

#### Agenda Cambridge COVID-19 Expert Advisory Panel 2 pm, Wednesday, May 26, 2021

Join with Google Meet

Join by phone

#### Welcome and Attendance

- 1) Clinical, case, vaccination and wastewater data update
- 2) Variant updates and global trends
  Daily COVID Cases in India, H5N8 outbreak article (see handouts)
- 3) Wastewater Surveillance discussion with Mariana Matos from Biobot (see handout)
- **4)** EAP Final Meeting on June 9th

#### Attachments:

- 1) Cambridge New Case Data (5/24/21)
- 2) MA Daily New Cases (5/24/21)
- 3) Cambridge Wastewater data (5/19/21)
- 4) INDIA Daily New Cases (5/24/21)
- 5) Highly Pathogenic Bird Flu Outbreak Already Reported in 46 Countries Science Alert (5/24/21)
- 6) Wastewater Surveillance Questions

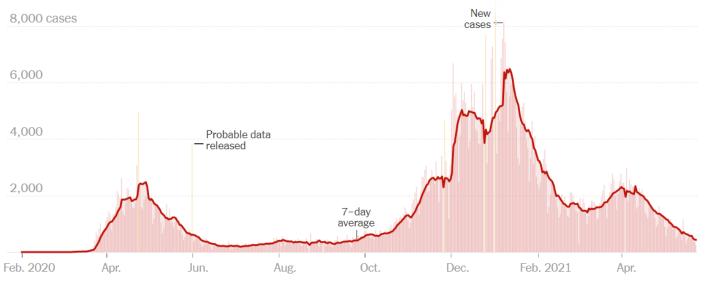




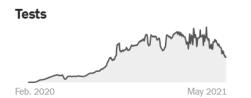
# MA Daily New COVID Cases 5\_24\_2021

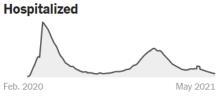
Updated May 25, 2021

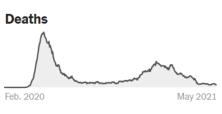




■ These are days with a reporting anomaly. Read more <u>here</u>.







	AVG. ON MAY 24	14-DAY CHANGE	TOTAL REPORTED
Cases	433	-51%	705,598
<b>T</b> .	47.000	040/	

### Vaccinations

**Fully vaccinated** 

51%

At least one dose

65%

See more details >

About this data

### Restrictions >

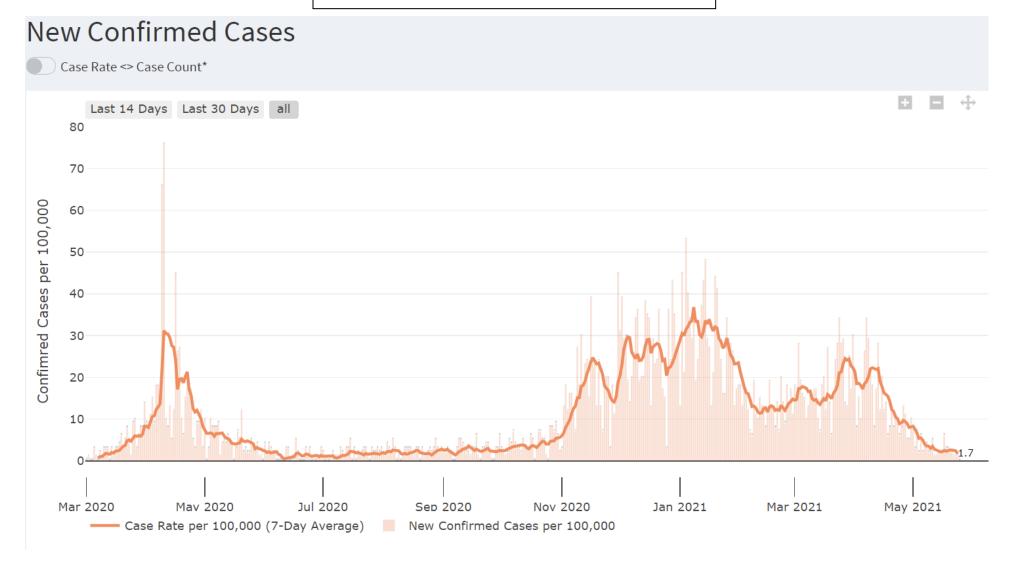
#### **Reopening May 29**

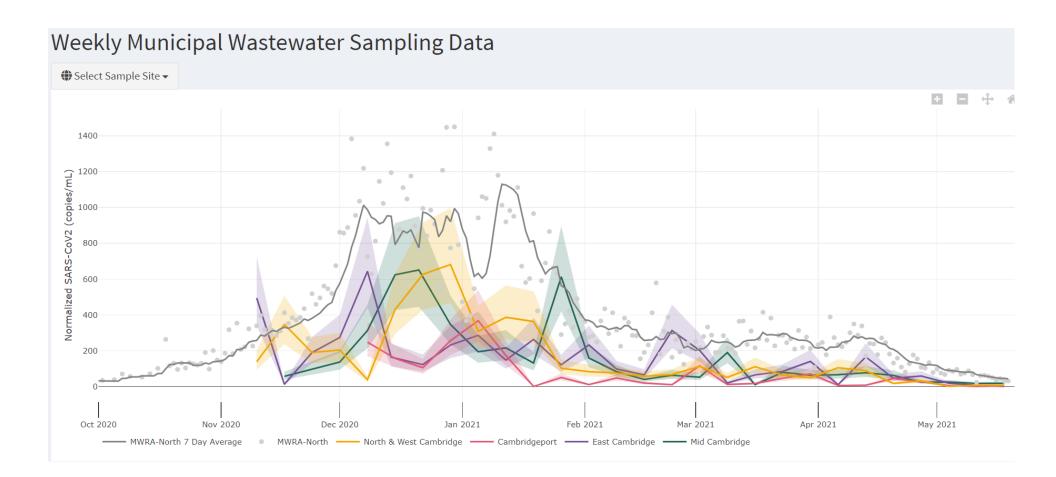
Masks required indoors

What's closed

Food and drink Bars

# Cambridge Daily New Cases 5/24/2021



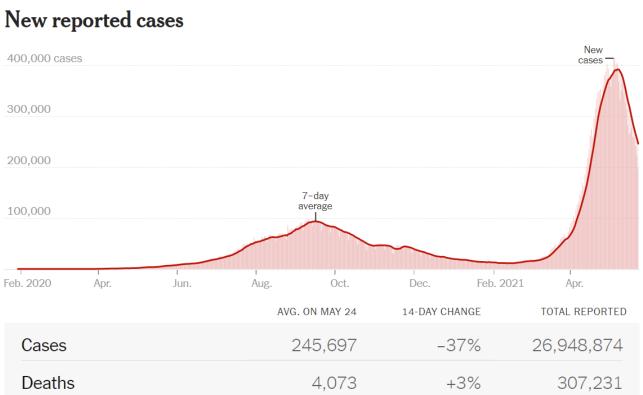


# Daily New COVID Cases in INDIA 5/25/21

### The New York Times

PLAY THE CROSSWORD

NEW: We are rolling out changes to our virus tracking pages. Read more here.



About this data

Q

### **Vaccinations**

**Fully vaccinated** 

3%

At least one dose

11%

See more details >

About this data

### Latest trends

 An average of 245,697 cases per day were reported in India in the last week. Cases have decreased by 37 percent from the average two weeks ago. Deaths have increased by 3 percent.



# Highly Pathogenic Bird Flu Outbreak Already Reported in 46 Countries, Scientists Warn

A pathologist swabs a wild duck for H5N8 in Rostock, Germany in 2014. (Carsten Koall/Getty Images)

**HEALTH** 

PETER DOCKRILL

24 MAY 2021

While the world was distracted with the rampant spread of a novel <u>coronavirus</u>, 2020 also witnessed an explosion in another deadly pathogen that could pose a threat to global public health.

<u>H5N8</u>, a subtype of highly pathogenic avian influenza virus (HPAIV), was identified decades ago, but during 2020 a series of emerging and ongoing H5N8 outbreaks in avian populations across dozens of countries have led to the death or slaughter of millions of birds worldwide.

"The affected geographic regions have been expanding continuously, and at least 46 countries have reported highly pathogenic H5N8 AIV outbreaks," virus researchers Weifeng Shi and George F. Gao write in a new perspective article in *Science*, warning of the dangers of H5N8 if we don't closely monitor and contain this worrisome trend.

While the most vulnerable animals to H5N8 are different kinds of birds (including farmed chicken and ducks, but also wild and migratory birds), human cases of the virus have also been discovered in recent times.

An outbreak of the avian flu in Russia in December 2020 jumped to poultry workers, with seven people on a farm in southern Russia showing signs of the infection – representing the first time H5N8 had ever been found in humans.

While that was a first for H5N8, it certainly wasn't a first for clades and subclades related to H5N8, nor for avian flu <u>viruses</u> in general.

"To date, there have been a total of 862 laboratory-confirmed human cases of infection with H5N1 reported to the <u>World Health Organization</u> (WHO), including 455 deaths," <u>Shi and Gao explain</u>. "These cases were from 17 countries, with ~76 percent from Egypt and Indonesia."

But zoonotic risks are only part of the problem with H5N8 and its ilk. In most of the recent outbreaks, a clade of H5N8 called 2.3.4 has become the dominant pathogen worldwide, first seen in a Chinese wet market in 2010.

"Clade 2.3.4 H5 AIVs, particularly the H5N8 subtype, have clearly displayed a propensity for rapid global spread in migratory birds," the researchers write, noting that these viruses also display evidence of constant evolution, genetically reassorting themselves with parts of other AIV subtypes.

Shi and Gao – respectively from China's Shandong First Medical University and the Chinese Center for Disease Control and Prevention – were among some of the first scientists to document the novel coronavirus in early 2020.

They note that the subsequent <u>COVID-19</u> <u>pandemic</u> – and the prevention and control measures world populations enacted in response – saw a sharp reduction in the spread of seasonal human influenza A and B viruses in the last year.

Nonetheless, in the same timeframe, a number of highly pathogenic H5Ny AlVs, including H5N1, H5N2, H5N5, and H5N8 subtypes, spread across China, South Africa, Europe, Eurasia, and elsewhere.

At the same time, <u>research has shown</u> that clade 2.3.4 viruses show particular cell-binding adaptations that could pose greater risks for human transmission, including potentially human-to-human transmissibility.

In all, the researchers say we need to significantly step up our surveillance of HPAIVs in poultry farms now, before these pathogens fly the coop.

"Because of the long-distance migration of wild birds, the innate capacity for reassortment of AIVs, the increased human-type receptor binding capability, and the constant antigenic variation of HPAIVs, it is imperative that the global spread and

potential risk of H5N8 AIVs to poultry farming, avian wildlife, and global public health are not ignored," <u>Shi and Gao write</u>.

The findings are reported in *Science*.



#### Wastewater Surveillance Questions and Topics

May 25, 2021

- \* Is there a plan to continue developing variant detection protocols for <a href="mailto:emerging strains">emerging</a> <a href="mailto:strains">strains</a> like B.1.617.2? We've discussed the challenges, once a variant become dominant (see B.1.1.7), since it no longer adds to our understanding of emerging and changing risks. Perhaps it makes more sense to use the regional signal for variants rather than samples from small catchment areas. There is frequently insufficient RNA to run for variants as it is.
- \* Is there any prospect of a deployable sampling protocol that isolates our <a href="https://high-risk\_locations">high-risk\_locations</a> (based on patterns observed over the past 15 months)? We have a small number of clusters lie sewersheds draining 3 of our larger long-term care facilities near Fresh Pond, and the public/subsidized housing cluster on Rindge Ave. Understanding that it introduces "hunches" and inconsistent surveillance, it seems like we should be able to focus on hotspots a little more when we are in surge.
- \* Any prospect of measuring antibody levels to observe the reduction of immune protection? Because long-term immunity isn't always reflected in antibody counts this might be misleading or if minimal value.
- \* Any other metrics of public health value we could start to collect during the same sampling events (weekly). Presumably the collection is the great proportion of the time/cost/effort and perhaps we can leverage that and show more value to the City of Cambridge.
- \* How much work has Biobot done on the temporal and transmission rate predictability of the viral counts in wastewater? Is the lag between wastewater signal spikes and case spikes highly variable from on district to another? Is it more reliable when drawing samples from a larger sewershed like MWRA?
- \* Regarding the temporal predictability, has the lag window between a wastewater spike and a case spike changed with any of the variants of concern?
- \* What is Biobot's experience with testing whole buildings. Is it useful in a workplace environment vs a residence? How large does the building population need to be and what proportion need to be infected for high signal to noise?

Looking forward to our discussion tomorrow.

Sam



