COVID-19: Variants Update

Date: 21 May 2021

During the COVID-19 pandemic, the Ministry of Health has seen high interest in all aspects of the virus from not only the scientific and health community but the general public as well. This update is designed to provide new information on variants of the virus that are of interest or concern. The first three pages of this update are provided as a brief overview with the full technical report available for download, including a full glossary and references.

Information gathered in the last week is provided in red text.

Background

SARS-CoV-2, the virus that causes COVID-19, can undergo genetic mutations. These can occur naturally over time or from selective pressures. While the vast majority of mutations do not change the virus in any meaningful way, some mutations, particularly those relating to virus’s spike protein, could affect the transmissibility of the virus, disease severity, and the effectiveness of treatments or vaccines. There is concern that if infection of SARS-CoV-2 persists for extended periods of time, such as within an immunocompromised person, it could serve as a way for mutations to accumulate.

Mutation nomenclature (i.e., how mutations are named) describes what has occurred at a specific location of the viral genome. For example, the ‘E484K’ mutation means that at the position 484, the amino acid changed from glutamic acid (E) to lysine (K). When a deletion occurs, the location is provided (e.g., deletion 144). Mutations constitute different lineages of the virus, commonly referred to as ‘variants’. A variant is referred to as a ‘strain’ when it becomes sufficiently different from its patent virus, either by showing distinct physical properties or behaving in a pathologically or immunologically different way.

Potentially problematic variants that may have concerning epidemiological, immunological, or pathogenic properties are raised for formal investigation by two main investigative groups - the Public Health England Variant Technical Group and the SARS-CoV-2 Interagency Group in collaboration with the Centers for Disease Control and Prevention (CDC) in the United States (US).

New variants are discovered through whole genome sequencing – a laboratory testing process, for which most countries have had low testing capacity prior to the COVID-19 pandemic. New Zealand now sequences all viable SARS-CoV-2 samples, however, the use and application of whole genome sequencing has varied between countries, and globally genomic surveillance of SARS-CoV-2 remains limited. The Global Initiative on Sharing Avian Influenza Data (GISAID) is a consortium that promotes and provides open access to genomic sequence data. Despite its original purpose for sharing avian (bird) flu data, it has proved to be beneficial in the fight against SARS-CoV-2. Submission of SARS-CoV-2 sequences to this repository has been key in tracking emerging variants. The US reports weekly published sequences from the National SARS-CoV-2 Strain Surveillance (NS3) programme, CDC contracts, and other sequencing efforts here and sequencing information from the UK can be found here.

Within this document, we will provide information on how “variants under investigation” (VUI), “variants of interest” (VOI), and “variants of concern” (VOC) are identified and describe what is known about their current epidemiological spread, before reviewing the emerging evidence and research on transmissibility, disease severity, vaccine protection, treatment effectiveness, and immune escape properties.
New information in this update

- Up to 17 May 2021, whole genome sequencing in New Zealand has identified the following VOCs:
  - 173 sequences of B.1.1.7. There is no change in B.1.1.7 sequences since the previous update
  - 28 sequences of B.1.351. There is no change in B.1.351 sequences since the previous update
  - 5 sequences of P.1. There is no change in P.1 sequences since the previous update
  - 12 sequences of B.1.617.2. This is an increase of two B.1.617.2 sequences since the previous update

- Public Health England reported among contacts that had not travelled, the secondary attack rate for B.1.617.2 was 11.5% (95% CI: 9.6-13.9%), which is similar to the secondary attack rate of 10.0% (95% CI: 9.9-10.1%) for B.1.1.7

- Based on the mutations present in B.1.617 and its increased growth rate, Public Health England reported ‘high confidence’ that B.1.617.2 is at least as transmissible as B.1.1.7. Therefore, it is estimated that B.1.617.2 has an increased transmissibility of at least 40% compared to previously circulating, non-B.1.1.7, variants.

- There was a 6.8-fold reduction in neutralisation of the VUI B.1.617.1 among convalescent sera and vaccinated individuals with the Pfizer and Moderna vaccines. It was noted that despite the reduction, B.1.617.1 was still neutralised in all vaccinated individuals meaning mRNA vaccines are likely able to still confer immunity against the variant.

- A study reported on neutralising antibodies against B.1.1.7, B.1.351, and P.1 from sera of individuals vaccinated with the Moderna (mRNA-1273) vaccine. While B.1.351 had the greatest impact on neutralisation, a 3 to 15-fold reduction, binding and functional antibodies against the three VOCs were still present after six months.

- A phase 3 trial of the Novavax (NVX-CoV2373) vaccine among 15,187 participants reported a vaccine efficacy of 86.3% (71.3-93.5%) against symptomatic B.1.1.7 with onset 7 days after the second dose.

- A follow-up to the study in Manaus, Brazil, where the P.1 variant predominates, estimated that approximately 17% of infections in the second wave (from November 2020 onwards) were reinfections, presumed to be infections of the P.1 variant. However, there are several limitations to this study: not a population-wide sample (238 blood donors), small sample (10 reinfections), whole genome sequencing was not used to determine variant type; P.1 was assumed, given the geographical location, which may include some non-P.1 cases.

- The FDA has reviewed data evaluating the combination of casirivimab and imdevimab against B.1.1.7, B.1.351, P.1, B.1.427, B.1.429, and B.1.526 and report minimal impact (≤2 fold change) on antibody neutralisation activity

- Up to date information on global cases can be found at:
  - B.1.1.7 (cov-lineages.org and outbreak.info)
  - B.1.351 (cov-lineages.org and outbreak.info)
  - P.1 (cov-lineages.org and outbreak.info)
  - B.1.617.2 (cov-lineages.org and outbreak.info)
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VOC Summary

Current VOCs have “evidence of an increase in transmissibility, more severe disease (increased hospitalisations or deaths), significant reduction in neutralisation by antibodies generated during previous infection or vaccination, reduced effectiveness of treatments or vaccines, or diagnostic detection failures”. Table 1 collates key information on nomenclature, transmissibility, severity, immune evasion and countries in which the variants have been identified.

Table 1. Summary of characteristics for Variants of Concern as of 21 May 2021, red text denotes new information, red highlights note variables of particular concern.

<table>
<thead>
<tr>
<th>Lineage</th>
<th>B.1.1.7</th>
<th>B.1.351</th>
<th>P.1</th>
<th>B.1.617.2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Country first identified</td>
<td>United Kingdom ‘Kent Variant’</td>
<td>South Africa</td>
<td>Brazil</td>
<td>India</td>
</tr>
<tr>
<td>Other names</td>
<td>501Y.V1, VOC-202012/01, VOC-20DEC-01</td>
<td>501Y.V2, VOC-202012/02, VOC-20DEC-02</td>
<td>501Y.V3, B.1.1.28.1, VOC-202101/02, VOC-21JAN-02</td>
<td>VOC-21APR-02</td>
</tr>
<tr>
<td>Transmissibility</td>
<td>• ~40-80% more transmissible (R0 ~3.5-5.2)*</td>
<td>• Not well established. Preliminary estimate ~50% more transmissible</td>
<td>• Not established. Preliminary estimates 40%-160% more transmissible</td>
<td>• Not well established. However, it is believed to be at least as transmissible as B.1.1.7 (approximately 40%) with ‘high confidence’ by Public Health England in the UK</td>
</tr>
<tr>
<td>Severity</td>
<td>• Mortality: 60-70% increased mortality compared to previous variants • Hospitalisation risk: 30-70% increased risk</td>
<td>• Mortality: Not well established. One report of no increased risk of mortality • Hospitalisation: Not well established. One report of approximately 3.6 times risk of hospitalisation</td>
<td>• Mortality: Not established. One report of no increased risk of mortality • Hospitalisation: Not well established. One report of approximately 2.6 times risk of hospitalisation</td>
<td>• Mortality: Not well established • Hospitalisation: Not well established</td>
</tr>
<tr>
<td>Immune evasion</td>
<td>Minimal</td>
<td>Moderate-Strong</td>
<td>Moderate-Strong</td>
<td>Not well established. Some preliminary laboratory evidence of minimal to moderate reduction in neutralisation. No estimates of vaccine efficacy or effectiveness</td>
</tr>
<tr>
<td>Countries reporting sequences</td>
<td>133</td>
<td>89</td>
<td>49</td>
<td>52</td>
</tr>
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*Assuming R0 for original SARS-CoV-2 of approximately 2.5 to 2.9