Variants of SARS-CoV-2

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June 2021
There are many, many variants of SARS-CoV-2

Genomic epidemiology of novel coronavirus - Global subsampling

Showing 4001 of 4001 genomes sampled between Dec 2019 and Jun 2021.
The SARS-CoV-2 Genome

Non-structural proteins

ORF1a

ORF1b

Structural proteins

Spike

E

M

N

E = Envelope
M = Membrane
N = Nucleocapsid
The SARS-CoV-2 Structure
Current variants are not the first and won’t be the last

D614G
Current variants are not the first and won’t be the last

Prevalence of D614G on GenBank, January to May 2020

D614G

Some variants are concerning or interesting

Increased transmissibility  Increased disease severity  Evades vaccine-induced immunity  Evades infection-induced immunity  Evades therapeutics  Evades diagnostics

Note, some SARS-CoV-2 risk assessment frameworks include zoonotic emergence and transmission from animals to humans, but this is not routine and usually a lower priority than those domains listed above.
Some variants are concerning or interesting

<table>
<thead>
<tr>
<th>Lineage</th>
<th>Public name</th>
<th>GISAID</th>
<th>Nextstrain</th>
<th>CDC Designation</th>
<th>WHO Designation</th>
<th>Concerns</th>
</tr>
</thead>
<tbody>
<tr>
<td>PANGOLIN</td>
<td></td>
<td></td>
<td></td>
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</tr>
<tr>
<td>B.1.1.7</td>
<td>Alpha</td>
<td>GRY (formerly GR/501Y.V1)</td>
<td>20I/S:501Y.V1</td>
<td>Concern</td>
<td>Concern</td>
<td></td>
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<tr>
<td>B.1.351</td>
<td>Beta</td>
<td>GH/501Y.V2</td>
<td>20H/S:501Y.V2</td>
<td>Concern</td>
<td>Concern</td>
<td></td>
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<tr>
<td>P.1</td>
<td>Gamma</td>
<td>GR/501Y.V3</td>
<td>20J/S:501Y.V3</td>
<td>Concern</td>
<td>Concern</td>
<td></td>
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<tr>
<td>B.1.427/B.1.429</td>
<td>Epsilon</td>
<td>GH/452R.V1</td>
<td>20C/S.452R</td>
<td>Concern</td>
<td>Interest</td>
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<tr>
<td>B.1.617.2</td>
<td>Delta</td>
<td>G/452R.V3</td>
<td>21A/S:478K</td>
<td>Concern</td>
<td>Concern</td>
<td></td>
</tr>
</tbody>
</table>
Some variants are likely to be ‘of high consequence’

“A variant of high consequence has clear evidence that prevention measures or medical countermeasures have significantly reduced effectiveness relative to previously circulating variants.

Currently there are no SARS-CoV-2 variants that rise to the level of high consequence.”

We are seeing a profound reduction in COVID-19 incidence Citywide
Despite a large increase in the relative proportion of Variants of Concern
B.1.617.2 (Delta) – vaccine efficacy (Pfizer)

Bernal et al. 2021 Effectiveness of COVID-19 vaccines against the B.1.617.2 variant. medRxiv
Summary of SARS-CoV-2 variants

• It’s complicated!
• It’s ever-changing!
  • With time, there will be more data on known variants, and new variants detected
• So far, COVID-19 vaccines protect against all known variants
  • There is a difference in amount of protection across vaccines, variants and number of doses
  but any dose of any EUA-approved vaccine offers some protection against all known lineages of SARS-CoV-2
• No variants detected so far have been designated a “variant of high consequence”
• CDPH has expertise and is building more
  • Testing and lab-based surveillance team = designated medical director, molecular laboratory
director, lab-based surveillance director, epidemiologist, director of planning, research and development
  • If we don’t know, we can ask CDC and WHO
• Regional Innovative Public Health Laboratory (RIPHL): healthcare leaders and partners
CDPH’s goal is to receive a:

1. Representative sample
2. Submitted routinely
3. With power to detect low frequency lineages
4. And monitor trends.
RIPHL will be a critical resource for future work in emerging infections, antimicrobial resistance, healthcare associated infections

- Provide a key set of tools that will continue to grow as science and pathogens evolve

- Strengthen Chicago’s capacity to respond to emerging infectious diseases challenges, antimicrobial resistance, healthcare-associated infections