Quick SARS-CoV-2 surveillance in the central European region using SGTF and a panel of seven mutation of concern RT-PCR SNP assays

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Introduction

Several SARS-CoV-2 variants have emerged that have been designated either as Variants of Concern (VOC) or Variants of Interest (VOI). VOC/VOI have Mutations of Concern (MOC) in the S-protein such as N501Y that confer increased transmissibility, and E484K/Q and K417T/N that can lead to immune escape.

Whole genome sequencing (WGS) is the conventional method for strain surveillance. However, WGS is not easily scalable for testing large numbers of samples and turnaround times (TAT) of ≥3 days can be prohibitive for swift reactions by public health care systems to contain the spread.

The S-gene Target Failure (SGTF) of the TaqPath™ COVID-19 CE-IVD RT-PCR Kit serves as a proxy for H69_V70Del seen in B.1.1.7 variant.

Aim

In this study, we evaluated SGTF along with a panel of 7 MOCs (SGTF+MOC) for strain surveillance and lineage assignment of circulating SARS-CoV-2 strains, the results for which can be made available in < 24 hours.

The workflow was directly compared to WGS to assess the accuracy for discrimination of VOC/VOI.

Methods

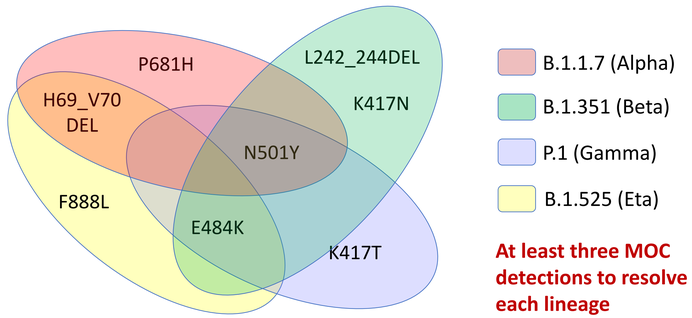

Figure 1. Mutations of Concern (MOC). 7 MOCs were chosen according to the VOC/VOI circulating in the area and used in combination to resolve each lineage. As a proxy for the H69_V70Del mutation, the S-gene target failure (SGTF) on the TaqPath™ CE-IVD kit was used.

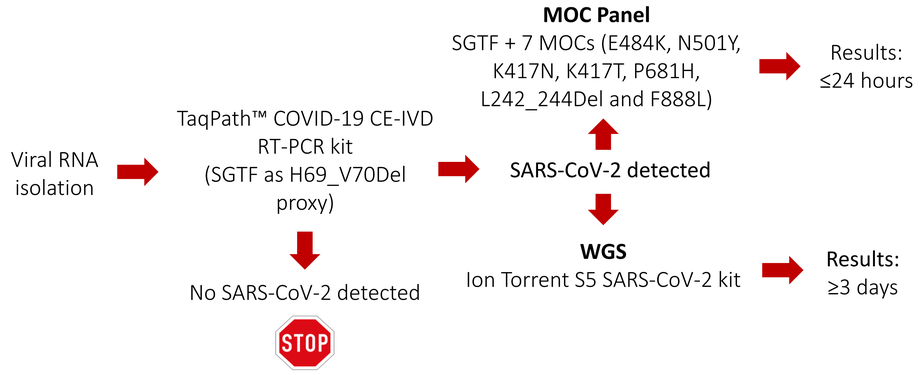

Figure 2. VOC/VOI identification workflow. 580 SARS-CoV-2 positive samples naso- and oropharyngeal samples were analysed using the TaqPath™ COVID-CE-IVD RT-PCR kit and were chosen for a paired analysis using WGS and MOC panel.

Results

SARS-CoV-2 lineages identified in the alpine region of Austria and Italy (January – May 2021)

WGS		MOC Panel	
B.1.1.7 (Alpha)	314	B.1.1.7 (Alpha)	314
B.1.351 (Beta)	23	B.1.351 (Beta)	23
P.1 (Gamma)	3	P.1 (Gamma)	3
B.1.525 (Eta)	10	B.1.525 (Eta)	10
B.1.177	35	Other Lineages	230
B.1.258	180		
Other (minor)	15		
Total determined	580	Total determined	580

Table 1. Paired analysis showed 100% agreement between the MOC panel and WGS.

Conclusions

Mutation of Concern Panel

Reliable (100% accuracy) and swift (TAT≤24hours) identification of lineages imposing highest threat in the region of interest

Whole Genome Sequencing

Monitoring for novel or undetermined strains

Fine tuning for further mutation assay panel modifications/updates