

DOMINANCE OF NEW VARIANTS DURING THE SARS-COV-2 EPIDEMIC IN SWITZERLAND

Martina L Reichmuth MSc^{1*}, Emma B Hodcroft PhD^{1,2}, Christian L Althaus PhD¹

¹ Institute of Social and Preventive Medicine, University of Bern, Bern, Switzerland

² Swiss Institute of Bioinformatics, Basel, Switzerland

*martina.reichmuth@ispm.unibe.ch; ISPM, Mittelstrasse 43, CH-3012 Bern

Abstract

The COVID-19 pandemic has led to the emergence of SARS-CoV-2 variants of concern (VoC), characterized by viral changes, i.e., increased transmissibility, immune evasion, or differences in severity. The potential impact of intervention strategies to mitigate the early spread of VoC is not fully understood. We used genomic data in combination with a transmission model to investigate the spread of Alpha and Delta in Switzerland.

First, we estimated the number and time of imports using two phylogenetic approaches i.e., a liberal and conservative approach. We created a phylogeny of Swiss sequences and the nearest available sequences to identify Swiss clusters based on imports. Second, we used the estimated number of imports to parameterize a dynamic transmission model that simulates the spread of VoCs in Switzerland.

We estimated 345 to 953 imports of Alpha and 38 to 120 of Delta into Switzerland. Incorporating the estimated imports into the transmission model resulted in a good description of the observed increase in the proportion of VoCs, particularly for the liberal scenario (Figure). Despite ten times fewer imports of Delta than Alpha, because of its increased transmissibility and the lower incidence when introduced, Delta dominated more quickly. In counterfactual scenarios, we investigated the impact of border closures and different levels of surveillance on the spread of VoCs.

We present an innovative framework to integrate genomic data into a dynamic transmission model of SARS-CoV-2. Quantifying the number of imports over time and investigating the potential impact of different interventions will help to inform surveillance strategies for international travelers as new VoCs emerge.

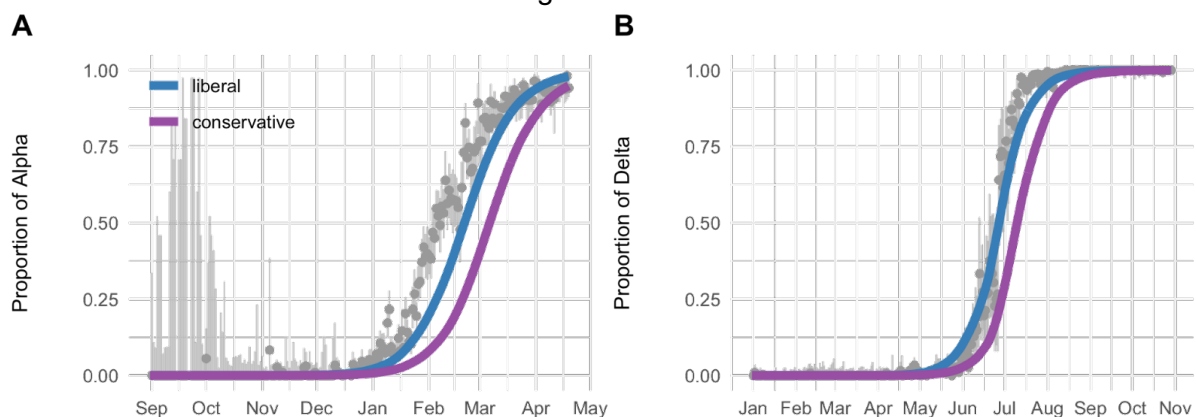


Figure. Increase in the proportion of Alpha and Delta among confirmed cases in Switzerland. Results of the transmission model using two phylogenetic approaches are shown as colored lines. Estimated proportions of VoCs based on sequenced samples are shown in gray.