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## INTRODUCTION

The importance of a rapid discrimination between a Wild Type SARS-CoV-2 infection and the (English)  $\alpha$  Variant B.1.1.7, in absence of a sequencing machine, for epidemiologic purposes.

## AIM

Research for a correlation between an abnormal curve of the S/RdRP in the trend of the amplification curves and the presence of a possible variant, as a rapid selection method for viral genome sequencing.

## METHOD

As the protocol of the Veneto region, 8 positive samples for SARS-CoV-2 are sent every week to the reference laboratory of the zooprophyllactic institute of the Venezie in order to monitor the presence of viral variants.

The samples first were processed using the Nimbus extractor and the Biorad CFX96 amplifier using the Allplex SARS-CoV-2 Seegene® kit which amplified the “S” gene in association with the RdRP gene and then sequenced. All samples sent to the reference laboratory had a CT (Threshold Cycles) below 26. The sequencing has been performed with Mi-Seq Illumina®.

150 samples, presenting an abnormal curve, has been sent to the Istitute in order to verify the belonging to the (English)  $\alpha$  Variant VOC-202012/01 (B.1.1.7) which involves mutations on the 'spike' protein, the one responsible for the adhesion of the virus to the host cell and the entry of viral RNA.

This variant under study possesses mutations in some amino acids of the spike protein that would make the virus more infectious than the virus belonging to the wt strain.

## RESULTS

After one careful re-evaluation of the amplification curves of the S/RdRP gene, it was observed that all the samples with the “ $\alpha$ ” variant had a less sigmoid curve and more at 45° compared to the normal strain curve WT. The difference in the curves of the two strains was illustrated in the two figures, respectively WT and then “ $\alpha$ ” strain.

All the 150 samples with an abnormal curve, sent to Zooprophyllactic Institute of the Venezie, have been confirmed as  $\alpha$  Variant.

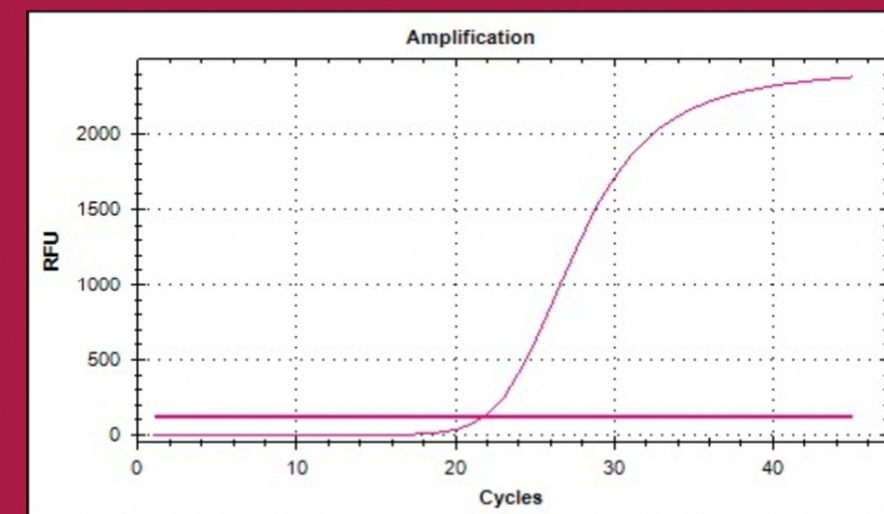


Figure 1: Wilde type amplification curve in SARS-CoV-2 of the S/RdRP gene

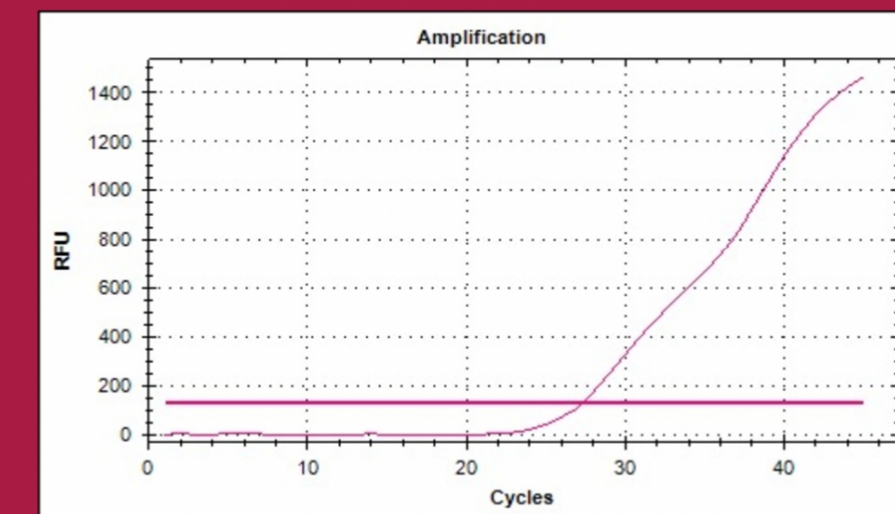


Figure 2: English variant B.1.1.7 amplification curve in SARS-CoV-2 of the S/RdRP gene

## CONCLUSIONS

Performing the routine analysis of the amplification curves allows for a quick screening of the samples before sequencing results for suspected  $\alpha$  variant.

This system can as well improve a faster identification of the contacts and the duration of isolation of quarantine in order to limit the diffusion of the variants as much as possible.

## REFERENCES

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