



Darmstadt, 22.03.2021

**Product Code:** PG6815 & PG6820 & PG6825

**Product Name:** RIDA®GENE SARS-CoV-2 &  
RIDA®GENE Flu & SARS-CoV-2

**Statement:** Detection of the SARS-CoV-2 variants B.1.1.7 & B.1.351 & B.1.1.28 P.1 & B.1.525 & gisaid\_hcov\_2021\_03\_16\_17

There has been an increase in COVID-19 cases in the UK since September, leading to increased epidemiological and virological investigations. Analysis of the data on the viral genome sequences revealed that a large proportion of the cases belonged to a new phylogenetic cluster. There are now initial indications (limited data) that this new SARS-CoV-2 variant B.1.1.7 is associated with increased case mortality. Furthermore, initial studies showed that this variant is even more contagious from person to person than the previously circulating variants. Infections with the SARS-CoV-2 variant B.1.1.7 have also been described in Germany since December 2020. In addition, cases have been reported in Denmark, the Netherlands and Belgium.<sup>1,2,3</sup>

Another virus variant, B.1.351, was first reported in South Africa in December 2020. Initial tests showed a potentially higher contagiousity for this variant as well. These studies also suggest that the protection provided by neutralizing antibodies against this variant may be reduced in people who were previously infected with the original variant or who received a vaccine based on the original variant.<sup>3</sup>

The SARS-CoV-2 variant B.1.1.28 P.1 circulated for the first time in the Brazilian state of Amazonas. Its changes are similar to the South African variant. An increased transmissibility and a possible reduction in the effectiveness of neutralizing antibodies in convalescent patients or vaccinated persons are discussed for this variant.<sup>3</sup>



In Germany, the SARS-CoV-2 variant B.1.525 is currently under observation. This variant has been detected for some time in Denmark and now for the first time in Germany.<sup>4</sup>

There is currently a report on a variant of the SARS-CoV-2 virus from Brittany, in which detection via PCR from a nasal swab is more difficult. No lineage number has yet been assigned for this variant.<sup>5</sup> The sequence of this variant is listed in the GISAID database with the number gisaid\_hcov\_2021\_03\_16\_17.

The RIDA®GENE SARS-CoV-2 assays (PG6815, PG6820, PG6825) detect SARS-CoV-2 over a specific area of the E gene (PG6815 & PG6820) or specific E gene & RdRP gene areas (PG6825).

Sequence alignments of the detection system used with the described sequences of variants B.1.1.7, B.1.351, B.1.1.28 P.1, B.1.525 & gisaid\_hcov\_2021\_03\_16\_17 showed no mismatches in the sequences. The detection of the above-mentioned SARS-CoV-2 variants are not influenced by the described mutations.

For further information, I am gladly at your disposal.

Kind regards

Dr. Anke Laux

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Literature:

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3. [https://www.rki.de/DE/Content/InfAZ/N/Neuartiges\\_Coronavirus/Virusvariante.html?sessionid=3DB10A96DE726B7AE1866B05B394309B.internet061?nn=2444038](https://www.rki.de/DE/Content/InfAZ/N/Neuartiges_Coronavirus/Virusvariante.html?sessionid=3DB10A96DE726B7AE1866B05B394309B.internet061?nn=2444038) Access 26.02.2021
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