

CORONASTEP Airport Report 02 (2023 - Weeks 02 to 07) SARS-CoV-2 Airport Sewage Surveillance in Luxembourg

Summary

The latest EU recommendations (https://health-security-committee-common-eu-approach-response-covid-19-situation-china-2023-01-05_en) state that EU/EEA countries should consider introducing or strengthening wastewater monitoring, especially in waters originating from airports with international flights and/or aircraft after long-haul flights, with a particular focus on passenger flights from China. However, the variants currently circulating in China are already circulating within the EU/EEA and no new variants have been detected so far.

Following these recommendations and at the request of the Health Directorate, LIST added an additional wastewater sampling point in the airport area.

In order to maximise the geographical coverage and the number of people captured, we have, in collaboration with SIDEST, defined a collection point in the sewage system of the airport area. This point captures both the wastewater from the aircrafts and that from the airport itself (option 3 in the EU guidelines 1).

In a similar way to what is done for the wastewater treatment plant monitoring network, sampling is carried out once a week over a 24-hour period, before being reported to LIST for analysis.

As requested in the EU guidelines¹, the following analyses are performed:

- Generic detection of SARS-CoV-2 by RT-qPCR (E gene)
- Search for specific mutations by RT-ddPCR
- High throughput sequencing to determine circulating variants and mutations. Sequencing is performed at LNS and bioinformatic analysis at LIST

Overall, the first results obtained confirm that so far, no new SARS-CoV-2 variants (or mutations) have been detected, but that all those currently circulating have been identified. This conclusion is based on the RT-ddPCR only. Indeed, the last sequencing results were unfortunately not meaningful at all, due to too low reads available. The main reason for this is certainly the lower amount of SARS-CoV-2 RNA detected in the latest analysed samples (see Table 1). It is also interesting to note that the detection levels observed in RT-ddPCR are also very weak.

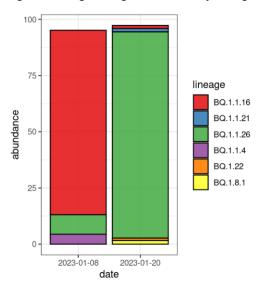
¹ European Commission. Adhoc guidance: Wastewater sampling of aircrafts and airports for SARS-CoV-2 surveillance. 10 January 2023. European Commission Brussels 2023.



Table 1: SARS-CoV-2 concentration (RT-qPCR) and mutations detected (RT-ddPCR) in the airport sewage samples.

Sampling date	SARS-CoV-2 concentration	Mutations detected by RT-ddPCR	Variants of concern carrying the mutation
08 January 2023	3.7 x 10 ⁴ genome copies / L	L452R	Omicron BA.4, BA.5, BQ.1
		LLPA24S	Omicron BA.2, BA.4, BA.5, BA.2.12.1, BA.2.75, BQ.1, XBB
		K417N	Omicron BA.1, BA.2, BA.4, BA.5, BA.2.12.1, BA.2.75, BQ.1, XBB
		R346T	Omicron XBB, BQ.1
19 January 2023	1.1 x 10 ⁴ genome copies / L	L452R	Omicron BA.4, BA.5, BQ.1
		LLPA24S	Omicron BA.2, BA.4, BA.5, BA.2.12.1, BA.2.75, BQ.1, XBB
		K417N	Omicron BA.1, BA.2, BA.4, BA.5, BA.2.12.1, BA.2.75, BQ.1, XBB
25 January 2023	2.0 x 10 ⁴ genome copies / L	L452R	Omicron BA.4, BA.5, BQ.1
		LLPA24S	Omicron BA.2, BA.4, BA.5, BA.2.12.1, BA.2.75, BQ.1, XBB
		K417N	Omicron BA.1, BA.2, BA.4, BA.5, BA.2.12.1, BA.2.75, BQ.1, XBB
		R346T	Omicron XBB, BQ.1
31 January 2023	4.3 x 10 ⁴ genome copies / L	L452R	Omicron BA.4, BA.5, BQ.1
		LLPA24S	Omicron BA.2, BA.4, BA.5, BA.2.12.1, BA.2.75, BQ.1, XBB
		K417N	Omicron BA.1, BA.2, BA.4, BA.5, BA.2.12.1, BA.2.75, BQ.1, XBB
		R346T	Omicron XBB, BQ.1
06 February 2023	6.0 x 10 ³ genome copies / L	L452R	Omicron BA.4, BA.5, BQ.1
		LLPA24S	Omicron BA.2, BA.4, BA.5, BA.2.12.1, BA.2.75, BQ.1, XBB
		K417N	Omicron BA.1, BA.2, BA.4, BA.5, BA.2.12.1, BA.2.75, BQ.1, XBB
		R346T	Omicron XBB, BQ.1
12 February 2023	7.6 x 10 ³ genome copies / L	L452R	Omicron BA.4, BA.5, BQ.1
		LLPA24S	Omicron BA.2, BA.4, BA.5, BA.2.12.1, BA.2.75, BQ.1, XBB
		K417N	Omicron BA.1, BA.2, BA.4, BA.5, BA.2.12.1, BA.2.75, BQ.1, XBB
		R346T	Omicron XBB, BQ.1

Figure 1: Pango lineages identified* by next generation sequencing in the airport sewage samples.



^{*}Please note that the quality of sequencing is not very good (not enough depth), which can lead to a lot of variance and uncertainty on the presented results.