

# GENETIC DIVERSITY OF SARS-CoV-2 IN CROATIA

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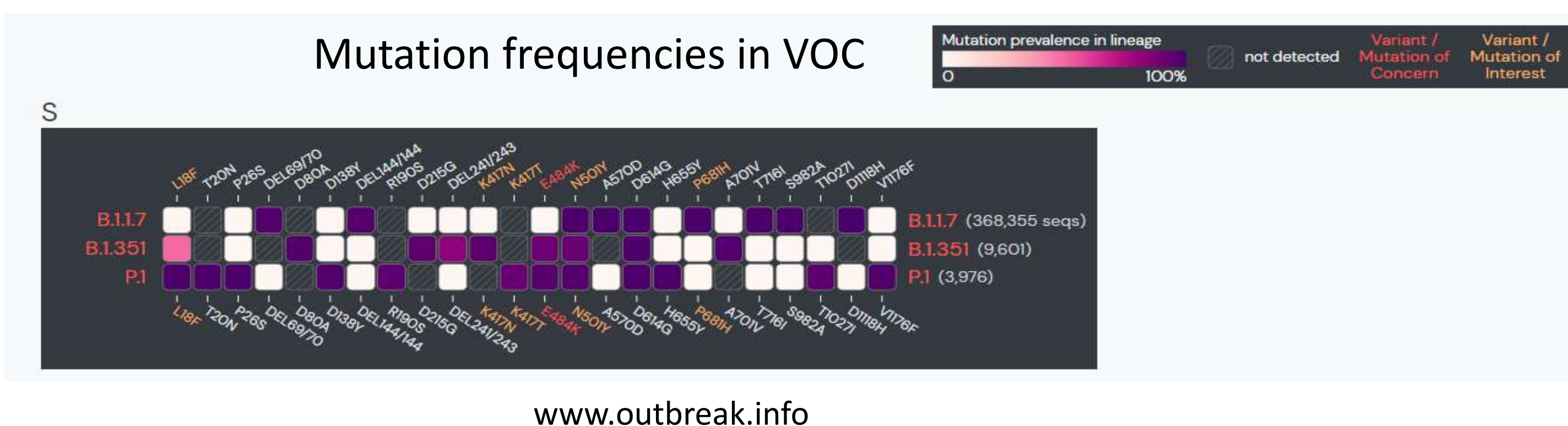
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## INTRODUCTION

- SARS-CoV-2 as an RNA virus with a large genome is subject to rapid mutation as it replicates. Among silent or deleterious mutations are the one that create variants with a selective advantage.
- In late 2020 and early 2021 emerged variants that appear to be more transmissible than existing strains, evade immunologic response and induce more severe disease. Three variants that rapidly became dominant in specific area and were designated variant of concern (VOC) are: VOC-202012/01 (B.1.1.7), 501Y.V2 (B.1.351) and P.1 (B.1.1.28.1).



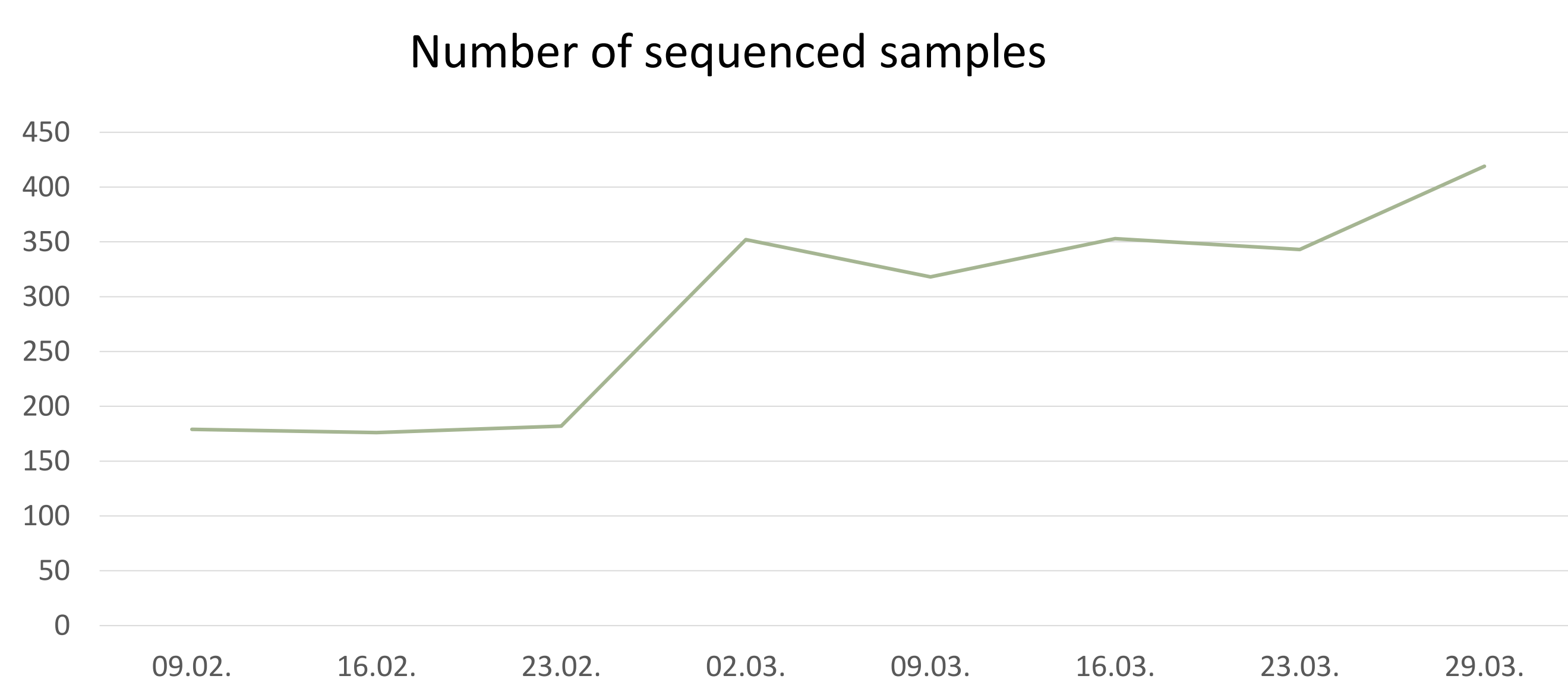
- GISAID acknowledges two more VOCs: GH/452R.V1 (B.1.429+B.1.427) and G/484K.V3 (B.1.525)

## AIM

- To monitor epidemiologic situation in Croatia
- To investigate virus transmission dynamics and introductions of novel genetic variants
- To assess the impact of mutations on the performance of molecular diagnostic, antigen characterisation and serological methods

## METHODS

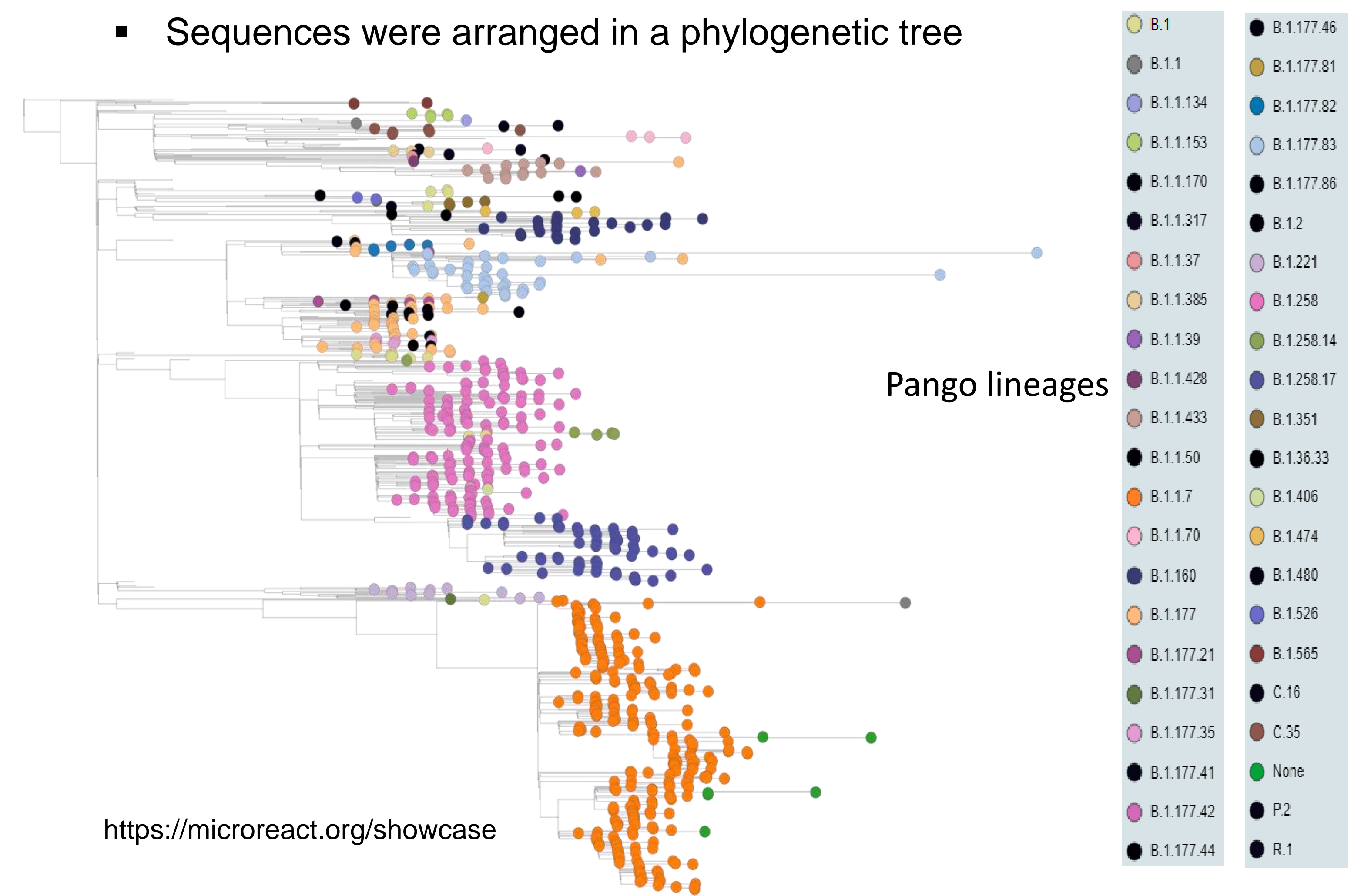
- Weekly based whole genome sequencing (WGS) was performed by a commercial laboratory with Illumina sequencing technology from 09.02.2021 on 5-10% SARS-CoV-2 positive samples in Croatia.



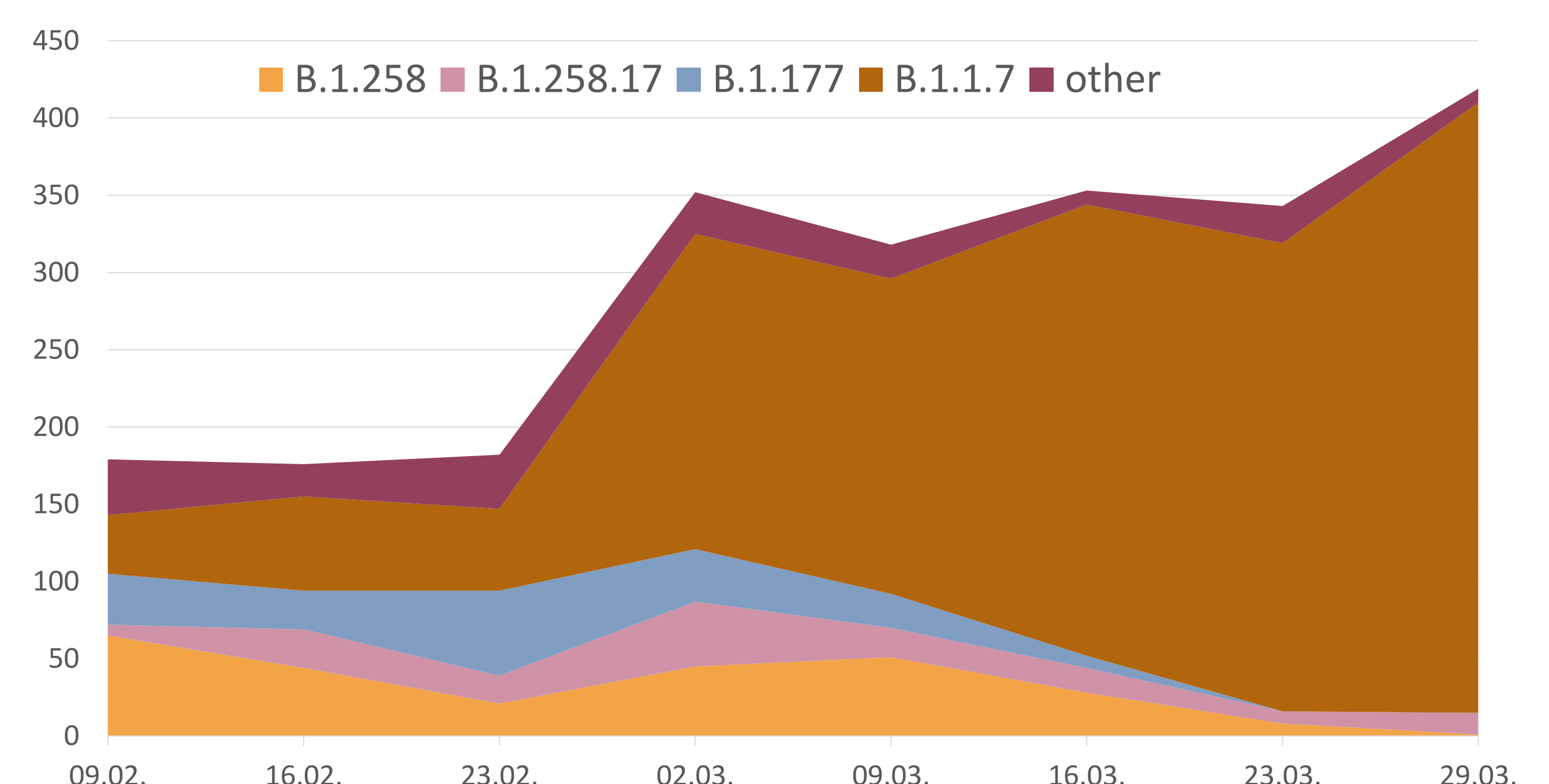
- Obtained sequences were uploaded to GISAID database and isolates were categorized in phylogenetic clades depending on single nucleotide polymorphism (SNP) present in the genome.
- By the end of March 2021 we processed 2632 samples. 1901 samples were successfully sequenced.

## RESULTS

- Sequences were arranged in a phylogenetic tree



- Delivered results showed marked continuous increase in B.1.1.7 presence from 21.23% in the first week of testing, to 94.27% in the last week of March



- Variant B.1.351 from GH clade was detected in 15 samples, mainly related to traveling abroad and their close contacts. B.1.526 detected in 4 samples, carries mutation essential for the loss of neutralizing activity of some monoclonal antibodies and is considered variant of interest.

## CONCLUSION

- Due to high transmissibility rate of VOC-202012/01 (B.1.1.7) by the end of March 2021 it became dominant SARS-CoV-2 lineage in Croatia.
- Between second and third wave of epidemic, virus lineages form clade G, GR and GV were dominant, but marked weekly increase of GRY clade indicated the beginning of the third epidemic wave in Croatia.

## REFERENCES

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