

New Zealand Wastewater Surveillance Programme COVID-19

Monthly Report November

Weeks ending 12 November to 03 December 2023

Report prepared 07 December 2023

Key Trends & Insights

For November, SARS-CoV-2 levels in wastewater averaged at 5.77 million genome copies per person per day (GC/p/d) compared to 3.07 GC/p/d in October. During this period, SARS-CoV-2 levels were highest in the week ending 03 December at 7.11 million GC/p/d.

100%

Sites (46/46) where SARS-CoV-2 was detected.

67%

NZ population covered by wastewater testing

EG.5

Most prevalent variant detected (33%)

- In November 2023, 273 samples were collected across Aotearoa. SARS-CoV-2 RNA was detected in 273/273 (100%) samples from 46/46 (100%) sites.
- SARS-CoV-2 levels generally increased during November and provided an early indication of a new wave of infections (followed by increases in reported cases and hospitalisations).
- As a group, the XBB family of lineages remains predominant (in weeks 43 to 46). The estimated national percentage of XBB (including XBB.1.5, XBB.1.16), EG.5, HK.1.2, HV.1 and JD.1.1 collectively were 78% and 77% in weeks 45 and 46, respectively.
- EG.5 was the most prevalent (33%) variant, with the national percentage peaking at 36% in week 45. Other tracked variants were at low levels throughout the period, although noting that the percentage of both BA.2.86 and its derived lineage JN.1 increased collectively to 9% in week 46.

National Results

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

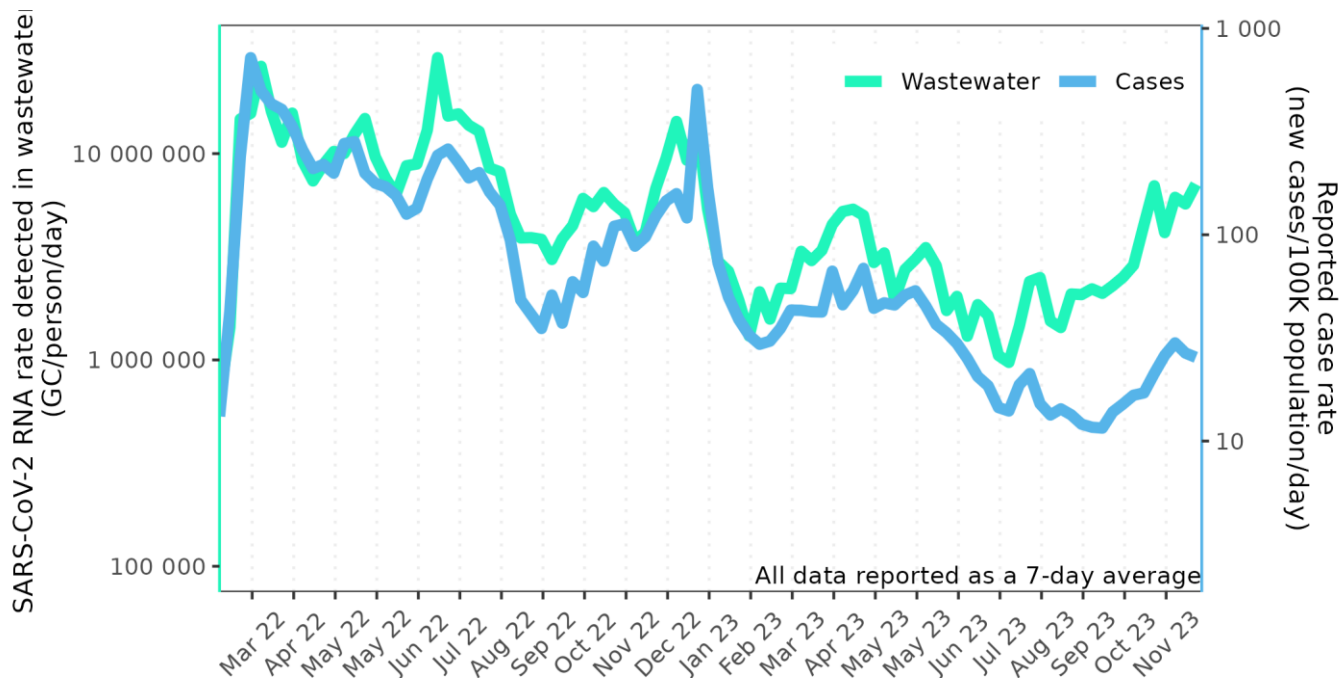


Figure 1. National timeseries of estimated SARS-CoV-2 wastewater rate (GC/person/day, green line) and reported case rate (new cases/100,000 population/day, blue line) on a log10 scale.

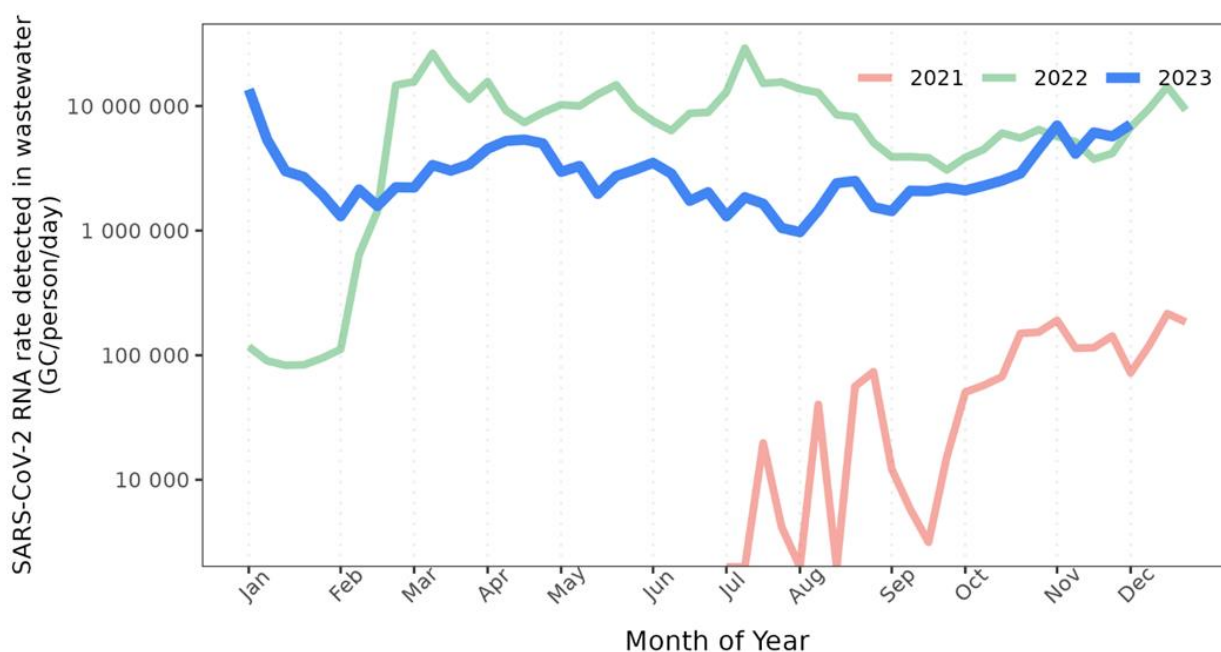


Figure 2. National timeseries of estimated SARS-CoV-2 wastewater rate (GC/person/day)

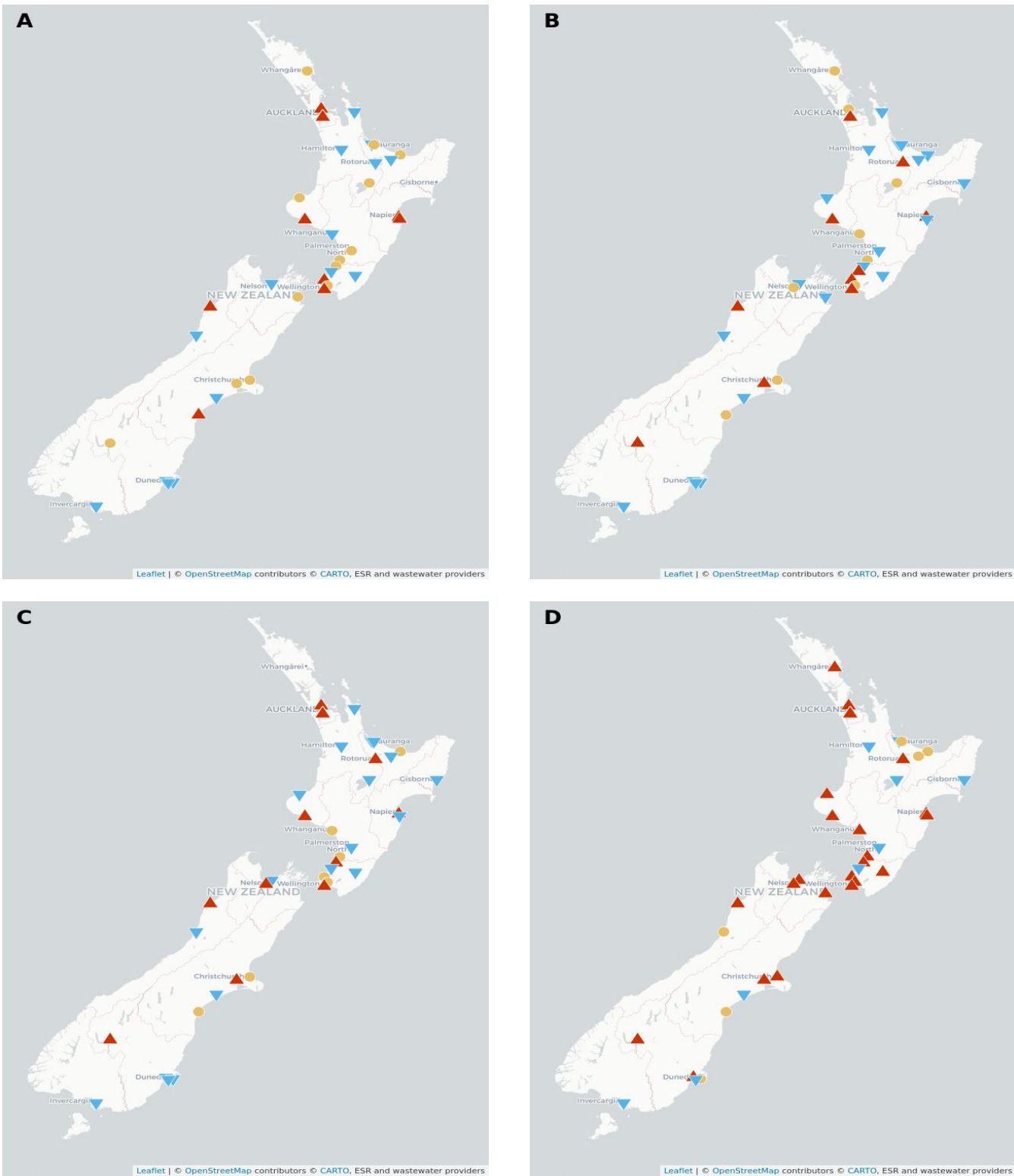


Figure 3. Comparison of SARS-CoV-2 levels for the week ending 3 December 2023, compared to levels measured: A) 1 week ago; B) 2 weeks ago; C) 4 weeks ago; D) 12 weeks ago. Only sites with results for both time points are included. When the viral quantity is 30% or more higher this is labelled as increased (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 four weeks of sampling (weeks 43 to 46) from up to 20 sentinel wastewater sites (Table 1) across New Zealand are reported.

The XBB family of lineages (which includes EG.5, HK.1.2, HV.1 and JD.1.1) was predominant (estimated total percentage between 76% and 78%) across this period (variants shown in shades of green, Figures 4 and 5, Table 1), noting that this month the descendant lineages XBB.1.5 and XBB.1.16 have been folded back into their parental lineage XBB. EG.5 was the most prevalent nationally in wastewater throughout this period, with national percentages ranging from 32% to 36% (Figures 4 and 5). The proportion of HK.3 (EG.5 group descendent) (11% to 15%) in weeks 43 to 46 was slightly lower than weeks 40 to 42 (14% to 20%).

The proportion of XBC decreased from 18% to 9% between weeks 43 to 46.

Other tracked variants were at low levels throughout the period, although noting that the percentage of both BA.2.86 and its derived lineage JN.1 increased collectively to 9% in week 46.

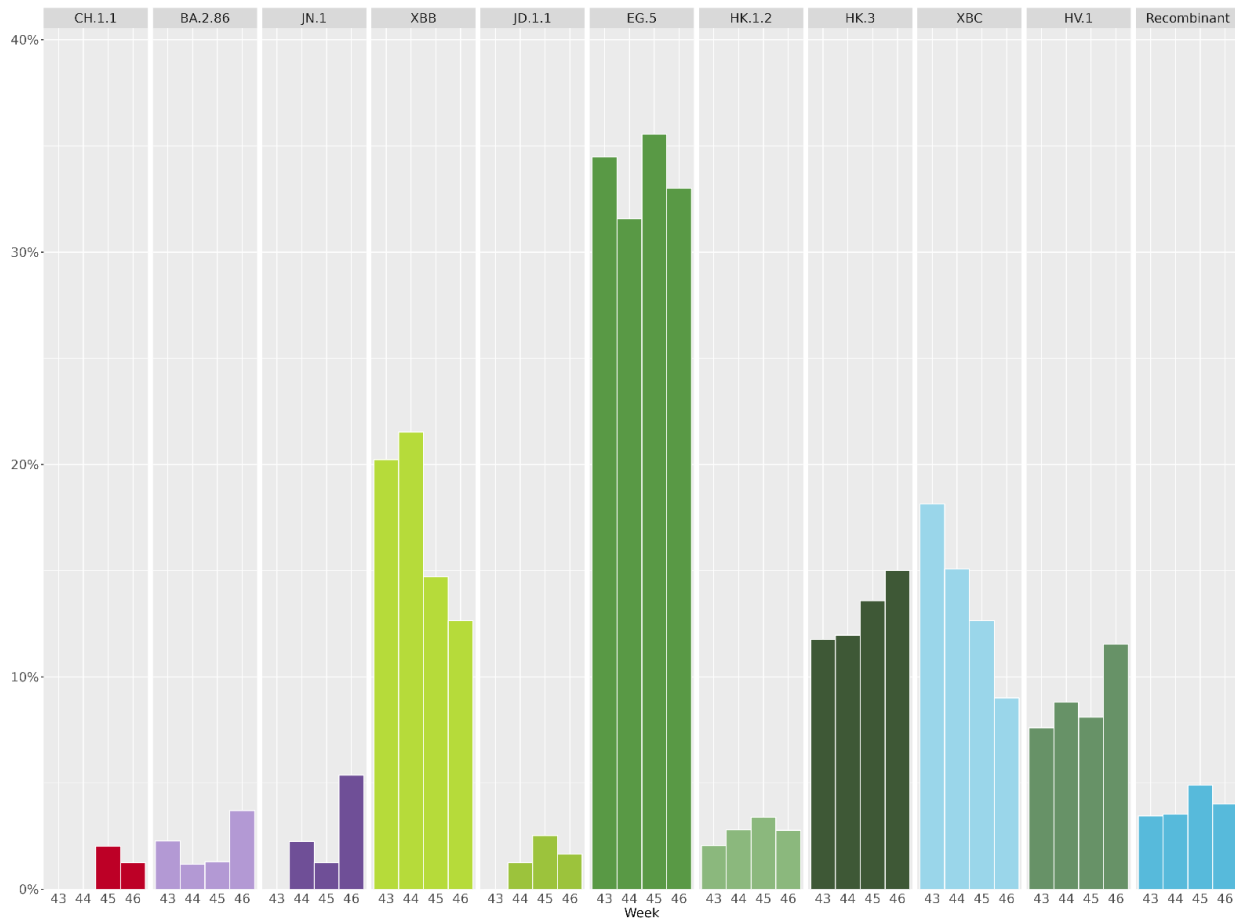


Figure 4. National percentage of each variant for week 43 (ending 29 October 2023) to week 46 (ending 19 November 2023).

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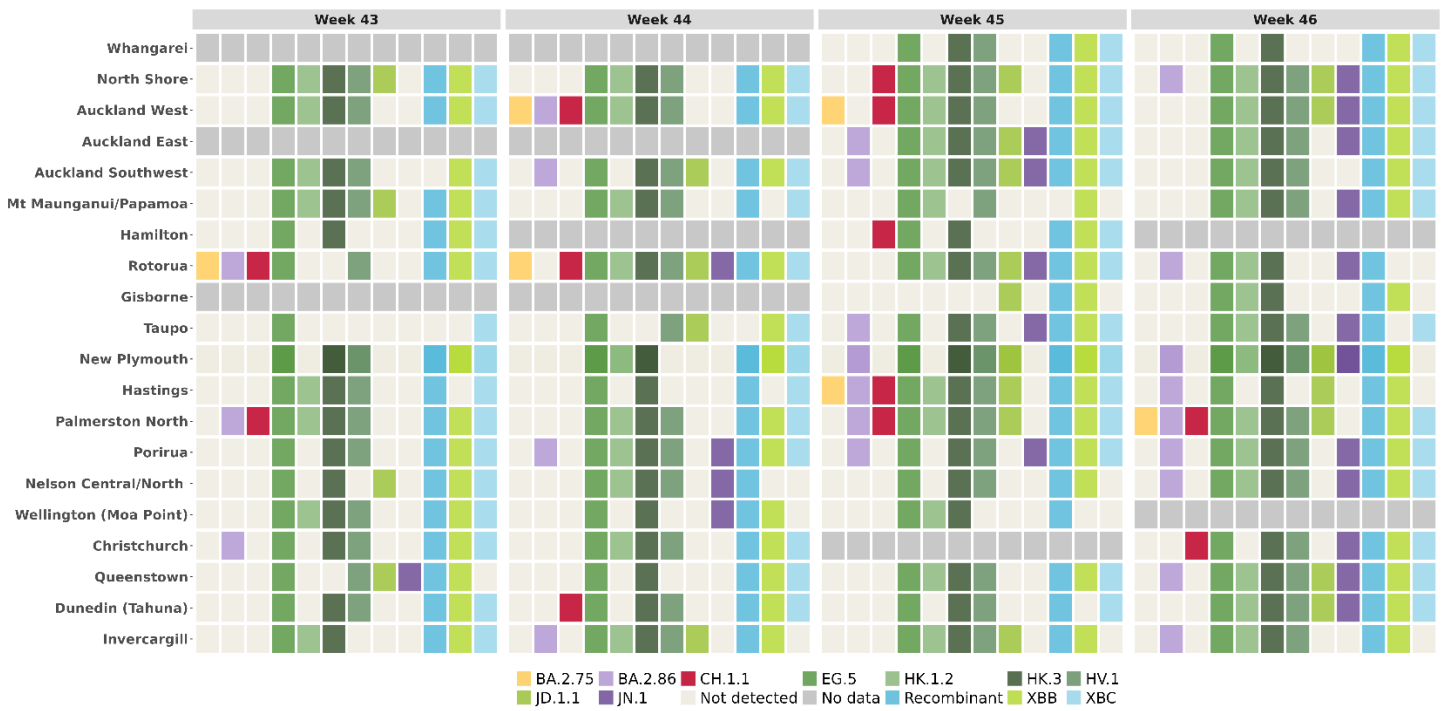


Table 1. Data from 20 wastewater sentinel sites sampled between week 43 (ending 29 October 2023) and week 46 (ending 19 November 2023). Coloured box denotes that the variant was detected at that site that week, cream box denotes that the variant was not detected, and grey box denotes site was not sampled that week.

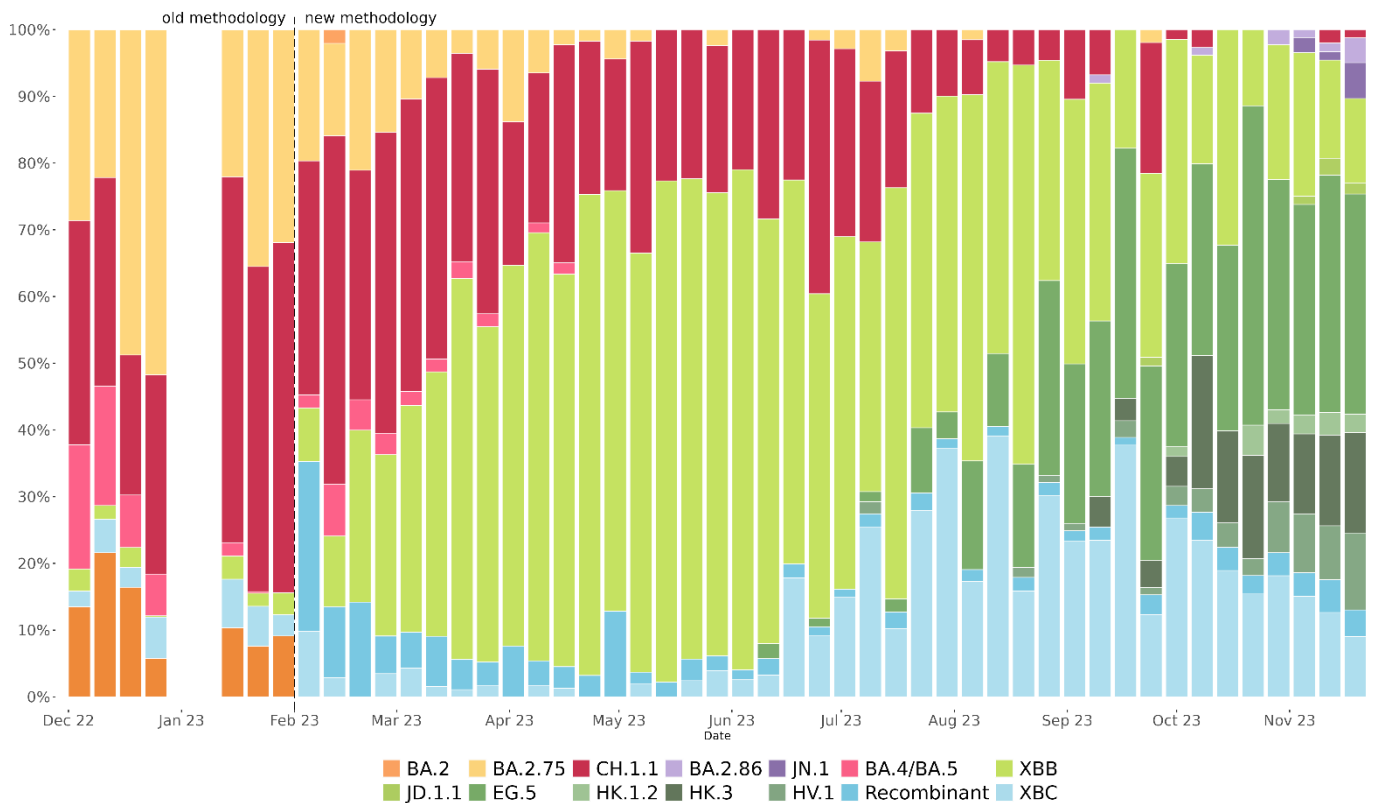


Figure 5. Estimated variant percentage over time at a national scale (average). Data are collected from up to 20 sentinel sites each week.

Instantaneous Reproduction Number

The model used to estimate the instantaneous reproduction number has been updated with more accurate distributions that describe the lags between infection, symptom onset, and reporting whereas the previous model used fixed values. Rather than using the 7-day average reported case and wastewater data, the model now uses daily data.

Daily wastewater and case data up to 01 December 2023 was used for the modelling. The uncertainty in these measures is denoted with 95% credible intervals (shown in green in Figure 6).

The estimate of the instantaneous reproduction number for 01 December 2023 (in week 48) was 1.00 (95% credible interval 0.71 – 1.38, Figure 6).

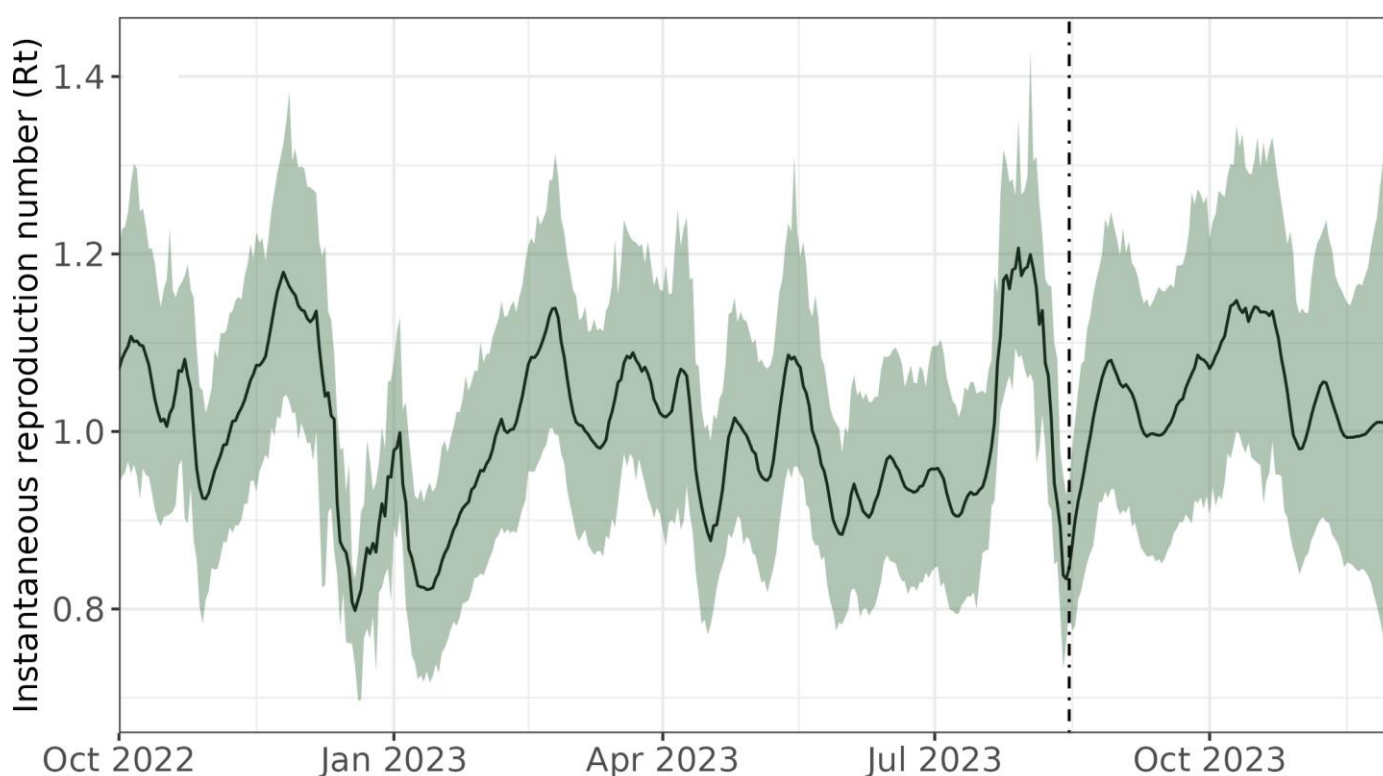


Figure 6. Estimates of instantaneous reproduction number. Black vertical lines represent when COVID-19 restrictions were lifted on 15 August 2023. Results assume the average total shedding per infection does not vary over time ($\alpha = 3 \times 10^9$). Black solid lines represent central estimates. Shaded regions show 95% credible intervals on the value of the hidden states (a,b).

Trends in Ministry of Health Regions

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

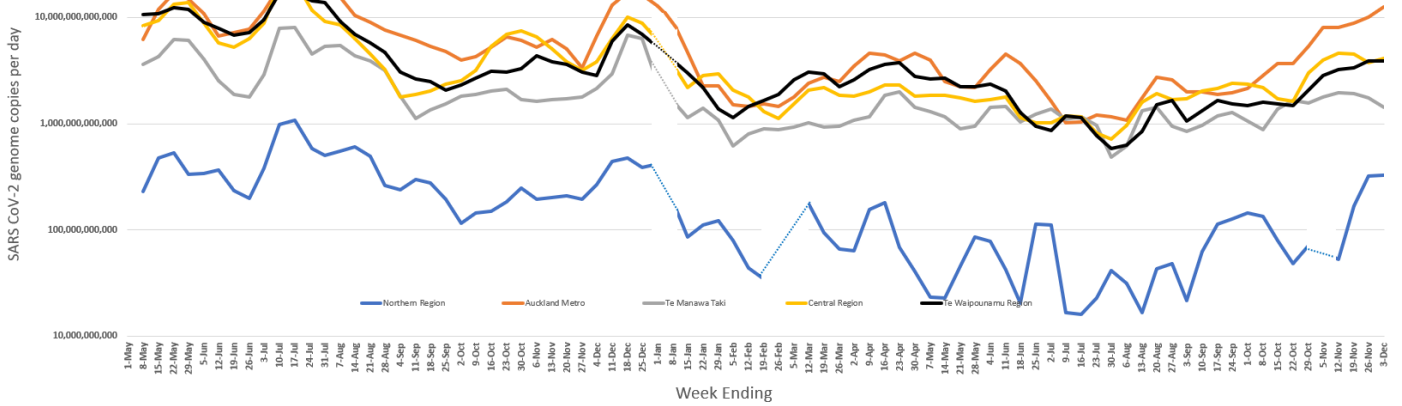


Figure 7. Two week rolling average of total SARS-CoV-2 genome copies detected per day in the five Ministry of Health regions. Dashed lines are inferred levels during periods when samples were either not collected (Christmas period) or insufficient numbers collected (due to weather impacts) for the region.

Glossary of Terms

Autosampler – an automatic water sampling machine that automatically collects water typically based on time or flow parameters.

Coronavirus disease 19 (COVID-19) – a respiratory illness caused by the virus SARS-CoV-2.

Grab sampler (Grab) – a grab sample is a sample physically taken from a sampler and consists of either a single discrete sample or multiple samples collected over a period.

Genome – The entire genetic code of an organism. In the case of SARS-CoV-2, the genome is ~30,000 nucleotides (or base pairs) in length. The process of obtaining the entire genome is called whole-genome-sequencing (WGS). It is achieved by sequencing SARS-CoV-2 in overlapping pieces and then ‘stitching’ them together (genome assembly). Sometimes genomes are tagged as *failed* or *partial*.

Genome copies per person per day – The raw data (genome copies per litre) is converted to a viral load of genome copies/person/day). This conversion considers the flow of wastewater entering the treatment plant and the population in the wastewater catchment (please note that this will not necessarily be the same as the population of the town/city). At the site level, GC/person/day is the average value of all samples collected within that week. When a site is sampled only once per week, the value of that sample is shown (as there is no average for the week). This approach allows for the aggregation at regional and national levels, and avoids small catchments being over-represented and large catchments being under-represented. This dashboard provides linear and log₁₀ unit options for data presentation.

Receptor binding domain (RBD) – a small part of the Spike protein that is instrumental in the virus attaching to the ACE2 receptor, a protein found on the outside of many human cells. Several key mutations have been identified here which determine a variant’s transmissibility and ability to evade immunity.

Ribonucleic acid (RNA) – is a nucleic acid, typically single-stranded – aids in cellular protein synthesis. In some viruses replace DNA as the primary source of genetic information such as SARS-CoV-2.

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) – the virus that causes the disease coronavirus disease 19 (COVID-19). SARS-CoV-2 is a single stranded RNA virus.

Subvariant – a sub-branch of a formally recognized variant. For example, BA.1 and BA.2 are classified as subvariants of Omicron; while BA.2.75 is a subvariant of BA.2. A sub-branch of a variant will remain unless the World health organization (WHO) elevates it to a distinct *variant status*.

Spike protein – a protein location on the outside of the SARS-CoV-2 virus that allows the virus to attach to, penetrate and infect cells. The spike protein is targeted by most vaccines. Changes to the spike protein can result in immune evasion.

Variant or Lineage – these are interchangeable terms that refer to a group of closely related viruses with a common ancestor. Several systematic methods of naming and classifying SARS-CoV-2 variants include the Pango (names like B.1.617.2) and Nextstrain (names like 21A) systems. The World Health Organization (WHO) also names various lineages of particular interest to public health.

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.

The wastewater analysis has been undertaken at ESR by a team including laboratory staff, data scientists, bioinformaticians, and other staff. Ongoing 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 10000 to over 1,000,000 individuals. The sites cover all regions of the country. Most major towns and all cities, as well as many smaller communities, are included. In early 2023, the wastewater catchment areas cover over 75% of the 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 vary 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 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 some wastewater treatment plants. When composite samplers are not available, 'grab' samples are collected. These range from a sample being taken at a single point in time, to 3 samples taken over 30 minutes, to samples collected over a day. 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 sampler. More variation may be expected with grab samples.

Laboratory analysis of wastewater samples: Samples are sent from each wastewater treatment plant to ESR. Processing of each sample 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 of 0.2 mL concentrate to give a final volume of 0.05 mL. 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) to convert RNA to complementary DNA (cDNA), followed by quantitative PCR (qPCR). RT-qPCR is 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 was a high likelihood of detecting viral RNA in wastewater (<https://doi.org/10.1016/j.watres.2021.118032>). Shedding by one individual may be detected in wastewater, but it does depend on many factors including the amount and duration of shedding. Very low levels 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 time period that the sample was being collected. In some cases, detections could also be due to the shedding of low levels of SARS-CoV-2 RNA by a recently recovered case. 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.

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 24 hours. This is a population-normalised viral load. Currently, the flow rate is the average annual flow rate, but will be replaced with daily flow rate when available (note that rainfall may significantly increase the flow rate at the inlet, diluting the sample, and may result in lower concentrations and 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. The effective reproduction (R_{eff}) number can be measured as either the instantaneous reproduction number (R_t), which measures transmission at a specific point in time; or the case reproductive number, which measures transmission for a specific cohort of individuals. The models described measure the instantaneous reproduction number (R_t). 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 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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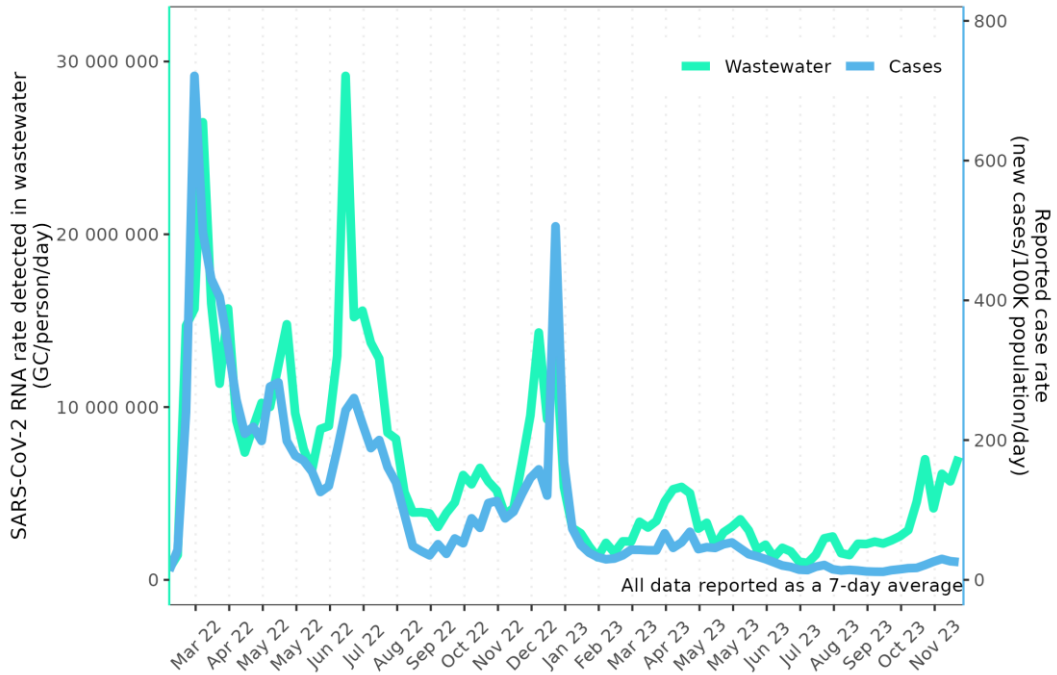
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Appendix A. National Results

Time series plotted on linear scale



Detections for the past 52 weeks

