

FACT SHEET

**(ARCHIVED)** Comparing SARS-CoV-2 Variants of Concern (VOCs)\* as of May 31, 2021

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This table compares characteristics of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Variants of Concern (VOCs). This table is current as of May 31, 2021 and will be updated as more information becomes available.

|  | <b>B.1.1.7</b>        | <b>B.1.351</b>              | <b>B.1.617<sup>†</sup></b>                               | <b>P.1</b>      |
|--|-----------------------|-----------------------------|--|-----------------|
| <b>Public Health England name</b>      | VOC-20DEC-01          | VOC-20DEC-02                | VOC-21APR-02   | VOC-21JAN-02    |
| <b>Nextstrain clade</b>                | 20I/S:501Y.V1         | 20H/S:501Y.V2               | 21A/S:154K (for B.1.617.1)<br>21A/S:478K (for B.1.617.2) | 20J/S:501Y.V3   |
| <b>World Health Organization label</b> | Alpha                 | Beta                        | Delta (for B.1.617.2)                                    | Gamma           |
| <b>Location first detected</b>         | United Kingdom (Kent) | South Africa (Eastern Cape) | India  | Brazil (Manaus) |
| <b>Detected in multiple countries?</b> | Yes                   | Yes                         | Yes  | Yes             |

|  | <b>B.1.1.7</b>   | <b>B.1.351</b>  | <b>B.1.617<sup>†</sup></b>                                 | <b>P.1</b>   |
|--|--|---|--|--|
| <b>Detected in Ontario?</b>                                    | Yes  | Yes   | Yes  | Yes  |
| <b>Increased transmissibility?</b>                             | Yes +55% <sup>‡</sup>  | Yes +58% <sup>‡</sup>   | Yes  | Yes +58% <sup>‡</sup>  |
| <b>Increased disease severity?</b>                             | Yes  | Unknown <sup>§</sup>  | Unknown <sup>§</sup>                                       | Unknown <sup>§</sup>   |
| <b>Impact on molecular tests?</b>                              | Yes <sup>¶</sup>   | No  | No   | No   |
| <b>Impact on antigen tests?</b>                                | No   | No  | Unknown <sup>§</sup> (but unlikely)                        | No   |
| <b>Impact on serological tests?</b>                            | Unknown <sup>§</sup>   | Unknown <sup>§</sup>  | Unknown <sup>§</sup>                                       | Unknown <sup>§</sup>   |
| <b>Immune escape?</b>  | No   | Yes   | Potential <sup>#</sup>                                     | Yes  |
| <b>Impact on vaccine effectiveness?</b>                        | No   | Yes <sup>**</sup> , <sup>††</sup>                                     | Potential impact <sup>††</sup>                             | Potential impact <sup>††</sup>                                 |
| <b>Notable mutations (key mutations in bold) <sup>††</sup></b> | <b>Δ69-70<sup>¶</sup></b> ,<br><b>N501Y<sup>§§</sup></b> D614G,<br>P681H/R | L18F, <b>K417N</b> ,<br><b>E484K</b> , <b>N501Y</b> ,<br>D614G, A701V | <b>L452R</b> , D614G, G142D<br><b>P681R</b> , <b>E484Q</b> | L18F, <b>K417T</b> ,<br><b>E484K</b> , <b>N501Y</b> ,<br>D614G |

Abbreviations: Δ, deletion; VOC, variant of concern

For additional information on VOCs and interpreting this table, please refer to PHO's [Companion Guide to Variants of Concern \(VOCs\)](#)<sup>1</sup>

\* VOCs are classified according to the [national definitions](#) for Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) variants established by the Canadian SARS-CoV-2 Variant Surveillance Group.<sup>2</sup>

<sup>†</sup> B.1.617 contains three sub-lineages (B.1.617.1; B.1.617.2; B.1.617.3) which differ by few potentially relevant mutations in the spike protein and their global prevalence of detection.<sup>3</sup> Designation of the sublineages in Canada may change as evidence on their attributes are being reviewed by the Canadian SARS-CoV-2 Variant Surveillance Group.<sup>2</sup>

<sup>‡</sup> Based on the odds ratio of secondary household transmission using a household study of VOC transmission in Ontario (forthcoming). For methods, see (<https://doi.org/10.1093/cid/ciab186>).<sup>4</sup>

<sup>§</sup> Unknown indicates that it is under investigation or there is currently no data for assessment.

<sup>¶</sup> Spike (S) gene target failure (SGTF) is observed for variants with the Δ69-70 mutation using some SARS-CoV-2 molecular assays that target this region of the S gene. These are multiple gene target assays that will still detect SARS-CoV-2 via the additional targets.

<sup>#</sup> Laboratory evidence suggests resistance to certain therapeutic monoclonal antibodies and/or slightly reduced neutralization by convalescent sera.

<sup>\*\*</sup> Reduced effectiveness to AstraZeneca and Johnson & Johnson.

<sup>††</sup> Laboratory evidence to suggest reduced effectiveness by AstraZeneca, Moderna mRNA-1273, and Pfizer-BioNTech vaccines.

<sup>†††</sup> Mutations in other genes are not represented in this table.

<sup>§§</sup> A small subset of B.1.1.7 variants have been found to have the E484K mutation.

## References

1. Ontario Agency for Health Protection and Promotion (Public Health Ontario). Companion guide to variants of concern (VOCs) [Internet]. Toronto, ON: Queen's Printer for Ontario; 2021 [cited 2021 Jun 08]. Available from: <https://www.publichealthontario.ca/-/media/documents/ncov/voc/2021/04/covid-19-companion-guide-variants.pdf?la=en>
2. Public Health Agency of Canada. SARS-CoV-2 variants: national definitions, classifications and public health actions [Internet]. Ottawa, ON: Government of Canada; 2021 [modified 2021 May 14; cited 2021 Jun 08]. Available from: <https://www.canada.ca/en/public-health/services/diseases/2019-novel-coronavirus-infection/health-professionals/testing-diagnosing-case-reporting/sars-cov-2-variants-national-definitions-classifications-public-health-actions.html>
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