Wastewater Sequencing Trend Report: Detection of SARS-CoV-2 Variants of Concern by Metagenomic Sequencing

Public Health Agency of Canada   **Agence de la santé publique du Canada**

Longitudinal wastewater sequencing data ending 2023-09-01.

The plots show the frequency of mutations associated with the SARS-CoV-2 Omicron lineage and its dominant sublineages (BA.5.2, BQ.1, and XBB) detected in wastewater samples collected from different sites using metagenomic sequencing. SARS-CoV-2 viral fragments present in the wastewater are isolated and sequenced to obtain a genomic "blueprint" of the virus. Each sublineage carries small differences in their genomic blueprint called mutations that can be queried using specialized software to identify the presence and abundance of different lineages. These figures show the relative abundance of the omicron sublineages BA.5.2, BQ.1, and XBB detected in each wastewater sample. The shaded areas in the plot show BA.5.2 in red, BQ.1 in green, and XBB in blue.

St. John's

St. John's
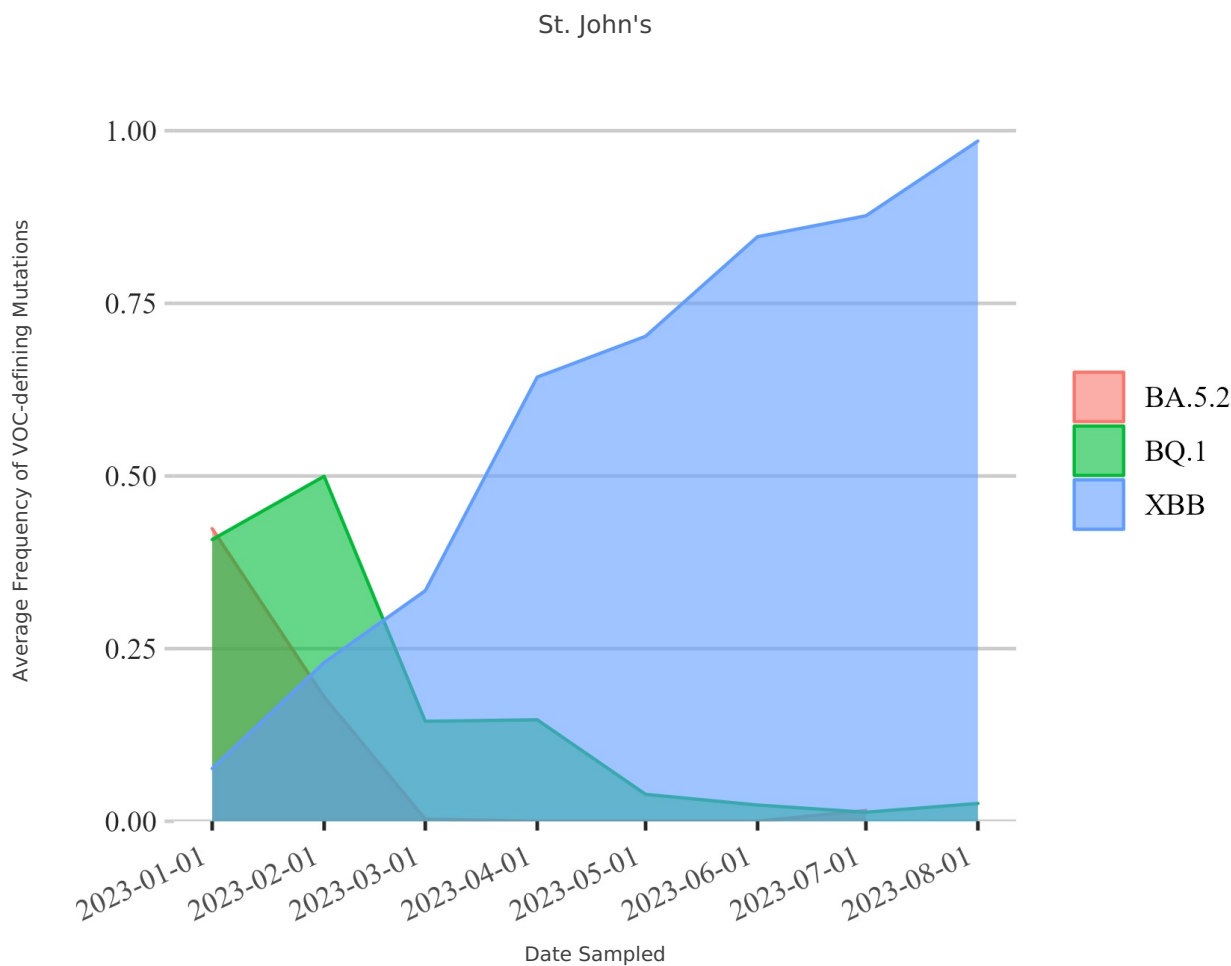
BA.5.2 sublineages were the dominant SARS-CoV-2 variant in summer through to January 2023. The mutations associated with BQ.1 sublineages began to increase in presence in September 2022, and was the dominant variant by the end of January, 2023. The mutations associated with XBB sublineages began to increase in presence at the end of December, 2022 and is now the dominant SARS-CoV-2 variants detected in the wastewater samples collected at this site.