The University of Washington COVID-19 community serosurvey: informing smart policy decisions

Keith R. Jerome, MD PhD

University of Washington

Fred Hutchinson Cancer Research Center

November 4, 2020

UW Medicine
LABORATORY MEDICINE
VIROLOGY

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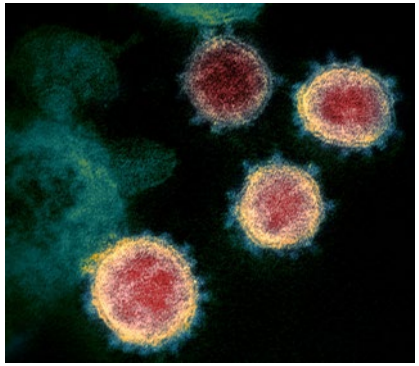
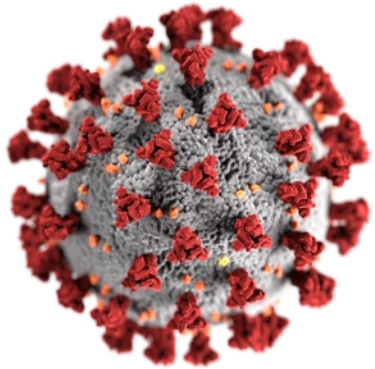
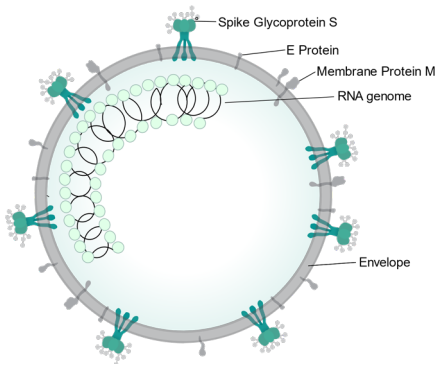
- The speakers, course director and planners at the Federation of State Medical Boards and Washington Medical Commission have nothing to disclose.

SARS-CoV-2

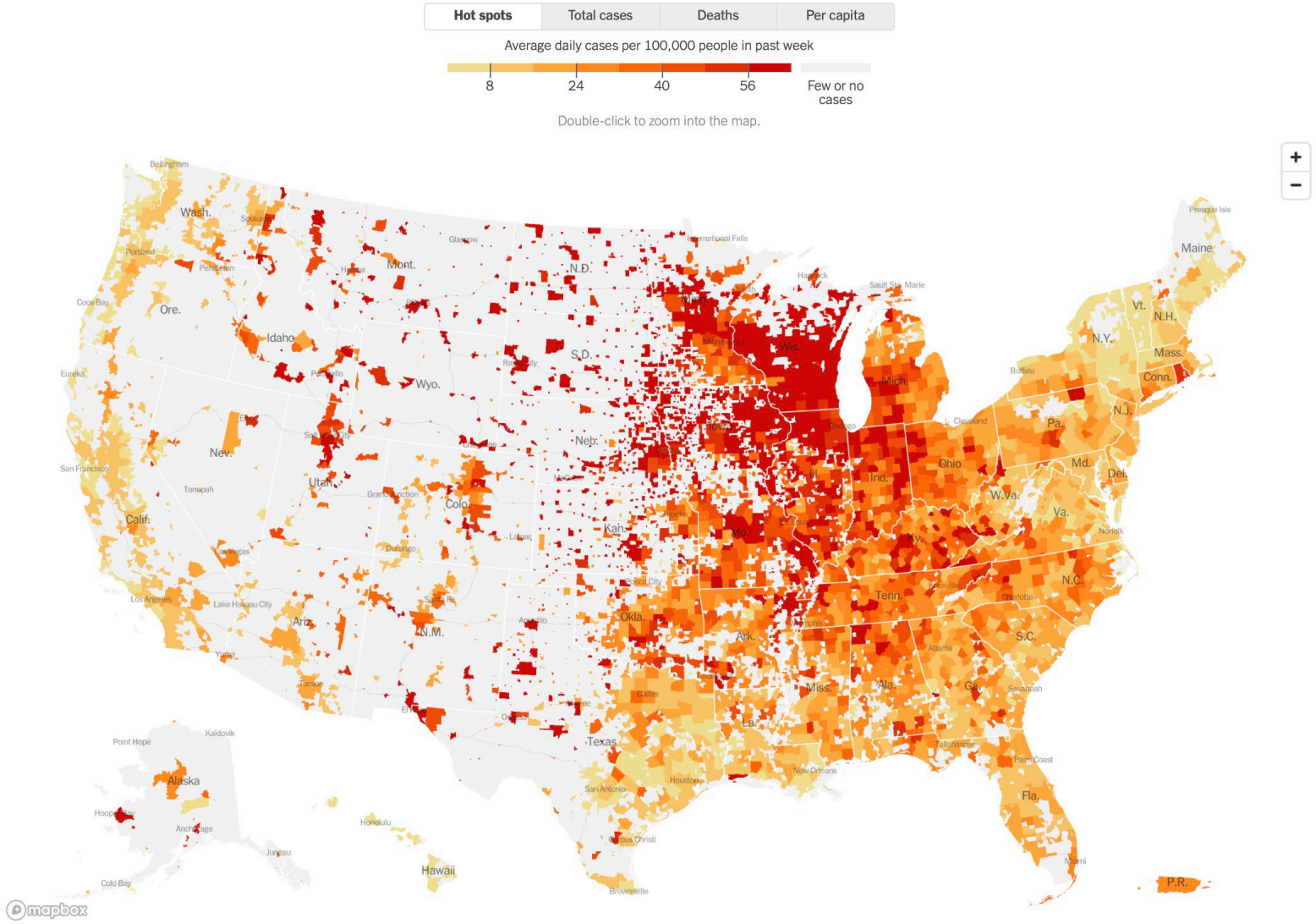


- Member of the coronavirus family, along with 229E, NL63, OC43, HKU1, MERS-CoV, and the original SARS-CoV.
- positive-sense single-stranded RNA virus (+ssRNA)
- ~30,000 bp genome
- Encode a proofreading 3′-to-5′ exoribonuclease, thus mutation rate is low
- four structural proteins: S (spike), E (envelope), M (membrane), and N (nucleocapsid)
- The causative agent of Coronavirus disease 2019 (COVID-19), first identified in December 2019 in Wuhan, China,



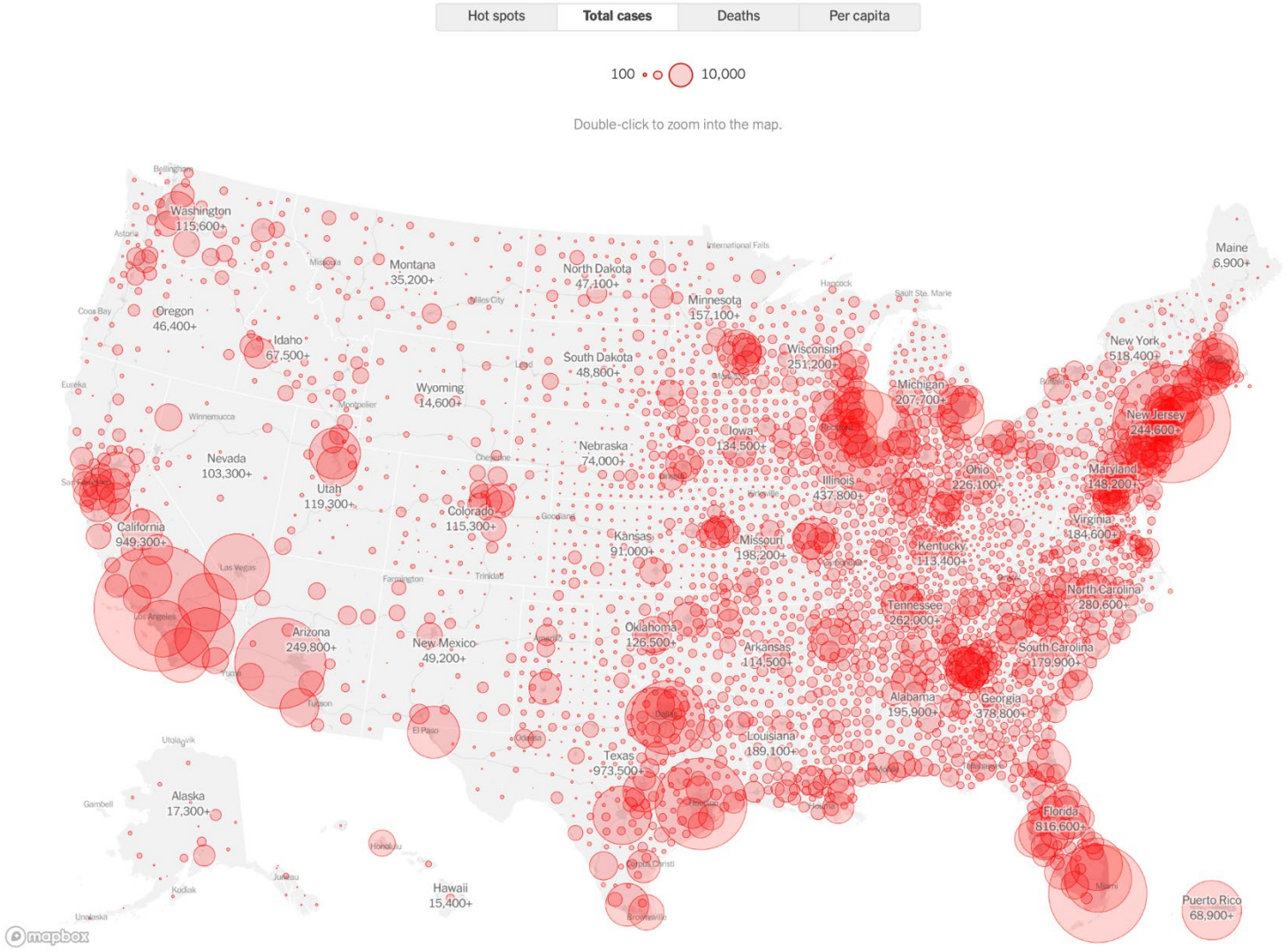


Current US case rates



NY Times, November 4, 2020

US distribution of cases



NY Times, November 4, 2020

Existing capabilities would have allowed discovery of SARS-CoV-2

ACCEPTED MANUSCRIPT

Metagenomic analysis reveals clinical SARS-CoV-2 infection and bacterial or viral superinfection and colonization

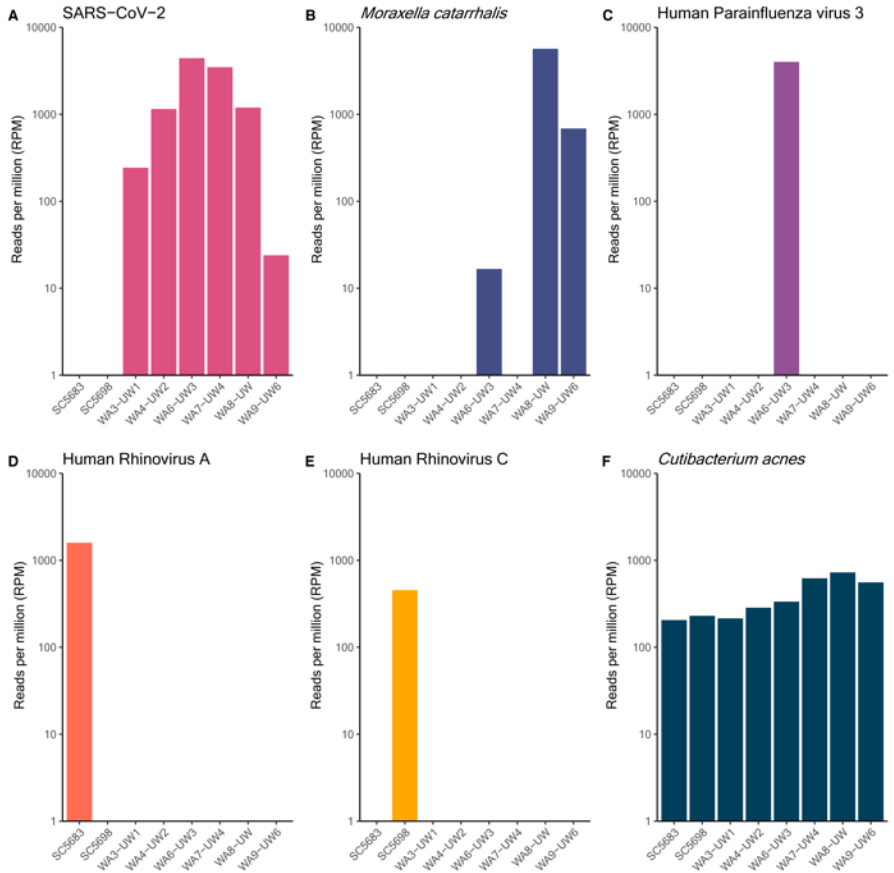
Vikas Peddu, Ryan C Shean, Hong Xie, Lasata Shrestha, Garrett A Perchetti, Samuel S Minot, Pavitra Roychoudhury, Meei-Li Huang, Arun Nalla, Shriya B Reddy, Quynh Phung, Adam Reinhardt, Keith R Jerome ✉, Alexander L Greninger ✉

Clinical Chemistry, hvaa106, https://doi-org.offcampus.lib.washington.edu/10.1093/clinchem/hvaa106

Published: 07 May 2020 **Article history** ▾

Sample	Total reads on sample	Percent of SARS-CoV-2 genome assembled	SARS-related coronavirus RPM	RdRp gene C_T
WA6-UW3	1,927,886	99.8	4423	20.7
WA9-UW6	5,756,216	99.0	24	29.5
WA7-UW4	1,770,266	98.7	3474	21.7
WA3-UW1	18,419,147	98.6	243	22.9
WA8-UW5	941,164	97.9	1194	24.8
WA4-UW2	2,713,586	97.6	1149	22.8
SC5683	1,728,462	0	0	NDT
SC5698	1,013,934	0	0	NDT

RdRp, RNA-dependent RNA polymerase.



The first UW SARS-CoV-2 genomes

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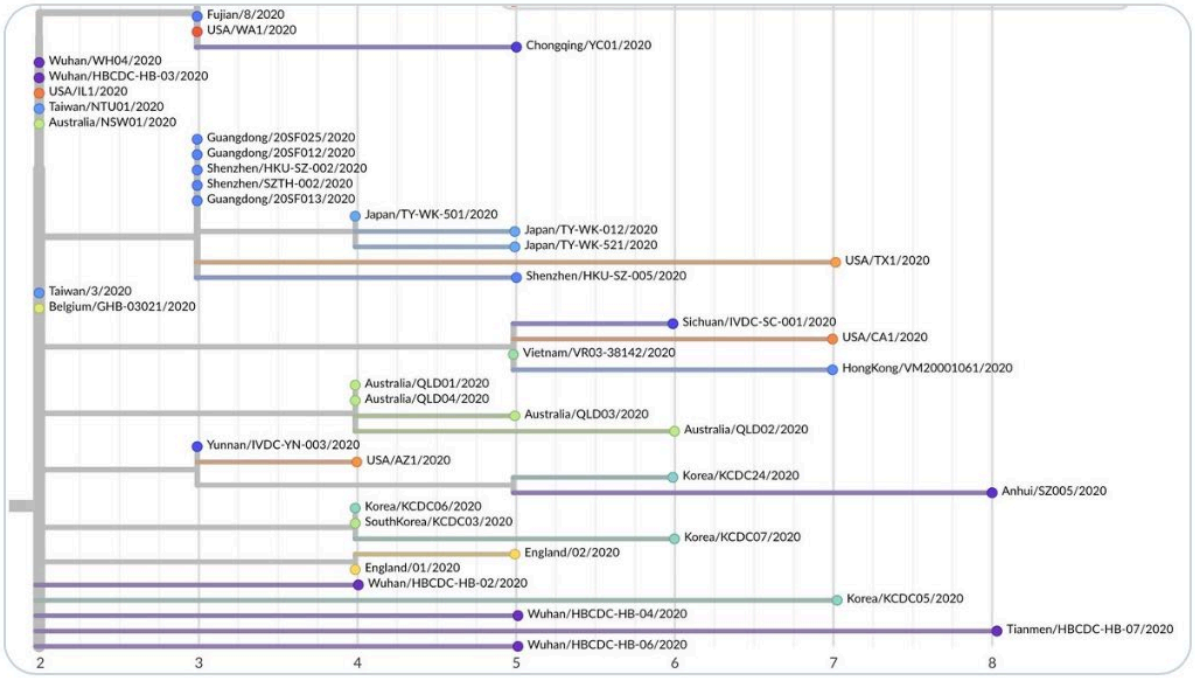
Thanks to rapid data sharing by @UWVirology via gisaid.org, we've updated the site with 2 additional #SARSCoV2 genomes from Washington State. These group with other locally acquired viruses into a single cluster. nextstrain.org/ncov?label=cla...



9 133 260

Sequencing provides understanding of COVID-19 spread

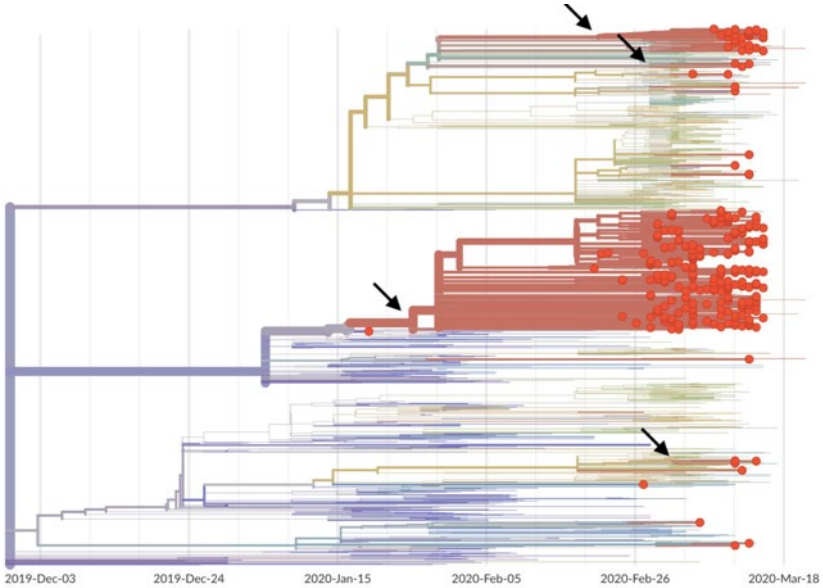


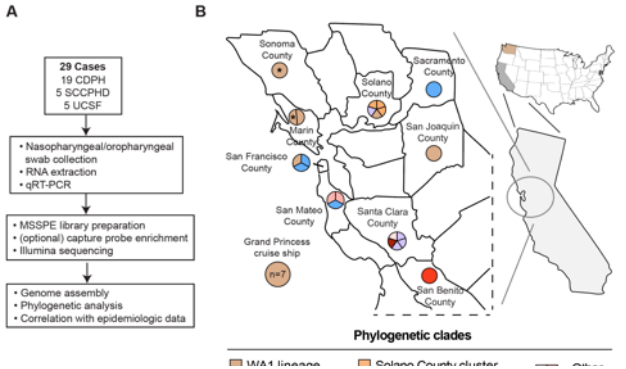
Figure 2. Phylogeny of 346 SARS-CoV-2 viruses collected from Washington State (red circles) on a background of globally collected viruses. Clustering of related viruses indicates community transmission after an introduction event. In addition to the estimated January introduction of the large outbreak clade we see later introduction events (marked by arrows) resulting in smaller community outbreaks.

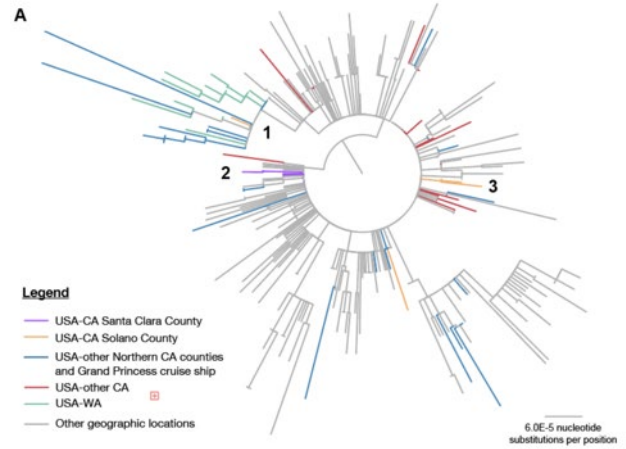
Cryptic transmission of SARS-CoV-2 in Washington State

Trevor Bedford*[§1,2,3], Alexander L. Greninger*[1,3], Pavitra Roychoudhury*[1,3], Lea M. Starita*[,2,3], Michael Famulare*[4], Meei-Li Huang[3], Arun Nalla[3], Gregory Pepper[3], Adam Reinhardt[3], Hong Xie[3], Lasata Shrestha[3], Truong N Nguyen[3], Amanda Adler[5], Elisabeth Brandstetter[3], Shari Cho[3], Danielle Giroux[3], Peter D. Han[3], Kairsten Fay[1], Chris D. Frazar[3], Misja Ilcisin[1], Kirsten Lacombe[5], Jover Lee[1], Anahita Kiavand[3], Matthew Richardson[3], Thomas R. Sibley[1], Melissa Truong[3], Caitlin R. Wolf[3], Deborah A. Nickerson[2,3], Mark J. Rieder[2,3], Janet A. Englund[3,5], the Seattle Flu Study Investigators, James Hadfield[1], Emma B. Hodcroft[6], John Huddleston[1,3], Louise H. Moncla[1], Nicola F. Müller[1], Richard A. Neher[6], Xianding Deng[7], Wei Gu[7], Scot Federman[7], Charles Chiu[7], Jeff Duchin[3,8], Romesh Gautom[9], Geoff Melly[9], Brian Hiatt[9], Philip Dykema[9], Scott Lindquist[9], Krista Queen[10], Ying Tao[10], Anna Uehara[10], Suxiang Tong[10], Duncan MacCannell[10], Gregory L. Armstrong[10], Geoffrey S. Baird[3], Helen Y. Chu*[2,3], Jay Shendure*[2,3,11], Keith R. Jerome*[1,3]

Version 2. medRxiv. 2020 Apr 6:2020.04.02.20051417. doi: 10.1101/2020.04.02.20051417.

Updated version in press, Science





Science

REPORTS

Cite as: X. Deng *et al.*, *Science* 10.1126/science.abb9263 (2020).

Genomic surveillance reveals multiple introductions of SARS-CoV-2 into Northern California

Xianding Deng[1,2*], Wei Gu[1,2*], Scot Federman[1,2*], Louis du Plessis[3*], Oliver G. Pybus[3], Nuno Faria[3], Candace Wang[1,2], Guixia Yu[1,2], Brian Bushnell[4], Chao-Yang Pan[5], Hugo Guevara[5], Alicia Sotomayor-Gonzalez[1,2], Kelsey Zorn[6], Allan Gopez[1], Venice Servellita[1], Elaine Hsu[1], Steve Miller[1], Trevor Bedford[7,8], Alexander L. Greninger[7,9], Pavitra Roychoudhury[7,9], Lea M. Starita[8,10], Michael Famulare[11], Helen Y. Chu[8,12], Jay Shendure[8,9,13], Keith R. Jerome[7,9], Catie Anderson[14], Karthik Gangavarapu[15], Mark Zeller[14], Emily Spencer[14], Kristian G. Andersen[14], Duncan MacCannell[16], Clinton R. Paden[16], Yan Li[16], Jing Zhang[16], Suxiang Tong[16], Gregory Armstrong[16], Scott Morrow[16], Matthew Willis[17], Bela T. Matyas[18], Sundari Mase[19], Olivia Kasirye[20], Maggie Park[21], Godfred Masinde[22], Curtis Chan[23], Alexander T. Yu[2], Shua J. Chai[2,15], Elsa Villarino[24], Brandon Bonin[25], Debra A. Wadford[1], Charles Y. Chiu[1,2,5†]

Spread of COVID-19 to US east coast

CellPress

Cell

Article

Coast-to-Coast Spread of SARS-CoV-2 during the Early Epidemic in the United States

Joseph R. Fauver,[1,22,*] Mary E. Petrone,[1,22] Emma B. Hodcroft,[2,3,22] Kayoko Shioda,[1] Hanna Y. Ehrlich,[1] Alexander G. Watts,[4] Chantal B.F. Vogels,[1] Anderson F. Brito,[1] Tara Alpert,[5] Anthony Muyombwe,[6] Jafar Razeq,[6] Randy Downing,[6] Nagarjuna R. Cheemarla,[7] Anne L. Wyllie,[1] Chaney C. Kalinich,[1] Isabel M. Ott,[8] Joshua Quick,[9] Nicholas J. Loman,[9] Karla M. Neugebauer,[5] Alexander L. Greninger,[10,11] Keith R. Jerome,[10,11] Pavitra Roychoudhury,[10,11] Hong Xie,[10] Lasata Shrestha,[10] Meei-Li Huang,[10,11] Virginia E. Pitzer,[1] Akiko Iwasaki,[12,13] Saad B. Omer,[1,14,15,16] Kamran Khan,[4,17,18] Isaac I. Bogoch,[18] Richard A. Martinello,[15,19,20] Ellen F. Foxman,[7,12] Marie L. Landry,[7,15,21] Richard A. Neher,[2,3] Albert I. Ko,[1] and Nathan D. Grubaugh[1,23,*]

Issues around COVID-19 diagnosis

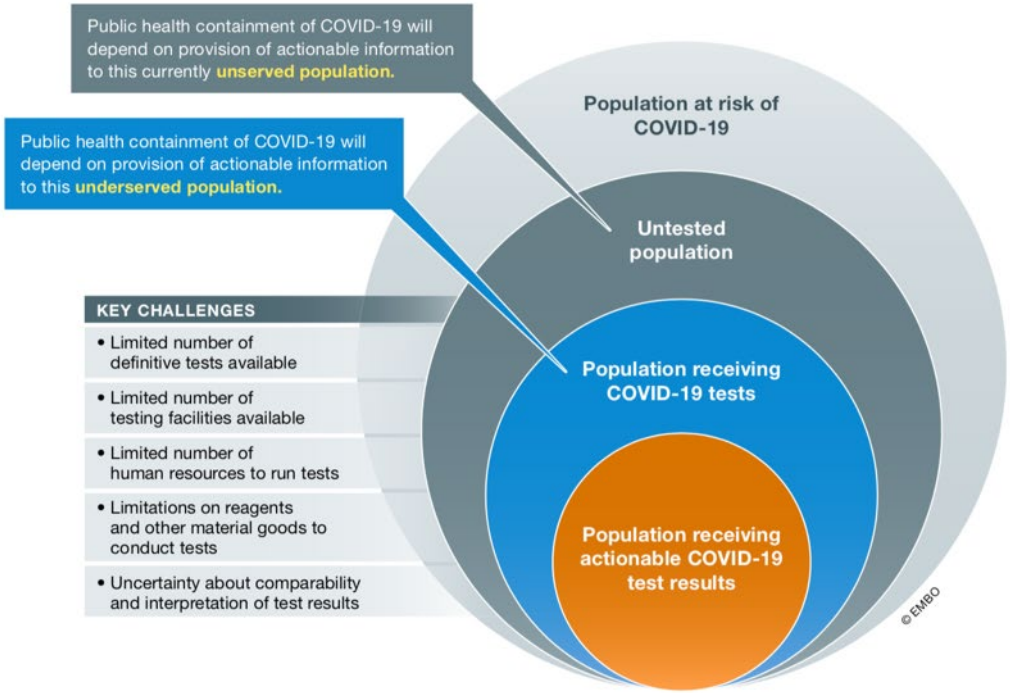


Figure 1. Critical gaps in population-level COVID-19 testing.

Illustration of contemporary challenges in providing testing to support public health containment of COVID-19 and key populations that are currently unserved or underserved by testing.

Correspondence

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EMBO Molecular Medicine

'All In': a pragmatic framework for COVID-19 testing and action on a global scale

Syril D Pettit[1,*], Keith R Jerome[2], David Rouquié[3], Bernard Mari[4], Pascal Barbry[4], Yasunari Kanda[5], Mineo Matsumoto[6], Susan Hester[7], Leah Wehmas[7], Jason W Botten[8] & Emily A Bruce[8]

Regulatory hurdles prevented early SARS-CoV-2 testing in the US

THE NEW YORKER

NEWS DESK

WHAT WENT WRONG WITH CORONAVIRUS TESTING IN THE U.S.

By Robert P. Baird
March 16, 2020

In February, as a first set of COVID-19 test kits sent out by the Centers for Disease Control failed to work properly, labs around the country scrambled to fill the void. Photograph Courtesy the C.D.C.

On February 5th, sixteen days after a Seattle resident who had visited relatives in Wuhan, China, was diagnosed as having the first confirmed case of COVID-19 in the United States, the Centers for Disease Control, in Atlanta, began sending diagnostic tests to a network of about a hundred state, city, and county public-health laboratories. Up to that point, all testing for

UW Virology was one of the first academic labs in the US to test for SARS-CoV-2

UW Medicine gets green light to test for coronavirus

March 4, 2020 at 5:30 pm | *Updated March 5, 2020 at 12:35 am*

1 of 3 | A medical lab scientist at UW Medicine in Seattle shows a collected nasal swab sample from Washington to be tested for the novel... (Ken Lambert / The Seattle Times) **More**

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THE CORONAVIRUS CRISIS

When Coronavirus Struck Seattle, This Lab Was Ready To Start Testing

March 5, 2020 · 5:53 PM ET

JON HAMILTON

3-Minute Listen + PLAYLIST

"Access to testing is really the major tool we have right now to fight this new coronavirus," says Dr. Keith Jerome, who runs a University of Washington lab in Seattle that can now test for the virus.

Jonathan Hamilton/NPR

Assay validation: sample types, stability, and quantitation

Journal of Clinical Virology 128 (2020) 104438

Contents lists available at ScienceDirect

Journal of Clinical Virology

journal homepage: www.elsevier.com/locate/jcv

Short communication

Validation of SARS-CoV-2 detection across multiple specimen types

Garrett A. Perchetti[a], Arun K. Nalla[a], Meei-Li Huang[a], Haiying Zhu[a], Yulun Wei[a], Larry Stensland[a], Michelle A. Loprieno[b], Keith R. Jerome[a,b], Alexander L. Greninger[a,b,*]

AMERICAN SOCIETY FOR MICROBIOLOGY | Journal of Clinical Microbiology

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Letter to the Editor

Stability of SARS-CoV-2 in PBS for Molecular Detection

Garrett A. Perchetti, Meei-Li Huang, Vikas Peddu, Keith R. Jerome, Alexander L. Greninger

DOI: 10.1128/JCM.01094-20

Journal of Clinical Virology 129 (2020) 104499

Contents lists available at ScienceDirect

Journal of Clinical Virology

journal homepage: www.elsevier.com/locate/jcv

Short communication

Multiplexing primer/probe sets for detection of SARS-CoV-2 by qRT-PCR

Garrett A. Perchetti[a], Arun K. Nalla[a], Meei-Li Huang[a], Keith R. Jerome[a,b], Alexander L. Greninger[a,b,*]

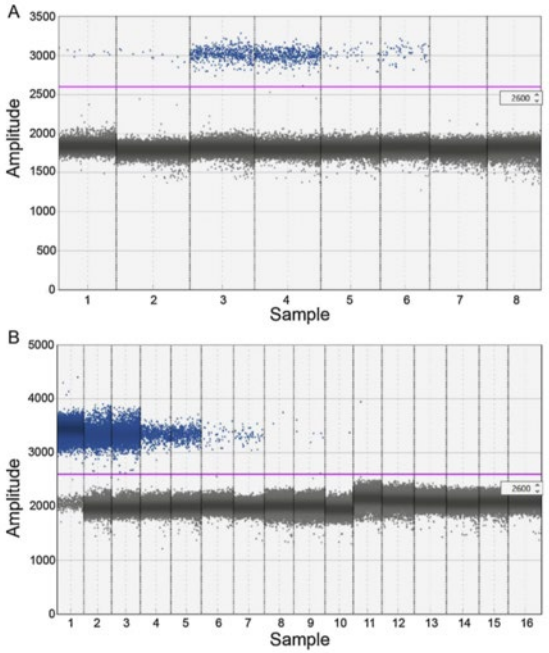


Table 1
Limits of detection for SARS-CoV-2 by specimen type.

	Sample Type																			
	NP Swab		BAL		Sputum		Plasma		CSF		Stool**		PBS		VTM/UTM		HBSS (Hanks')			
Target	N1	N2	N1	N2	N1	N2	N1	N2	N1	N2	N1	N2	N1	N2	N1	N2	N1	N2		At LoD
Dilution	1e'5	2e'5	1e'5	2e'5	1e'5	1e'5	5e'4	1e'5	1e'5	1e'6	1e'5	1e'5	1e'5	1e'5	1e'5	1e'5	1e'5	1e'5		
Copies/ Reaction*	10	5	10	5	10	10	20	10	10	1	10	10	10	10	10	10	10	10		
Mean C_T	33.8	35.1	33.8	35.4	34.5	35.4	34.4	34.9	35.5	36	35.7	36.2	35	34.8	34.6	34	34.8	34.8		
Pos. Detected	20/20	20/20	20/20	20/20	19/20	19/20	20/20	20/20	19/20	20/20	20/20	20/20	20/20	20/20	20/20	20/20	20/20	20/20		
Dilution	2e'5	5e'5	2e'5	5e'5	1e'6	1e'6	1e'5	2e'5	2e'5	1e'7	1e'6	1e'6	2e'5	2e'5	1e'6	1e'6	1e'6	1e'6		Beyond LoD
Copies/ Reaction*	5	2	5	2	1	1	10	5	5	0.1	1	1	5	5	1	1	1	1		
Mean C_T	35.9	36.4	35.6	36.9	36.5	37.2	35.4	36.5	36.5	38.3	37.1	37.8	35.7	36.4	37.2	37.5	36.5	36.1		
Pos. Detected	18/20	17/20	18/20	16/20	8/20	14/20	17/20	18/20	14/20	1/20	5/20	8/20	18/20	18/20	7/20	14/20	17/20	18/20		
Unique Specimens	77		104		47		100		100		60		N/A		N/A		N/A			Specificity
Unique Respiratory Pos.	20		25		16		N/A		N/A		N/A		N/A		N/A		N/A			

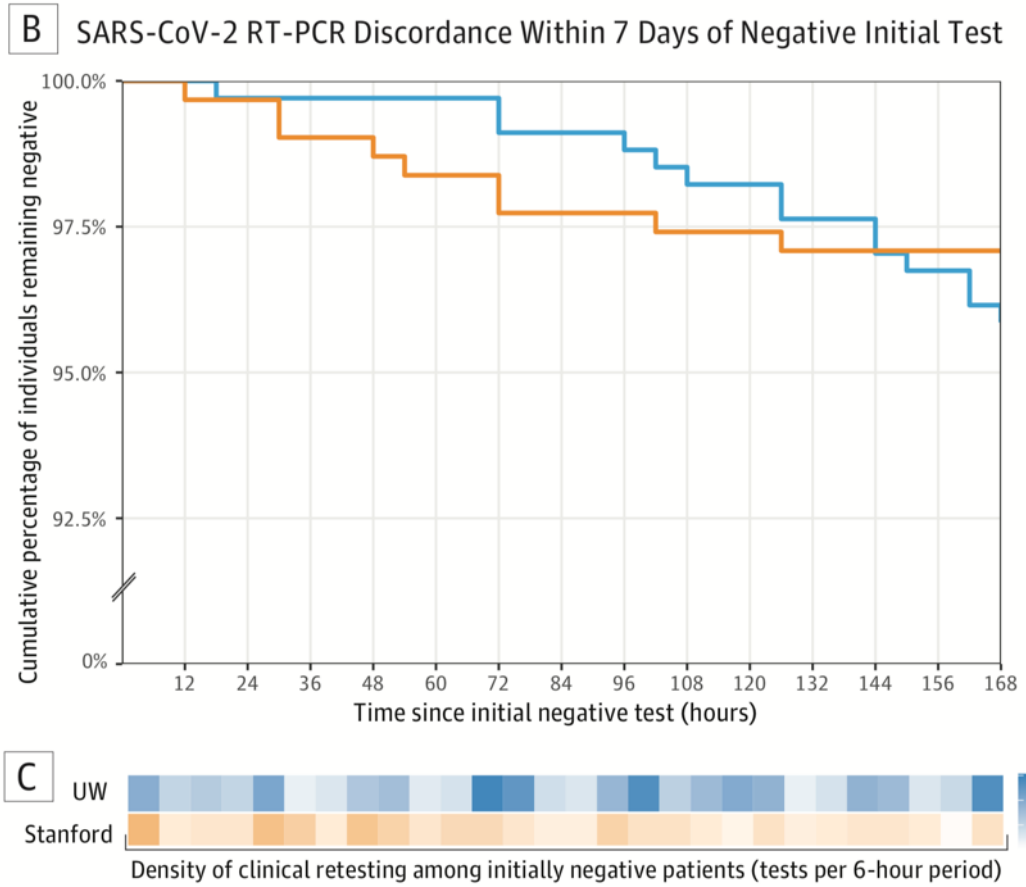
Abbreviations: NDET, Not detected; CT, cycle threshold; NP nasopharyngeal; BAL, bronchoalveolar lavage; PBS, phosphate buffered saline; VTM, viral transport medium; UTM, universal transport medium; HBSS, Hanks' balanced buffer solution; CSF, cerebral spinal fluid; rxn, reaction.
Conversion of copies/rxn to copies/mL is a factor of 50.
*Estimated copies/rxn were quantified using digital droplet PCR of SARS-CoV-2 dilutions series in duplicates.
**Stool serial dilutions are adjusted as 20 uL of stool sample was already diluted with 180uL STAR buffer for extraction (1:10 dilution).

Table 1
Clinical LDT CT comparison to triplex assay.

Target	Mean C_T	Median C_T	Range C_T
N1 LDT	24.0	23.0	14.0-36.3
N1 Triplex	23.1	22.2	13.7-36.5
N2 LDT	24.0	23.0	13.8-39.5
N2 Triplex	25.4	24.9	14.0-39.6

Abbreviations: C_T, cycle threshold, LDT, laboratory developed test.
Positive or inconclusive SARS-CoV-2 samples (n = 183) tested by triplex have comparable mean and median C_T values to LDT.

False negatives are rare with SARS-CoV-2 RT-PCR



ACCEPTED MANUSCRIPT

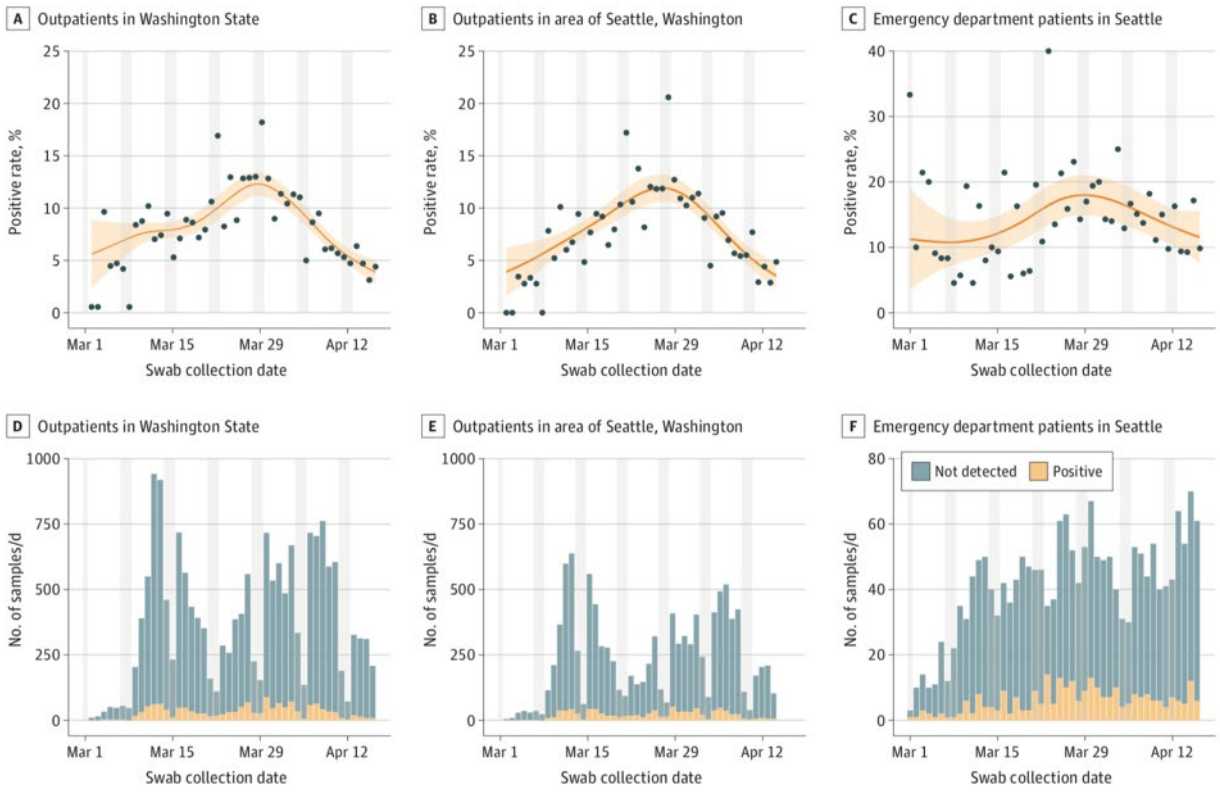
Occurrence and Timing of Subsequent SARS-CoV-2 RT-PCR Positivity Among Initially Negative Patients

Dustin R Long, MD, Saurabh Gombar, MD, PhD, Catherine A Hogan, MD, MSc, Alexander L Greninger, MD, PhD, Vikas O'Reilly Shah, MD, PhD, Chloe Bryson-Cahn, MD, Bryan Stevens, MD, Arjun Rustagi, MD, PhD, Keith R Jerome, MD, PhD, Christina S Kong, MD, James Zehnder, MD, Nigam H Shah, MD, PhD, Noel S Weiss, MD, DrPH, Benjamin A Pinsky, MD, PhD ✉, Jacob Sunshine, MD, MSc
Author Notes

Clinical Infectious Diseases, ciaa722, https://doi-org.offcampus.lib.washington.edu/10.1093/cid/ciaa722

Washington state flattened the curve

Figure. SARS-CoV-2 Positivity Rates and Amount of Samples Tested at Outpatient and Emergency Department Settings in Washington State



Research Letter

ONLINE FIRST FREE

May 8, 2020

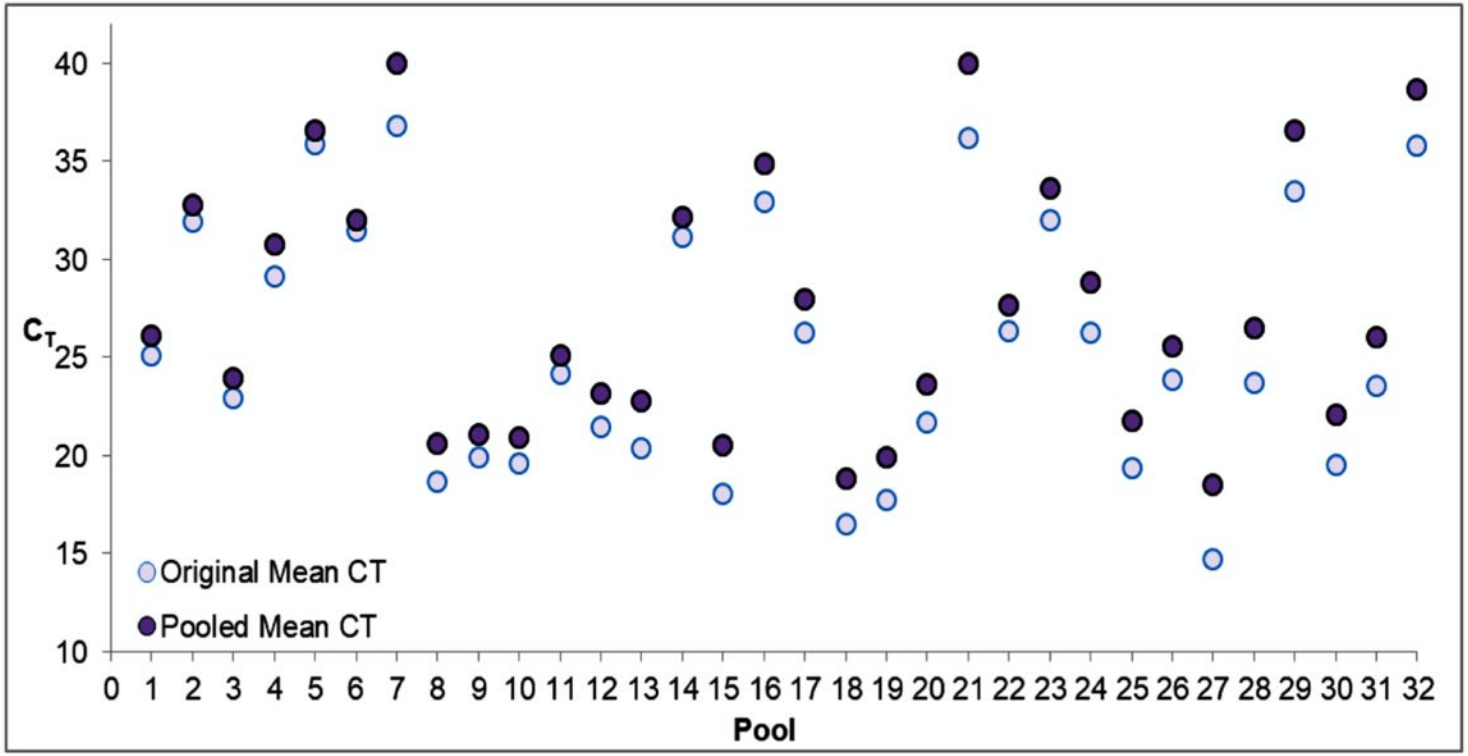
Changes in SARS-CoV-2 Positivity Rate in Outpatients in Seattle and Washington State, March 1-April 16, 2020

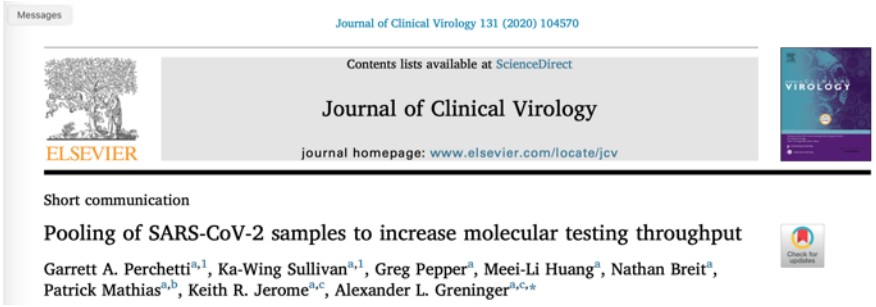
April Kaur Randhawa, PhD[1]; Leigh H. Fisher, PhD[1]; Alexander L. Greninger, MD, PhD[2]; Shuying Sue Li, PhD[1]; Jessica Andriesen, PhD[1]; Lawrence Corey, MD[1]; Keith R. Jerome, MD, PhD[2]

Author Affiliations | Article Information

JAMA. Published online May 8, 2020. doi:10.1001/jama.2020.8097

Expanding access to COVID testing: sample pooling





Messages

Journal of Clinical Virology 131 (2020) 104570

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Short communication

Pooling of SARS-CoV-2 samples to increase molecular testing throughput

Garrett A. Perchetti[a,1], Ka-Wing Sullivan[a,1], Greg Pepper[a], Meei-Li Huang[a], Nathan Breit[a], Patrick Mathias[a,b], Keith R. Jerome[a,c], Alexander L. Greninger[a,c,*]

We're not done with SARS-CoV-2

UW Medicine

UW Virology COVID-19 Dashboard

Overview

This dashboard shows the overall daily testing volumes for COVID-19 performed at UW Virology in UW Medicine's Department of Laboratory Medicine. Greater than 95% of the testing volume reported in this dashboard is performed for individuals whose samples were collected in the state of Washington. We receive test orders from a variety of settings and locations including inpatients, outpatients, employee health, and community health screening settings. This dashboard excludes testing performed for individuals whose samples we have received for research studies.

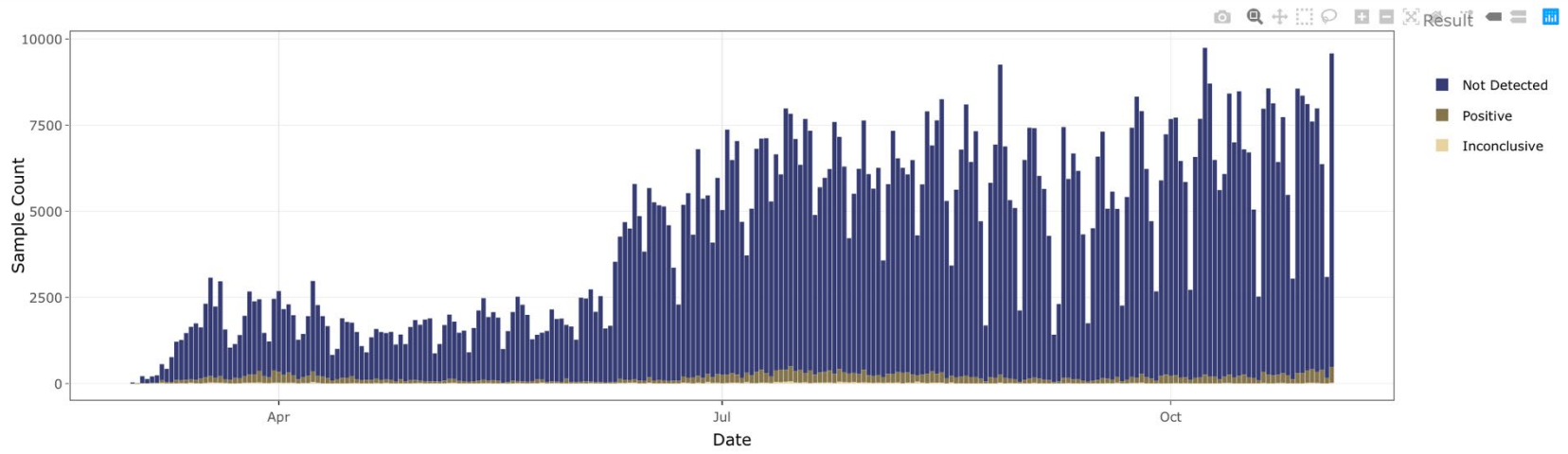
Inconclusive and positive results are added together to compute the positivity rate.

Note: Starting on 10/22, the top level counts have been shifted from counting the number of individuals tested to capturing the number of samples tested.

Data Last Updated: 2020-11-03

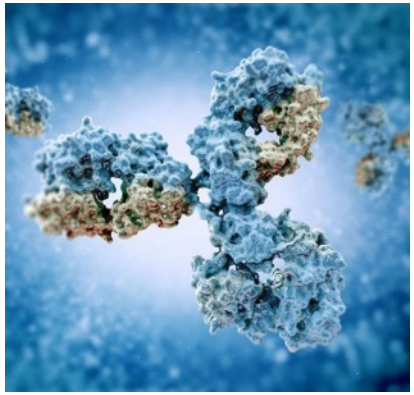
Total samples tested to date:	Total positive/inconclusive samples:	Overall test positivity rate:
1,047,994	43,522	4.2%
Daily samples tested on 2020-11-03:	**Daily positive/inconclusive samples on 2020-11-03:**	**Sample positivity rate on 2020-11-03:**
9,560	471	4.9%

Daily Statistics



Serologic assays for COVID-19 and their utility

- Testing for antibody gives a historic record of infection status
- Population-based studies of SARS-CoV-2 seroprevalence
- Inform public health policy/recommendations
- In very select circumstances, as an adjunct to primary diagnosis
- Counseling of individuals regarding risk status?
- Input into back-to-work and similar decisions?



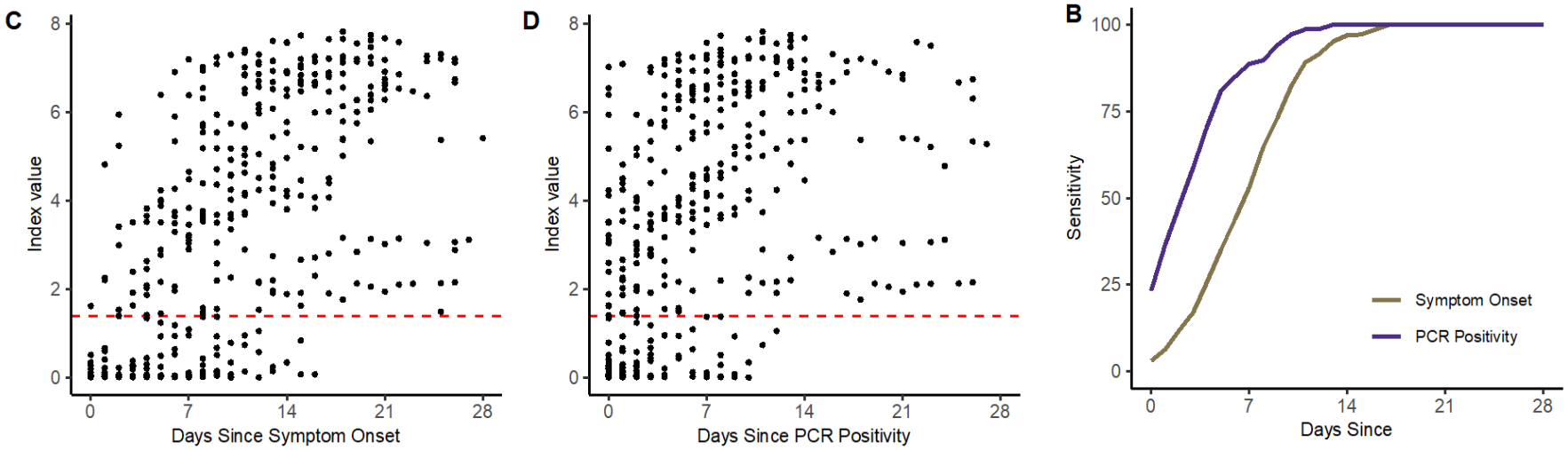
Desirable characteristics for a SARS-CoV-2 serologic assay

- Good sensitivity
- Excellent specificity
- Correlation with meaningful immunity
- High throughput
- Compatibility with existing instrumentation

Technical aspects of the Abbott SARS-CoV-2 IgG assay

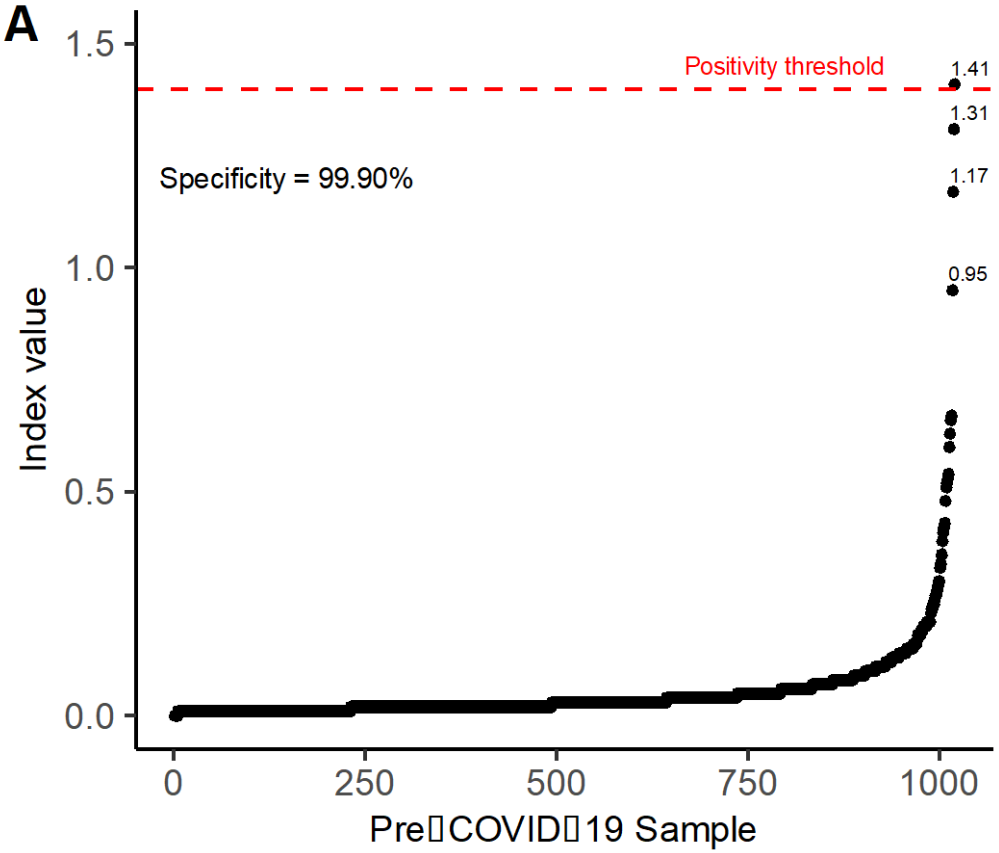
- Chemiluminescent microparticle immunoassay (CMIA) used for the qualitative detection of IgG antibodies to SARS-CoV-2
- Specifically detects antibodies to the nucleocapsid protein of SARS-CoV-2
- Performed on human serum and plasma using the automated ARCHITECT iSystem immunoanalyzer.
- iSystem analyzers are common in labs throughout the country
- Potential throughput of >3000 samples/day/analyzer

Sensitivity of the Abbott SARS-CoV-2 IgG assay



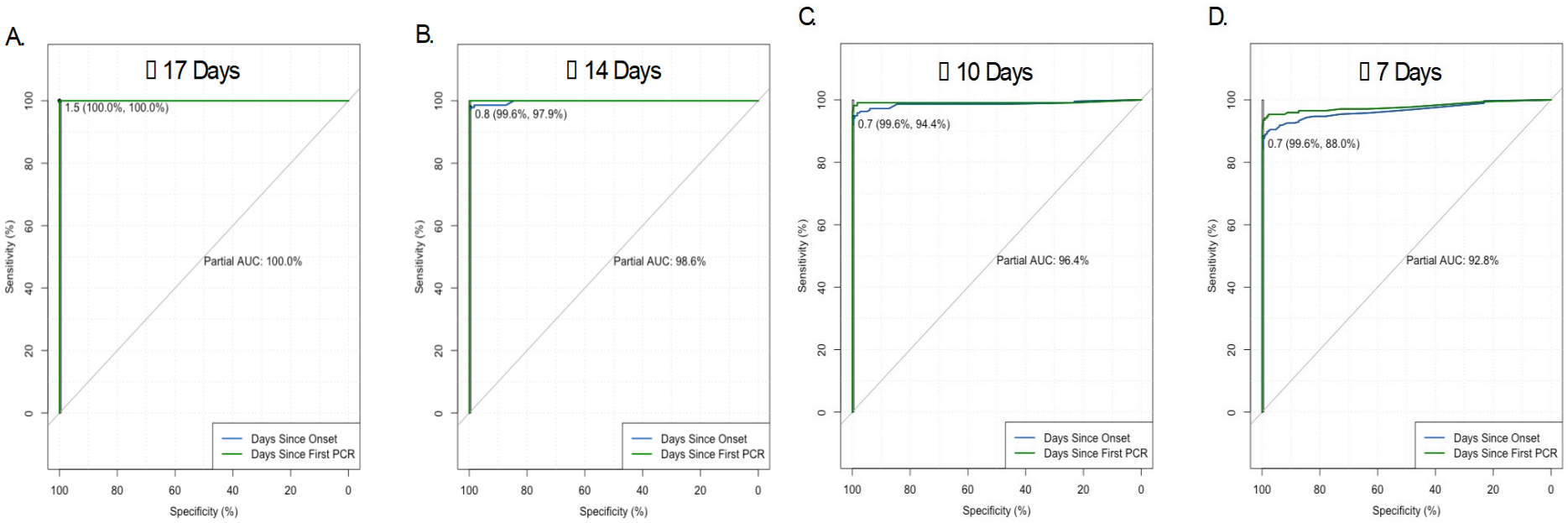
Based on 125 hospitalized UW Medicine patients testing RT-PCR positive for SARS-CoV-2

Specificity of the Abbott SARS-CoV-2 IgG assay



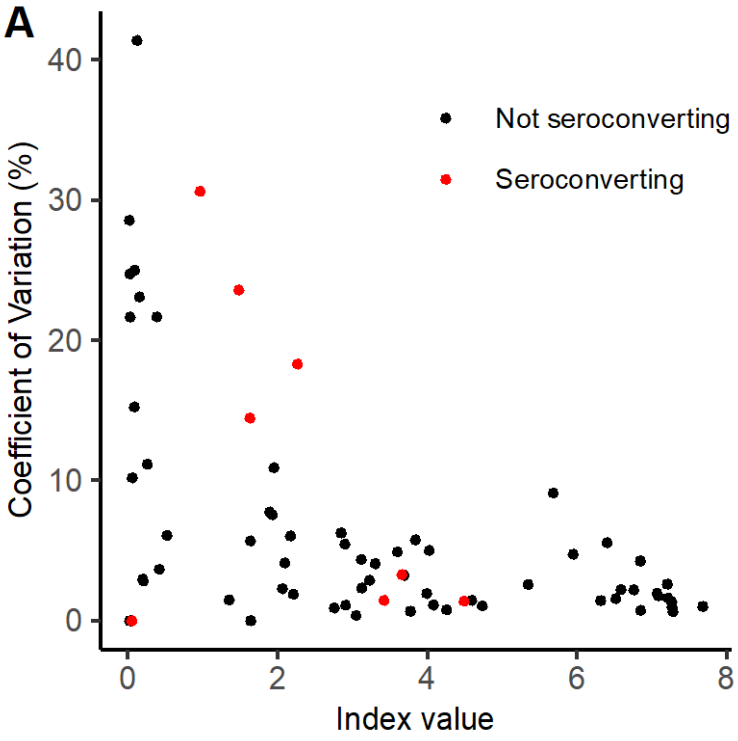
Based on 1020 samples sent to UW Virology for HSV Western blot in 2018 and 2019

Receiver operating characteristic (ROC) curves

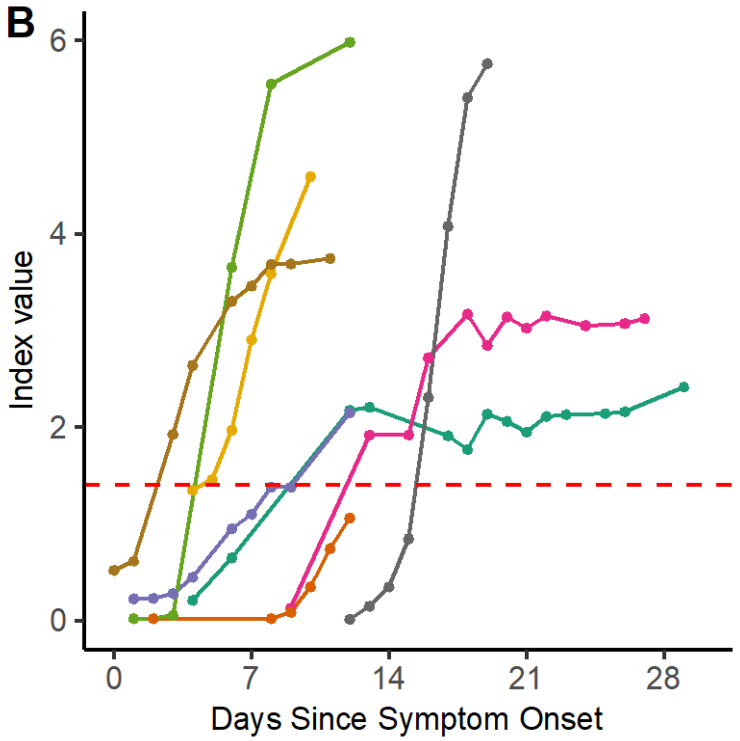


Optimal cutoff 1.42-1.49

Assay reproducibility and performance during seroconversion



Patients with at least 3 samples available from the same day



Patients with at least 5 sample on different days and suspected seroconversion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Immunoassays

Performance Characteristics of the Abbott Architect SARS-CoV-2 IgG Assay and Seroprevalence in Boise, Idaho

Andrew Bryan, Gregory Pepper, Mark H. Wener, Susan L. Fink, Chihiro Morishima, Anu Chaudhary, Keith R. Jerome, Patrick C. Mathias, Alexander L. Greninger

DOI: 10.1128/JCM.00941-20

Neutralizing antibodies are protective against COVID-19

NY Times

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Virology

Neutralizing antibodies correlate with protection from SARS-CoV-2 in humans during a fishery vessel outbreak with high attack rate

Amin Addetia, Katharine H. D. Crawford, Adam Dingens, Haiying Zhu, Pavitra Roychoudhury, Meei-Li Huang, Keith R. Jerome, Jesse D. Bloom, Alexander L. Greninger

DOI: 10.1128/JCM.02107-20

Table 2. Summary table of infection status of crew members for which pre-departure serology testing was performed.

		Pre-departure	
		Neutralizing Ab (+)	Neutralizing Ab (-)
On boat	Infected	0	103
	Not Infected	3	14

p=0.0024

Seroprevalence in Boise Idaho, one week in late April 2020

	Total (%)	Positive (%)
Total	4856 (100%)	87 (1.8%)
Reported Gender		
Female	2631 (54.2%)	42 (1.6%)
Male	2035 (41.9%)	40 (2.1%)
Unknown	190 (3.9%)	5 (2.6%)
Age (years)		
0-19	240 (4.9%)	1 (0.4%)
20-29	301 (6.2%)	7 (2.3%)
30-39	831 (17.1%)	13 (1.6%)
40-49	1102 (22.7%)	18 (1.6%)
50-59	1142 (23.5%)	22 (1.9%)
60-69	888 (18.3%)	22 (2.5%)
70-79	327 (6.7%)	3 (0.9%)
80+	25 (0.5%)	1 (4%)

Additionally, of 34192 samples tested to date in routine operations at UW Virology, 4.8% have been positive


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Immunoassays

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Seroprevalence estimates to date

- Boise, Idaho (late April): 87/4856 positive (1.8%)
- Clinical testing to date: 1217/27898 positive (4.4%)
- UW Medicine patients only: 246/4278 positive (5.8%)
- Fred Hutch return to work study: 6/481 positive (1.25%)
- UW Medicine employee study underway (n~18,000)

- None of these are necessarily reflective of the general population of WA state, or the distribution of COVID-19 between geographic regions or racial/ethnic/socioeconomic subgroups

Washington seroprevalance study

- Partnership between WA state authorities, Paul G. Allen Family Foundation, and UW Medicine
- 8000 participants; all will receive initial virologic (PCR) and serologic testing for COVID-19, with followup serologies at 2 and 4 months later, and PCR testing for any symptoms of COVID-like illness
- Random address-based household sampling, supplemented by other approaches as needed
- Local sampling by study field teams in collaboration with county-level health authorities
- Participating counties chosen to reflect geographic diversity of Washington
- Targeted oversampling to ensure statistically robust data for ethnic and racial subgroups (in collaboration with county, tribal, and community groups)

Objectives

Primary Objectives:

- **Estimate the prevalence of COVID-19 in WA State (using qPCR and serology)**
- Estimate of COVID-19 prevalence at the county-level [within selected counties]
- Estimate the prevalence of COVID-19 in WA State among underrepresented groups:
  - Hispanic/Latina/Latino/Latinx
  - American Indian/Native American
  - African American

Objectives cont.

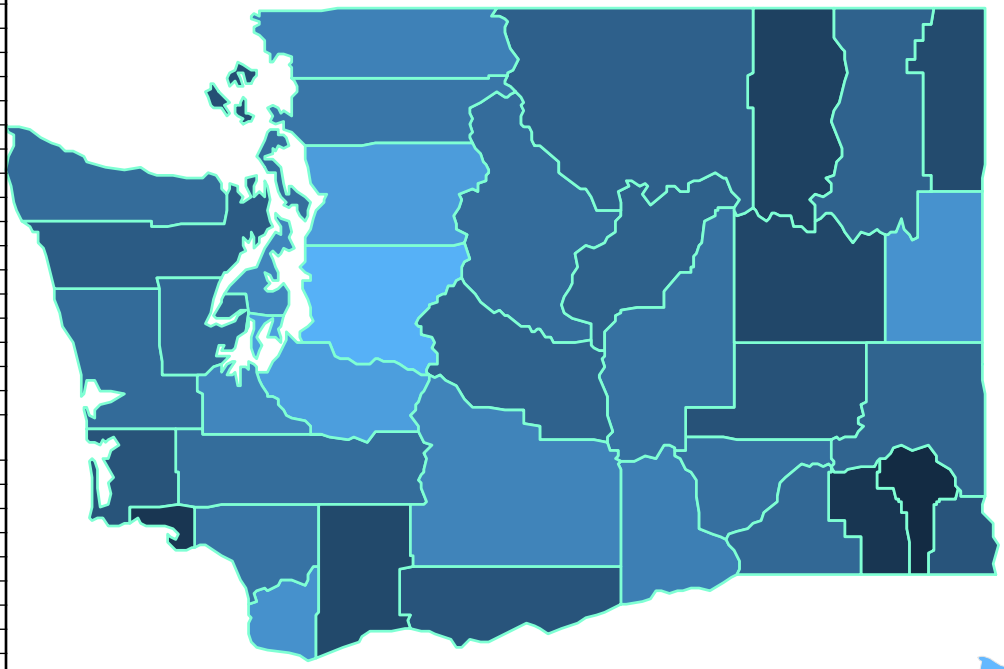
Secondary Objectives:

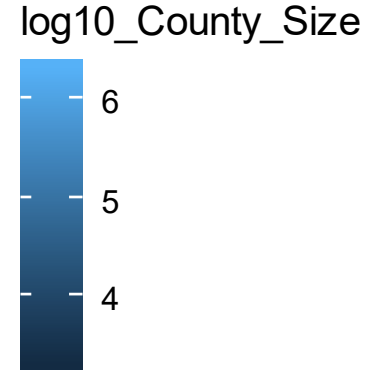
- Estimation of the temporal trend for increasing seropositivity over the study period, at the statewide
- and county levels
- Examine immune factors associated with COVID-19

Population Size of Each WA County

OFM* 2019 Estimates

county	rank	size	prop	cum prop
Washington		7546410.00		
King	1	2226300.00	0.30	0.30
Pierce	2	888300.00	0.12	0.41
Snohomish	3	818700.00	0.11	0.52
Spokane	4	515250.00	0.07	0.59
Clark	5	488500.00	0.06	0.65
Thurston	6	285800.00	0.04	0.69
Kitsap	7	270100.00	0.04	0.73
Yakima	8	255950.00	0.03	0.76
Whatcom	9	225300.00	0.03	0.79
Benton	10	201800.00	0.03	0.82
Skagit	11	129200.00	0.02	0.84
Cowlitz	12	108950.00	0.01	0.85
Grant	13	98740.00	0.01	0.86
Franklin	14	94680.00	0.01	0.88
Island	15	84820.00	0.01	0.89
Lewis	16	79480.00	0.01	0.90
Chelan	17	78420.00	0.01	0.91
Clallam	18	76010.00	0.01	0.92
Grays Harbor	19	74160.00	0.01	0.93
Mason	20	64980.00	0.01	0.94
Walla Walla	21	62200.00	0.01	0.94
Whitman	22	50130.00	0.01	0.95
Kittitas	23	46570.00	0.01	0.96
Stevens	24	45570.00	0.01	0.96
Douglas	25	42820.00	0.01	0.97
Okanogan	26	42730.00	0.01	0.97
Jefferson	27	31900.00	0.00	0.98
Asotin	28	22520.00	0.00	0.98
Klickitat	29	22430.00	0.00	0.98
Pacific	30	21640.00	0.00	0.99
Adams	31	20150.00	0.00	0.99
San Juan	32	17150.00	0.00	0.99
Pend Oreille	33	13740.00	0.00	0.99
Skamania	34	12060.00	0.00	1.00
Lincoln	35	10960.00	0.00	1.00
Ferry	36	7830.00	0.00	1.00
Wahkiakum	37	4190.00	0.00	1.00
Columbia	38	4160.00	0.00	1.00
Garfield	39	2220.00	0.00	1.00

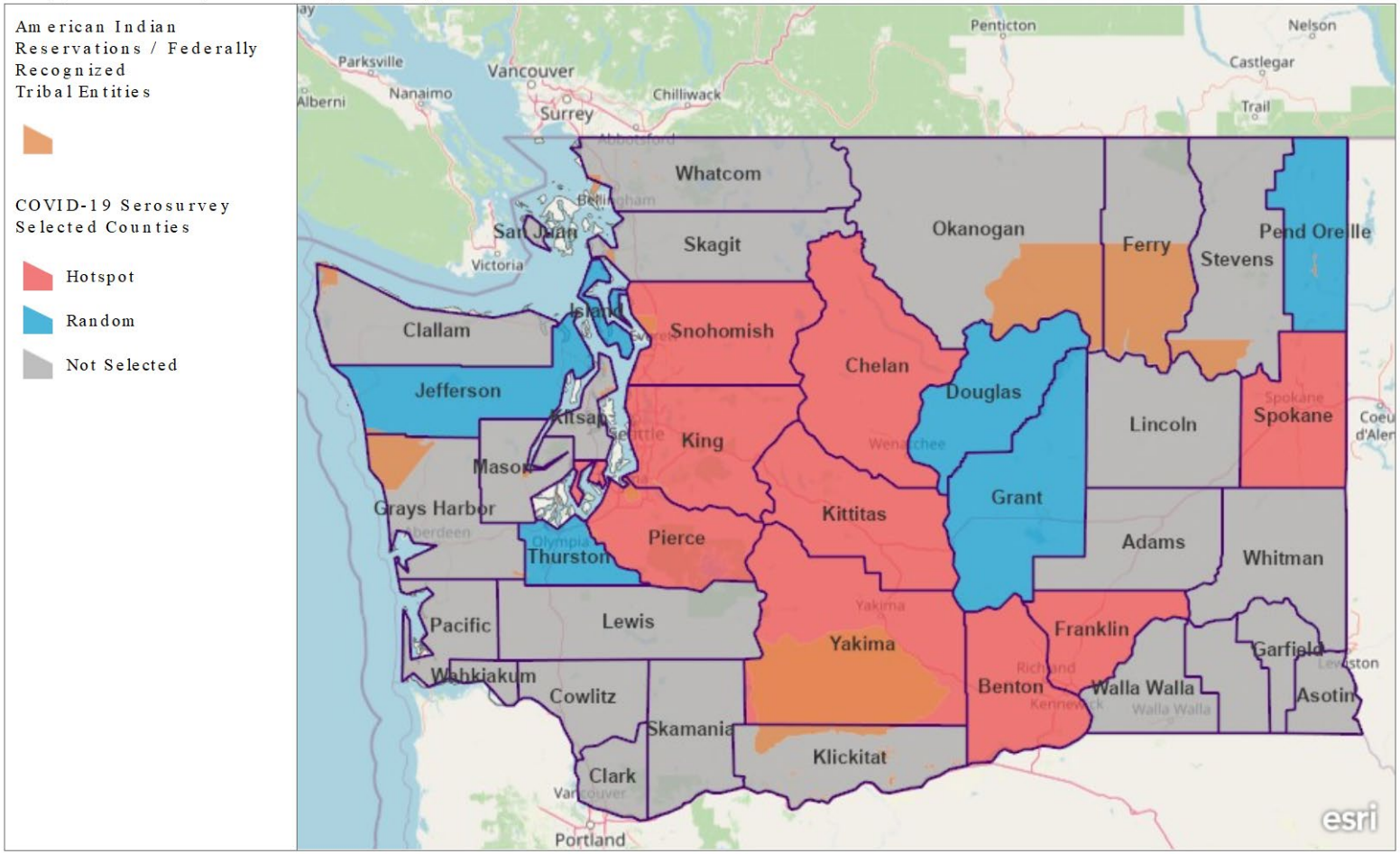




Counties listed in proposal account for ~ 73% of WA state population

**Washington State Office of Financial Management*

County selection



Selected counties for WA Serosurvey with tribal jurisdictions and census tract display options

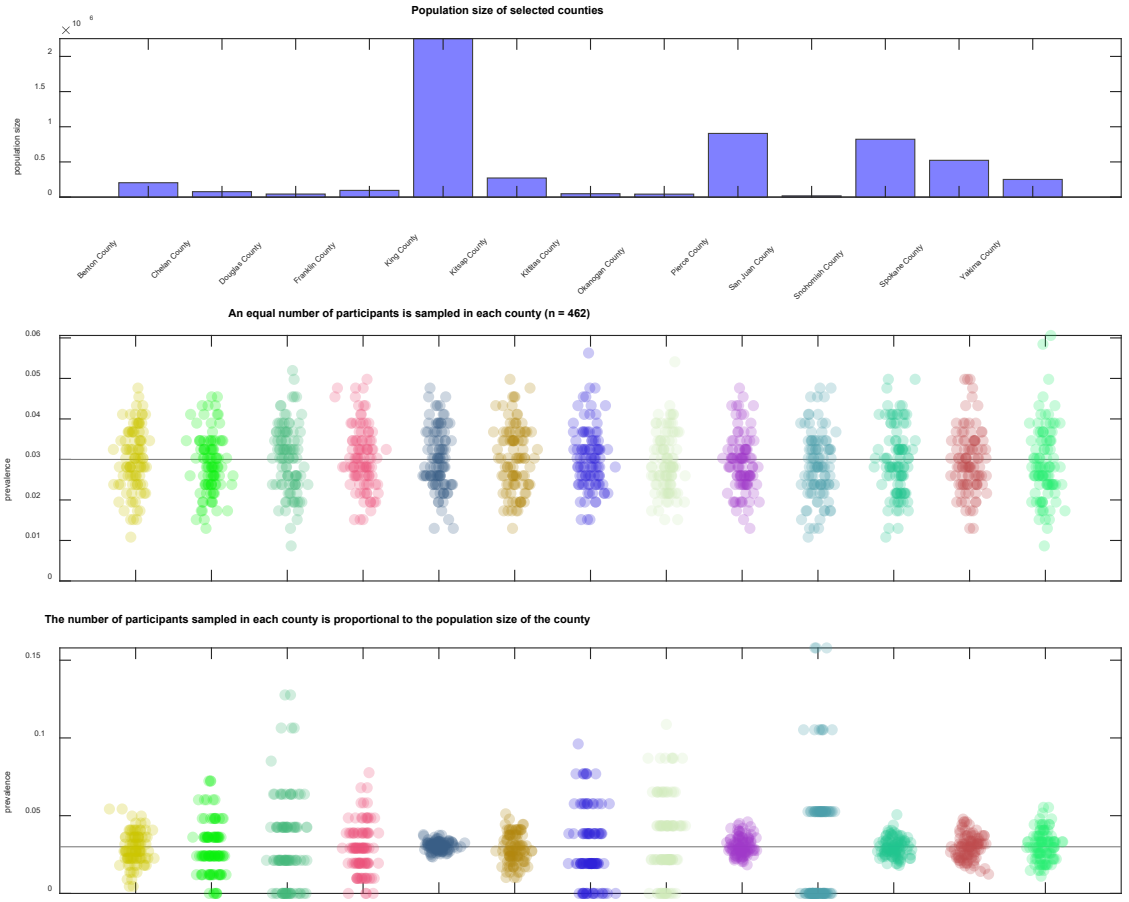
Estimation of the Prevalence Under Two Sampling Strategies

Assumptions:

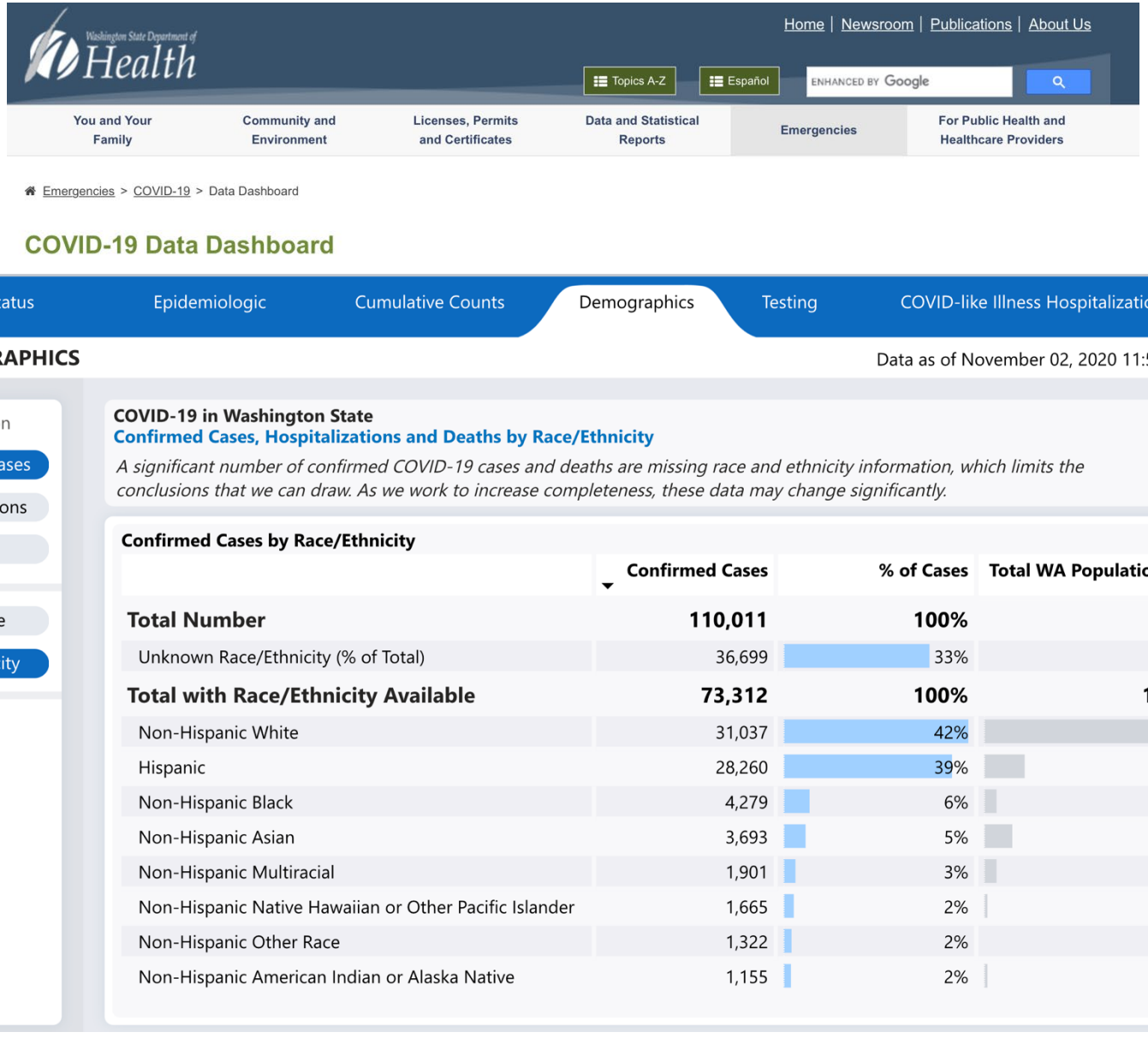
- Prevalence = 3.0%
- Simple random sample within each county
- N = 6,000 (additional 1,000 for oversampling would improve prevalence estimates)
- Sample size per county:
  - (i) Equally sized (n = 462)
  - (ii) Proportional to county size

Main conclusion:

- Proportional sampling would poorly estimate prevalence in the smallest counties (e.g., San Juan (n = 17,150), Douglas (n = 42,820),)



Racial/ethnic disparities in COVID-19 cases



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COVID-19 Data Dashboard

Current Status | Epidemiologic | Cumulative Counts | Demographics | Testing | COVID-like Illness Hospitalizations

DEMOGRAPHICS

Data as of November 02, 2020 11:59PM PT

Select an Option

- Confirmed Cases
- Hospitalizations
- Deaths

- Sex & Age
- Race/Ethnicity

COVID-19 in Washington State

Confirmed Cases, Hospitalizations and Deaths by Race/Ethnicity

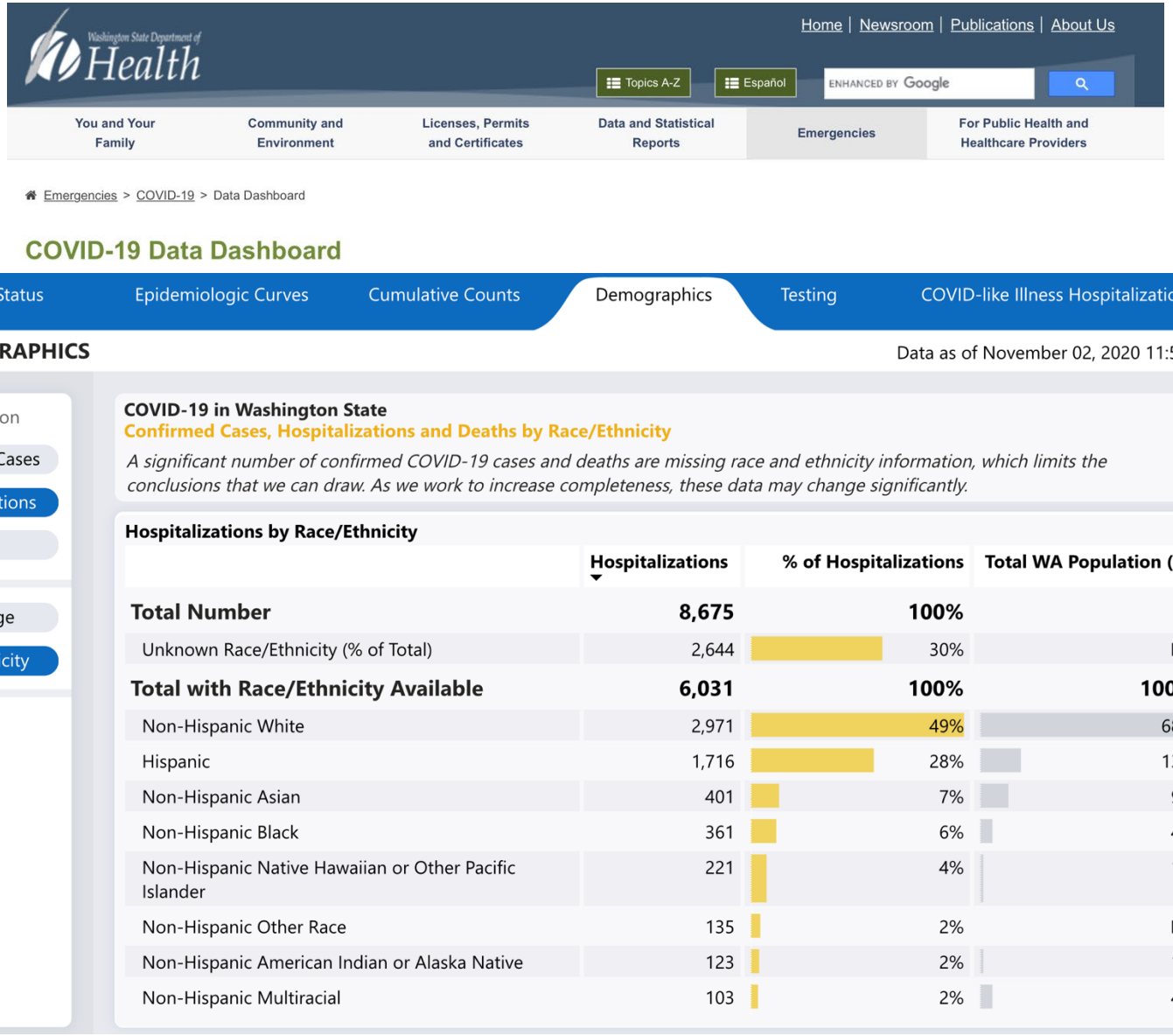
A significant number of confirmed COVID-19 cases and deaths are missing race and ethnicity information, which limits the conclusions that we can draw. As we work to increase completeness, these data may change significantly.

Learn More

Confirmed Cases by Race/Ethnicity

	Confirmed Cases	% of Cases	Total WA Population (%)
Total Number	**110,011**	**100%**	
Unknown Race/Ethnicity (% of Total)	36,699	33%	NA
Total with Race/Ethnicity Available	**73,312**	**100%**	**100%**
Non-Hispanic White	31,037	42%	68%
Hispanic	28,260	39%	13%
Non-Hispanic Black	4,279	6%	4%
Non-Hispanic Asian	3,693	5%	9%
Non-Hispanic Multiracial	1,901	3%	4%
Non-Hispanic Native Hawaiian or Other Pacific Islander	1,665	2%	1%
Non-Hispanic Other Race	1,322	2%	NA
Non-Hispanic American Indian or Alaska Native	1,155	2%	1%

Racial/ethnic disparities in COVID-19 hospitalizations



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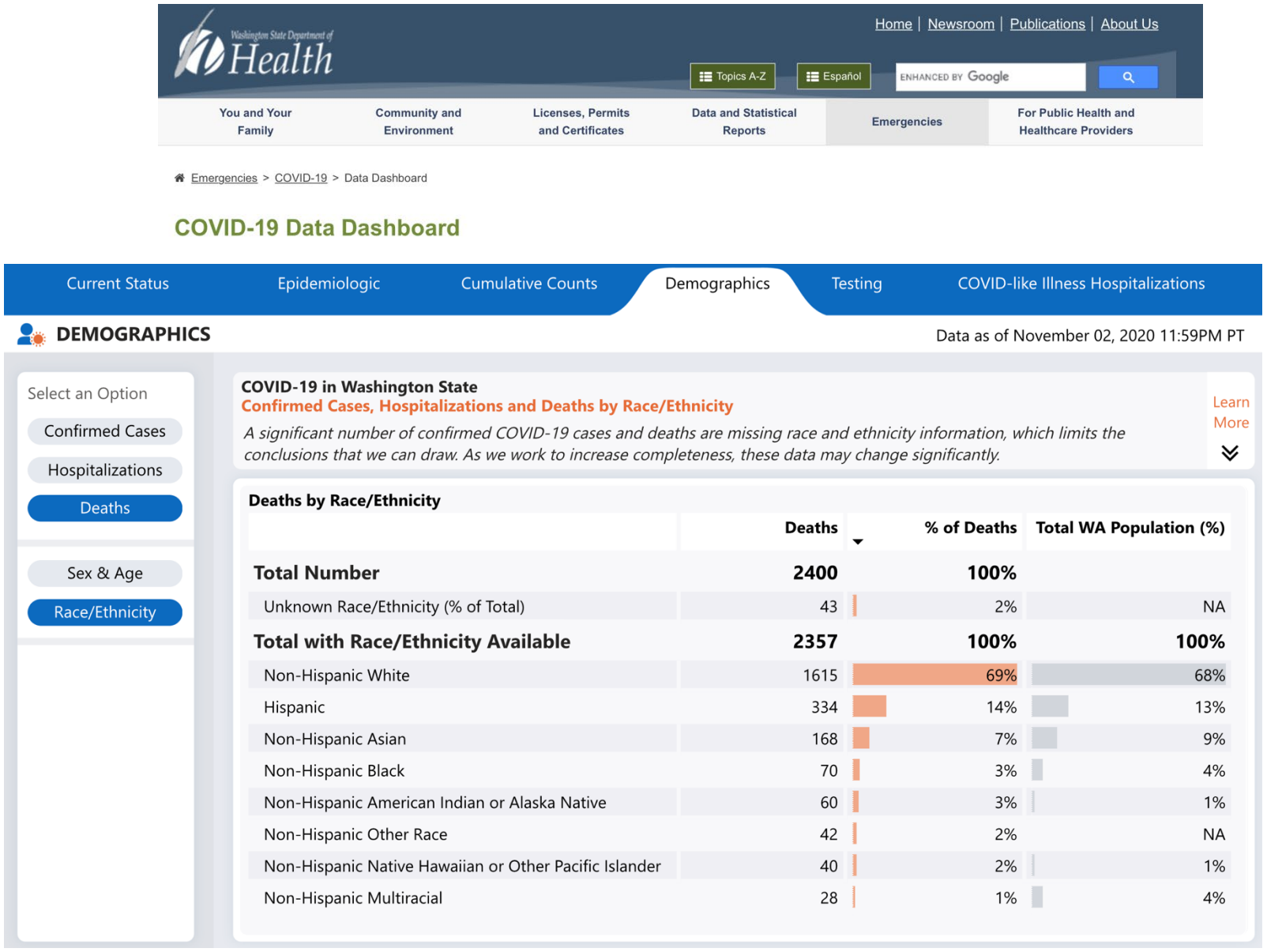
A significant number of confirmed COVID-19 cases and deaths are missing race and ethnicity information, which limits the conclusions that we can draw. As we work to increase completeness, these data may change significantly.

Learn More

Hospitalizations by Race/Ethnicity

	Hospitalizations	% of Hospitalizations	Total WA Population (%)
Total Number	**8,675**	**100%**	
Unknown Race/Ethnicity (% of Total)	2,644	30%	NA
Total with Race/Ethnicity Available	**6,031**	**100%**	**100%**
Non-Hispanic White	2,971	49%	68%
Hispanic	1,716	28%	13%
Non-Hispanic Asian	401	7%	9%
Non-Hispanic Black	361	6%	4%
Non-Hispanic Native Hawaiian or Other Pacific Islander	221	4%	1%
Non-Hispanic Other Race	135	2%	NA
Non-Hispanic American Indian or Alaska Native	123	2%	1%
Non-Hispanic Multiracial	103	2%	4%

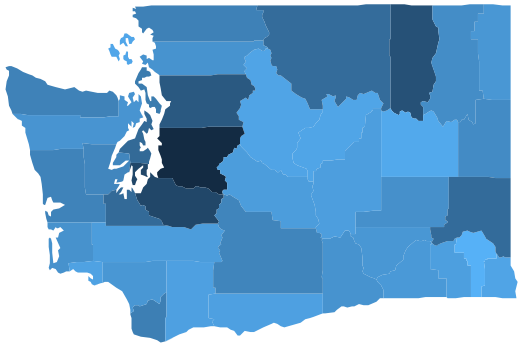
Racial/ethnic disparities in COVID-19 deaths



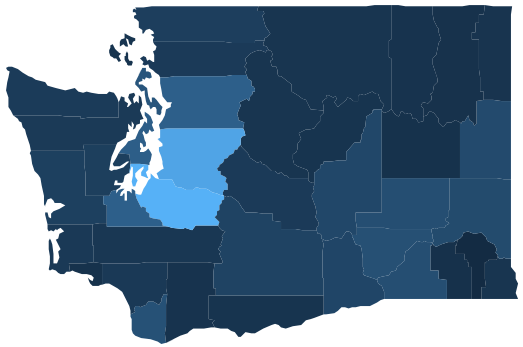
	Deaths	% of Deaths	Total WA Population (%)
Total Number	**2400**	**100%**	
Unknown Race/Ethnicity (% of Total)	43	2%	NA
Total with Race/Ethnicity Available	**2357**	**100%**	**100%**
Non-Hispanic White	1615	69%	68%
Hispanic	334	14%	13%
Non-Hispanic Asian	168	7%	9%
Non-Hispanic Black	70	3%	4%
Non-Hispanic American Indian or Alaska Native	60	3%	1%
Non-Hispanic Other Race	42	2%	NA
Non-Hispanic Native Hawaiian or Other Pacific Islander	40	2%	1%
Non-Hispanic Multiracial	28	1%	4%

Distribution of Races Across Washington State Counties

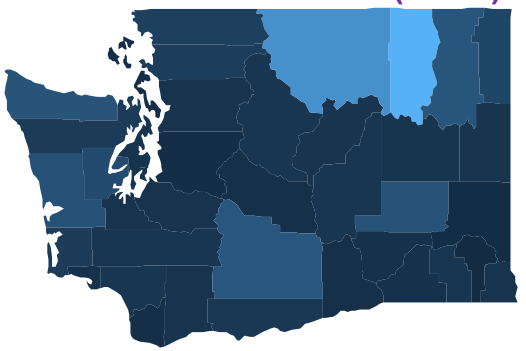
White



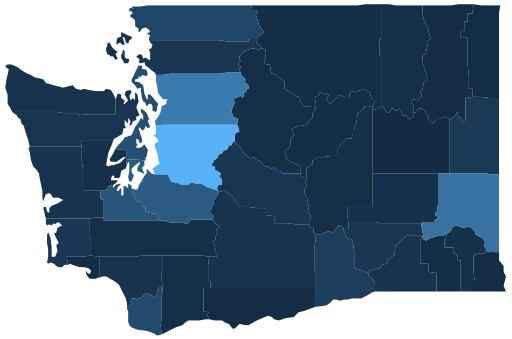
Black



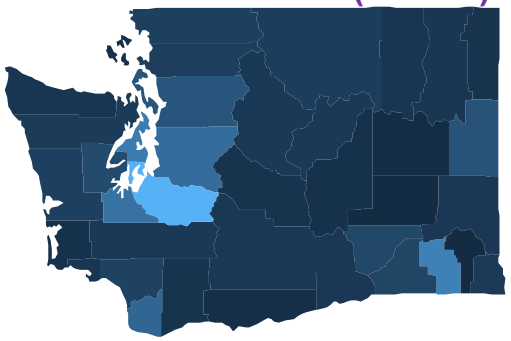
American Indian or Alaskan Native (AIAN)



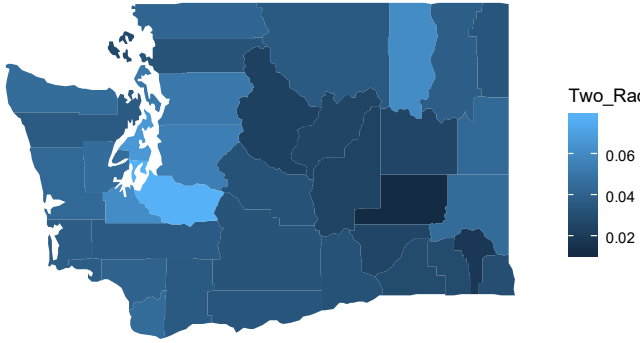
Asian



Native Hawaiian or Other Pacific Islander (NHOPI)



Two or More Races



Local Health Jurisdictions

Public health entities can support the survey:

- Provide local context
- Engage appropriate county authorities
- Media and social media platforms
- Medical/paramedical human

resources to contribute to fieldwork under the training and guidance of our staff

- Return of results for participants*
- Potential resources for specific response efforts
  - I.e. individuals such as Washington State Service Corps to call non-respondent households

Local Health Jurisdictions

- Non-selected counties and LHJs
  - Available for laboratory sub-contracts
- Selected counties
  - Please send liaison contact to cheryld5@uw.edu
  - Liaison to meet on survey LHJ sub-committee
    - Share best practices
    - Common challenges
    - Technical input
- Tribal health authorities
  - Letter to Tribal Chairs, Meeting with American Indian Health Commission

Methods: County and Sub-county Selection

- Cluster-based household survey
- County is primary sampling unit, followed by Census Tracts

Sub-county selection*

- ≤8 Census tracts / county = sample all tracts in the county,
- >8 = # of tracts to obtain sample size
- ~15 households per census tract

*Sub-county strategy

Target number of realized households and numbers of census tracts by county in order to attain desired sample sizes by county

County	Tract	Number of tracts to sample	Sample size per county	targeted # households/tract	targeted # of people/tract
Benton	37	10	300	15	30
Chelan	14	10	300	15	30
Douglas	8	8	300	19	38
Franklin	13	10	300	15	30
Grant	16	10	300	15	30
Island	21	10	300	15	30
Jefferson	7	7	300	22	43
King	397	48	1447	15	30
Kittitas	8	8	300	19	38
Pend Oreille	5	5	300	30	60
Pierce	172	22	666	15	30
Snohomish	149	21	625	15	30
Spokane	105	15	448	15	30
Thurston	49	10	314	15	30
Yakima	45	10	300	15	30

Methodology - CASPER Methods

30 x 7 design

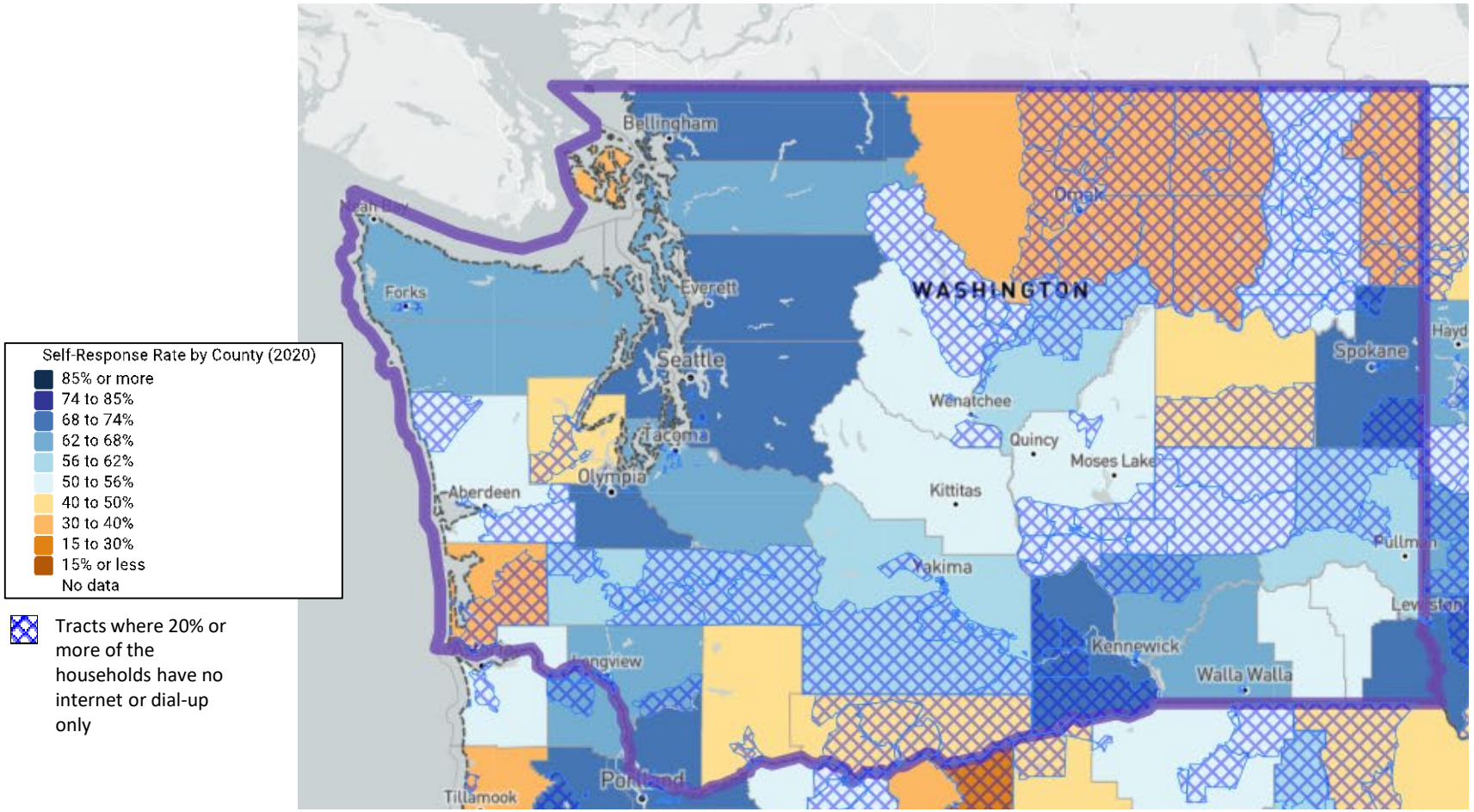
- 30 clusters (census tracts or block groups)
- 7 houses per cluster
- Census tracts or block groups with more houses are more likely to be selected two or three times
- Household-level assessment
- Field teams sample houses
- Cross-sectional
- Questionnaire only

Methodology – Considerations for CASPER

- CASPER proposes stratification to obtain adequate sample size within categories like urban/rural
- Stratification by multiple characteristics is complex
- Officially, “CASPER” or “CASPER-modified” is not appropriate if individuals are the ultimate sampling unit
  - However, the toolkit, guidance, and forms will be helpful
- Non-CASPER surveys households can be pre-sampled with GIS resources
- Panel/longitudinal approaches

Thomas Yung, 2008

Response Rates – US Census – July 2020



American Indian/Alaska Native Engagement

- Letter via our Government Liaison to Tribal Chairs of Federally Recognized Tribal Jurisdictions overlapping the sampled area:
  - Confederated Tribes of the Chehalis Reservation
  - Hoh Indian Tribe
  - Kalispel Tribe of Indians
  - Muckleshoot Indian Tribe
  - Nisqually Indian Tribe
  - Puyallup Tribe
  - Quinault Indian Nation
  - Tulalip Tribes
  - Confederated Tribes and Bands of the Yakama Nation
- GOIA
- LHJ/Tribal Health Officer Meeting in late September
- American Indian Health Commission
- NATIVE; Seattle Indian Health Board
- IRBs – Northwest Indian Health Board; Northwest Indian College IRB

Household-level Implementation

Household selection

- Traditionally, field teams still needed for assessment of “destroyed” or “inaccessible structures”

Specimen collection

- Individual unit as the USU more efficient and allow potential analysis of household clustering
- Consenting of <18 years may be more feasible at household
- Return of results

Questionnaire collection

- Confidentiality

Methodology – Questionnaire Development

Questionnaire

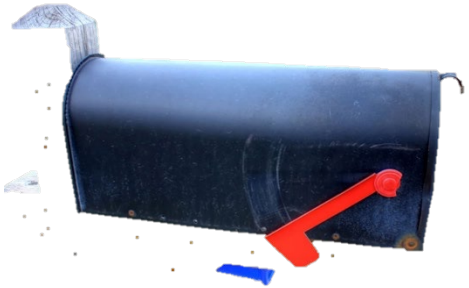
- Length (CASPER is two pages for printed, examples ~35 questions)
- Content
  - Demographics
  - Symptoms
  - Exposure
    - Structural (e.g. income status, employment, place of employment)
    - Community/Intrapersonal (e.g. caretaking responsibilities, family/community gatherings and assistance, known contacts)
    - Individual (e.g. mask wearing, recreation choices/behaviors)
  - Knowledge

Questionnaire Implementation

Questionnaire

- All eligible adults (recommended)
- Children
- Tablets
  - Can scan a specimen sticker
- Platform (REDCap, ODK)
- Data server and location
- Training and staff
- Pre-interview remotely when possible
  - Mail
  - Telephone
  - Digital survey

Survey Implementation



Mailed invitation to randomly sampled addresses

Participant fills out an online questionnaire

Email/Telephone contact

No response/no contact

Schedule window of time for specimen collection

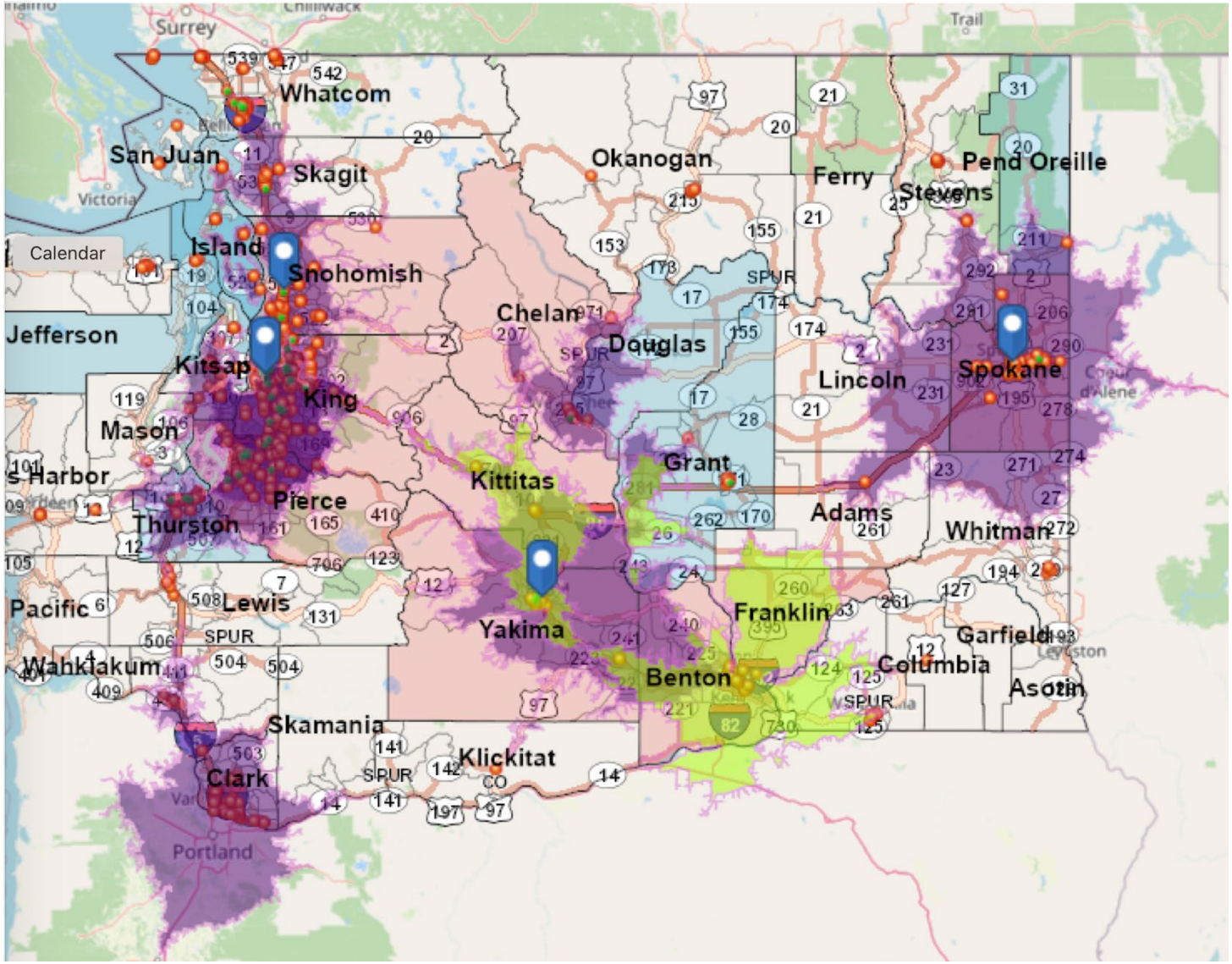
Knock on unit entrance

Verification of those who scheduled specimen collection; Full or partial interview for first contact or incomplete questionnaires

Current symptoms assessment for everyone

Venipuncture and Nasal Swab (NP/AN)

Driving times for UW field teams



Methodology – Longitudinal Considerations

Longitudinal visits 2 and 3

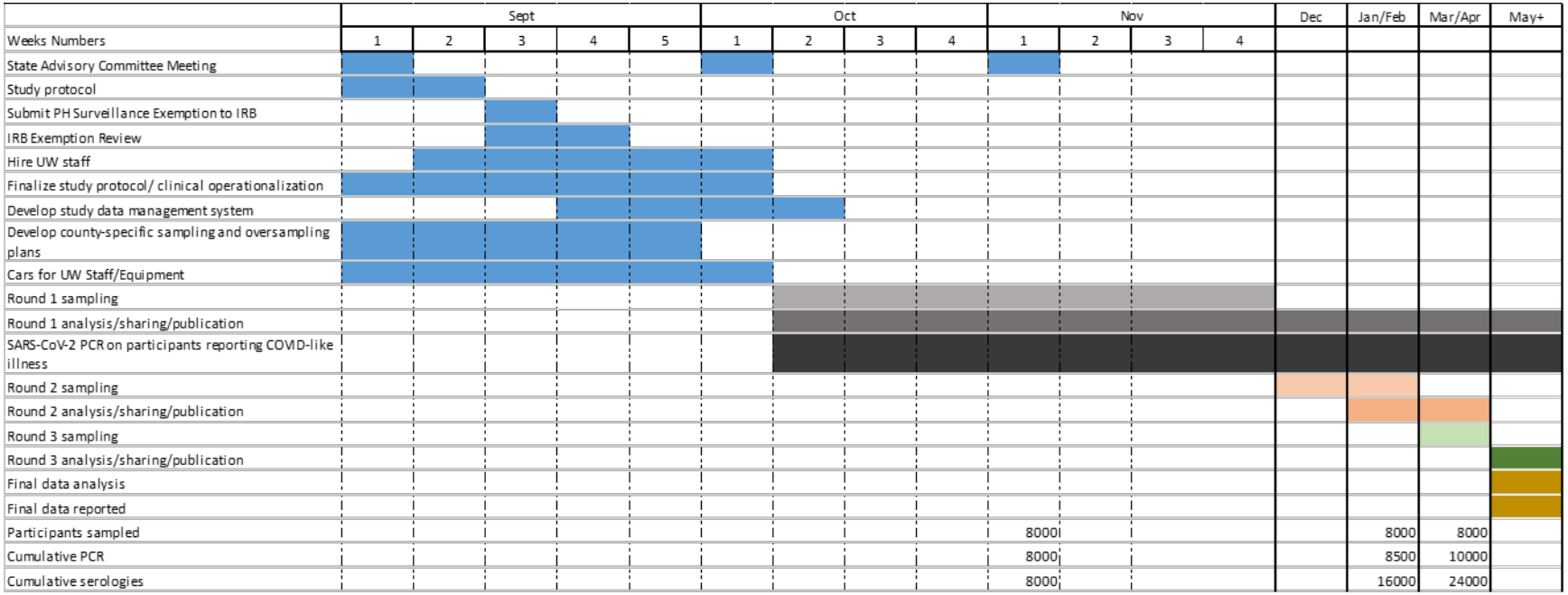
- Maintain individuals previously enrolled in the study
  - Incentive structure for 2nd and 3rd participation
- Replace individuals
  - Challenge: sampling structure with some individuals in a household repeating and others not
  - Household refusal, a priori design to select new households
  - Additional cross-sectional surveys as needed

When?

Wave 1: Fall, November start, rollout first to populous areas

Wave 2: Winter, beginning 2021

Wave 3: Spring, March, April 2021



General thoughts on the next stages of the pandemic

- Demand for RT-PCR testing continues to increase as school and economic activity resumes, as additional waves of infection occur
- Demand for serology likely to increase now that data is available that positivity correlates with protection from disease
- Therapeutic pipeline is uncertain (late diagnosis, substantial immunopathological component)
- The current vaccine effort is very impressive and generally progressing well

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