

Overview and Recommendations on Worrying SARS-CoV-2 Virus Variants (VOC)

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Abstract

This work introduces briefly an overview and recommendations on worrying SARS-CoV-2 Virus variants, that can be interpreted as the most spread ones till now. They are: Lineage B.1.1.7, Lineage B.1.351, and Lineage P.1. It is also displayed their observations and development in definite locations in Germany as an exemplary version.

1. Introduction

SARS-CoV-2 (Severe acute respiratory syndrome corona virus type 2) is a new corona virus (genus: Betacoronavirus, subgenus: Sarbecovirus) that was identified as the cause of the COVID-19 disease in early 2020. Corona viruses are widespread among mammals and birds [1,2]. They are assigned to the Corona viridae (suborder: Cornidovirineae, order: Nidovirales, area: Riboviria), in which the large subfamily Orthocoronavirinae includes four genera: Alpha-, Beta-, Gamma-, and Deltacoronavirus. Due to their homologous recombination ability, corona viruses can expand their host range relatively easily and jump over the species boundary [3].

2. Virus variants

Virus variants of concern (VOC) are virus variants that differ significantly from conventional virus variants in terms of their pathogen properties such as transferability, virulence or susceptibility to the immune response of recovered or vaccinated people. The ECDC currently lists the following VOCs:

2.1 Lineage B.1.1.7 [4,5]:

In December 2020, British authorities reported this new SARS-CoV-2 virus variant that has been spreading in the UK since September 2020. According to the current state of knowledge, it is even more easily transmitted from person to person than previously circulating variants and has a higher reproductive number, so that its spread is more difficult to contain. With limited data, there are indications

that it could be associated with increased case mortality. So far there are no indications of a substantially reduced effectiveness of the vaccines. B.1.1.7 E484K is a special form of the variant that has been detected several times in Great Britain, but is currently still considered rare. It has an additional mutation (E484K), which also occurs in variants B.1.351 and P.1 (see below) and makes the virus less sensitive to neutralizing antibodies that have already formed. It is therefore suspected that the vaccines currently available against this variant may be less effective.

2.2 Lineage B.1.351 [6,7]:

This virus variant from South Africa was also reported for the first time in December 2020. This variant is also assumed to be more transferable. Several studies also indicate that people who were infected with the original variant or who received a vaccine based on it are less well protected against infection with B.1.351 - because the neutralizing antibodies that the immune system has produced against the altered virus are less effective.

2.3 Lineage P.1 [8,9]:

This SARS-CoV-2 variant, derived from line B.1.1.28, circulated for the first time in the Brazilian state of Amazonas and is similar in its changes to the South African variant. Increased transferability is also considered conceivable. Due to certain mutations such as E484K, which are also present in B.1.351, a reduction in the effectiveness of neutralizing antibodies in convalescent or vaccinated persons is being discussed for this variant.

B.1.1.7, B.1.351 and P.1 are spreading worldwide and in some countries with great dynamism. Whether and to what extent the new variants will impair the effectiveness of the available vaccines cannot yet be reliably assessed. These aspects are examined in numerous scientific studies. Molecular biological details on the variants are available under SARS-CoV-2: Basic virological data and virus variants.

3. Situation in Germany [10]

Infections with these three variants have also been known in Germany since December 2020: On December 24th, 2020, the state of Baden-Württemberg reported for the first time a detection of line B.1.1.7. B.1.1.7 is currently the most common of the three variants in Germany; large outbreaks with this variant are also known. It can be assumed that the proportion of B.1.1.7 in all SARS-CoV-2 infections will continue to increase. On January 12th, 2021, Baden-Württemberg reported for the first time about evidence of line B.1.351, cases and outbreaks are now known in several federal states. On January 22nd, 2021, the state of Hesse reported for the first time that the variant of line P.1 was verified. More cases and outbreaks are expected.

Since February 5, 2021, the RKI has published reports on the worrying variants in Germany, in particular B.1.1.7. How these new variants will affect the course of the pandemic in Germany is still unclear. However, it is foreseeable that they will make fighting the pandemic more difficult. It is therefore all the more important to consistently comply with the known rules - contact reduction, keep at least 1.5 meters away, observe hygiene rules, wear masks and ventilate - in order to generally prevent the transmission of SARS-CoV-2 and the spread of VOCs slow down and thus counteract the overuse of hospitals and health authorities. Travel should be avoided at all times at the moment.

4. Conclusion

It can be concluded that generally to prevent the transmission of SARS-CoV-2 and the spread of VOCs, the following may be taken into account: contact reduction, keep at least 1.5 meters away, observe hygiene rules, wear masks and ventilate and thus counteract the overuse of hospitals and health authorities. Travel should be avoided at all times at the moment.

5. References

- [1] Ackermann M.; Verleden S.E.; Kuehnel M.; Haverich A.; Welte T.; Laenger, F. Vanstapel A.; Werlein C.; Stark H. and Tzankov A.; "Pulmonary Vascular Endothelialitis, Thrombosis, and Angiogenesis in Covid-19". *N Engl J Med.* 383: 120-128, 2020.
- [2] Alm E.; Broberg E.K.; Connor T.; Hodcroft E.B.; Komissarov A.B.; Maurer-Stroh S.; Melidou A.; Neher R.A.; O'Toole A. and Pereyaslov D.; "Geographical and temporal distribution of SARS-CoV-2 clades in the WHO European Region". *January to June 2020. Euro Surveill*, 25, 2020.
- [3] Graham R.L. and Baric R.S.; "Recombination, reservoirs, and the modular spike: mechanisms of coronavirus cross-species transmission". *J Virol* 84: 3134-3146, 2010.
- [4] Leung K.; Shum M.H.H.; Leung G.M.; Lam T.T.Y. and Wu J.T.; "Early transmissibility assessment of the N501Y mutant strains of SARS-CoV-2 in the United Kingdom, October to November" (2021). *Eurosurveillance. European Centre for Disease Control and Prevention (ECDC).* 26 (1). ECDC, p. 9. (2020).
- [5] Voloch C.M.; da Silva Francisco R.; Jr.; de Almeida, L.G.P.; Cardoso, C.C.; Brustolini, O.J.; Gerder, A.L.; Guimaraes, A.P.C.; Mariani, D.; da Costa, R.M.; Ferreira, O.C.; Jr.; "Genomic characterization of a novel SARS-CoV-2 lineage from Rio de Janeiro". *Brazil. J. Virol.*; 2021.
- [6] Kiani A.K.; Dhuli K. and Anpilogov K.; "Natural compounds as inhibitors of SARS-CoV-2 endocytosis: a promising approach against COVID-19". *Acta Biomed.* 91, e2020008. 2020.
- [7] Liu Z.; VanBlargan L.A.; Bloyet L.M.; Rothlauf P.W.; Chen R.E.; Stumpf S.; et al.; "Identification of SARS-CoV-2 spike mutations that attenuate monoclonal and serum antibody neutralization". *Cell Host Microbe*; 29: 477-88.e4, 2021.
- [8] Tegally H.; Wilkinson E. and Giovanetti M.; "Emergence and rapid spread of a new severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2) lineage with multiple spike mutations in South Africa. *MedRxiv.*; 2020.
- [9] Xie M. and Chen Q.; "Insight into 2019 novel coronavirus-an updated intrim review and lessons from SARS-CoV and MERS-CoV, *IJID*", 94: 119-124, 2020.
- [10] Dejnirattisai W.; Zhou D.; Supasa P.; Liu C.; Mentzer A.J.; Ginn H.M.; et. al; "Antibody evasion by the P.1 strain of SARS-CoV-2". *Cell*, 2021.
- [11] Meyer E.; Steffen G.; Krings A.; Ullrich A.; Kollan C. and Dudareva S.; "Zimmermann R Zur Situation bei wichtigen Infektionskrankheiten in Deutschland". -im Jahr 2020. *Epid. Bull.*; 28: 3-19, 2021.