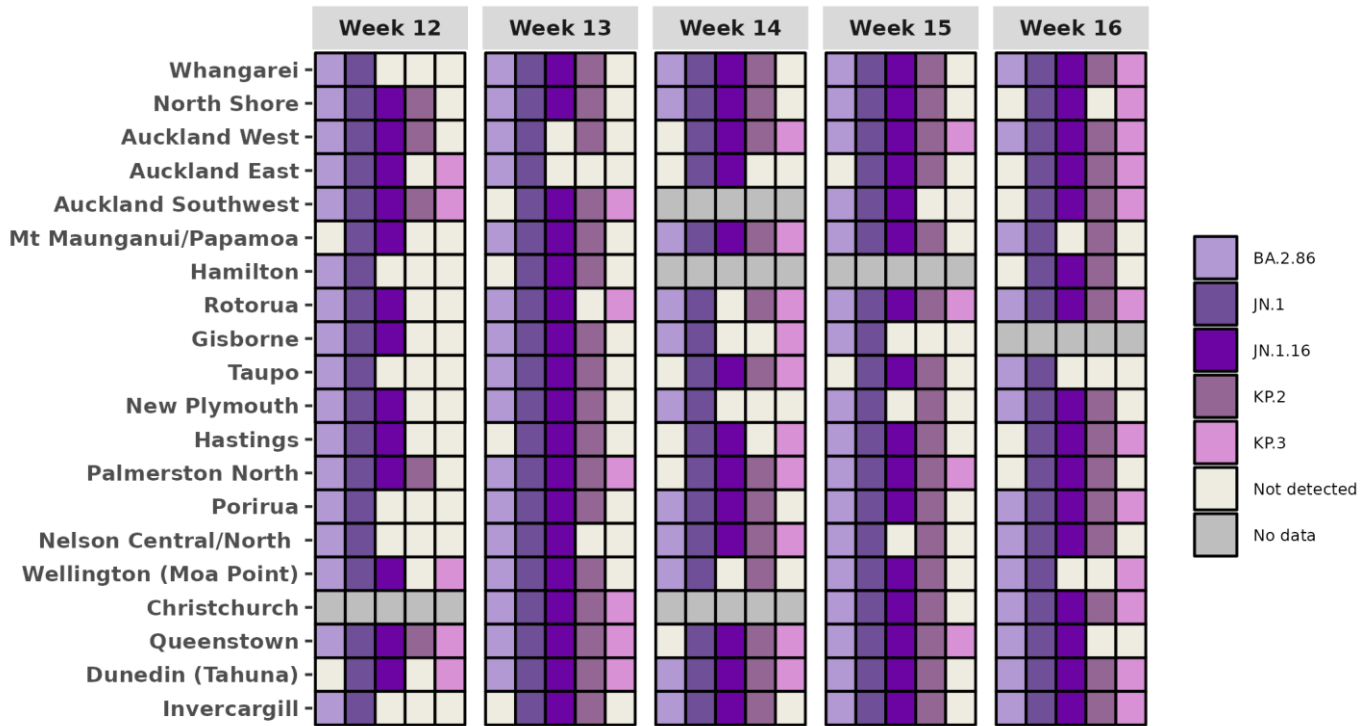


Table 1. Data from 20 wastewater sentinel sites sampled in week 12 (ending 24 March 2024) to week 16 (ending 21 April 2024). Coloured box denotes that the variant was not detected and grey box denotes site was not sampled or no sequencing result that week.

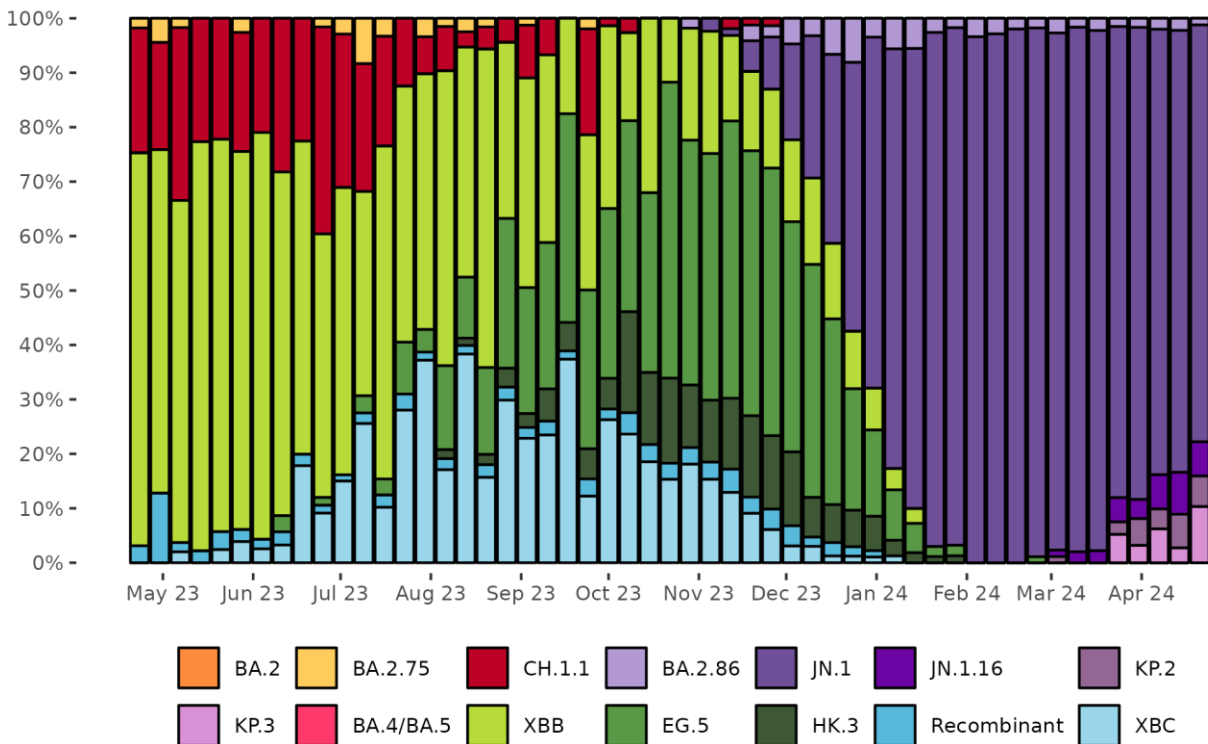


Figure 5. Estimated percentage over time at a national scale up to week 16 (ending 21 April 2024). Data are collected from up to 20 sentinel sites each week.

Instantaneous Reproduction Number

Daily wastewater and case data up to 28 April 2024 was used for the modelling. The uncertainty in these measures is denoted with 95% credible intervals (shown in green in Figure 6).

Instantaneous reproduction number: The estimate of the instantaneous reproduction number for 28 April 2024 (in week 17) was 1.09 (95% credible interval 0.77 - 1.55, Figure 6).

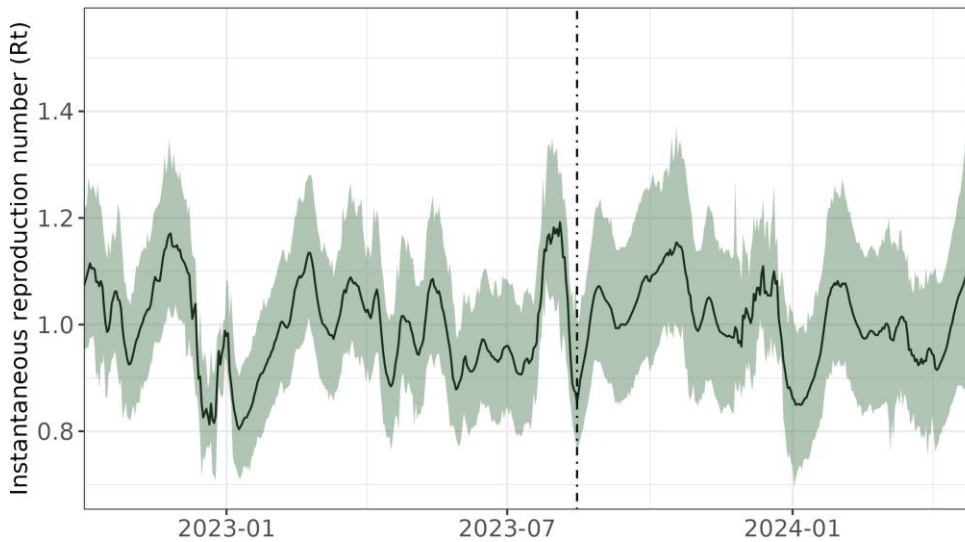


Figure 6. Estimates of instantaneous reproduction number. Black vertical lines represent when COVID-19 restrictions were lifted on 15 August 2023. Solid lines represent central estimates. Shaded regions show 95% credible intervals on the value of the hidden states.

Trends in Ministry of Health Regions

Regional analysis of the wastewater data is shown in Figure 7.

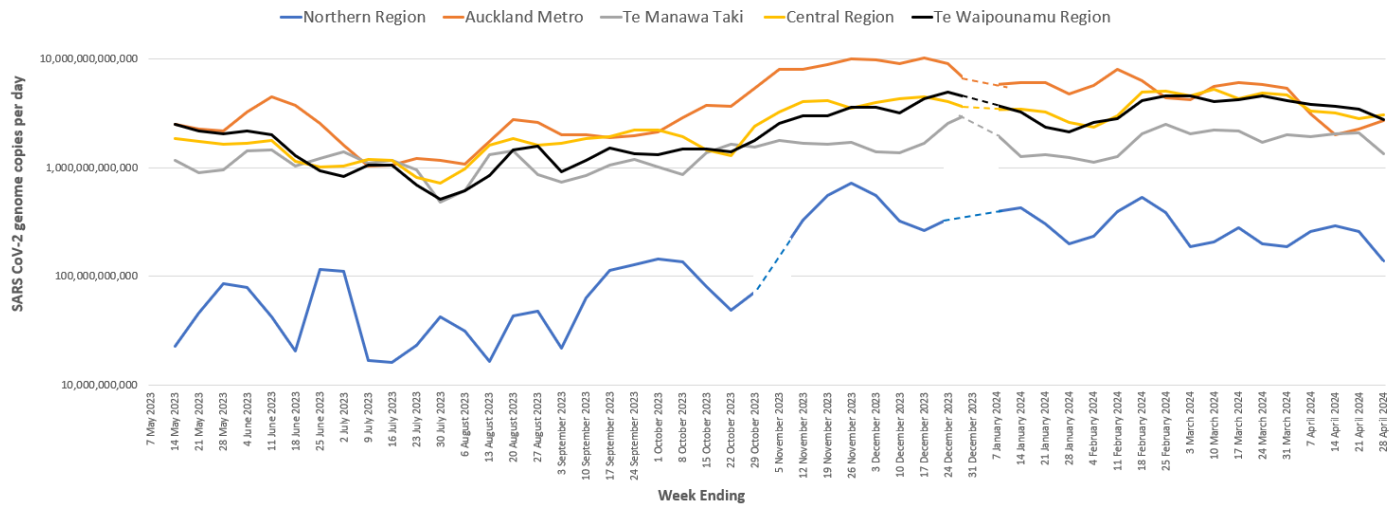


Figure 7. Two week rolling average of total SARS-CoV-2 genome copies detected per day in the five Ministry of Health regions for the last 12 months. Dashed lines are inferred levels during periods when samples were either not collected (Christmas period) or insufficient numbers collected (for example, due to weather impacts).

Acknowledgements

This work represents the combined efforts of many individuals and organisations.

We thank the teams across the country who are collecting the wastewater that underpins this work.

Wastewater analysis is undertaken at ESR by a team including laboratory staff, data scientists, bioinformaticians, and other staff. Support for this work from the Ministry of Health and ESR management is appreciated.

Notes

Sites and frequency of sample collection: The catchment population sites selected for the surveillance range from approximately 5,000 to over 680,000 individuals. The sites cover all regions of the country. Most major urban centres are included. As of early 2024, the combined wastewater catchment areas cover over 60% of the New Zealand population connected to wastewater treatment plants. The sites from which samples have been collected have varied over the last 12 months. New sites may be added over time, and/or sampling may reduce in frequency or cease for other sites. The selection and frequency of sampling varies depending on the local population, access to wastewater collection points, staff availability to collect samples and risk factors. When included, samples are collected at least weekly, with twice weekly sampling being most common.

Sampling method: The preferred option is to automatically collect a 24 hour 'composite' sample. This is where a pump automatically collects a small volume of wastewater every 15 minutes over 24 hours using a composite sampler. These samplers are available in many wastewater treatment plants. When composite samplers are not available, 'grab' samples are collected. These involve a sample being taken at a single point in time, or at intervals such as 3 samples taken over 30 minutes. Grab samples represent only the composition of the source at that time of collection and may not be as representative as a 24-hour composite sample. More variation may therefore be expected with grab samples.

Laboratory analysis of wastewater samples: Samples are sent from each wastewater treatment plant to ESR. Processing of each sample generally commences within an hour or two of receipt. Processing involves the concentration of virus from 250 mL sample to approx. 1 mL using centrifugation and polyethylene glycol. Viral RNA is then extracted from a small volume (0.2 mL) of concentrate to give a final volume of 0.05 mL of RNA. The presence of SARS-CoV-2 RNA is determined using RT-qPCR. SARS-CoV-2 is considered detected when any of the RT-qPCR replicates are positive.

RT-qPCR: Reverse transcription (RT) is used to convert RNA to complementary DNA (cDNA), followed by quantitative PCR (qPCR). RT-qPCR is a standard method used for detection and quantification of viral RNA.

Method sensitivity: The protocol used to concentrate SARS-CoV-2 from wastewater allows for the sensitive detection of SARS-CoV-2 by RT-qPCR. ESR has shown that when 10 individuals are actively shedding SARS-CoV-2 RNA in a catchment of 100,000 individuals, there is a high likelihood of detecting viral RNA in wastewater ([Publication](#)). <https://doi.org/10.1016/j.watres.2021.118032> Shedding by one infected individual may be detected via this wastewater testing method, but it does depend on many factors including the amount and duration of shedding. Very low levels of SARS-CoV-2 RNA in wastewater may be not able to be quantified (i.e., less than the limit of quantification - see below).

SARS-CoV-2 RNA detected (positive result): A positive detection in the wastewater indicates that at least one person has been shedding SARS-CoV-2 into the wastewater at some point during the period that the sample was being collected. The detection of SARS-CoV-2 RNA does not indicate that infectious virus is present.

SARS-CoV-2 RNA not detected (negative result): A negative result can occur because there are no active 'shedding' cases in the catchment or because the SARS-CoV-2 RNA concentration is too low to be detected, most likely because there are a very low number of cases in the wastewater catchment. Therefore, negative finding does not necessarily guarantee the absence of COVID-19 in the community in that location.

Viral loads and normalisation: When detected, the SARS-CoV-2 RNA concentration is calculated as genome copies per L of wastewater. This is then converted to a viral load of genome copies/day/person. This conversion considers the flow rate of wastewater entering the treatment plant (the influent) and the population in the catchment. The flow rate is the total volume (m³ per day) recorded at the inlet of the wastewater treatment plant over the 24 hours during which the sample was collected. This is a population-normalised viral load. When the actual daily flow rate is not available, the average daily flow rate is used instead. Note that rainfall may significantly increase the flow rate at the inlet, diluting the sample, and may result in lower concentrations and/or a false negative result.

Limit of quantification: The lowest concentration of the target that can be reliably quantified is referred to as the limit of quantification. For those samples where SARS-CoV-2 is detected but cannot be quantified, a value of 5 genome copies/mL wastewater is used. While a standard method is being used, virus recovery can vary from sample to sample, and this may affect the quantitation.

Wastewater Data Modelling: *Instantaneous reproduction number (R_t)*: The instantaneous reproduction number (R_t) represents the average number of secondary cases that will arise per primary infectious case. In general terms, an R_t above 1 would typically indicate an increasing number of infections in the population. The instantaneous reproduction number is calculated using a semi-mechanistic model that is fitted to (i) case numbers and (ii) wastewater quantitation, and incorporates information about shedding rates, infection generation times, and case ascertainment. Instantaneous reproduction number is estimated take into account any delays and omissions in self-reporting of cases. It should be noted that there is uncertainty in this measure, which is denoted with the 95% credible intervals.

Data subject to change: Data generated for the New Zealand Wastewater COVID-19 Surveillance Programme should be considered provisional and may be subject to change.

Data not shown: Results from certain samples may not be shown, as the result was either deemed invalid, or the sample could not be tested (e.g., leaked in transit, not labelled).

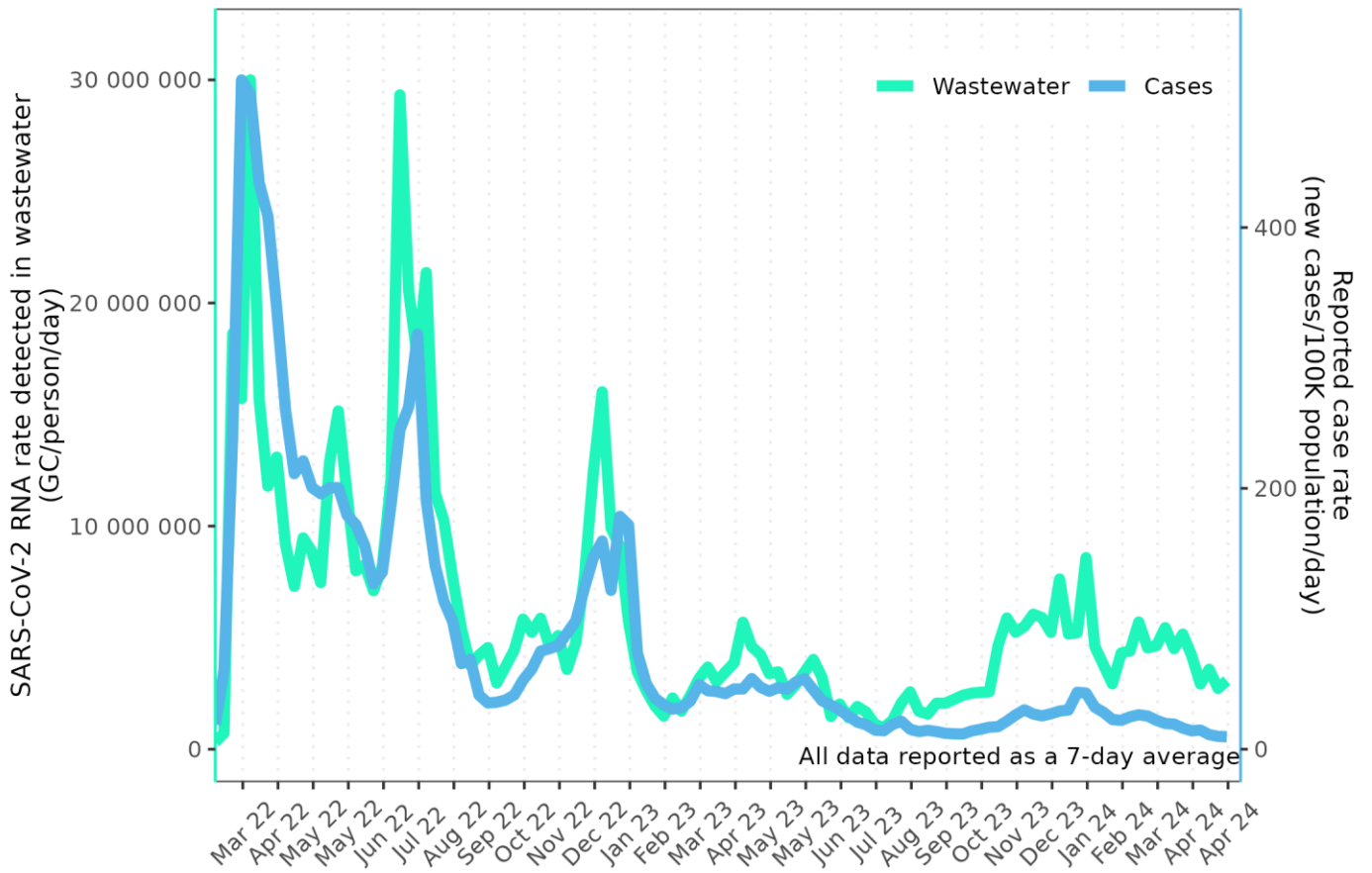
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Appendix A. National Results

Time series plotted on linear scale



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