World Health Organization

Statement of the WHO Working Group on COVID-19 Animal Models (WHO-COM) about the UK and South African SARS-CoV-2 new variants

23 December 2020 | Meeting report

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Background

The WHO-COM is an expert group of more than 150 scientists around the world with expertise in animal models of viral diseases. Since February 2020 the group has met weekly to discuss advances, foster collaborations, share resources and reagents and avoid duplication of effort. The WHO-COM met on 22 December 2020 to discuss action plans and current knowledge about the emerging SARS-CoV-2 variants containing multiple mutations in the viral spike protein and that are currently circulating in the UK and South Africa. The UK variant was identified through genomic sequencing and reported to WHO on 14 December 2020 and is referred to as SARS-CoV-2 VUI 202012/01 (B1.1.7). The South African variant is characterized by eight lineage-defining mutations in the spike protein including three key residues in the receptor binding domain (K417N, E484K and N501Y) and is referred to as lineage 501Y.V2. Epidemiological data suggests that these two variants may be associated with increased transmissibility. It is not known whether they may also result in increased pathogenicity, immune escape from current COVID-19 vaccines or lack of detection by established diagnostic methods. The WHO-COM group intends here to draft an action plan to test these hypotheses experimentally.

155 scientists participated in the meeting of Tuesday 22 December, 2020 to discuss the SARS-CoV-2 variants.

Meeting minutes

- Simon Funnell, co-chair of the WHO-COM group presented a summary of the current knowledge regarding the B1.1.7 variant in the UK including: i) Specific mutations in the spike, ORF1ab, ORF8 and N genes, S gene target failure in diagnostic tests, unanswered questions and possible approaches.
- Public Health England is working as fast as possible to distribute the new variant via dedicated repositories such as BEI, NIBSC, and EVA. Alex Sigal, who is growing the South African variant also pledged to distribute the virus among the group as soon as available.
- Additional resources available immediately to the group are plasmids to encode the mutant spike RBD. These plasmids generated by Florian Krammer (Mount Sinai) will be distributed to group members without the need of an MTA and may help immediately to assess important questions such as possible evasion from neutralizing antibodies present in convalescent or vaccinee sera.
- The group agreed that a high priority is to test the new variant against existing COVID-19 sera. This could be done with existing NHP sera (for example Vincent Munster, NIH and Vasan Vasan, CSIRO offered sera from ChadOx vaccinated monkeys) or with vaccinee sera. Regarding the latter, Mount Sinai and PHE have established a collaboration to test the new variant against sera from Pfizer vaccinees.
- With respect to the latter point, the group discussed ways to speed up sharing of sera without the need to execute MTAs with developers. Rather than obtaining sera from clinical trials, the proposal would be to obtain and share sera from vaccinees receiving EUA vaccines. Collection of these sera by key laboratories of the WHO-COM distributed worldwide would ensure rapid testing of possible immune escape by emerging SARS-CoV-2 variants.

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