

Fall 2021 Course Evaluations

Open: Wednesday November 24, 10:00 AM

Close: Wednesday December 8, 11:59 PM

evals.mcmaster.ca

#macevals2021





Continued Genomic epidemiology in the time of SARS-CoV-2

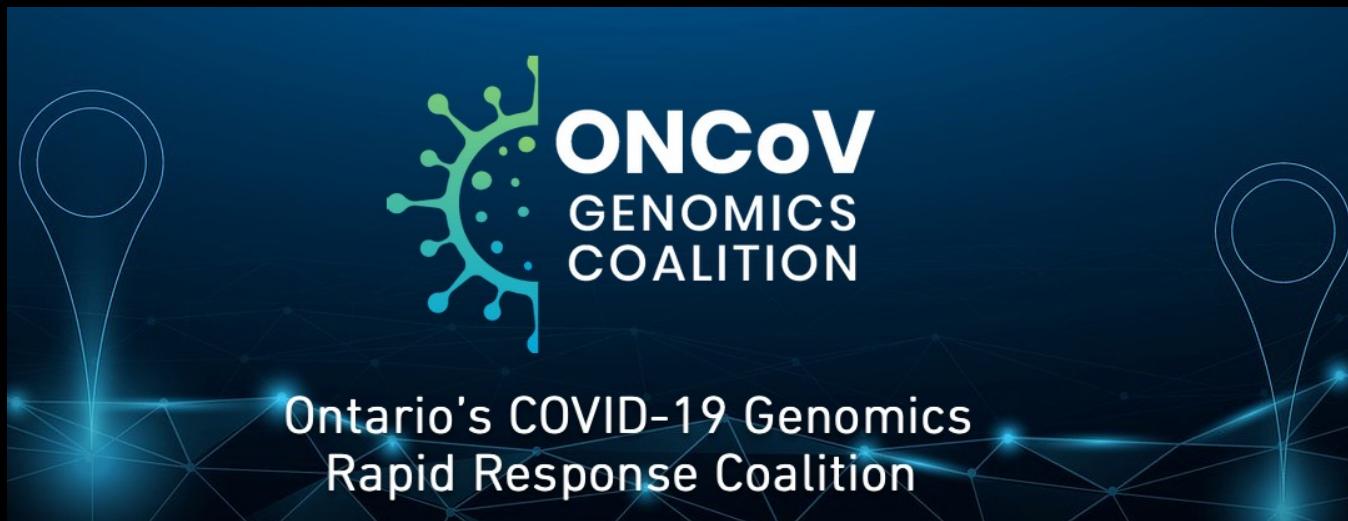
Jalees A. Nasir

Adapted from slides by Dr. Andrew G. McArthur

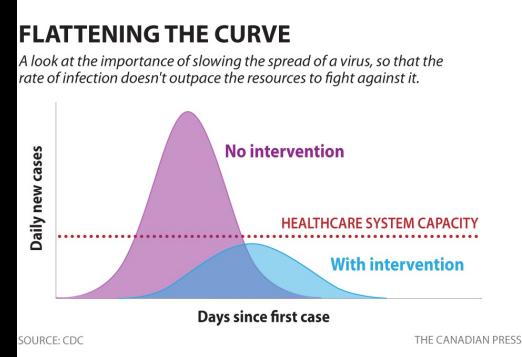
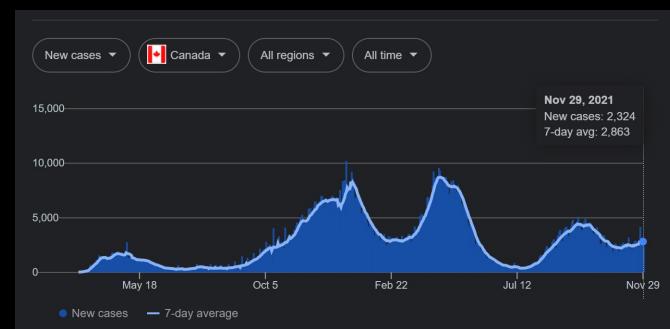
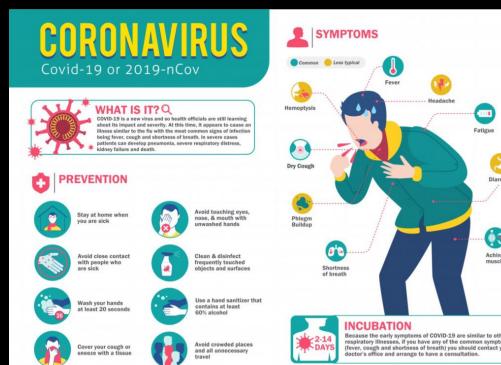
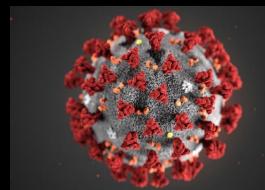
Michael G. DeGroote Institute for Infectious Disease Research
David Braley Center for Antibiotic Discovery
Department of Biochemistry & Biomedical Sciences
McMaster University, Canada

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SARS-CoV-2



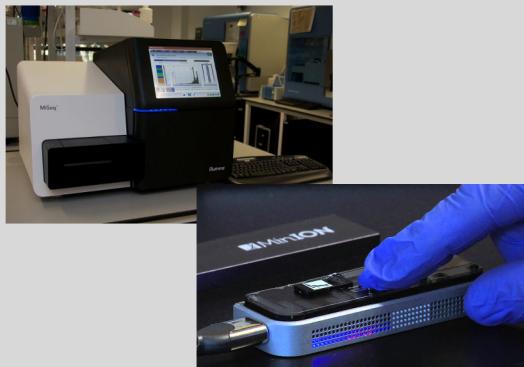
Antimicrobial Resistance

Newsweek: The Syrian Civil War Could Spell the End of Antibiotics



September 21, 2016

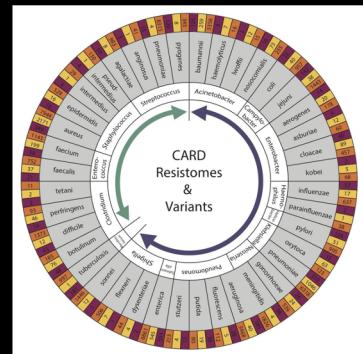
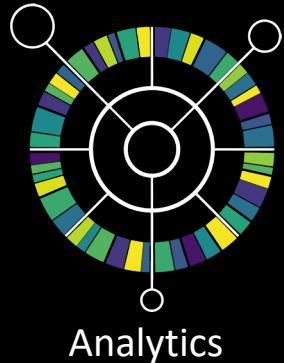
Newsweek visits the Doctors Without Borders Special Hospital for Reconstructive Surgery in Amman, [Jordan](#), to look into the growing number of Syrians who have acquired bacterial infections that are immune to almost all antibiotics. [View external media](#).



DNA Sequencing

DETECT

patient
diagnostics



Bioinformatics

Biocuration

DECODE

community
outbreaks



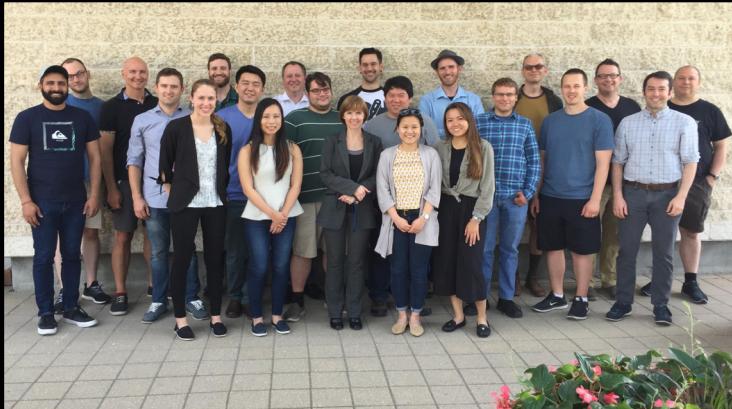
Johnson & Johnson



Public Health Agency Usage 2019

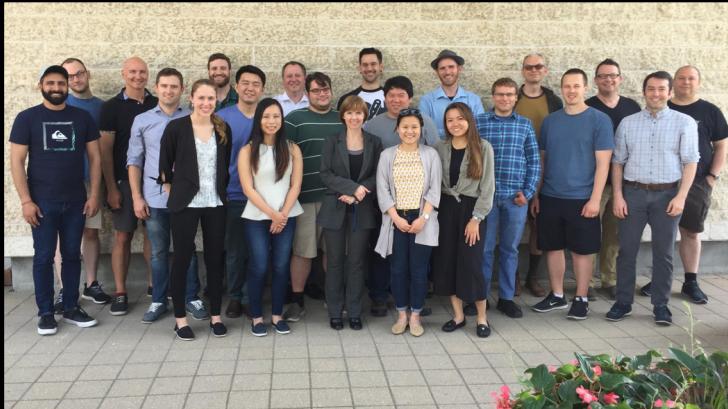
DEPLOY

national & international
surveillance



A screenshot of the GenEpiO website. The header features the text "GENOMIC EPIDEMIOLOGY ONTOLOGY" and a subtext "Working together to develop a more comprehensive controlled vocabulary for infectious disease surveillance and outbreak investigations". Below the header is a navigation bar with links: HOME, FAQ, CONSORTIUM, ONTOLOGY, BLOG, and GET INVOLVED. The main content area contains text about the project's goal and its GenEpiO consortium, along with a "get involved" link. To the right, there is a sidebar titled "RECENT POSTS" with three entries: "Just published: our article on contextual data for improved food safety and surveillance", "FoodOn is at the SeedsAndChips.com conference!", and "March 9, 2017: The FoodOn ontology alpha is launched!".

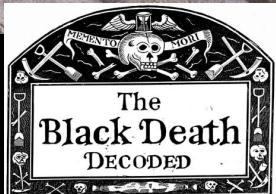
Integrated Rapid Infectious Disease Analysis (IRIDA) Platform - a Canadian-led open source, end-to-end platform for public health genomics



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Hendrick Poinar



AMR Bait Capture



Hendrick Poinar



Gerry Wright



Mike Surette



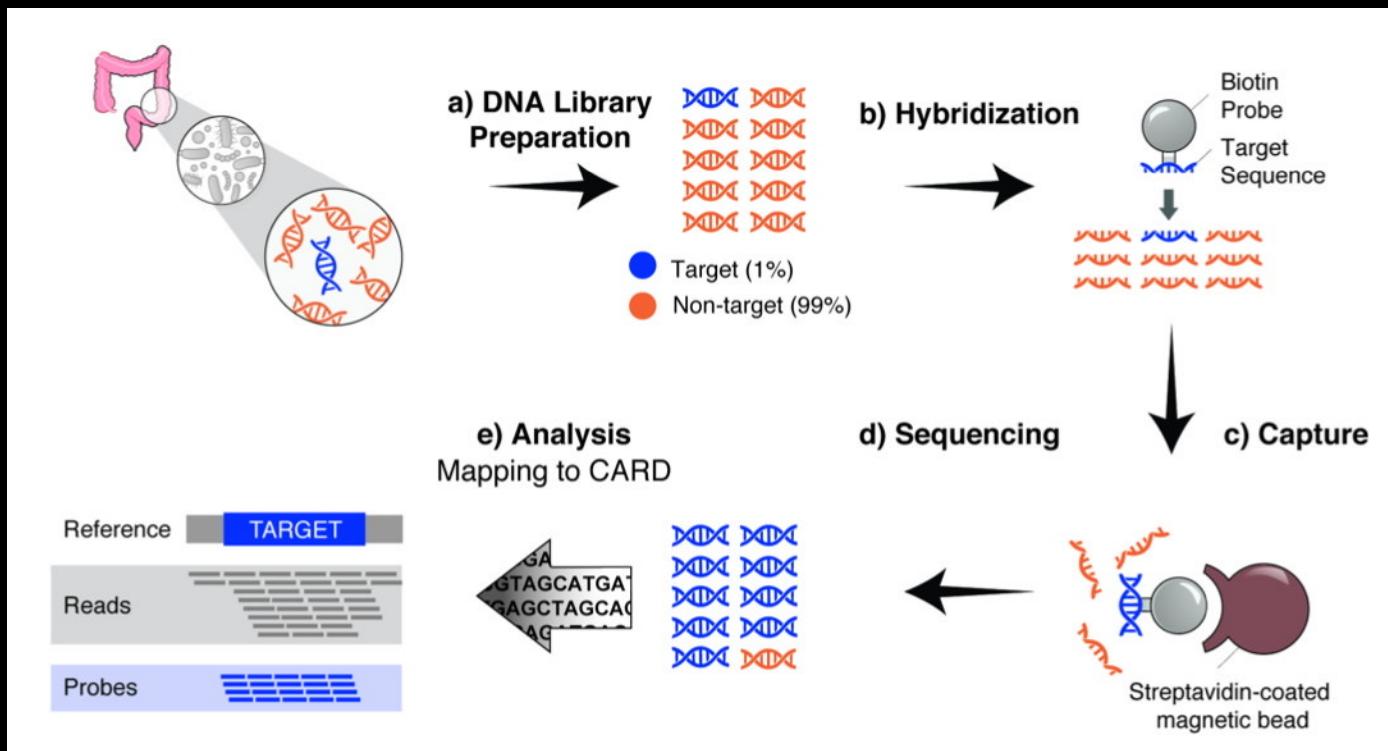
Allison Guitor, Ph.D. student
(Wright Lab)



Amos Raphenya
Lead CARD Developer



Brian Alcock
Lead CARD Curator



Summer 2019 – Viral Bait Capture



Hendrick Poinar



Jalees Nasir, PhD Student
(McArthur Lab)

- 3 million available virus sequences
- Existing design methods would result in over 85,000,000 hybridization baits

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Robert Kozak, Samira Mubareka (Sunnybrook Health Sciences)

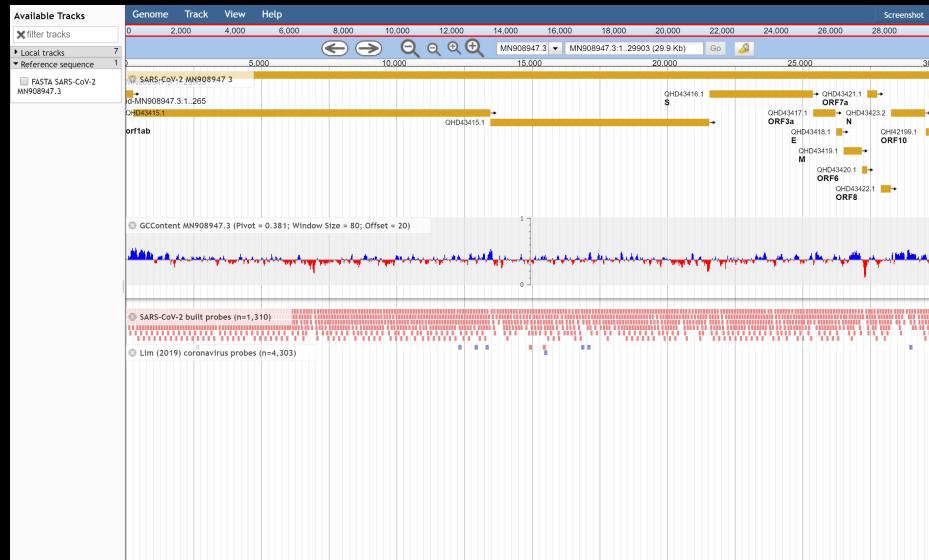
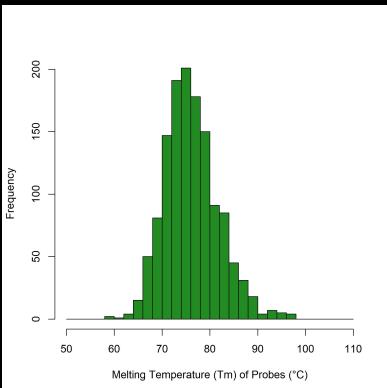
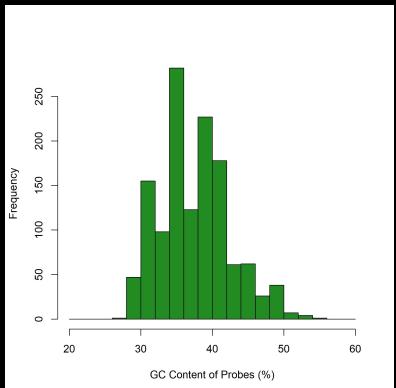
- Syndromic bait sets
- Focus on respiratory viruses first
- 30% are lacking diagnostic tools
- Include seasonal and other coronaviruses

Winter 2020 – SARS-CoV-2 Bait Capture



Jalees Nasir, PhD Student
(McArthur Lab)

- SARS-CoV-2 Bait Capture Probe Set
- <https://github.com/jaleezyy/covid-19-baits>
- Nasir, J.A., D.J. Speicher, R.A. Kozak, H.N. Poinar, M.S. Miller, & A.G. McArthur. 2020. Rapid design of a bait capture platform for culture- and amplification-free next-generation sequencing of SARS-CoV-2. *Preprints* 2020, 2020020385.

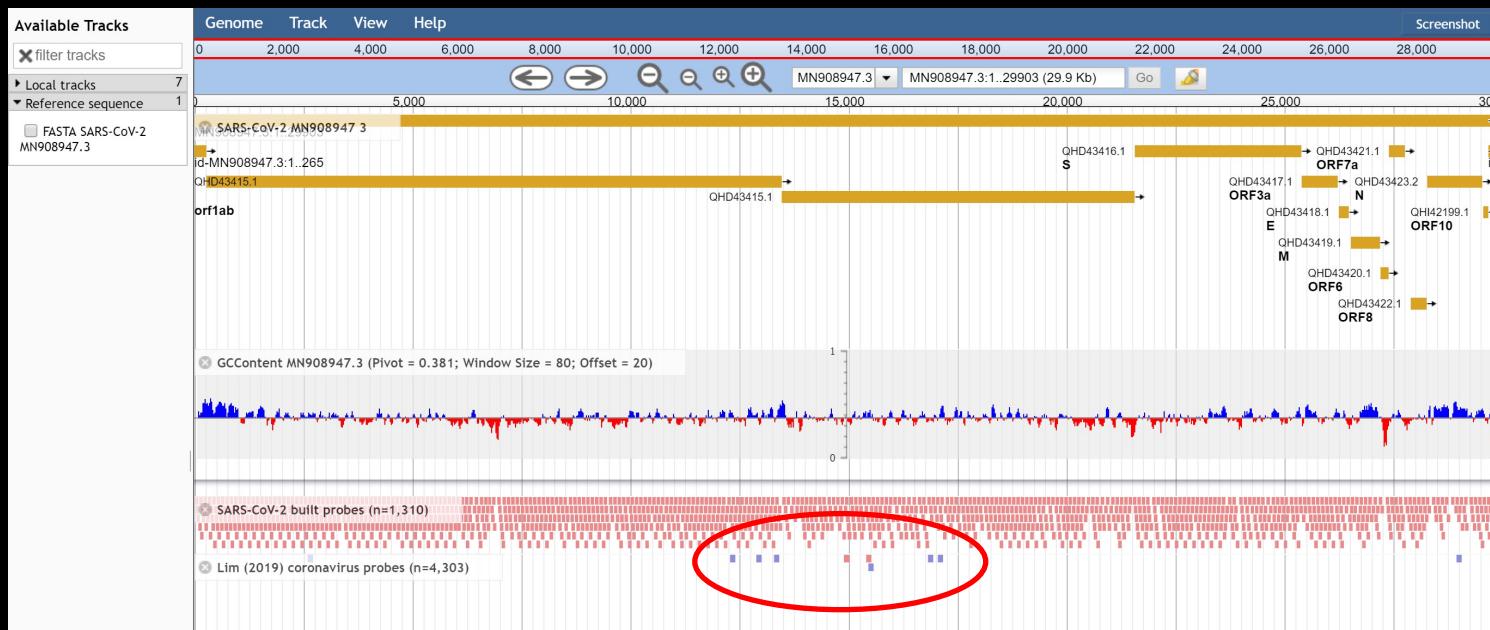


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Research team has isolated the COVID-19 virus

March 12, 2020



SHARE



Pictured left to right: Dr. Robert Kozak, Dr. Samira Mubareka, Dr. Arinjay Banerjee

A team of researchers from Sunnybrook, [McMaster University](#) and the [University of Toronto](#) has isolated severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the agent responsible for the ongoing outbreak of COVID-19.

Related stories

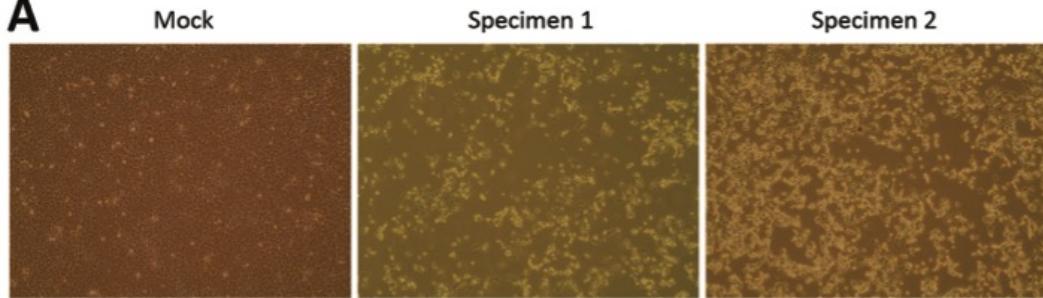
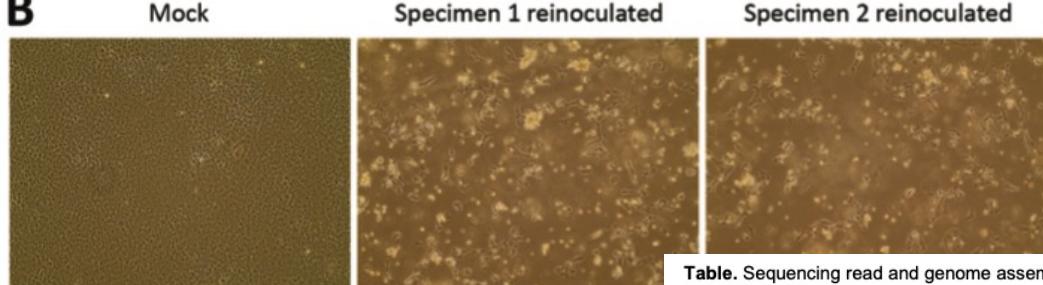
A**B**

Table. Sequencing read and genome assembly statistics used in study of isolation, sequence, infectivity, and replication kinetics of SARS-CoV-2*

Metric or mutation	SARS-CoV-2/SB2	SARS-CoV-2/SB3 TYAGNC
Number of paired reads	730,137 bp	690,167 bp
Reads from SARS-CoV-2	94.0%	94.4%
Number of assembly contigs	1	1
Assembly N50	29,494 bp	29,369 bp
Average depth of coverage of reads	7940.0-fold	7550.1-fold
Total assembly length	29,494 bp	29,369 bp
SARS-CoV-2 assembly completeness	98.6%	98.2%
Unresolved 5' sequence	262 bp	272 bp
Unresolved 3' sequence	200 bp	205 bp
Pos. 884 (orf1ab polyprotein)		R207C (<u>CGT</u> → <u>TGT</u>)
Pos. 1397 (orf1ab polyprotein)	V378I (<u>GTA</u> → <u>ATA</u>)	V378I (<u>GTA</u> → <u>ATA</u>)
Pos. 2832 (orf1ab polyprotein)	K856R (<u>AAG</u> → <u>AGG</u>)	
Pos. 3040 (orf1ab polyprotein)		Y925Y (<u>TAC</u> → <u>TAT</u>)
Pos. 8327 (orf1ab polyprotein)	18.1% of reads suggest L2688F (<u>CTT</u> → <u>TTT</u>)	M2796I (<u>ATG</u> → <u>ATT</u>)
Pos. 8653 (orf1ab polyprotein)	5.6% of reads suggest K3363T (<u>AAG</u> → <u>ACG</u>)	
Pos. 10353 (orf1ab polyprotein)		
Pos. 11074 (orf1ab polyprotein)	10.2% of reads suggest +TTT and a deletion between positions 10809 and 13203	
Pos. 11083 (orf1ab polyprotein)	L3606F (<u>TTG</u> → <u>TTT</u>)	L3606F (<u>TTG</u> → <u>TTT</u>)
Pos. 25413 (orf3a protein)		36.7% of reads suggest I71 (<u>ATC</u> → <u>ATT</u>)
Pos. 28688 (nucleocapsid phosphoprotein)	L139L (<u>TTG</u> → <u>CTG</u>)	L139L (<u>TTG</u> → <u>CTG</u>)

*Predicted mutations are relative to the MN908947.3 SARS-CoV-2 genome (29,903 bp). Mutations within codons are underlined. All mutations were predicted by 100% of sequencing reads mapping to that position, unless otherwise noted. None of the mutations with support from <100% of sequencing reads appeared in the final assembled genome consensus sequences. Substitutions in boldface have been observed in direct sequencing of patient isolates (S. Mubareka, A.G. McArthur, unpub. data). orf1ab, open reading frame 1ab; pos., position; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.



Why sequence SARS-CoV-2?

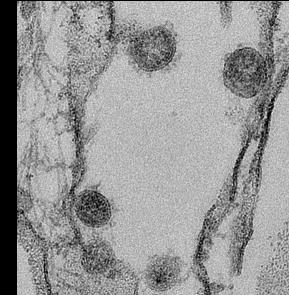
- Validation of *in vitro* experiments



*Image courtesy of
Arinjay Banerjee*

Why sequence SARS-CoV-2?

- Validation of *in vitro* experiments
- Diagnostic escape
- Vaccine escape



*Image courtesy of
Arinjay Banerjee*

Why sequence SARS-CoV-2?

- Validation of *in vitro* experiments
- Diagnostic escape
- Vaccine escape
- Changing biology – infectivity, virulence
- Re-infection & immunity
- Environmental transmission



*Image courtesy of
Arinjay Banerjee*



Allison McGeer - Mount Sinai Hospital

Why sequence SARS-CoV-2?

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- Global and community transmission
- Outbreak dynamics



Image courtesy of
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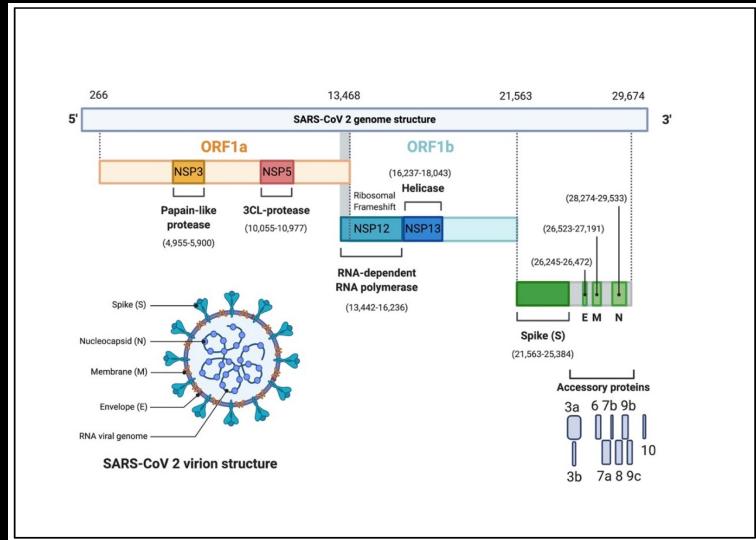


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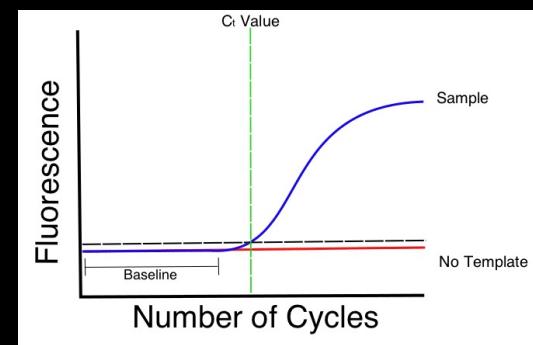


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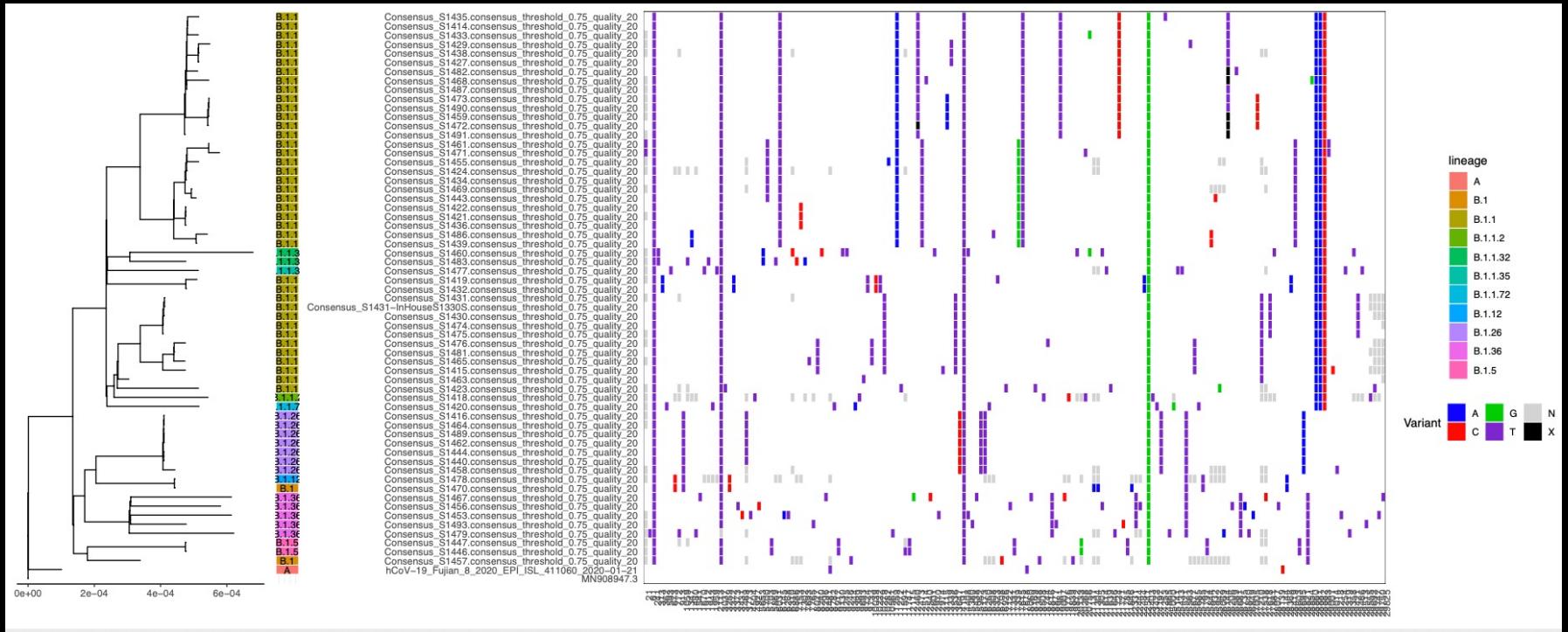
Diagnostic Escape Mutations



- SeeGene; Assay: Allplex COVID assay - can detect 3 different genes - RdRp, Envelope and Nucleocapsid
- Roche; Assay: Cobas SARS-CoV-2 assay - can detect 2 genes, ORF1ab gene (Target 1) and Envelope gene (Target 2)
- Altona Diagnostics; Assay: RealStar SARS-CoV-2 assay - can detect the Spike and Envelope gene
- BGI Genomics; MGI SARS-CoV-2 Assay – detects the ORF1ab gene
- Hamilton Regional Laboratory Medicine Program; Assay: SARS-CoV-2 – detects 2-3 different viral genes
- Public Health Ontario Laboratory; Assay: SARS-CoV-2 – detects 2 different viral gene targets

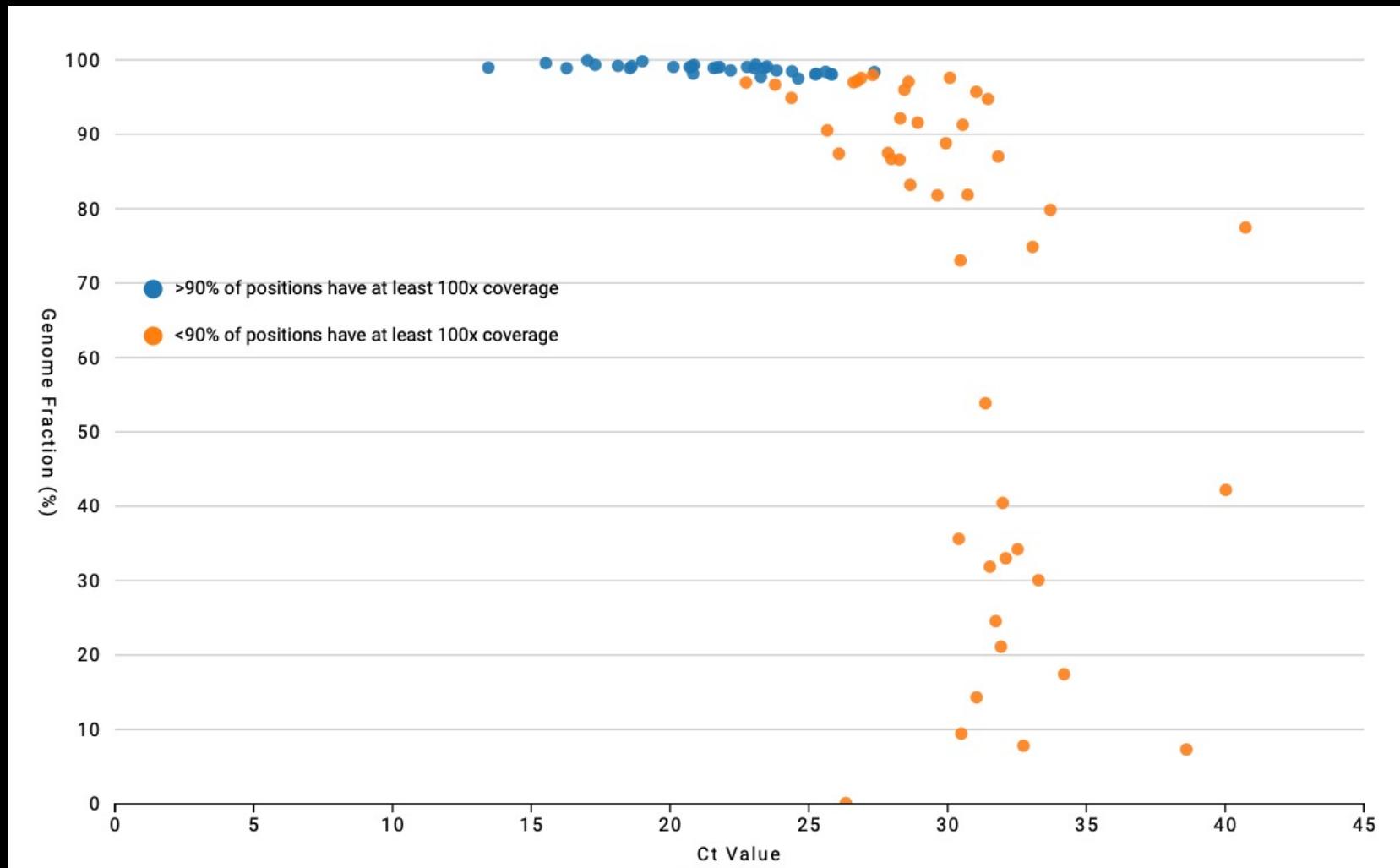
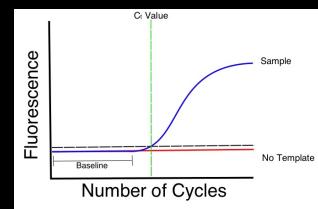


What is the risk for mutations?

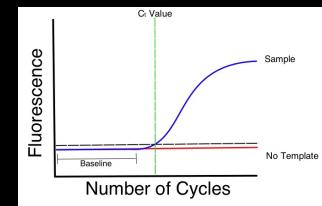
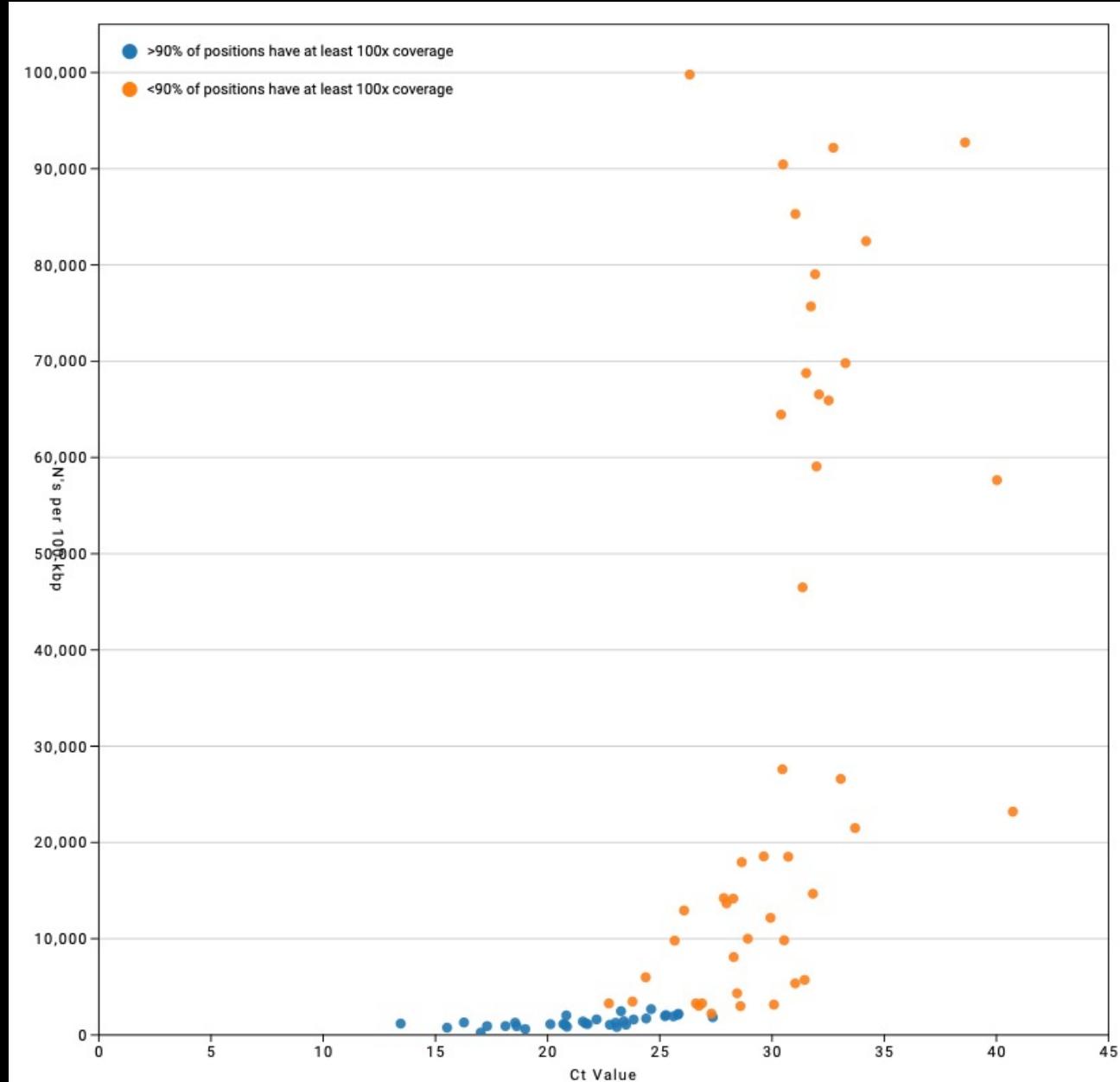


- ~28,000 bp genome
- Intrinsic mutation rate is low due to nonstructural protein 14 (nsp14): 3'-to-5' exoribonuclease (ExoN) and guanine-N7-methyltransferase (N7-MTase) activities
- Risk of diagnostic mutations low
- Risk of mutations that change biological properties low – **selective pressures?**
- Genome analysis must be intolerant of sequencing error!

Problems with Sequencing Error



Problems with Sequencing Error



What is the risk for Escape Mutations? - 1st Wave

Population Biology

What is the intrinsic mutation rate	low
How much time has passed, i.e., generations of replication	not much
How big is the population, i.e., how many have been infected?	33M+
Is the population expanding or contracting? Bottlenecks?	varies
Potential for recombination?	needs assessment
Selective pressures?	D614G <i>increased thermostability*</i>

What is the risk for Escape Mutations? - 2nd, 3rd , 4th Waves

Population Biology

What is the intrinsic mutation rate	low
How much time has passed, i.e., generations of replication	> 1.5 years
How big is the population, i.e., how many have been infected?	262M+
Is the population expanding or contracting? Bottlenecks?	regional waves
Potential for recombination?	Minimal
Selective pressures?	new mutations <i>re-infection increased transmission convalescent serum superior ACE2 binding vaccination escape?</i>

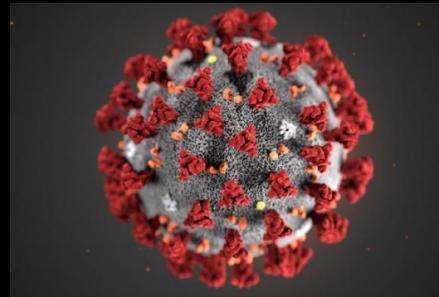
How do we sequence SARS-CoV-2?



Mike Surette



Hooman Derakhshani
(PDF, McMaster)

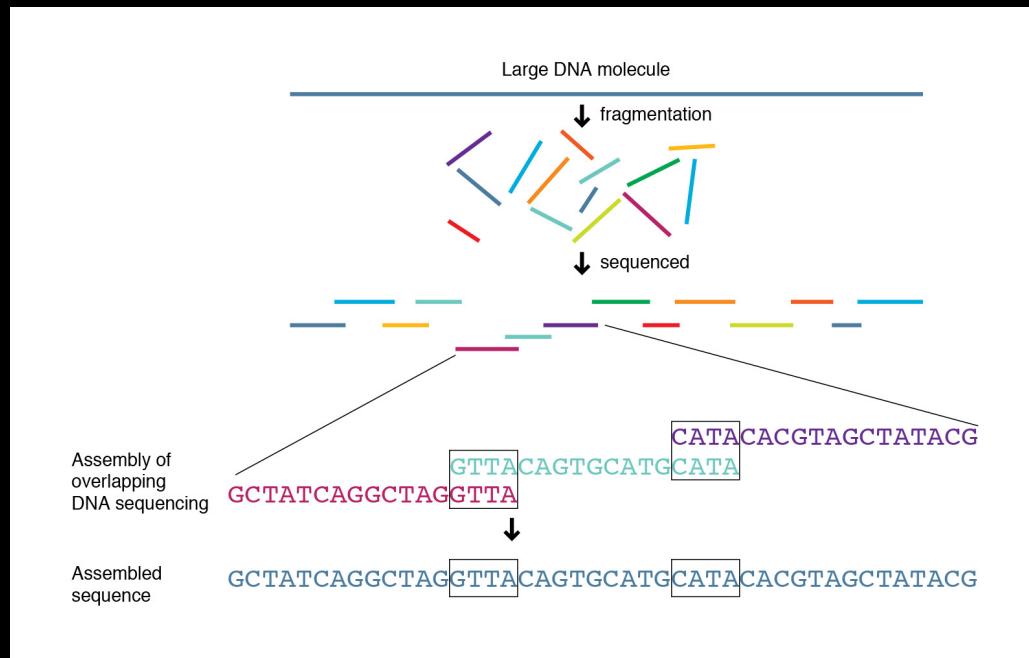


Patryk Aftanas
(Sunnybrook)

How do we sequence SARS-CoV-2?

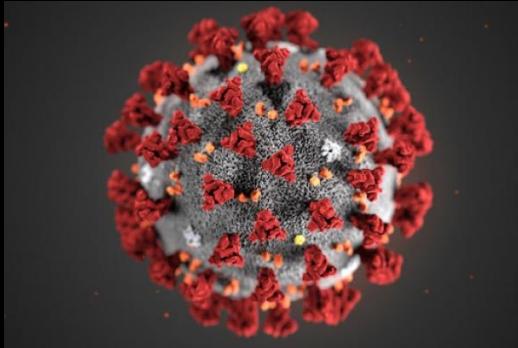


E. coli



- Culture to obtain large amount of clean DNA of pathogen
- Random fragmentation of DNA – each part of the genome is equally sampled
- Graph based computational assembly of the consensus genome
- Highly redundant sequencing of each nucleotide; at least 100x
- Sequencing error is nearly random; overcome by redundancy

How do we sequence SARS-CoV-2?



BSL3

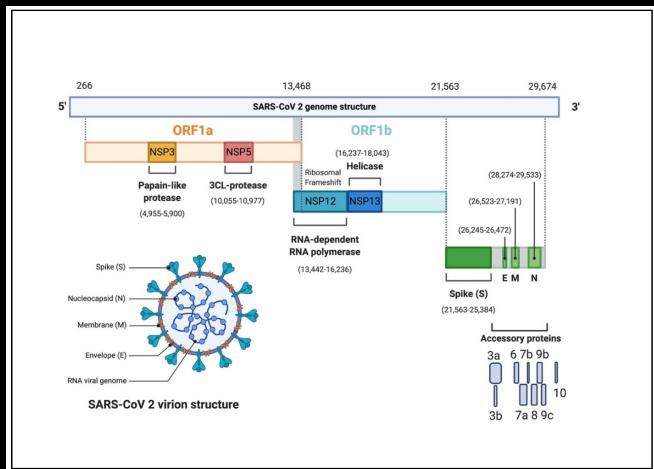


Arinjay Banerjee and friends

How do we sequence SARS-CoV-2?

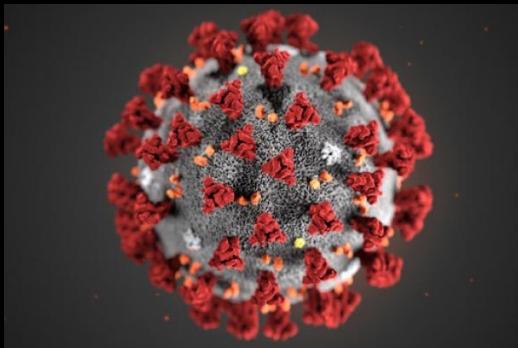


Overlapping PCR Amplicons → Illumina Sequencing



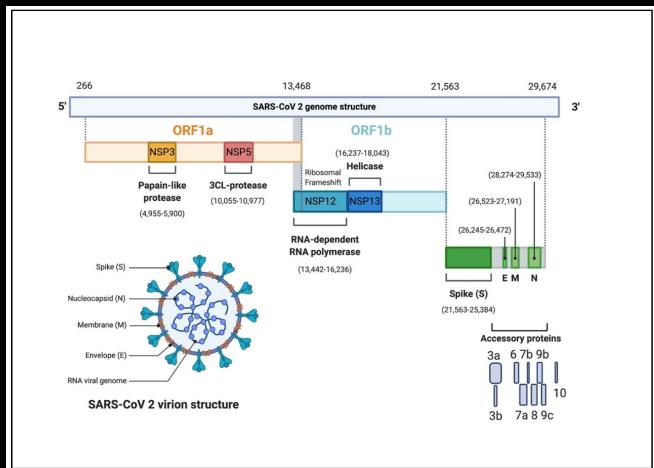
- Liverpool – 30 amplicons
- ARTIC3 – 98 amplicons

How do we sequence SARS-CoV-2?



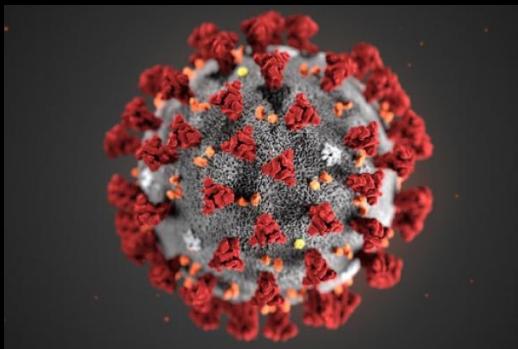
→ cDNA
reverse transcriptase

Overlapping PCR Amplicons → Illumina Sequencing



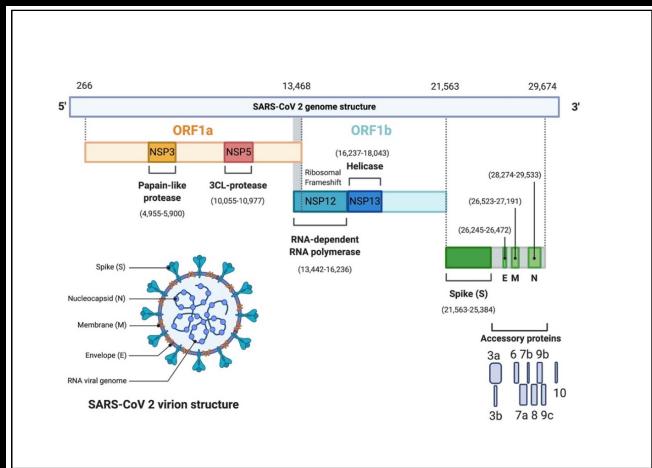
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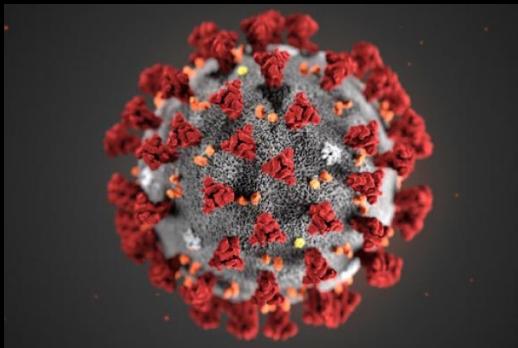
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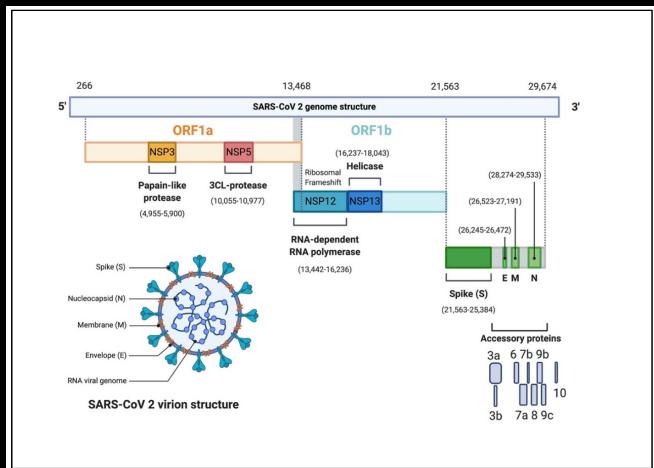
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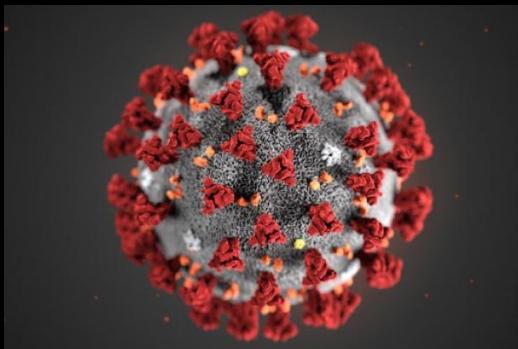
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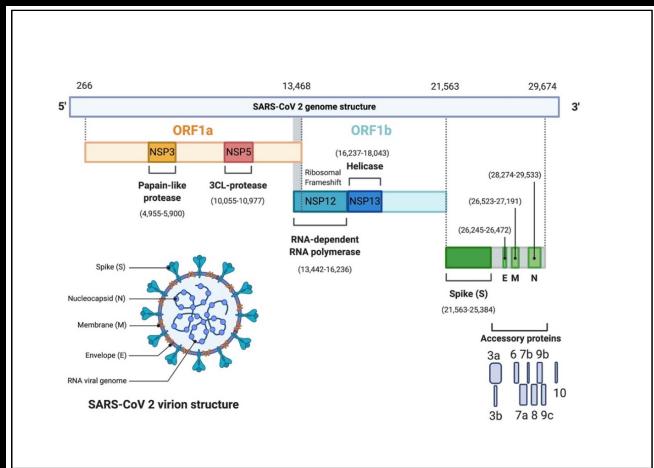
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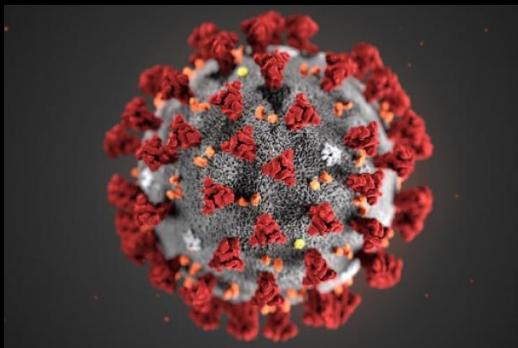
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- 10x coverage

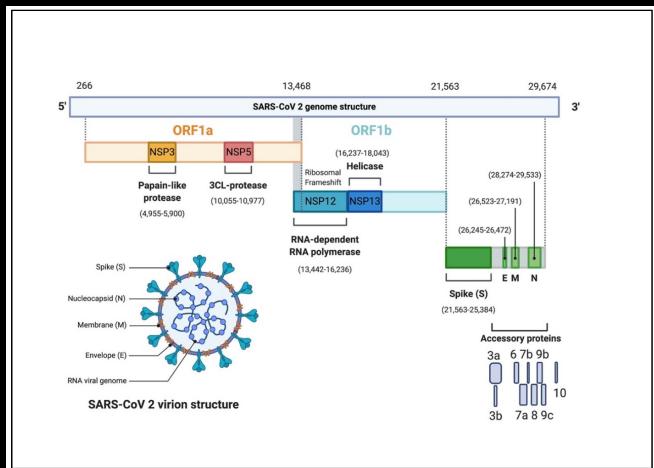
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SIGNAL: SARS-CoV-2 Illumina GeNome Assembly Line

<https://github.com/jaleezyy/covid-19-signal>



Jalees Nasir



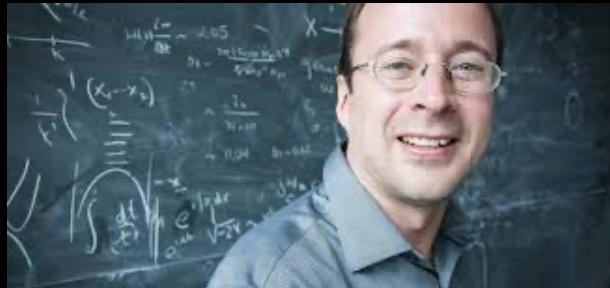
Amos Raphenya



Finlay Maguire (Dalhousie)



Natalie Knox (PHAC)



Kendrick Smith (Perimeter Institute)

*J.A. Nasir
R.A. Kozak
P. Aftanas
A.R. Raphenya
K.M. Smith
F. Maguire
H. Maan
M. Alruwaili
A. Banerjee
H. Mbareche
B.P. Alcock
N.C. Knox
K. Mossman
B. Wang
J.A. Hiscox
A.G. McArthur
S. Mubareka*

SIGNAL: SARS-CoV-2 Illumina GeNome Assembly Line

<https://github.com/jaleezyy/covid-19-signal>



Jalees Nasir



Amos Raphenya

Predicted mutations					
evidence	position	mutation	freq	annotation	gene
RA	241	C→T	100%	F3F (TT <u>C</u> →TT <u>T</u>)	Wuhan_probe → Wuhan_probe
RA	1,499	T→C	11.9%	S412P (T <u>C</u> T→CCT) ‡	orf1ab → orf1ab polyprotein
RA	1,500	C→T	11.9%	S412F (T <u>C</u> T→T <u>T</u>) ‡	orf1ab → orf1ab polyprotein
RA	1,503	A→T	11.9%	Y413F (T <u>A</u> T→T <u>T</u>)	orf1ab → orf1ab polyprotein
RA	1,508	Δ1 bp	11.9%	coding (1243/13203 nt)	orf1ab → orf1ab polyprotein
RA	1,510	T→C	11.9%	G415G (GG <u>T</u> →GG <u>C</u>)	orf1ab → orf1ab polyprotein
RA	3,037	C→T	100%	F924F (TTC→TT <u>T</u>) L256L (CTA→T <u>T</u> A)	orf1ab → Spike_F1 → orf1ab polyprotein Spike_F1
RA	7,388	G→A	14.3%	A2375T (GCC→ACC) G1706D (GGC→GAC)	orf1ab → Spike_F1 → orf1ab polyprotein Spike_F1
RA	14,408	C→T	100%	P4046L (CCT→CIT) P314L (CCT→CIT)	Spike_F1 → orf1ab → Spike_F1 orf1ab polyprotein
RA	23,403	A→G	100%	D614G (GA <u>T</u> →GG <u>T</u>)	S → surface glycoprotein
RA	23,677	T→A	35.8%	V705V (GT <u>T</u> →GT <u>A</u>)	S → surface glycoprotein
RA	26,715	T→G	9.3%	F65V (ITT→GT <u>T</u>)	M → membrane glycoprotein
RA	26,720	G→A	9.4%	V66V (GT <u>G</u> →GT <u>A</u>)	M → membrane glycoprotein
RA	26,722	Δ1 bp	9.7%	coding (200/669 nt)	M → membrane glycoprotein
RA	26,723	Δ1 bp	9.7%	coding (201/669 nt)	M → membrane glycoprotein
RA	28,881	3 bp→AAC	100%	coding (608-610/1260 nt) coding (1-3/22 nt)	N → nucleocapsid phosphoprotein N_gene-F → N_gene-F

Sample: S8

Data Volume [[trim_galore.log](#)]

Raw Data (read pairs)	27121
Raw Data (base pairs)	16326842
Post Primer Removal (read pairs)	27121
Post Primer Removal (base pairs)	16094033
Post Trim (read pairs)	27060

Quality Control Flags

Genome Fraction greater than 90%	PASS
Depth of coverage >= 2000x	FAIL
All variants with at least 90% frequency among reads	WARN
Reads per base sequence quality	PASS
Sequencing adapter removed	PASS
At least 90% of positions have coverage >= 100x	FAIL
At least 90% of positions have coverage >= 1000x	WARN

FASTQC Flags [[R1_val_1_fastqc.html](#) | [R2_val_2_fastqc.html](#)]

Per base sequence content	FAIL
Per sequence GC content	FAIL
Per tile sequence quality	WARN
Sequence Length Distribution	WARN

Kraken2 [[report](#)]

Reads SARS-CoV-2 (%)	93.57
----------------------	-------

QUAST [[report.html](#)]

Genome Length (bp)	29825
Genome Fraction (%)	94.937
N's per 100 kbp	4818.11
Genomic Features	
Mismatches per 100 kbp	24.66
Indels per 100 kbp	0.0
Average Depth of Coverage	
Fraction with 0 coverage	0.011
Fraction with 1x-10x coverage	0.04
Fraction with 11x-100x coverage	0.103
Fraction with 101x-1000x coverage	0.79
Fraction with 1001x-2000x coverage	0.057
Fraction with 2001x-10000x coverage	0.0
Fraction with > 10000x coverage	0.0
5' Ns	19
3' Ns	0

Variants in Consensus Genome (iVar)

C241T C3037T C14408T A23403G T23677A G28881A G28882A G28883C

J.A. Nasir

R.A. Kozak

P. Aftanas

A.R. Raphenya

K.M. Smith

F. Maguire

H. Maan

M. Alruwaili

A. Banerjee

H. Mbareche

B.P. Alcock

N.C. Knox

K. Mossman

B. Wang

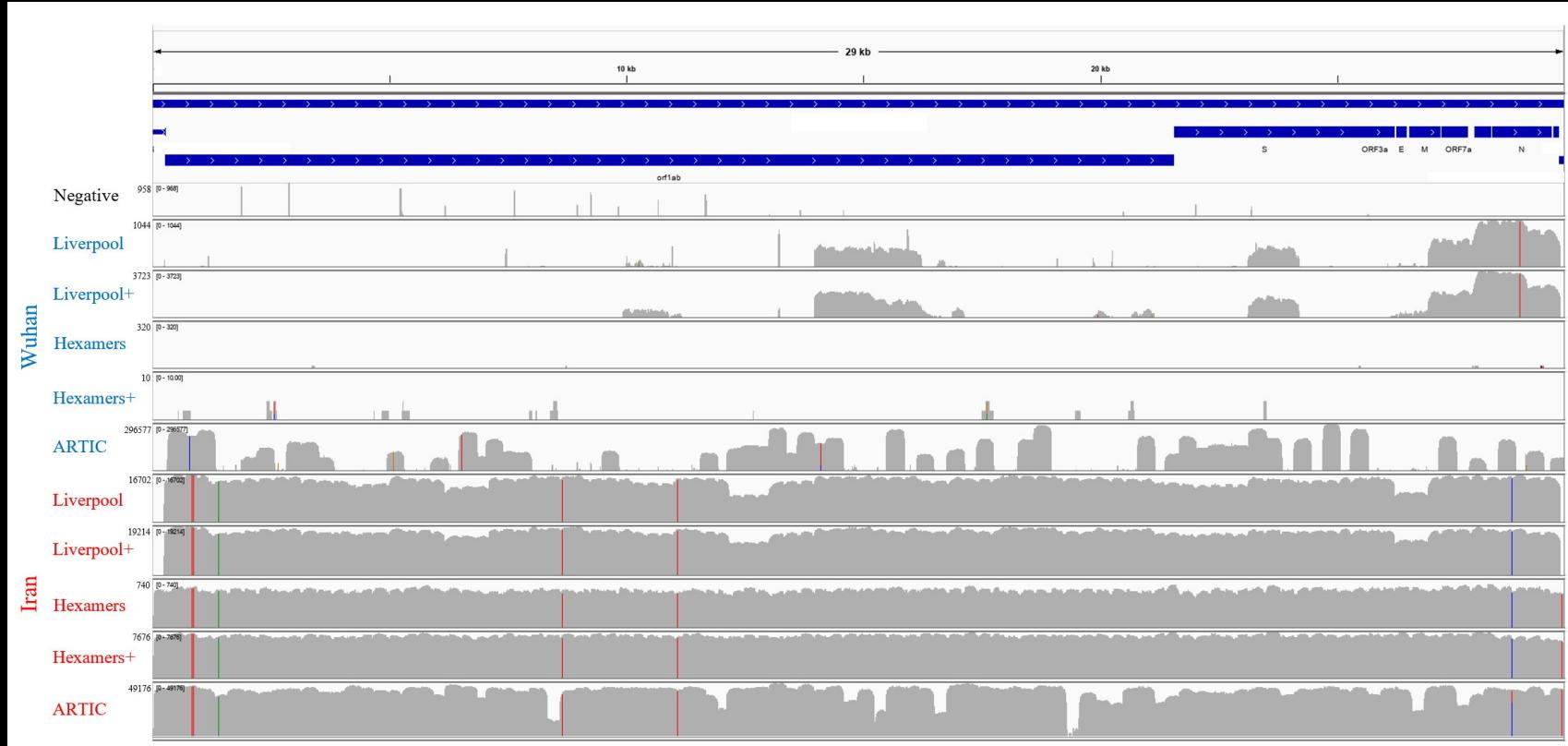
J.A. Hiscox

A.G. McArthur

S. Mubareka

SIGNAL: SARS-CoV-2 Illumina GeNome Assembly Line

<https://github.com/jaleezyy/covid-19-signal>



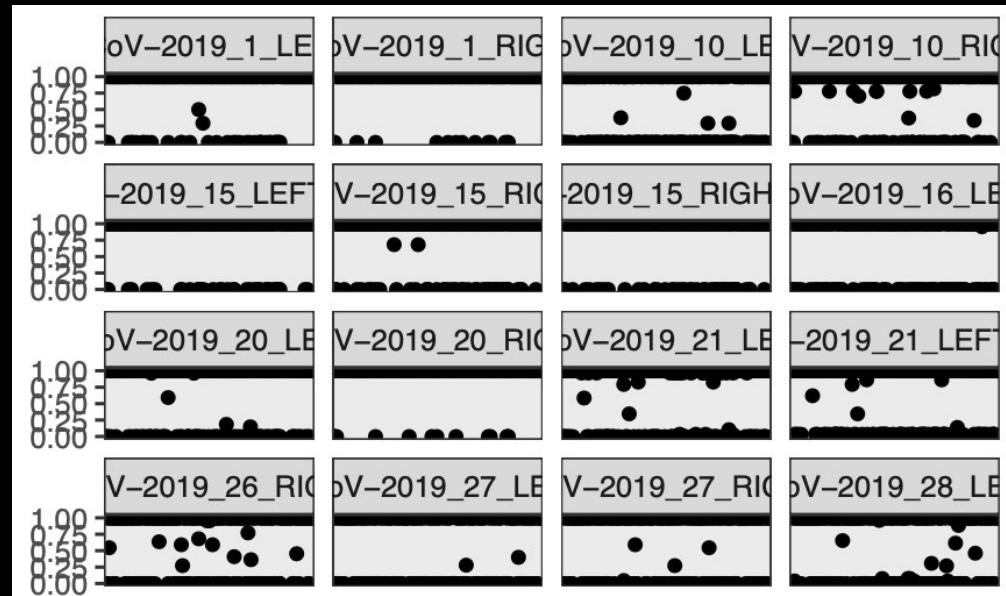
- Viral concentration (Ct value) is the most important predictor of success
- ARTIC3 provides highest depth of coverage of the SARS-CoV-2 genome; but dropped amplicons
- LIVERPOOL provides the most even coverage of the SARS-CoV-2 genome
- Bait capture enrichment provides results on par with sequencing amplicons
- Bait capture very useful for determining PCR artifacts

NCoV-Tools: Quality control for SARS-CoV-2 sequencing

<https://github.com/jts/ncov-tools>



Jared Simpson (OICR)





CanCOGeN



Mike Surette



Hooman Derakhshani



Andrew McArthur



Amos Raphenya



Ahmed Draia



Emily Panousis



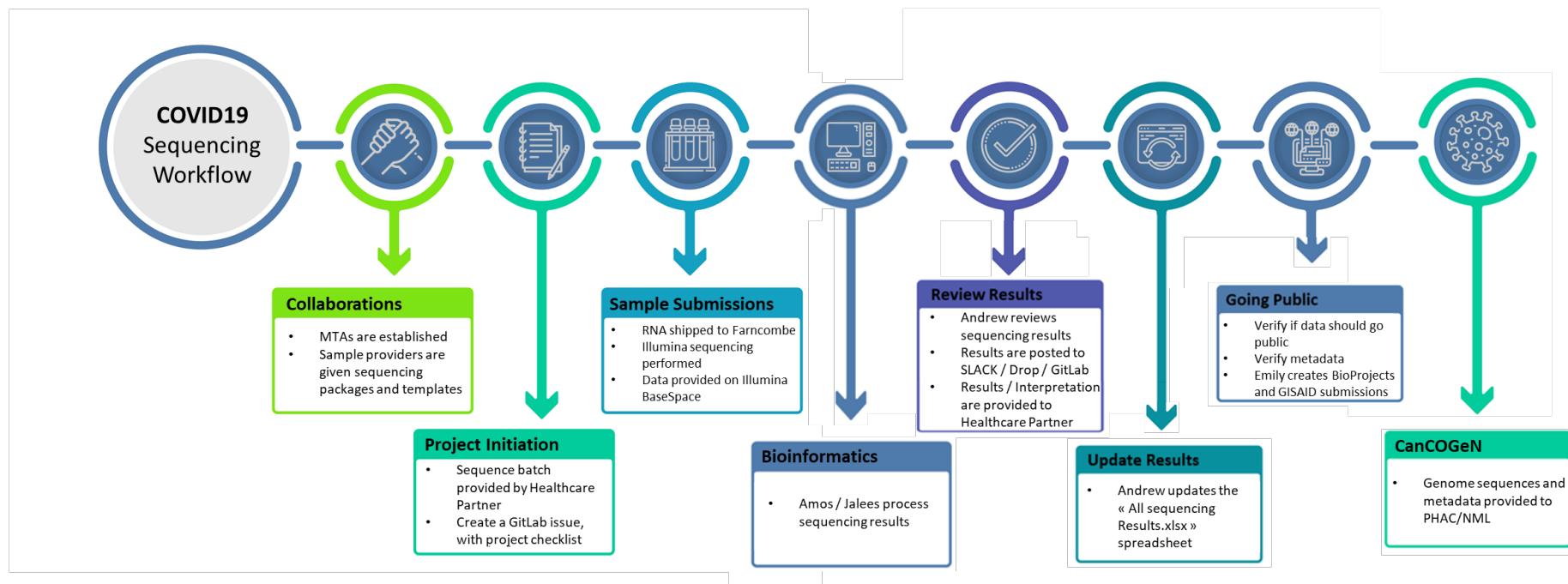
Ontario's COVID-19 Genomics Rapid Response Coalition



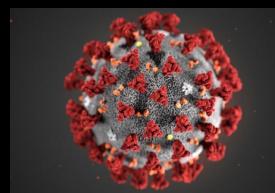
Ahmed Draia



Emily Panousis



McMaster – Sunnybrook



4,837 genomes sequenced

2,148 in GISAID (713 pending)

- current success rate >90%

- often 6 days from swab to GISAID, sometimes <4 days

Until recent retrospective data dumps... (late 2020)

- ~20% of national data

- ~50% of Ontario data

Currently... (late 2021)

- ~1-2% of national data

- ~6.3% of Ontario data

Hamilton

London

Ottawa

Toronto (Sunnybrook & Mt. Sinai)

Brampton / Etobicoke

Windsor

North Bay & Sudbury via Canadore College

Public Health Ontario overflow

Dynacare

Pearson Airport

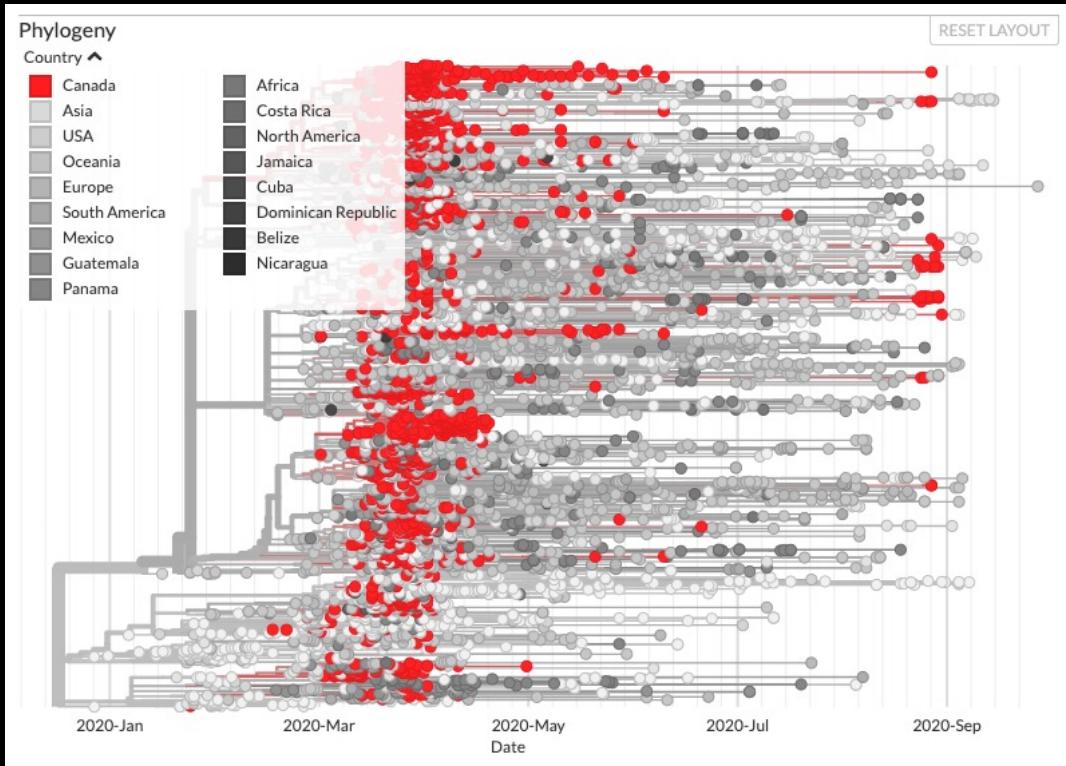
Institutional Outbreaks

- *Hamilton General*

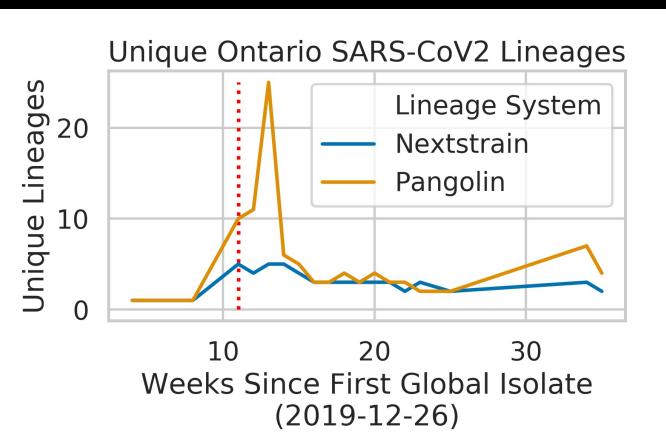
- *Juravinski*



The First Wave in Canada



Finlay Maguire (Dalhousie)



What do we know for Hamilton/Ontario?



June 2020 – LTC & Hospital Outbreak

B.1.1

* no community data

November 2020 – Point Prevalence (80 positives)

19 different variants (5 predominant)

December 2020 – Juravinski Outbreak

B.1.564.1 + 7 other variants

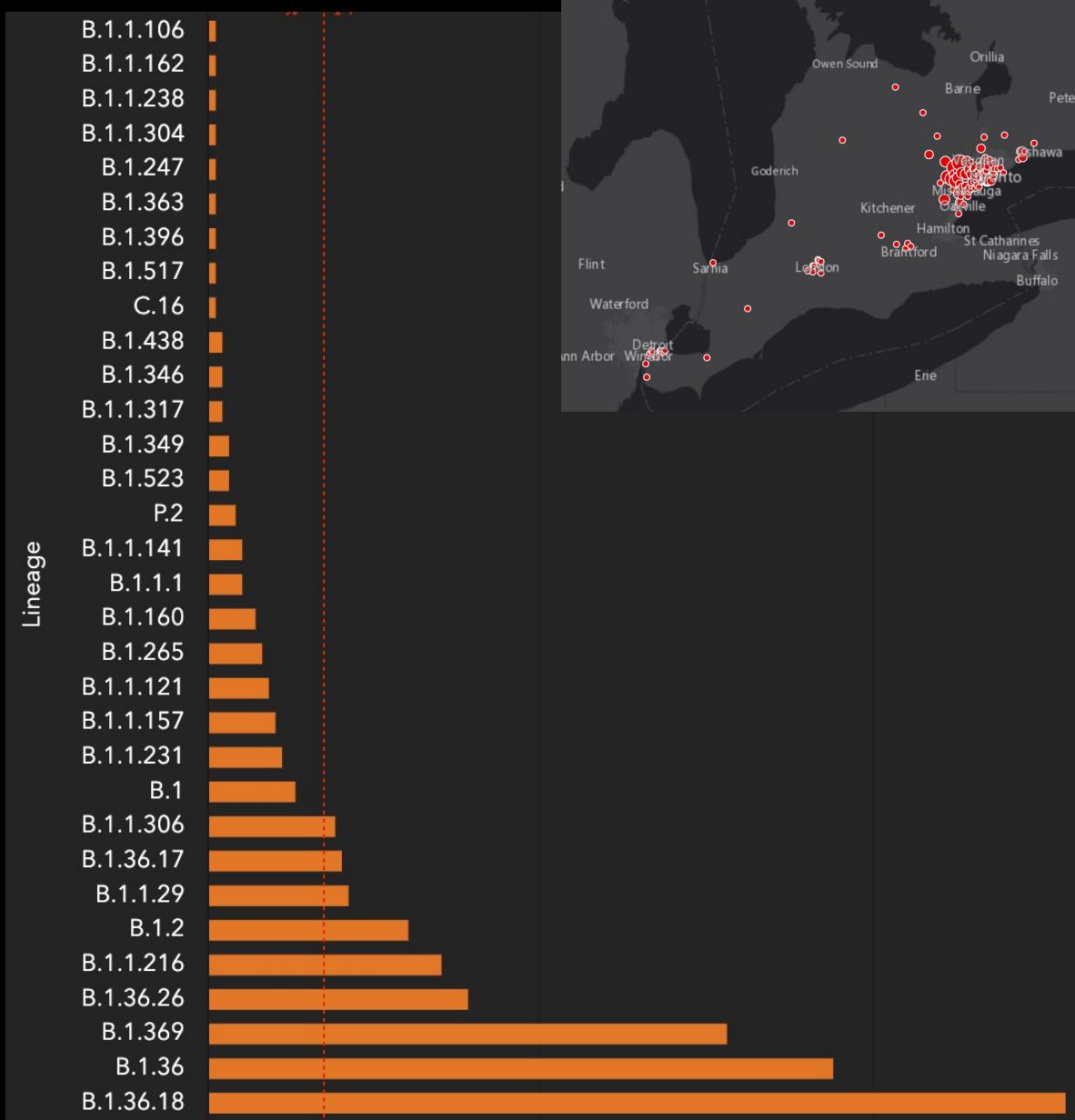
January 2021 – PHO Point Prevalence

~77% samples confirmed B.1.1.7

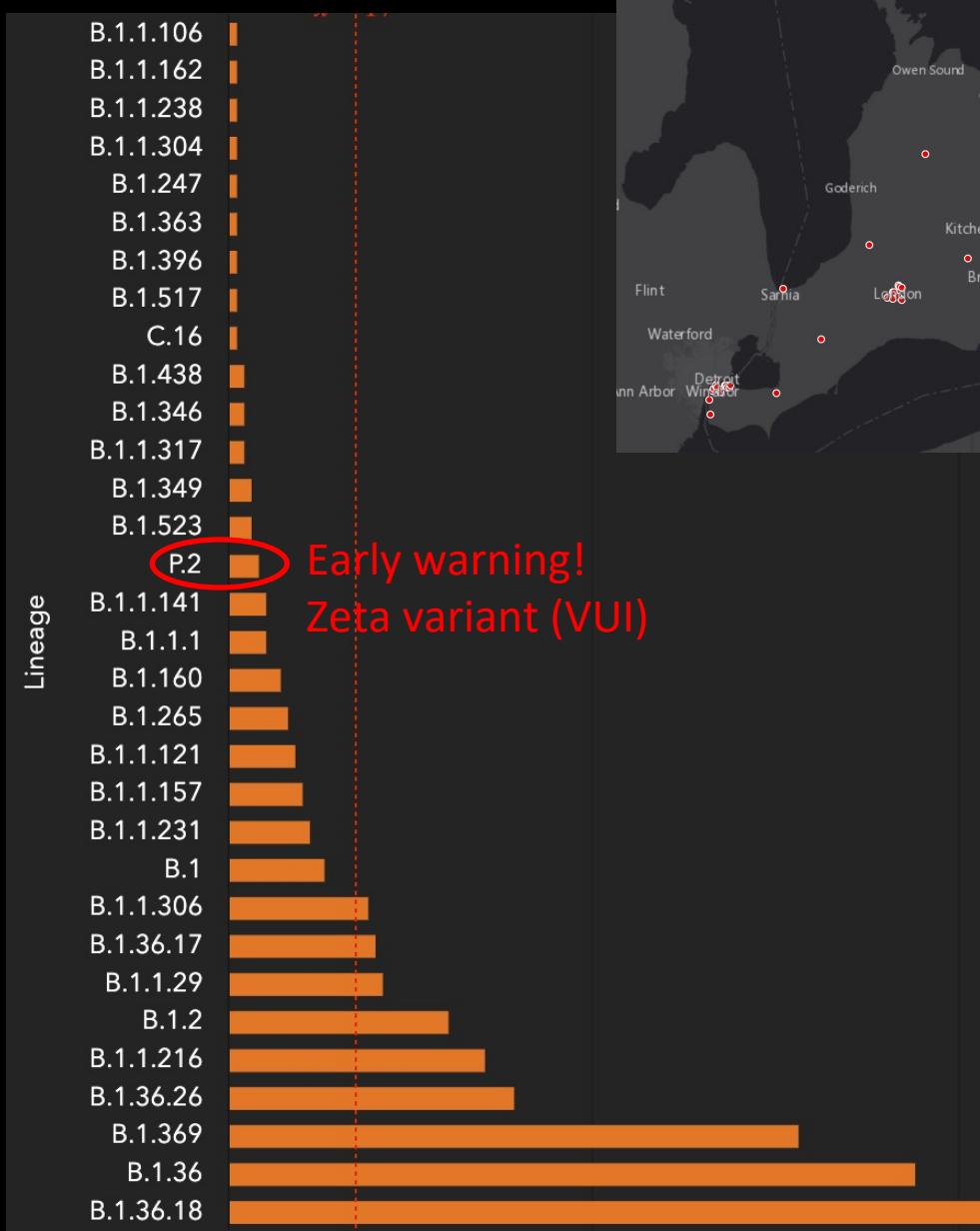
February 2021 – Vulnerable Community Outbreak

R.1 + 3 other variants

November 24, 2020 'Point Prevalence'



November 24, 2020 'Point Prevalence'

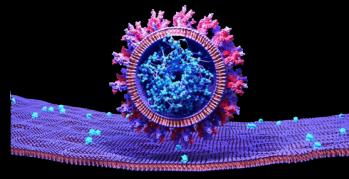


Ontario SARS-CoV-2 Point Prevalence Study – January 2021



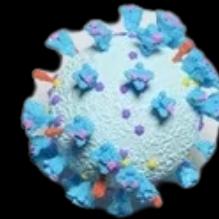
2,570 samples received and screened for N501Y

~3,003 SARS-CoV-2 samples were reported in Ontario on January 20th 2021



1
4.4% of screened samples had N501Y mutation

80.5% of these were from the Simcoe Muskoka District Health Unit



~77% of samples positive for N501Y were confirmed to be Alpha (B.1.1.7) Variants by WGS

PANGO Lineage detection

Canada's Third Wave & Variants of Concern

Alpha (B.1.1.7)	32 defining mutations	8 spike mutations	~50% incr. transmissibility 30-70% incr. mortality 50:50 male:female ratio
Beta (B.1.351)	21 defining mutations	9 spike mutations	likely incr. transmissibility
Gamma (P.1)	17 defining mutations	10 spike mutations	incr. transmissibility?

Canada's Third Wave & Variants of Concern

- Alpha (B.1.1.7)** Novavax trial reports reduction in vaccine efficacy; origins in immunocompromised patient?
- Beta (B.1.351)** partial resistance in two randomized control trials (RCTs)
- Gamma (P.1)** unclear but associated with re-infection

Canada's Third Wave & Variants of Concern

Alpha (B.1.1.7)

H69-/V70-

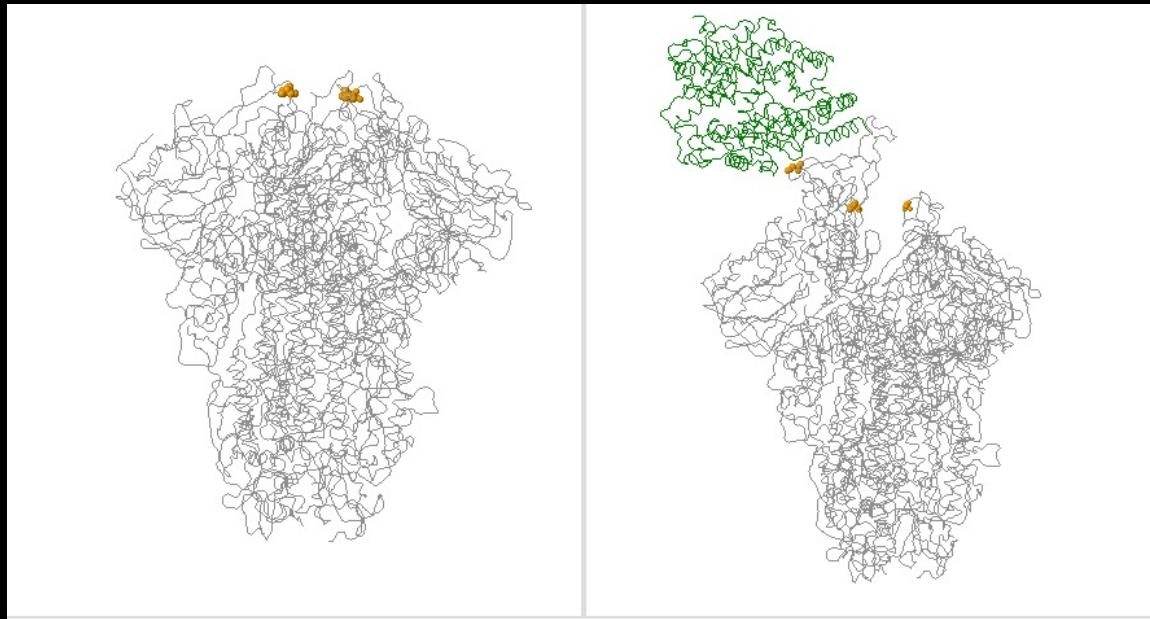
N501Y

Beta (B.1.351)

N501Y

Gamma (P.1)

N501Y



May increase ACE2 binding; ACE2 binding may be further increased by the presence of E484K; stabilized by the presence of K417N

May be associated with adaptation to rodents and mustelids (i.e. mink); animal reservoir?

Small but significant reduction in neutralization via Moderna and Pfizer-BioNTech vaccines.

Canada's Third Wave & Variants of Concern

Alpha (B.1.1.7)

H69-/V70- N501Y

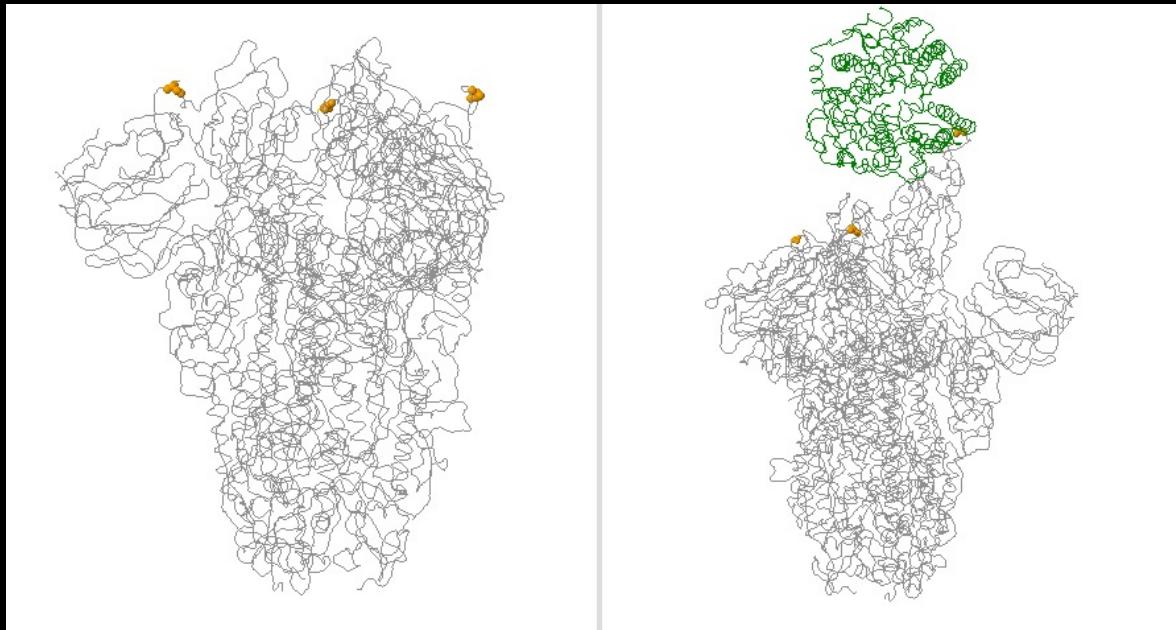
Beta (B.1.351)

N501Y E484K

Gamma (P.1)

N501Y E484K

receptor binding domain



may increase ACE2 binding, which may be further increased by the presence of S:N501Y, and stabilized by the presence of S:K417N

may significantly reduce convalescent serum neutralization

associated with re-infection

tests in people vaccinated with the Moderna and Pfizer-BioNTech vaccines suggest S:E484K and S:N501Y individually, and both together in combination with S:K417N, cause a small but significant reduction in neutralization

Canada's Third Wave & Variants of Concern

Alpha (B.1.1.7)

H69-/V70- N501Y

P681H

Beta (B.1.351)

N501Y E484K

furin cleavage site

Gamma (P.1)

N501Y E484K

receptor binding domain

directly adjacent to the SARS-CoV-2
S1/S2 furin cleavage site

may increase cleavability and
membrane fusion to enhance
infectivity

Canada's Third Wave & Variants of Concern

Alpha (B.1.1.7)	H69-/V70-	N501Y	E484K	P681H
Beta (B.1.351)		N501Y	E484K	<i>furin cleavage site</i>
Gamma (P.1)		N501Y	E484K	<i>receptor binding domain</i>

Canada's Third Wave & Variants of Concern

Alpha (B.1.1.7)	H69-/V70-	N501Y	E484K	P681H
Beta (B.1.351)		N501Y	E484K	<i>furin cleavage site</i>
Gamma (P.1)		N501Y	E484K	
<i>receptor binding domain</i>				

Table 1. Variant lineage, designation and status as of 6 May 2021

Lineage	Designation	First detected in sequence from	Status
B.1.1.7	VOC-20DEC-01	UK	VOC
B.1.351	VOC-20DEC-02	South Africa	VOC
P.1	VOC-21JAN-02	Japan ex Brazil	VOC
B1.1.7 with E484K	VOC-21FEB-02	UK	VOC
P.2	VUI-21JAN-01	Brazil	VUI
A.23.1 with E484K	VUI-21FEB-01	UK	VUI
B.1.525	VUI-21FEB-03	UK	VUI
B.1.1.318	VUI-21FEB-04	UK England	VUI

Business Standard

AstraZeneca vaccine 80% effective against B1.617.2 variant: UK study

Across UK, case numbers of the B1.617.2 variant had risen by 2,111 over the past week to hit 3,424 cases

Topics

Coronavirus | Coronavirus Tests | Coronavirus Vaccine

Spike: T19R, 156del, 157del, R158G, L452R, T478K, D614G, P681R, D950N

B.1.617.2 (Delta) VOC lacking N501Y or E484K

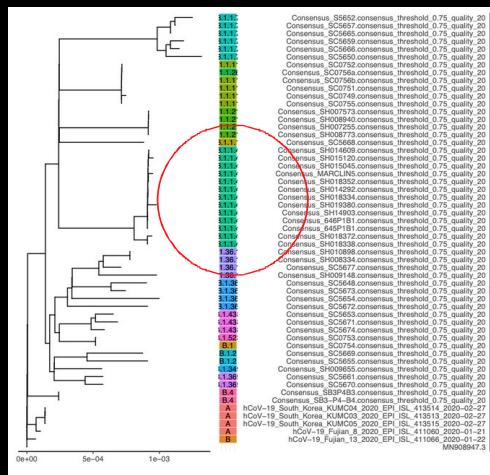
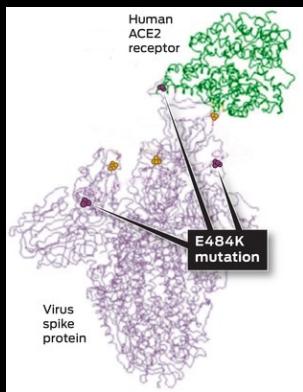


Hamilton R.1 Outbreak



January/February 2021 - Burden fell on a community experiencing homelessness

Lineage	Most common countries	Earliest date	# designated	# assigned	Description	WHO Name
R.I	Japan 71.0%, United States of America 23.0%, Sweden 2.0%, Germany 1.0%, Austria 1.0%	2020-01-14	72	10719	Alias of B.I.I.316.I, Sublineage of B.I.I.316 with 3 additional spike mutations, circulating in a number of countries. pango-designation issue #17	



E484K, G769V and W152L Mutations

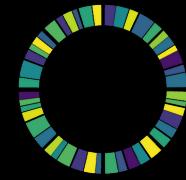
"Escape mutations" that pose a threat to our current diagnostic methods

R.1 identified in a shelter outbreak in Hamilton

Localized outbreak, spread limited in rest of the city

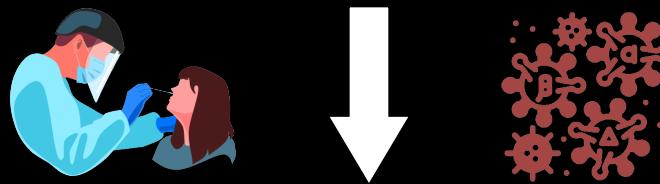
Culturing of R.1 Variant

Implications in determining functional ability of this variant



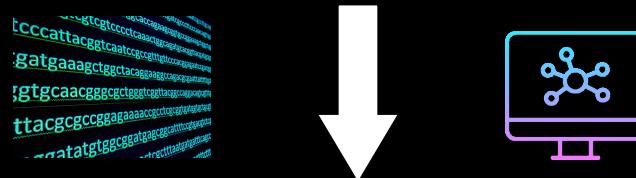
The game plan: genomic surveillance teamwork

Samples collected and sequenced by HHS

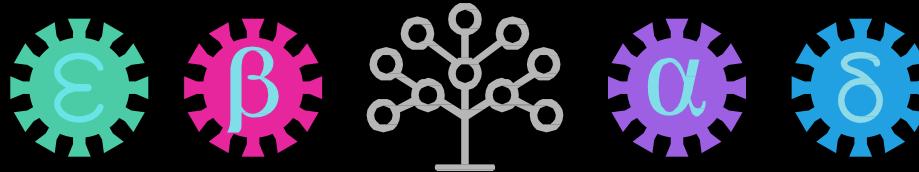


Raw Data sent to McArthur Lab Weekly

Consensus genomes run through SIGNAL and PANGOLIN



PANGO Lineage Reports Generated



Weekly lineage reports helped Hamilton be reclassified as a Delta hotspot



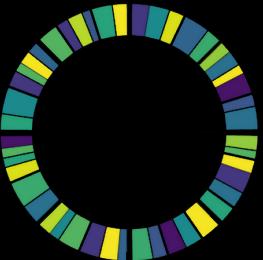
NEWS ▾ WEATHER TRAFFIC SHOWS ▾ MORNING LIVE SCHEDULE SHOP LOCAL

Home > News > Local News > Hamilton added as Delta variant hot spot as province opens up 2nd...

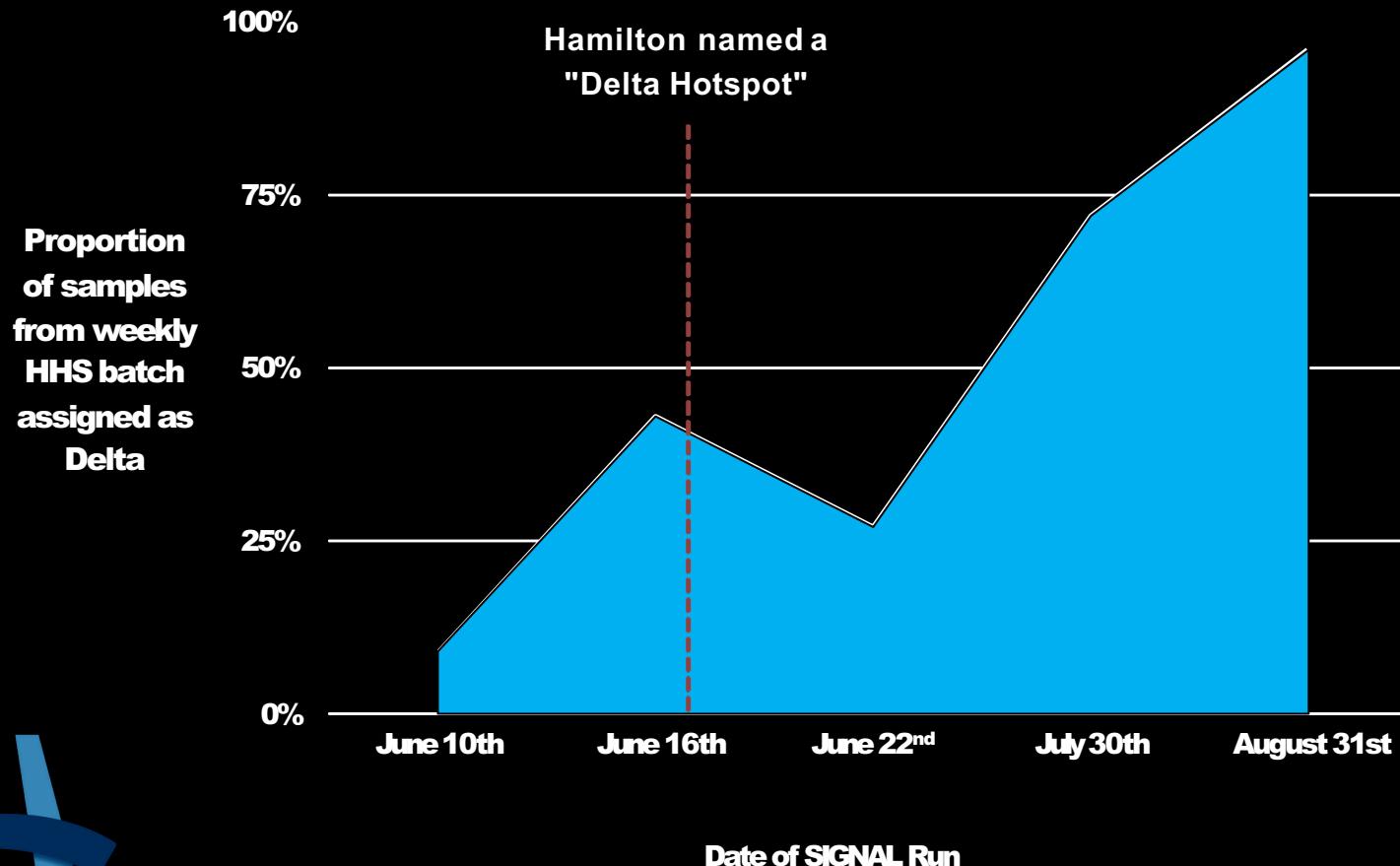
News Local News Top News Story

Hamilton added as Delta variant hot spot as province opens up 2nd dose eligibility

By **Andrea Lawson** - June 17, 2021, 12:45 pm



Delta Variant in Hamilton: Summer 2021



Thanks!

McArthur Lab

- Amos Raphenya, Emily Panousis, Ahmed Draia, Dr. McArthur

McMaster

- Mike Surette, Hooman Derakhshani, Arinjay Banerjee, Farncombe Sequencing Team, MILO, CSU, HiREB, Gina Mannen, Gerry Wright, Karen Mossman

ONCoV, ONS2, Sunnybrook

- Jared Simpson, Samira Mubareka, Rob Kozak, Robyn Lee, Ramzi Fattouh, Hamza Mbareche, Kyuganya Nirmalarajah, Patryk Aftanas , and so many more...

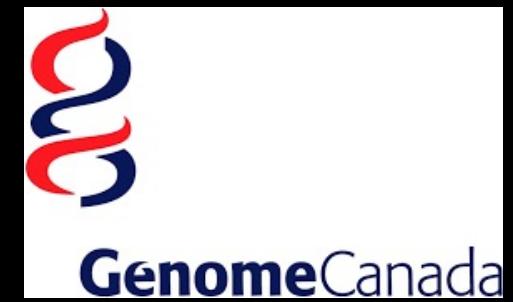
CanCOGeN

- Gary Van Domselaar, Natalie Knox, and the many working groups (QC & BC especially!)

The ‘Hackers’

- Finlay Maguire, Kendrick Smith, Hassaan Maan, Bo Wang, DNAStack

Thanks!



End