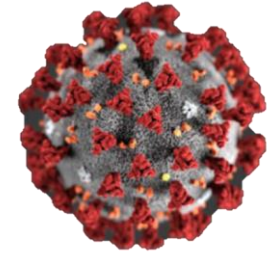


New Hampshire Coronavirus Disease 2019 Weekly Partner Call



December 2, 2021

Ben Chan
Elizabeth Talbot
Beth Daly
Lindsay Pierce

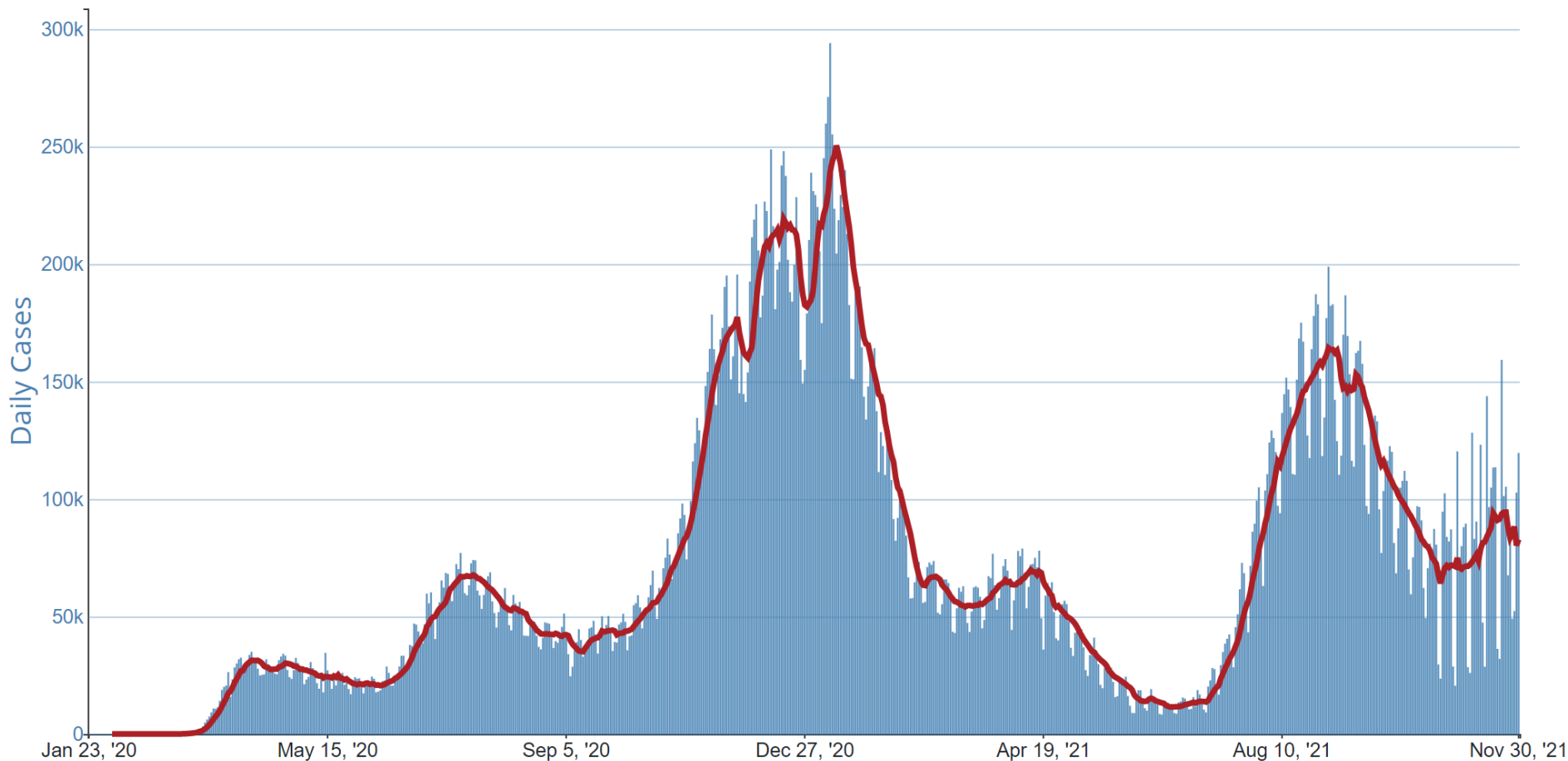
Thursday noon-time partner calls will focus on science, medical, and vaccine updates with time for Q&A

Agenda

- Epidemiology Update
- Omicron Variant
- Questions & Answers (Q&A)

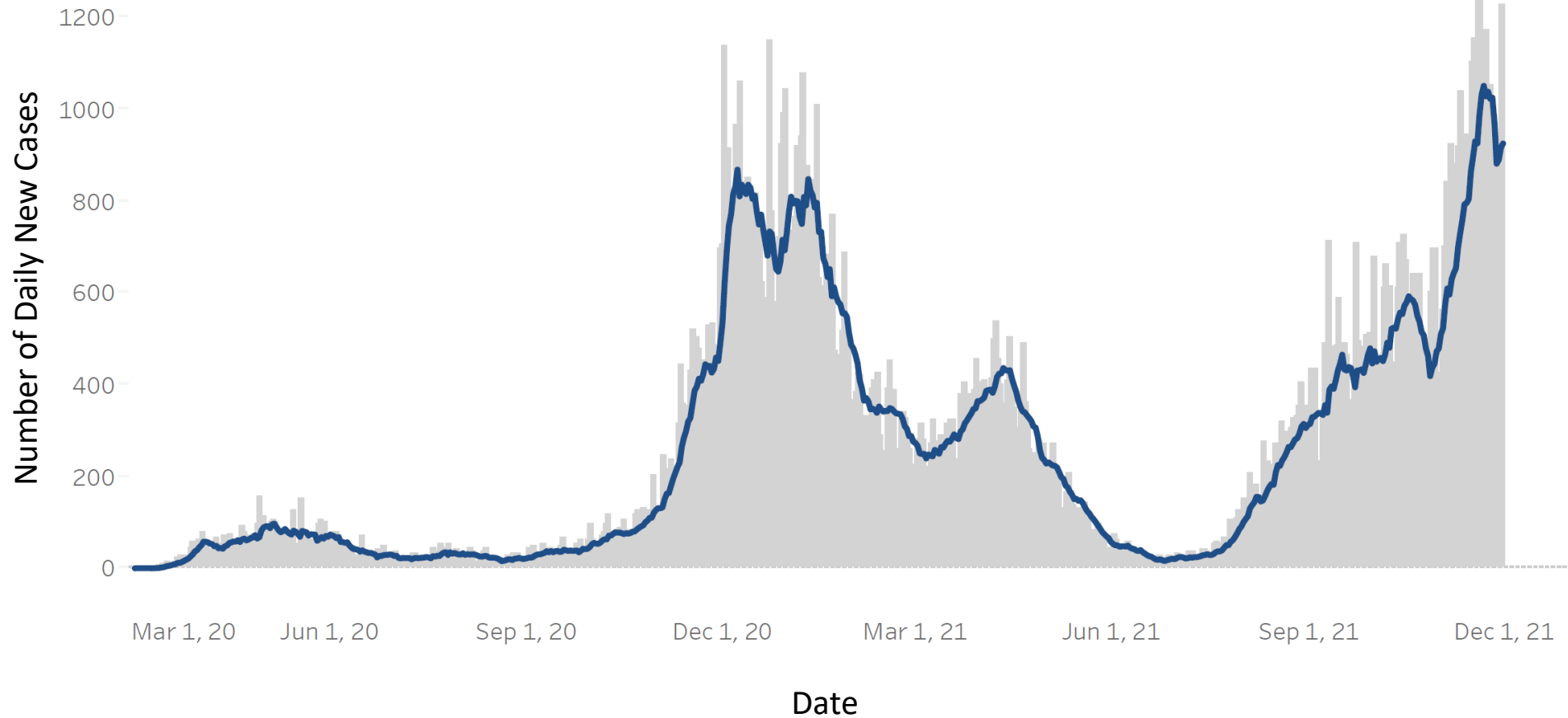
Epidemiology Update

U.S. National Daily Incidence of COVID-19



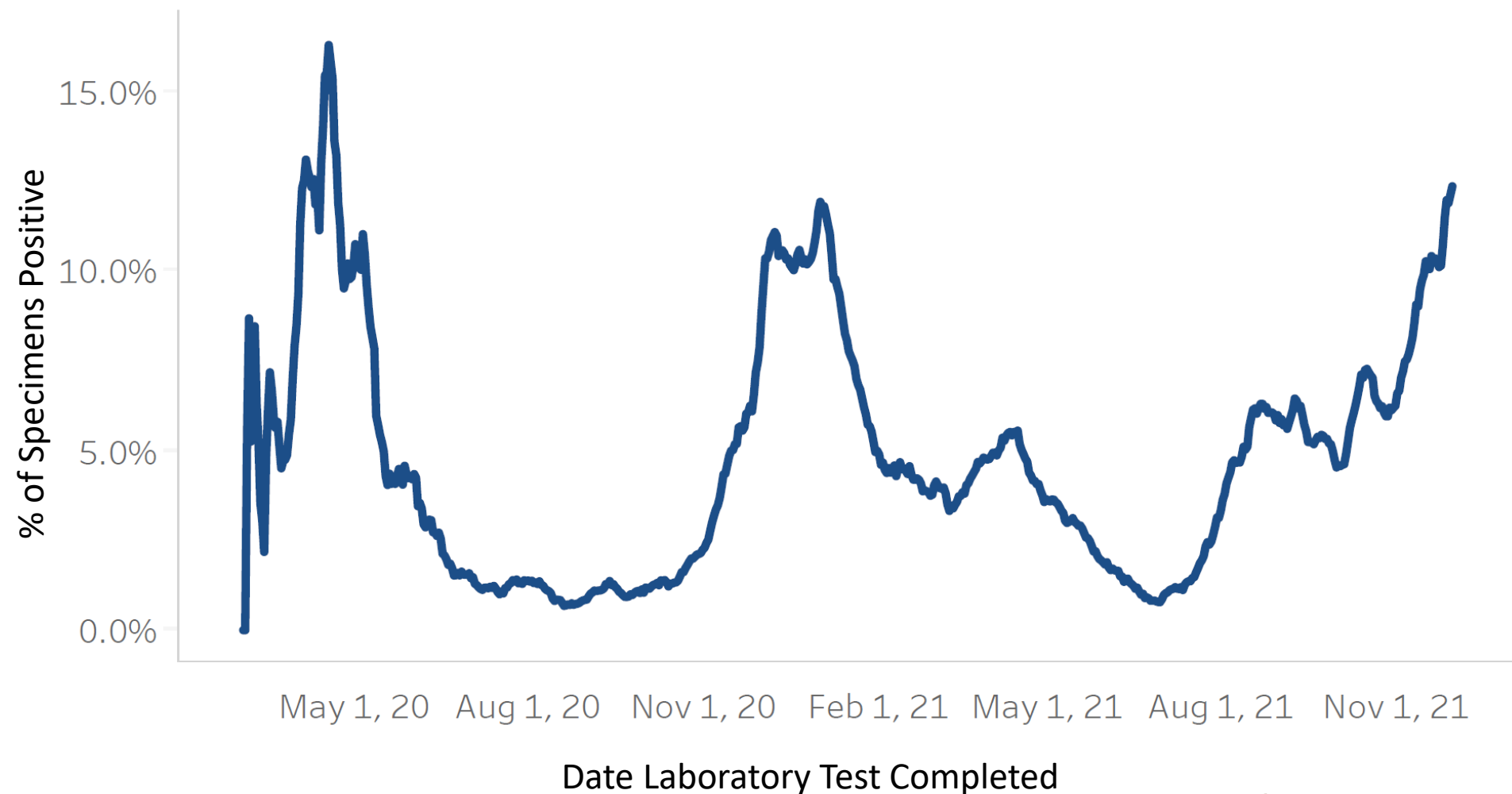
https://covid.cdc.gov/covid-data-tracker/#trends_dailytrendscases

Number of New COVID-19 Cases per Day in NH



<https://www.nh.gov/covid19/dashboard/overview.htm#dash>

% of Tests (Antigen and PCR) Positive for COVID-19 (7-Day Average)



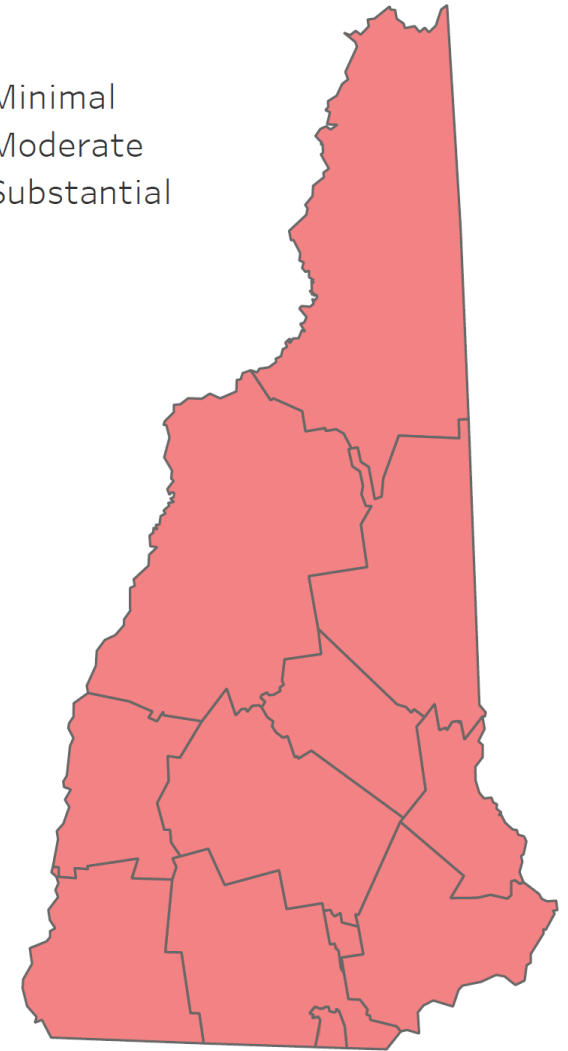
<https://www.nh.gov/covid19/dashboard/overview.htm#dash>

Level of Community Transmission in NH

Statewide
Level of
Transmission

Substantial

- Minimal
- Moderate
- Substantial



New Cases per 100k
over 14 days

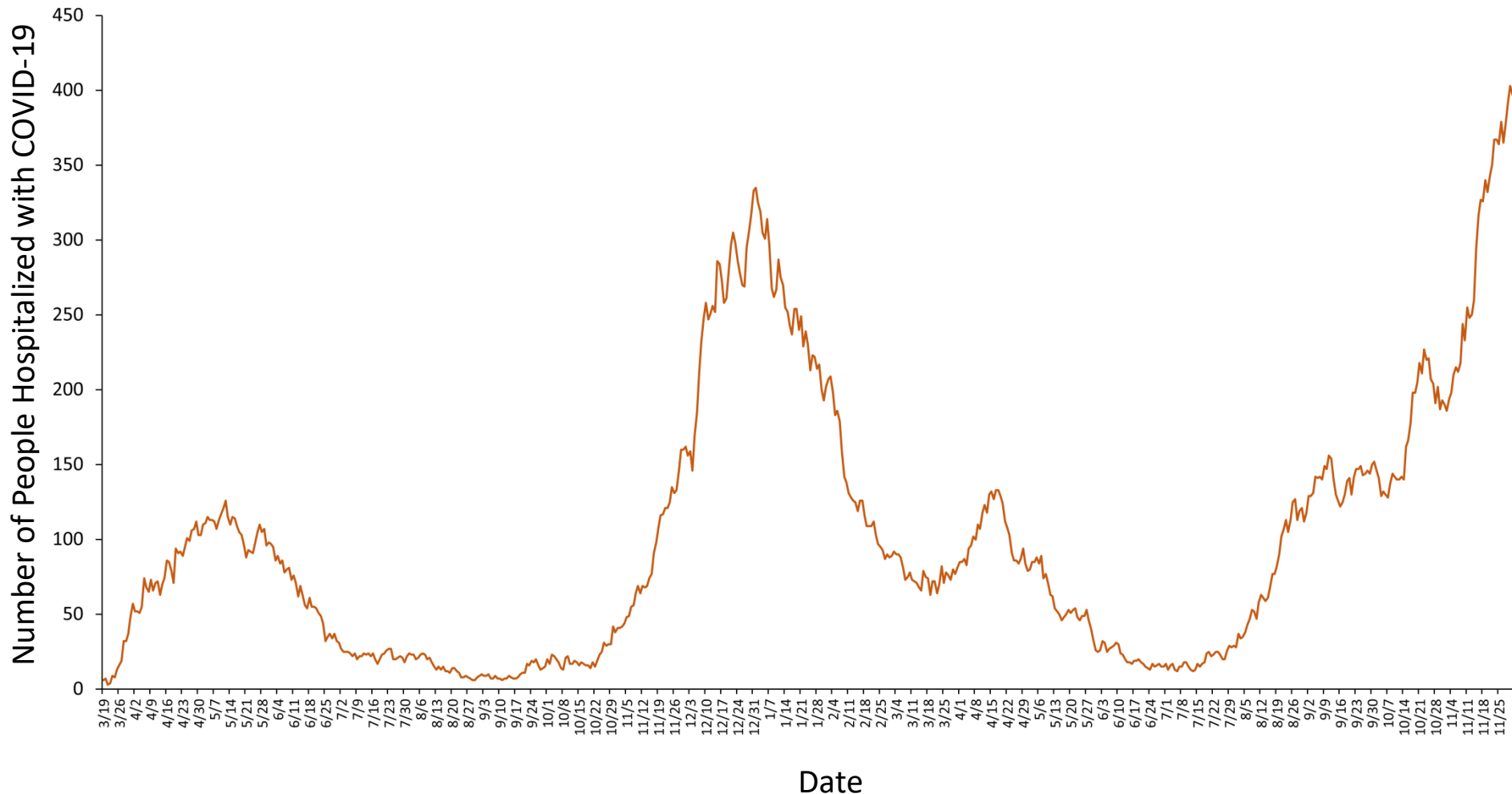
1,009.5

7-Day Total Test
Positivity Rate

12.4%

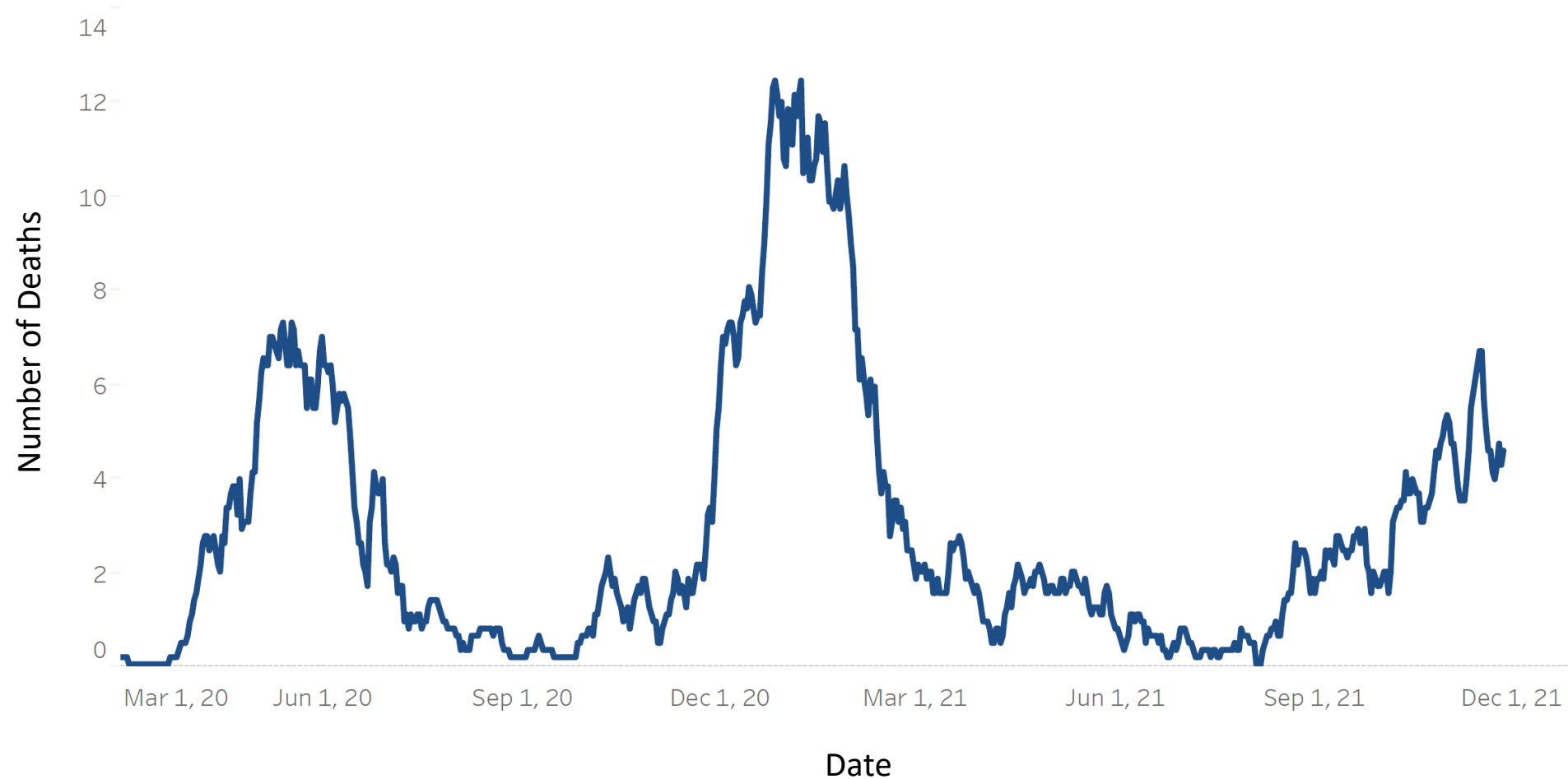
Data as of: 12/1/2021

Number of People Hospitalized with COVID-19 Each Day in NH (Hospital Census)



<https://www.nh.gov/covid19/dashboard/overview.htm#dash>

Average Number of COVID-19 Deaths per Day in NH (Based on Date of Death)



<https://www.nh.gov/covid19/dashboard/overview.htm#dash>

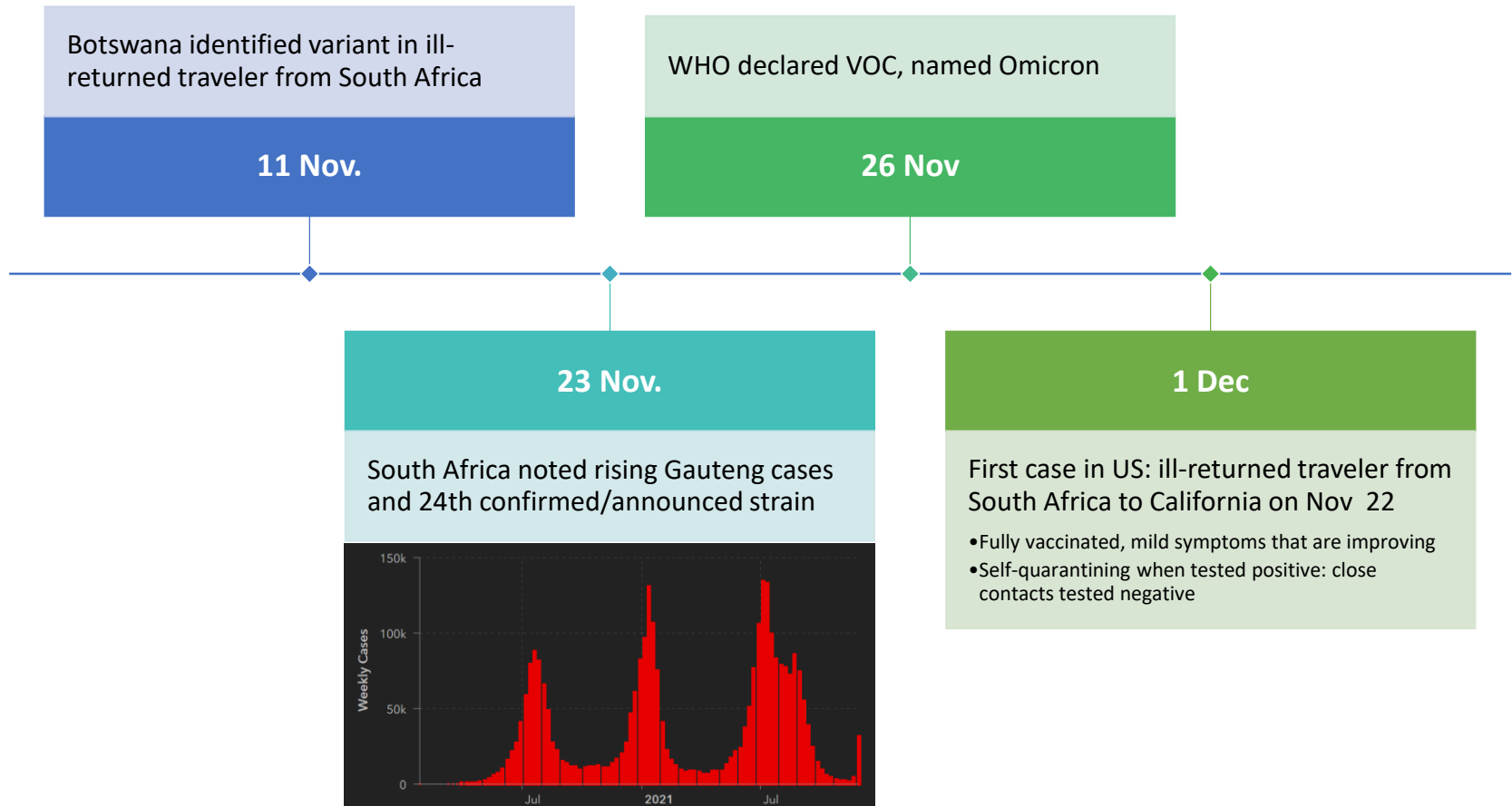
Omicron Variant

COVID-19 Omicron

1. What we know
2. What we don't know (and when we might know it)



B.1.1.529 is Named VOC Omicron

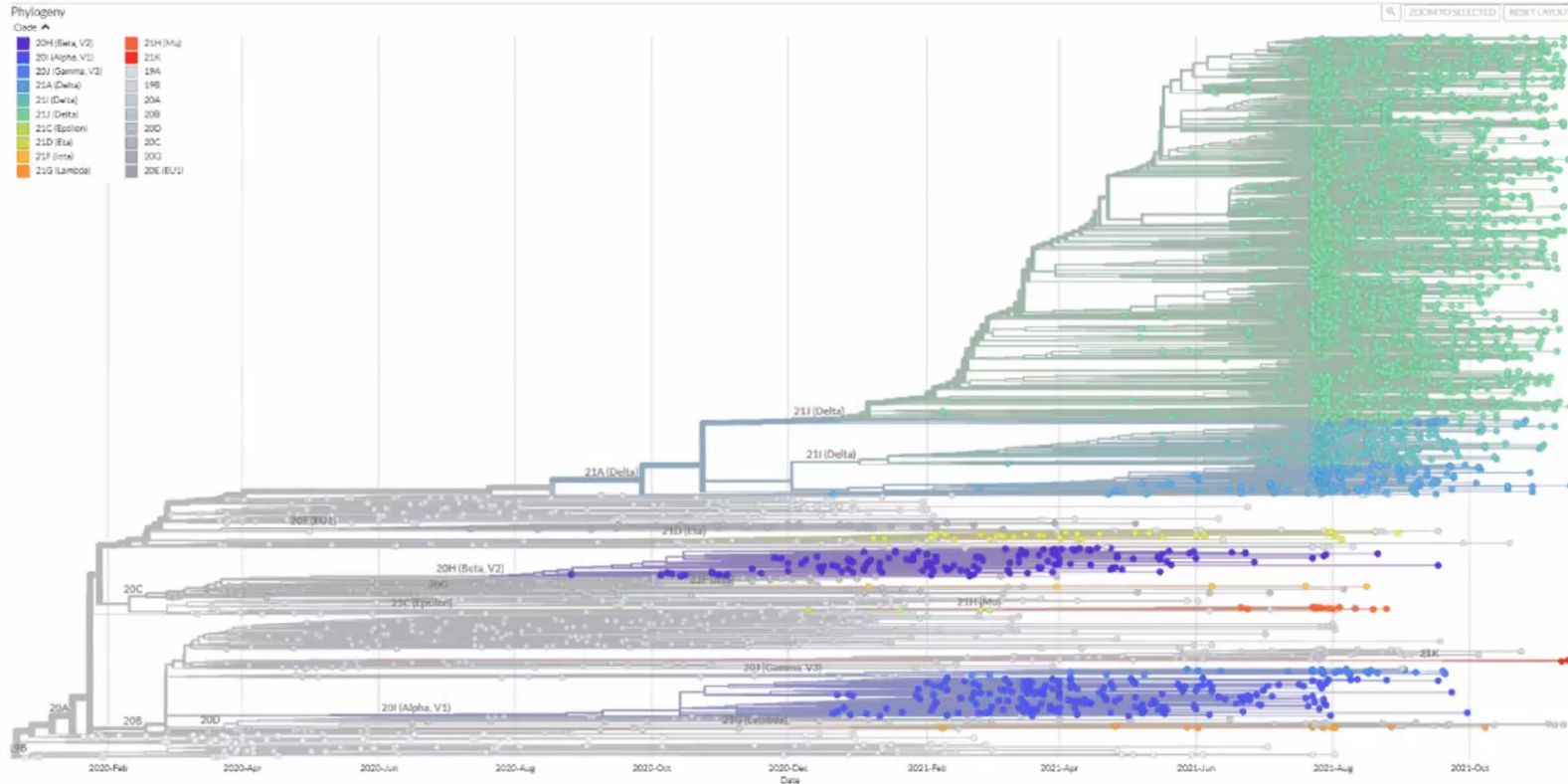


Omicron Not Derived From Delta or Other VOCs

Genomic epidemiology of novel coronavirus - Africa-focused subsampling

Built with nextstrain/ncov. Maintained by the Nextstrain team. Enabled by data from GISAID

Showing 3719 of 3719 genomes sampled between Dec 2019 and Nov 2021.



Omicron

[Nextstrain / ncov / gisaid / africa](https://nextstrain.org/ncov/gisaid/africa)

Thanks to R. Neher and E. Hodcroft



Nov 30: U.S.
SARS-CoV-2
Interagency
Group Classified
Omicron a VOC

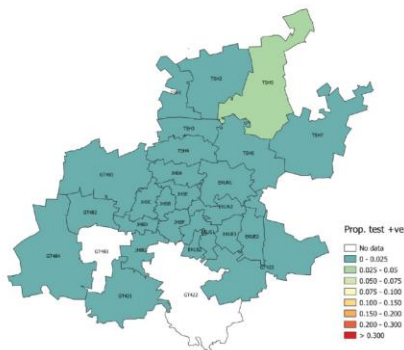
- Detection in multiple countries, including among those without travel history
- Transmission and displacement of Delta in South Africa
- Number and locations of substitutions in the spike protein
- Available data for other variants with fewer substitutions in the spike protein indicating a reduction in neutralization by vaccinee and convalescent sera and certain monoclonal antibody treatments

What is the Concern?

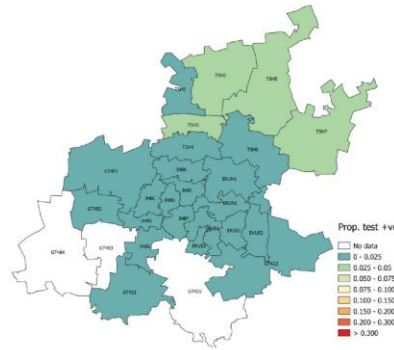
High number of mutations, some unusual, some concerning for predicted

- Immune evasion
- Increased transmissibility: $R_e = 1.47$; Gauteng $R_e = 1.93$

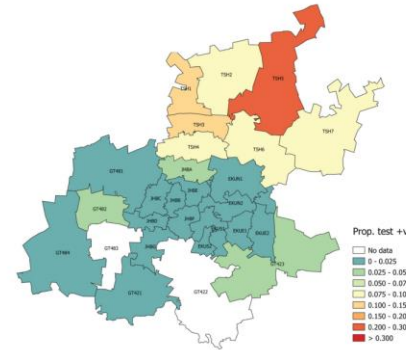
Early signs from diagnostic laboratories that Omicron has rapidly increased in Gauteng and may already be present in most other provinces



Week 44 (31 Oct – 6 Nov)

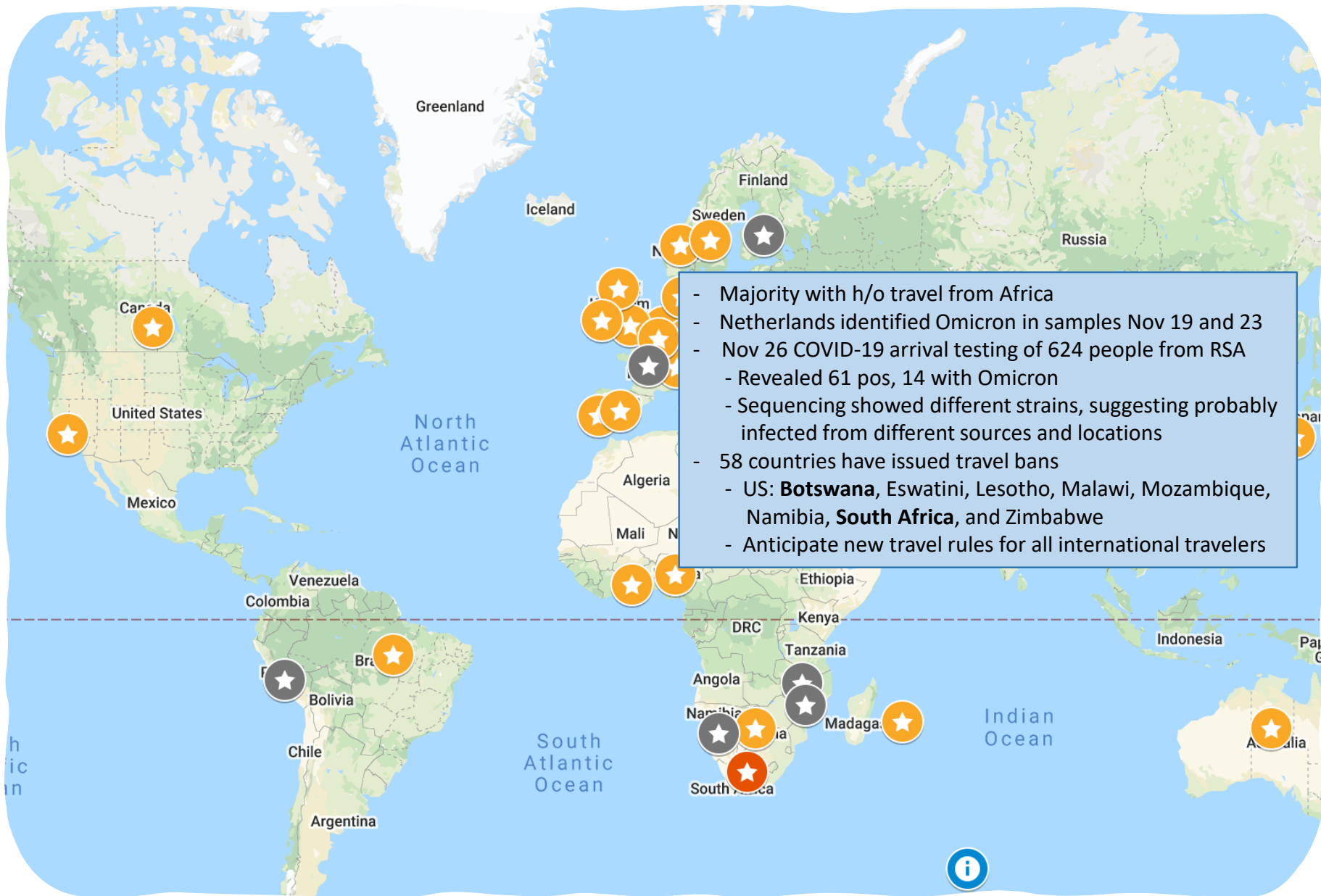


Week 45 (7-13 Nov)



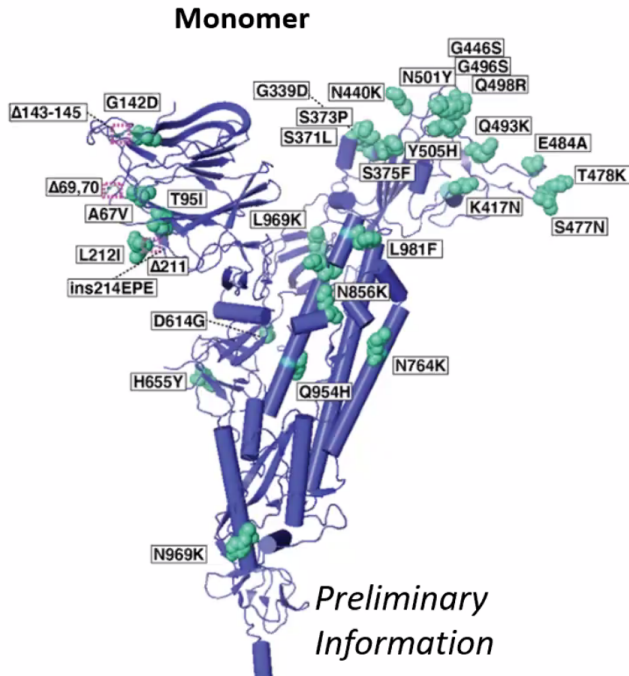
Week 46 (14-20 Nov)

RSA test pos jumped
16.5% Dec 1, from
10.7% Nov 30



Omicron Tracker

Omicron Has Many Concerning Spike Mutations

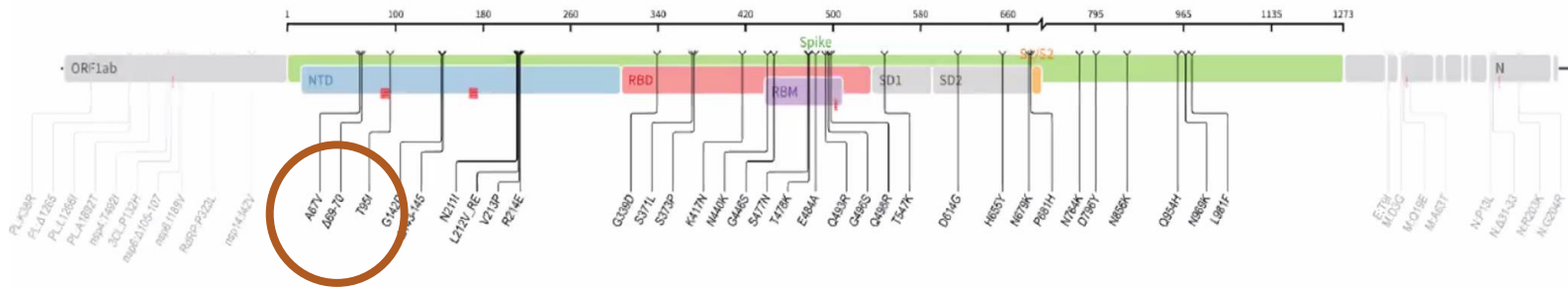


Has substitutions, insertion, and deletions

- S mutations likely impact
 - Binding with the hACE2 (Transmission?)
 - Fusion (Transmission?)
 - S1/S2 cleavage site changes
- May reduce neutralization by therapeutic antibodies and polyclonal antibodies induced by natural infection or vaccination
 - No data in the context of this Spike yet
- Insertion and deletions in S gene
 - Del 69/70 may lead to target failure in some rt-RTPCR assays

Infection and clinical illness: Omicron Variant

- The variant has infected:
 - Fully vaccinated persons (unknown regarding boosted persons)
 - Persons recovered from Delta variant SARS-CoV-2 infection
- No systematically collected data yet on:
 - Spectrum of signs, symptoms, and severity
- South African public health authority has not officially reported any increase in the proportions of hospitalizations, ICU admissions, or deaths
- WHO reported Dec 1, reports of Omicron range from mild to severe, but full clinical profile poorly understood
 - Hospitalizations rising in RSA may be result of more cases not higher severity



- Unusually large number of mutations across the SARS-CoV-2 genome
 - **45-52 amino acid changes including deletions**, of which 26-32 are in the spike gene
- Some mutations well characterized with known phenotypic impact, but many others rarely observed until now and not well characterized
- Known mutations have raised theoretical concerns that the Omicron variant might:
 - Be more infectious and transmissible than the Delta variant
 - Resist neutralization by vaccine- and infection-induced antibodies
 - Resist treatment with therapeutics
 - Evade innate immunity

PCR-based proxy for new variant

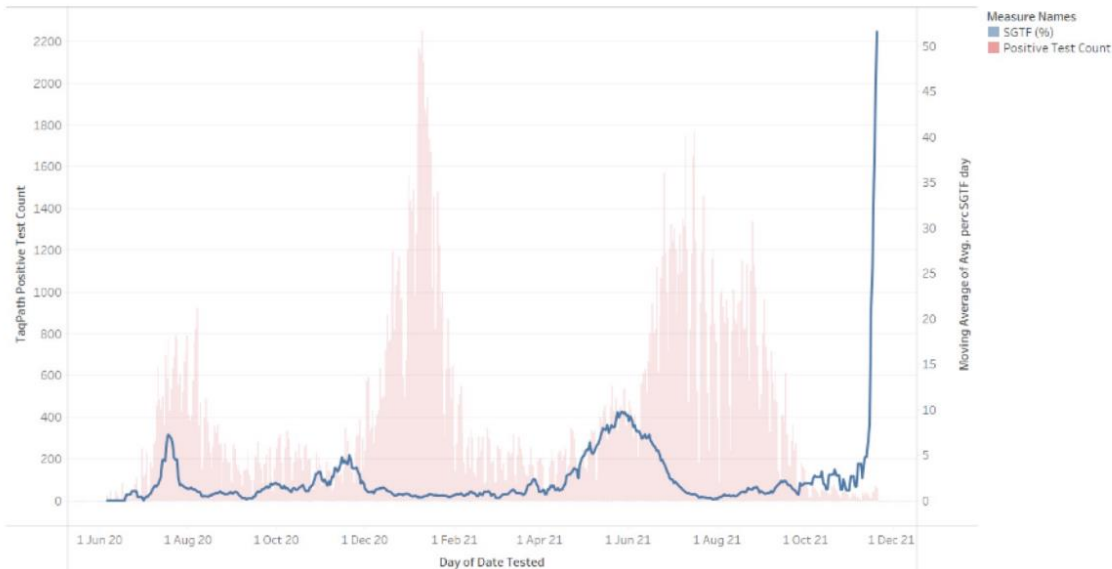
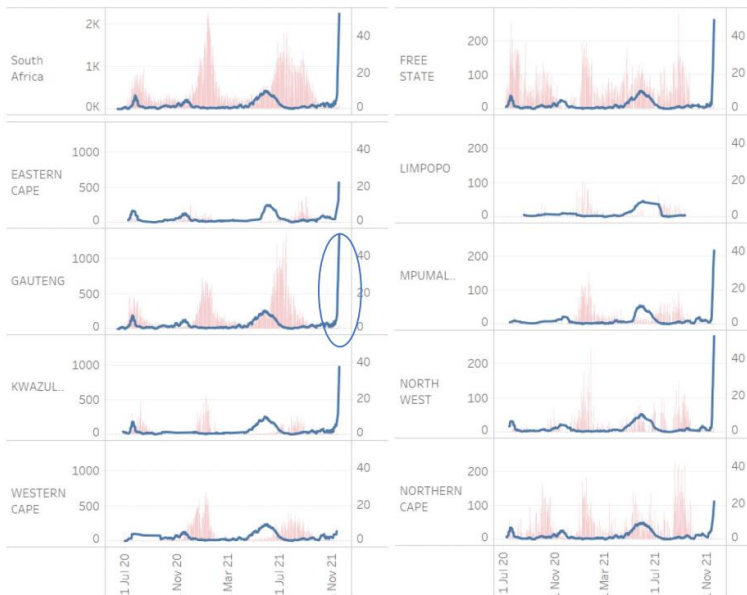


Figure 9: S-gene dropout (%) of cases with high VL (Ct value<30 for ORF or N gene). The red bars are the number of tests reporting the presence of SARS-CoV-2 (daily) on the TaqPath assay. The solid blue line is the moving median of S-gene dropout (%).

*Current (end of Nov '21) dramatically increasing trend in the proportion of SGTF (Ct value<30 for ORF or N gene)

- Variant can be detected with one particular PCR assay (before whole genome sequencing)
- New increase in S-gene dropout noted by NHLS and private labs very recently - from mid-November
- Now rapidly increasing in most provinces

S gene target failure by province



- Rapid increase in proportion with SGTF noted across multiple provinces (caution low number of tests in most provinces)
- 77 samples with SGTF sequenced from Gauteng (samples collected 12-20 Nov) – 77/77 (100%) were B.1.1.529
- Hundreds of recently collected samples being sequenced currently by NGS-SA labs – results available by end of week (today we received 70 samples from Gauteng 67/70 were SGTF and sequencing tonight, in KZN approximately 20%).

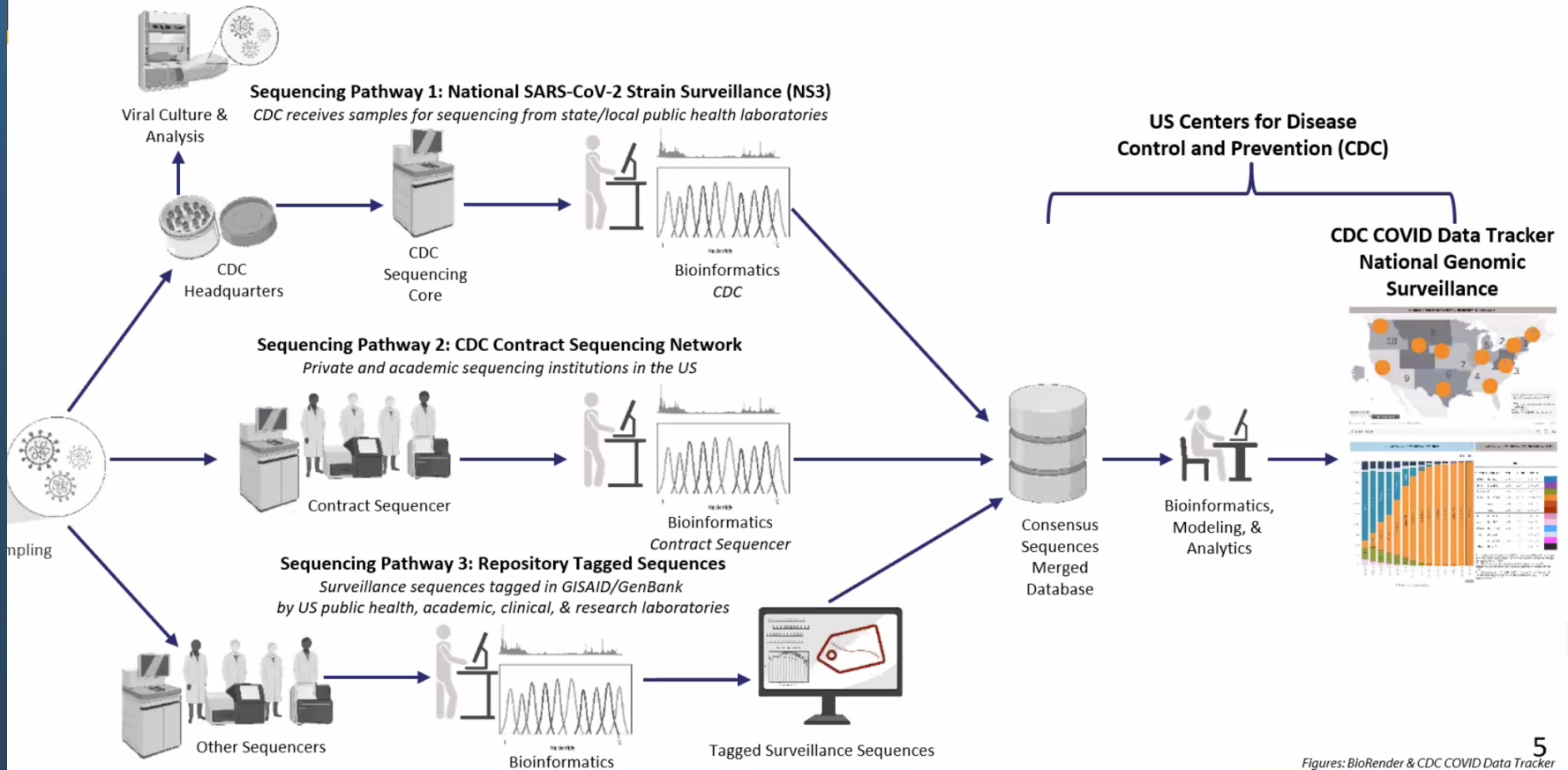
Courtesy of Lesley Scott and NHLS team

Vaccines and therapeutics

- Vaccines:
 - Expect decreased neutralization from vaccine and prior infection
 - Expect vaccines to remain effective against severe illness and death
 - Effects on cellular immunity unknown
- Monoclonals:
 - No virus-specific data for FDA-authorized and available monoclonals
- Antivirals:
 - No virus-specific data for remdesivir, molnupiravir, and PAXLOVID™

National SARS-CoV-2 Genomic Surveillance System: Data Workflow

November 2021



Delta >99.9% of US strains
 Enhancing SGTF interrogation

Summary

- Omicron has emerged in RSA, identified on 5 continents, [first case in US](#)
- High number mutations – novel and known concerning for predicting increased transmissibility and immune evasion
 - One mutation allows it to be detected/tracked by S-gene target failure on TaqPath
 - Demonstrating sustained increased incidence in Gauteng RSA, increased R_e
- Mutation profile predicted to give significant immune evasion and enhanced transmissibility: urgent work already started to understand full significance
- International travel disrupted
- With Omicron identified and Delta-driven global surge continuing, vaccines remain critical
 - mRNA vaccine modifications possible, if needed

Work needed to understand phenotypic impact: “We know *more* about what we *don't* know than what we *do* know”



Transmissibility



Vaccines



Risk of reinfection



Disease severity



Diagnostics

Q&A

Healthcare Provider & Public Health Partner Calls

- **1st and 3rd Thursday** of each month from 12:00-1:00 pm
(Next call will be December 16th)
- Webinar/call information (stays the same):
 - Zoom link: <https://nh-dhhs.zoom.us/j/94059287404>
 - Webinar ID: 940 5928 7404
 - Passcode: 353809
 - Telephone: 646-558-8656