

#### CDC Organizational Update and Status of Foodborne Illness Trends

Robert Tauxe, MD, MPH Director Division of Foodborne, Waterborne, and Environmental Diseases

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#### **CDC Organizational Updates**

- New Division: Coronavirus and Other Respiratory Viruses Division (CORVD)
- National Wastewater Surveillance System → Division for Infectious Disease Readiness & Innovation (DIDRI)
- Division of Parasitic Diseases and Malaria → National Center for Emerging and Zoonotic Infectious Diseases

#### **DFWED Staffing Updates**

- New leadership in Enteric Diseases Epidemiology Branch
  - Jennifer Cope
  - Kristina Angelo
- Beau Bruce has transitioned to the Center for Forecasting and Outbreak Analytics, and Patricia Griffin has retired
- Megin Nichols (Deputy Director) has returned from her detail to the Office of Tribal Affairs and Strategic Alliances (OTASA)



## Cronobacter

- Summer 2023: Invasive infant infections with *Cronobacter* was added to list of nationally notifiable diseases in collaboration with the Council of State and Territorial Epidemiologists
- Effective on January 1, 2024, with state-by-state action to add to their process
- Waiting for final OMB approval to collect this information

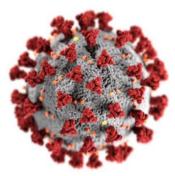
# National Notifiable Diseases Surveillance System and Collaboration for Prevention

- Accurate estimates of the yearly number of U.S. cases
- Information on where diseases occur, how they are transmitted, common risk factors, and opportunities for prevention
- CDC will continue working with partners on all aspects of *Cronobacter* surveillance



### Impact of COVID-19 on Surveillance and Reporting

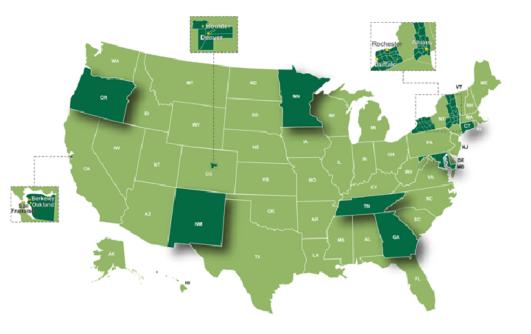
- COVID-19 was a major stress on the system
- Factors connected to COVID-19 influencing transmission, detection, and reporting:
  - Interventions to limit the spread of COVID-19
  - Decreases in international travel
  - Changes in healthcare-seeking behaviors and diagnostic testing practices
  - Reduced capacity for health department staff to investigate illnesses and collect, clean, and transmit data
- Surveillance rebounding to pre-pandemic levels of reporting



#### FoodNet

- Active population-based surveillance
- Collaboration among CDC, 10 FoodNet sites, FDA, USDA/FSIS
- 8 pathogens commonly spread through food and pediatric hemolytic uremic syndrome
- Reliable and up-to-date data on illness trends online for 1996 – 2022

#### FoodNet Surveillance Area





### **2022 FoodNet Annual Report**

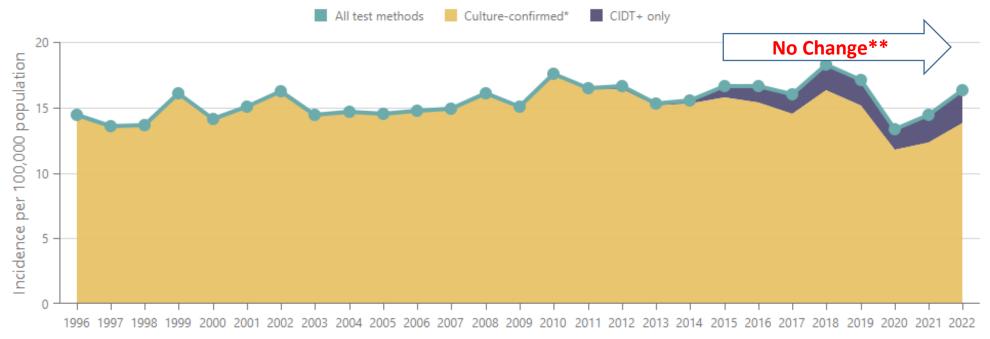
Measuring progress toward foodborne illness prevention

Pathogen	Change from baseline	Rate in 2022 per 100,000 people	<b>Target rate</b> based on Healthy People 2030 goals
Campylobacter	7%	17.4	10.9
Cyclospora	430%	0.6	None
Listeria	No change	0.26	0.22
Salmonella	No change	14.5	11.5
Shigella	No Change	3.9	None
<b>STEC</b> Shiga toxin-producing <i>E. coli</i>	No change	4.6	3.7
Vibrio	54%	0.9	None
Yersinia	144%	1.9	None

Rates & targets are numbers of infections per 100,000 people per year. They include domestically acquired infections detected by culture or culture-independent methods. Targets based on Healthy People 2030 goals, which were set using average annual incidences during 2016–2018. No change indicates that the 95% credible interval of the percentage change included zero. For more information, visit cdc.gov/FoodNet.

#### Salmonella Infections

- HP 2030 target of 11.5 infections per 100,000 population (incidence rate, or IR)
- Relative to the 2016-2018 baseline used for measuring progress toward HP 2030, in 2022 there was:
  - No change in the total number of infections (IR=16.3)
  - No change in the number of domestically acquired infections (IR=14.5)

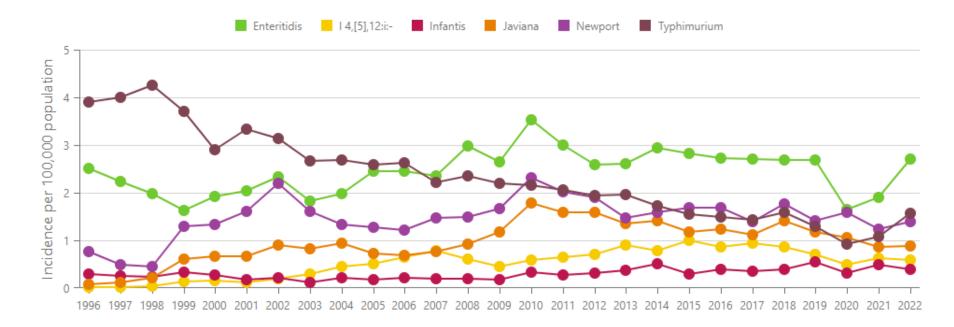


\* Culture-confirmed includes those infections confirmed by culture only or by culture following a positive CIDT.

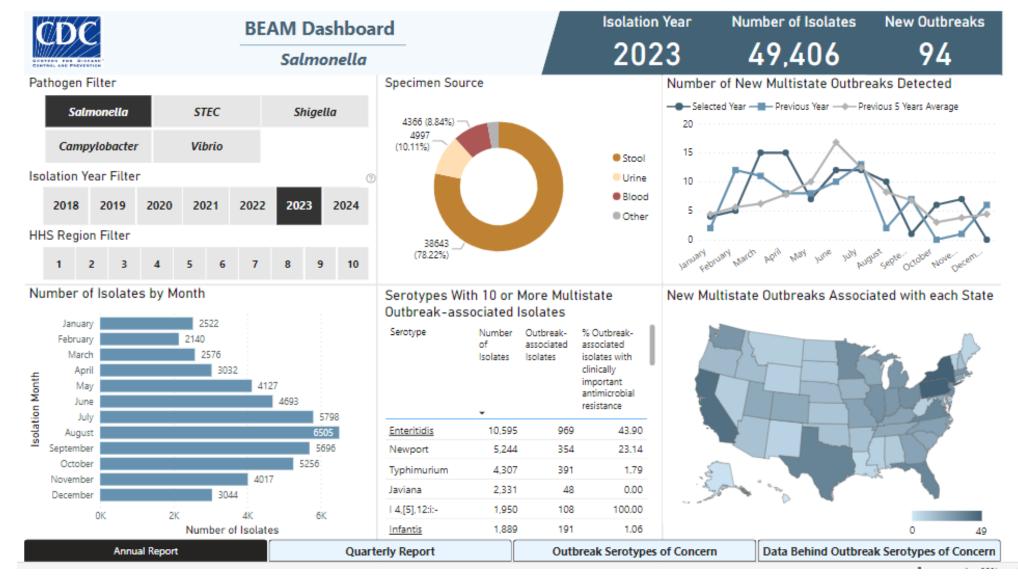
\*\* This graph shows data for domestically-acquired and international-associated infections. When subset to only domestically-acquired infections, we still see no change in incidence in 2022 relative to the 2016-2018 baseline.

#### Salmonella Serotypes

- Relative to the 2016-2018 baseline used for measuring progress toward HP 2030, in 2022 there was:
  - 18% decrease in the incidence of *S*. Typhimurium infections
  - 34% decrease in the incidence of *S.* I 4,[5],12:i:- infections
  - No change in the incidence of S. Infantis, S. Newport or S. Enteritidis infections



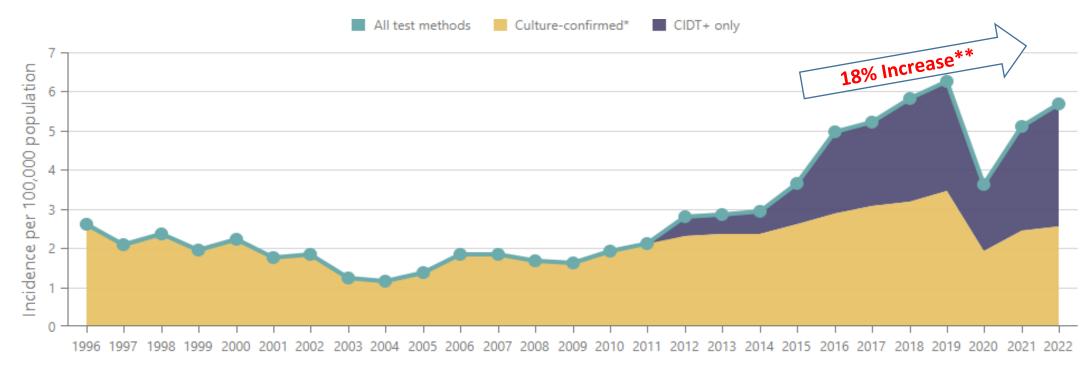
#### **BEAM Dashboard:** Salmonella 2023



https://www.cdc.gov/ncezid/dfwed/BEAM-dashboard.html

### Shiga-toxin Producing E.coli Infections

- HP 2030 target of 3.7 infections per 100,000
- Relative to the 2016-2018 baseline used for measuring progress toward HP 2030, in 2022 there was:
  - 18% increase in the total number of infections (IR=5.7)
  - No change in the number of domestically acquired infections (IR=4.6)

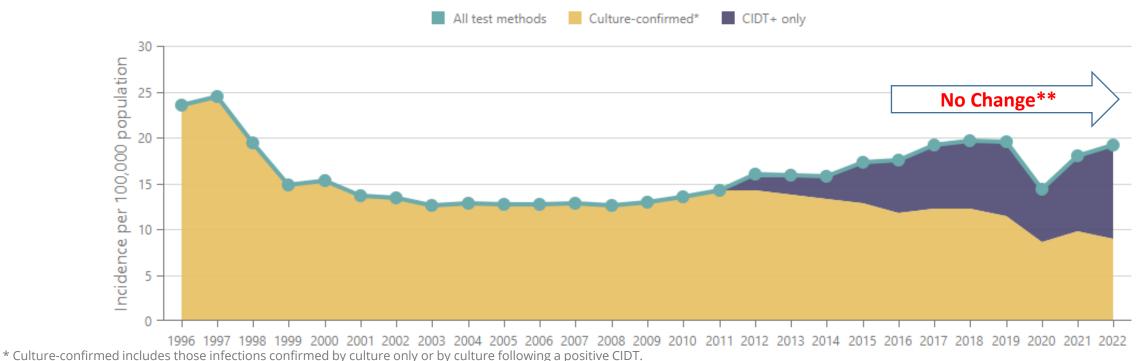


\* Culture-confirmed includes those infections confirmed by culture only or by culture following a positive CIDT.

\*\* This graph shows data for domestically-acquired and international-associated infections. When subset to only domestically-acquired infections we see no change in incidence in 2022 relative to the 2016-2018 baseline as opposed to an increase

### **Campylobacter** Infections

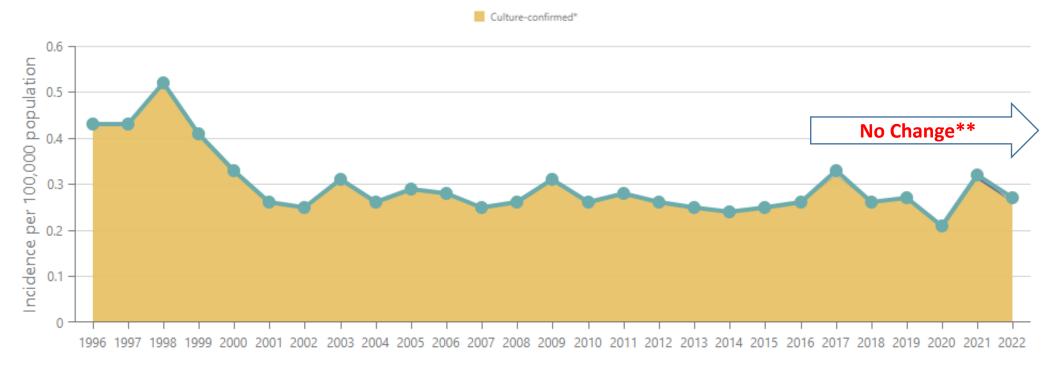
- HP 2030 target of 10.9 infections per 100,000
- Relative to the 2016-2018 baseline used for measuring progress toward HP 2030, in 2022 there was:
  - No change in the total number of infections (IR=19.2)
  - 7% increase in the number of domestically acquired infections (IR=17.4)



\*\* This graph shows data for domestically-acquired and international-associated infections. When subset to only domestically-acquired infections we see a 7% change in incidence in 2022 relative to the 2016-2018 baseline

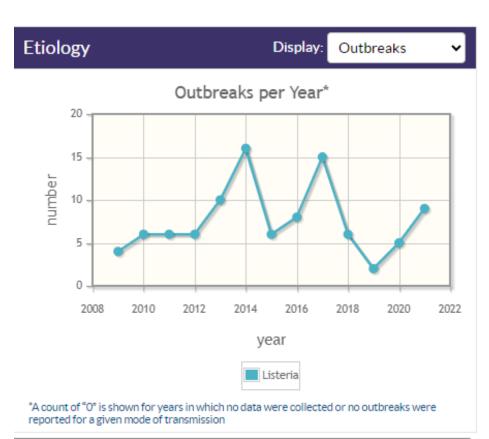
#### **Listeria** Infections

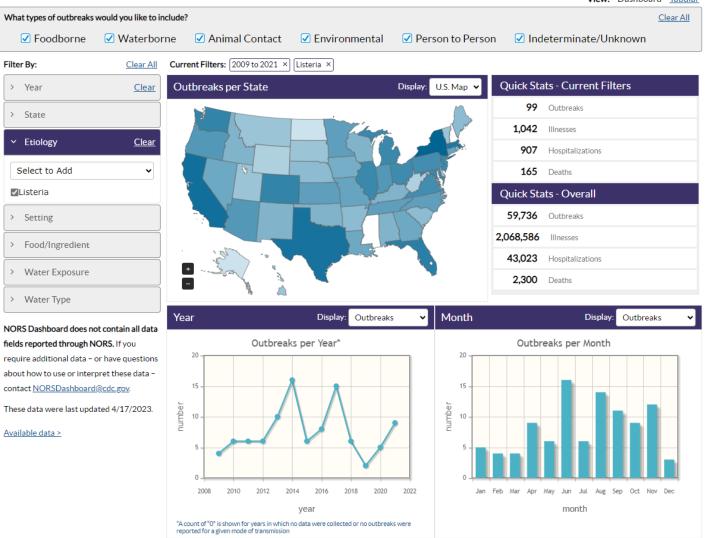
- HP 2030 target of 0.22 infections per 100,000
- Relative to the 2016-2018 baseline used for measuring progress toward HP 2030, in 2022 there was:
  - No change in the total number of infections (IR=0.3)
  - No change in the number of domestically acquired infections (IR=0.3)



\*\* This graph shows data for domestically-acquired and international-associated infections. When subset to only domestically-acquired infections, we still see no change in incidence in 2022 relative to the 2016-2018 baseline

### National Outbreak Reporting System (NORS) Dashboard: Listeria monocytogenes





https://wwwn.cdc.gov/norsdashboard/



## PulseNet 2.0

#### Modernization of PulseNet's analytical platform:

- PulseNet relies on, BioNumerics, which reaches End of Life December 2024 and needs to be replaced
- A new platform is being developed; no existing system meets all PulseNet needs

## PulseNet 2.0 – A Path Forward for Modernization

- New system addresses pain points with previous software
- Takes advantage of Enterprise cloud services at CDC for data storage and data visualization
- Technical solution will take advantage of open-source containerization and workflow management tools
- Highly scalable and adaptable as technology and requirements change



# Whole Genome Sequencing in PulseNet Reveals New Patterns

- Better cluster detection in PulseNet than before
- Better observation of patterns in the epidemiological landscape including REP strains
- Focused investigation may identify points of prevention.



#### **Expanding Use of WGS to More Pathogens**

- Began with *Listeria monocytogenes*, STEC, and *Salmonella*
- Now expanding to
  - More bacterial pathogens *Shigella, Campylobacter, Vibrio, Yersinia enterocolitica,* and *Cronobacter*
  - Beyond bacteria
    - Parasitic agents: Cryptosporidium, Cyclospora, Giardia, Naegleria
    - Fungal agents: Candida auris
- PulseNet International is also moving to WGS

## **Culture-Independent Diagnostic Tests (CIDTs)**

- Drastic increase in use of CIDTs in clinical labs to identify enteric pathogens
- Burden of bacterial culture shifted to public health laboratories
  - Isolates needed for WGS and AR determination methods
- CDC responses
  - Preserve access to isolates by identifying efficient workflows
  - Develop culture independent subtyping methods
  - Monitor and describe CIDT usage trends (FoodNet)
  - Investigate impact of CIDT usage on our understanding of illness epidemiology

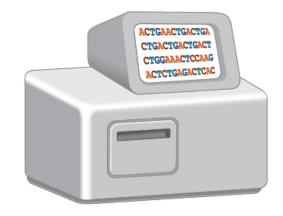
## **Highly Multiplexed Amplicon Sequencing (HMAS)**

#### HMAS allows us to:

- Skip the isolation step
- Sequence only what you need
- Process more samples together

#### **Benefits:**

- Applicable to any pathogen if:
  - It can be amplified
  - Subtyping targets identified
  - Specific primers designed
- Backwards compatibility with WGS
- Assay design can support disambiguation of pathogens from gut commensals
- Consumable \$/sample ~\$65 from lib prep-sequencing
- Requires only 1 major new instrument with multiple public health implications



#### **Foodborne Disease Prevention: Evolving Public Health Tools**

- We have more work to do in reaching HP 2030 targets
- Whole genome sequence-based surveillance is now improving outbreak detection, investigation, and prevention
- Outbreak investigations point to continuing and novel risks
- Attention on strains that re-occur, emerge or persist may focus prevention
- Empower public health, regulators, industry, academia, and consumers to drive down incidence of foodborne infections

#### Thank you!

For more information, contact CDC 1-800-CDC-INFO (232-4636) TTY: 1-888-232-6348 www.cdc.gov

The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention.



