CITY OF MILWAUKEE HEALTH DEPARTMENT UPDATE

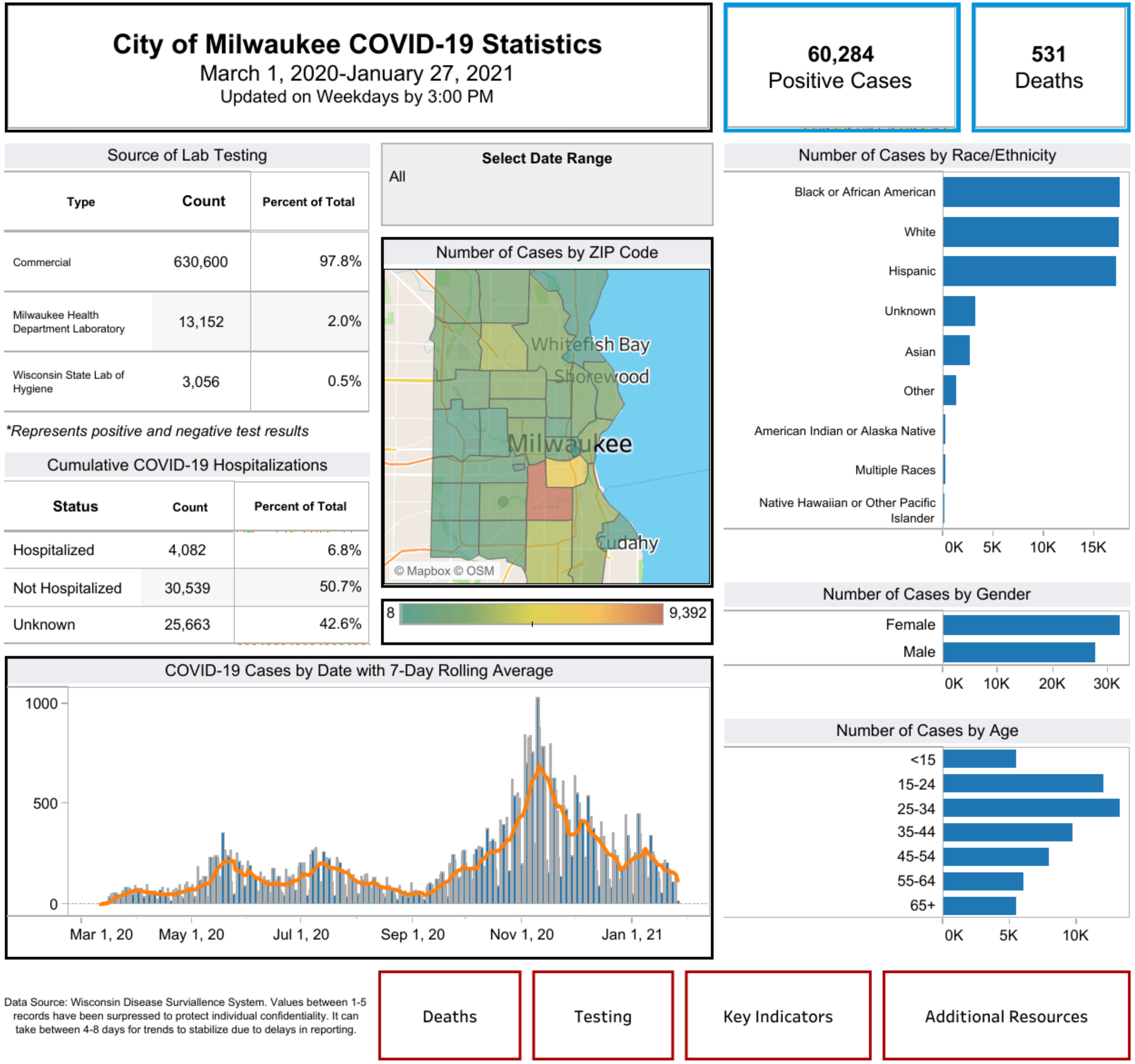
Marlaina Jackson, MPA

Interim Commissioner of Health

Public Health and Safety Committee January 2021

AGENDA

- Dashboard/Gating Criteria/Order 4.2
- New Variant
- Enforcement
- Testing and Tracing Update
- Vaccination Update



City of Milwaukee COVID-19 Statistics

March 1, 2020-January 27, 2021

Updated on Weekdays by 3:00 PM

60,284
Positive Cases

531
Deaths

Source of Lab Testing

Type	Count	Percent of Total
Commercial	630,600	97.8%
Milwaukee Health Department Laboratory	13,152	2.0%
Wisconsin State Lab of Hygiene	3,056	0.5%

**Represents positive and negative test results*

Cumulative COVID-19 Hospitalizations

Status	Count	Percent of Total
Hospitalized	4,082	6.8%
Not Hospitalized	30,539	50.7%
Unknown	25,663	42.6%

Select Date Range

All

Number of Cases by ZIP Code

COVID-19 Cases by Date with 7-Day Rolling Average

Number of Cases by Race/Ethnicity

Number of Cases by Gender

Number of Cases by Age

Data Source: Wisconsin Disease Surviallence System. Values between 1-5 records have been surpressed to protect individual confidentiality. It can take between 4-8 days for trends to stabilize due to delays in reporting.

Moving Milwaukee Forward Safely

Gating Metric Review October 1-January 21

CITY OF MILWAUKEE
HEALTH DEPARTMENT

Metric	Status – Oct 1	Status – Oct 8	Status – Oct 15	Status – Oct 22	Status – Oct 29	Status – Nov 5	Status – Nov 12	Status – Nov 19	Status – Dec 3	Status – Dec 10	Status – Dec 17	Status – Jan 7	Status – Jan 14	Status – Jan 21
** This statistic uses an industry standard of p<0.05 for statistical significance; this enables us to report the statistic with confidence or accuracy														
Cases	Yellow Slope of 0.17, no statistically significant trend	Yellow Slope of -0.01, no statistically significant trend	Red Slope of 0.27, statistically significant trend	Red Slope of 0.21, statistically significant trend	Red Slope of 0.29, statistically significant trend	Red Slope of 0.41, statistically significant trend	Red Slope of 0.66, statistically significant trend	Yellow Slope of -0.06, no statistically significant trend	Yellow Slope of 0.25, no statistically significant trend	Yellow Slope of 0.03, no statistically significant trend	Green Slope of -0.22, statistically significant trend	Red Slope of 0.37, statistically significant trend	Yellow Slope of -0.04, no statistically significant trend	Green Slope of -0.22, statistically significant trend
** Measured as the ability for residents to access a COVID-19 lab test														
Testing	Green Average of 2,426 tests per day. Average of 8.4% positive	Green Average of 2,680 tests per day. Average of 7.7% positive	Red Average of 2,857 tests per day. Average of 10.2% positive	Red Average of 2,974 tests per day. Average of 10.9% positive	Red Average of 2,861 tests per day. Average of 12.2% positive	Red Average of 3,382 tests per day. Average of 14.7% positive	Red Average of 4,018 tests per day. Average of 19.1% positive	Red Average of 4,267 tests per day. Average of 15.5% positive	Red Average of 2,680 tests per day. Average of 14.6% positive	Red Average of 3,456 tests per day. Average of 13.3% positive	Red Average of 3,332 tests per day. Average of 11.1% positive	Red Average of 2,341 tests per day. Average of 11.0% positive	Green Average of 2,881 tests per day. Average of 9.7% positive	Green Average of 2,775 tests per day. Average of 8.2% positive
Care: Percentage of COVID+ hospital beds PPE: Hospital systems reaching Personal Protective Equipment (PPE) goals														
Care ***	Green 6%	Green 6%	Green 7%	Yellow 11%	Yellow 14%	Yellow 17%	Red 21%	Red 25%	Red 23%	Red 21%	Yellow 19%	Yellow 14%	Yellow 12%	Yellow 11%
Safety (PPE) ***	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow
** Week 1: 16.05% of COVID+ cases received a contact attempt by MHD staff within 24 hours of the case being reported Weeks 2-23: COVID+ residents assigned to MHD for follow-up were successfully reached within 3 contact attempts Weeks 24+: COVID+ residents assigned to MHD for follow-up that were successfully reached within 2 days of assignment														
Tracing	Yellow 83.5%	Yellow 85.2%	Yellow 81.7%	Yellow 73.3%	Yellow 58.2%	Red 45.3%	Yellow 53.0%	Yellow 61.0%	Yellow 66.8%	Yellow 72.6%	Yellow 73.7%	Yellow 72.1%	Yellow 74.8%	Yellow 72.0%

***Methodology for testing, cases, and tracing metrics were adjusted based on best practices for the city of Milwaukee*

****Based on Milwaukee County Dashboard Data*

ENFORCEMENT

ENFORCEMENT EFFORTS

- Total number of covid complaints received **1,589**
- Total number investigated **1230**
- Total number not in compliance **102**
- Total number of citations issued **29**
- Citations in progress **7**

Enforcement Process Update:

- Several citations issued based on MPD referral
- Ability to cite off citizen complaint (only if willing to testify) – best to have photo/video time stamped footage
- Contract with field observation vendor in process

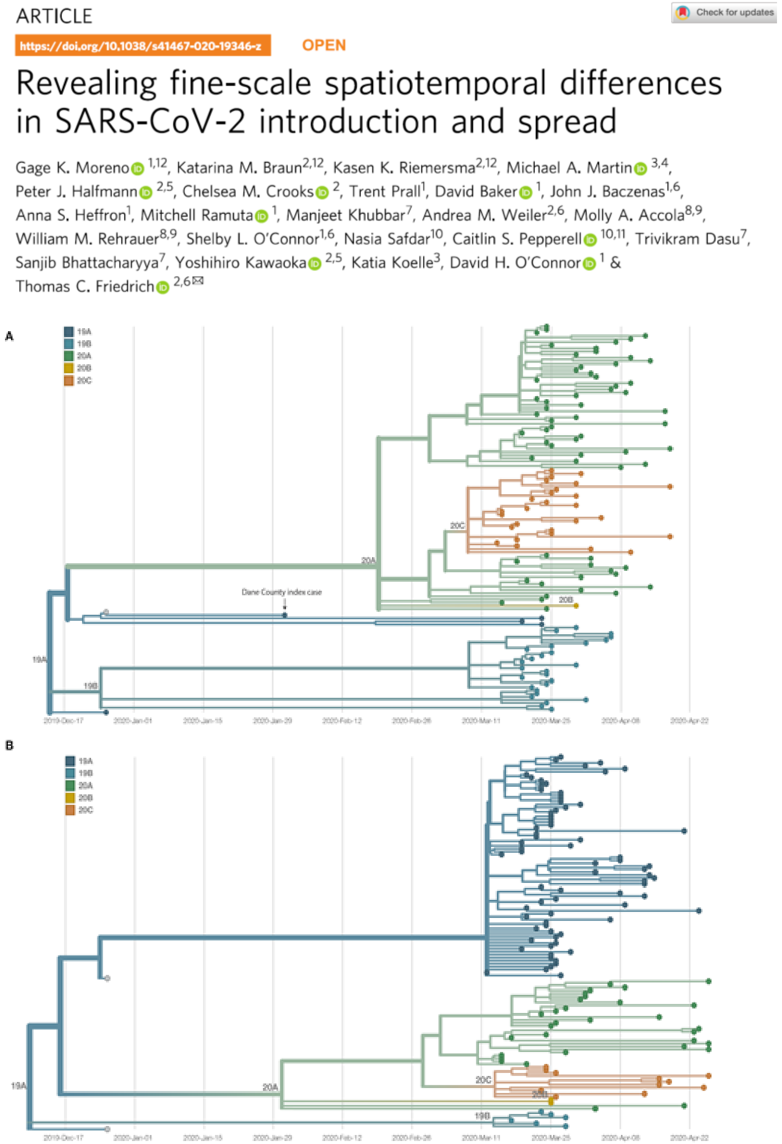
COVID-19 VARIANT

CITY OF MILWAUKEE
HEALTH DEPARTMENT

SARS-COV-2 GENOMIC SURVEILLANCE

- Early importation: Madison, Dane County had the 12th documented case in U.S.
- MHD Laboratory, and UW-Madison conducting whole genome sequencing from Milwaukee and Dane County- since March 2020
  - WSLH covering the whole state thru WI Clinical Lab Network
- State epidemiologist directs clinical labs to provide residual test-positive specimens to expand statewide sequencing capacity
- So far 2,966 sequences submitted to GISAID- Global initiative on sharing all influenza data- A global repository for SARS-CoV-2 sequence data
- Current emphasis: Surveillance, rapid turnaround to detect novel variants, investigate potential immune failure

Nature Comm. 2020 Nov 3;11(1):5558. doi: 10.1038/s41467-020-19346-z.



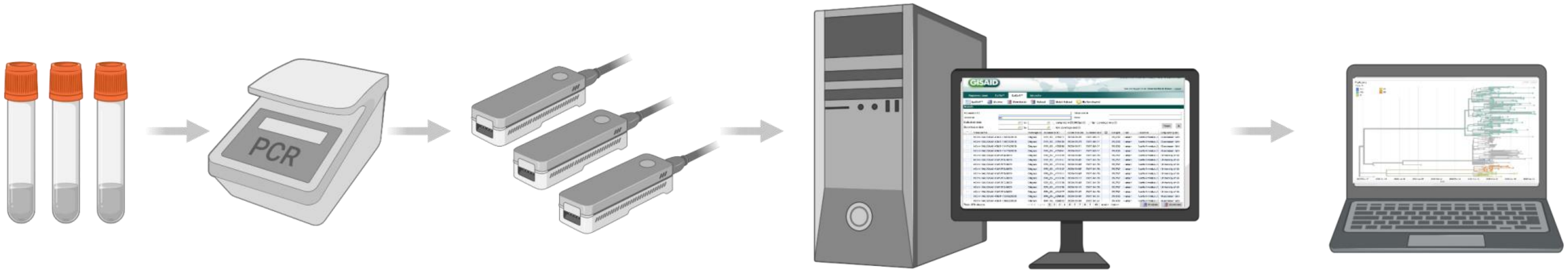
ARTICLE

https://doi.org/10.1038/s41467-020-19346-z OPEN

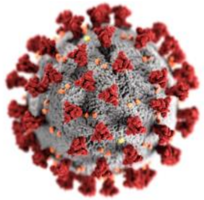
Revealing fine-scale spatiotemporal differences in SARS-CoV-2 introduction and spread

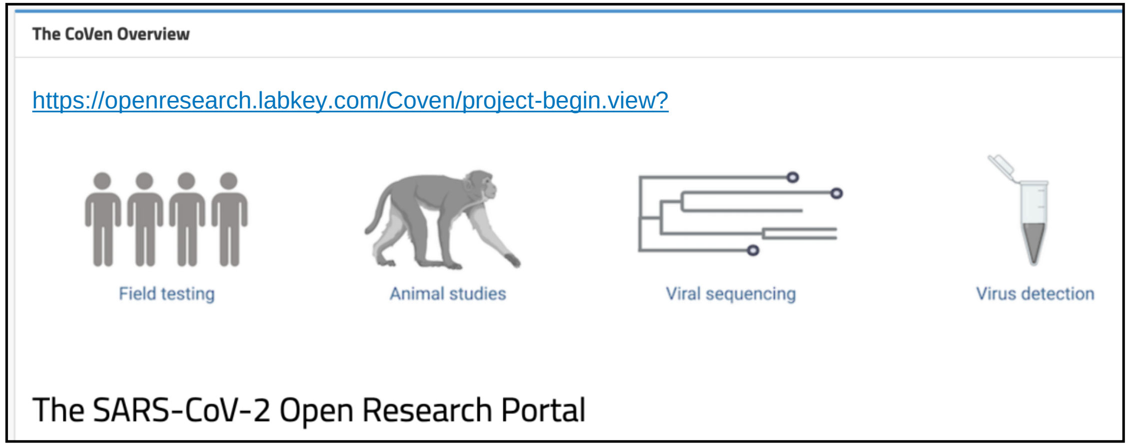
Gage K. Moreno[1,12], Katarina M. Braun[2,12], Kasen K. Riemersma[2,12], Michael A. Martin[3,4], Peter J. Halfmann[2,5], Chelsea M. Crooks[2], Trent Prall[1], David Baker[1], John J. Baczenas[1,6], Anna S. Heffron[1], Mitchell Ramuta[1], Manjeet Khubbar[7], Andrea M. Weiler[2,6], Molly A. Accola[8,9], William M. Rehrauer[8,9], Shelby L. O'Connor[1,6], Nasia Safdar[10], Caitlin S. Pepperell[10,11], Trivikram Dasu[7], Sanjib Bhattacharyya[7], Yoshihiro Kawaoka[2,5], Katia Koelle[3], David H. O'Connor[1] & Thomas C. Friedrich[2,6]✉

WHOLE GENOME SEQUENCING AND DATA ANALYSIS



SARS-CoV-2 genome (~29.9 Kb) is a single-stranded RNA, composed of 13–15 protein-coding genes

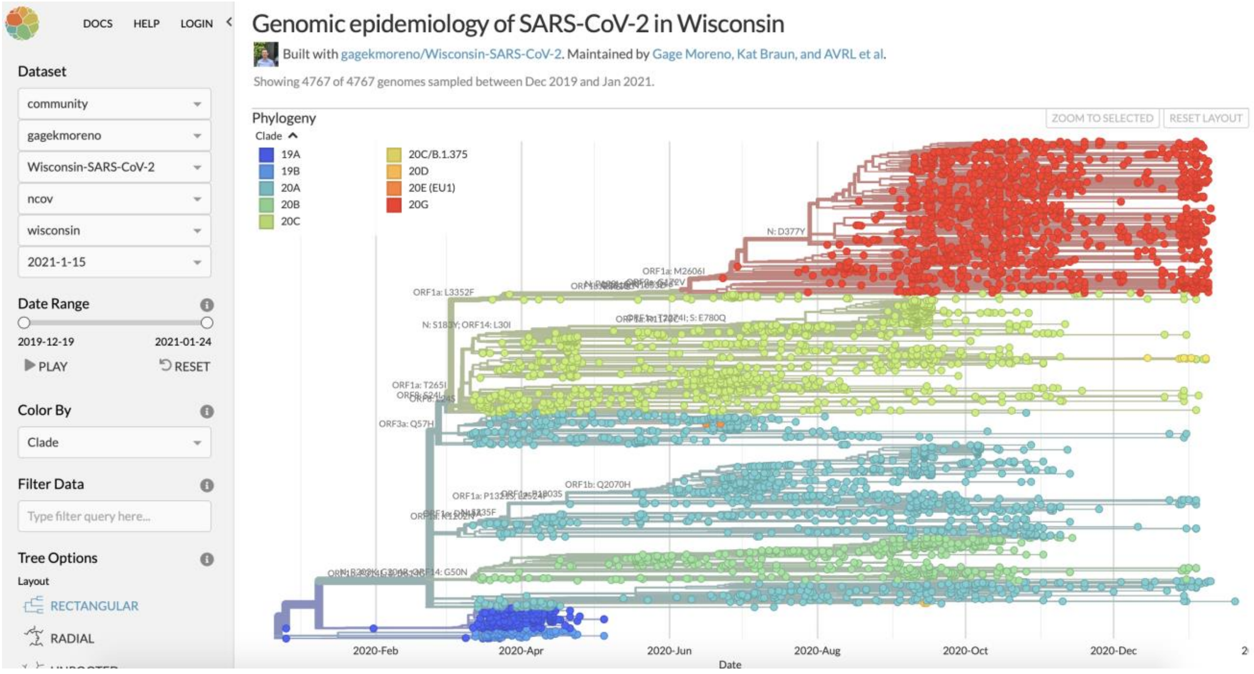




The CoVen Overview

https://openresearch.labkey.com/Coven/project-begin.view?

The SARS-CoV-2 Open Research Portal



Genomic epidemiology of SARS-CoV-2 in Wisconsin

Built with gagekmoreno/Wisconsin-SARS-CoV-2. Maintained by Gage Moreno, Kat Braun, and AVRL et al.

Showing 4767 of 4767 genomes sampled between Dec 2019 and Jan 2021.

Dataset: community, gagekmoreno, Wisconsin-SARS-CoV-2, ncov, wisconsin, 2021-1-15

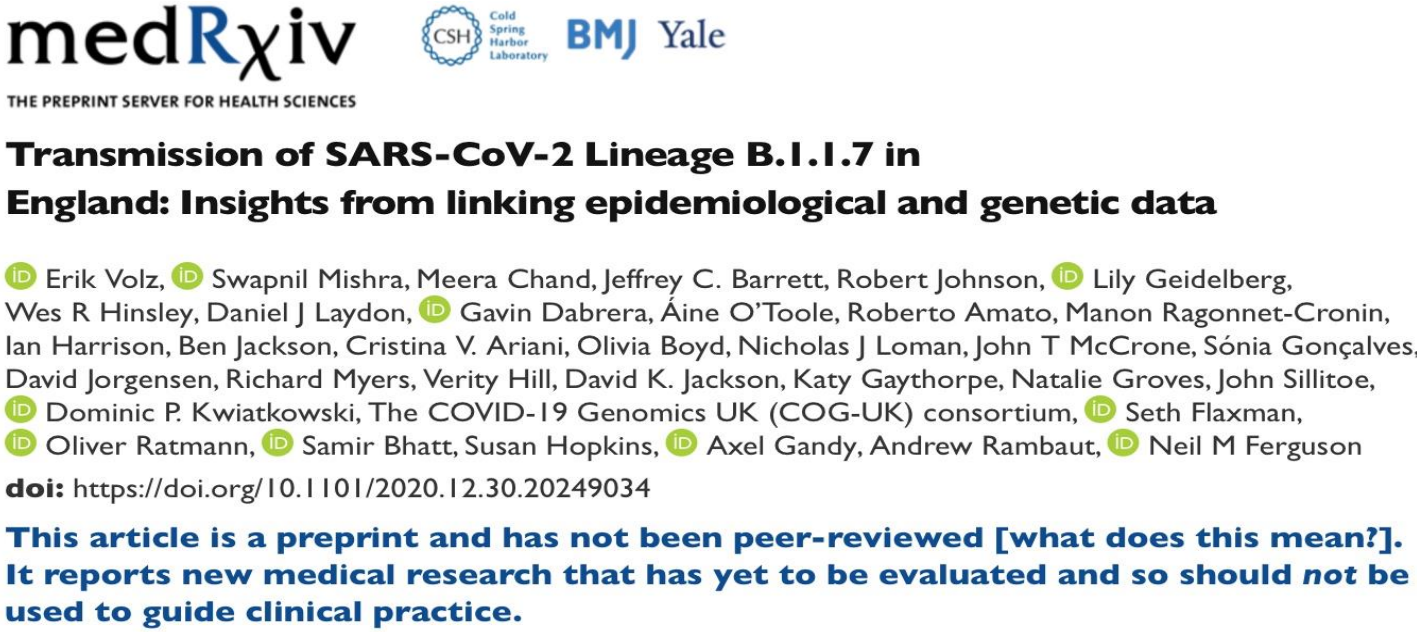
Date Range: 2019-12-19 – 2021-01-24

Color By: Clade

Filter Data: Type filter query here...

Tree Options

Layout: RECTANGULAR, RADIAL



medRxiv
THE PREPRINT SERVER FOR HEALTH SCIENCES

CSH Cold Spring Harbor Laboratory BMJ Yale

Transmission of SARS-CoV-2 Lineage B.1.1.7 in England: Insights from linking epidemiological and genetic data

Erik Volz, Swapnil Mishra, Meera Chand, Jeffrey C. Barrett, Robert Johnson, Lily Geidelberg, Wes R Hinsley, Daniel J Laydon, Gavin Dabrera, Áine O'Toole, Roberto Amato, Manon Ragonnet-Cronin, Ian Harrison, Ben Jackson, Cristina V. Ariani, Olivia Boyd, Nicholas J Loman, John T McCrone, Sónia Gonçalves, David Jorgensen, Richard Myers, Verity Hill, David K. Jackson, Katy Gaythorpe, Natalie Groves, John Sillitoe, Dominic P. Kwiatkowski, The COVID-19 Genomics UK (COG-UK) consortium, Seth Flaxman, Oliver Ratmann, Samir Bhatt, Susan Hopkins, Axel Gandy, Andrew Rambaut, Neil M Ferguson

doi: https://doi.org/10.1101/2020.12.30.20249034

This article is a preprint and has not been peer-reviewed [what does this mean?]. It reports new medical research that has yet to be evaluated and so should *not* be used to guide clinical practice.

- "There is a consensus among all analyses that the [**variant of concern B.1.1.7**] has a substantial transmission advantage…" September 2020

- As of Jan 13, 76 cases of B.1.1.7 have been detected in 10 U.S. states
- B.1.1.7 is more efficiently transmitted compared to circulating SARS-CoV-2 variants, but no data on increased mortality
- U.S. prevalence of B.1.1.7is less than 0.5% (based on cases identified by S-gene target failure (SGTF) in one of the RT-PCR diagnostic assays

- **B.1.351**- South Africa- October 2020
- **P.1** - Brazil and Japan- January 2021

Centers for Disease Control and Prevention
MMWR
Morbidity and Mortality Weekly Report
Early Release / Vol. 70 January 15, 2021

Emergence of SARS-CoV-2 B.1.1.7 Lineage — United States, December 29, 2020–January 12, 2021

Summer E. Galloway, PhD[1]; Prabasaj Paul, PhD[1]; Duncan R. MacCannell, PhD[2]; Michael A. Johansson, PhD[1]; John T. Brooks, MD[1]; Adam MacNeil, PhD[1]; Rachel B. Slayton, PhD[1]; Suxiang Tong, PhD[1]; Benjamin J. Silk, PhD[1]; Gregory L. Armstrong, MD[2]; Matthew Biggerstaff, ScD[1]; Vivien G. Dugan, PhD[1]

On December 14, 2020, the United Kingdom reported a SARS-CoV-2 variant of concern (VOC), lineage B.1.1.7, also referred to as VOC 202012/01 or 20I/501Y.V1.* The B.1.1.7 variant is estimated to have emerged in September 2020 and has quickly become the dominant circulating SARS-CoV-2 variant in England (*1*). B.1.1.7 has been detected in over 30 countries, including the United States. As of January 13, 2021, approximately 76 cases of B.1.1.7 have been detected in 10 U.S. states.† Multiple lines of evidence indicate that B.1.1.7 is more efficiently transmitted than are other SARS-CoV-2 variants (*1*–*3*). The modeled trajectory of this variant in the U.S. exhibits rapid growth in early 2021, becoming the predominant variant in March. Increased SARS-CoV-2 transmission might threaten strained health care resources, require extended and more rigorous implementation of public health strategies (*4*), and increase the percentage of population immunity required for pandemic control. Taking measures to reduce transmission now can lessen the potential impact of B.1.1.7 and allow critical time to increase vaccination coverage. Collectively, enhanced genomic surveillance combined with continued compliance with effective public health measures, including vaccination, physical distancing, use of masks, hand hygiene, and isolation and quarantine, will be essential to limiting the spread of SARS-CoV-2, the virus that causes coronavirus disease 2019 (COVID-19). Strategic testing of persons without symptoms but at higher risk of infection, such as those exposed to SARS-CoV-2 or who have frequent unavoidable contact with the public, provides another opportunity to limit ongoing spread.

Global genomic surveillance and rapid open-source sharing of viral genome sequences have facilitated near real-time detection, comparison, and tracking of evolving SARS-CoV-2 variants that can inform public health efforts to control the pandemic. Whereas some mutations in the viral genome emerge and then recede, others might confer a selective advantage to the variant, including enhanced transmissibility, so that such a variant can rapidly dominate other circulating variants. Early in the pandemic, variants of SARS-CoV-2 containing the D614G mutation in the spike (S) protein that increases receptor binding avidity rapidly became dominant in many geographic regions (*5*,*6*).

In late fall 2020, multiple countries reported detecting SARS-CoV-2 variants that spread more efficiently. In addition to the B.1.1.7 variant, notable variants include the B.1.351 lineage first detected in South Africa and the recently identified B.1.1.28 subclade (renamed "P.1") detected in four travelers from Brazil during routine screening at the Haneda (Tokyo) airport.§ These variants carry a constellation of genetic mutations, including in the S protein receptor-binding domain, which is essential for binding to the host cell angiotensin-converting enzyme-2 (ACE-2) receptor to facilitate virus entry. Evidence suggests that other mutations found in these variants might confer not only increased transmissibility but might also affect the performance of some diagnostic real-time reverse transcription–polymerase chain reaction (RT-PCR) assays¶ and reduce susceptibility to neutralizing antibodies (*2*,*3*,*5*–*10*). A recent case report documented the first case of

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* https://www.gov.uk/government/news/phe-investigating-a-novel-variant-of-covid-19.

† https://www.cdc.gov/coronavirus/2019-ncov/transmission/variant-cases.html.

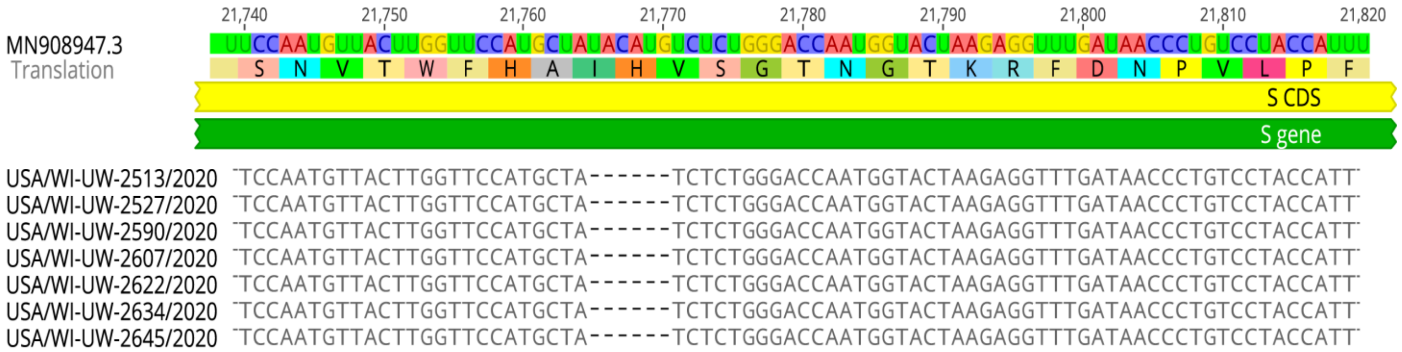
§ https://www.japantimes.co.jp/news/2021/01/11/national/science-health/new-coronavirus-variant-japan/.

¶ https://www.fda.gov/news-events/press-announcements/fda-issues-alert-regarding-sars-cov-2-viral-mutation-health-care-providers-and-clinical-laboratory?utm_medium.

U.S. Department of Health and Human Services
Centers for Disease Control and Prevention

SARS-COV-2 VARIANTS IN WISCONSIN

- On Jan 12, DHS reported B.1.1.7 variant strain of SARS-CoV-2 in Eau Claire, WI (sequenced by a private reference lab)
- Detected viruses encoding S Δ69-70 circulating in Wisconsin, but we have not detected B.1.1.7 in any of those 2,966 genomes so far
- Spread of B.1.1.7 (“UK variant”) in Wisconsin is likely, though currently rare in detection



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MN908947.3          UUCCAAUGUUACUUGGUUCCAUGCUAUACAUGUCUCUGGGACCAAUGGUACUAAGAGGUUUGAUAACCCUGUCCUACCAUUU
Translation          S N V T W F H A I H V S G T N G T K R F D N P V L P F
USA/WI-UW-2513/2020 TCCAATGTTACTTGGTTCCATGCTA------TCTCTGGGACCAATGGTACTAAGAGGTTTGATAACCCTGTCCTACCATT
USA/WI-UW-2527/2020 TCCAATGTTACTTGGTTCCATGCTA------TCTCTGGGACCAATGGTACTAAGAGGTTTGATAACCCTGTCCTACCATT
USA/WI-UW-2590/2020 TCCAATGTTACTTGGTTCCATGCTA------TCTCTGGGACCAATGGTACTAAGAGGTTTGATAACCCTGTCCTACCATT
USA/WI-UW-2607/2020 TCCAATGTTACTTGGTTCCATGCTA------TCTCTGGGACCAATGGTACTAAGAGGTTTGATAACCCTGTCCTACCATT
USA/WI-UW-2622/2020 TCCAATGTTACTTGGTTCCATGCTA------TCTCTGGGACCAATGGTACTAAGAGGTTTGATAACCCTGTCCTACCATT
USA/WI-UW-2634/2020 TCCAATGTTACTTGGTTCCATGCTA------TCTCTGGGACCAATGGTACTAAGAGGTTTGATAACCCTGTCCTACCATT
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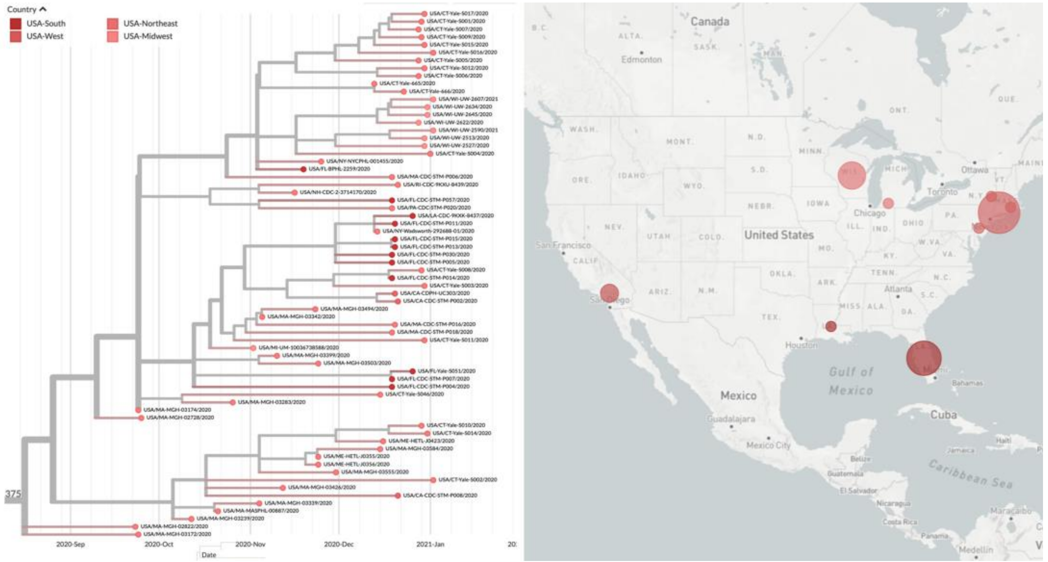


MHDL- in-house sequencing, qualified and trained staff

- Adding Bioinformatics (data analysis) position
- Epidemiologist's contribution to identify hot spots

SUMMARY

- Emerging SARS-CoV-2 variants could— but may not— undermine the performance of diagnostics, therapeutics, or vaccines
- Long-term capacity for genomic surveillance is critical to detect the emergence and spread of 'variants of concern'
- Continued adaptation of SARS-CoV-2 to its hosts (both human and animal) is inevitable- but which variants to be concerned about may only become clear with more genomic and epidemiological data
- Efforts that can limit the spread of the B.1.1.7 variant at the personal level- universal and increased compliance with public health mitigation strategies
- Increased ongoing vaccination efforts likely add to achieve higher population-level immunity.
- Enhancing community messaging for personal protection, increase testing (all options available) and encourage vaccination

TESTING AND TRACING

TESTING & TRACING

Response to Community Need

- Community sites
  - Northwest Health Center
  - Southside Health Center
  - American Family Field

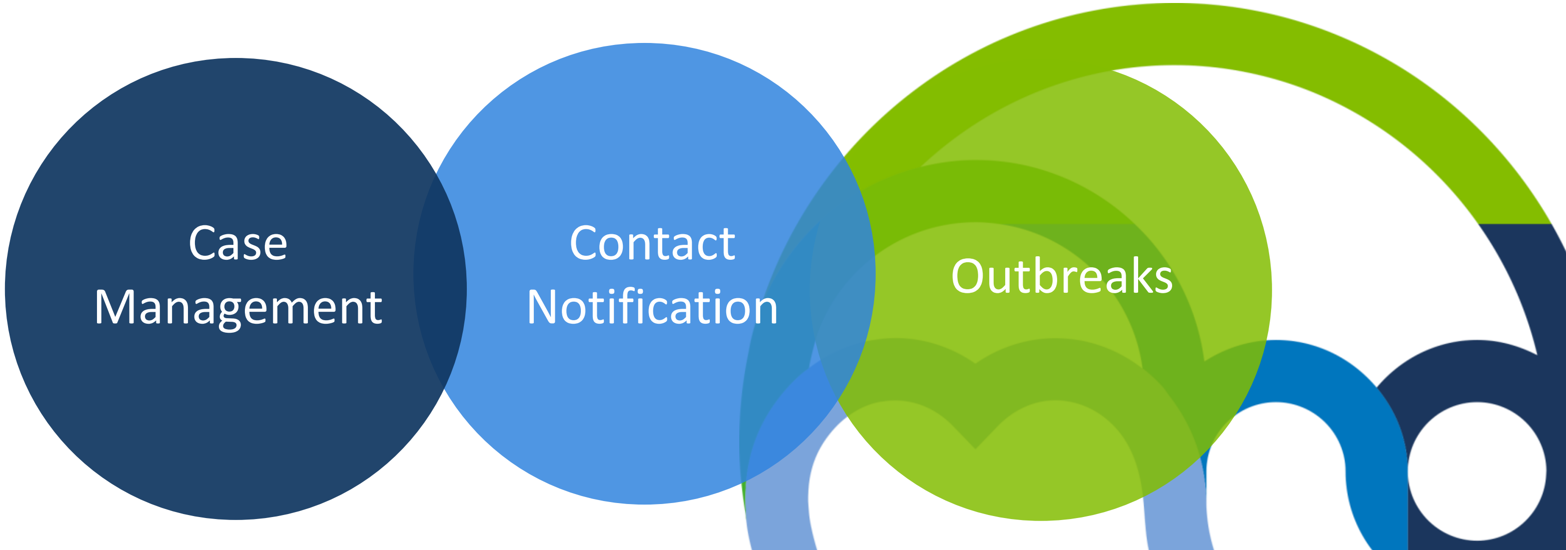
211 Hotline

Test Results and Questions

Supports for Isolation/Quarantine

Vaccine Navigation

- Contact Tracing
  - 200 trained tracers



Case Management

Contact Notification

Outbreaks

COVID-19 VACCINE

OVERVIEW

COVID-19 VACCINE

- Phase 1
  - Wisconsin Center
  - Ability to vaccinate many in a short amount of time
  - Meets physical criteria for space
  - Respond to built-up demand

- Phase 2
  - Mobile strategy
  - Community partnerships
  - Vaccinate closer to home

UPDATES

COVID-19 VACCINE

- Started vaccinating on 1/7/21
- Beginning second doses this week
- Phase 1a, plus additional groups per DHS guidance
- Working with DER for phasing of city employees

Scheduling

Registration

Consent

Vaccination

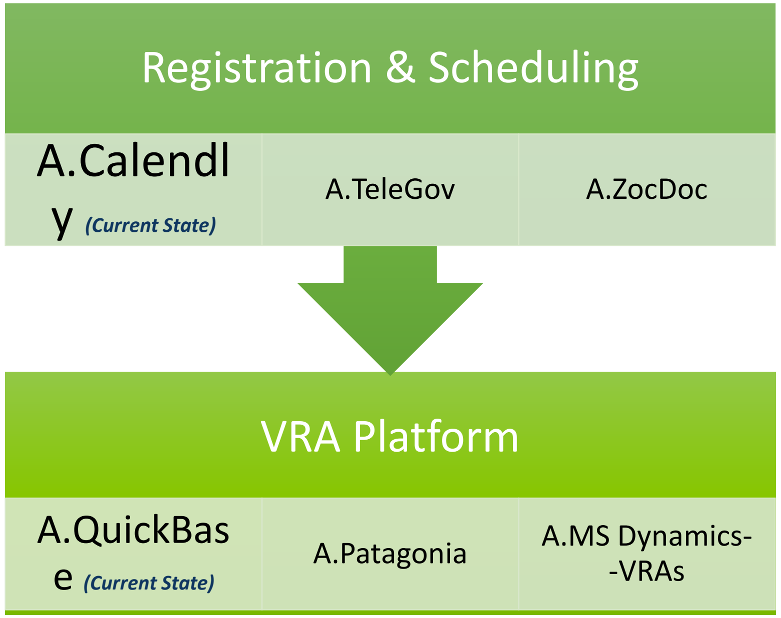
Observation

Reporting

VACCINATION

CURRENT STATE & STRATEGIES

Strategies



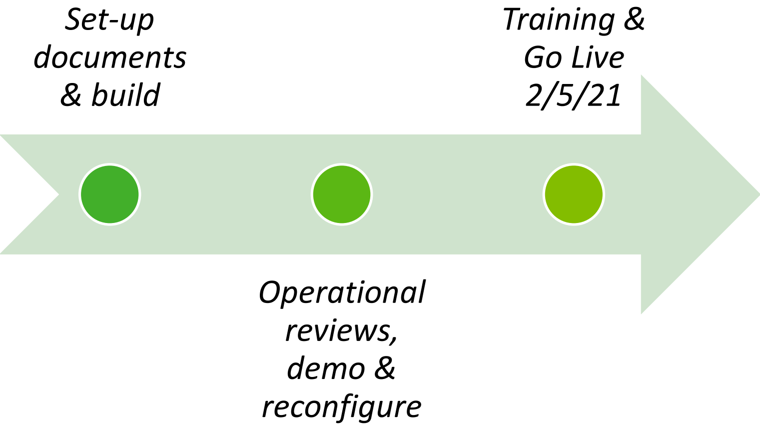
Registration & Scheduling

A.Calendly ***(Current State)***	A.TeleGov	A.ZocDoc

VRA Platform

A.QuickBase ***(Current State)***	A.Patagonia	A.MS Dynamics--VRAs

Registration & Scheduling

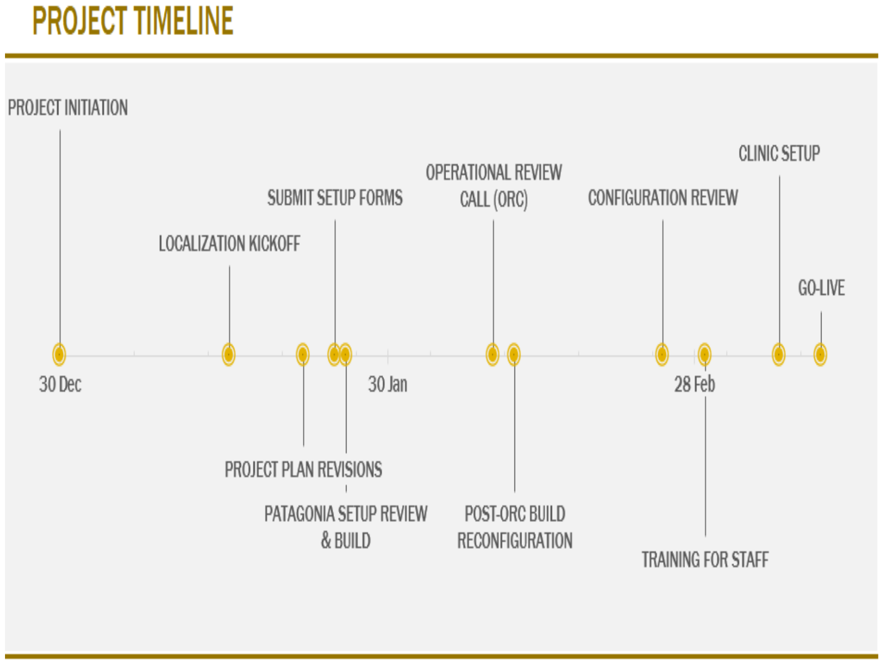


Set-up documents & build

Operational reviews, demo & reconfigure

Training & Go Live 2/5/21

Mass Immunizations Project Overview



Rapid Implementation Cycle

COMMUNICATIONS/OUTREACH

METHODOLOGY

- Current State
  - Scheduling System Link
    - Identified groups
- Future State (Week of 2/1)
  - New Scheduling System Link
    - High volume registration
    - Demographic data for evaluation
  - Hotline
    - Available for individuals without internet access

VACCINE OUTREACH

#CRUSHCOVIDMKE TOOLKIT IN DEVELOPMENT

Stickers, buttons

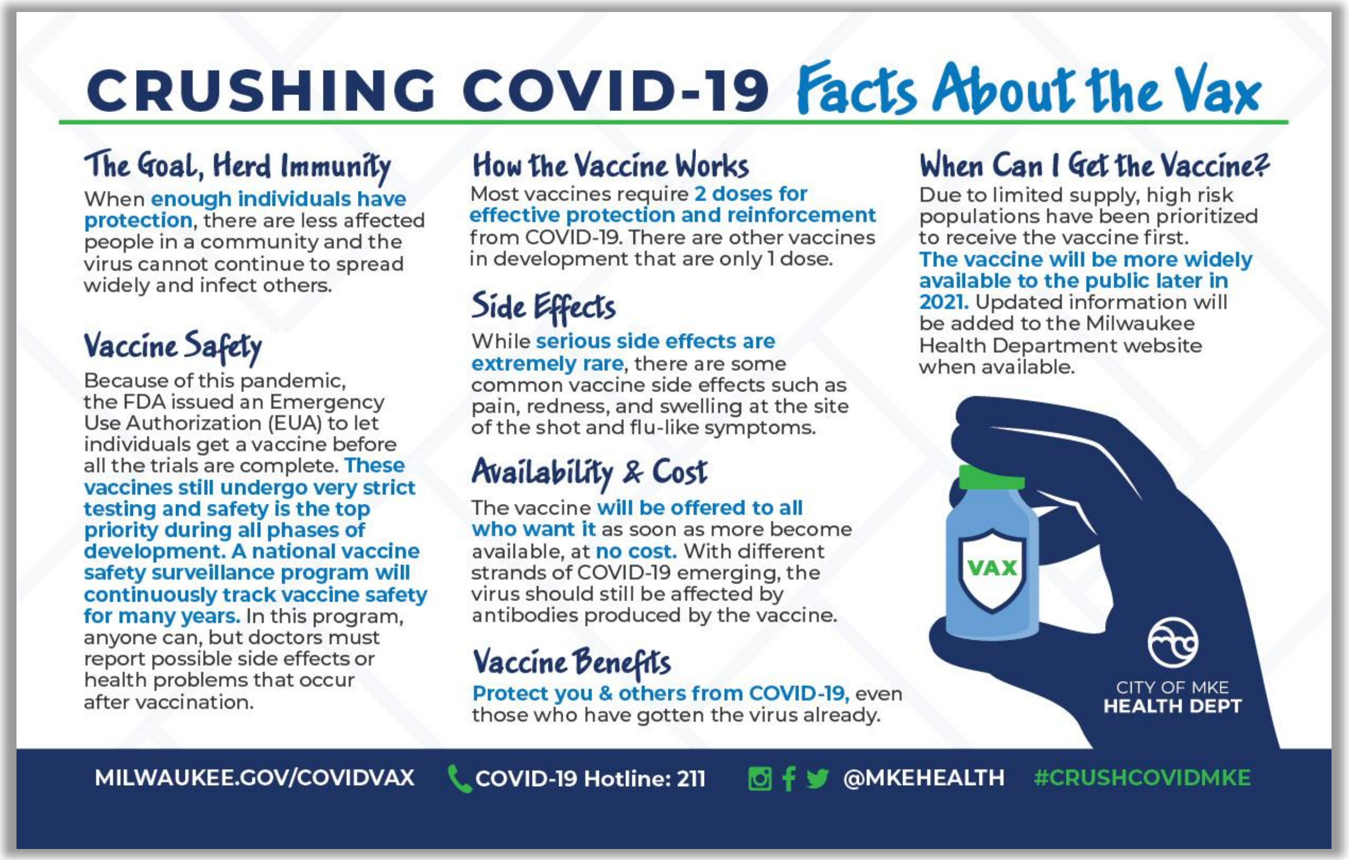
- Similar to Voting stickers, printed badges/tokens encourages vaccination support

Facebook Profile Picture Frame and social profile images

- Overlays on your FB profile image
- “Before” version – PLEDGE TO GET THE SHOT
- “After” version – I GOT THE SHOT

VACCINE FACTS

Goal is to myth-bust, encourage vaccination and provide safety information. Prints and Digital graphics in circulation



CRUSHING COVID-19 Facts About the Vax

The Goal, Herd Immunity

When **enough individuals have protection**, there are less affected people in a community and the virus cannot continue to spread widely and infect others.

Vaccine Safety

Because of this pandemic, the FDA issued an Emergency Use Authorization (EUA) to let individuals get a vaccine before all the trials are complete. **These vaccines still undergo very strict testing and safety is the top priority during all phases of development. A national vaccine safety surveillance program will continuously track vaccine safety for many years.** In this program, anyone can, but doctors must report possible side effects or health problems that occur after vaccination.

How the Vaccine Works

Most vaccines require **2 doses for effective protection and reinforcement** from COVID-19. There are other vaccines in development that are only 1 dose.

Side Effects

While **serious side effects are extremely rare**, there are some common vaccine side effects such as pain, redness, and swelling at the site of the shot and flu-like symptoms.

Availability & Cost

The vaccine **will be offered to all who want it** as soon as more become available, at **no cost.** With different strands of COVID-19 emerging, the virus should still be affected by antibodies produced by the vaccine.

Vaccine Benefits

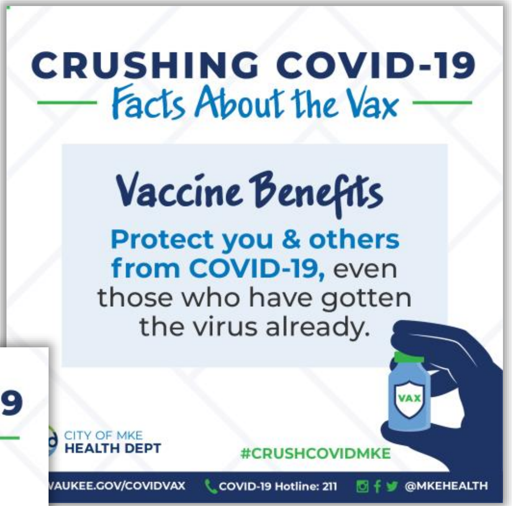
Protect you & others from COVID-19, even those who have gotten the virus already.

When Can I Get the Vaccine?

Due to limited supply, high risk populations have been prioritized to receive the vaccine first. **The vaccine will be more widely available to the public later in 2021.** Updated information will be added to the Milwaukee Health Department website when available.

CITY OF MKE HEALTH DEPT

MILWAUKEE.GOV/COVIDVAX ☎ COVID-19 Hotline: 211 @MKEHEALTH #CRUSHCOVIDMKE



CRUSHING COVID-19
Facts About the Vax

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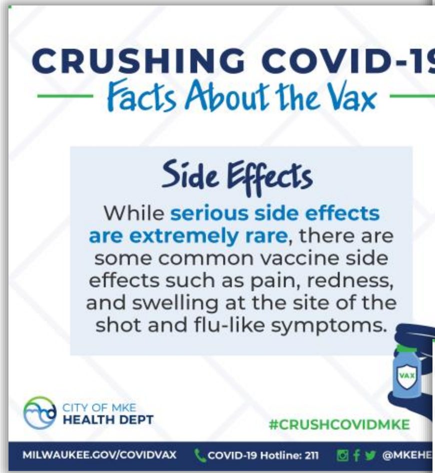
CITY OF MKE HEALTH DEPT

#CRUSHCOVIDMKE

AUKEE.GOV/COVIDVAX ☎ COVID-19 Hotline: 211 @MKEHEALTH



CRUSHING COVID-19
Facts About the Vax

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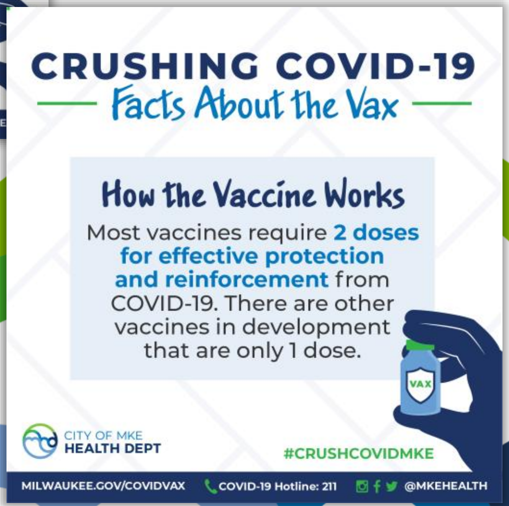
CITY OF MKE HEALTH DEPT

#CRUSHCOVIDMKE

MILWAUKEE.GOV/COVIDVAX ☎ COVID-19 Hotline: 211 @MKEHE



CRUSHING COVID-19
Facts About the Vax

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CITY OF MKE HEALTH DEPT

#CRUSHCOVIDMKE

MILWAUKEE.GOV/COVIDVAX ☎ COVID-19 Hotline: 211 @MKEHEALTH

VACCINE TOWN HALL

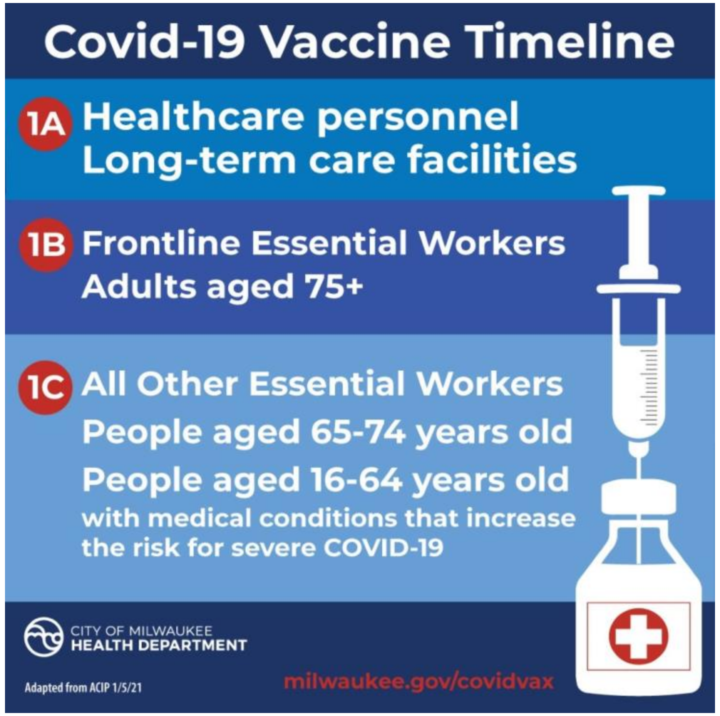
SAVE THE DATE: COVID-19 Vaccine Virtual Town Hall
Wednesday, February 10, 2021 at 6pm

This town hall will be the first of many to identify and address misconceptions and concerns around vaccine safety and effectiveness. Presenters will provide the latest information on the safety, process and timeline for the COVID-19 vaccine.

- Mayor Tom Barrett, Mayor of City of Milwaukee
- Marlaina Jackson, Interim Commissioner of City of Milwaukee Health Department
- Heather Paradis, MD, MPH, Deputy Commissioner of Medical Services
- Moderator - Anthony Atkins, TMJ4

milwaukee.gov/covidvax

SOCIAL GRAPHICS



Covid-19 Vaccine Timeline

1A Healthcare personnel
Long-term care facilities

1B Frontline Essential Workers
Adults aged 75+

1C All Other Essential Workers
People aged 65-74 years old
People aged 16-64 years old
with medical conditions that increase
the risk for severe COVID-19

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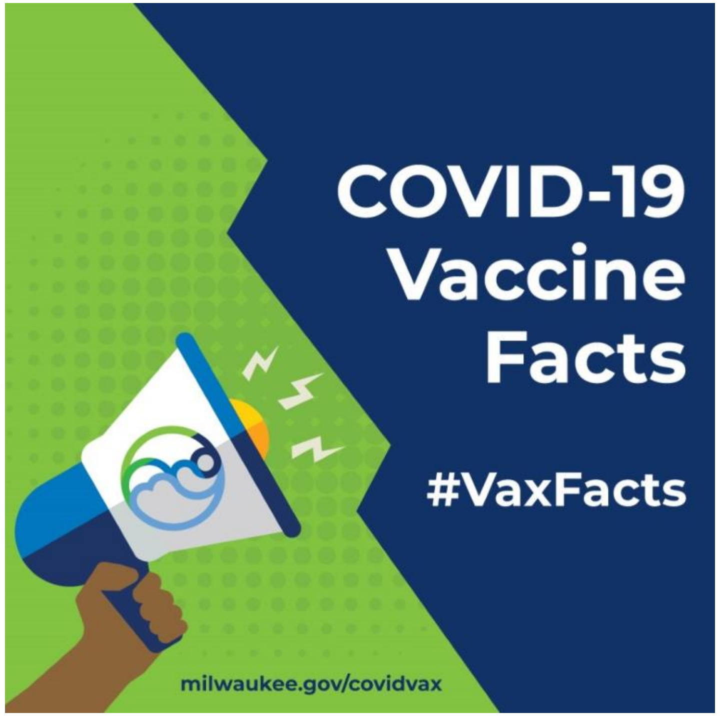
Adapted from ACIP 1/5/21

milwaukee.gov/covidvax



THANK YOU

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HEALTH DEPARTMENT