

Emergence of a novel SARS-CoV-2 strain in Southern California, USA

Dr. Jasmine Plummer

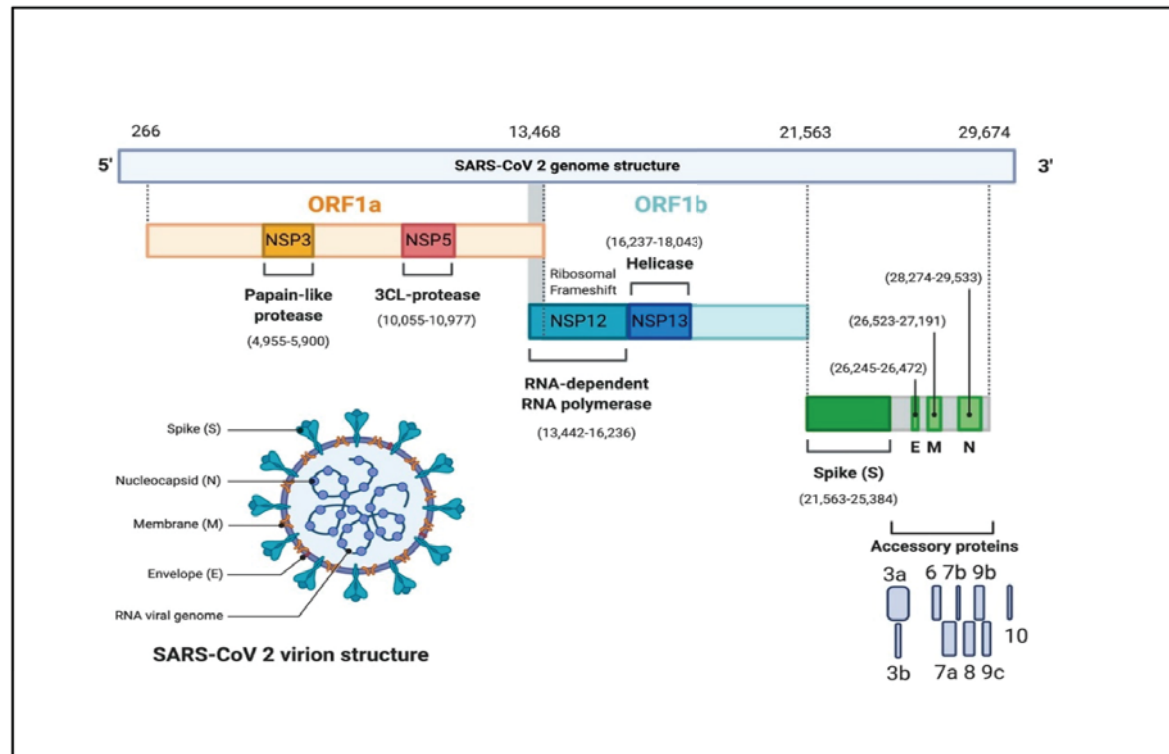
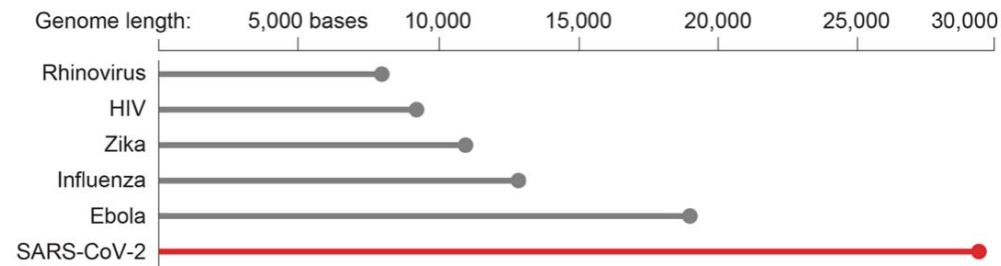
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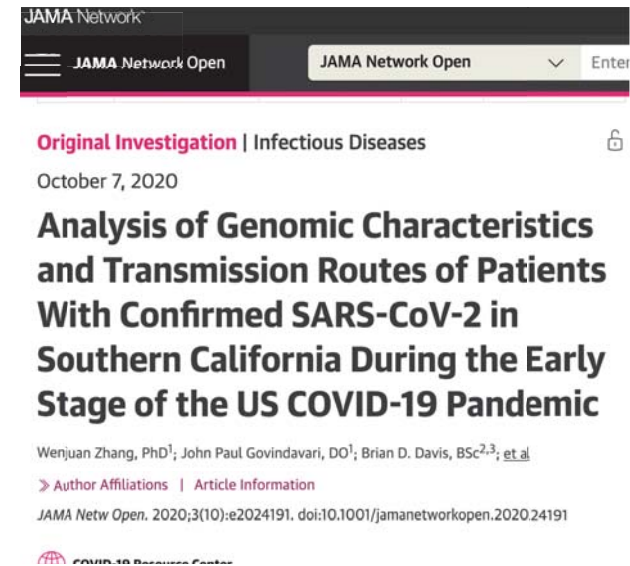
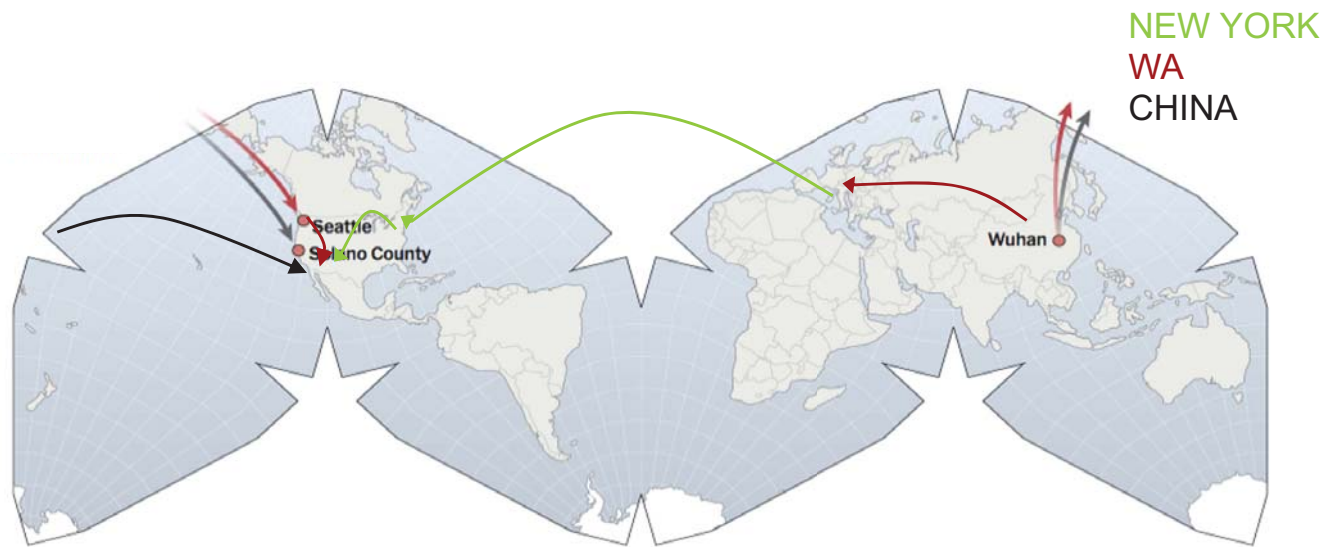
Coronavirus, COVID-19, SARS-CoV-2, variants and evolution

- SARS-CoV-2 is the coronavirus which causes COVID-19, the disease associated upon infection
- Variant is a change at the DNA level
- All living things acquire these changes over time, viruses evolve
- The distinction between a variant and a strain is based on if the virus behaves in a distinct way, the designation becomes strain
- We can use these changes to track the spread of viruses by looking at what SARS-CoV-2 looks like from people in a given area or location using a technology called Next Generation Sequencing
- Sequence COVID-19+ people and look to see what their SARS-CoV-2 DNA sequence looks like, who looks more like who.

SARS-CoV-2 genome



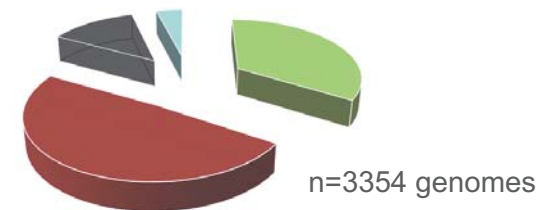
Possible transmission routes: early in Los Angeles pandemic



Can we use genomic sequencing to analyze possible transmission routes to local US West Coast population (Cedars)?

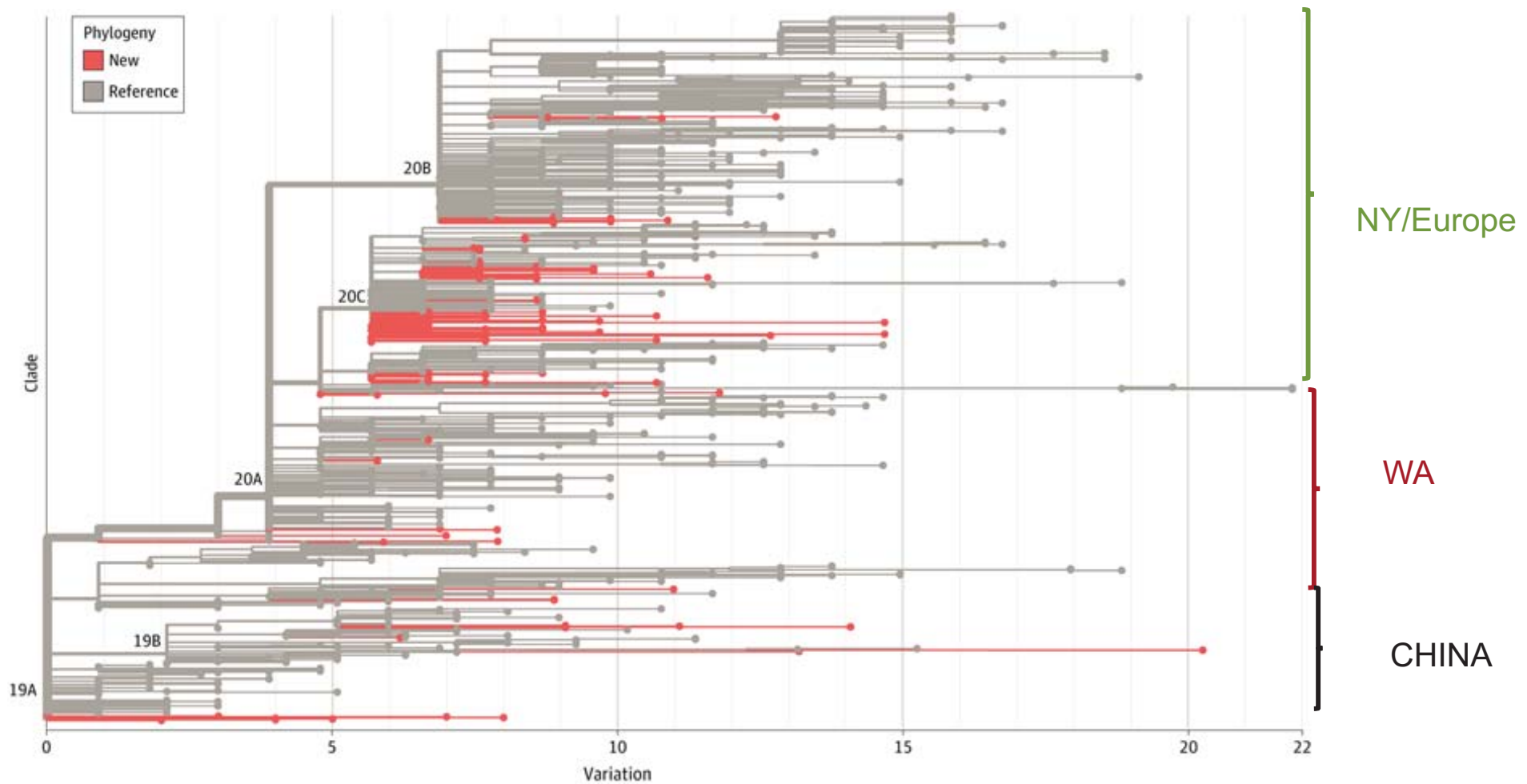


Dr. Wenjuan Zhang
Dr. Eric Vail



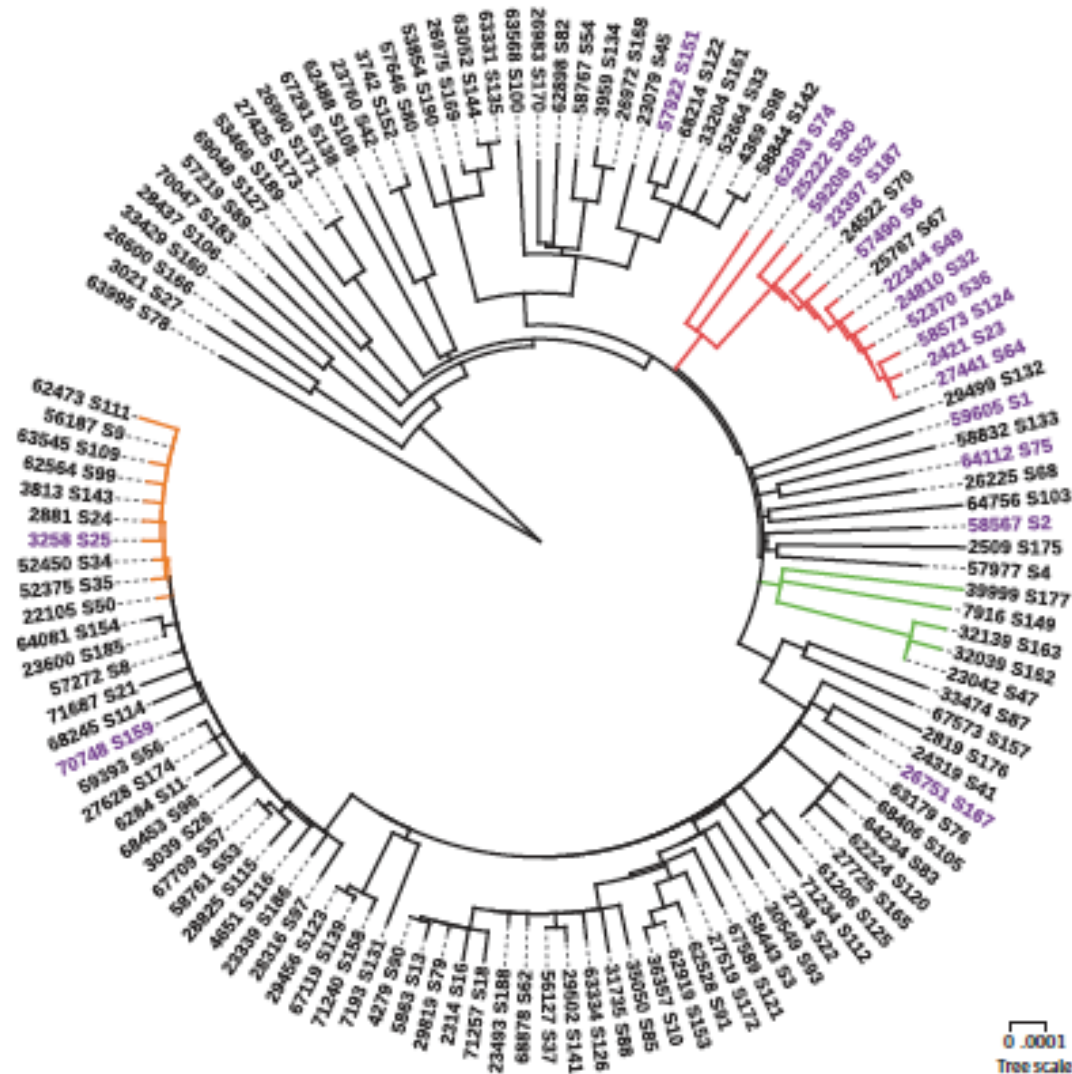
- New York
- Washington
- China
- Cedars Sinai

More samples look like NY compared WA and China



Zhang et al., 2020

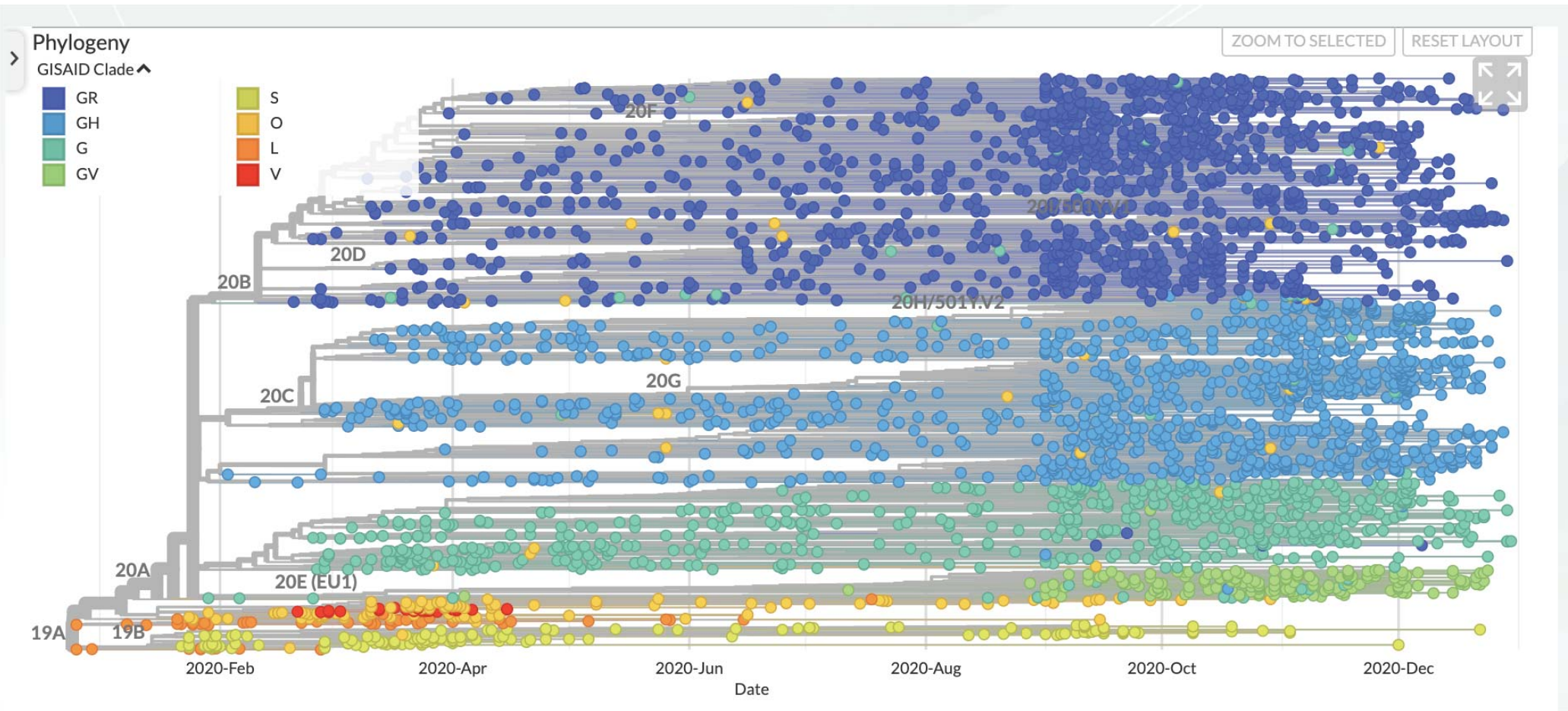
Can we track the spread in a local population?



- Yes!
- We can see differences down to 1bp and track to a single postal code
- More precise to agnostically track spread

Zhang et al., 2020

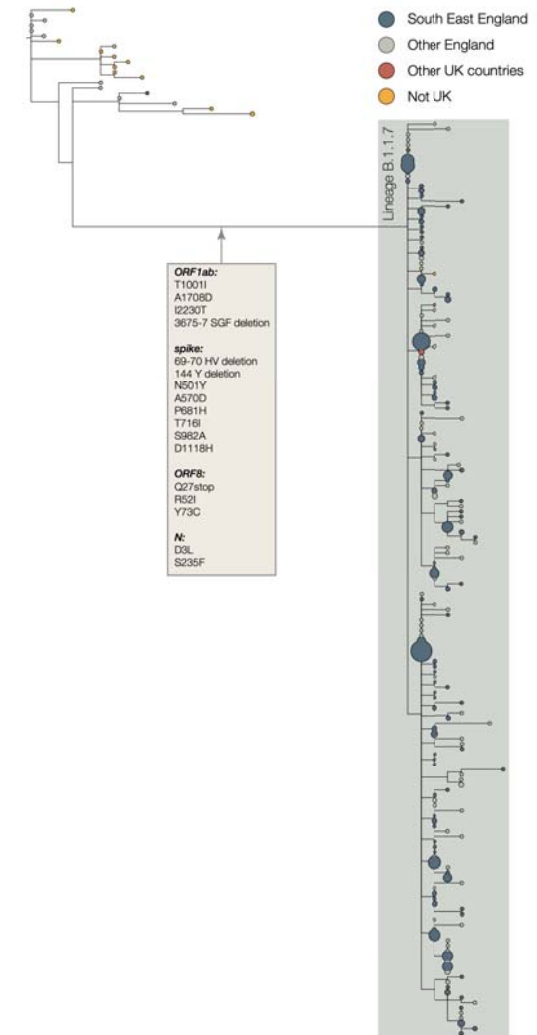
Global effort to sequence patient samples >400,000 deposited to date



www.gisaid.org

UK variant aka B.1.17 lineage, 20B/501Y.V1

- Mutation in the receptor binding domain (RBD) of the spike protein N501Y
- First emerged in the UK during September 2020.
- Since December 20, 2020, several countries have reported cases of the B.1.1b.1.7 lineage, including the United States and Canada.
- This variant is associated with increased transmissibility (i.e., more efficient and rapid transmission)
- Early reports found no evidence to suggest that the variant has any impact on the severity of disease or vaccine efficacy



www.cdc.gov

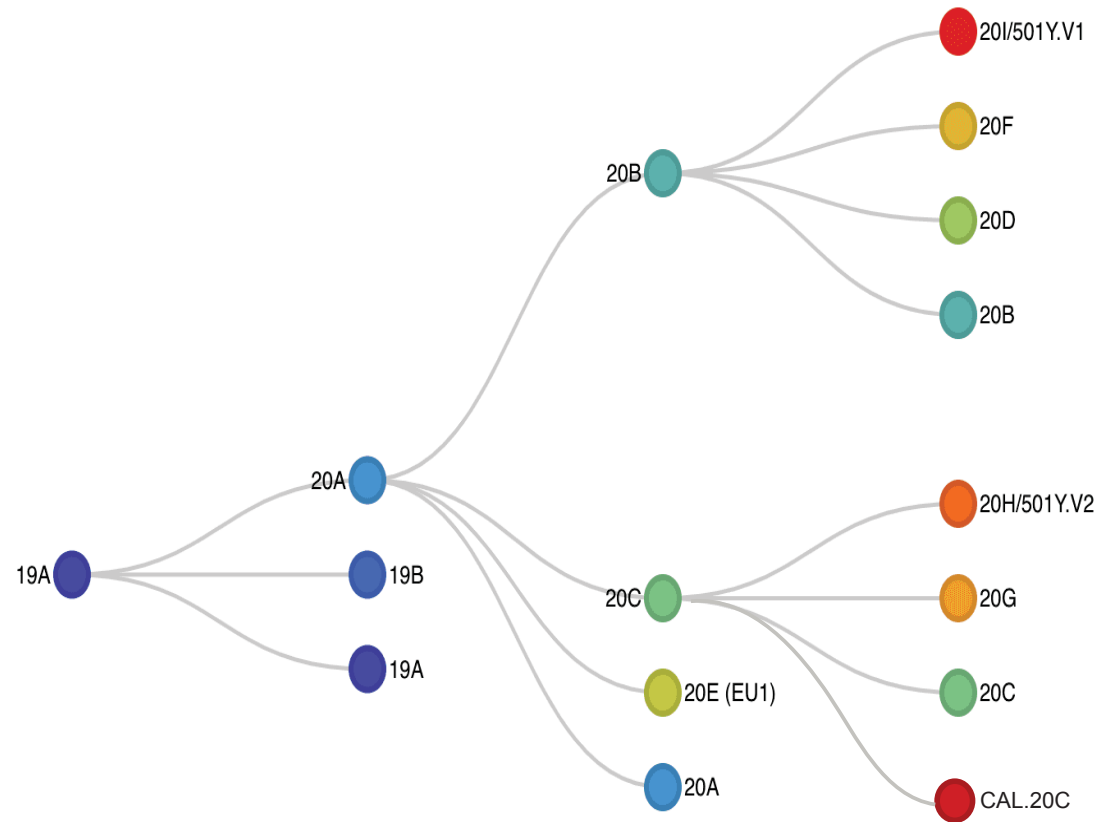
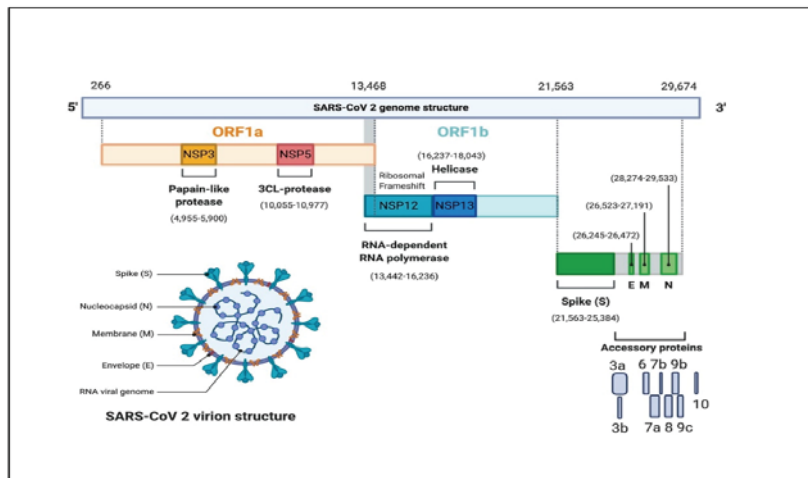
B.1.351 lineage (a.k.a. 20C/501Y.V2)

- Multiple mutations in the spike protein, including K417N, E484K, N501Y.
- Emerged independently, this variant does not contain the deletion at 69/70.
- This variant was first identified beginning of October 2020, in Nelson Mandela Bay, South Africa and now detected outside of South Africa, including the United States
- The variant identified in Zambia in late December 2020, appears to be the predominant variant in the country.
- Currently there is no evidence to suggest that this variant has any impact on disease severity.
- There is some evidence to indicate that one of the spike protein mutations, E484K, may affect neutralization by some polyclonal and monoclonal antibodies

www.cdc.gov

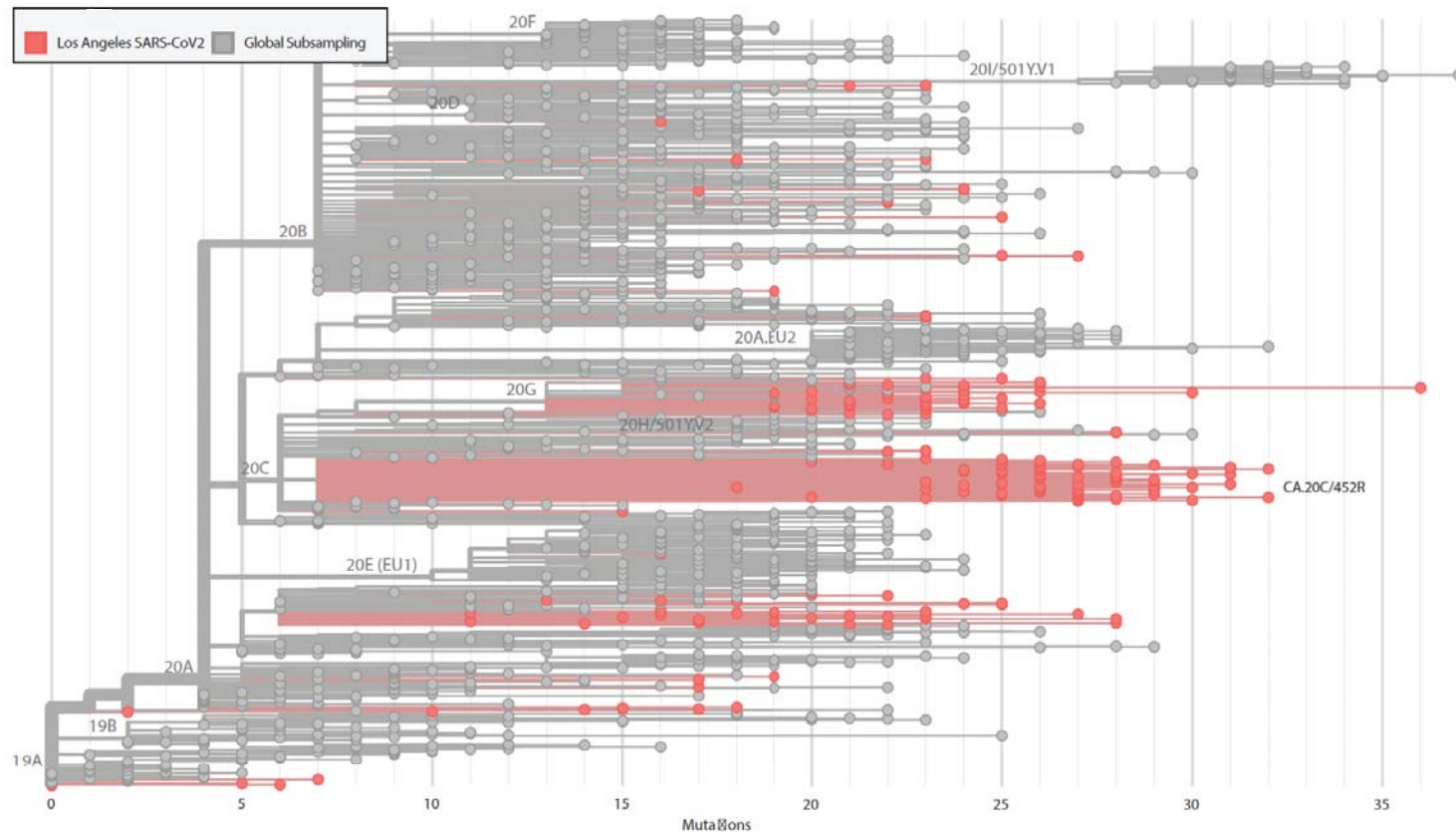
California strain aka CAL.20C, B.1.429

- mainly defined by the following 5 mutations (ORF 1a:I4205V, ORF1b:D1183Y. S: S131; W152C; L452R).

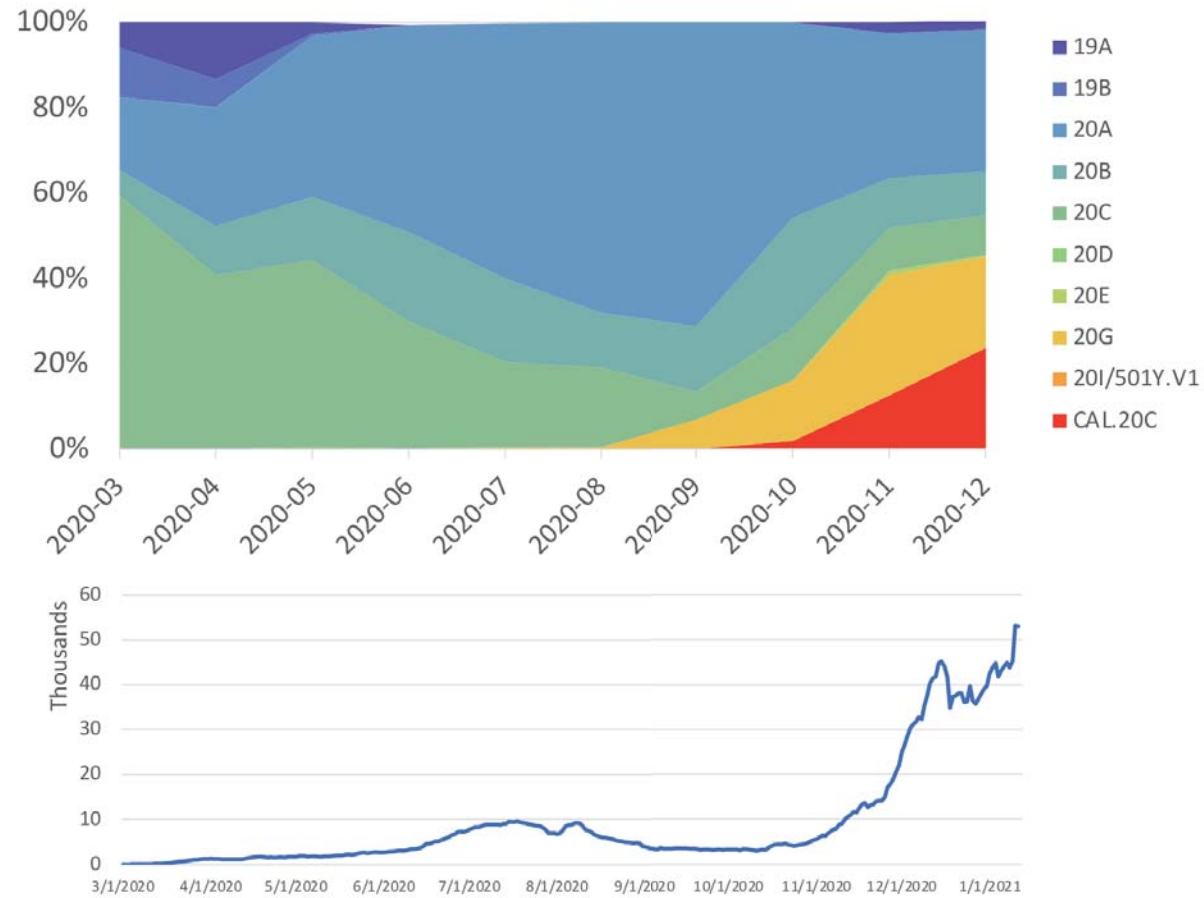


California variant's (CAL.20C) emergence

- First appearing in July, 1 out of 1230
- 36.4% in our own-study population (185 Cedars samples) collected from end of November to end of December
- Analyzed public data (4337 samples) we found it in ~25% mainly in Southern California but also in the entire state and surrounding state



CAL.20C in Southern California



Viral Evolution-why do variants matter?

- Ability to spread more quickly in people.
- Ability to cause either milder or more severe disease in people.
- Ability to evade detection by specific viral diagnostic tests.
- Decreased susceptibility to therapeutic agents such as monoclonal antibodies.
- Ability to evade natural or vaccine-induced immunity.
- **MORE STUDIES NEEDED-** Cedars is currently looking into answering these questions in regards to the California strain.

What does this mean?

- **Viruses evolve but SARS-CoV-2 by comparison mutates quite slowly**
- **Wash hands**
- **Wear a mask**
- **Socially distance**
- **Stay home where possible**
- **Doing these four things TOGETHER, we can help curb the spread**

Acknowledgments

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Stephanie Chen, Brian Davis, Kane Ong, Dr Yizhou Wang



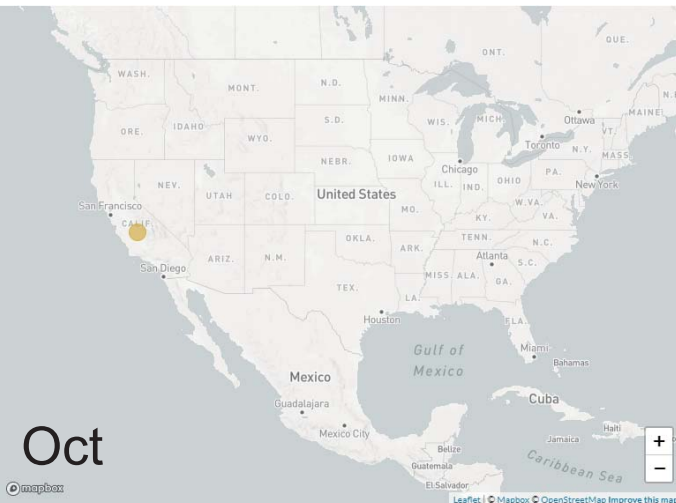
Funding

Department of Pathology

Department of Biomedical Sciences



CAL.20C across the US



CAL.20C from Oct to today (1/22/21) across US and Oceania

California strain: current numbers

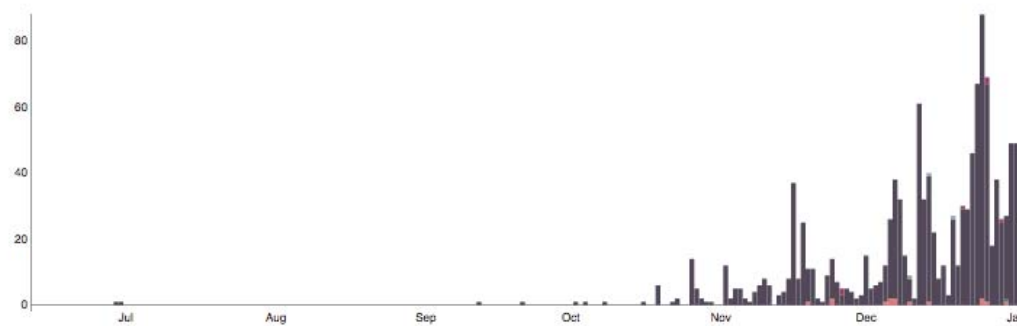
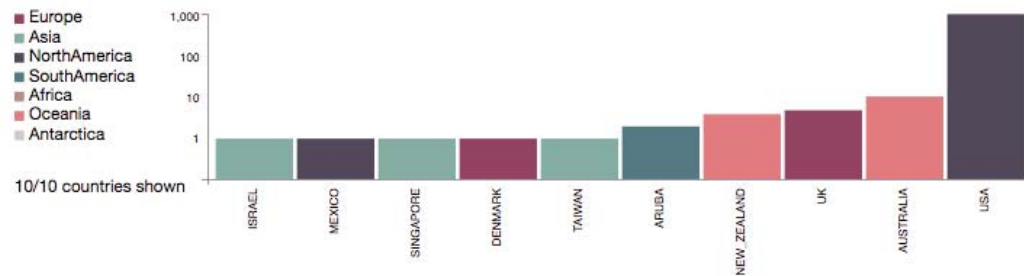


Table 1 | Summary of lineage & sub-lineages

Search for lineage...

Lineage	Most common countries	Earliest date	Count	Travel History	Description
B.1.429	USA 98.0%, Australia 1.0%, UK 0.0%, New_Zealand 0.0%, Aruba 0.0%	2020-07-13	1217		A lineage predominantly circulating in California but with exports to other countries. Characterised by the spike L452R mutation but also has spike:W152C orf1ab:D5584Y and N:T205I.

www.pangolin.org