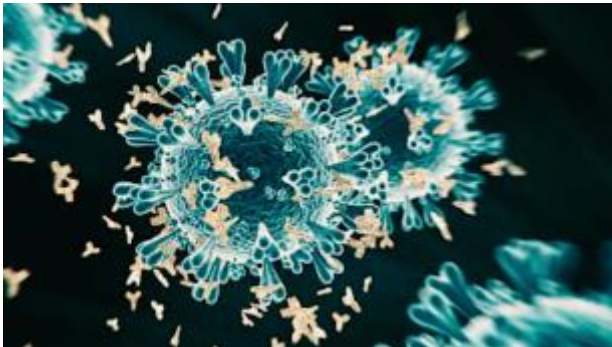


Spot report: Lambda, the Newest WHO Variant of Interest

The Lambda variant has now been found in 29 different countries, seven of them in Latin America and it is the dominant strain in Peru.

The Lambda variant, or the C.37 strain, designated a variant of interest by the WHO on 15 June 2021, was first identified in Peru in August 2020. It is widespread across Argentina, Brazil, Colombia, Ecuador, and Mexico, and has since spread to the UK.



Dr Maria Van Kerkove, WHO Technical Lead on COVID-19, has said that the WHO is currently tracking this strain to see if it should be upgraded to a variant of concern.

“It would become a variant of concern if it has demonstrated properties of increased transmissibility, increased severity, or has some kind of impact on our counter-measures,” said Van Kerkove during a 2 July briefing.

Countries around the world, including Russia, Portugal, and South Africa, are currently scrambling to control the Delta variant, reported to be more deadly and infectious than any other variant. From July, ASEAN country reported increasing number of mortality and morbidity as well.

Variant is Potentially More Infectious

A pre-print analysis published on 3 July, though yet to be peer-reviewed, of the spike proteins on the SARS-CoV-2 Lambda variant showed a two-fold increase in infectivity, due to a mutation of the virus called the L452Q mutation.

In addition to testing the infectivity of the variant, researchers from the NYU Grossman School of Medicine also tested the effectiveness of mRNA vaccines Pfizer and Moderna against the C. 37 strain.

Though the virus with the Lambda spike protein demonstrated “a partial resistance to neutralization by vaccine-elicited antibodies” results “suggest that vaccines in current use will remain effective against the lambda variant”.



Further Research Needed to Ascertain Effectiveness of Vaccines

However, another pre-print paper found the Lambda variant to have mutations with increased resistance to the vaccine, CoronaVac.

Researchers examined the impact of the lambda variant on infectivity and antibodies produced by the COVID-19 vaccine CoronaVac, using plasma samples from healthcare workers in Santiago, Chile, who received the two-doses of CoronaVac.

They found that the Lambda spike protein had increased infectivity when compared to the Alpha or Gamma variants.

The antibodies produced by CoronaVac decreased by a factor of 3.05 from the Lambda spike protein, while antibodies decreased by a factor of 2.33 for the Gamma spike, and 2.03 for the Alpha spike.

“These data reinforce the idea that massive vaccination campaigns in countries with high SARS-CoV-2 circulation must be accompanied by strict genomic surveillance,” the paper said.

Chile leads in its vaccination program with over 50% of its population vaccinated, the vast majority (78.2%) receiving CoronaVac.

In another large study of the efficacy of the vaccine on 10.2 million Chileans, it was found that CoronaVac was 65.9% effective in preventing infection, 87.% effective in preventing hospitalization and 86% effective in preventing death after two doses, according to a report published in the New England Journal of Medicine (NEJM) on Thursday.

However, further research will be needed to determine the effectiveness of vaccines against the new variant, according to the NEJM.

ACMM Recommendation

ASEAN still fight with Viral Variants that cause more infectious and spread faster. Shared developing knowledge about prevention, mitigation, vaccine research and Intervention strategies should be done for disease control and living well in COVID era together.

Reference

<https://www.cnbc.com/2021/07/09/covid-heres-what-you-need-to-know-the-lambda-variant.html>

<https://www.csis.org/programs/southeast-asia-program/projects/southeast-asia-covid-19-tracker>

<https://edition.cnn.com/2021/08/07/health/lambda-coronavirus-variant-wellness-explainer/index.html>

<https://healthpolicy-watch.news/lambda-new-variant-interest-29-countries/>

<https://www.nejm.org/doi/full/10.1056/NEJMoa2107715>

<https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/>