Brief note of the extraordinary meeting of NERVTAG subgroup on SARS-CoV-2 variant B.1.1.529

Date & Location: 15:00 – 16:00, 25 November 2021 - Via telecon only
In attendance: *NERVTAG Chair:* Peter Horby (PH) *NERVTAG Members:* Julian Hiscox (JHi), John Edmunds (JE), Wendy Barclay (WB), Ravi Gupta (RG) *NERVTAG Secretariat: UKHSA* - Ruth Parry (RP), Stephen Barnard (SB); DHSC - Emma Sherwood (ES) *Invited experts/presenters:* UKHSA - Meera Chand (MCh); University of Edinburgh/ COG UK - Andrew Rambaut (AR), Imperial College, London - Paul Kellam (PK) *DHSC Observers:* Sadia Dorsani (SD), Jonathan Van Tam (JVT)
Apologies: NA

Brief summary of NERVTAG subgroup opinion.

The sub-group considered available information on:

1. The genomic characteristics of B.1.1.529

2. The epidemiology of B.1.1.529 available from genomic surveillance and from the press conference given by the South African Health Authorities this morning.

3. The South African context, with respect to recent prior circulation of SARS-CoV-2 variants and levels of population immunity.

The observations of the NERVTAG sub-committee are as follows:

4. The number of B.1.1.529 cases has rapidly increased in one area of SA (Gauteng). Although B.1.1.529 now represents the dominant genotype in this area, there are likely biases in sampling (over-sampling in areas most affected by B.1.1.529), so the true proportion of cases that are B.1.1.529 in this area is uncertain.

5. The mutations observed in B.1.1.529 include some that are known to be associated with enhanced transmissibility.

6. SA estimates an R-value of 1.9 for B.1.1.529 in Gauteng.

7. B.1.1.529 has a genotype that would lead to failure to detect the S gene target in PCR assays (S gene target failure – SGTF). To the best of the subgroup's knowledge, there are no other prevalent SARS-CoV-2 variants in South Africa (SA) with SGTF.

8. 100% of SGTF samples sequenced in the recent period in SA have been confirmed as B.1.1.529.

9. It is therefore a reasonable assumption, at this stage, that SGTF in SA is currently a reliable marker of the variant B.1.1.529.

10. Samples with SGTF are being detected in multiple provinces of SA.

11. **Conclusion: the subgroup concludes that it is highly likely that B.1.1.529 is a 'fit' virus that is undergoing extensive community transmission in SA, and possibly elsewhere.**

12. The R-value estimate of 1.9 is occurring against a background of high levels of immunity following the recent wave (wave number 3) of Delta variant infections in SA and an active immunisation programme.

13. The multiple mutations observed in the B.1.1.529 spike glycoprotein, the major target for neutralising antibodies (including monoclonal antibodies), are highly likely to result in reduced neutralising ability of antibodies raised to earlier variants and vaccination.

14. Although there is not yet any direct experimental evidence of immune escape, the genotype and the epidemiology in SA are highly suggestive that B.1.1.529 is an antigenically divergent variant that is able to successfully infect previously infected or vaccinated individuals.

15. There are currently insufficient data to make any comments on disease severity associated with B.1.1.529.

16. Whilst we do not know the effect of the B1.1.529 mutations on the vaccine efficacy (VE) against severe disease, it is possible that VE against severe disease could be reduced.

17. **Conclusion: the subgroup concludes that if introduced into the UK, B.1.1.529 would likely be capable of initiating a new wave of infections. We cannot exclude that this wave would be of a magnitude similar, or even larger, than previous waves.**

18. **Conclusion: Although data on disease severity associated with B.1.1.529 are not yet available, a large wave of infections will be accompanied by a wave of severe cases and the subgroup cannot rule out that this may be sufficient to overwhelm NHS capacity**

19. Although computational analyses are ongoing, the multiple mutations observed in the B.1.1.529 spike glycoprotein are likely to render many of the currently available monoclonal antibodies ineffective.

Despite current uncertainty about the characteristics of B1.1.529, there are sufficiently worrying signals for the subgroup to advise that:

20. **Introduction of B.1.1.529 into the UK might have very serious consequences and, therefore, early and robust actions to prevent introduction and onward transmission are warranted.**

21. **Actions should be taken to enhance the early detection of B.1.1.529 in the UK and, if necessary, to implement containment measures.**

22. **Acceleration of the vaccine boosting campaign should be considered, which might provide some residual or significant VE against B1.1.529, and at a minimum would help control concurrent Delta impact.**

23. **The optimal use of available antiviral products should be reconsidered in light of the new threat posed by B.1.1.529.**

24. **Actions should be taken to enhance the characterisation of B.1.1.529 e.g. computational biology, obtaining live virus samples and constructing pseudoviruses.**

25. **Preparations should be made for the modification of countermeasures i.e. vaccines and monoclonal antibodies.**

END

Signed off by Chair, following review by subgroup members. Full Minutes of the meeting will be prepared and published in due course