How RT-PCR Testing Allows Labcorp to Perform National SARS-CoV-2 Pandemic Surveillance

Brian Krueger, PhD Associate Vice President, Research and Development Center for Esoteric Testing / Center for Molecular Biology and Pathology

4/23/2021

labcorp

Labcorp: Leading Laboratory Service Provider

- •Large scale national molecular testing
- •PIXEL at home collection kits expand reach
- •National laboratory information system
- •Specimen tracking
- •Sample meta data attached to each sample





SARS-CoV-2 RT-PCR Test Development Timeline





LabCorp COVID-19 RT-PCR Test

- A high throughput implementation of the CDC RT-PCR Test
- Development
 - Extraction:
 - Roche MagnaPure 96 samples per hour
 - ThermoFisher KingFisher MagMax-96 samples per hour
 - Hamilton MagEx 192 samples per hour
 - Detection
 - QuantStudio 7 384-well
 - Multiplex Assay (384 samples, 1 rxn per sample) ~
 6,000 samples/instrument/day





LabCorp COVID-19 RT-PCR Test

- Assay Multiplex Development began in February
 - Launched on manual SinglePlex because of quick access to reagents
- Assay Multiplexed by changing Fluorescent dyes
 - N1 FAM
 - N2 Yakima Yellow
 - RP Cy5
- Automated on Hamilton Star Liquid Handlers
 - 1,152 rxns/instrument/hr
- More than half of Labcorp SARS-CoV-2 testing is performed on the Labcorp COVID-19 RT-PCR Test
 - >40M tests performed since March 2020



Supply Chain Constraints DEFINED the Pandemic

- Swabs
 - Cotton Swabs (qTips)
 - Foam Swabs
 - 3D Printed Swabs
- Transport Media
 - UTM
 - Saline
- Extraction Methods
- 1-Step RT Enzymes
- Heat/Quick Extraction
- Saliva Collection





LabCorp Total Unique RT-PCR Positives





PCR Testing vs Genome Sequencing

- •Our PCR testing detects 2 locations in the SARS-CoV-2 Genome
- •Both are in the N protein, or Nucleocapsid Protein
 - -Resides inside of the viral particle and protects the Viral genome
- •Genome Sequencing determines the genetic code of the entire virus



Image: https://www.scientificanimations.com, CC BY-SA 4.0





Molecular RT-PCR Testing Workflow Enables Viral Genome Surveillance



Sequencing and Analysis Pipeline

Condensed Plate of Positive High Value Samples Whole Genome Tiled Amplification (2 Pools of Overlapping 1.2kb Amplicons)

PacBio Sequel II



Phylogenetic Assignment



Alignment and Variant Calling





What's a viral genome?





What's a viral genome?

- •Viruses evolve within the host
- •New mutations arising continuously
- •A host has a population of viruses, many of which can have distinct genetic differences





Large Variant Detection and Phasing



Images: Liz Tseng, PacBio



Sequencing Library Protocol



Freed, et al, 2020 – DOI: 10.1093/biomethods/bpaa014 Labcorp optimized protocol is available on the PacBio website



Analysis Pipeline

CSH Spring bioRviv	Home about submit news & notes alerts / rss channels		lerts / rss Channels
Laboratory	Search		Q
THE PREPRINT SERVER FOR BIOLOGY			Advanced Search
ioRxiv is receiving many new papers on coronavirus SARS-CoV-2. A reminder: these are p	preliminary reports that have not bee	en peer-reviewed. They should not	be regarded as conclusive, guide clinical
practice/health-related behavior, or be reported in news media as established information.			
New Results	• Comment on this paper	G Previous	Next 🗲
CEConsta versatile VCE based consensus sequence generat		Postod February 27, 2021	
CrCons: a versaule VCr-based consensus sequence general	or for small	Posted Pebruary 27, 2021.	
genomes			Email
🖻 Elizabeth Tseng, 📵 Qiandong Zeng, 💿 Lax Iyer		Download PDP	Anter Share
doi: https://doi.org/10.1101/2021.02.26.433111			Citation Tools
This article is a preprint and has not been certified by peer review [what does this mean?].			
		Tweet Like 0	
Abstract Info/History Metrics	Preview PDF		
		COVID-19 SARS-CoV-2 preprints from	
Abstract		medRxiv and bioR	xiv
We had developed VCFCons to address urgent need for a robust co	onsensus sequence	Subject Area	
generator for SARS-CoV-2 viral surveillance, which presented seve	ral unique	Bioinformatics	
requirements including: (a) low coverage areas should be noted w	ith 'N's (b) low		
frequency or suspicious variant calls need to be filtered. We have f	ound that while		
are evicting tools such as bothools can approve the desired one	ound that, while	Subject Areas	
some existing tools such as bottools can generate the desired con-	sensus sequence, it		

For Internal Use Only – Not For Distribution

Acc

.....

Pilot Surveillance Study

•70,000 SARS-CoV-2 positive samples banked from March, 2020 – Dec, 2020

•Initial pilot study of 10,000 early pandemic samples (March 15, 2020 - May 21, 2020)

• Developed a model for national viral genome surveillance Feb 23, 2020 Mar 15, 2020

Sequencing Project Begins



Dec 7, 2020 ASM Presentation of Pilot Study Data

Dec 27, 2020 Awarded CDC Sequencing Contract



Pilot Study Sample Collection

SARS-CoV-2 Mutations Over Time





S:D614G Spread During the Early Pandemic When Few Were Looking





New Variants of Concern

•B.1.1.7 lineage (201/501Y.V1)



- -Emerged in the UK September 2020
- -Likely has increased transmissibility
 -Detected in the US Dec 29,2020

•P.1 lineage (20J/501Y.V3)



- -Brazilian origin
- -Likely increased transmissibility and antibody resistance
- -Detected in the US Jan 25, 2020
- •B.1.351 lineage (20H/501Y.V2)
 - -South African origin
 - -Likely increased transmissibility and antibody resistance
 - -Detected in the US Jan 28, 2020



Image: https://www.scientificanimations.com, CC BY-SA 4.0





19

Spike Mutations Can Reduce Immunity to the Virus

Convalescent Plasma (Immunity from viral infection)

Vaccine Plasma (Immunity from vaccination)



Wang et al, 2021, https://doi.org/10.1101/2021.01.25.428137



Overview of Current CDC Sequencing Results

- •Sampling from ~3,500 samples every week
 - -CDC Baseline Study
 - -Minimum of 10 per state
 - •~60% Full genomes, +~30% Lineage typed
 - -Results reported weekly on CDC SPHERES calls
- •Share Summary statistics, CCS BAMs and FASTA consensus
- •Tracking individual mutations and viral lineages
- •Aiding in CDC response and national action planning for containment of new mutants





CDC Sequencing by Week

750-1500 1500-3000 3000+ <25 25-50 50-100 100-200 200-400 400-750 • . .*





CDC Clade Distribution





The New York Times

Overview of Cur

Covid-19 Live Updates: Variant Found in South Africa Now Detected in U.S.

Sampling from ~10
CDC Baseline Stud
Minimum of 10 p
~60% Full genon
Results reported ¹

- •Share Summary sta
- Tracking individual
- •Aiding in CDC resp

The variant that emerged in South Africa is reported in the U.S. for the first time.





ew variants



Geographic Focused Surveillance





Geographic Focused Surveillance





The New York Times

Overview of C⁴

Sampling from ~
-CDC Baseline St
-Minimum of 10
~60% Full gen
-Results reporte

- •Share Summary
- Tracking individu
- •Aiding in CDC re:

labcorp





Variants of Concern

Variants of Concern (12/19/20 - 12/26/20)+/-



VOC





_____b.1.1.7 _____b.1.351 _____P.1

Variants of Concern – B.1.526 E484K





B.1.526 - E484K

 Dec 19 Dec 26 Jan 02
 Jan 09 Jan 16
 Jan 23
 Jan 30
 Feb 06
 Feb 13
 Feb 20
 Feb 27
 Mar 06
 Mar 13
 Mar 20
 Mar 27
 Apr 03

 2020
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021
 2021

-NJ -NY -USA



A Change in the Clade Distribution?





B.1.1.7 Cases Are Increasing, Total Cases Have Plateaued



B.1.1.7 vs Cases

Total b.1.1.7



UP IN THE BLUE SEATS A NEW YORK RANGERS HOCKEY PODCAST





🛣 тірз

Pandemic (

Bill Gates' daughter jokes on social media about getting COVID-19 vaccine



Mayor, police chief and clerks all arrested in small lowa town



Mom who went viral pushing dairy truck through snow gets year's supply of milk



UK company Scancell developing vaccine to fight COVID-19 variants



•Labcorp ha: SARS-CoV-2

- •Scalable to
- •Proven suc(
- Pacific Bios
 genotypes

•Labcorp an beginning c

labcorp



By Aaron Feis

Seven new highly contagious COVID-19 variants found across US

February 15, 2021 | 1:16pm | Updated

G 💟 🖓 😂 🚯









Acknowledgements



Molecular Micro and Genetics R&D

Mike Levandoski PhD Scott Parker John Pruitt Kim Wagner Ayla Burns Thomas Urban PhD Amanda Suchanek PhD **Center for Bioinformatics**

Lax Iyer PhD Qian Zeng PhD Stan Letovsky PhD

DNA Identity

Brian Norvell Jon Williams PhD

Marcia Eisenberg, PhD Chief Scientific Officer



Elizabeth Tseng PhD George Yuan PhD Kristina Weber PhD Jason Underwood PhD Andy Larrea PhD Jonas Korlach PhD



CENTERS FOR DISEASE CONTROL AND PREVENTION

Duncan MacCannell PhD Dhwani Batra PhD Scott Sammons PhD



How RT-PCR Testing Allows Labcorp to Perform National SARS-CoV-2 Pandemic Surveillance

Brian Krueger, PhD Associate Vice President, Research and Development Center for Esoteric Testing / Center for Molecular Biology and Pathology Brian.Krueger@labcorp.com



h2so4hurts in /in/BrianKruegerPhD

labcorp