



25^{es}
journées annuelles
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Sequencing SARS-CoV-2 Variants in Quebec Wastewater: A Tool Under Development

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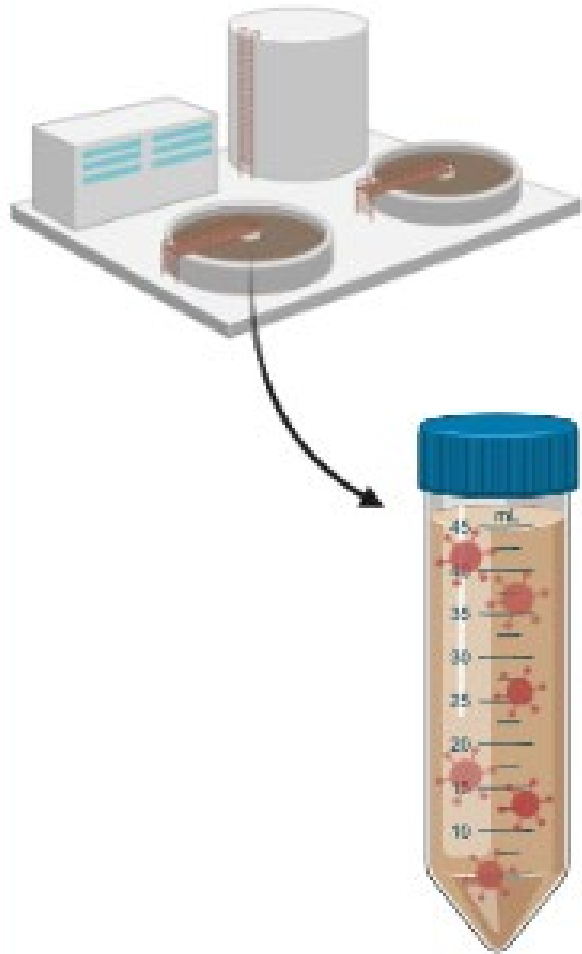
Laboratoire de santé publique du Québec, Institut national de santé publique du Québec

The COVID wastewater surveillance program in Quebec

- ▶ Public-academic partnership, launched in February 2022
 - ▶ INSPQ, MSSS, MELCCFP, CentrEau-Covid, McGill Genome Centre
- ▶ Deployment in 15 cities across Quebec
- ▶ Analyses in 4 laboratories
- ▶ Includes as an objective the monitoring of epidemiological trends of the virus and its variants to support public health interventions

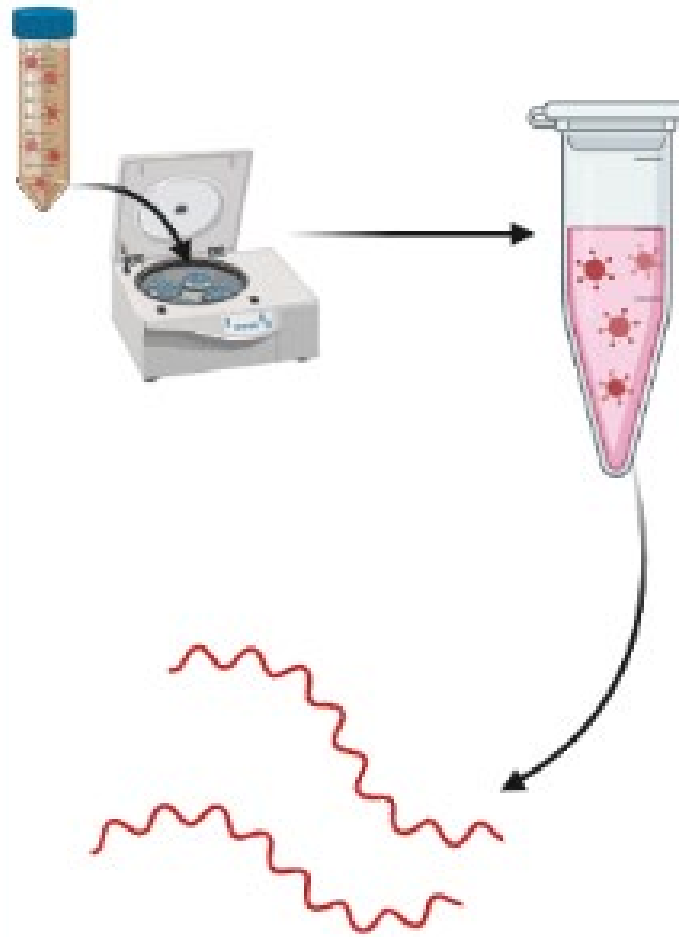
1

Prélèvement aux stations d'épuration



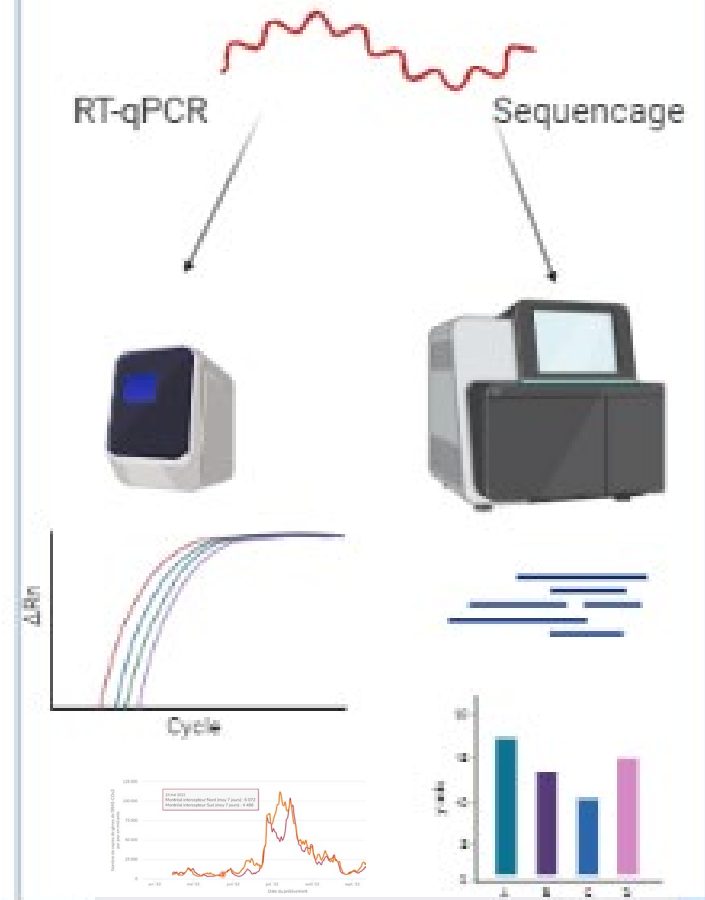
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Filtration des échantillons et extraction de l'ARN




3

Quantification de SARS-CoV-2 et identification des lignées par RT-qPCR et séquençage



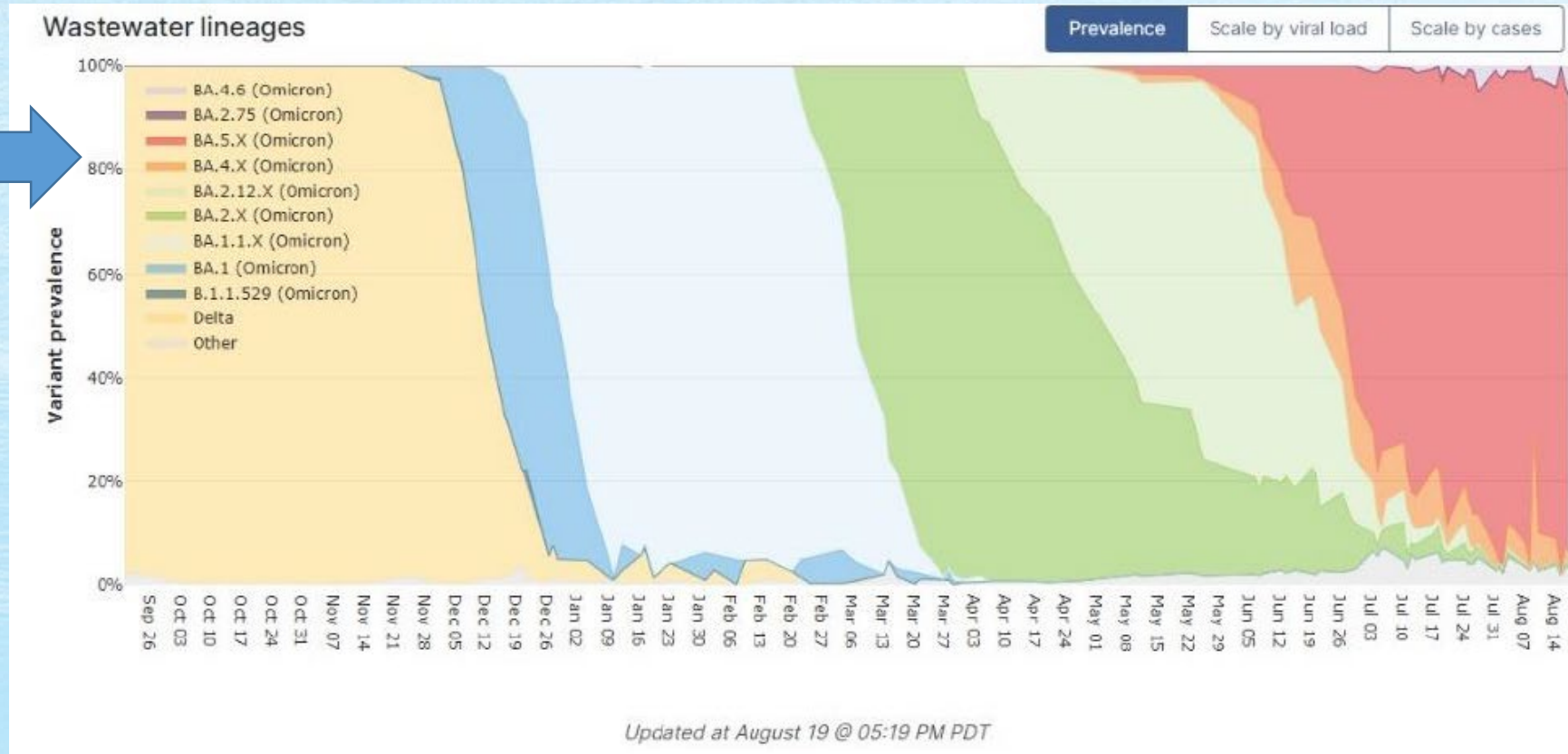
Sequencing of variants in wastewater: what's being done elsewhere



What's being done elsewhere: highlights

- ▶ SARS-CoV-2 monitoring in wastewater in ≥ 70 countries
- ▶ Graphs showing the proportions of variants over time
- ▶ Presentation of data on a weekly basis in most cases
- ▶ Data presented mostly by city, but various levels of aggregation (country, state, city, station) in some cases
- ▶ Most jurisdictions have data on known variants in high proportions or of public health interest
- ▶ Emerging sublineages in small proportions rarely reported
- ▶ Approximately a two-week delay between sampling and data release

The example of San Diego, CA



Lines under surveillance reported

Presentation of data by various indicators

Short duration between sampling and data submission

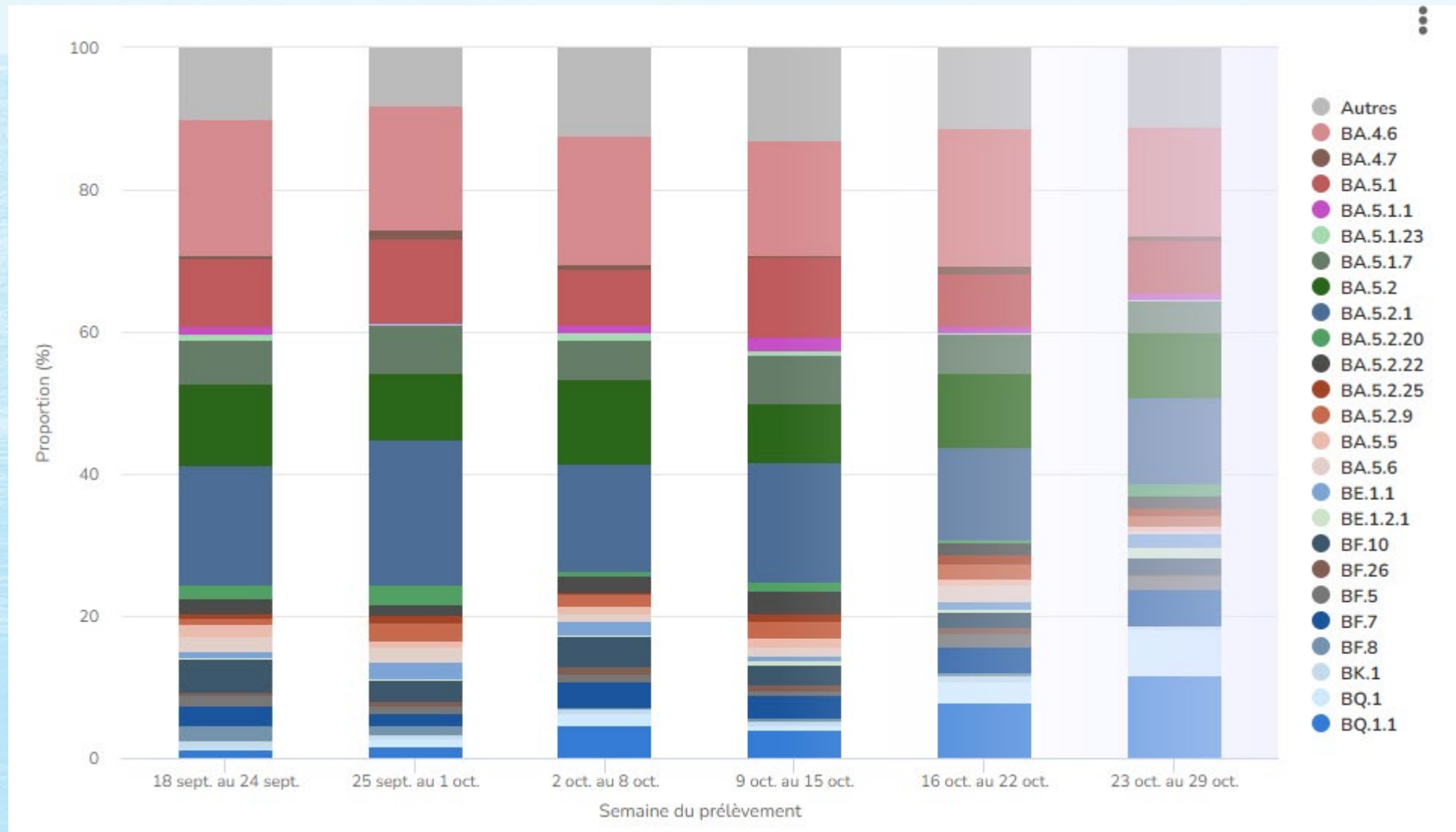
The background features a stylized seascape with a light blue sky, a greenish-blue horizon, and a foreground of overlapping geometric shapes in various shades of blue and teal. A small white sailboat is visible in the lower right, and a large orange triangle is on the right edge.

Sequencing of variants in wastewater: developments in Quebec

Current surveillance of SARS-CoV-2 variants

- ✓ Objective: monitor the evolution of SARS-CoV-2 variants in Quebec and detect the circulation of new variants that could have an impact on the management of the COVID-19 pandemic.
- ✓ Based mainly on representative sequencing of clinical samples (approx. 600–700 sequences/week).
- ✓ Sampling strategy enables detection of the appearance of a lineage with a prevalence of 2.5%, as well as a variation in the prevalence of a lineage from 1% to 3%.
- ✓ Median time between sampling and results: 10 days.

Sequencing data from clinical samples



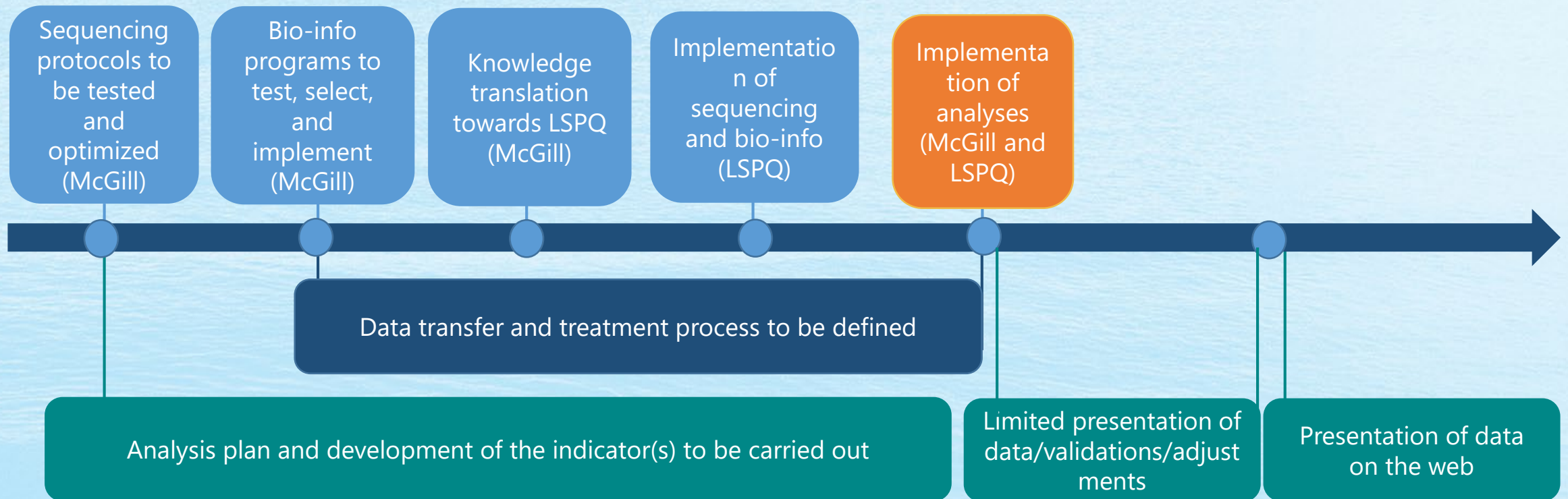
Objectives of variant sequencing in wastewater

- ✓ Wastewater could provide a complementary source of data if clinical samples decrease (representativeness of the population).

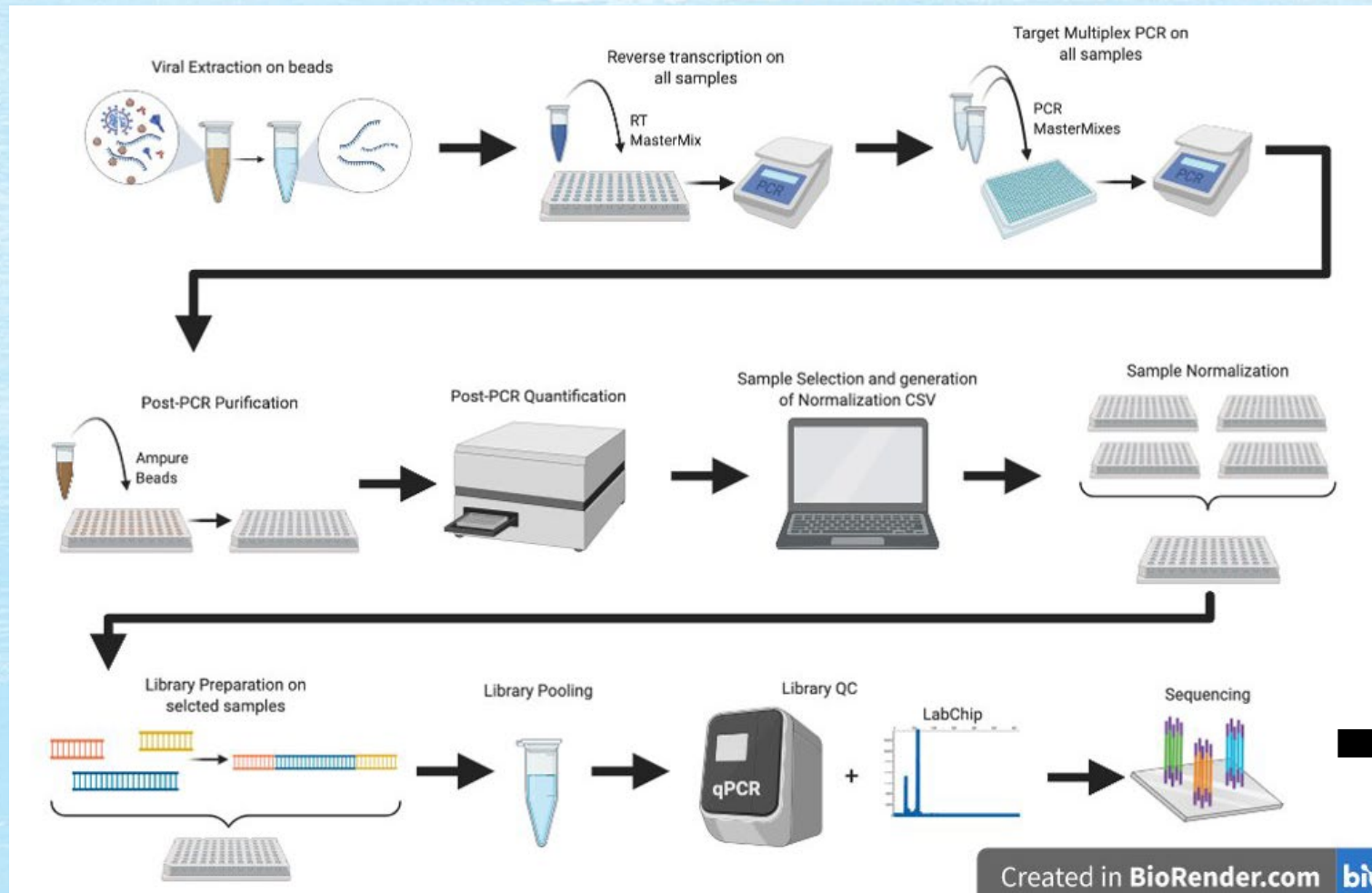
(Preliminary) objectives:

- ✓ Monitor changes in the proportion of major variants circulating in wastewater;
- ✓ Identify emerging lineages;
- ✓ Report the proportion of certain mutations of interest that have a suspected or documented epidemiological or clinical impact (e.g., increased transmissibility or virulence; immune escape or resistance to COVID-19 therapies).

Stages of development in Quebec



Sequencing technique at a glance



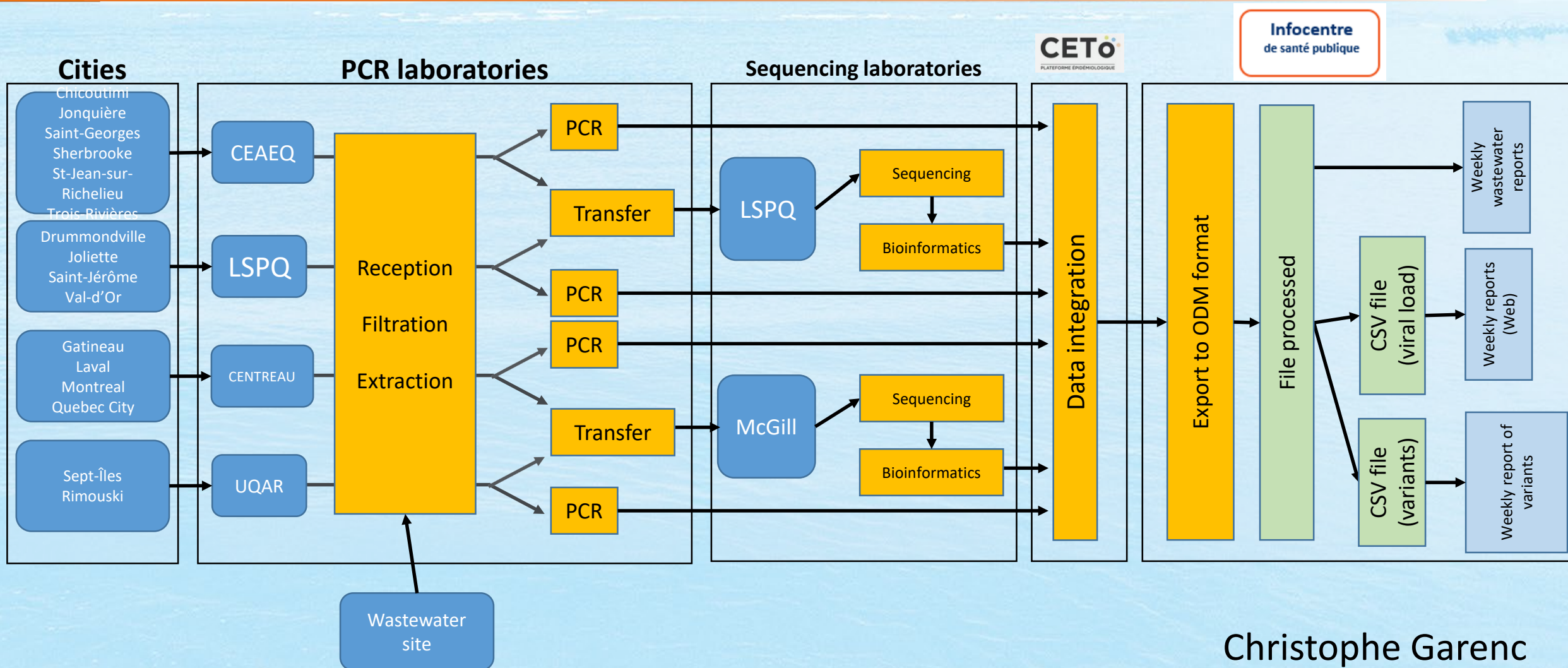
Next generation amplicon-based sequencing (ARTIC V.4.1 primers)

McGILL
GENOME
CENTRE

Bioinformatics analyses
Steven Sutcliffe, PhD

Anne-Marie Roy; Ju-Ling Liu, PhD

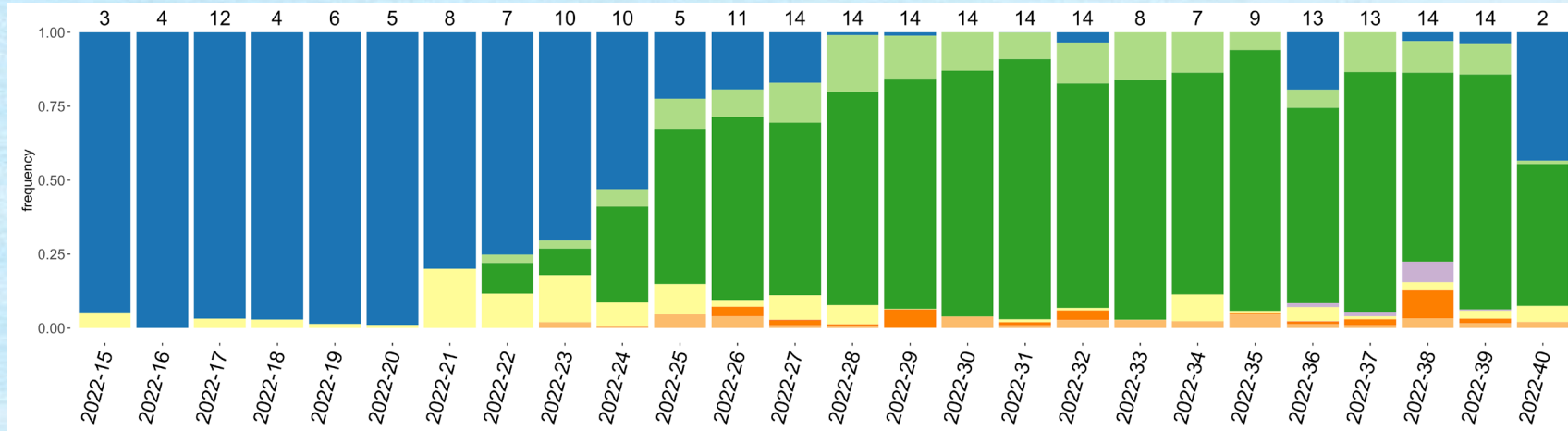
Global mapping of data-related processes



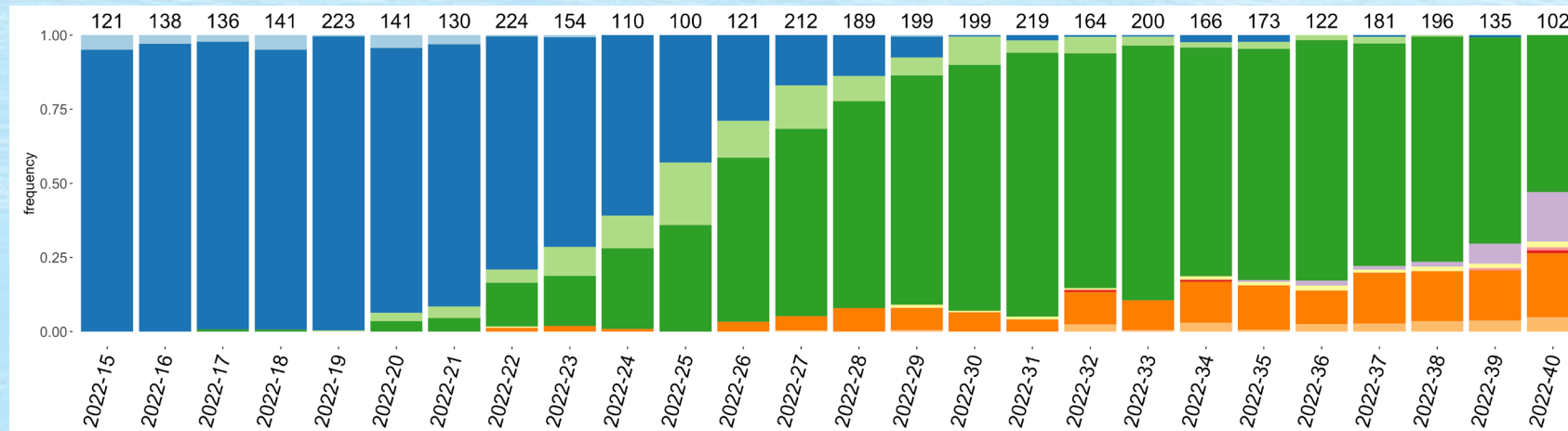
Preliminary results

Montreal:

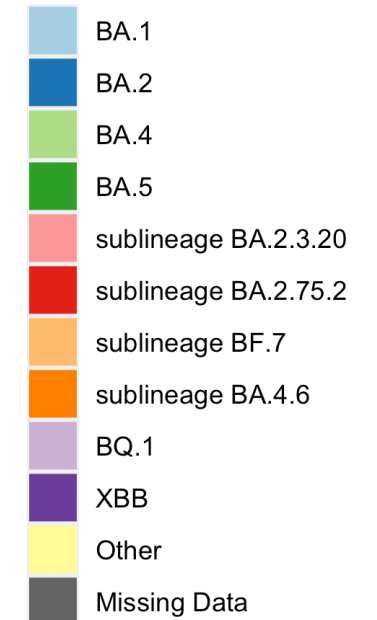
Wastewater



Clinical data



lineage



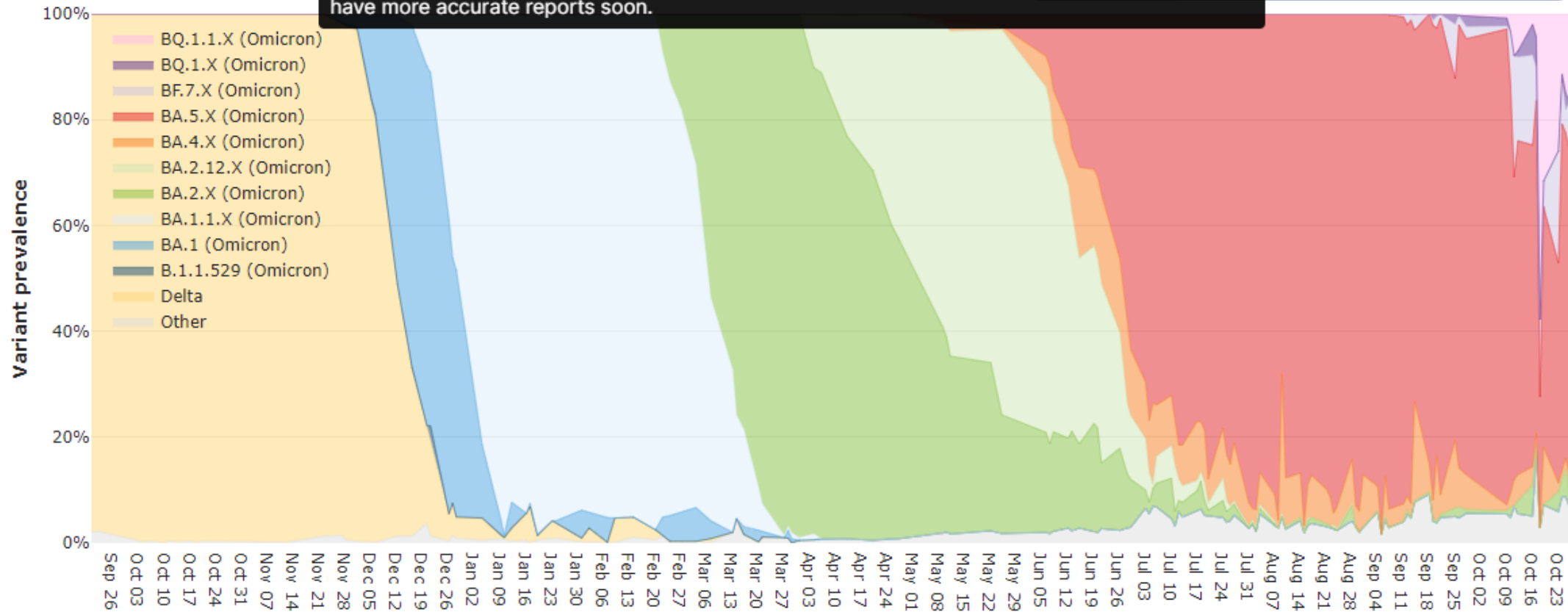
Limitations and ways to optimize

Wastewater lineages

Due to the low viral load at the most recent dates, there is considerable uncertainty in the variant calls shown in the lower graph. We are actively investigating this problem and aim to have more accurate reports soon.

Scale by viral load

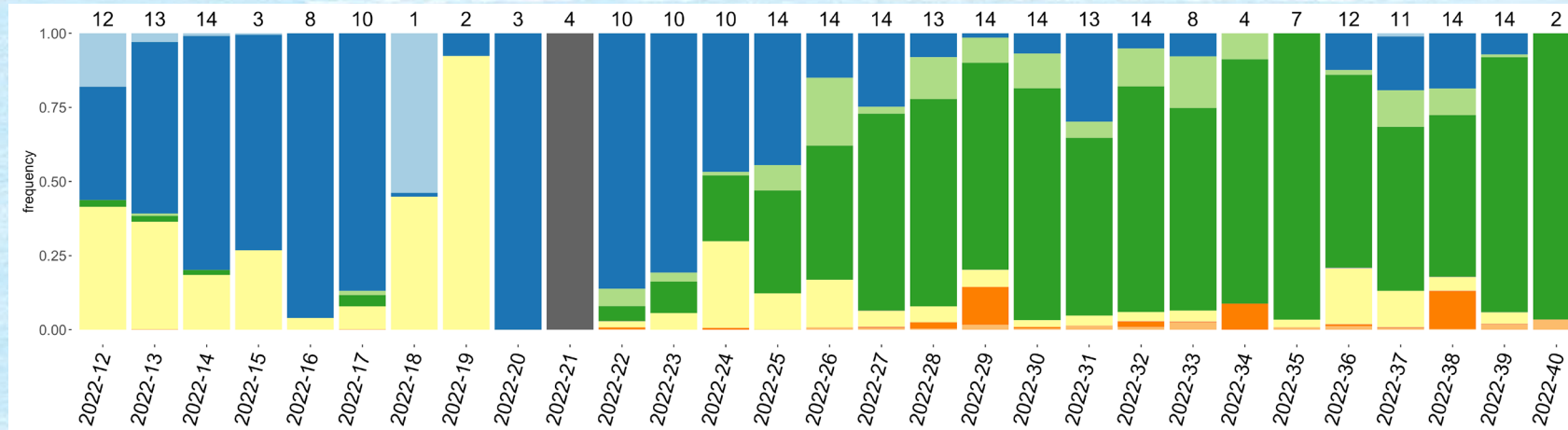
Scale by cases



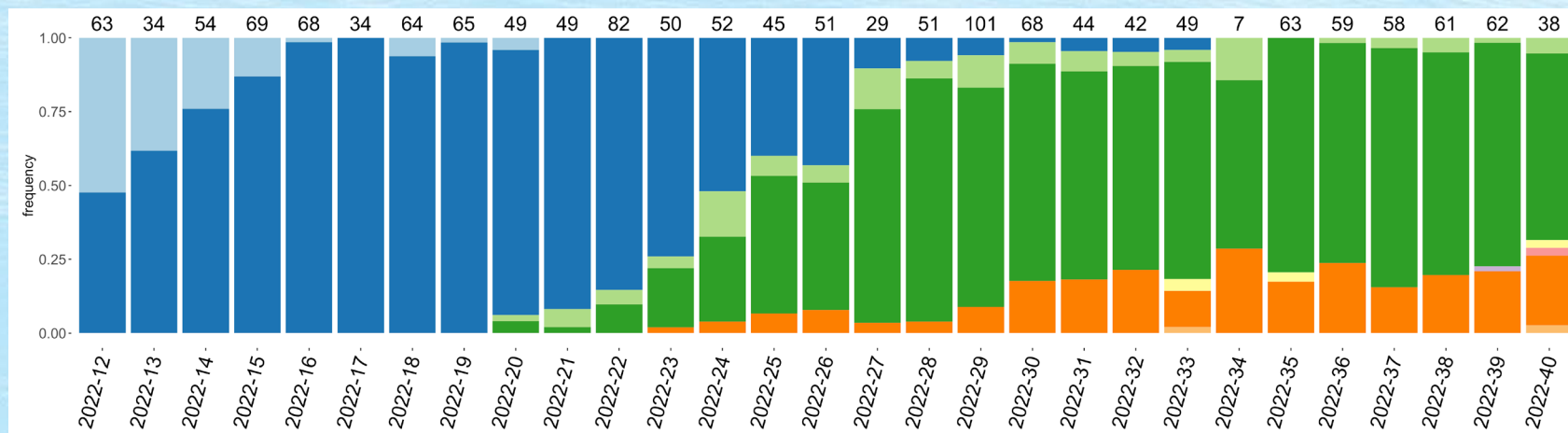
Limitations and ways to optimize

Quebec City:

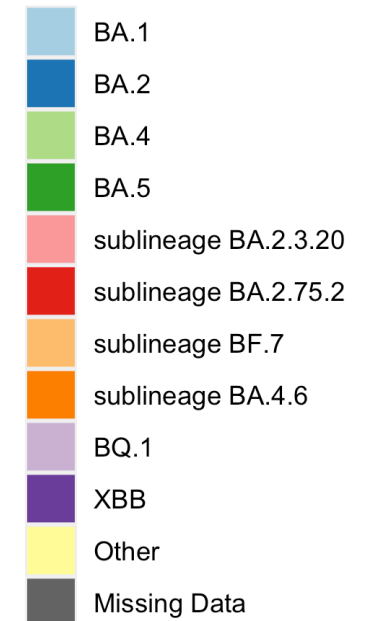
Wastewater



Clinical data

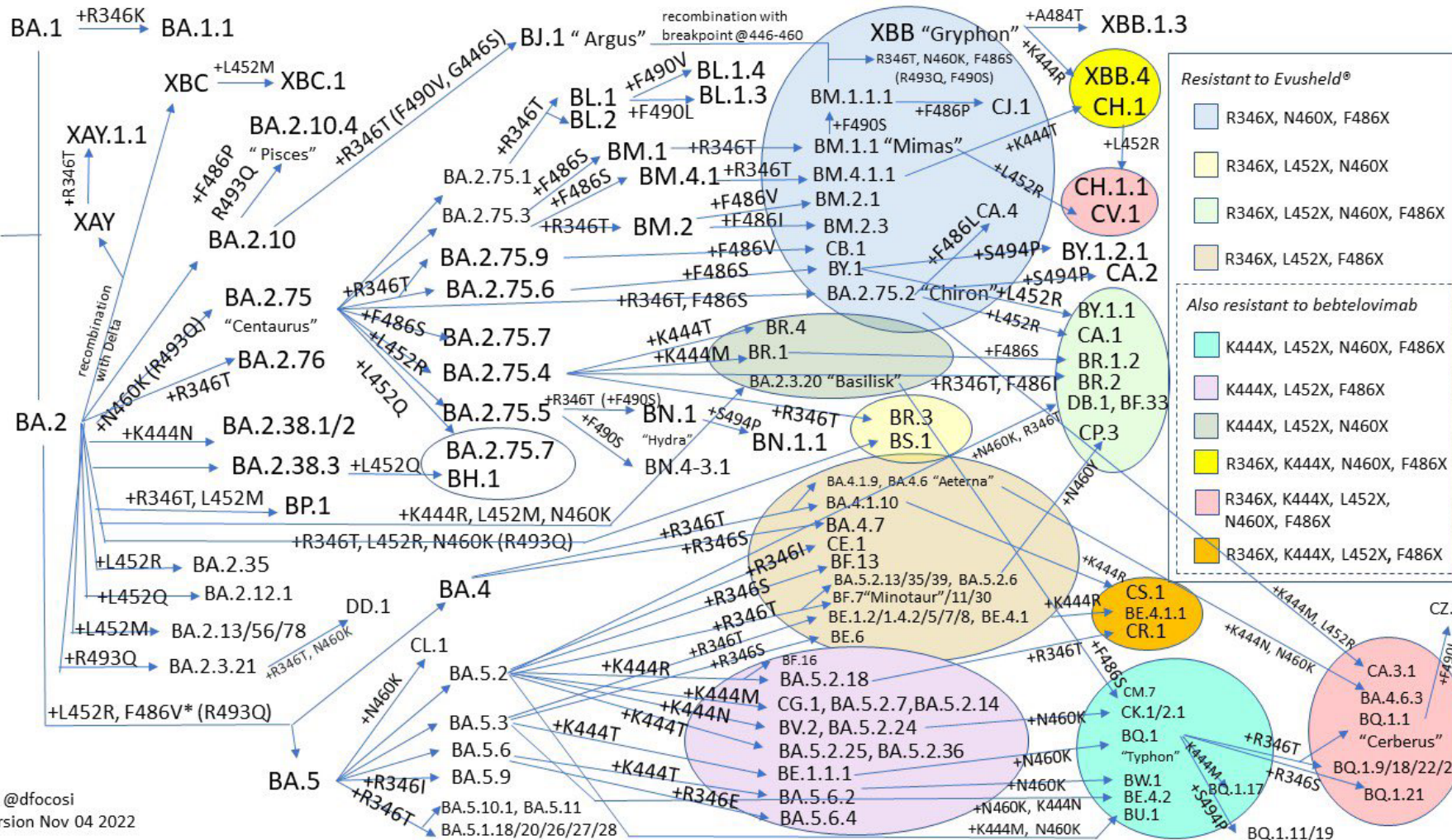


lineage



Steven Sutcliffe, PhD

Limitations and ways to optimize



✓ Evolving convergence: different lineages have the same mutations = difficult to identify in wastewater.

✓ Analysis of the proportion of mutations of interest rather than lineages (under development).

In conclusion

- ✓ Wastewater sequencing will detect and describe SARS-CoV-2 variants in an urban environment.
- ✓ Sequencing of individual clinical samples provides higher quality sequence data (better resolution for lineage identification), but the reliance of monitoring on these samples alone presents a weakness (limited access to PCR tests).
- ✓ Sequencing of SARS-CoV-2 in wastewater should be a complementary tool to sequencing of clinical samples.



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Questions?