# Article information:

ACE2 binding and antibody evasion in enhanced transmissibility of XBB.1.5 - The Lancet Infectious Diseases
[https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(23)00010-5/fulltext](https://www.thelancet.com/journals/laninf/article/PIIS1473-3099%2823%2900010-5/fulltext)

# Article summary:

1. XBB.1.5 is a subvariant of the recombinant mutant XBB that has shown a substantial growth advantage compared to other SARS-CoV-2 strains.

2. XBB.1.5 carries a Ser486Pro mutation on the spike protein, which may be responsible for its enhanced transmissibility.

3. XBB.1.5 has stronger immune escape ability but weaker ACE2 binding affinity than BQ.1.1, making it more likely to cause the next global wave of COVID-19 infections.

# Article rating:

Appears well balanced: The article presents the information in a reliable and balanced way, without biases and prejudices. The claims made in the article are well supported and, where applicable, all sides of the argument are given opportunity to present their point of view. The article appears trustworthy and reliable.

# Article analysis:

The article “ACE2 binding and antibody evasion in enhanced transmissibility of XBB.1.5” from The Lancet Infectious Diseases provides an overview of the potential role of the Ser486Pro mutation in the spike protein of SARS-CoV-2 strain XBB 1.5 in its enhanced transmissibility and increased prevalence over other strains such as BQ 1.1 and XBB 1, as well as its ability to evade neutralisation by plasma and serum from vaccinated or convalescent individuals and monoclonal antibodies (mAbs). The article is based on data from vesicular stomatitis virus-based pseudovirus neutralisation assays, surface plasmon resonance experiments, and deep mutational scanning studies, all of which are reliable sources for scientific research on SARS-CoV-2 variants and their effects on human health outcomes such as transmission rates and vaccine efficacy against them.

The article does not appear to be biased or one-sided in its reporting; it presents both sides equally by providing evidence for both the increased prevalence of XBB 1.5 over other strains due to its enhanced transmissibility, as well as its ability to evade neutralisation by plasma and serum from vaccinated or convalescent individuals and mAbs due to its Ser486Pro mutation in the spike protein receptor binding domain (RBD). It also acknowledges limitations in its analysis due to lack of data on BQ 1.1 breakthrough infection in individuals who were convalescent, which could have provided further insight into the scale of immune evasion by XBB 1.5 for this group had it been available for analysis at the time of writing this article

The article does not appear to contain any promotional content or partiality towards any particular strain or vaccine; rather it provides an objective overview of current scientific evidence regarding SARS-CoV-2 variants and their effects on human health outcomes such as transmission rates and vaccine efficacy against them based on reliable sources such as vesicular stomatitis virus-based pseudovirus neutralisation assays, surface plasmon resonance experiments, and deep mutational scanning studies mentioned above

The article does not appear to omit any points of consideration or evidence for claims made; rather it provides detailed information about each source used for analysis (e.g., vesicular stomatitis virus-based pseudovirus neutralisation assays) along with relevant results obtained from each source (e

# Topics for further research:

* SARS-CoV-2 variants and transmission rates
* SARS-CoV-2 variants and vaccine efficacy
* Ser486Pro mutation and ACE2 binding
* Ser486Pro mutation and antibody evasion
* Vesicular stomatitis virus-based pseudovirus neutralisation assays
* Deep mutational scanning studies and SARS-CoV-2 variants

# Report location:

<https://www.fullpicture.app/item/63d8c442e5d538480ebce19499b98641>