

Analysis of SARS-CoV-2 B.1.1.7 Variant Mutation Trends

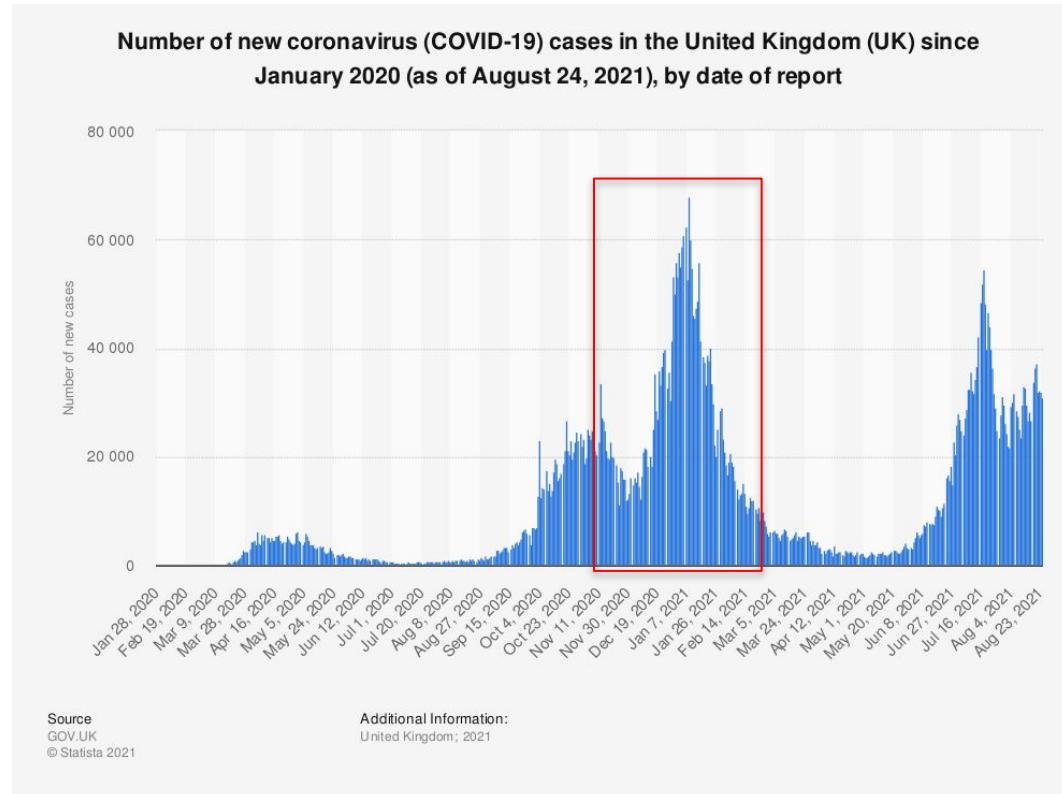
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Julianne Jimenez

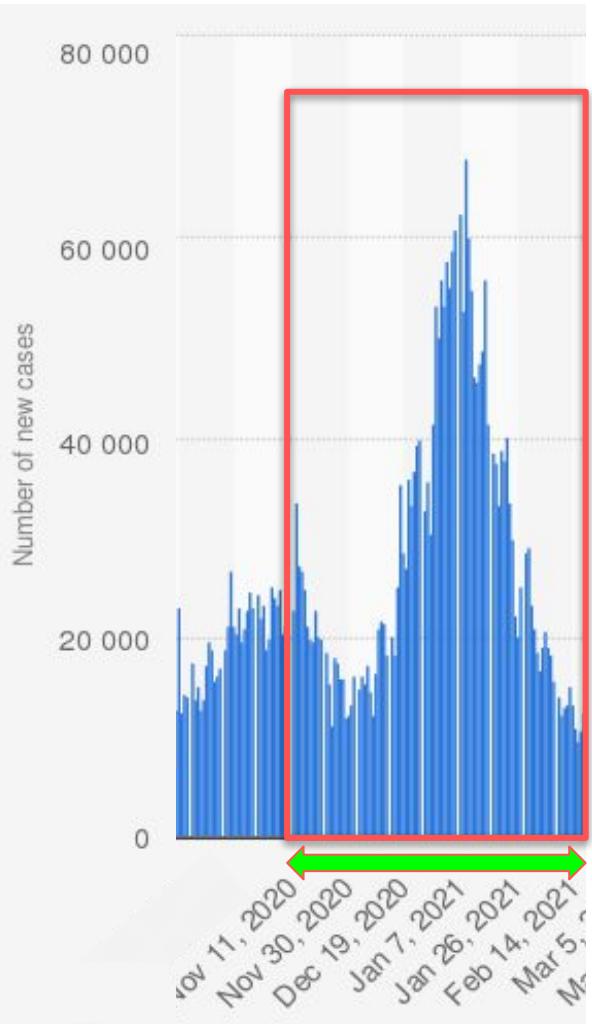
SARS-CoV-2

- SARS-CoV-2 is a coronavirus that causes the respiratory illness COVID-19.
- COVID-19 was first discovered in Wuhan, China and since then different variants of SARS-CoV-2 have arose due to the mutations in virus' genome.
- The first variant was detected in the United Kingdom in the winter of 2020, named Alpha.
- The Alpha variant is known to have nearly 50% increased transmission and it potentially attributes to increased fatality rates.

United Kingdom Spike in Cases

After the detection of first alpha variant, UK had a spike in COVID cases in the winter of 2020.





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Science News

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Alpha variant of COVID-19 spread via 'super-seeding' event in UK, research finds

Date: July 22, 2021

Source: University of Oxford

Summary: The rapid spread of the Alpha variant of COVID-19 in the UK resulted from biological changes in the virus and was enhanced by large numbers of infected people 'exporting' the variant around the country, in what the researchers call a 'super-seeding' event.

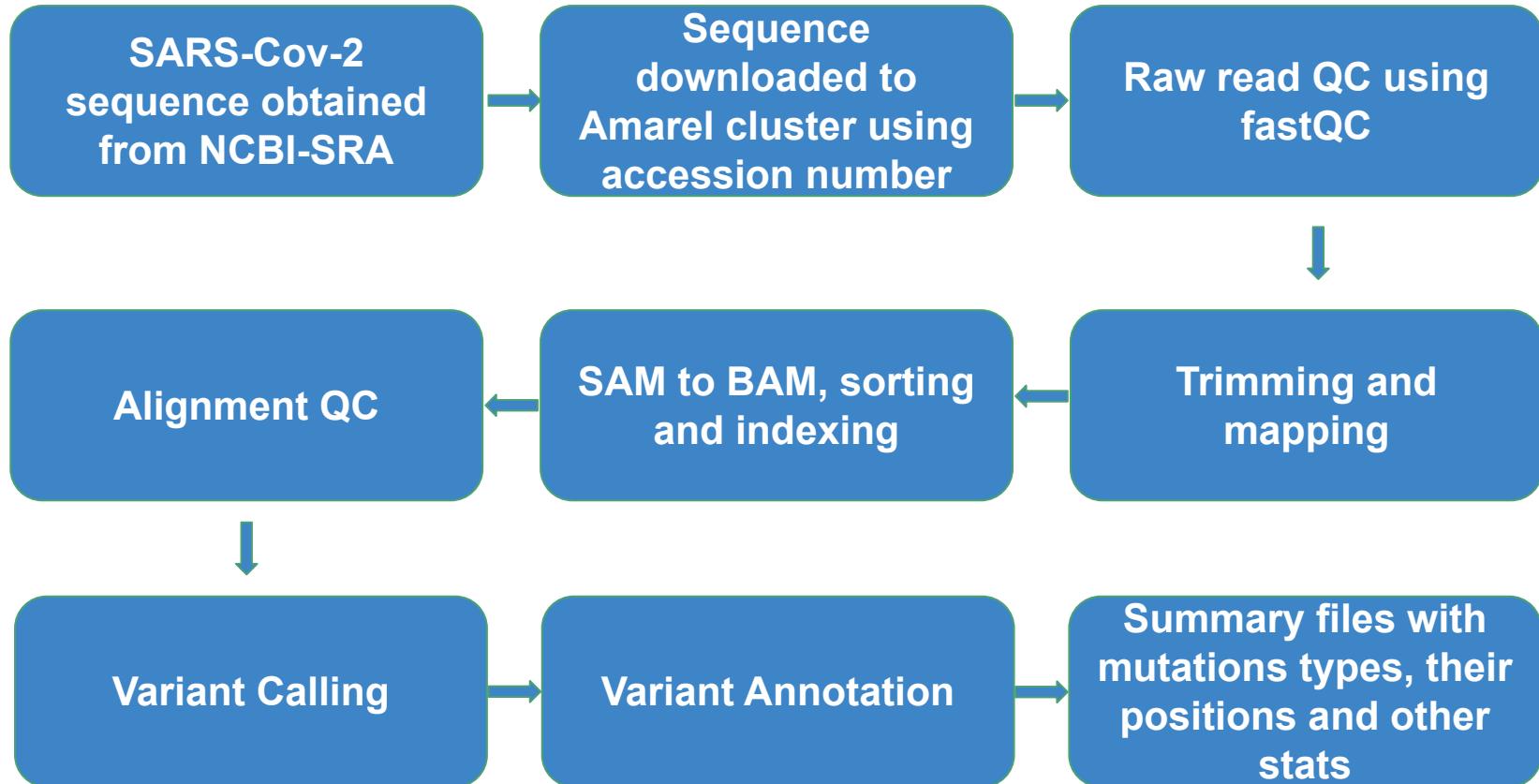
Question

Did the rate of mutation in SARS-CoV-2 change during these four months and if so, was there a correlation between this change and infection rate?

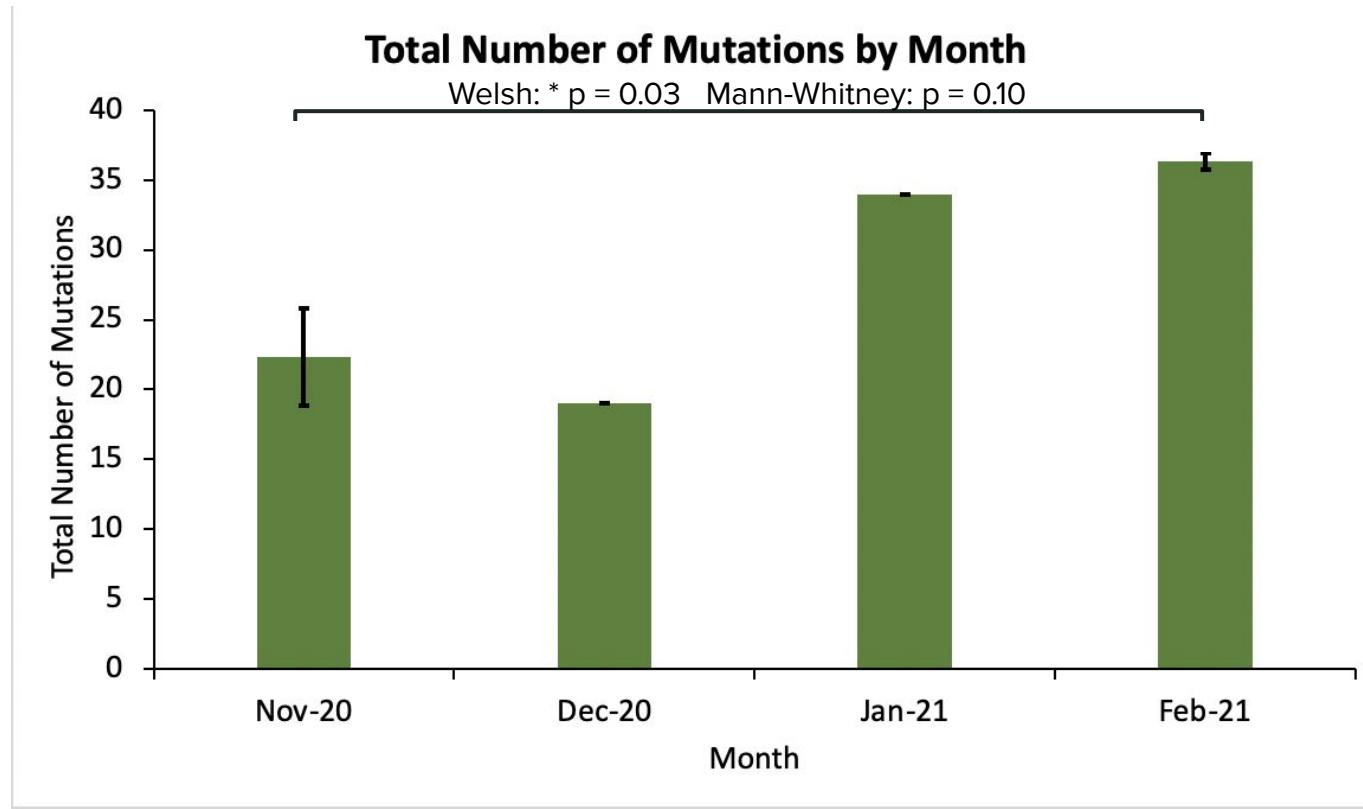
Hypothesis

We hypothesize that the rate of mutation of the SARS-CoV-2 virus will be directly proportional to the increase in cases.

Methods

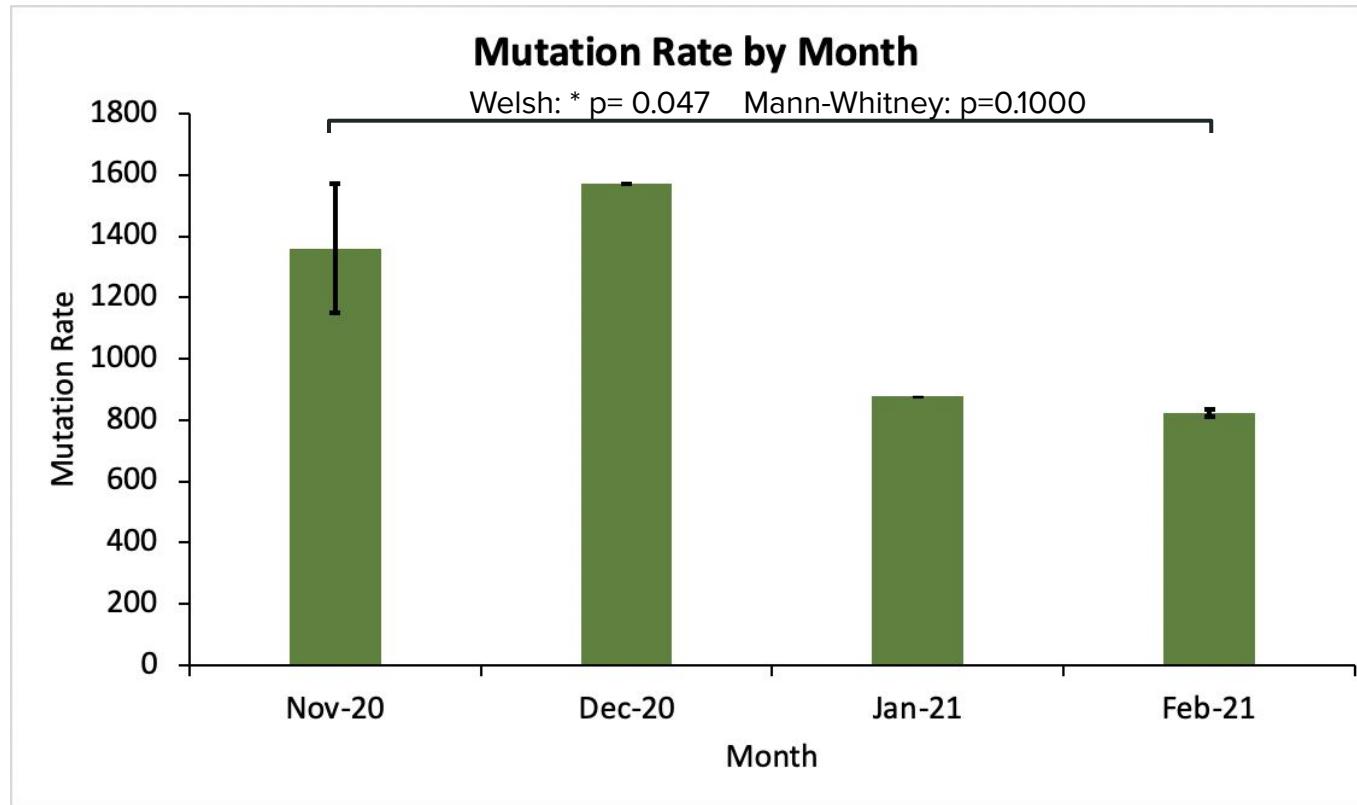


Number of Mutations by Month

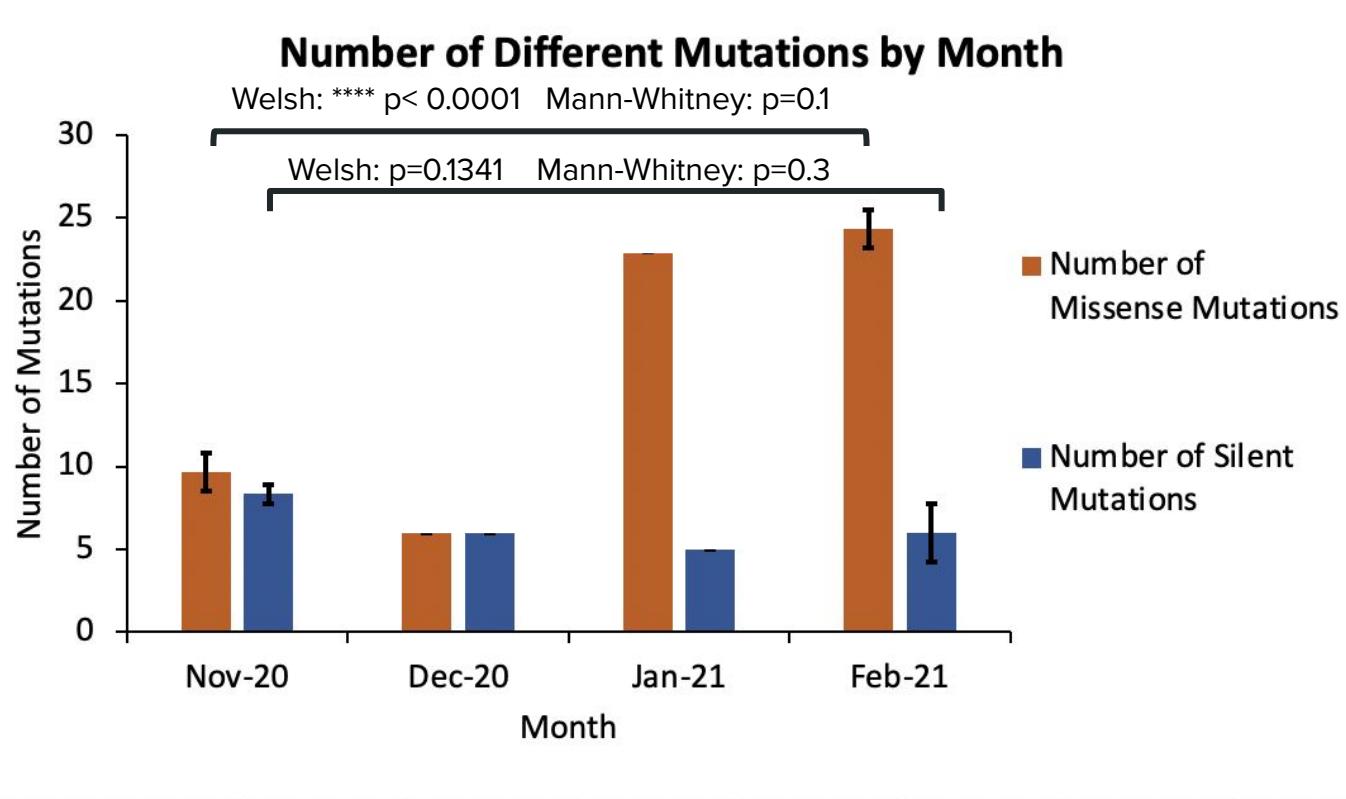


Rate of Mutations by Month

Mutation Rate Formula:
Total # nucleotides / Total # mutations

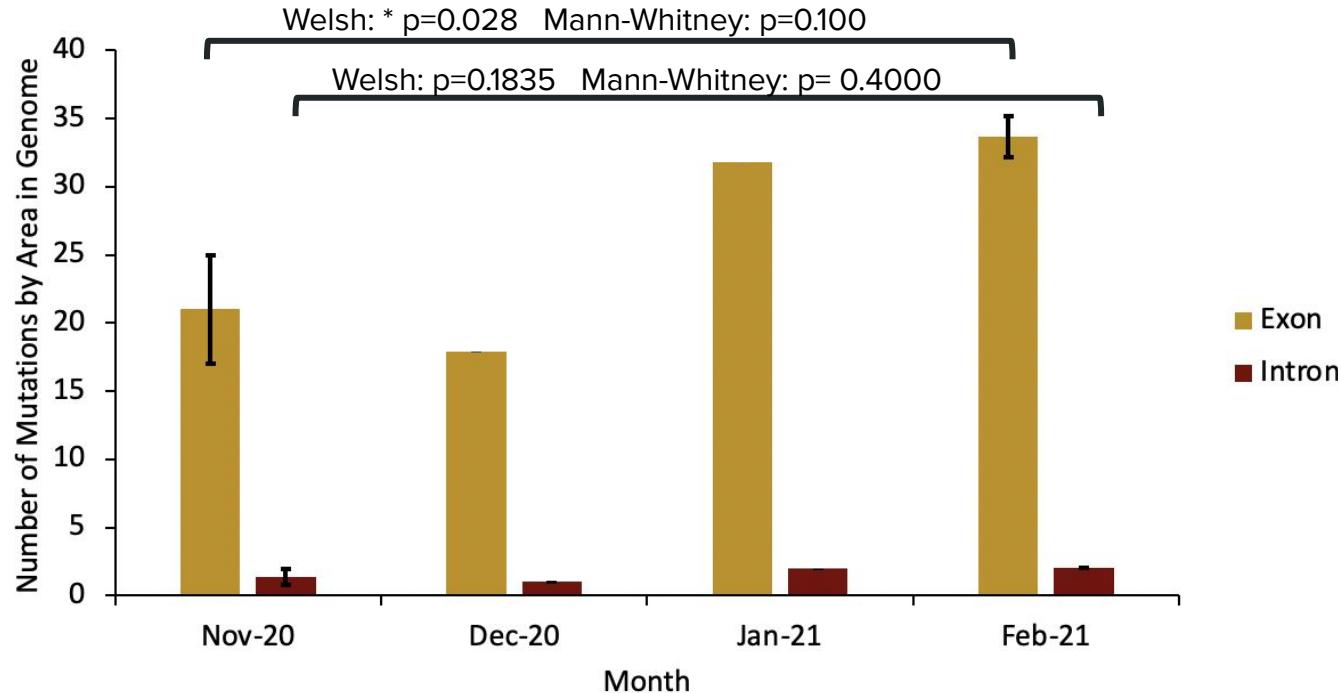


Number of Different Mutations by Month



Location of Mutations in the Genome

Number of Mutations in Different Areas of Genome by Month



Conclusions and Future Directions

- A trend showed an increase in missense mutations in January and February, which explains the increased infection rate in January and February.
- Since most of the mutations were on exons, it suggests that the transcription of mRNA will be affected, changing the functioning of proteins produced.
- Most of the mutations were on the exons, and since exons code for proteins, mutations in the exons were likely beneficial for the virus.
- In the future, we will analyze three or more SARS-CoV-2 sequence samples from each month to perform statistical analysis and draw proper conclusions.

References

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Acknowledgements

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