

## **Recommendation RAG testing for protocol sequencing SARS-CoV-2 – 22/12/20**

A SARS-CoV-2 variant, referred to as SARS-CoV-2 VUI 202012/01 (Variant Under Investigation, year 2020, month 12, variant 01), has been identified through viral genomic sequencing in the United Kingdom, defined by multiple spike protein mutations. This identification of a mutant strain is the result of a very strong genomic surveillance in the UK. The spread of this new variant was triggered by a sudden surge of cases in Southeast England and London, with large outbreaks in schools and hospitals, despite lockdown measures. Similar mutations possibly occur elsewhere but go unnoticed.

It was observed in the UK that, due to the 69-70 deletion, this variant was associated with a particular pattern of the Thermo Fisher TaqPath multiplex assay (positive result, but S gene not detected), used also by the Belgian Platform Bis labs and other clinical laboratories. In the UK, this specific pattern and its proportion increased over the time, together with the spread of the variant of concern.

In an assessment of the risk for Belgium on 20/12, it was recommended to urgently reinforce laboratory characterization and enhanced genomic surveillance in Belgium, with the elaboration of a plan and protocol (collaboration NRC and Sciensano).

The RAG testing supports this recommendation. The genomic surveillance should allow to describe a baseline of circulating strains, in a representative sample of the general population, including specific groups such as elderly, homeless people, migrants, etc. Specific attention should also be given to groups at high risk for generating mutations, such as patients in clinical trials, immunocompromised patients, etc..

The protocol should therefore establish criteria of people (from a variety of settings and of all age groups) to be included in the surveillance.

To establish the baseline surveillance, a collection of up to 1000 samples a week is proposed, with continuous evaluation, and possible adaptation of this number after 2 months.

In addition, sequencing should also be carried out in large outbreak settings (especially in nursing homes, hospitals and schools), in response to other epidemiological changes, or in case of laboratory issues regarding test performance.

Although the 69-70 deletion in the mutant strain can occur among other variants of the virus, we suggest to perform in Belgium a confirmatory test (whole genome or specific PCR to be validated) for all samples harboring this specific PCR result. Diagnostic companies including Thermo Fisher should directly warn their users of the consequences of the circulation of this new variant on their test results. And the AFMPS should ask the diagnostic companies present on the Belgian market what impact the presence of the UK variant could have on the results of their molecular tests. This list with potential problems of detection by test should be available on the Sciensano website.

Close monitoring of COVID-19 vaccinated individuals should also be set up, to identify vaccination failure and breakthrough infections and confirm or exclude vaccine escape mutants in these settings.

Finally, it is recommended to inform all the laboratories on this variant and gather all information on different strains already available at the laboratories.