Transmission of SARS-CoV-2 variants in Switzerland

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Summary

- **The proportion of SARS-CoV-2 variants (501Y, B.1.1.7) among confirmed cases rapidly increases in Geneva, Zurich, and in Switzerland overall.**
- **We estimate an increase in transmissibility of around 50% for the new SARS-CoV-2 variants (501Y, B.1.1.7).**
- **These findings underline the importance of efficient control measures in order to prevent an increase in SARS-CoV-2 incidence in Switzerland.**

Results

Three recently detected variants (B.1.1.7, B.1.351, P.1) of SARS-CoV-2 are currently being detected in various countries worldwide. Two of these variants (B.1.1.7, B.1.351) have also been detected in Switzerland.

We aim at tracking the spread of these variants in the cantons of Geneva and Zurich and in Switzerland overall (Figure 1). As a comparison, we also provide an analysis of the spread of B.1.1.7 in Denmark. Finally, we estimate the current proportion of the variants among all samples and their increased transmissibility (Figure 2).

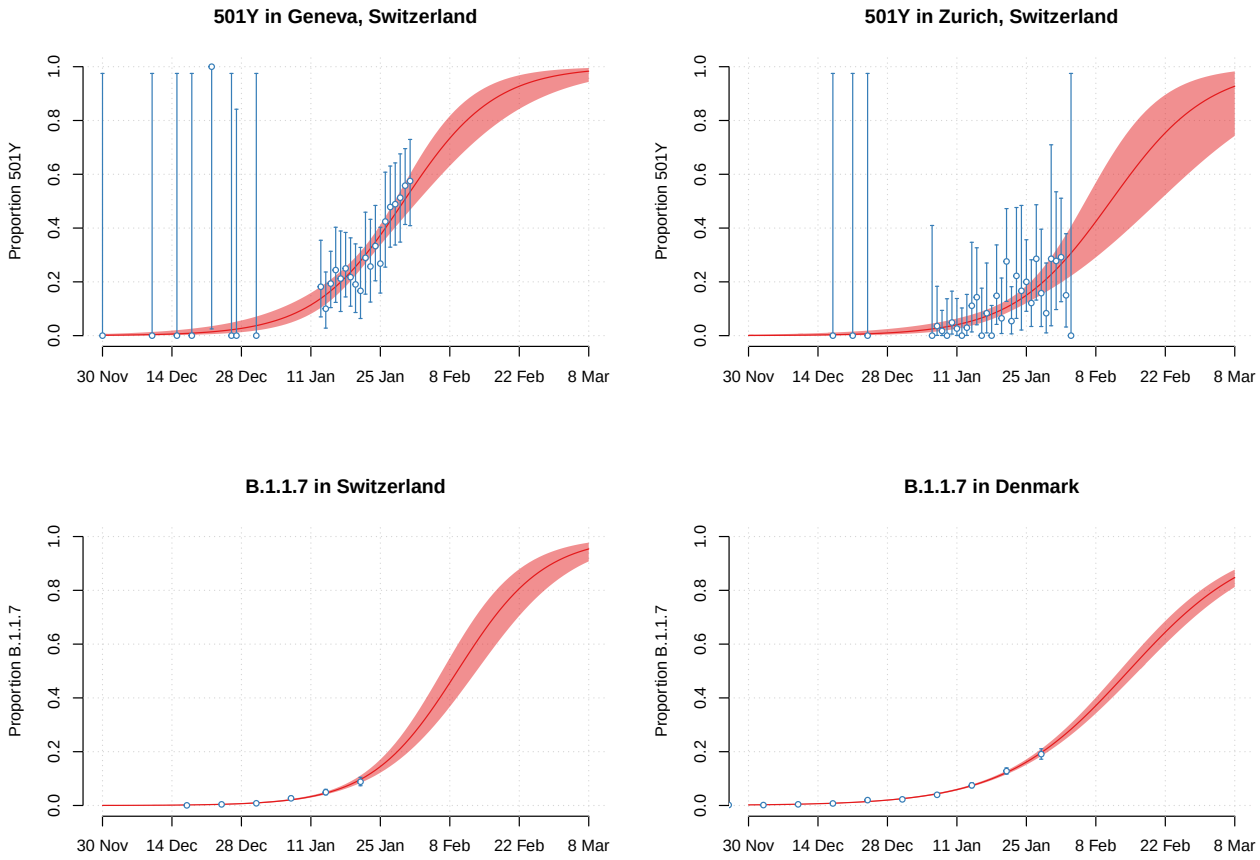

Figure 1. Increase in the proportion of SARS-CoV-2 variants in Switzerland and Denmark. Error bars and shaded areas correspond to the 95% confidence intervals of the data (blue) and model (red), respectively.

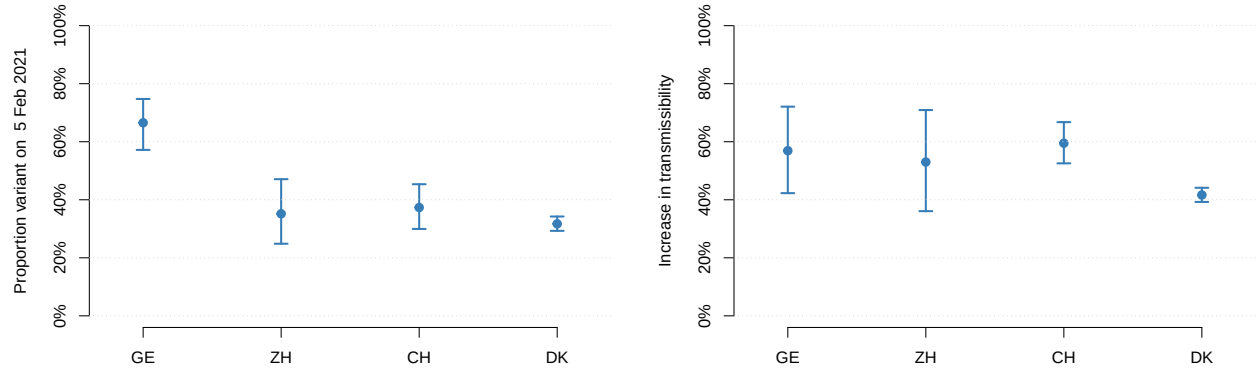

Figure 2. Estimated proportion of the variant on 5 February 2021 (left) and increase in transmissibility (right). Error bars correspond to the 95% confidence intervals.

The proportion of the variants rapidly increases in all regions. Fitting a logistic growth model to the data allows to quantify and project the increase in the proportion of the new variants (see Volz et al. for further details). We estimate the **proportion of the variants** by 5 February 2021 at:

- 67% (95% CI: 57%-75%) for 501Y in Geneva,
- 35% (95% CI: 25%-47%) for 501Y in Zurich,
- 37% (95% CI: 30%-45%) for B.1.1.7 in all of Switzerland,
- 32% (95% CI: 29%-34%) for B.1.1.7 in Denmark.

Note that due to the delay from infection to sample collection, the shown increase and the estimated proportions of the new variants reflect the epidemic situation from one to two weeks ago.

Assuming an effective reproduction number *Re* around 1 and a generation time of 5.2 days (Ganyani et al.), we estimate the following **increase in transmissibility** of the new variants compared to previously circulating variants:

- 57% (95% CI: 42%-72%) for 501Y in Geneva,
- 53% (95% CI: 36%-71%) for 501Y in Zurich,
- 59% (95% CI: 53%-67%) for B.1.1.7 in all of Switzerland,
- 42% (95% CI: 39%-44%) for B.1.1.7 in Denmark.

These estimates are in good agreement with earlier findings for B.1.1.7 in the UK (Volz et al., Davies et al., Leung et al.). The estimate for B.1.1.7 in Denmark appears to be somewhat lower than the estimates for Switzerland. This could be due to the following reasons. First, *Re* was relatively low in Denmark at the end of December 2020 and in early January 2021 (https://ibz-shiny.ethz.ch/covid-19-re-international/) which would result in a slower increase in the proportion of the new variant and consequently a biased estimated of the increase in transmissibility. Second, the increase of new variants could at least partly be driven by immune escape and Denmark has arguably a lower overall infection attack rate than Switzerland. Third, data from Switzerland could be biased towards higher coverage of new variants due to current outbreak investigations. In contrast, Denmark sequences a considerable proportion of all confirmed SARS-CoV-2 cases and their sample might thus be more representative.

Taken together, these findings underline the importance of efficient control measures in order to prevent an increase in SARS-CoV-2 incidence in Switzerland.

Data

We use the following four data sets for our analysis:

- **Geneva, Switzerland:** We use samples that were sent to the Geneva University Hospitals for primary diagnosis of SARS-CoV-2. All positives were re-screened for 501Y using RT-PCR (mostly B.1.1.7). To cover the period of November and December 2020, we use sequence data from randomly chosen samples from Geneva that were submitted to GISAID by the Swiss Viollier Sequencing Consortium from ETH Zurich (download here).
- **Zurich, Switzerland:** We use samples from SARS-CoV-2-positive cases from the University Hospital Zurich and test centers at Spital Limmattaal and Spital Männedorf that were re-screened for 501Y using RT-PCR at the Institute of Medical Virology, University of Zurich (download here).
- **Switzerland:** We use data on the frequency of B.1.1.7 among randomly chosen SARS-CoV-2 samples that underwent genetic characterization and are provided by the Swiss Viollier Sequencing Consortium from ETH Zurich and the Swiss National COVID-19 Science Task Force (download here).
- **Denmark:** We use data on the frequency of B.1.1.7 among sequenced genomes from the Danish Covid-19 Genome Consortium (download here).

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