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SARS-CoV-2 evolution on a dynamic immune landscape

Inhalt

Since the onset of the pandemic many SARS-CoV-2 variants have emerged exhibiting substantial evolution in the virus'spike protein, the main target of neutralizing antibodies. A plausible hypothesis proposes that the virus evolves to evade antibody-mediated neutralization (vaccine- or infection-induced) to maximize its ability to infect an immunologically experienced population. Because viral infection induces neutralizing antibodies, viral evolution may thus navigate on a dynamic immune landscape that is shaped by local infection history. We developed a comprehensive mechanistic model, incorporating deep mutational scanning data, antibody pharmacokinetics, and regional genomic surveillance data, to predict the variant-specific relative number of susceptible individuals over time. We show that this quantity precisely matched historical variant dynamics, predicted future variant dynamics and explained global differences in variant dynamics. Our work strongly suggests that the pandemic continuously shapes variant-specific population immunity, which determines a variant's ability to transmit, thus defining variant fitness. The model can be applied to any region by utilizing local genomic surveillance data, allows contextualizing risk assessment of variants and provides information for vaccine design.

Keywords

SARS-CoV-2, antibody waning, immune escape, population immunity, cross-neutralization, evolutionary dynamics, mechanistic modeling

Registration ID

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Professional Status of the Speaker

Senior Scientist

Junior Scientist Status

No, I am not a Junior Scientist.

Track Klassifizierung: Pandemic Prepardness & Prevention

Typ des Beitrags: Both options possible