GENOMIC ANALYSIS REPORT
SARS-CoV-2 Surveillance

Report date: 28 January 2025

Summary

- XEC is the dominant lineage in clinical surveillance samples, with approximately 62% of samples tested over the past 2 weeks assigned this lineage.
- KP.3.1.1 is the second highest lineage proportion with approximately 24%.
- XEC and KP.3.1.1 are the dominant lineages across the 5 wastewater collection sites.

(Please see sampling strategies for data caveats)

SARS-CoV-2 Whole Genome Sequencing

Results

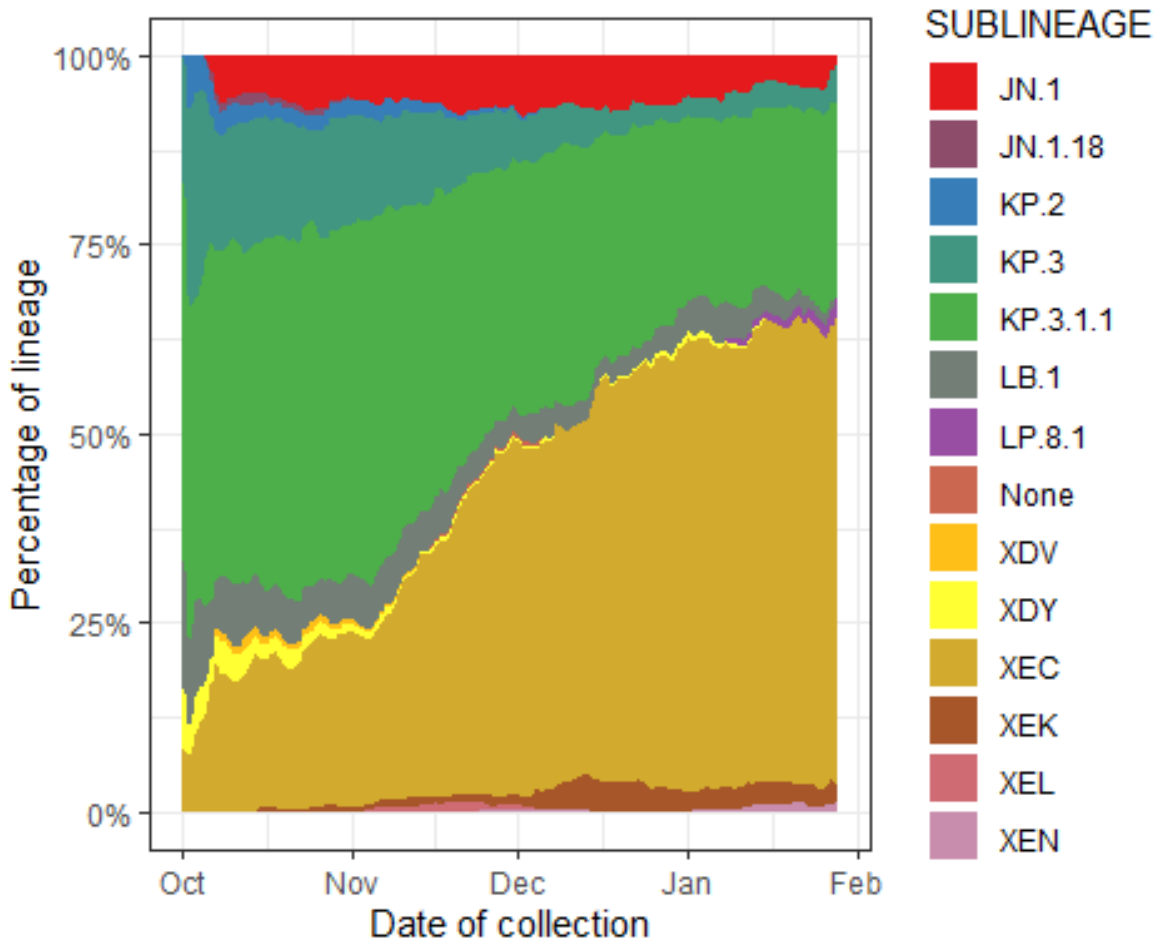

Figure 1: Proportion of Omicron lineages recently sequenced in Queensland for the reporting period [2024-10-01,2025-01-28].
Recent data to be interpreted with caution due to sequencing lag.

Table 1: Proportion of sequences represented by each Hospital and Health Services (HHS) area for the reporting period [2024-10-01,2025-01-28].

Region	Hospital and Health Service (HHS)	Number of sequences for reporting period	Percentage of total sequences for reporting period
Central	Wide Bay	99	7.7%
Central	Central Queensland	47	3.7%
Central	South West	22	1.7%
Central	Central West	4	0.3%
North	Cairns and Hinterland	88	6.9%
North	Townsville	67	5.2%
North	Mackay	64	5.0%
North	Torres and Cape	21	1.6%
North	North West	3	0.2%
South East	Metro South	245	19.1%
South East	Metro North	165	12.9%
South East	Gold Coast	149	11.6%
South East	Darling Downs	116	9.0%
South East	Sunshine Coast	110	8.6%
South East	West Moreton	78	6.1%
Overseas	Overseas	4	0.3%
Interstate	Interstate	1	0.1%

Sampling Strategy:

Community samples are sourced from cases who test positive for SARS-CoV-2 via PCR and may not necessarily reflect the distribution of all cases in Queensland. The current surveillance strategy selects samples based on stratification of recent positive SARS-CoV-2 cases based on risk factors. There is a lag between the date a swab sample is taken from a patient and the date that the results of WGS are reported.

SARS-CoV-2 Wastewater Surveillance

Results

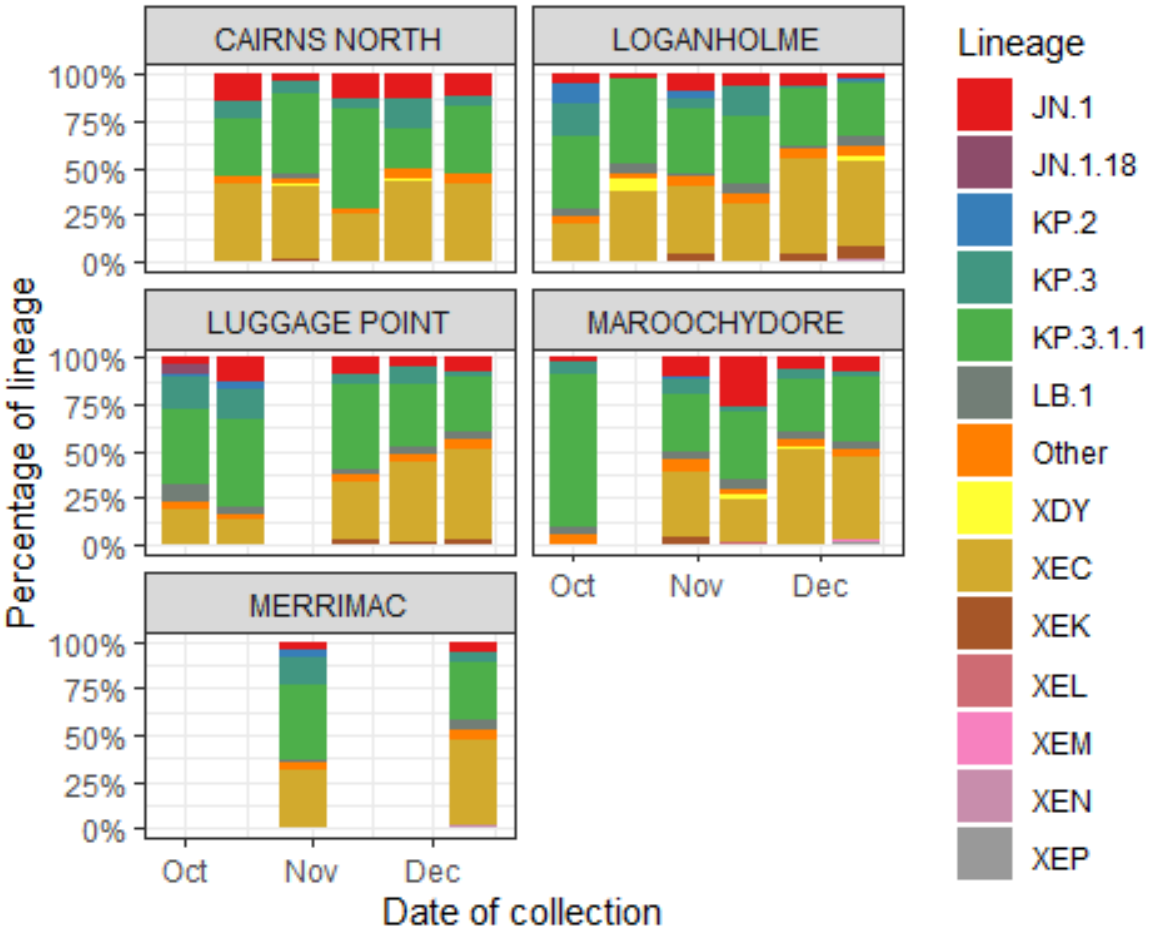

Figure 2: Proportion of lineages in Wastewater samples over time.
Note that there is irregularity in the sampling frequency between sewage treatment plant sites. Please note the methods and analysis has not yet been fully validated and results should be interpreted accordingly. Preliminary validation work has demonstrated that agreement between lineage abundances appear to decrease down the lineage hierarchy, and between lineages that are similar genomically. Note the quality of sequencing data generated from wastewater samples is reduced when compared to that generated from clinical samples due to the nature of the sample type.

Table 2: Description of the waste water surveillance collection sites..

Collection Site	Area Serviced	Residential Population (2021 Census)
Luggage Point	Brisbane CBD and surrounding suburbs, including most areas between Upper Kedron, Nudgee Beach, Port of Brisbane, and Mount Gravatt	580,000
Cairns North	Cairns CBD, as well as most areas between Edge Hill, Holloways Beach, Kamerunga and Redlynch	48,000
Maroochydore	Most areas between Mooloolaba, Sippy Downs, Bli Bli and Marcoola	110,000
Loganholme	Most of the Logan Local Government Area	220,000
Merrimac	Most areas between Broadbeach Waters, Nerang, Reedy Creek and Miami	160,000

Sampling Strategy:

Trends are presented for samples from the Luggage Point, Maroochydore, Merrimac, Cairns North and Loganholme sewage treatment plants. 24hr composite samples are collected fortnightly and are represented on the bar charts above. Gaps in data are due to failure of sample delivery or sample processing.

Table 3: SARS-CoV-2 Variants of Interest (VOIs) & Variants Under monitoring (VUMs) – Nomenclature, genetic features and date or designation.

*Lineage	Lineage heritage	Epidemiology and risk assessment info
JN.1*	Descendant of BA.2.86	This lineage was assigned as a VOI by WHO on 18 December 2023. The earliest sample was collected 25 August 2023 in Europe. It has grown rapidly globally and represents the vast majority of BA.2.86* reported to GISAID as of late December 2023. And it has been reported from 59 countries. Initial risk assessment from WHO on 18 December 2023 has found high risk of growth advantage, moderate risk of antibody escape and low risk of severity of this lineage.
KP.2*	Descendant of JN.1, which is a sublineage of BA.2.86	This lineage was first reported in January 2024 and assigned as a VUM by WHO on 03 May 2024.
KP.3*	Descendant of JN.1, which is a sublineage of BA.2.86	This lineage was first reported in February 2024 and assigned as a VUM by WHO on 03 May 2024.
JN.1.18*	Descendant of JN.1, which is a sublineage of BA.2.86	This lineage was first reported in November 2023 and assigned as a VUM by WHO on 03 May 2024.
LB.1*	Descendant of JN.1, which is a sublineage of BA.2.86	This lineage was first reported in February 2024 and assigned as a VUM by WHO on 28 June 2024.
KP.3.1.1*	Descendant of KP.3, which is a descendant of JN.1, which is a sublineage of BA.2.86	This lineage was first reported in January 2024 and assigned as a VUM by WHO on 19 July 2024.
XEC*	Recombinant lineage of KS.1.1 (JN.1.13.1.1.1) and KP.3.3 (breakpoint 21738-22599)	This lineage was first reported in May 2024 and assigned as a VUM by WHO on 24 September 2024. The initial risk evaluation on 9 December 2024 by WHO has found low level of risk in antibody escape and low level of risk in severity and clinical considerations, despite high level of risk in growth advantage of this lineage.
LP.8.1*	Descendant of JN.1, which is a sublineage of BA.2.86.	This lineage was first reported in July 2024 and assigned as a VUM by WHO on 24 January 2025.

*Includes descendant lineages, except those individually specified elsewhere in the table.
SARS-CoV-2 lineages are reported based on the variants of concern and variants under monitoring list https://www.who.int/activities/tracking-SARS-CoV-2-variants and may be present in the surveillance and wastewater samples before they are reported. This is done to ensure consistency in reporting and manage the large number of sublineages.

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