

Genomic surveillance of SARS-CoV-2 in Belgium

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

**Situation update – 30 of November 2021
(report 2021_57)**

Executive summary

66,978 Belgian sequences of SARS-CoV-2 are now publicly available on GISAID; compared to last week's report, 2,331 sequences have been added.

1,243 sequences of positive SARS-CoV-2 samples collected between 15/11/2021 and 28/11/2021 have at this stage been analysed in the context of baseline surveillance. Among these, B.1.617.2 (*Delta*) and its sublineages represented 99,9% of the circulating strains. Omicron (B.1.1.259) has been identified for the first time in Belgium during the last week, in one single patient / infection. In addition, one additional infection with an S gene dropout has been detected among the household members of the first patient and one non-linked patient was confirmed by sequencing. Several suspect cases, spread across all regions of the country, are currently being evaluated.

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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>

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1. Monitoring of VOCs in Belgium

While first identified on 6 April 2021 in Belgium, the B.1.617.2 Variant of Concern (Delta) remains the dominant lineage in the country, representing 99.9% of the baseline surveillance samples sequenced (see Figure 1). One Omicron infection was reported from a sample from a returning traveller (Egypt; return travel on November 11th) who developed symptoms on the 22nd of November 2021.

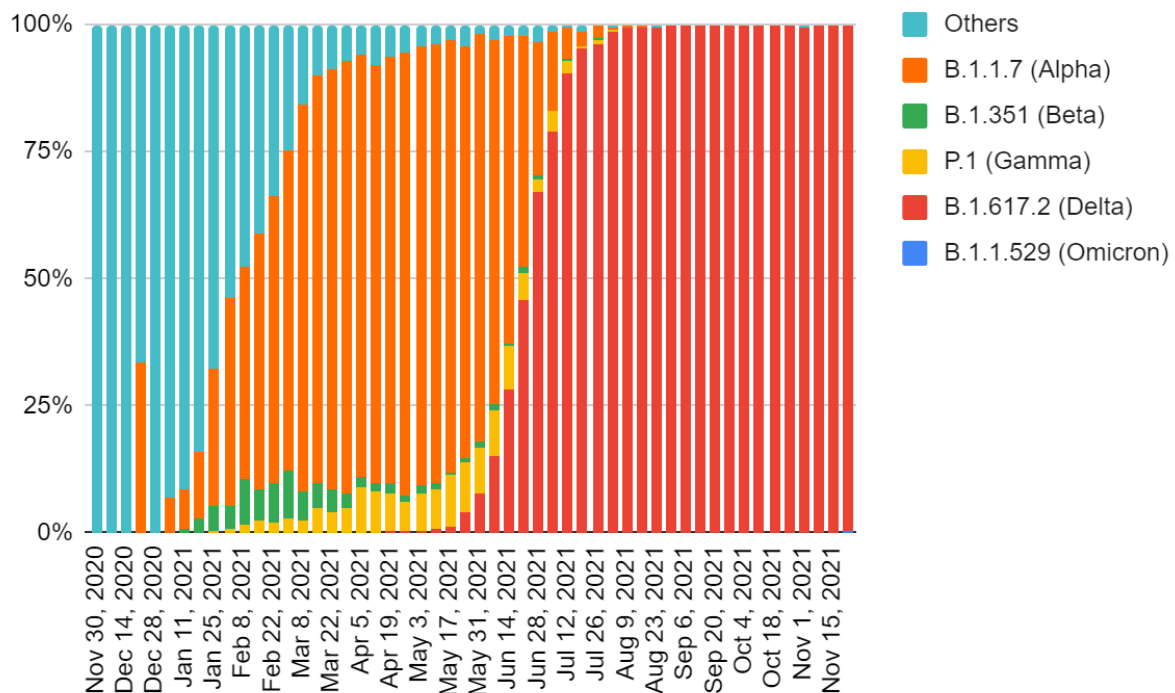


Figure 1: Weekly evolution of the frequency of variants of concern reported by the baseline surveillance network using a whole genome sequencing (WGS) approach.

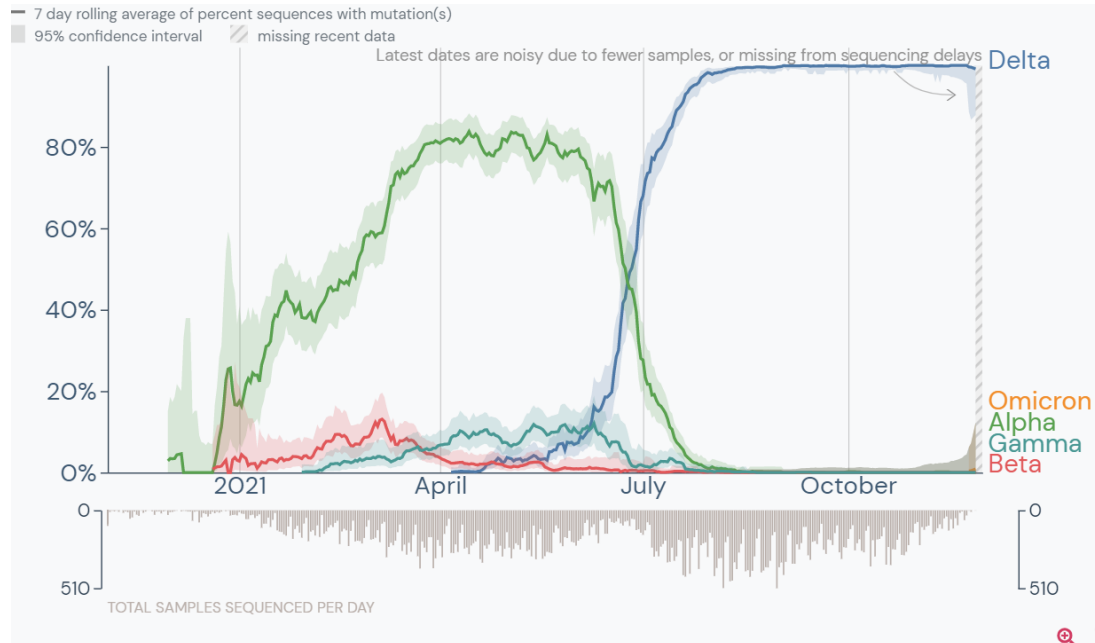


Figure 2: Evolution of the proportion of Variants of Concern in Belgium during the past year.

2. Current status with regard to Omicron in South Africa

The data originating from South Africa are still limited at this stage, and it remains therefore difficult to have a clear assessment with regard to the virulence of this new variant of concern, its immune escape and its transmissibility. The evaluation hereunder is therefore a preliminary assessment that will need to be revised as more information and research become available.

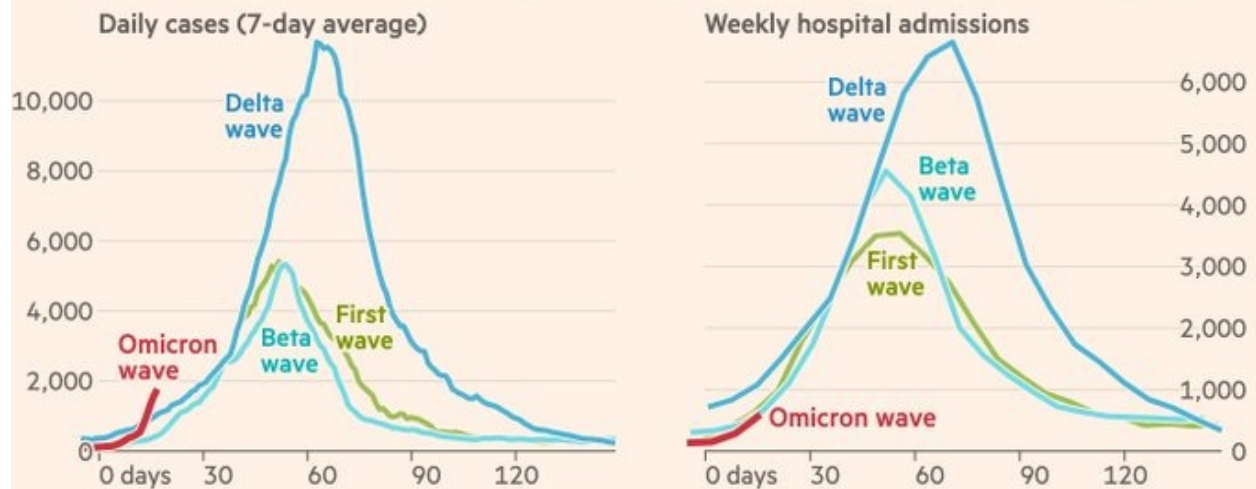
2.1. Virulence

While initial reports have mentioned limited observations with regard to the virulence of this new variant, it also appears that these initial observations did not include sufficient patients representing the different age categories.

The Financial Times has published preliminary hospitalisation data from the Gauteng province (Figure 3) and has compared these numbers with the previous waves. These data tend to show an increase of hospitalized patients following a rapid increase of infections. From these observations, it also appears that the number of Omicron infections have increased more rapidly than during the previous waves. The fact that the ratio between the number of hospitalizations against the number of documented infections seems to be lower compared to the previous waves may be due to decreased virulence, recent acceleration of vaccination campaigns, or due a more intense testing capacity compared to the previous waves. The combination of these hypotheses may also explain these early observations.

Covid cases are rising faster in South Africa's Gauteng province than during previous waves, and hospital admissions are on pace with past climbs

Cases and hospital admissions in Gauteng province, by number of days since each wave began



Source: FT analysis of data from South Africa's National Institute for Communicable Diseases
FT graphic by John Burn-Murdoch / @jburnmurdoch
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Figure 3: COVID cases and hospital admissions in the Gauteng Province of South Africa (Source: Financial Times).

2.2. Immune escape

The numerous mutations in the Spike gene which characterize the Omicron variant will inevitably lead to a certain level of immune escape. This phenomenon is intuitively illustrated by the rapid spread of this variant in the South African population, which has been intensively exposed during the three previous waves. The impact of this new variant on vaccine efficacy has yet to be fully measured, and these estimations will require three levels of assessment. For the moment, results of preliminary investigations are, e.g., only available for modelling work such as the analyses performed by the research team of Jesse Bloom (Fred Hutchinson Cancer Research Center, USA; see the report 2021_56 of last week).

a. Antibody neutralization tests

Antibody neutralization tests have to be conducted to assess to what extent this new variant is able to escape vaccine-induced immunity and immunity acquired through a previous infection. Those tests consist of confronting the cultured variant to sera of antibodies of convalescent or vaccinated people.

The virus could not yet be cultured in any of the European countries, but it should be a matter of days before these experiments can start. The results of those tests are not expected to be available for at least another 2 weeks.

b. Animal models

The National Reference Laboratory will investigate the possibility to evaluate the cross protection developed through vaccination and previous infections on validated animal models (hamsters). These studies should provide more observations within two months.

c. Real-life observations

The most reliable source of information will originate from observations of the different countries. The quality of the data shared by other countries will be crucial to estimate the potential impact of this variant on European countries. African countries will probably be the first experiencing a rise of Omicron infections. Unfortunately, the low vaccination coverage on the African continent and its limited laboratory capacities will make these first estimations less transferrable to western European countries, and will inevitably generate a delay in our ability to precisely estimate the risk associated with this variant in highly vaccinated countries.

2.3. Transmissibility

The apparent rapid increase in the detection frequency of Omicron in the first impacted regions in South Africa could be the result of a potentially significant transmission advantage of Omicron compared to Delta, a transmission advantage that can be the result of an enhanced immune escape and/or an enhanced intrinsically transmissibility (its capacity to spread within a population). Disentangling the relative impact of those two different aspects will require modelling analyses as well as the outcomes of the neutralization tests mentioned above. It is indeed crucial to estimate to what extent the transmission advantage of Omicron, if confirmed, is mainly due or not to its capacity to evade immunity.

3. Update on the detection of Omicron around the World

Since last Thursday, many countries around the world have now reported Omicron cases. Because of (i) heterogeneous genomic surveillance capacities and (ii) the time needed to confirm the nature of the variant through a sequencing process, it is highly likely that Omicron is already present, and potentially circulating locally, in several other countries.

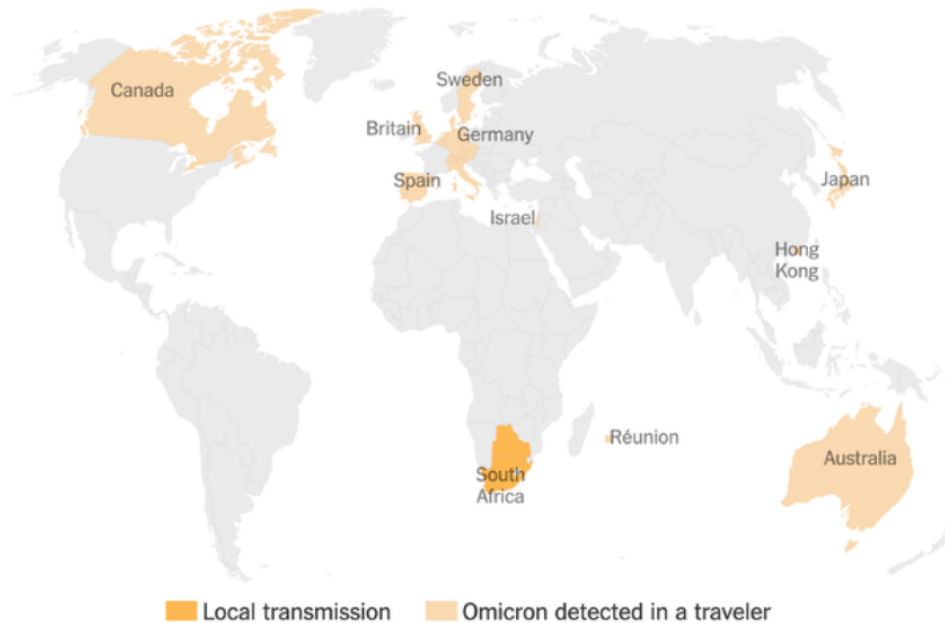


Figure 4: countries having reported Omicron case(s) on the 30/11/21 (detected in returning traveller or local transmission in the case of South Africa; source: NY Times). N.B.: while not reported on this map, Brazil has now also reported two cases.

4. Current status with regard to Omicron in Belgium

Although the first Belgian Omicron infection was documented from a traveller returning from Egypt (via Turkey), the relatively long delay between the travel and the onset of symptoms (10 days), and the current absence of documented Omicron cases in Egypt or Turkey raise a number of uncertainties. From a phylogenetic point of view, there is insufficient information at this point to clearly determine the origin of the Belgian Omicron case. Based on a phylogenetic analysis on November 29th (see Figure X), it seems that the Belgian case does not cluster with any other known European cases (1 from Italy, 1 from Austria, and 2 from England). If more data would become available, in the form of Omicron genomes from Egypt and Belgium for example, we may be able to perform a more accurate analysis. A follow-up analysis will be performed with additional European genomes (and an otherwise also updated data set).

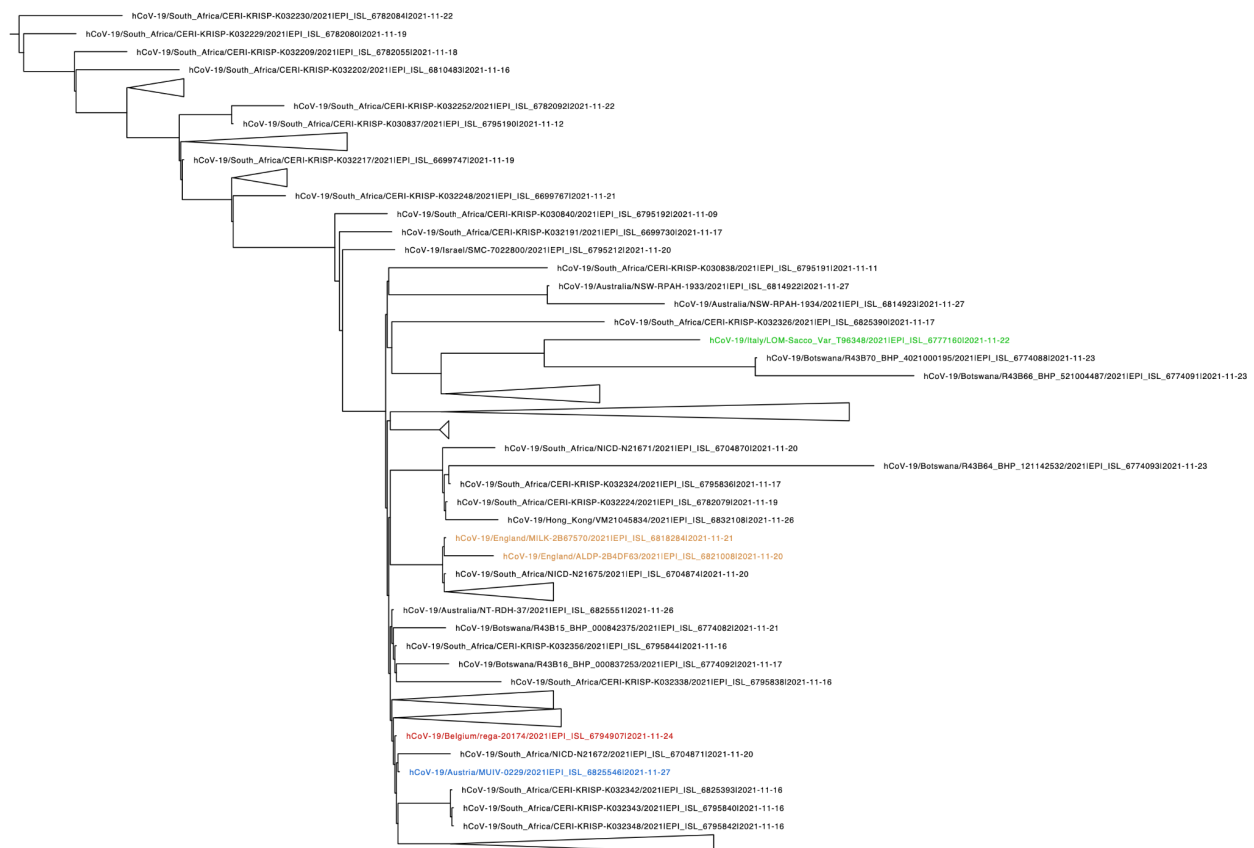


Figure 5. With the limited available data on November 29th, phylogenetic reconstructions would point to the European cases being imported cases from South Africa via international travel. More data from both African and European countries are needed to perform a more accurate analysis.

At the time of writing this report, we could not collect all epidemiological and travel information related to the second Omicron patient confirmed by sequencing. More information will be provided in the next report.