

Technical Briefing

05.02.2021

Following recent articles published by German online newspapers relating to a so called “Norwegian-Luxembourgish” SARS-CoV-2 variant, B.1.1.6, the LNS would like to clarify the confusion created concerning these reports.

The SARS-CoV-2 virus is an RNA virus, which is known to evolve and mutate at a high rate, hence it would be easy to characterize and differentiate the geographical spread over time. In the ongoing and rapidly changing epidemic a nomenclature system can facilitate real-time epidemiology by providing commonly agreed labels to refer to viruses circulating in different parts of the world, thereby revealing the links between outbreaks that share similar virus genomes.

The group of genetically closely related variants is called lineage, which is designated a letter (A, B, or others) followed by a number and any evolution of this parent lineage is added with another number (e.g. B.1.1.7), this is mainly to facilitate geographical tracing. The lineages are called after the country or the region that it first emerged (e.g. South African variant or B.1.135)

All diagnostic laboratories around the globe submit their sequences via a tool (Pangolin; Phylogenetic Assignment of Named Global Outbreak LINeages) in order to assign lineages to query sequences as described in Rambaut et al 2020 (<https://cov-lineages.org/lineages.html>)

Unfortunately due to the similarities in this numbering system the reporting of B.1.1.6 was an error during editing the article as this sequence has no reported sequence in the international database although is claimed to be of US origin. After consultation with German health authorities, it was confirmed that there was a reporting error in the numbering and that B.1.1.6 should instead be B.1.160.

B.1.160 is a large European lineage representing an EU/EEA and UK multi-country cluster which involves Belgium, France, Germany, and the United Kingdom. It is characterized by a spike protein mutation S: S477N, occurring in combination with N: M234I, A376T, ORF1a: M3087I, ORF1b: A176S, and most also with ORF1b: V767L K1141R, E1184D. It is one of many variants in Luxembourg and was the most prevalent variant until recently and has been circulating in Luxembourg since September 2020. Hence, variant B.1.160 has not emerged in Luxembourg and is not known to be more transmissible and we have noticed a decrease in its prevalence in the pool of samples referred to our laboratories last week.

[B.1.160](#)

Denmark 27.0%, UK 19.0%, Switzerland
15.0%, France 11.0%, Luxembourg 10.0%

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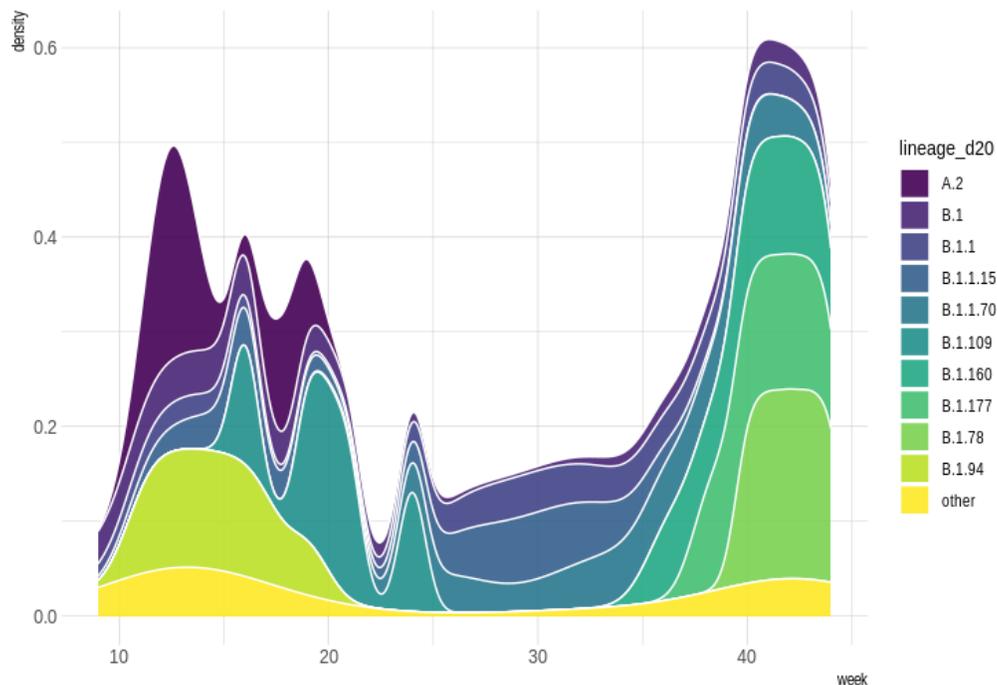
Large European lineage, sequences from
BeNeLuX, Denmark, Switzerland, Hungary
and UK.

Source : (<https://cov-lineages.org/lineages.html>)

The National reference laboratory of the Acute Respiratory Infection at LNS continues to improve its sequencing pool of samples to reach real-time epidemiology by and of February by implementing four axes of sequencing activities

- 1) Sequencing all hospitalized positive cases
- 2) Sequencing all positive cases from airport testing
- 3) Sequencing all outbreaks and identified clusters
- 4) Population sequencing of representative samples from different regions and age groups.

We will continue to report the SARS-CoV-2 dynamics in Luxembourg every Thursday via our ReViLux newsletter(<https://lins.lu/en/departement/departement-of-microbiology/revilux/>).



SARS-CoV-2 variants dynamics in Luxembourg (LNS-Dr Malte Herald)