Relative transmission rates of SARS-CoV-2 variants in the US and Its Dynamics
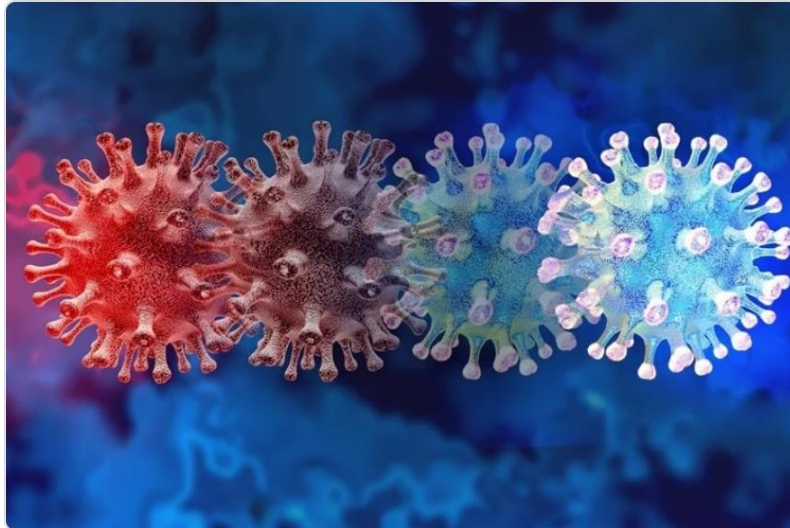
A team of researchers from the University of Washington recently investigated the transmission dynamics of severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) variants and reported that the variants showed consistent differences in their transmission rates.

Introduction

The emergence of (SARS-CoV-2) variants of concern (VOCs) and variants of interest (VOIs) has pressed the scientific community to understand and possibly predict the transmission rates of variants. Prior studies that tried to address the frequency dynamics of variants using sequence data could not establish the epidemiological dynamics because frequency alone cannot determine the rate of transmission of SARS-CoV-2.

Study

In the present study, researchers developed two models of variant-specific effective reproduction number (Rt) – a free Rt model and a fixed growth advantage model. The effective reproduction number (Rt) is the average number of infections caused by an infectious individual in a given outbreak. The team used confirmed case data between January 2021 and October 2021 to define variant specific Rt as well as the frequencies of other variants in the United States (US).

In the free Rt model, the effective reproduction number of each variant was independent of other variants for a non-linear relationship between growth rates of different variants over a certain period. In the fixed growth advantage model, each variant had its multiplicative growth advantage.

In the free Rt model, the effective reproduction number was parameterized with an exponential spline basis. In the fixed growth advantage model, the fitness of variants was parameterized. These models governed by two parameters, i.e., the effective reproduction number and generation time (length of infection and transmissibility throughout infection), defined those variant generated infections independent of one another.

The researchers studied 7 VOIs and VOCs of SARS-CoV-2, Alpha, Beta, Gamma, Delta, Epsilon, Iota, and Mu, to estimate their Rt by using daily case counts updated on the US Centers for Disease Control (CDC). The sequence count data was obtained from Nexstrain-curated datasets for each variant. Eta,

Lambda, Kappa, and Theta variants were not included in the study due to selection criteria, which eliminated them from the analysis along with non-variant viruses.

Results

The non-variant viruses showed a declining trend after January 2021, while Alpha and Gamma variants caused surges until May 2021 with Rt > 1. With the arrival of the Delta variant, the effective reproduction number remained high until September 2021. Subsequently, by employing the fixed growth advantage approach on these observed trends, it was reported that all VOCs except the Epsilon variant showed a shared positive growth advantage. Iota and Delta variants showed larger growth advantages over non-variants compared to other variants which had modest growth over non-variants.

The study provided insights into the structured relationship between effective reproduction numbers to estimate fixed variant-specific growth advantages. The model, which partitioned case count data based on variant frequency in sequence data, effectively represented SARS-CoV-2 variant dynamics. During Spring in the US, the increase in cases could be attributed to the prevalence of Alpha, Beta, Gamma, and Iota variants. With the numbers subsiding, the arrival of Delta variant with a growth advantage significantly drove the massive surge in cases in the Summer. With this approach to evaluating variant-specific Rt, researchers showed that the Delta variant was growing rapidly in May across US states way before the surge in numbers due to Delta was evident.

Conclusion

The approach designed by the researchers in this study accounted for fitness differences between genetic variants to remain prepared for effective epidemic management. These analyses provide a general mechanism to understand the emergence of new and highly transmissible variants and could act as an alert for imminent epidemics.

The analysis of growth rates of SARS-CoV-2 variants using differences in effective reproduction number rather than the frequency of variants could potentially help in evolutionary forecasting of SARS-CoV-2 variants because this method reports the frequency of co-circulating variants by addressing population-level transmission dynamics. However, this would require the development of new techniques to quantify population-level immunity and the escape potential of existing and emerging variants. Furthermore, this approach can be used to analyze the role of specific mutations that define a variant or lineage in governing the changes in effective reproduction number. In conclusion, the findings of the study revealed the transmission dynamics of SARS-CoV-2 variants that could help tackle local and regional epidemics.

Source:

https://www.news-medical.net/news/20211214/Dynamics-and-relative-transmission-rates-of-SARS-CoV-2-variants-in-the-US.aspx