

Information concerning the Mutations

At the end of December 2019 in the Chinese metropolis of Wuhan, numerous cases of pneumonia of unknown cause occurred.¹ At the beginning of January 2020, Chinese authorities identified a novel coronavirus (SARS-CoV-2) as the cause of these illnesses.¹ The disease caused by SARS-CoV-2 was officially named COVID-19 (“coronavirus disease 2019”) and is transmitted from human to human.² Due to this pathogen’s novelty, the epidemic rapidly evolved into a pandemic.

There have already been 100,200,107 cases recorded worldwide (as of January 28, 2021).³ At the end of January 2020, the first cases were confirmed in Germany as well. Germany has had 2,178,828 cases so far (as of January 28, 2021).⁴ The WHO declared a Public Health Emergency of International Concern on 2020-01-31.¹

There has been an increase in COVID-19 cases in the UK since September, leading to increased epidemiological and virological investigations. Analysis of the viral genome sequences revealed that a large proportion of the cases belonged to a new phylogenetic cluster. The new variant is characterized by several spike protein mutations (deletion 69-70, deletion 144, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H) as well as mutations in other genomic regions (ORF1ab, ORF8, N-Gene). There are initial indications (limited data) that this new SARS-CoV-2 variant B.1.1.7 is associated with increased case mortality. Furthermore, initial studies have shown that it is even easier transmissible from person to person than previously circulating variants. Infections with the above-mentioned variants were identified in Germany since December 2020. Some cases with the new variant have been reported in Denmark, the Netherlands and Belgium.^{5,6,7}

Another virus variant, B.1.351, was first reported in South Africa in December 2020. Initial tests showed for this variant, too, a potentially higher transmissibility. Initial studies also suggest that protection by neutralizing antibodies against this variant could be reduced in people who were previously infected with the original variant or who received a vaccine based on the original variant.⁷

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.⁷

References:

- 1) https://www.rki.de/DE/Content/InfAZ/N/Neuartiges_Coronavirus/nCoV.html. Last accessed: 16.09.2020
- 2) <https://www.spiegel.de/wissenschaft/medizin/covid-19-weltgesundheitsorganisation-verkuendet-neuen-namen-des-coronavirus-a-810ce436-7081-43d2-b8e0-f0b315503e0b>. Last accessed: 12.02.2020
- 3) <https://covid19.who.int/>. Last accessed: 28.01.2021
- 4) https://www.rki.de/DE/Content/InfAZ/N/Neuartiges_Coronavirus/Fallzahlen.html. Last accessed: 28.01.2021
- 5) <https://www.ecdc.europa.eu>. Last accessed: 21.12.2020
- 6) https://www.cogconsortium.uk/wp-content/uploads/2020/12/Report-1_COG-UK_19-December-2020_SARS-CoV-2-Mutations.pdf. Last accessed: 21.12.2020
- 7) https://www.rki.de/DE/Content/InfAZ/N/Neuartiges_Coronavirus/Virusvariante.html;jsessionid=3DB10A96DE726B7AE1866B05B394309B.internet061?nn=2444038. Last accessed: 28.01.2021