Genomic surveillance of SARS-CoV-2 in Belgium

Report of the National Reference Laboratory (UZ Leuven & KU Leuven)

Situation update – 23 of November 2021
(report 2021_55)

Executive summary

64,647 Belgian sequences of SARS-CoV-2 are now publicly available on GISAID; compared to last week's report, 939 sequences have been added.

773 sequences of positive SARS-CoV-2 samples collected between 08/11/2021 and 21/11/2021 have at this stage been analysed in the context of baseline surveillance. Among these, B.1.617.2 (*Delta*) and its sublineages represented 100% of the circulating strains. AY.43 currently represents 40% of the circulating strains, remaining at a stable level compared to the past weeks.

The genomic diversity of SARS-CoV-2 in Belgium is comparable with the situation described over the last 16 weeks.

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With the collaboration of the laboratories of UCL, ULB, UMons, UNamur, ULiège, UGent, UZA/UAntwerpen, Jessa ZH, AZ Delta, AZ Klina, IPG, AZ St Lucas Gent, OLVZ Aalst, Briant network, ZNA, AZ St Jan Brugge, UZ Brussel, LHUB-ULB, and UZ Leuven/KU Leuven; and Sciensano HealthData.

Previous reports can be downloaded using the following link:
https://www.uzleuven.be/nl/laboratoriumgeneeskunde/genomic-surveillance-sars-cov-2-belgium

Table of contents

1. Monitoring of VOCs in Belgium

While first identified on 6 April 2021 in Belgium, the B.1.617.2 Variant of Concern (Delta) is now the dominant lineage in the country, representing 99.9% of the baseline surveillance samples sequenced (see Figure 1). One isolated Alpha infection was reported on 9 November 2021.

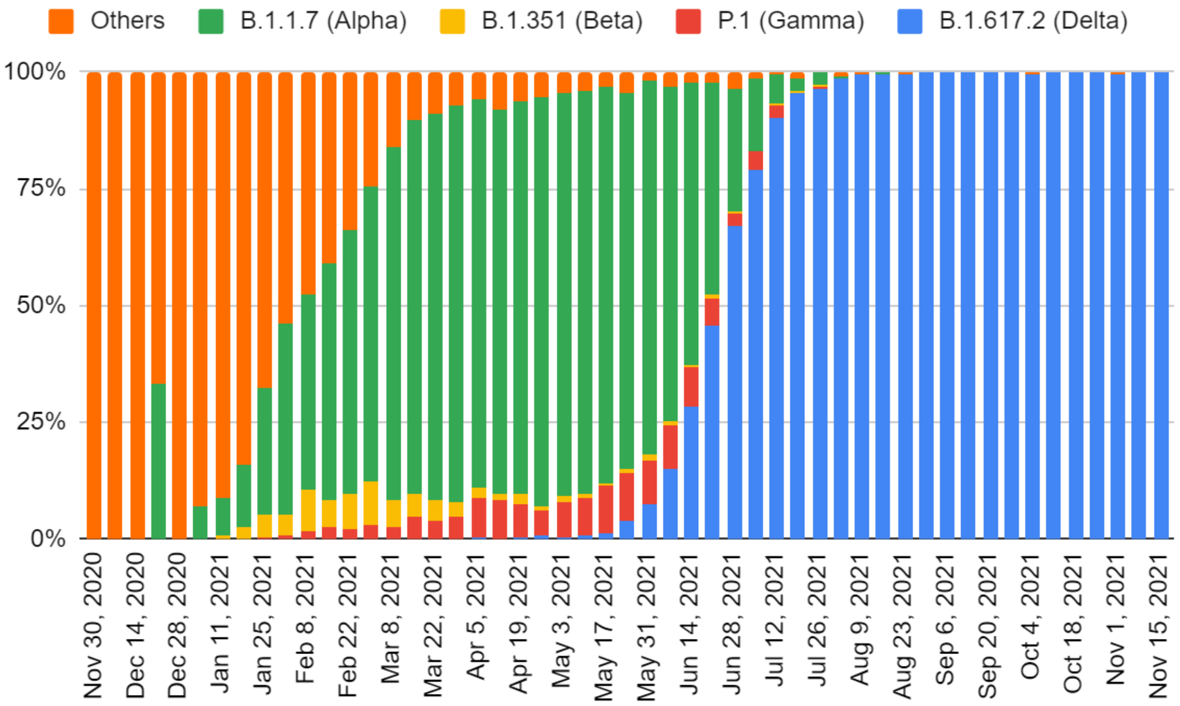

Figure 1: *Weekly evolution of the frequency of variants of concern reported by the baseline surveillance network using a whole genome sequencing (WGS) approach.*

The main dates related to the introduction and evolution of variants of concern identified in Belgium are listed below.

Alpha:	1st detected	30 Nov 2020
	50%	week of 7/2/2021
	Peak (87%)	week of 26/4/2021
	Last detected	week of 27/9/2021
	Total sequenced: 21,206	
Beta:	1st detected	20 Dec 2020
	Peak (9%)	week of 1/03/2021
	Last detected	week of 26/7/2021
	Total sequenced: 1,131	
Gamma:	1st detected	week of 25/11/2021
	Peak (10%)	week of 17/05/2021
	Last detected	week of 9/8/2021
	Total sequenced: 2,037	
Delta:	1st detected	6 Apr 2021
	50%	week of 28/6/2021
	>95%	Since week of 19/7/2021
	Total sequenced: 31,165	

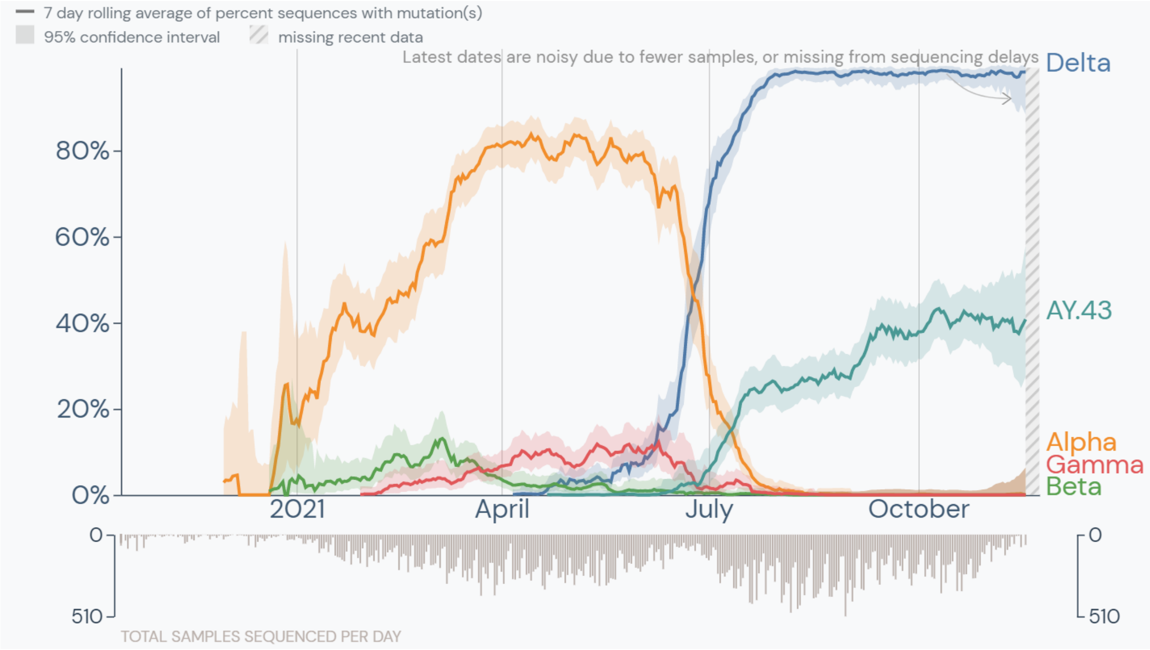

Figure 2: *Evolution of the proportion of Variants of Concern and AY.43 (sublineage of Delta) in Belgium during the past year.*

2. Post-vaccination outbreaks in highly vaccinated nursing homes

The National Reference Center has investigated the virological and immunological characteristics of three nursing homes which have experienced SARS-CoV-2 outbreaks with high attack rates and mortality despite a relatively complete vaccination coverage among residents and staff. The results of this study will shortly be sent for peer-review. We list the main findings below.

2.1. Virological investigation

From a virological point of view, these three outbreaks were caused by single introductions of three different variants (Gamma, Delta and Mu). The virus was detected in the environment (collective rooms used by residents or staff) during several weeks after the start of the outbreak.

These observations underline the importance of maintaining systematic prevention measures, including increased ventilation.

2.2. Predictors of fatal disease

Our analysis highlighted that, among infected residents, those with the highest level of active intracellular viral replication had a higher chance of fatal outcome.

These findings support the potential utility of antiviral treatments for fragile populations, as a complement to vaccination for preventing severe evolution after exposition to the virus.