The genetic epidemiology of the LA COVID-19 outbreak

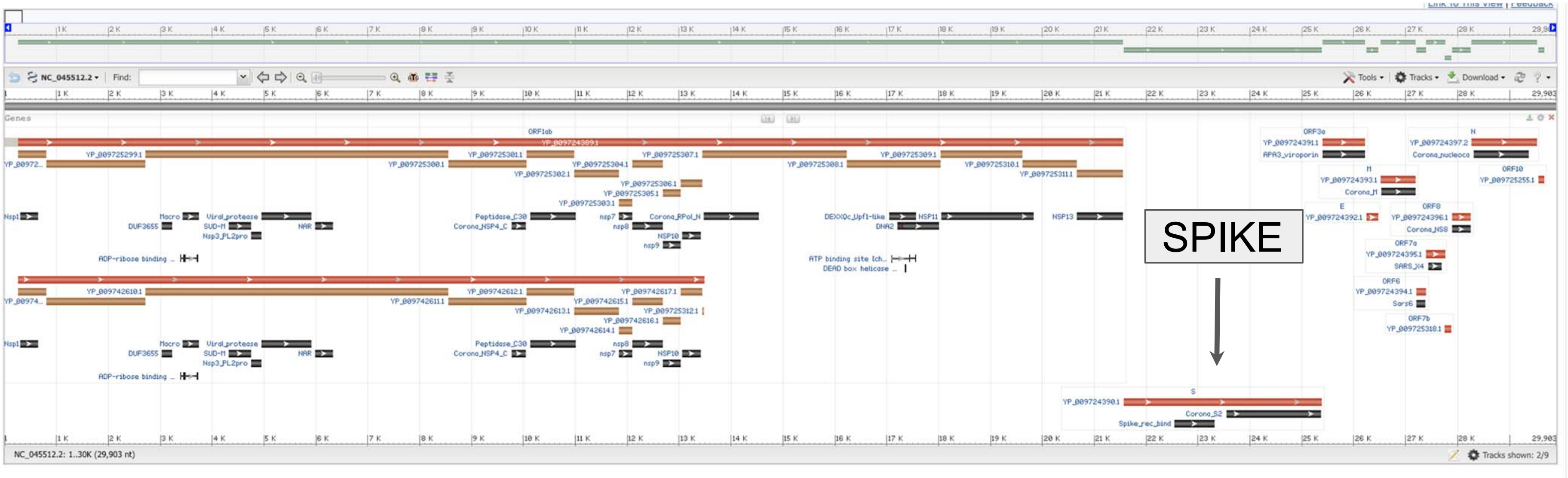
Leonid Kruglyak

Key points

- LA is a major global hub, and has seen many introductions of SARS-CoV-2 from all over the world
- New B.1.1.7 lineage from the UK is more transmissible, raising the reproductive number R and acting as an accelerant in the pandemic
- This lineage is either already here at a low frequency, or will be here very soon
- Once it’s introduced, it rapidly becomes the dominant lineage
- Strong public health measures are needed to keep cases from growing even faster

The SARS-CoV-2 genome

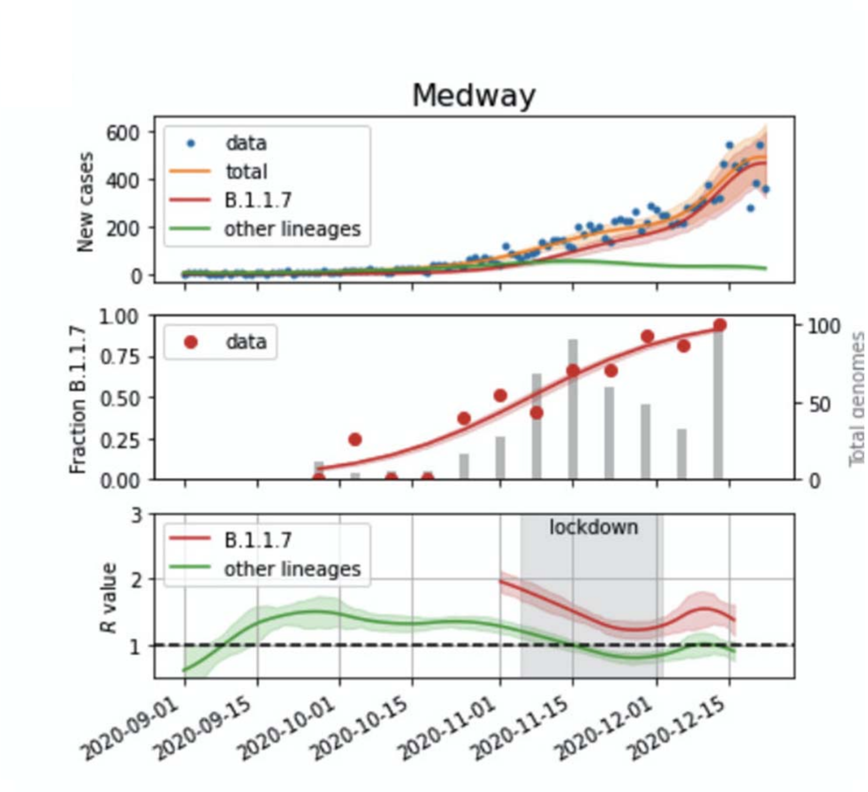
- The RNA sequence of the virus was sequenced and made available to the public in early January 2020
- The genome is 29,903 bases (letters) long
- The genome encodes instructions for building the virus



579.7798 (2020): 265-269.

Viral genome evolution

- Virus sometimes makes mistakes (mutations) when copying itself, leading to new lineages
- Many viral lineages are now circulating
- Most mutations have not changed infectivity or severity
- UK lineage B.1.1.7 is an exception, appearing to be ~1.5 times more infectious



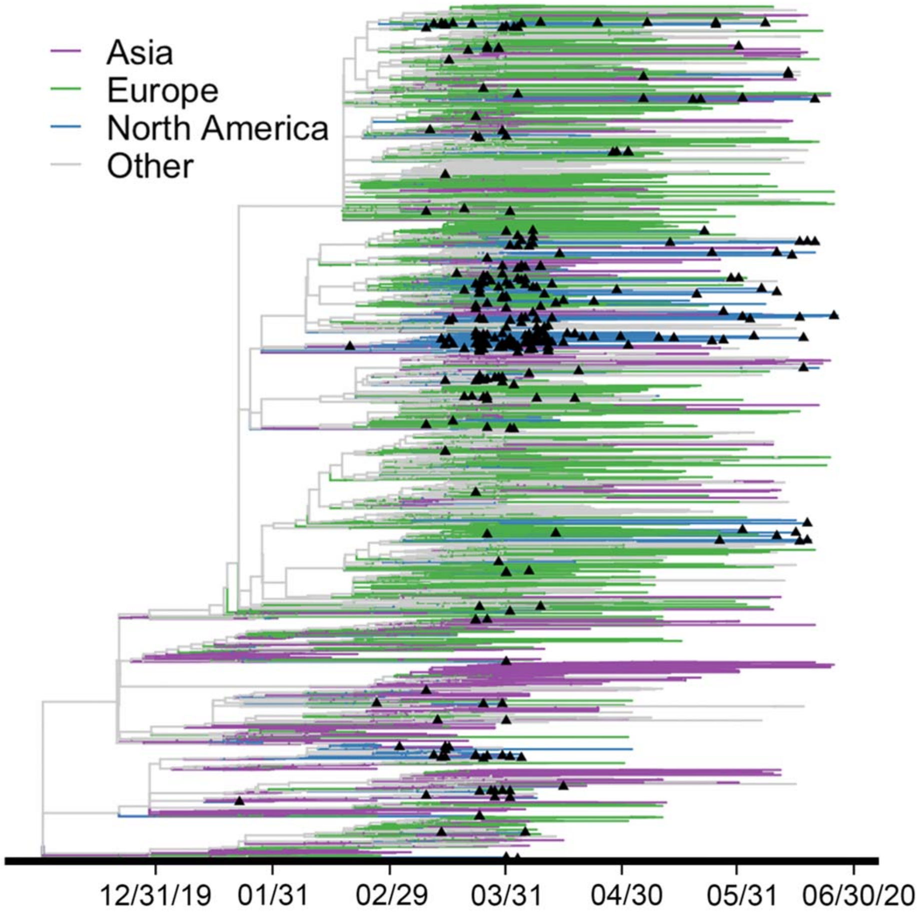
https://virological.org/t/lineage-specific-growth-of-sars-cov-2-b-1-1-7-during-the-english-national-lockdown/575

UCLA Health SARS-CoV-2 genomes

- 142 viral genomes from patient samples
- All samples were collected before June 30, 2020

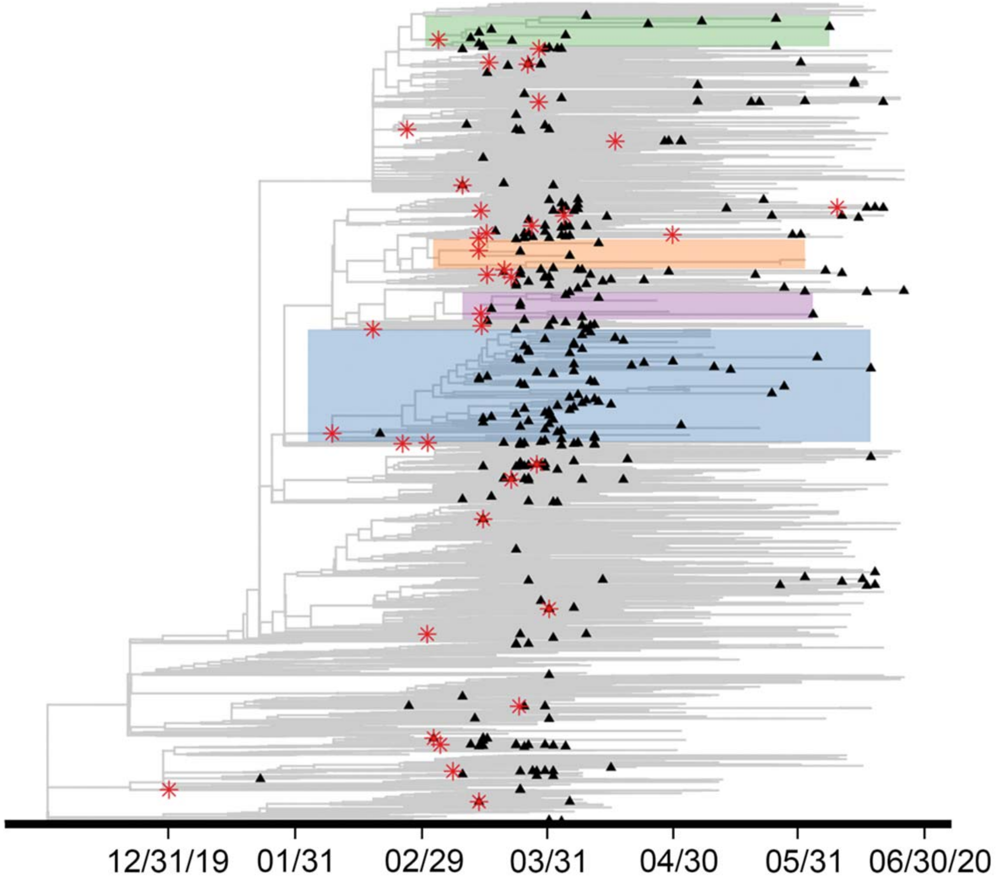
SARS-CoV-2 has been introduced into LA County many times

- Combined 142 unique UCLA SAR-CoV-2 genomes with 144 publicly available LA County genomes
- These 286 LA County genomes were clustered with 3,809 genomes from around the world that are available on GISAID
- LA county genomes are distributed throughout the tree, consistent with multiple introductions

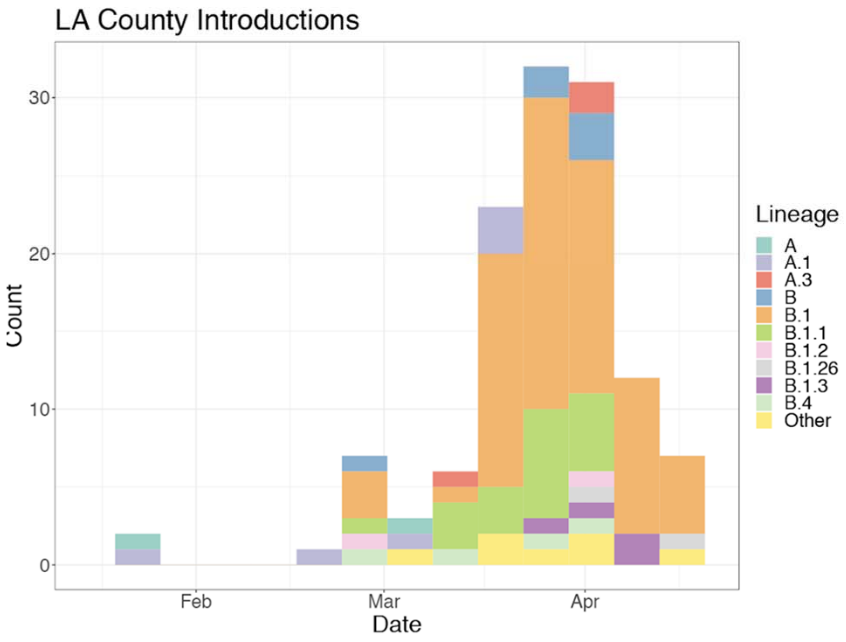


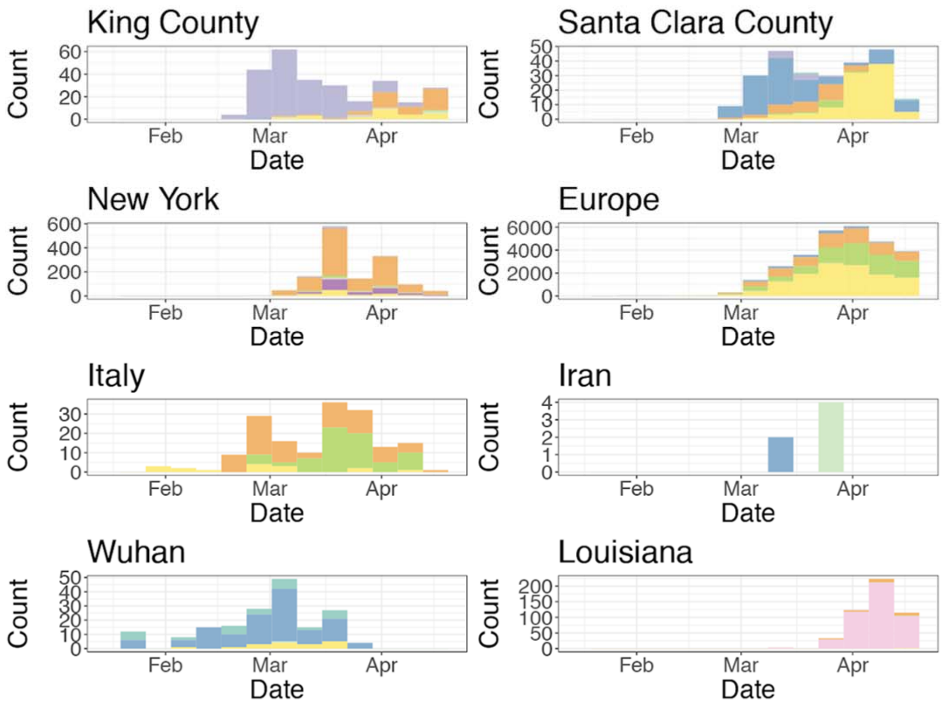
SARS-CoV-2 has been introduced into LA County many times

- We identified 34 introductions of SARS-CoV-2 that resulted in observed community transmission
- One introduction related to a large outbreak cluster (blue) containing 66 LA genomes



17 distinct lineages related to global and early U.S. outbreaks were introduced into LA County before April 19


LA County Introductions


King County

Santa Clara County

New York

Europe

Italy

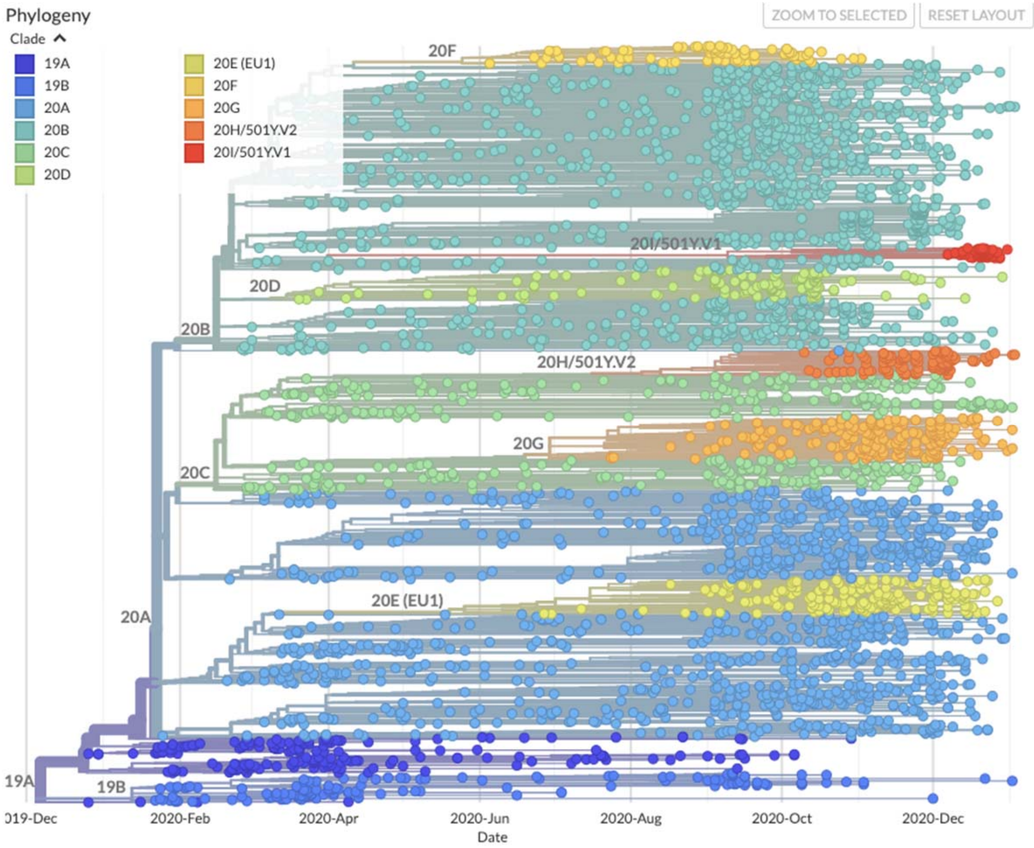
Iran

Wuhan

Louisiana

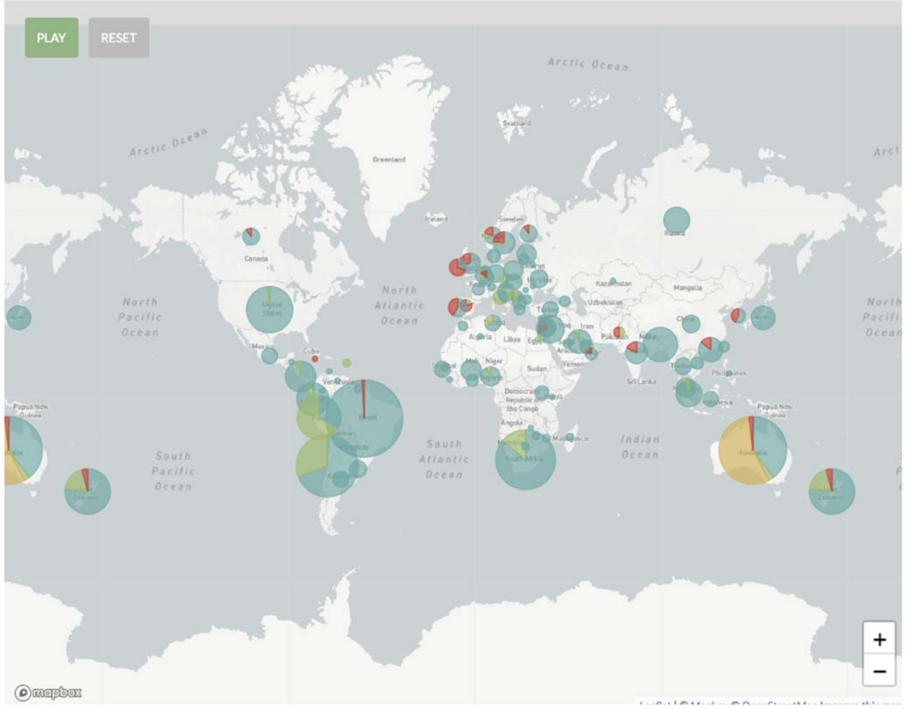
Global view of SARS-CoV-2 genomes

- >300,000 SARS-Cov-2 genomes have been deposited in the publicly accessible GISAID database
- Red strain is UK lineage B.1.1.7



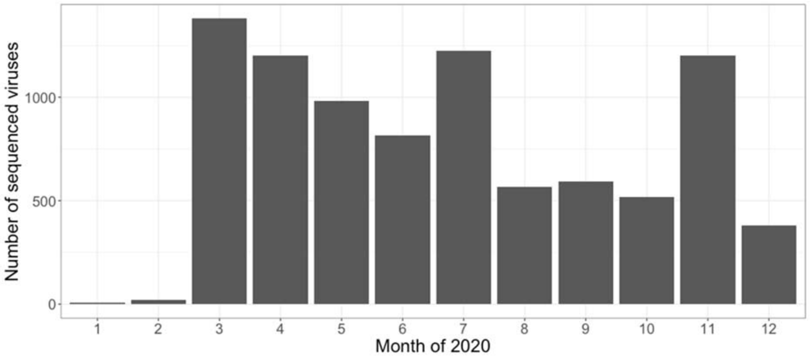
B.1.1.7 is still rare in the US

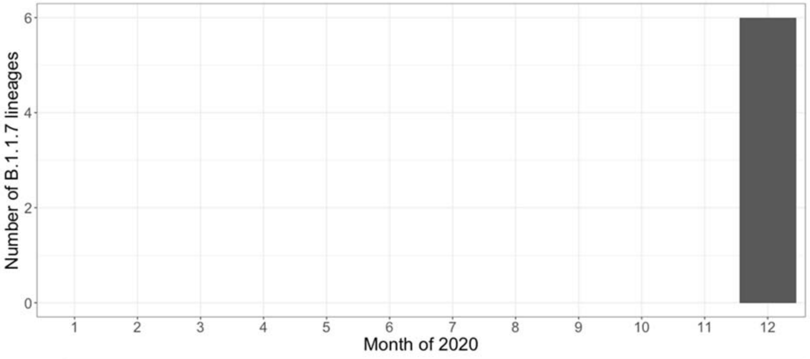
- The B.1.1.7 lineage is common in UK, parts of Europe and Asia
- The B.1.1.7 lineage is still rare in the US **(72 known cases as of today)**
- However, SARS-CoV-2 sequencing is extremely patchy in the US

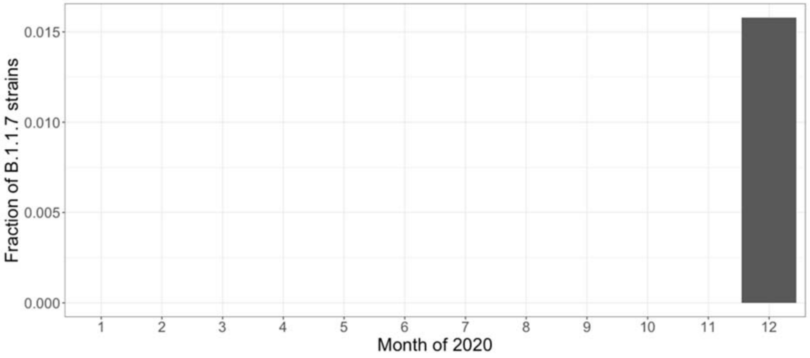


B.1.1.7 in California

- Hundreds of strains sequenced each month
- 32 B.1.1.7 isolates seen in CA (28 in San Diego County)
- No B.1.1.7 lineages identified in Los Angeles County yet but it’s likely only a matter of time

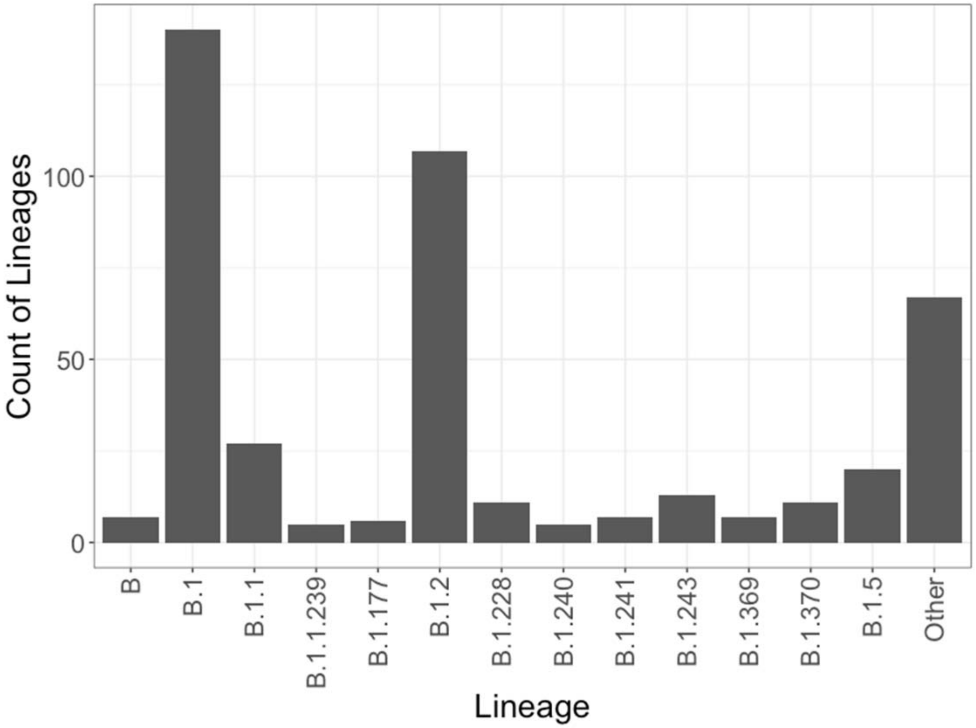




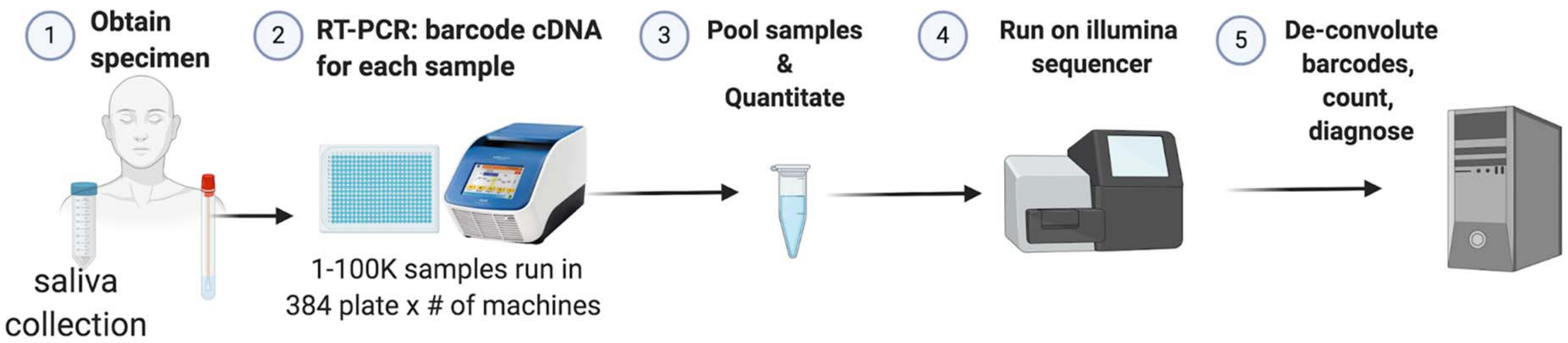


Recent Sampling of SARS-CoV-2 genomes from Los Angeles County

- 423 genomes deposited from LA deposited in November, December 2020, and January 2021
- Sequenced by the Center for Personalized Medicine, Children's Hospital of Los Angeles, and the Anderson lab at Scripps Research San Diego
- 13 lineages with at least 5 representatives
- 46 lineages with fewer than 5 representatives



UCLA SwabSeq Testing Technology



① Obtain specimen

saliva collection

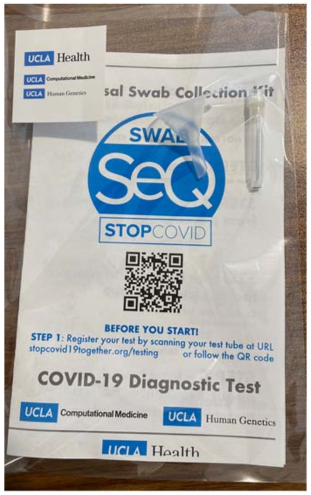
② RT-PCR: barcode cDNA for each sample

1-100K samples run in 384 plate x # of machines

③ Pool samples & Quantitate

④ Run on illumina sequencer

⑤ De-convolute barcodes, count, diagnose



Major differences from traditional PCR testing:

- Works straight from saliva or nasal swab samples
- Thousands of tests done in parallel by DNA sequencing
- Efficient, inexpensive, fewer supply chain bottlenecks

SwabSeq IP freely available under Open Covid Pledge

UCLA SwabSeq Lab

- Started developing test April 2020
- CLIA: October 30 2020
- First Day of CLIA Testing: November 10, 2020
- Total # of samples resulted in 2020: 7108

- 2021: First week of testing: resulted 7500 samples
- 83 positives (asymptomatic screening)

- Plan to sequence viral genomes from positive samples starting this week

Acknowledgements

James Boocock
Longhua Guo
Yi Yin
Joshua Bloom

Jonathan Flint
Eleazar Eskin
Val Arboleda

Shangxin (Shaun) Yang
Omai Garner
Evann E. Hilt

Key points

- LA is a major global hub, and has seen many introductions of SARS-CoV-2 from all over the world
- New B.1.1.7 lineage from the UK is more transmissible, raising the reproductive number R and acting as an accelerant in the pandemic
- This lineage is either already here at a low frequency, or will be here very soon
- Once it’s introduced, it rapidly becomes the dominant lineage
- Strong public health measures are needed to keep cases from growing even faster