

# Identifying common mutations in SARS-CoV-2, B.1.1.7 and B.1.617.2 variants

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## Coronavirus 2019 and SARS-CoV-2

Coronavirus Disease 2019 (COVID-19) caused by infection of Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) first emerged in October 2019.

COVID-19's ability to transmit has led to a global pandemic that continues to spread.

This virus has undergone mutations and created variants of the original virus which have different symptoms and different rates of morbidity, prevalence, and mortality than the original virus.

## Objective

Our goal is to use variant analysis techniques to identify the location of these mutations and compare and analyze the similarities between the Alpha variant and Delta variant.

## Hypothesis

We hypothesize that the Alpha and Delta variants will have one of the same mutations on the spike gene of the SARS-CoV-2 genome.

## B.1.1.7: Alpha variant

The B.1.1.7 (Alpha) was first reported in United Kingdom in September 2020.

This variant is different than the original because of a 6 nucleotide deletion mutation in the SARS-Cov-2 genome which prevents the amplification of s(pike) gene target resulting in S-gene Target Failure (SGTF).

## B.1.617.2: Delta variant

The B.1.617.2 (Delta) was first reported in India in December 2020.

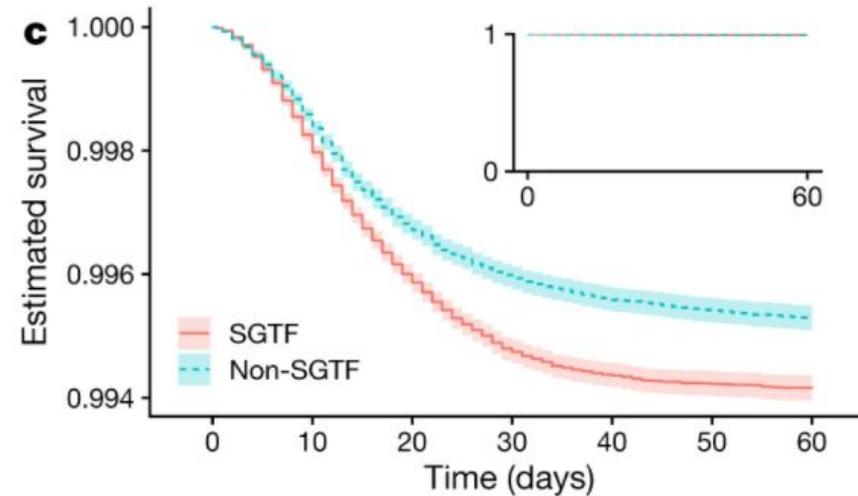
In the United States, this variant was first detected in March 2021 and is one of the most dominant SARS-CoV-2 strains in the US. Current studies indicate that the Delta variant has higher morbidity and mortality rates than the original SARS-CoV-2 virus.

This variant has ten mutations (T19R, (G142D\*), 156del, 157del, R158G, L452R, T478K, D614G, P681R, D950N) in the spike protein.

# S-gene

The S-gene is important for receptor recognition and cell membrane fusion in SARS-CoV-2. Mutations in the S-gene have caused the gene to not be expressed in the Alpha and Delta variant. When this gene is not expressed it is called S(pike)- gene Target Failure (SGTF).

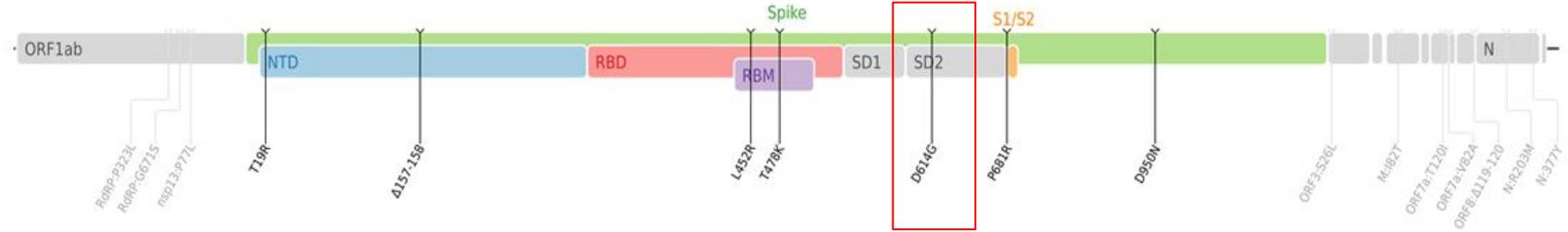
Evidence indicates that cases of Covid-19 of the Alpha variant with SGTF have higher rates of mortality and have lower estimated rates of survival than the cases of original strain.



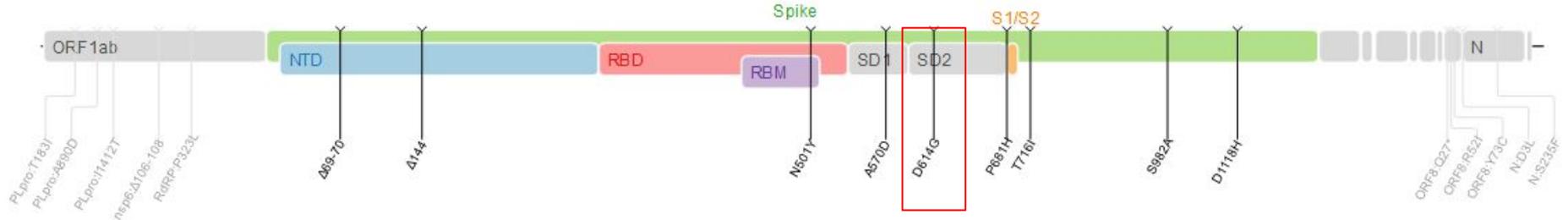
Davies et al. (2021). Increased mortality in community-tested cases of SARS-CoV-2 lineage B.1.1.7. <https://doi.org/10.1101/2021.02.01.21250959>

Based on this information, we will be comparing the genome of the Alpha variant to Delta variant to identify any similarities and possibly pinpoint the location of a mutation.

## Alpha



## Delta



# Sample collection

Open-source sharing of viral genome sequences have allowed researchers to track emerging SARS-CoV-2 variants.

In this study, we compared genomic sequences of SARS-CoV-2 variants, Alpha (SRR13744683) and Delta (SRR14401829), to investigate and identify common mutations that are associated with mortality rates

Samples were collected from the NCBI SRA site for genomic sequences.

# Method- GATK pipeline with COVID-19 genome

## Quality assessment

- Fastqc and trimmomatic in order to filter data

## Read alignment

- Mapping using bwa

## Variant Identification -> annotation

- Variant calling using gatk environment and variant annotation

## Visualization

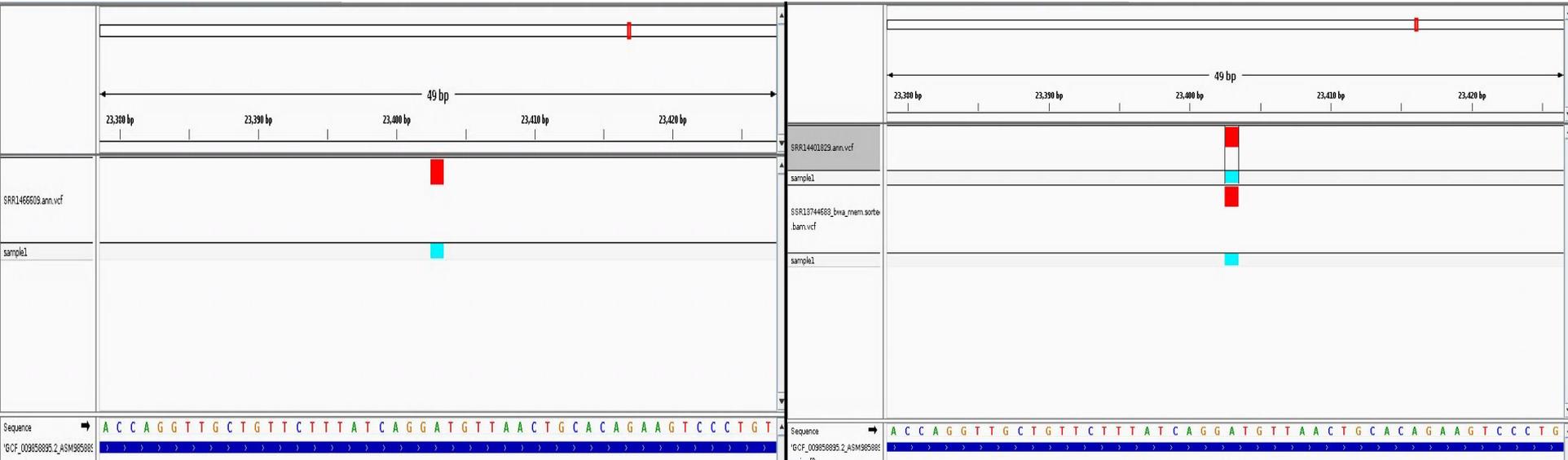
- Visualized our analysis in the form of a report and DNA sequence

# Location 23,403 bp: Original vs. Variants

- Comparison between samples from Delta and Alpha SARS\_CoV-2 in location 23,403bp
- Both samples take place at the same base pair with same mutation
  - Potential lethality is taken place in this position.
  - n=1

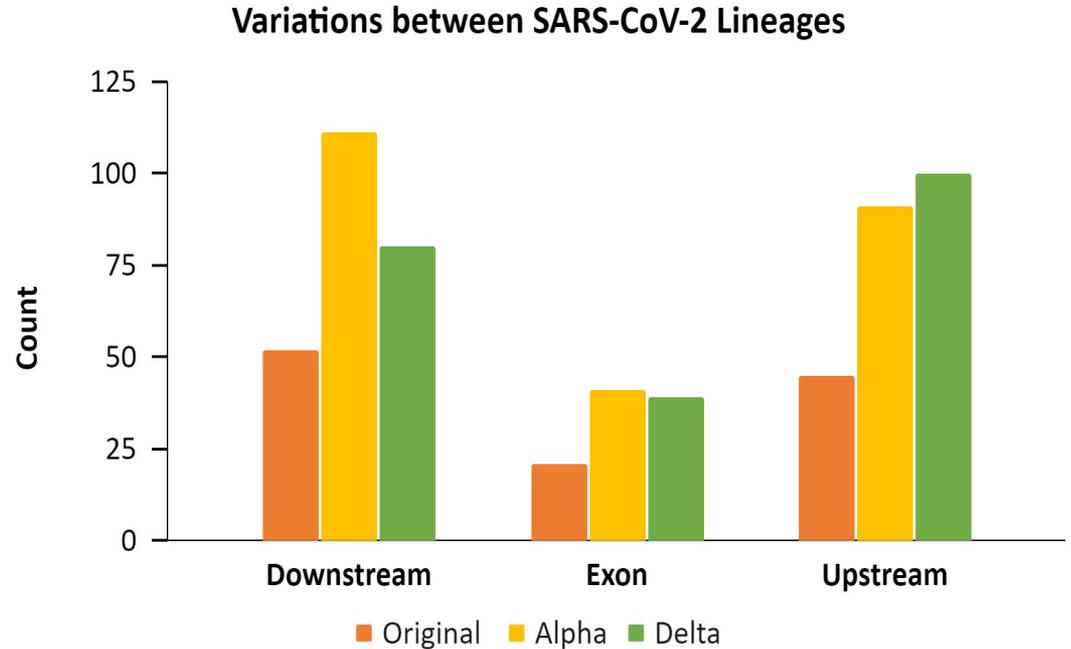
Original

Top: Delta Sample  
Bottom: Alpha Sample



# Report Comparison

- Difference in variation counts are taken place
- S gene is associated with upstream
  - Main focus
  - Most variation is taken place in delta variant

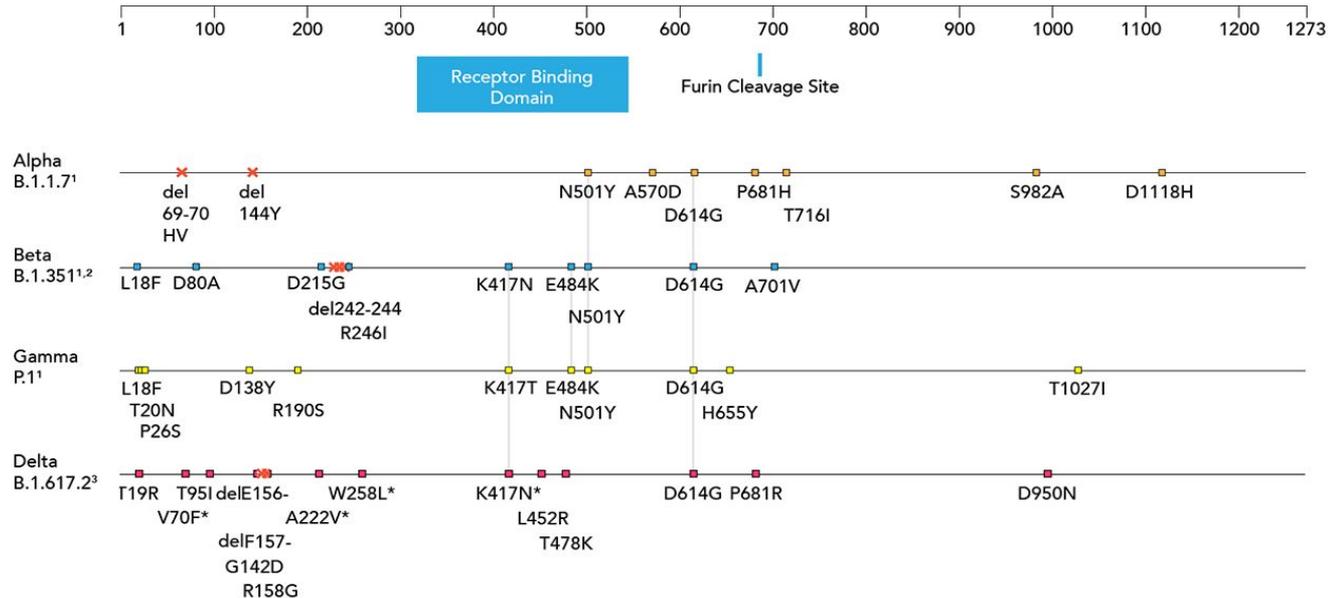


# Conclusion

- At base pair 23,403 there is a missense mutation in both Alpha and Delta variants.
- The SARS-CoV-2 Variant Alpha lineage B.1.1.7 is an older variant and has less upstream variation than the newer more prevalent Delta
- The three samples' mutations take place in the same region
  - There is a difference in the amount of mutations taken place
  - Provides a potential location for looking into mutations in variants
- Pinpointing the exact variants proved to be very difficult
- Expert research confirmed our hypothesis

# Discussion

- Location 23,403 bp is the missense mutation D614G.
- This is the only mutation that is consistently exhibited from the Alpha Variant to the Delta Variant



\*Detected in some sequences but not all.

<sup>1</sup>[https://cov-lineages.org/global\\_report.html](https://cov-lineages.org/global_report.html)

<sup>2</sup><https://doi.org/10.1101/2021.01.25.428137>

<sup>3</sup><https://www.cdc.gov/coronavirus/2019-ncov/variants/variant-info.html>

# Future Applications

- This was a week long project with two days of work but with more time we would compare even more variants to test for the presence of this same mutation.
- The same method we implemented can be used in the future to test newer variants, to understand how the virus is mutating and if new variants are mutating from older variants.
- This technique can also be used with other genes to identify similar mutations between variants.

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Questions?

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