Pennsylvania
Department of Health

Integrated surveillance for antimicrobial resistance in enteric bacteria, Pennsylvania

How collaboration with NARMS strengthens core surveillance and training

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Disclaimer: The findings and conclusions are those of the author and do not necessarily represent the official position of the Pennsylvania Department of Health, federal agencies or collaborators.

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Context

Pennsylvania mandate · 28 Pa. Code Chapter 27

One Health

Humans CDC **Retail food** FDA **Animals** USDA

National · National Notifiable Diseases Surveillance System

Global · International Health Regulations (2005)



Alexander D. Langmuir (left), CDC chief epidemiologist, with colleagues, 1955. Source: CDC Public Health Image Library

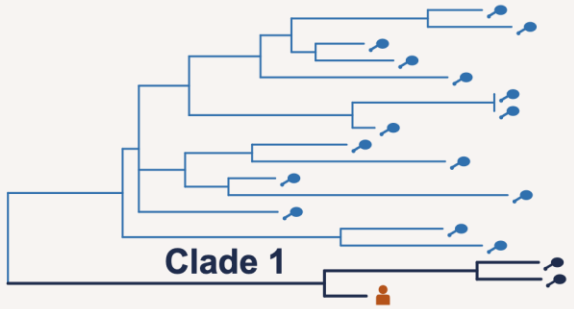
Antiquity	→ Middle Ages	→ 1800s	→ 1950s	→ Today
Hippocrates	Venice quarantine	William Farr	Alexander Langmuir	Microbial genomics [1–5]

NARMS collaboration builds on surveillance infrastructure centuries in the making

Supporting regulatory oversight · Uncovering sources of enteric pathogens

1 Example 1 · State-led

Salmonella from patients matched strains in retail poultry: Reading within 5 alleles, Infantis within 10



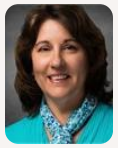
Patient Retail meat · Clade 1 in dark blue

S. Reading tree (n = 18); M'ikanatha et al. Open Forum Infect Dis 2021

≤10 alleles patient and retail chicken *S.* Infantis; both carried *bla*CTX-M-65 and *gyrA* D87Y

16 of 102 sequenced clinical and retail meat isolates carried resistance mechanisms to ceftriaxone, preferred for severe infections in children

2017 matching *S.* Reading strains were in retail ground turkey, before the multistate outbreak was recognized in 2018



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Genomic links between meat and patients can flag sources before outbreaks

2 Example 2 · State-led with federal partners

Conventional poultry had 2.6× higher odds of multidrug-resistant *Salmonella* compared with reduced-use alternatives (aOR 2.61)

46,937 retail poultry samples tested (2008–2017)

Metric	Reduced-use	Conventional	Impact
***Salmonella* prevalence**	**5.1%**	**8.6%**	Lower overall contamination
Multidrug resistance (MDR)	**14.1%**	**29.5%**	aOR 2.61



Yin et al. Int J Food Microbiol 2021



Xin Yin
Doctoral student, PA Dept. of Health



Heather Tate
Co-mentor, FDA NARMS



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Co-mentor, PA Dept. of Health

Production claims correlate with lower resistance, but evidence suggests contamination persists in retail poultry

3 Example 3 · Academic collaboration

Salmonella presented substantial clinical severity, with nearly half of patients hospitalized

Clinical burden and severity (N = 82)

46% hospitalized (38 of 82 patients)

12% invasive infections (10 of 82; 8 with bacteremia, all hospitalized)

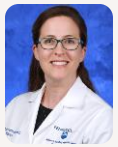
6% required intensive care (5 of 82; 1 death)

Diagnostic and treatment impact

79% of empiric antibiotic treatments changed after laboratory confirmation



Hackman et al. Open Forum Infect Dis 2022;9(Suppl 2):ofac492.1634



Nicole Hackman
Pediatrics, Penn State Hershey



Sameera Sayeed
Microbiologist, PA Bureau of Labs



Louise Watkins
CDC NARMS

Salmonella invasiveness and frequent antibiotic modification (≈80%) underscore the need for timely laboratory diagnosis

4 Example 4 · Academic collaboration

Salmonella Baildon in wastewater was within 0–1 SNP of restaurant outbreak isolates



M'ikanatha et al. J Clin Microbiol 2024



Nicholas Cesari
Enteric Disease Outbreak Team, PA Dept. of Health



Edward Dudley
Food Science, Penn State

Raw sewage

8 *S.* Baildon from 2 wastewater treatment plants (June 2022)

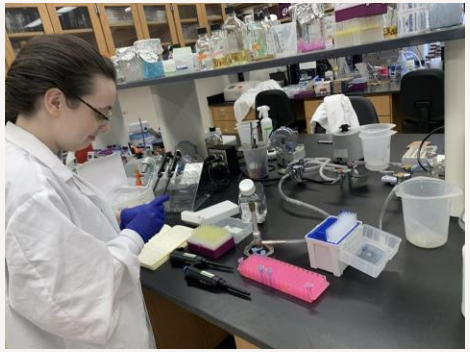
8 of 43 total *Salmonella* isolates

0–1
SNP
nearly identical genomes

Clinical outbreak

42 outbreak isolates linked to May 2022 restaurant exposure

46 total clinical *S.* Baildon isolates



Erin Nawrocki, prepares sewage samples, Dudley Lab, Penn State

High sensitivity (75%)

of wastewater samples were positive for *Salmonella*

Rare serotype (<1%)

of U.S. clinical salmonellosis cases are *S.* Baildon; wastewater mirrored a local outbreak

Findings suggest wastewater genomic monitoring complements conventional enteric disease reporting, though robust data remain essential

5 Example 5 · Academic collaboration

Salmonella Dublin genomes were highly clonal across hosts, but antimicrobial resistance profiles varied



Kenney, M'ikanatha, Ganda. Appl Environ Microbiol 2025



Sophia M. Kenney
Graduate student, lead author



Erika Ganda
Animal Science, Penn State

Study scope

2,150 U.S. genomes (2002–2023)

93% within 20 SNPs of another strain

Resistance markers by source

Marker	Bovine	Human	Environ.
IncA/C2 plasmid	**14.3%**	4.8%	2.0%
***gyrA* D87N**	6.5%	**19.0%**	**18.8%**

Shared lineages suggest need for One Health antimicrobial stewardship in human and veterinary settings

6 Example 6 · Academic collaboration

Multidrug-resistant *Salmonella* was rare in wild birds

7 of 375 isolates across 41 states

375
Wild bird isolates
41 states, 1978–2019

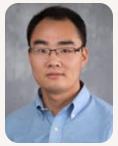
1.9%
Resistant to ≥3 antimicrobial classes
7 of 375

1.9%
Resistant to ≥3 heavy metals
7 of 375

0
Resistant isolates from songbirds
all from raptors and water birds



Fu et al. Environ Microbiol 2022



Yezhi Fu
Postdoc, Penn State; now Sun Yat-sen Univ.



Edward Dudley
Food Science, Penn State



Pine siskin, a wild songbird. Image: CDC

Wild birds are not a major reservoir of multidrug-resistant *Salmonella*

Summary

Take-home points

- **Genomic surveillance:** Comparing retail meat and clinical isolates identifies transmission pathways prior to outbreaks.
- **Production claims vs. safety:** Labeling claims correlate with resistance patterns but do not guarantee pathogen-free products.
- **Susceptibility and clinical care:** Given the potential severity of *Salmonella*, susceptibility profiling directly guides targeted therapy.
- **One Health lineages:** Shared bacterial lineages necessitate unified antimicrobial stewardship across veterinary and human medicine.

Acknowledgments and references

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Background (slide 3)

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Examples 1–6

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