

Transmission characteristics of SARS-CoV-2 variants of concern: A rapid scoping review

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Summary

Most of the limited evidence on VOC transmission has not been peer reviewed. The majority focuses on B.1.1.7, and evidence is very limited for B.1.351 and P.1. Heterogeneity and inconsistency in VOC testing and study methods make it difficult to interpret and compare data across studies.

Based on findings from eight studies, B.1.1.7 transmission risk appears to be higher than non-VOCs. B.1.351 and P.1 may be more transmissible than non-VOCs, based on one study each.

Increased viral load (using Ct as a proxy measure) and increased ACE2 binding may increase transmission risk, but studies of these mechanisms use inconsistent methods, so it is difficult to draw any meaningful conclusions.

VOC definitions vary, but often include three main characteristics: (1) Phylogenetic distinction from non-VOCs; (2) Mutations of biological significance; and (3) Rapid spread, dominance, and/or selective advantage over other variants.

Potential Implications

- **Continued monitoring and sharing of VOC data remains important**
- **Continued systematic sequencing of VOCs, with a focus on standardized testing, will facilitate future data comparison**
- **VOCs appear to be as transmissible or more transmissible than non-VOCs, so existing public health guidelines remain important**
- **Synergizing and sharing information about public health precautions in response to VOCs will help improve epidemiological research**

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What is the current situation?

As of March 2021, three SARS-CoV-2 variants of concern (VOCs) have been identified: B.1.1.7 (UK variant), B.1.351 (South Africa variant), and P.1 (Brazil variant). VOCs can potentially cause changes in transmissibility, clinical presentation, and severity, and they may have an impact on countermeasures.

What are the review questions?

This rapid scoping review identified evidence related to the following questions:

1. How much more transmissible are the VOCs?
2. Why are they more transmissible?
3. What criteria are used to define new VOCs?

How was the review conducted?

An information specialist designed a broad, comprehensive search to retrieve all published, preprint, and grey literature related to the VOC in MEDLINE, Embase, the Cochrane Library, Epistemonikos' L·OVE on COVID-19, medRxiv, and bioRxiv (Feb 21, 2021), Google, Twitter, and relevant websites (Feb 26-Mar 1, 2021). Animal studies and studies only reporting on predictive modelling data were excluded. Title/abstract screening was completed by one reviewer; full text screening and data extraction were completed by one reviewer and verified by a second. Data extraction was undertaken in consultation with infectious disease specialists and microbiologists. Critical appraisal was not conducted.

What did the review find?

The search retrieved 1,863 records, of which 23 reports (13 preprints, 3 peer-reviewed journal articles, 7 grey literature sources) were included in this review.

Transmissibility: Compared to non-VOCs, B.1.1.7 transmission risk ranges from 45-71% higher, the R_0 ranges from 75-78% higher, and the R_t values range from 1.1-2.8. It appears there is an additive transmission effect, where B.1.1.7 is not only replacing previous infections, but is also associated with a growth in the number of infections. One study found that B.1.351 might be more transmissible (55% higher transmission risk; $R_t = 1.55$) than non-VOCs, and one study estimated that P.1 might be 1.1-2.2 times more transmissible than non-VOCs.

Mechanism of transmission: It is difficult to draw conclusions about the underlying mechanisms of VOC transmissibility from the existing data. There is variation in methods, measures and reporting across studies and limited evidence, particularly on P.1 and B.1.351. Some evidence suggests VOC viral load may be higher, using RT-PCR Ct values as a proxy measure. Other studies have proposed that VOCs might evade immune system response through increased ACE2 binding.

VOC definition: Three characteristics are used in multiple reports: (1) Phylogenetic distinction from non-VOCs; (2) Mutations of biological significance; and (3) Rapid spread, dominance, and/or selective advantage over other variants.