



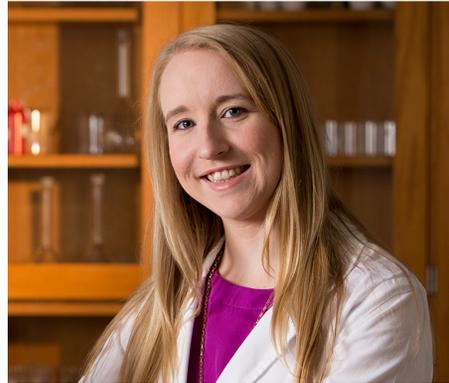
# REP Codes, NCBI Pathogen Detection, and SEDRIC

Jack Marr, MPH

June 24, 2025

# Introductions

Lauren Hudson, PhD



- Research Assistant Professor
- Dept. of Food Science
- University of Tennessee
- lkhudson@utk.edu

Jack Marr, MPH



- Epidemiologist
- Foodborne and Enteric Diseases
- Tennessee Department of Health
- jack.marr@tn.gov

# Agenda

- REP Codes
  - Understanding REP codes
  - Local REP codes, investigation, and monitoring
- **BREAK**
- NCBI Pathogen Detection
  - Cluster detection
  - Notification set-up
- SEDRIC
  - Cluster detection
  - Historical outbreaks and serotypes/species
- Next session, Discussion

# Learning Objectives

<b>REP codes</b>	Explain what REP codes are
	Understand benefits of tracking and investigating REP codes
	Identify, investigate document local REP codes
<b>NCBI</b>	Utilize the NCBI Pathogen Detection Portal for cluster investigation
	Set up email notifications for new isolates in cluster
<b>SEDRIC</b>	Utilize SEDRIC for cluster detection and investigation
	Utilize SEDRIC to obtain historical context for rare serotypes
<b>Overall</b>	Choose the appropriate cluster detection/identification tool (e.g., NCBI Pathogen Detection, SEDRIC) to use in different contexts

The logo consists of a red square containing the white letters 'TN' in a serif font. Below the red square is a thin dark blue horizontal bar.

**TN**

# Reoccurring, Emerging, and Persisting Enteric Bacterial Strains

# What are REP Codes?

- “Group of bacteria, closely related by whole genome sequencing, that continues to cause illness over time”
  - Intentionally vague
- Since 2019, CDC has used the PulseNet system to identify and monitor REP strains of several major pathogens, including:
  - *Salmonella enterica*
  - *E. coli* O157:H7
  - *Listeria monocytogenes*
  - *Campylobacter jejuni*

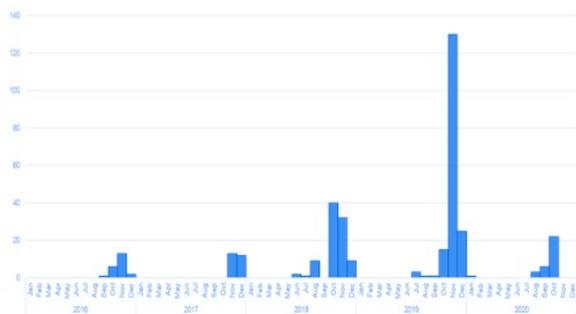
# What are REP Codes?

- Typical PH response – acute, investigation tied to single source, low genetic diversity to be specific
- ✨ Not! Like! Other! Bacteria! 🧴
  - **Reoccurring:** Repeatedly causing acute outbreaks separated by periods with no/low illness
  - **Emerging:** Previously novel or rare strains
    - (Show potential to) increase in cases
  - **Persisting:** Causing illnesses consistently over a long period of time
- Category may not be straight forward or change over time

<https://www.cdc.gov/foodborne-outbreaks/php/rep-surveillance/index.html>

# REP Strains

## Reoccurring Strain



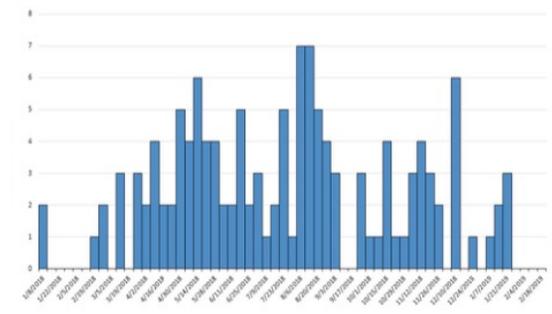
Strain that periodically causes a substantial number of illnesses, typically in outbreaks, separated by periods when it is not isolated from people or it causes very few illnesses

## Emerging Strain



Strain that causes illnesses that have increased in frequency, or have the potential to increase in frequency, over time

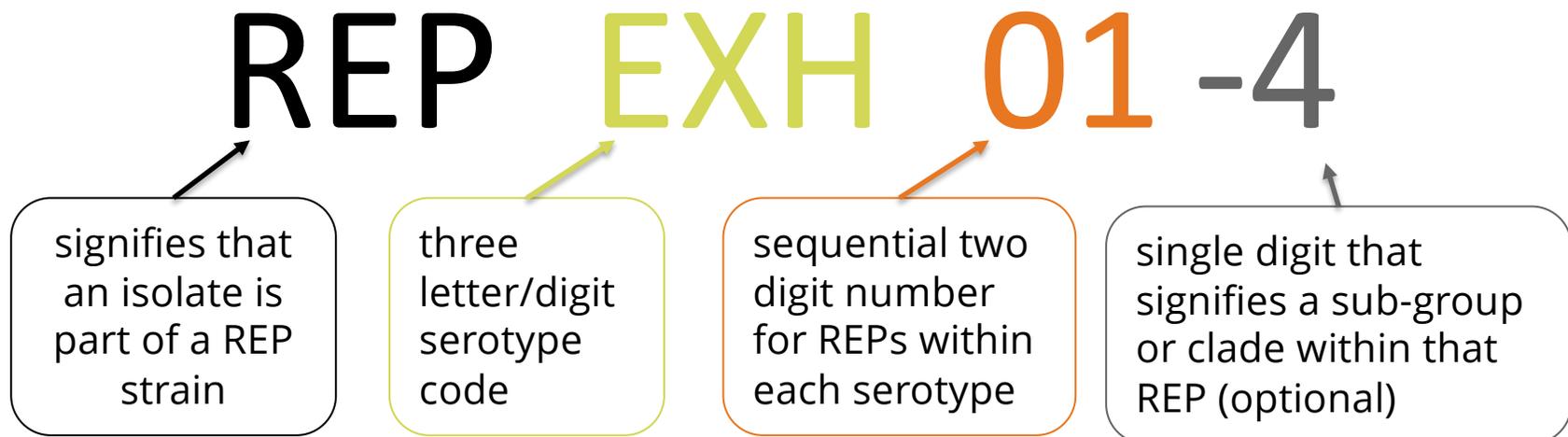
## Persisting Strain

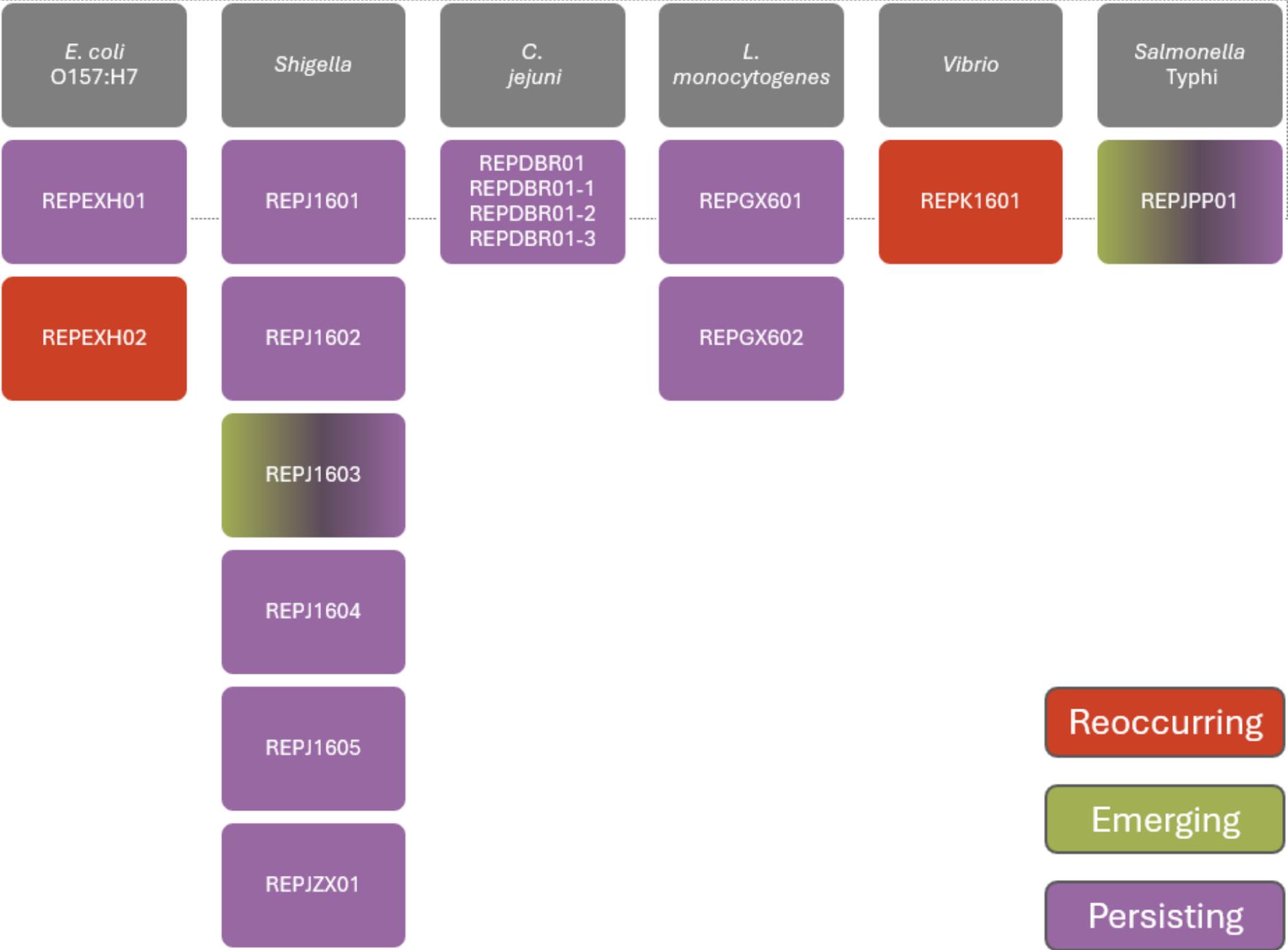


Strain that causes illnesses consistently over time, although the frequency of illnesses may fluctuate

# REP Strains

- Identifying a strain as a REP strain is based on many factors, including:
  - the number of illnesses, if increasing
  - the characteristics of the strain (e.g., multidrug resistance, high virulence, increased transmissibility)
  - if the strain is the cause of large or frequent outbreaks



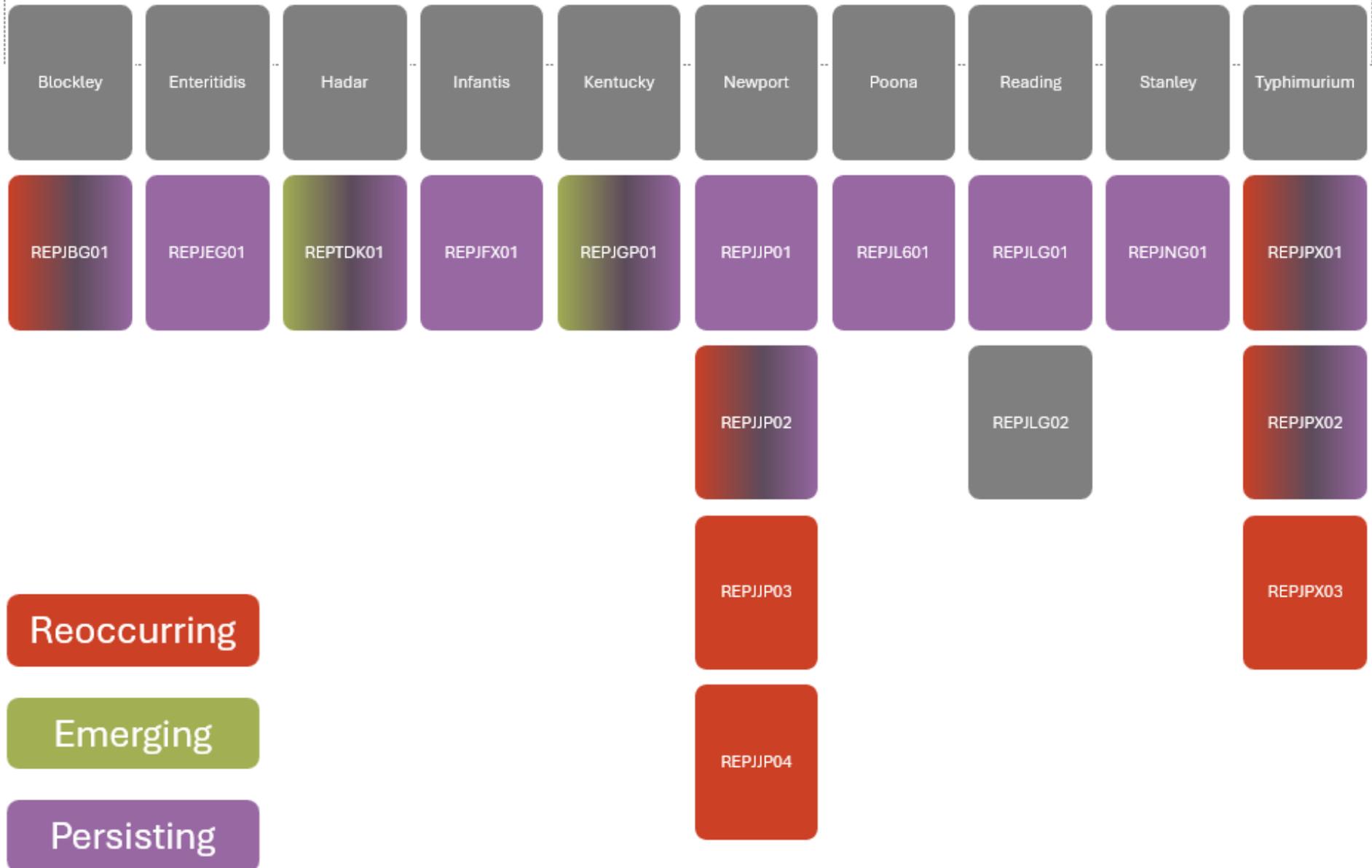


Reoccurring

Emerging

Persisting

# nontyphoidal *Salmonella*



# Emerging Illness – REPJPP01

## HIGHLIGHTS

- REPJPP01 is an emerging strain of extensively drug-resistant *Salmonella* Typhi, the bacteria that cause typhoid fever. This strain has caused illnesses in the United States since 2018.
- REPJPP01 has caused illness in travelers to Pakistan and neighboring countries and in people who did not leave the United States.
- Getting vaccinated against typhoid fever before international travel – especially to South Asia – and following safe eating and drinking habits while traveling can prevent illness.

What makes this “emerging”?

- ID’ed in Pakistan, now found in more countries including US not related to travel
- Antibiotic resistance – ceftriaxone initially, now some XDR

*Did you know: bacteria in REPJPP01 are within 13 alleles?*

# Persistent Illness – REPJPP01

## HIGHLIGHTS

- REPEXH01 is a persistent strain of Shiga toxin-producing *E. coli* O157:H7 bacteria that has caused illnesses and outbreaks in the United States.
- This strain has caused many outbreaks linked to different sources, such as recreational water, ground beef, and romaine lettuce.
- Additional research could help determine where this strain is coming from and how to prevent future illnesses.

What makes this “persistent”?

- Multiple outbreaks
- Variety of sources
- Unclear where strain is coming from

*Did you know: REPEXH01 includes 634 PN cases and 14 outbreaks!*

## Knowledge Check

REP stands for:

- A. Repeating, Emerging, and Persisting
- B. Repeating, Enteric, and Persisting
- C. Reoccurring, Emerging, and Persisting
- D. Reoccurring, Emerging, Problematic

## Knowledge Check

REP codes include:

- A. Three letter or digit serotype code
- B. R, E, or P for type of REP code
- C. Two-digit number for strains within each serotype
- D. A and B
- E. A and C

## Knowledge Check

**True or False:** REP strains can belong to more than one classification (i.e. reoccurring, emerging, persisting)

**True!**



**TN**

**TN REP Strain - Shiga toxin-producing *E. coli* Cluster with unknown link, 2023 to 2024\***

# Local REP Codes

- Currently, CDC monitors and tracks all REP codes in US through SEDRIC
- States can use the core principles of REP codes for themselves!
  - Reoccurring STEC cluster in TN

SALM1.0 - 6788.1.1.4x	SALM1.1-
58.68.73.1993	SALM1.1-
58.68.73.1993.2457	SALM1.1-
58.68.73.1993.2457.109548	SALM1.1-
58.68.73.1993.2457.114195	SALM1.1-
58.68.73.1993.2457.14658	SALM1.1-
58.68.73.1993.2457.164384	SALM1.1-
58.68.73.1993.2457.17700	SALM1.1-
58.68.73.1993.2457.18082	SALM1.1-
58.68.73.1993.2457.18439	SALM1.1-
58.68.73.1993.2457.25526	SALM1.1-
58.68.73.1993.2457.3078	SALM1.1-
58.68.73.1993.2457.38755	SALM1.1-
58.68.73.1993.2457.42783	SALM1.1-
58.68.73.1993.2457.49319	SALM1.1-
58.68.73.1993.2457.56160	SALM1.1-
58.68.73.1993.2457.5954	SALM1.1-
58.68.73.1993.2457.8056	SALM1.1-

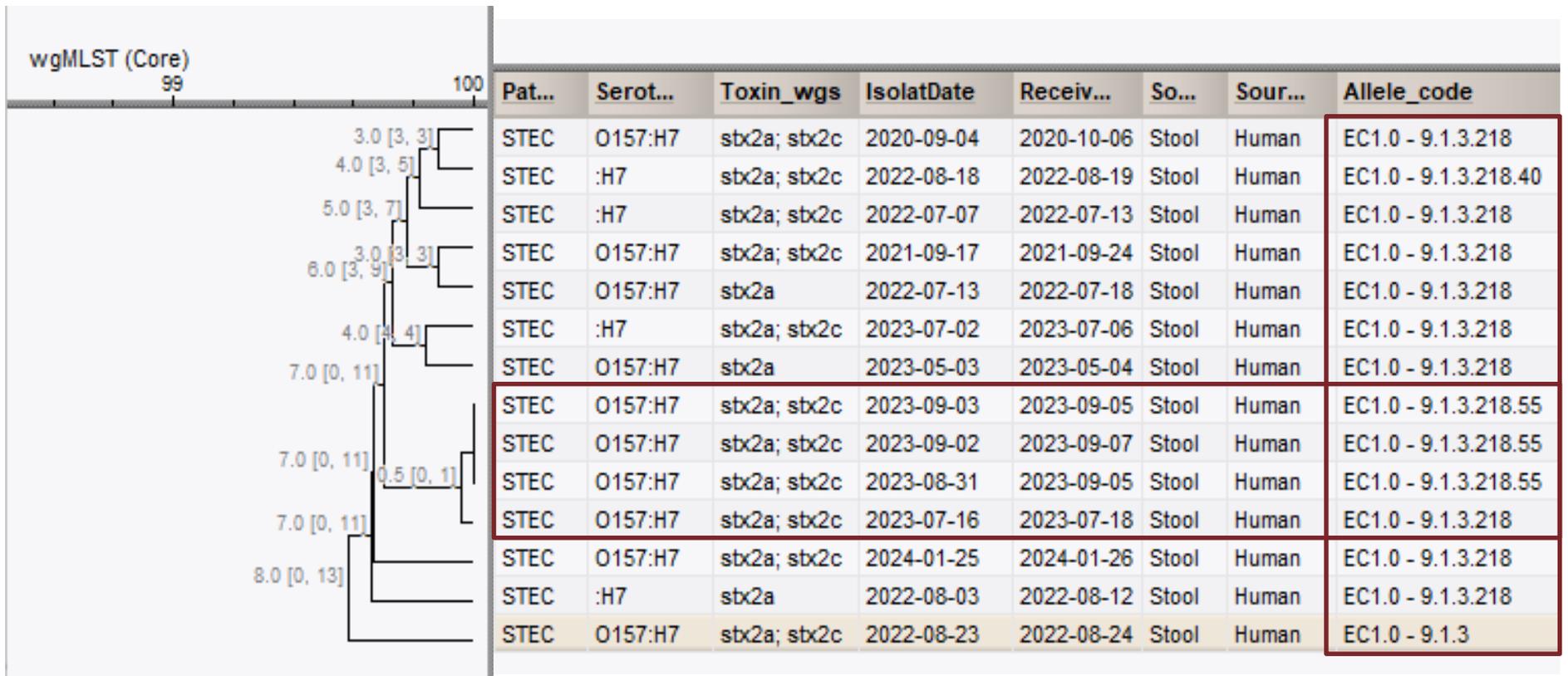
*REPJPP01  
allele codes*

58.68.73.1993.2457.8114	SALM1.1-
58.68.73.1993.2457.8376	SALM1.1-
58.68.73.1993.2457.89476	SALM1.1-
58.68.73.1993.2457.89534	SALM1.1-
58.68.73.1993.2457.89929	SALM1.1-
58.68.73.1993.2457.90628	SALM1.1-
58.68.73.1993.2457x	SALM1.1-
58.68.73.1993.2457x.14658	SALM1.1-
58.68.73.1993.2457x.164384	SALM1.1-
58.68.73.1993.2457x.18082	SALM1.1-
58.68.73.1993.2457x.213038	SALM1.1-
58.68.73.1993.2457x.3078	SALM1.1-
58.68.73.1993.2457x.47093	SALM1.1-
58.68.73.1993.2457x.5954	SALM1.1-
58.68.73.1993.2457x.8376	SALM1.1-
58.68.73.1993.33058	

# Notification and Review

- TDH was notified in May 2023, of a hospitalized STEC O157 case who developed hemolytic uremic syndrome (HUS) and subsequently passed away
  - Classified as a public health incident
- Review of cases in BN
  - Had the same or similar allele code to the 2023 case, but **not highly related (within 13 alleles)**
    - Multiple commonalities, particularly age
- In the late summer of 2023, received more cases with the same allele code including an outbreak at a daycare

# Case Investigations



\*Allele codes previous version

# Case Investigations

EC1.0 - 9.1.3.218 allele code\* with 15 TN cases

- Four cases belong to a daycare-related outbreak

17/18 are in children

Middle and West Tennessee

12/17 were hospitalized, 9 had HUS

Two deaths

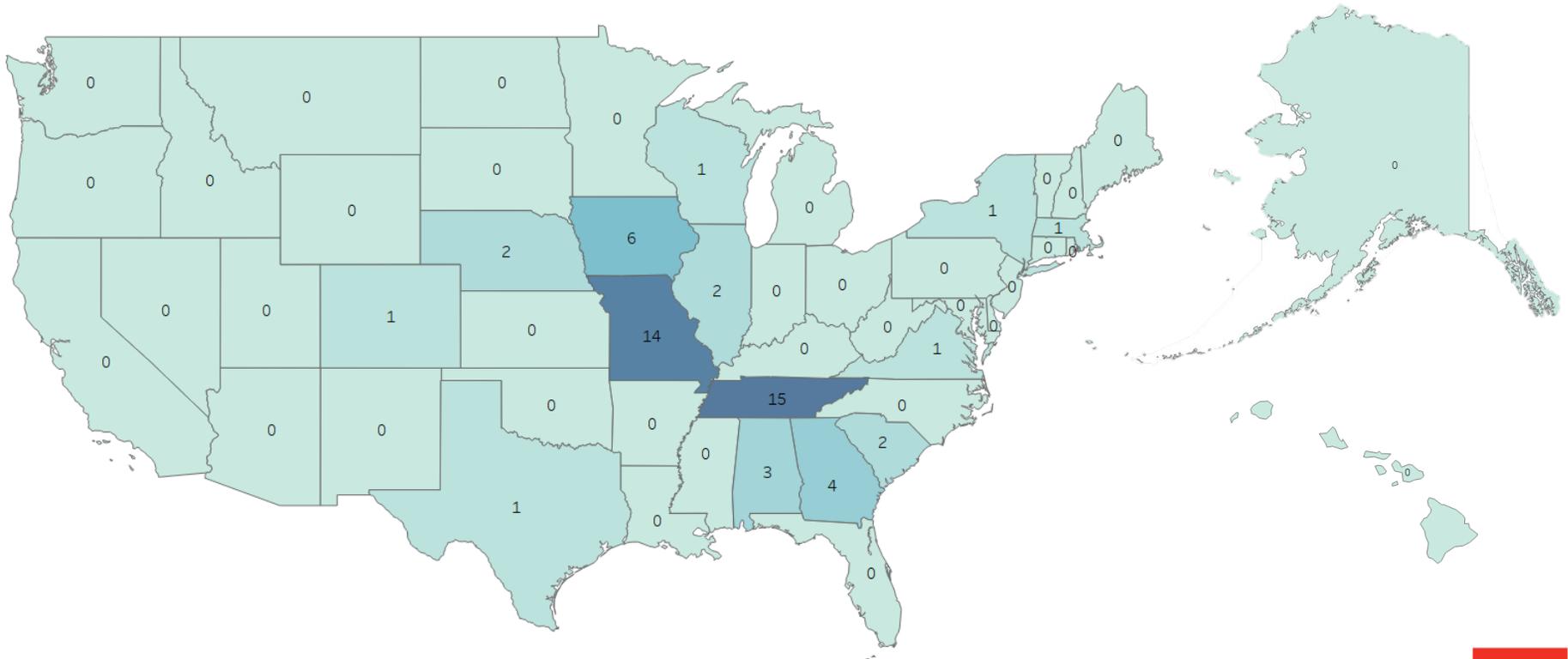


No signal or suspect source

*\*Allele codes previous version*

# Out of State Cases

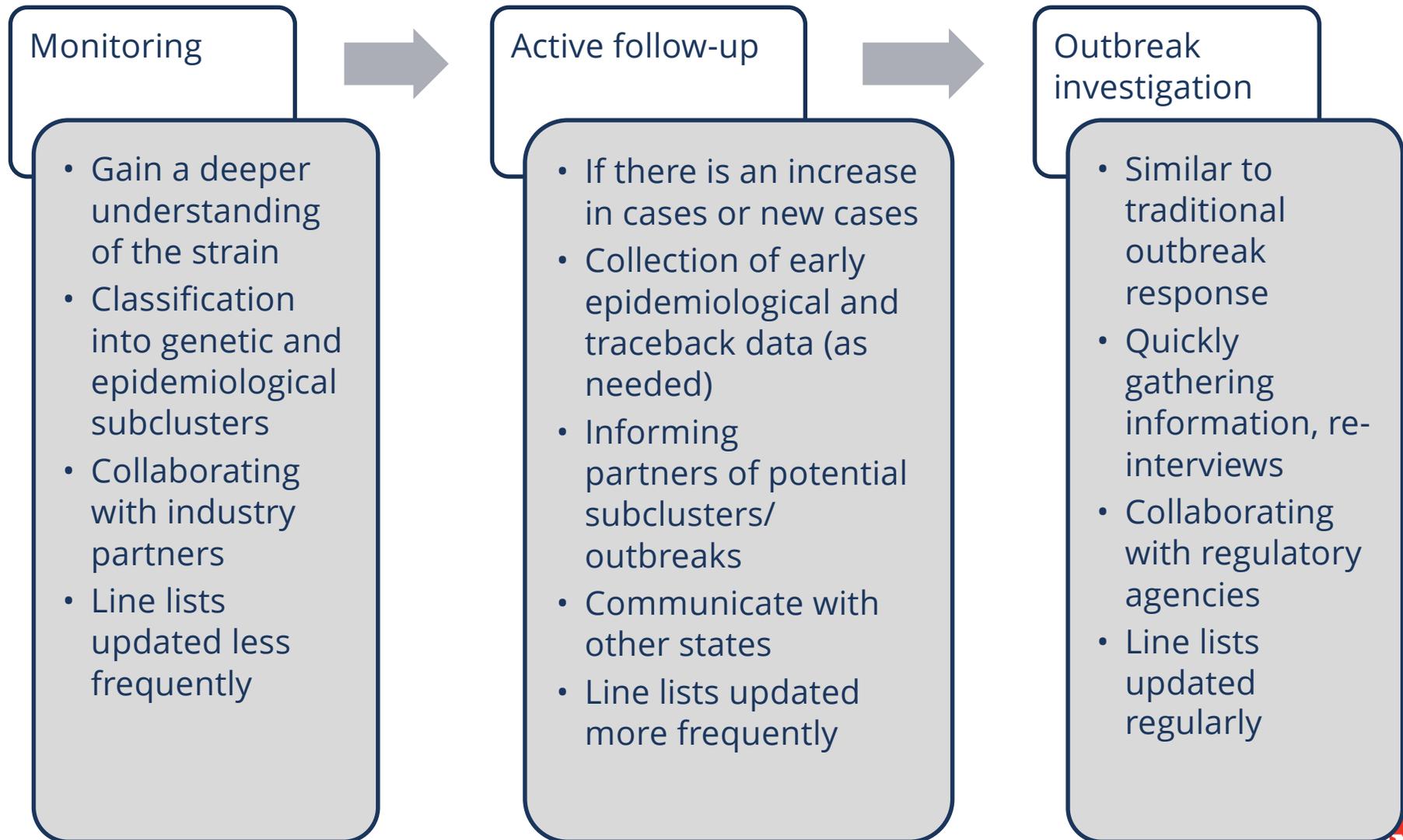
- As of 05/02/2024 there are 38 cases in 13 states
  - MO 14, IA 6, GA 4, AL 3, IL 2, NE 2, SC 2, CO 1, MA 1, NY 1, TX 1, VA 1, WI 1



## Conclusions – STEC cases

- Local REP code?
  - ✓ Reoccurs yearly between June and September
  - ✓ Geographically centered on West/Mid TN, nearby states
  - ✓ Severe illness among consistent group
- Atypical investigation
  - Primarily data review mixed with outbreak investigation
  - Large allelic difference vs. more specific parameters

# Monitoring & Investigating REP Strains



# Why Investigate REP Strains?

- Track how REP strains change over time
- Collaborate on measures to reduce spread
- Better understand transmission routes and sources
  - Prior investigation of settings, other factors
- Streamline future outbreak investigations involving the same strain
  - Guiding hypothesis generation
  - Create focused or supplemental questionnaires and/or to prioritize questions about related exposures during interviews

# Documentation and tracking

- Multistate REP codes tracked via internal REDCap
  - With all other local/MS clusters
- TN Local REP codes are not tracked
  - For future local REP codes – will likely implement similar system
  - Do keep records and files in usual secure drive
  - No naming convention yet
- Other state testimonials

# Documentation and tracking

<b>Investigation Status:</b>	<input type="text" value="Closed"/>   Change to CLOSED when investigation is complete.
Date Investigation Closed:	<input type="text" value="10-11-2023"/>  <input type="text" value="Today"/> M-D-Y
Reason Investigation Closed:	<input type="text" value="REP strain investigation complete"/>
<b>Date First Identified/CDC Notification:</b>	<input type="text" value="09-22-2023"/>  <input type="text" value="Today"/> M-D-Y
<b>Source of Notification:</b>	<input type="text" value="CDC"/>
<b>Cluster Jurisdiction:</b>	<input type="text" value="Multistate - CDC REP Strain"/>
<b>Organism:</b>	<input type="text" value="Listeria"/>
Species/Serotype:	<input type="text" value="monocytogenes"/>
Serotype Notes:	<input type="text" value="possibly linked to queso fresco-type soft cheeses"/> 
<b>Allele Code:</b>	<input type="text" value="LMO1.1 - 1.72.1.2"/>
<b>REP Code:</b>	<input type="text" value="REPGX602"/>

The logo consists of a red square containing the white letters 'TN' in a serif font. Below the red square is a thin dark blue horizontal bar.

TN

TM

# NCBI Pathogen Detection Tool with *Salmonella* Stanley Example

# Cluster Identification

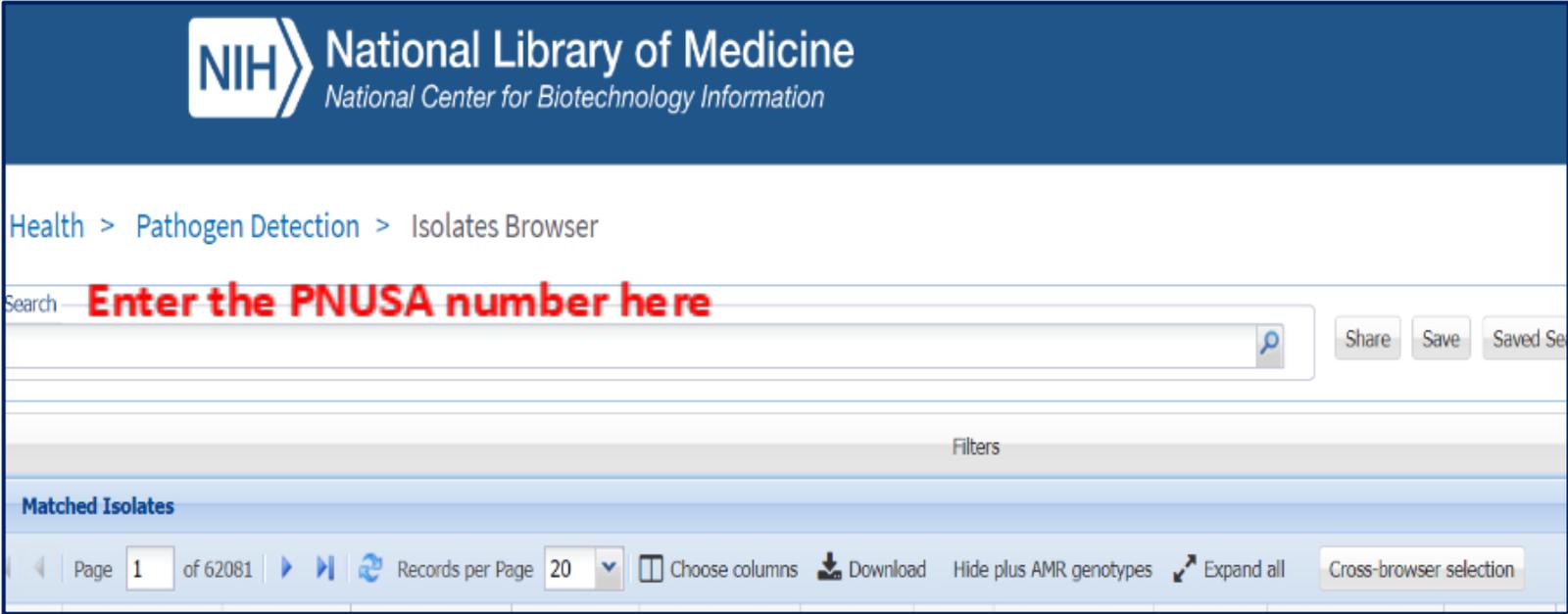
- *Salmonella* Stanley cluster, 0 alleles apart
  - Case A: 4-year-old boy in Northeast Tennessee
  - Case B: 58-year-old woman in West Tennessee
- Common exposure to small turtles
- NCBI and SEDRIC used to find more cases
  - Pulled cases within 20 SNPs in last year
  - One WA case with turtle exposure



# Using NCBI Pathogen Detection Isolates Browser

Search for cases in the National Center for Biotechnology Information (NCBI) Isolates Browser by using the **WGS ID** or **PNUSA #** into search bar to determine if there are any current or historical human, animal, or environmental on a national level are closely related to the cases in the cluster being investigated.

**Lookup: PNUSAS266798, PNUSAS266800**



The screenshot shows the NCBI Pathogen Detection Isolates Browser interface. At the top, the NIH logo and "National Library of Medicine National Center for Biotechnology Information" are displayed. Below this, the breadcrumb navigation reads "Health > Pathogen Detection > Isolates Browser". A search bar is present with the text "Enter the PNUSA number here" in red. To the right of the search bar are buttons for "Share", "Save", and "Saved Se". Below the search bar is a "Filters" section. The main content area is titled "Matched Isolates" and includes a pagination bar showing "Page 1 of 62081", a "Records per Page" dropdown set to "20", and buttons for "Choose columns", "Download", "Hide plus AMR genotypes", "Expand all", and "Cross-browser selection".

# Using NCBI Pathogen Detection Isolates Browser

Health > Pathogen Detection > Isolates Browser

Search  
PNUSAS306567

Filters

### Matched Clusters

#	Organism groups	SNP cluster	Matched isolates	Matched clinical isolates	Matched environmental isolates	Total isolates
1	Salmonella enterica	<a href="#">PDS000029636.628</a>	1	1	0	3013

**Click on the blue hyperlink to view the SNP tree**

### Matched Isolates

Page 1 of 1 | Records per Page 20 | Choose columns | Download | Hide plus AMR genotypes | Expand all | Cross-browser selection

#	Organism group	Strain	Isolate identifiers	Serovar	Isolate	Create date	Locat...	Isolation source	Isolation ...	SNP cluster	Mi
1	Salmonella ente...	PNUSAS306...	PNUSAS306567 SRS15338680	Newport	<a href="#">PDT001444502.1</a>	2022-10-06	USA		clinical	<a href="#">PDS000029636.628</a>	

# NCBI – Finding Neighbors

- Make a note of the PNUSA numbers of any isolates that are closely related in time and in SNP distance.
- The information in NCBI does not tell you what state an isolate (may say for environmental or animal isolates) is from.
- The **neighbors** button can automatically select closely related isolates.

Health > Pathogen Detection > Isolates SNP Tree Viewer

**SNP distances between selected isolates shown here**  
Salmonella - 3013 isolates  
PDG000000002.2497 / PDS000029636.628

**Isolates Selected** ✕ Clear

Distance between selected isolates :  
minimum = 11 SNPs, maximum = 11 SNPs, average = 11 SNPs

Target creation date range :  
2021-10-30 to 2022-08-02

Group by: Creation date

Isolation type	Location	Create ...	Min-same	Min-diff	Actions
<b>Year: 2022</b>					
clinical	USA	2022-0...	9	16	 
<b>Year: 2021</b>					
clinical	USA	2021-1...	10	17	 

**SNP tree showing selected isolates**

Filters

Share Show Table Labels Load Labels Neighbors Common subtree Watch Watched isolates

Spacing ▾ Export ▾ Search & Highlight in Tree

clinical, 2018-01-18, USA, stool, PNUSA010234, PDT000197088.2  
clinical, 2017-08-11, USA, stool, 2015AM-1894, PDT000232843.2  
clinical, 2017-04-05, USA, stool, PNUSA010896, PDT000200331.2  
clinical, 2021-08-18, USA, PNUSA0221272, PDT001110886.1  
clinical, 2021-01-22, PNUSA189962, PDT000939762.1  
clinical, 2017-08-11, USA, stool, 2015AM-1894, PDT000232843.2  
clinical, 2019-05-24, USA, PNUSA076272, PDT000505342.1  
clinical, 2018-05-29, USA, PNUSA077034, PDT000509560.1  
clinical, 2022-06-14, PNUSA276637, PDT001327890.1  
clinical, 2018-10-25, USA, PNUSA058828, PDT000396457.1  
clinical, 2022-08-08, USA, PNUSA288936, PDT001379751.1  
clinical, 2017-01-04, USA, stool, PNUSA006456, PDT000176336.2  
clinical, 2017-01-30, USA, stool, PNUSA006252, PDT000183174.2  
clinical, 2017-03-31, USA, stool, PNUSA010511, PDT000198463.2  
clinical, 2018-12-12, USA, PNUSA063511, PDT000416713.1  
clinical, 2018-09-25, USA, PNUSA054635, PDT000384422.1  
clinical, 2018-11-07, USA, PNUSA060372, PDT000403865.2  
clinical, 2017-04-05, USA, stool, PNUSA010892, PDT000200319.2  
clinical, 2017-04-05, USA, stool, PNUSA010889, PDT000200334.2  
clinical, 2018-03-22, USA, stool, PNUSA035800, PDT000296807.2  
clinical, 2022-10-06, USA, PNUSA306567, PDT001444502.1  
clinical, 2019-12-12, USA, 2016AM-0581, PDT000644025.1  
clinical, 2022-09-19, USA, PNUSA301261, PDT001425151.1  
clinical, 2021-10-30, USA, PNUSA240458, PDT001164774.1  
clinical, 2022-06-02, USA, PNUSA267829, PDT001377431.1

**Can find additional isolates on tree by putting in PNUSA # in this search bar or using the neighbor button.**

# NCBI – Download Data

The screenshot displays the NCBI interface for downloading data. A table of Salmonella isolates is shown, with columns for #, Organism group, Strain, Isolate identifiers, Serovar, Isolate, Create date, Location, Isolation source, and Isolation ... . The table contains 5 rows of data. A 'Download' button is highlighted in the top right corner of the table. A 'Download' dialog box is open, showing options for downloading the selected data. The dialog box includes a 'Selected only' checkbox, a 'Data type' dropdown menu set to 'Table', a 'Type' dropdown menu set to 'Excel (.csv)', and a 'Name' text box containing 'isolates.csv'. The dialog box also indicates that 2 isolate record(s) will be downloaded. The 'Download' and 'Cancel' buttons are visible at the bottom of the dialog box.

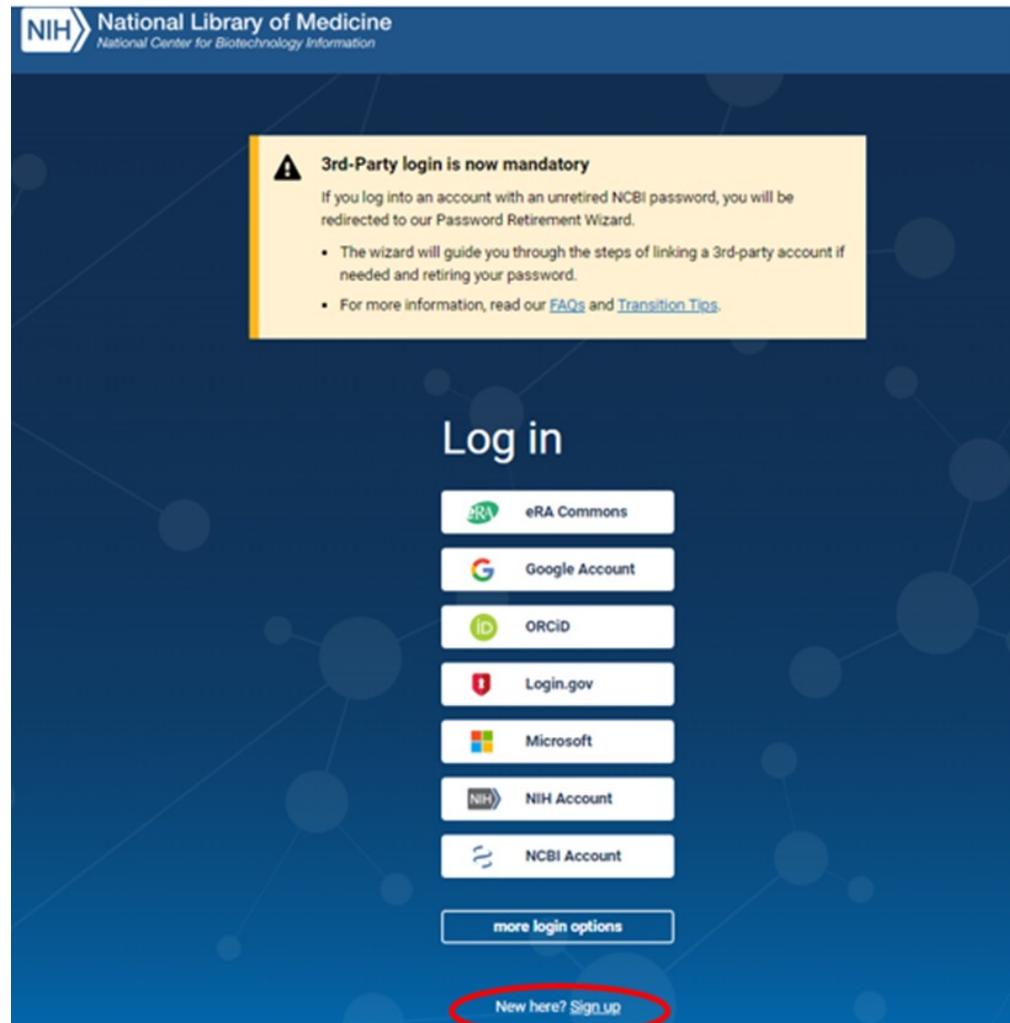
#	Organism group	Strain	Isolate identifiers	Serovar	Isolate	Create date	Location	Isolation source	Isolation ...
<input checked="" type="checkbox"/>	Salmonella ente...	PNUSAS266...	PNUSAS266798 SRS12658296	Stanley	PDT001290457.1	2022-04-19	USA		clinical
<input checked="" type="checkbox"/>	Salmonella ente...	PNUSAS266...	PNUSAS266800 SRS12658294	St...					clinical
<input type="checkbox"/>	Salmonella ente...	PNUSAS033...	PNUSAS033797 SRS3022036						clinical
<input type="checkbox"/>	Salmonella ente...	534775	534775 534775.biosample SRS3392885	St...				human	clinical
<input type="checkbox"/>	Salmonella ente...	531229	531229 531229.biosample SRS3547989	St...				human	clinical

Download dialog box details:

- Selected only:
- Data type: Table
- Type: Excel (.csv)
- Name: isolates.csv
- 2 isolate record(s)
- Buttons: Download, Cancel

# Using NCBI Pathogen Detection Isolates Browser

To get notified of new isolates added to a cluster in NCBI, please create an account first or sign in if you have an account.



The screenshot shows the NCBI login page. At the top left is the NIH logo and the text "National Library of Medicine National Center for Biotechnology Information". A yellow warning box in the center contains the following text:

**⚠ 3rd-Party login is now mandatory**  
If you log into an account with an unretired NCBI password, you will be redirected to our Password Retirement Wizard.

- The wizard will guide you through the steps of linking a 3rd-party account if needed and retiring your password.
- For more information, read our [FAQs](#) and [Transition Tips](#).

Below the warning box is the "Log in" section, which includes a list of login options:

- eRA Commons
- Google Account
- ORCID
- Login.gov
- Microsoft
- NIH Account
- NCBI Account

There is a "more login options" button below the list. At the bottom of the page, the text "New here? [Sign up](#)" is circled in red.

# Using NCBI Pathogen Detection Isolates Browser

- Above the tree there is an icon that looks like an eye and is labeled **“Watch”**.
- Click it and then name the isolate/cluster a unique name so you’re able to identify what cluster it is in reference to (ex. S. Liverpool cluster).
- Adjust the SNP distance to get notified of any isolates related to the one being watched within the threshold. Click **“Save”**.

The screenshot shows the NCBI Pathogen Detection Isolates Browser interface. At the top, there is a toolbar with several buttons: Share, Hide Table, Labels, Load Labels, Neighbors, Common subtree, Watch, and Watched isolates. The 'Watch' and 'Watched isolates' buttons are highlighted with red boxes. Below the toolbar, there is a search bar and a 'Spacing' dropdown menu. The main area displays a phylogenetic tree on the left and a 'Watched Isolates' table on the right. The table has columns for '#', 'Name', 'Original accessions', 'Distance', 'Original', 'Current', 'Cluster', and 'Delete'. The 'Delete' column contains trash icons for each row. The 'Watched Isolates' table is also highlighted with a red box.

#	Name	Original accessions	Distance	Original	Current	Cluster	Delete
1	TN22-032	5	5	🔍	🔍		🗑️
2	Stanley	15	8	🔍	🔍	🌲	🗑️
3	test	2	4	🔍	🔍	🌲	🗑️

## Knowledge Check

Isolates can be searched for in NCBI with:

- A. PNUSA or WGS IDs
- B. Lab accession number
- C. Investigation ID
- D. None of the above

## Knowledge Check

**True or False:** Only one isolate can be searched for at a time in NCBI.

**False!**

## Knowledge Check

What button does NOT appear in NCBI?

- A. Neighbors
- B. Watch
- C. Watched Isolates
- D. Show State Origin
- E. Labels

The logo consists of a red square containing the white letters 'TN' in a bold, serif font. Below the red square is a thin blue horizontal bar.

TN

**SEDRIC Cluster  
Detection with  
*Salmonella* i4:i- Example**

# Background

- On October 15, 2024, the TN FED Program identified 2 genetically related cases of Salmonella I 4:i- residing in Shelby County
- By December 10, 2024, 9 cases were identified via NCBI:
  - 5 Memphis/Shelby Co. (MSR)
  - 1 Illinois
  - 1 Mississippi
  - 1 Ohio
  - 1 Texas

# Laboratory Analysis

9

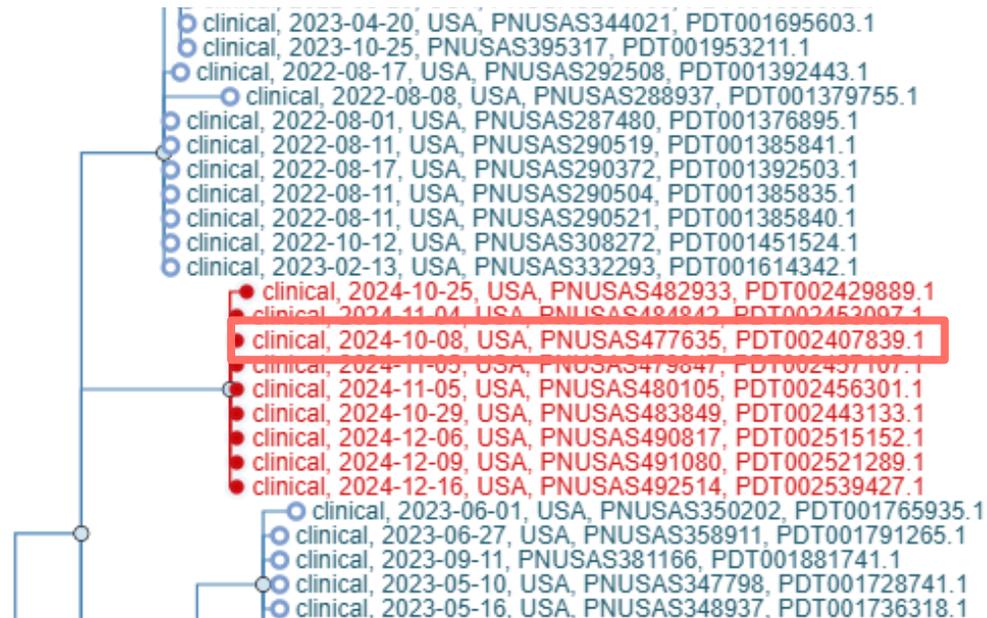
## Isolates Selected ✕ Clear

Distance between selected isolates :

**minimum = 0 SNPs, maximum = 1 SNPs, average = 0 SNPs**

Target creation date range :

**2024-10-08 to 2024-12-16**



# SEDRIC isolates

- Use PNUSA number
  - ID isolates, demos, basic information
  - Find state contact for additional information

**Public Health Contacts**

**Filters**

First Name: contains search  
Last Name: contains search  
State: IL X  
Contact Type: any of these contact types  
Email Address: contains search  
Government Level: any of these levels

Copy Emails Draft Email New Edit Delete

First Name	Last Name	Email Address	Primary Phone	State	Level	Contact Type	Position	Comments	Updated
[REDACTED]	[REDACTED]	[REDACTED]	[REDACTED]	IL	State	VET;Outbreaks;List Outbreaks;Zoonoti Outbreaks;Water Outbreaks	NORS Admin/SPHV	VET; Listeria contact	2024-04-29

PNUSAS477635

# SEDRIC

- How to find
  - Historical information, rare serotypes
    - Can search for a serotype or species with SEDRIC event filter to find historical outbreaks

The screenshot displays the SEDRIC search interface. At the top, there is a search bar with a magnifying glass icon, a dropdown menu set to 'All', and the search query 'salmonella stanley'. Below the search bar, there are navigation tabs: 'All' (2.60M), 'Objects' (2.60M), 'Object types' (2), and 'Artifacts' (14). The 'Objects' tab is selected. On the left side, there is a sidebar with 'Object type filters'. It includes a search box for filters, a filter for 'FDA Cara Outbr...' with a warning icon and a count of 5, and a filter for '1. SEDRIC Event' with a globe icon and a count of 3.40k. The main content area shows a list of results under the heading '1. SEDRIC EVENT 3.40k'. Two results are visible: '2403MLJNG-1' with Serotype: Stanley and Pathogen: Salmonella, and '2405MLJNG-2' with Serotype: Stanley and Pathogen: Salmonella.

- Other cases: use cluster detection tool!

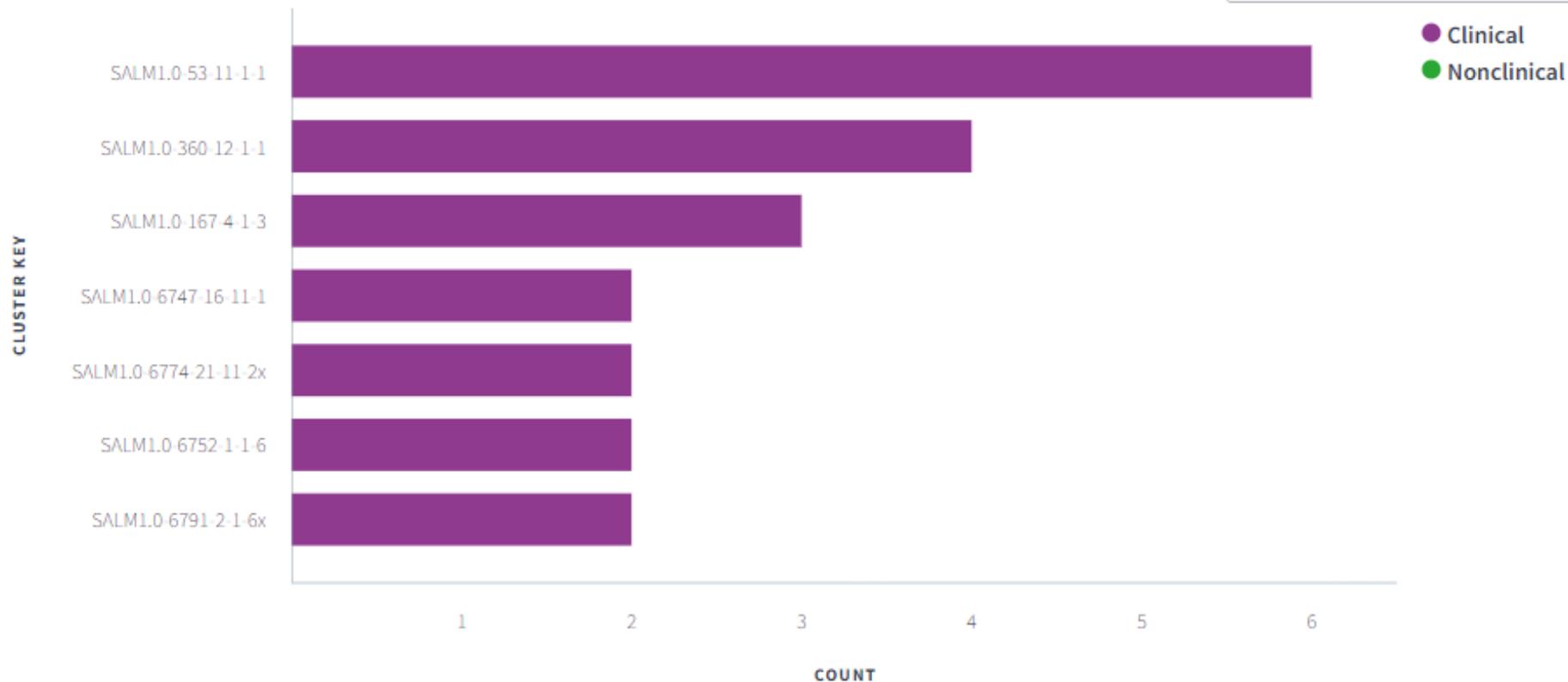
# SEDRIC Cluster Detection

- On main page, select SEDRIC, then Cluster Detection
- Settings
  - 3 month window with two isolates minimum
    - Min. of 4 allele digits for Salmonella, STEC
    - Min. of 5 allele digits for Salmonella for Enteritidis, Javiana, Newport, Typhimurium, I4i-, Campylobacter
    - X codes – Checking NCBI for these to identify sub-clusters, SNP threshold for x code clusters
- Threshold for investigation may increase/decrease based on season and capacity
  - Highly clonal serotypes/species = higher threshold

# SEDRIC Cluster Detection

## Detected Clusters

Stratify by:



# SEDRIC Cluster Detection

## Selected Isolates

<input type="checkbox"/>	Key	▲ Outbreak	◅ Allele Code	◅ Serotype	◅ WGS ID	◅ Isolation Date
<input type="checkbox"/>	TN_██████████	2404MLAFR-1	SALM1.0 - 2871.1.1.19.1.1	Africana	PNUSAS432729	2024-04-09
<input type="checkbox"/>	TN_██████████	2404MLAFR-1	SALM1.0 - 2871.1.1.19.1	Africana	PNUSAS436186	2024-04-22
<input type="checkbox"/>	TN_██████████	2404MLAFR-1	SALM1.0 - 2871.1.1.19.1.1	Africana	PNUSAS437316	2024-04-27
<input type="checkbox"/>	TN_██████████	2404MLAFR-1	SALM1.0 - 2871.1.1.19.1.1	Africana	PNUSAS437319	2024-04-03
<input type="checkbox"/>	TN_██████████	2404MLAFR-1	SALM1.0 - 2871.1.1.19.1.1	Africana	PNUSAS437327	2024-04-26

# Pros and cons

- Cons
  - Fewer clusters detected compared to PN 2.0
    - Typically highly clonal species/serotypes e.g. Enteriditis
    - Some shorter allele codes can be missed
  - Cannot detect *Shigella*, non-jejuni *Campylobacter* clusters
- Pros
  - Easier access than PulseNet!
  - Higher threshold, lower number of clusters to investigate
  - Can include additional states, demographic filters

# NCBI and SEDRIC Investigation Summary

## NCBI

- Search using PNUSA #s/WGS ID
- SNP-based dendrogram trees
- Used to find related national and environmental isolates (“neighbors”)
- Can “watch” isolate and get emails when new related isolates are added
- No state or demographic information, public access

## SEDRIC

- Limited access
- Search using PNUSA numbers found in NCBI, serotype, or allele code
- No dendrogram trees; use cluster detection application with allele distance
- Great for finding related national, historical, and environmental isolates by allele code/serotype (if uncommon)
- Demographic, state and sometimes exposure information are available
- Find state or national contacts to find for additional data

## Knowledge Check

What information can you find in SEDRIC?

- A. Basic demographic data of isolates
- B. Contact information
- C. Isolates with a specific allele code
- D. All of the above
- E. None of the above

## Knowledge Check

Connect the data system with units of genetic difference.

PulseNet ————— Alleles

NCBI Allele Codes  
SED RIC SNPs

# Final Session

- Tuesday July 1<sup>st</sup> 1-2PM EST
- Please complete survey!
- Topics
  - Data visualization
    - Tableau
    - SatScan
  - Communication
    - Communicating WGS results
    - Standard phrasing
  - PulseNet 2.0
    - How to get access

# Questions?