



Pork Safety- *Salmonella* Outbreaks and Risk Assessment

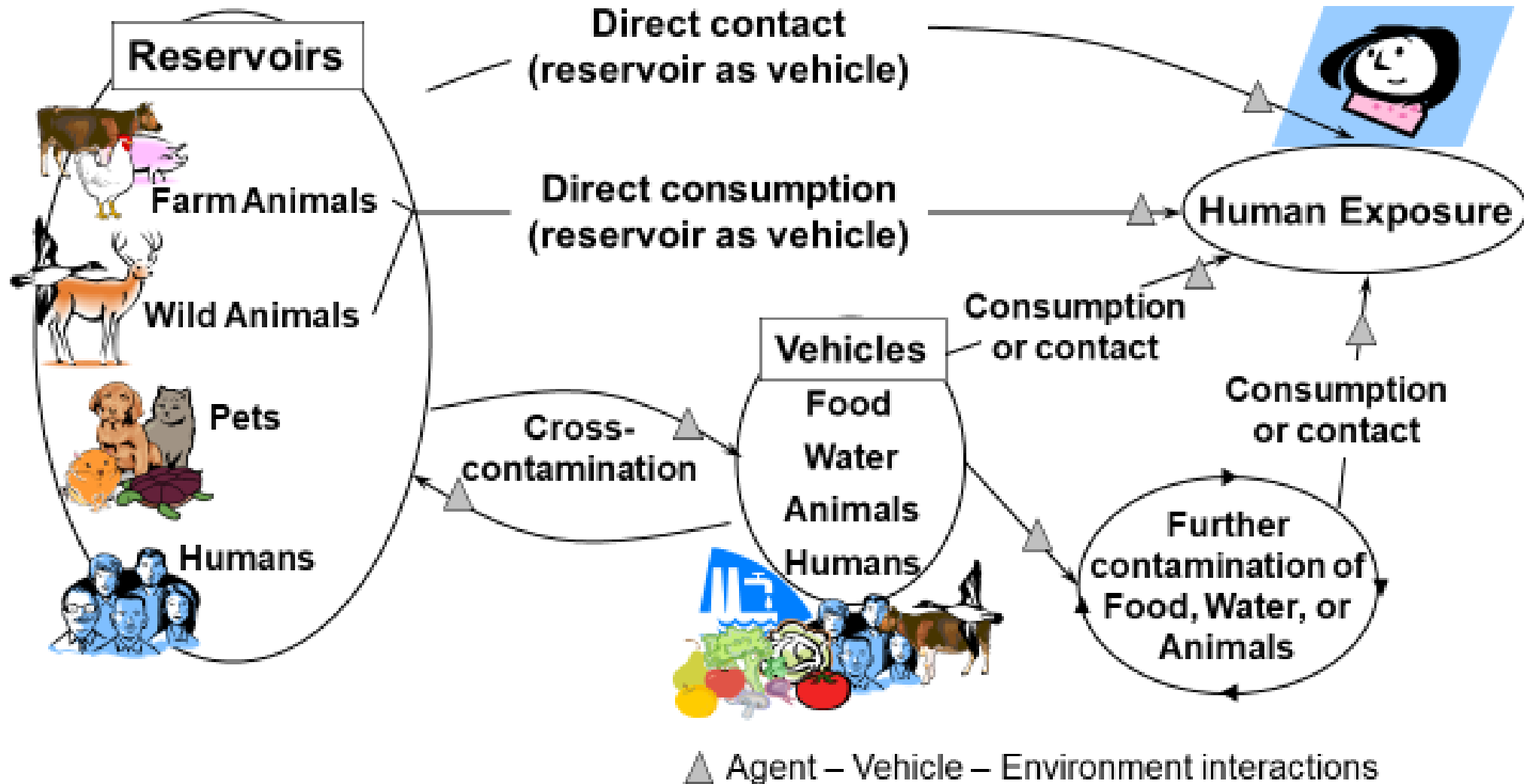
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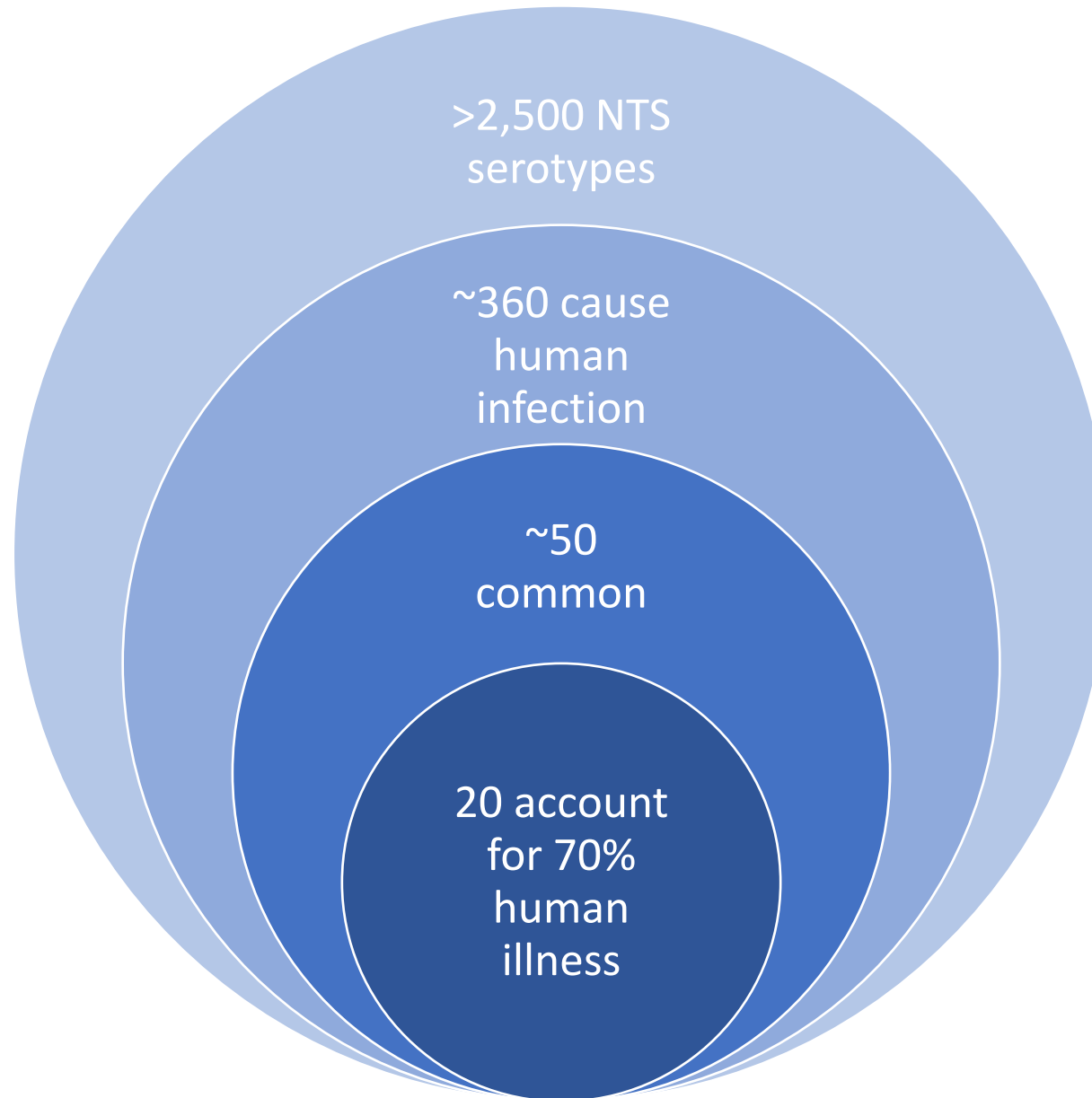
**MINNESOTA INTEGRATED
FOOD SAFETY CENTER OF EXCELLENCE**

UNIVERSITY OF MINNESOTA • MINNESOTA DEPARTMENT OF HEALTH

Salmonella: A One Health Wonder

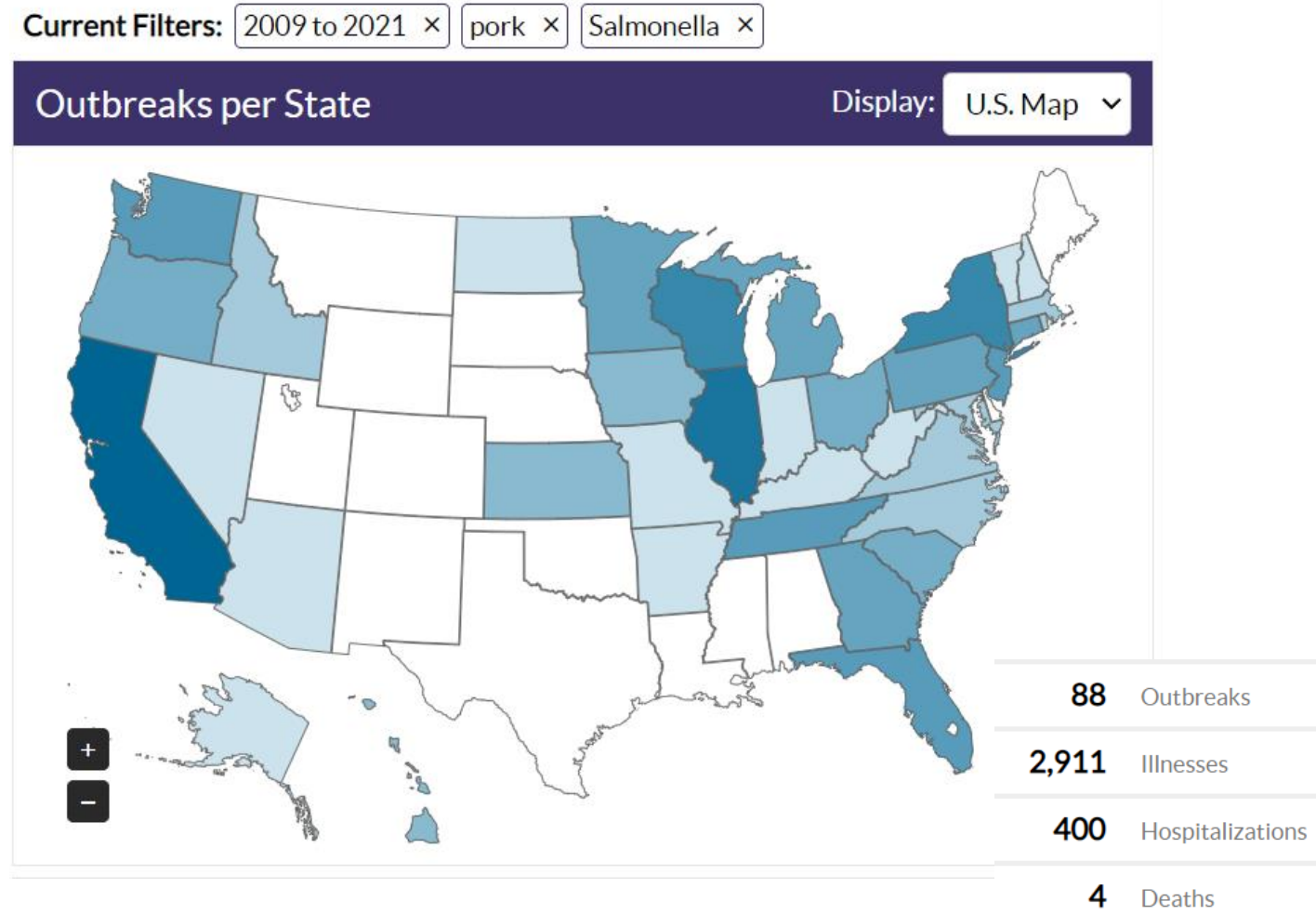


CDC. National *Salmonella*
Surveillance Overview.
Atlanta, Georgia: US
Department of Health and
Human Services, CDC, 2011.



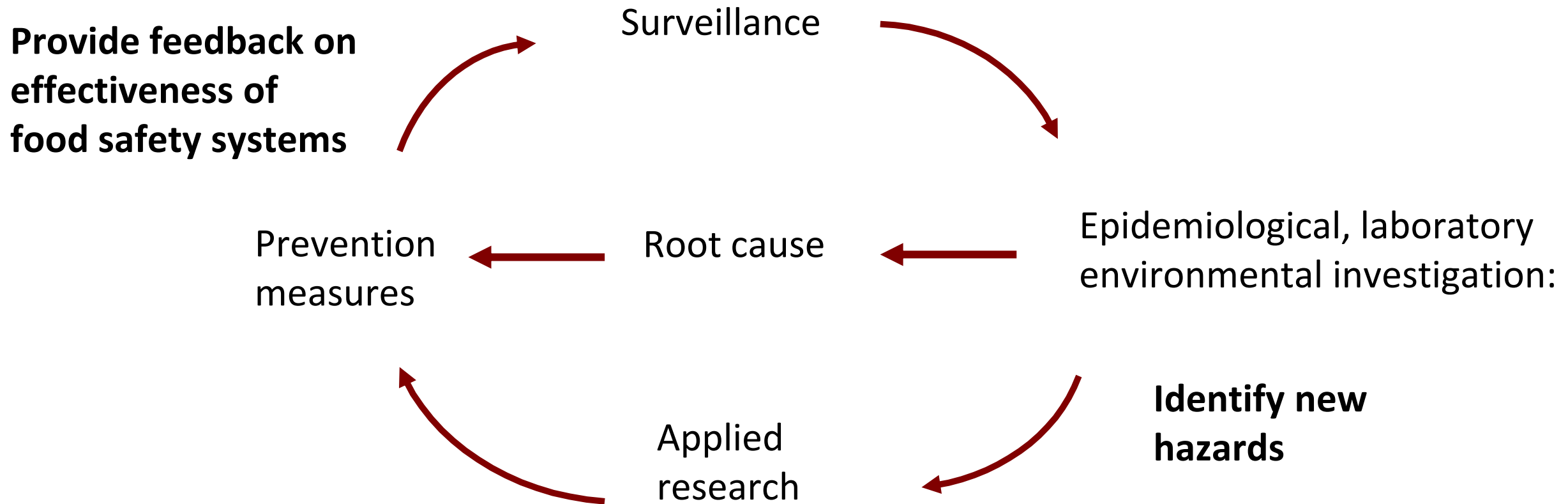
Salmonella Outbreaks and Risk Assessments

- Overview of public health surveillance
 - Transformative effect of whole genome sequencing
- Importance for source attribution and risk assessments
- Impact for industry



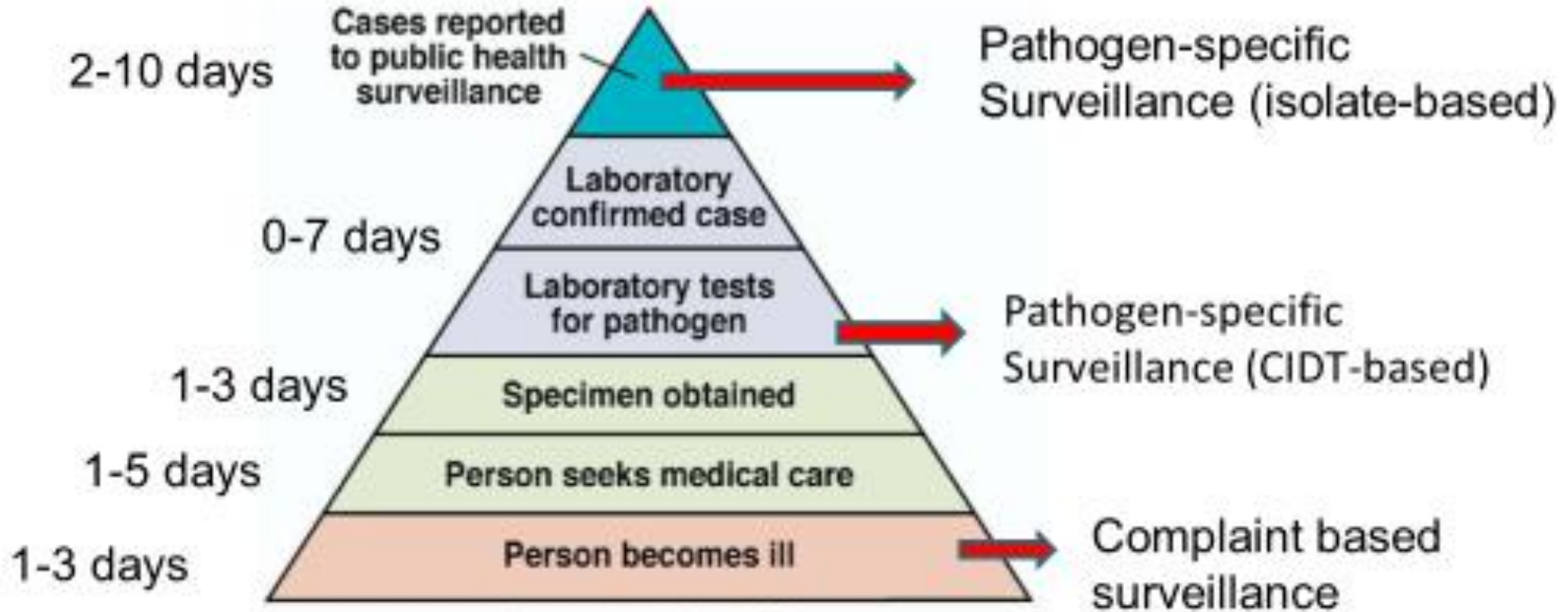
The Cycle of Public Health Prevention

Humans are the ultimate bioassay for the food supply



Primary Sources for Outbreak Detection

Cumulative: 2-4 weeks



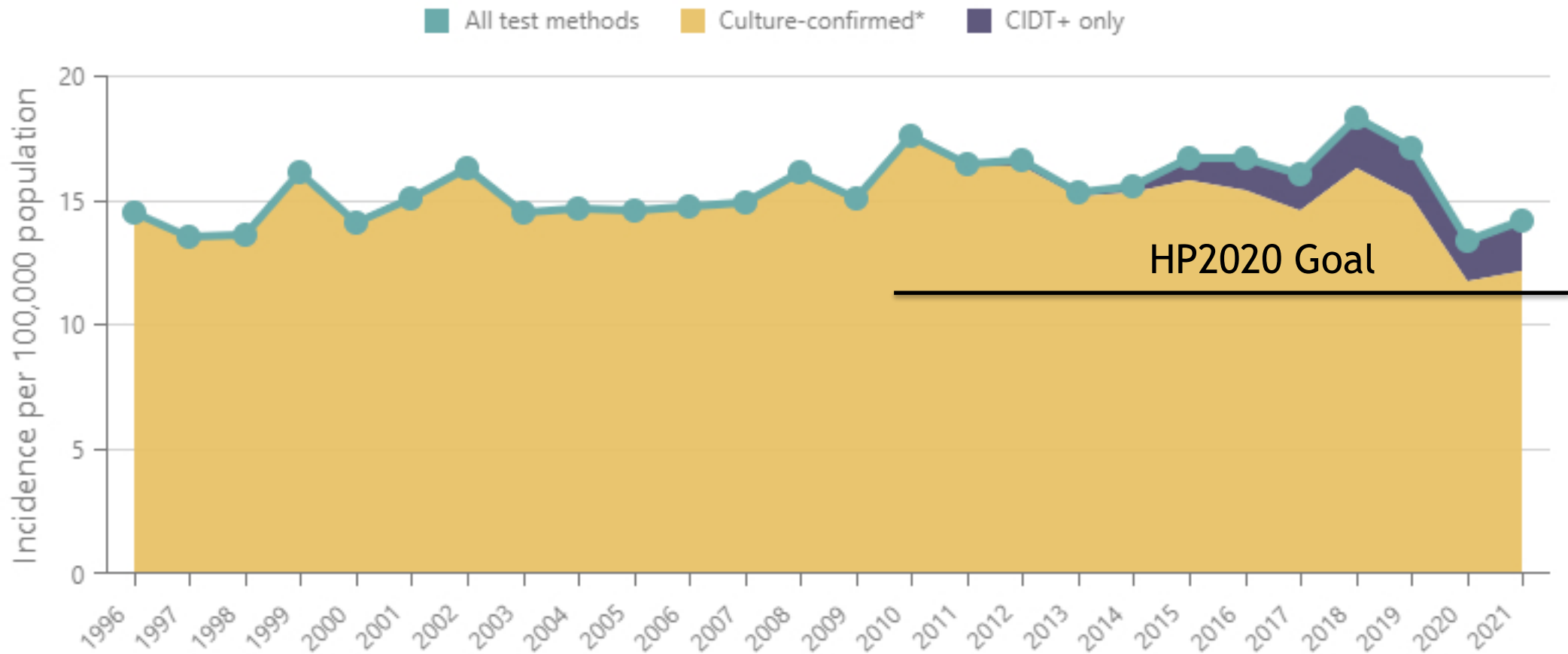
Source: adapted from CDC,
http://www.cdc.gov/foodnet/surveillance_pages/burden_pyramid.htm,
accessed Sept 4, 2008

Salmonella infections by year; 1996-2021

Incidence per 100,000 population – FoodNet sites; all test methods

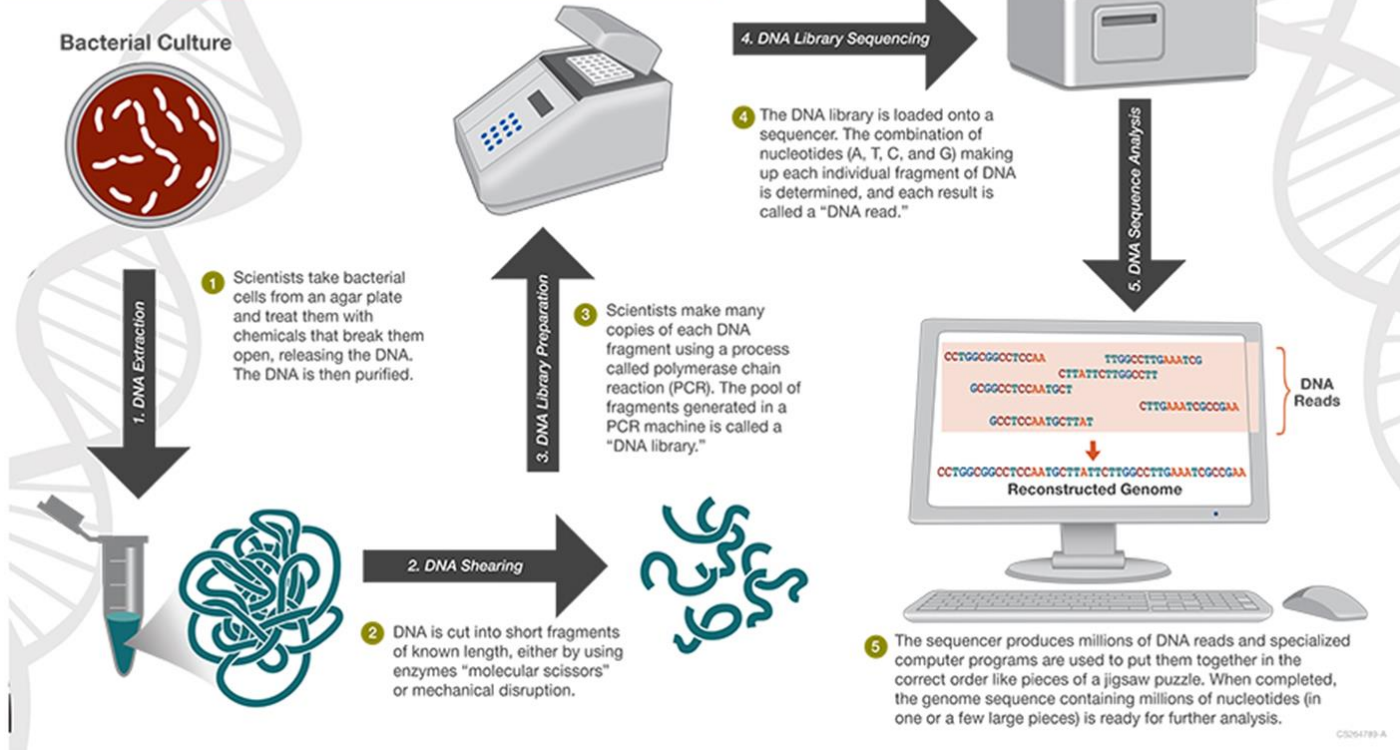
* Culture-confirmed includes those infections confirmed by culture only or by culture following a positive CIDT.

Source: FoodNet, Centers for Disease Control and Prevention

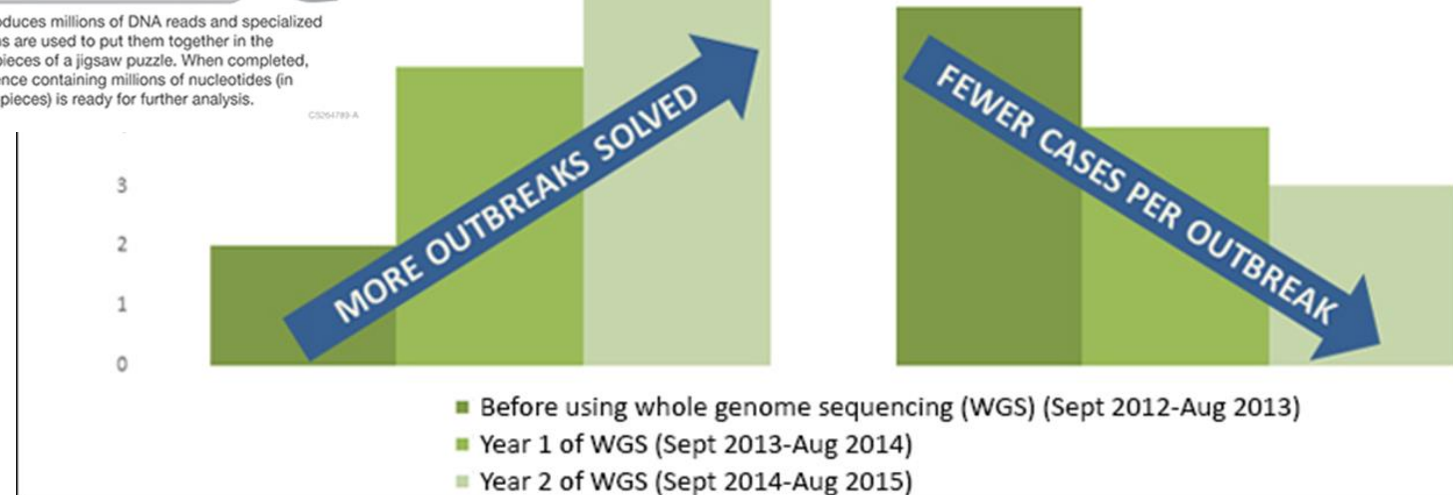


The Whole Genome Sequencing (WGS) Process

WGS is a laboratory procedure that determines the order of bases in the genome of an organism in one process. WGS provides a very precise DNA fingerprint that can help link cases to one another allowing an outbreak to be detected and solved sooner.



Whole genome sequencing improves the detection and investigation of foodborne outbreaks





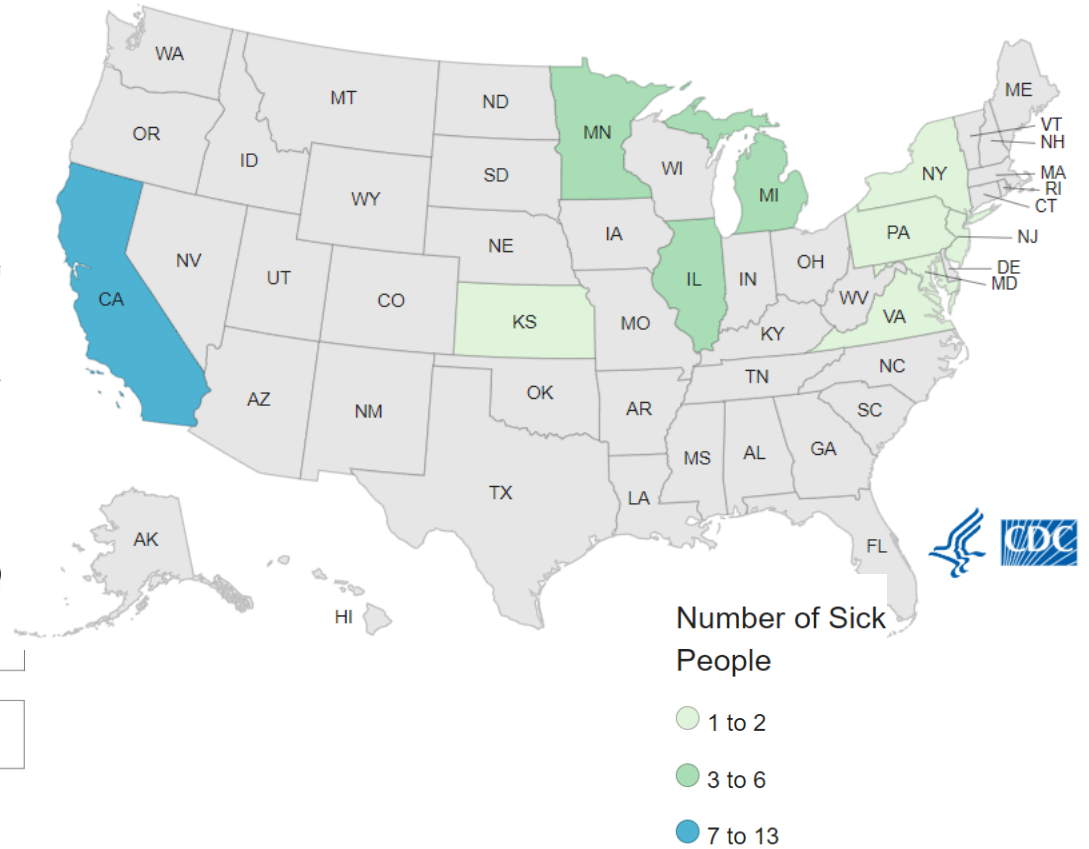
Increasing the specificity of food exposure information provided by case-patients is as important as increasing the specificity of the case definition.

The National Molecular Subtyping Network for Foodborne Disease Surveillance



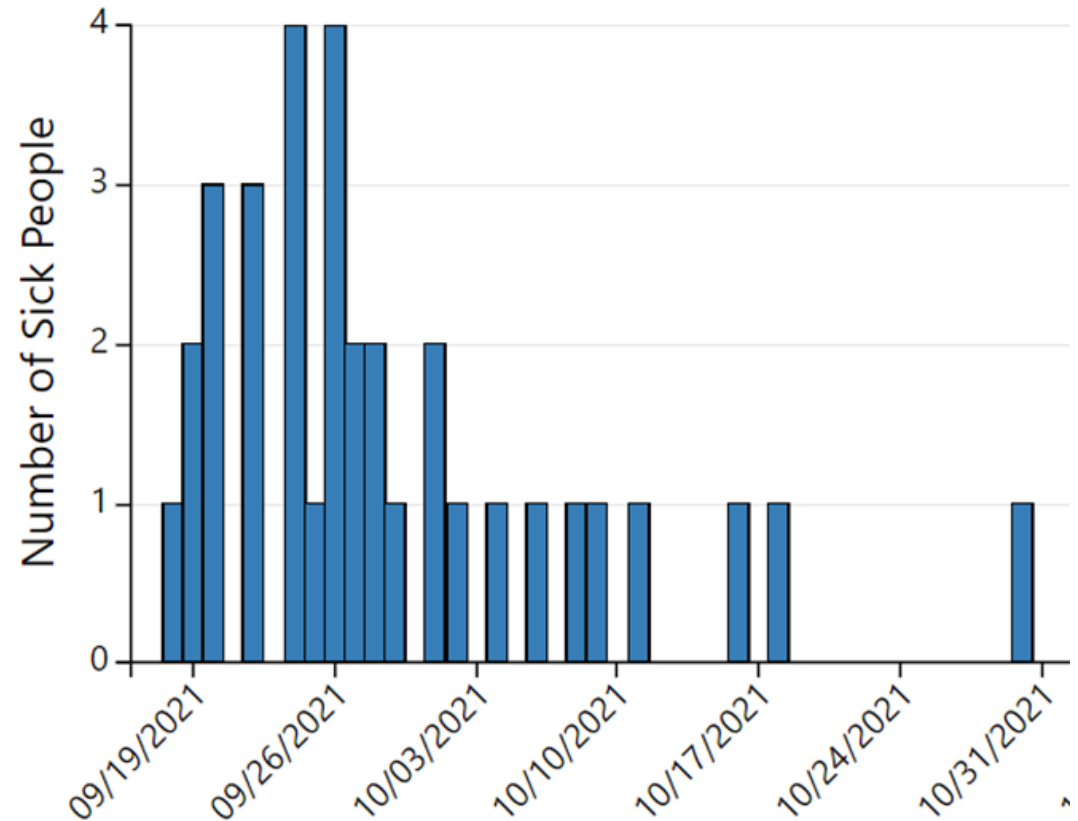
August 2002

Salmonella Outbreak Linked to Salami Sticks

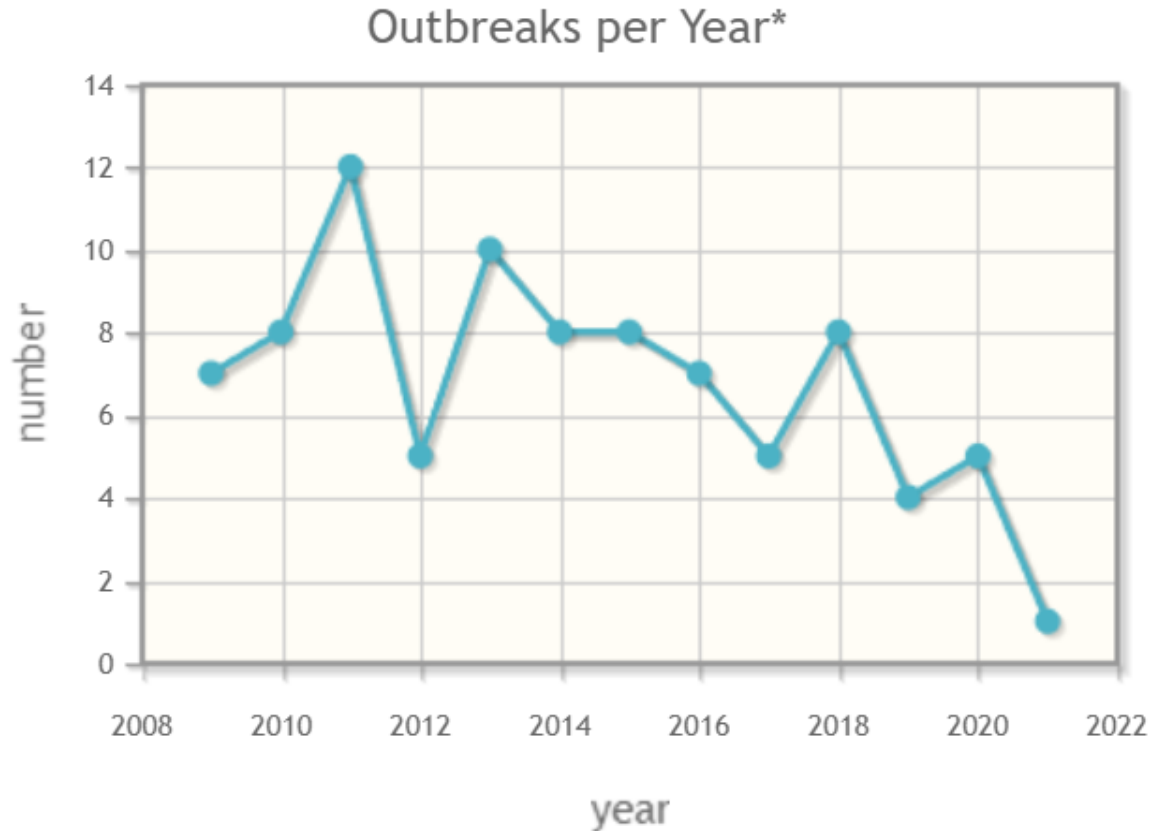


Salmonella Outbreak Linked to Salami Sticks

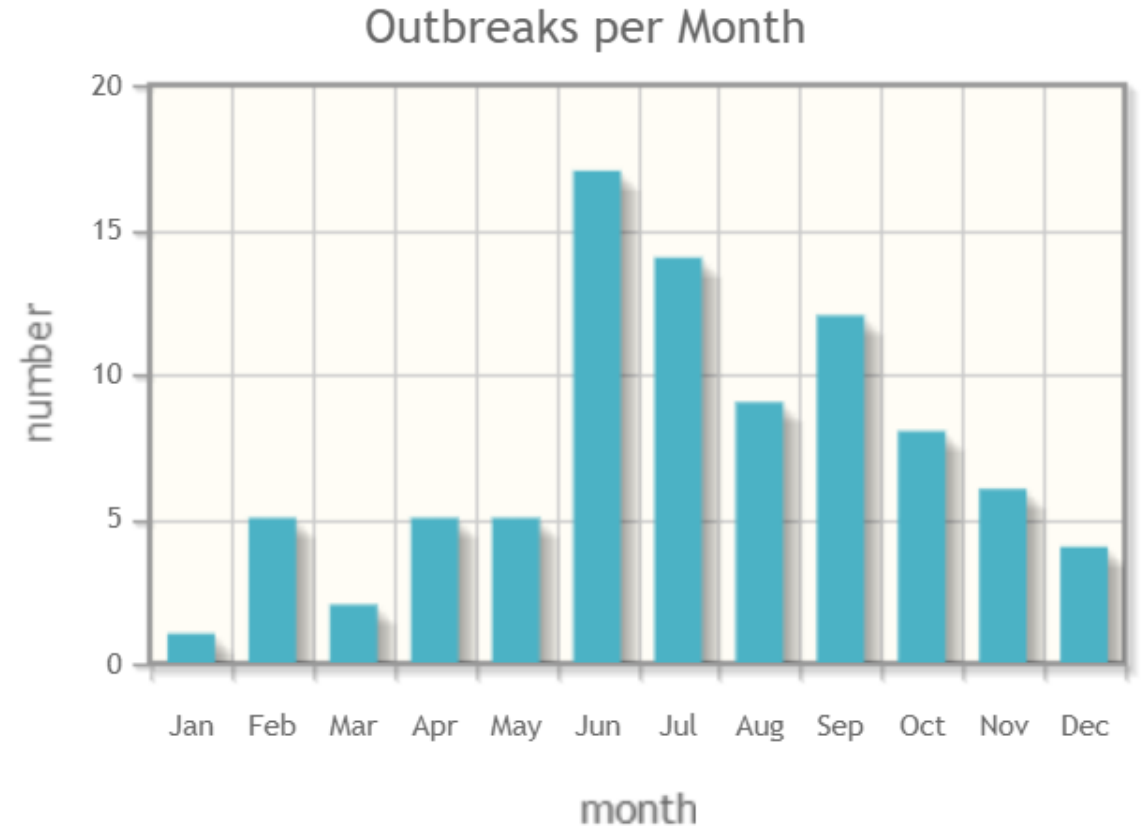
- 34 ill
- Age 1 to 75 years, 79% <18
- 58% female
- 7 hospitalized, no deaths
- 27 interviewed, 26 (96%) ate salami sticks, 25 (93%) named same brand
- *Salmonella* in 2 unopened packages (S. Derby) not closely related to samples from sick people
- 119,091 pounds of products recalled



Salmonella Outbreaks Associated with Pork, US, 2009-2021



- Overall decline, more multistate outbreaks



- Summertime seasonality

Salmonella Outbreaks Associated with Pork, US, 2009-2021

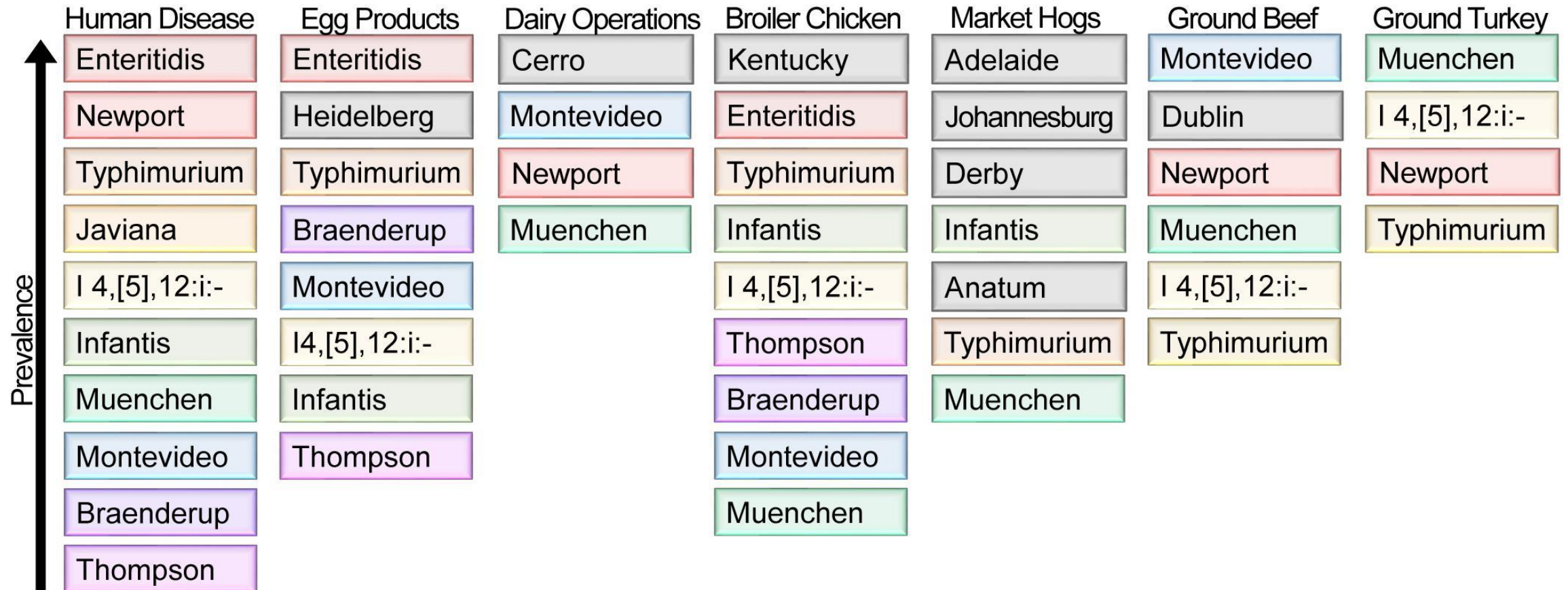
Food Vehicle	No. Outbreaks
Pork	20
Pork, roasted	15
Pork, BBQ	15
Carnitas	14
Pulled pork	6
Sausage	5
Whole hog	3
Other	10

- Description of food vehicles lacks specificity, some include other ingredients

Salmonella Outbreaks Associated with Pork, US, 2009-2021

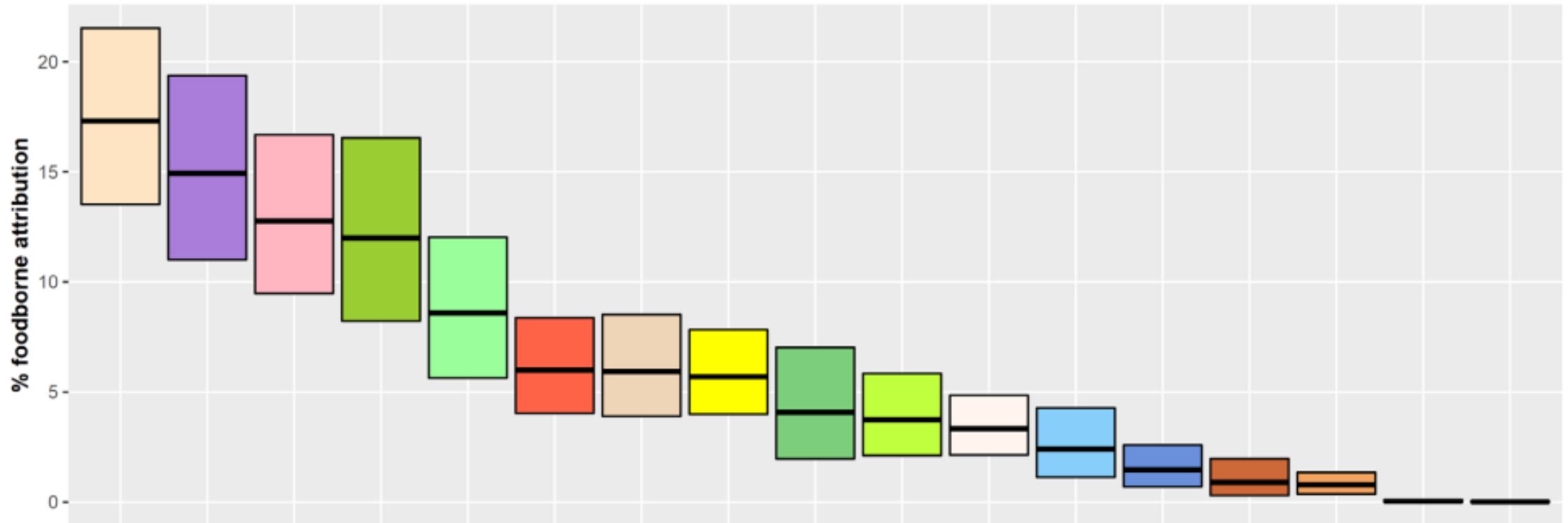
Serotype	No. Outbreaks
I 4,[5],12:i:-	18
Typhimurium	15
Infantis	9
Enteritidis	8
Newport	6
Derby, Agona	4 each
Adelaide, Mbandaka, Uganda	3 each
Other (15 serotypes)	24

- Wide variety of *Salmonella* serotypes associated with outbreaks.
Top 3 serotypes account for almost half of outbreaks.



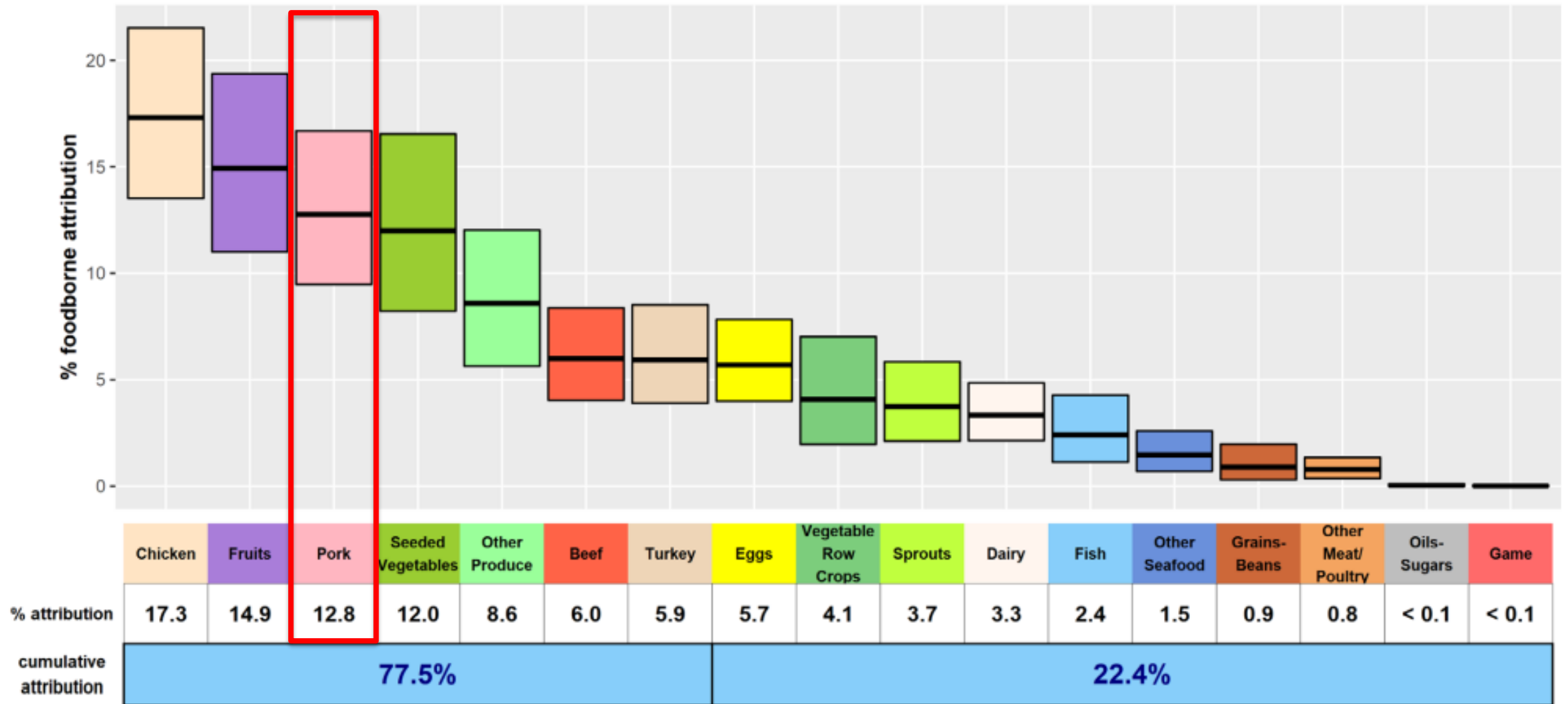
Cheng RA, Eade CR, Wiedmann M. 2019. Embracing diversity: differences in virulence mechanisms, disease severity, and host adaptations contribute to the success of nontyphoidal Salmonella as a foodborne pathogen. *Front Microbiol* 10:1368.

Salmonella Attribution to Food Categories, 2020



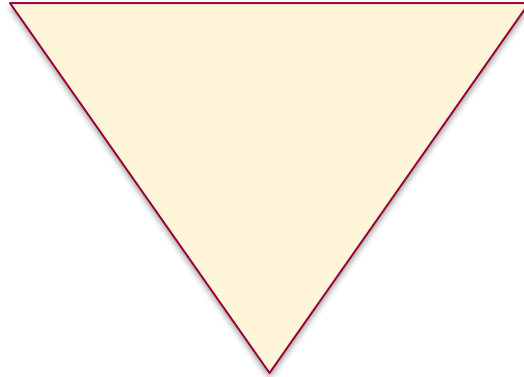
	Chicken	Fruits	Pork	Seeded Vegetables	Other Produce	Beef	Turkey	Eggs	Vegetable Row Crops	Sprouts	Dairy	Fish	Other Seafood	Grains-Beans	Other Meat/Poultry	Oils-Sugars	Game
% attribution	17.3	14.9	12.8	12.0	8.6	6.0	5.9	5.7	4.1	3.7	3.3	2.4	1.5	0.9	0.8	< 0.1	< 0.1
cumulative attribution	77.5%								22.4%								

Salmonella Attribution to Food Categories, 2020



Risk Assessment Models

Top-down models:



Number of human illnesses



Attribution estimates

% human illnesses due to pork

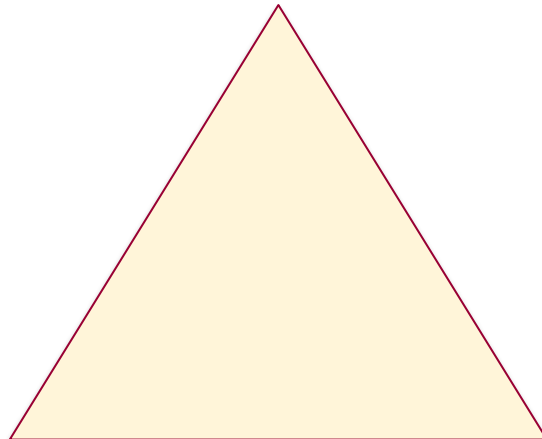
Number human illnesses due to pork



Preparation and consumption scenarios

Prevalence of *Salmonella* in pork

Bottom-up models:



FSIS Raw Product Sampling and Testing

- 52 week “moving window” testing approach
- Frequency dependent upon daily production volume
- Increased NTS prevalence in ground products
- HACCP Plans



USDA FSIS Quarterly Sampling Reports on Salmonella. Q1, 2023

Product	Number of Samples	Number of Positives	Percent Positive
Young Chicken Carcasses	2442	117	4.79%
Chicken Parts (legs/breast/wings)	3698	306	8.27%
Comminuted Chicken	471	127	26.96%
Mechanically Separated Chicken	30	26	86.67%
Total for Raw Chicken	6663	580	8.70%
Young Turkey Carcasses	412	0	0.00%
Comminuted Turkey	301	50	16.61%
Mechanically Separated turkey	22	12	54.55%
Total for Raw Turkey	735	62	8.44%
Raw ground beef - Retail	126	5	3.97%
Raw ground beef	2617	28	1.07%
Total for Raw Beef	4302	76	1.77%
Comminuted pork	1545	246	15.92%
Pork Cuts	576	41	7.12%
Total for Raw Pork	2121	287	13.53%

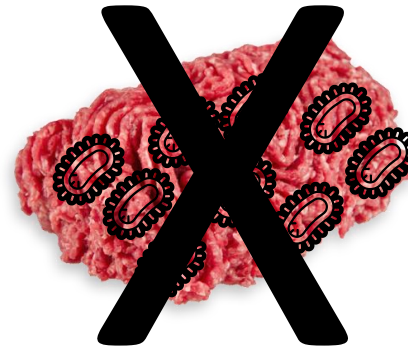
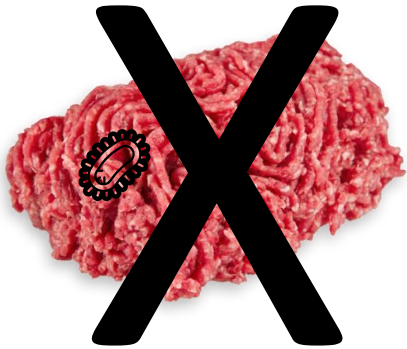
Limitations in Prevalence-Based Performance Standards

Prevalence: $3/8 = 37.5\%$



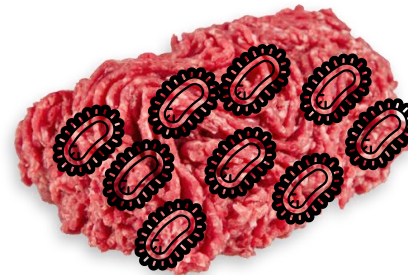
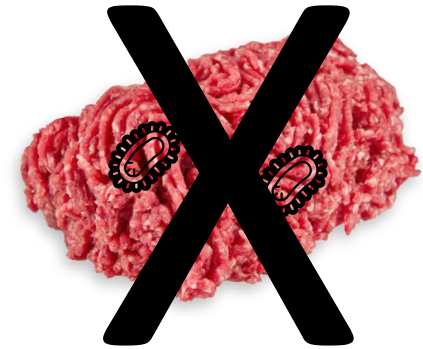
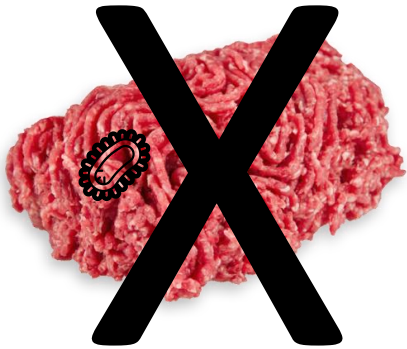
Limitations in Prevalence-Based Performance Standards

Prevalence: $1/6 = 16.7\%$

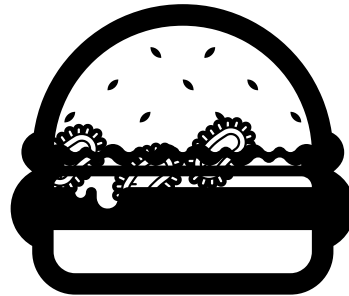


Limitations in Prevalence-Based Performance Standards

Prevalence: $1/6 = 16.7\%$



Limitations in Prevalence-Based Performance Standards



Ground Pork Risk Assessment

- Assess the public health impact of contaminated ground pork lots
 - higher levels of *Salmonella* contamination are more likely to produce illness
- Investigate various consumption and risk reduction scenarios
- Explore the impact of cross-contamination events during product preparation

High Virulence Criteria

- Listed as a top 10 serotype isolated from human illnesses according to the most recent CDC *Salmonella* Annual Report

OR

- Identified as an outbreak causing serotype by the National Outbreak Reporting System

AND

- Was not individually over-represented in risk estimates using CDC and FoodNET serotype reporting data

FSIS Enumeration Data

446 *Salmonella* enumerated samples (2010-2020)

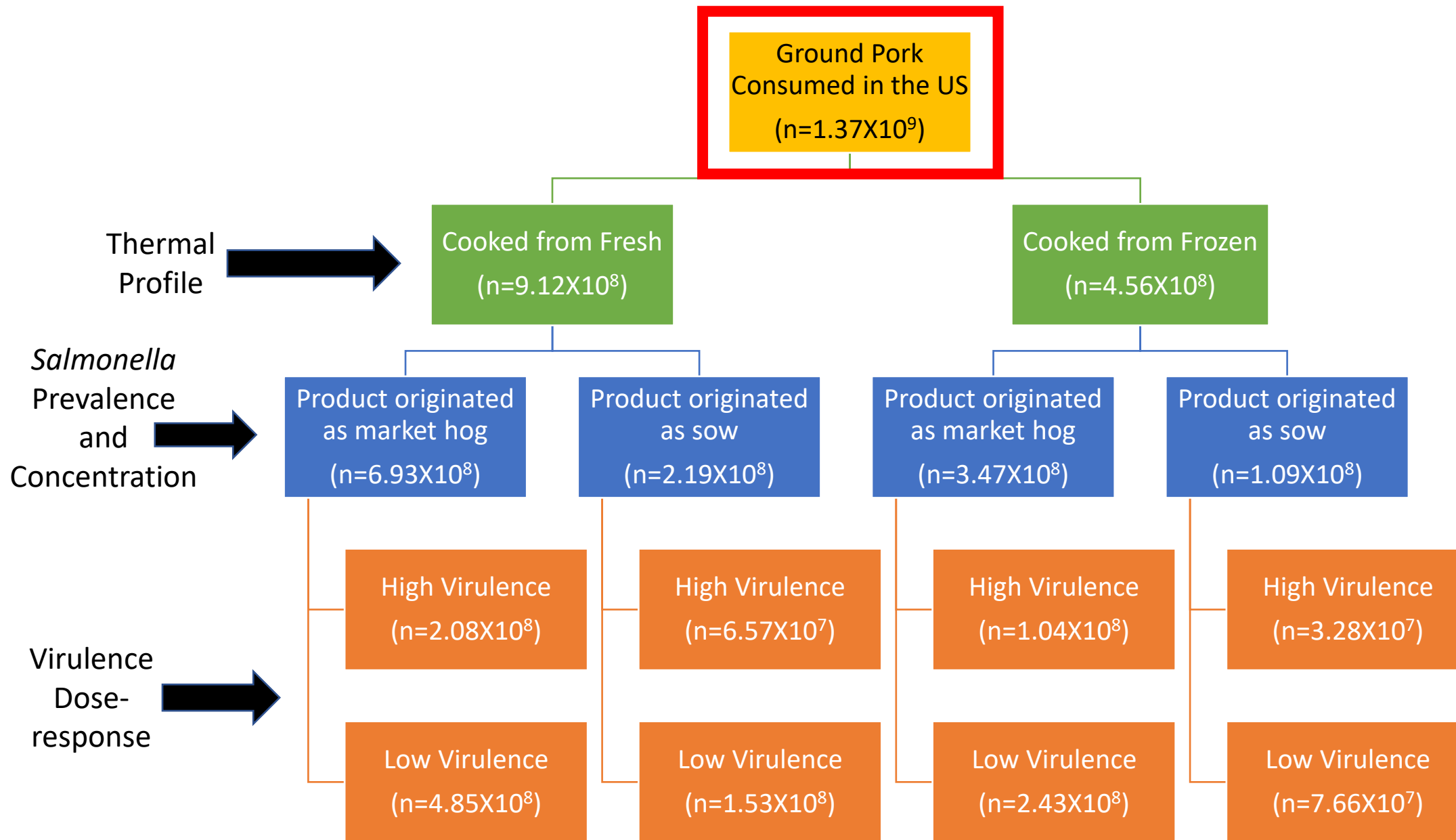
- *Salmonella* prevalence varied from 15.6% (MH) – 43.5% (Sow)
- 30% met high virulence criteria

Very low *Salmonella* prevalence in production lots sampled

- >1 MPN/g = 3% production lots

Average concentration:

- Market Hog: 0.18 MPN/g (SD: 1.15 MPN/g)
- Sow: 1.06 MPN/g (SD: 15.2 MPN/g)



Results

Table 1. Risk estimate comparisons after removal of ground pork lots based on relative *Salmonella* characteristics

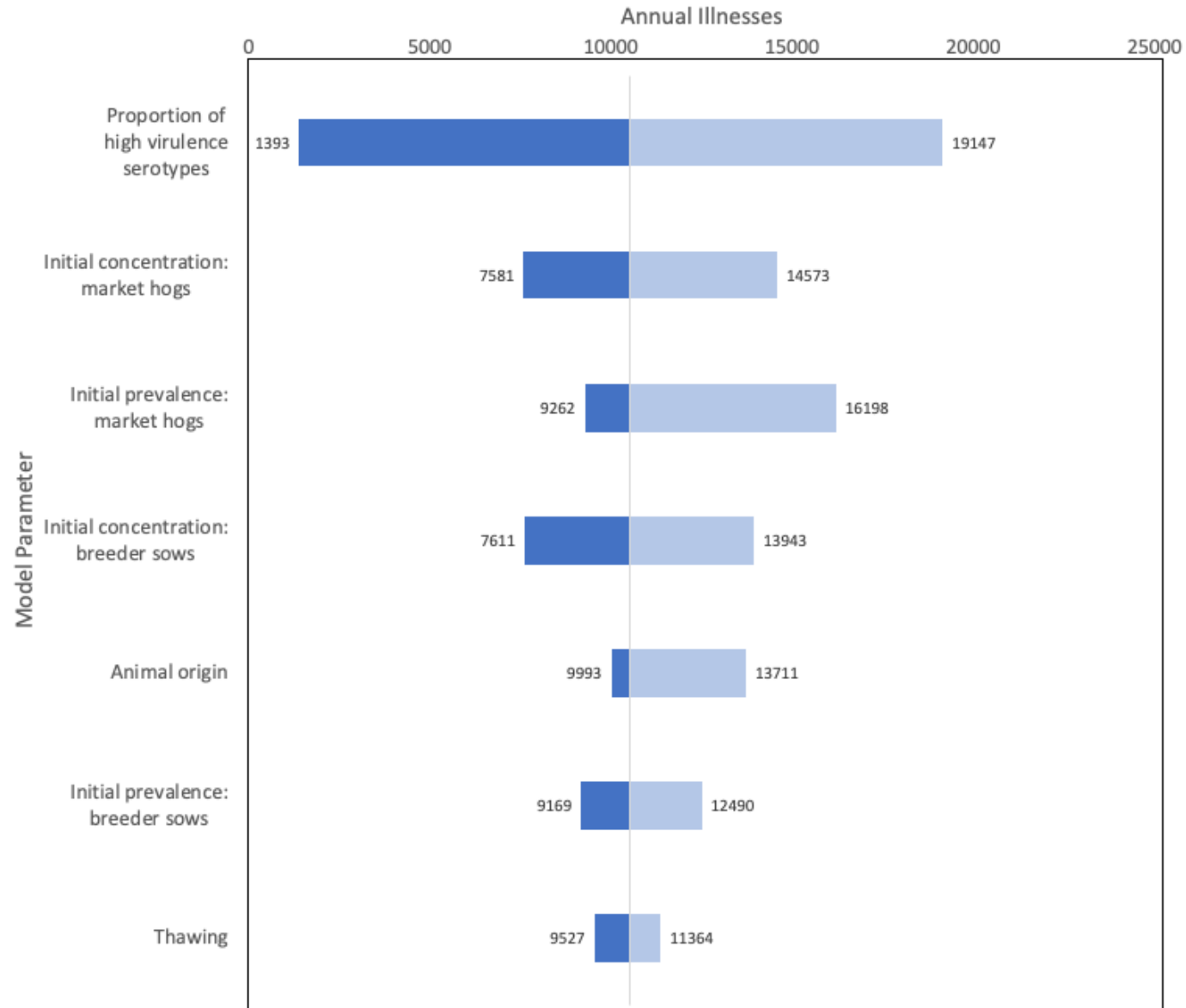
Model	Annual Illnesses*	Reduction from Baseline (%)
Baseline	10,590	-
>1 MPN/g removed	5,632	46.8
Highly virulent lots removed	90	99.2

*Unadjusted for under-reporting

Table 2. Annual salmonellosis illness estimates separated by ground pork consumption scenarios and virulence profile at baseline

Consumption Scenario	Annual Illnesses by Virulence Profile		
	High-virulence (90% CI)	Low-virulence (90% CI)	Total
Market Hog, Fresh (n=6.93X10 ⁸)	16 (4, 148)	2110 (1300, 3070)	2126 (1304, 3218)
Market Hog, Frozen (n=3.47X10 ⁸)	40 (8, 282)	4030 (2480, 5860)	4070 (2488, 6142)
Sow, Fresh (n=2.19X10 ⁸)	12 (3, 105)	1500 (923, 2180)	1512 (926, 2285)
Sow, Frozen (n=1.09X10 ⁸)	22 (6, 200)	2860 (1760, 4160)	2882 (1766, 4360)
Total	90 (21, 735)	10500 (6463, 15270)	10,590 (6484, 16005)

Tornado diagram illustrating sensitivity analysis of ground pork baseline model



Project Highlights:

~10,600 annual cases of salmonellosis attributable to ground pork

Removing >1 MPN/g resulted in a ~50% reduction in illnesses

Sow products have higher initial *Salmonella* prevalence and concentration

Most ground pork products originated as market hogs (76%)

Presence of highly virulent *Salmonella* was the most impactful model parameter

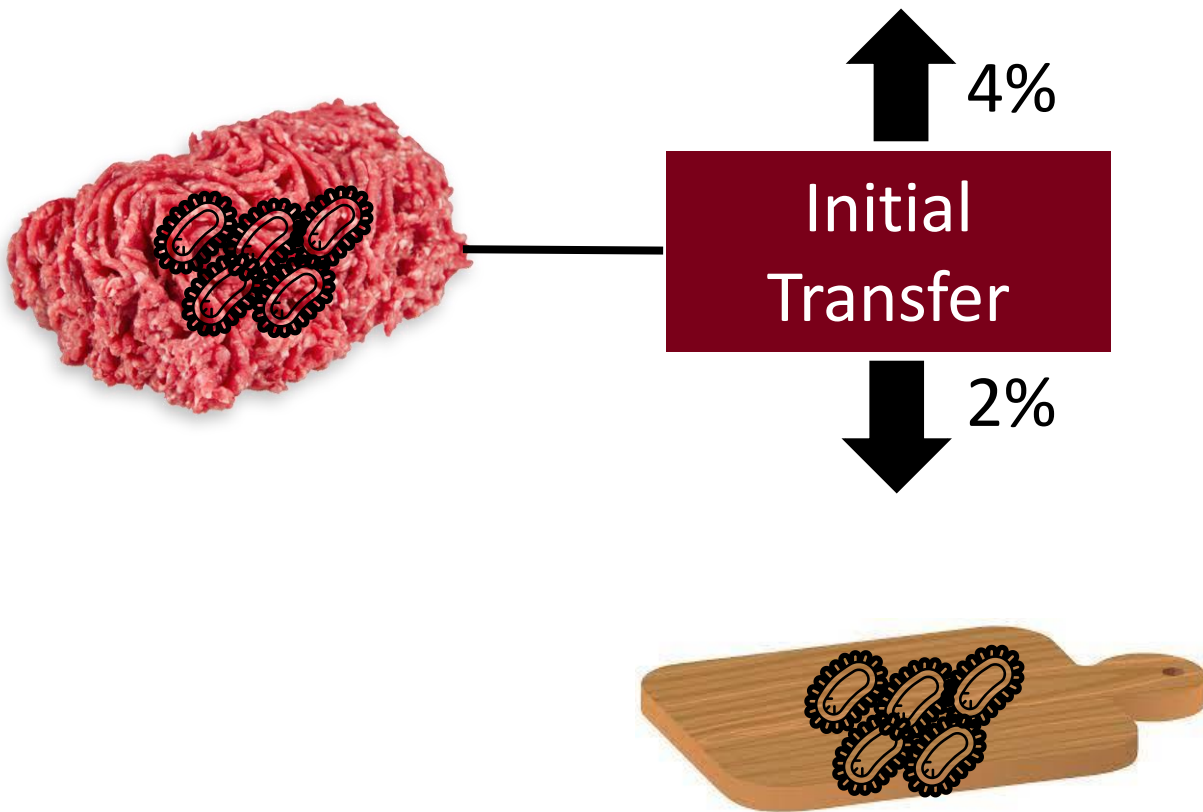
Cross-contamination Events Modeled:

Wachtel, M. R., McEvoy, J. L., Luo, Y.,
Williams-Campbell, A. M., & Solomon, M. B.
(2003).



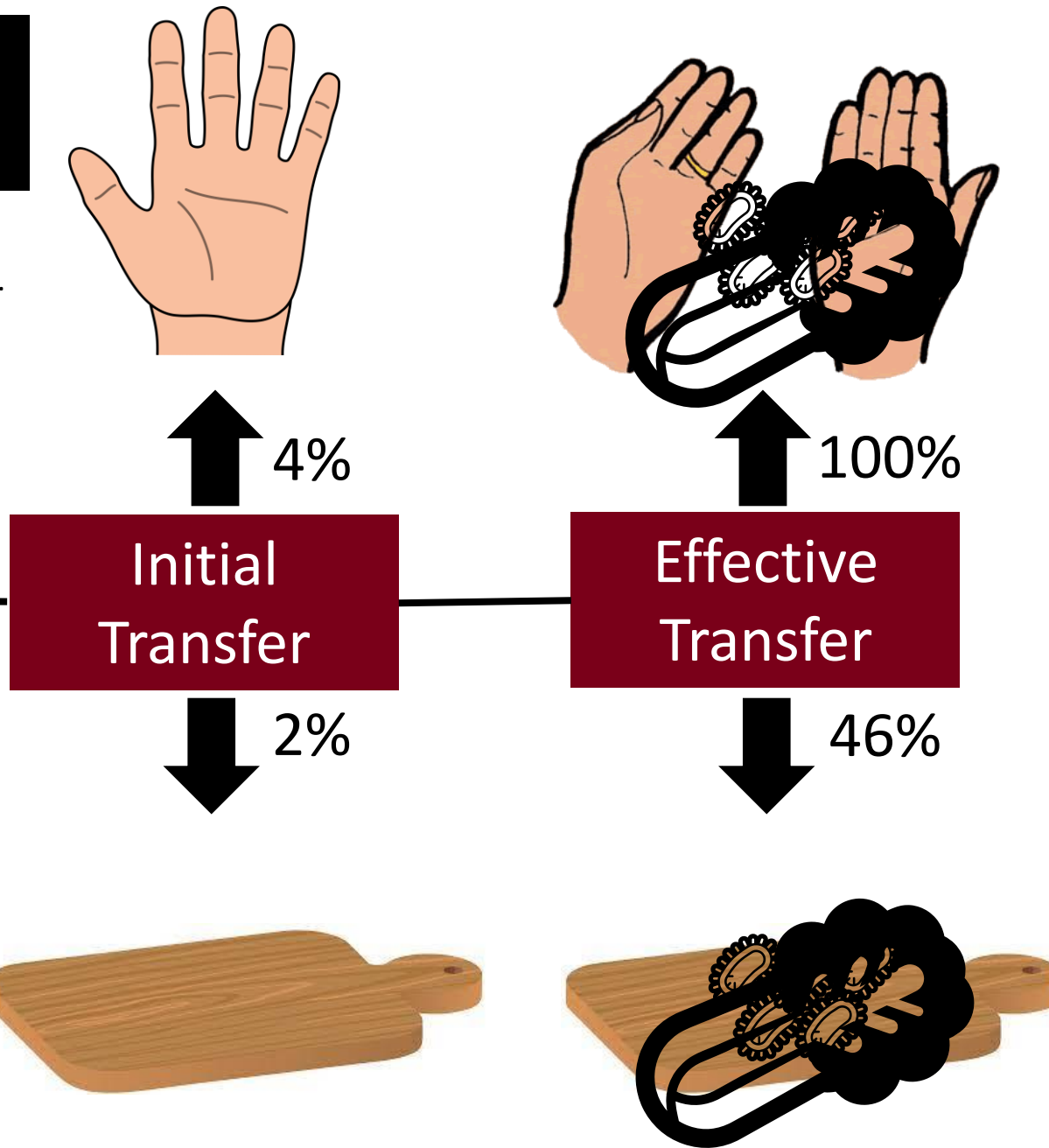
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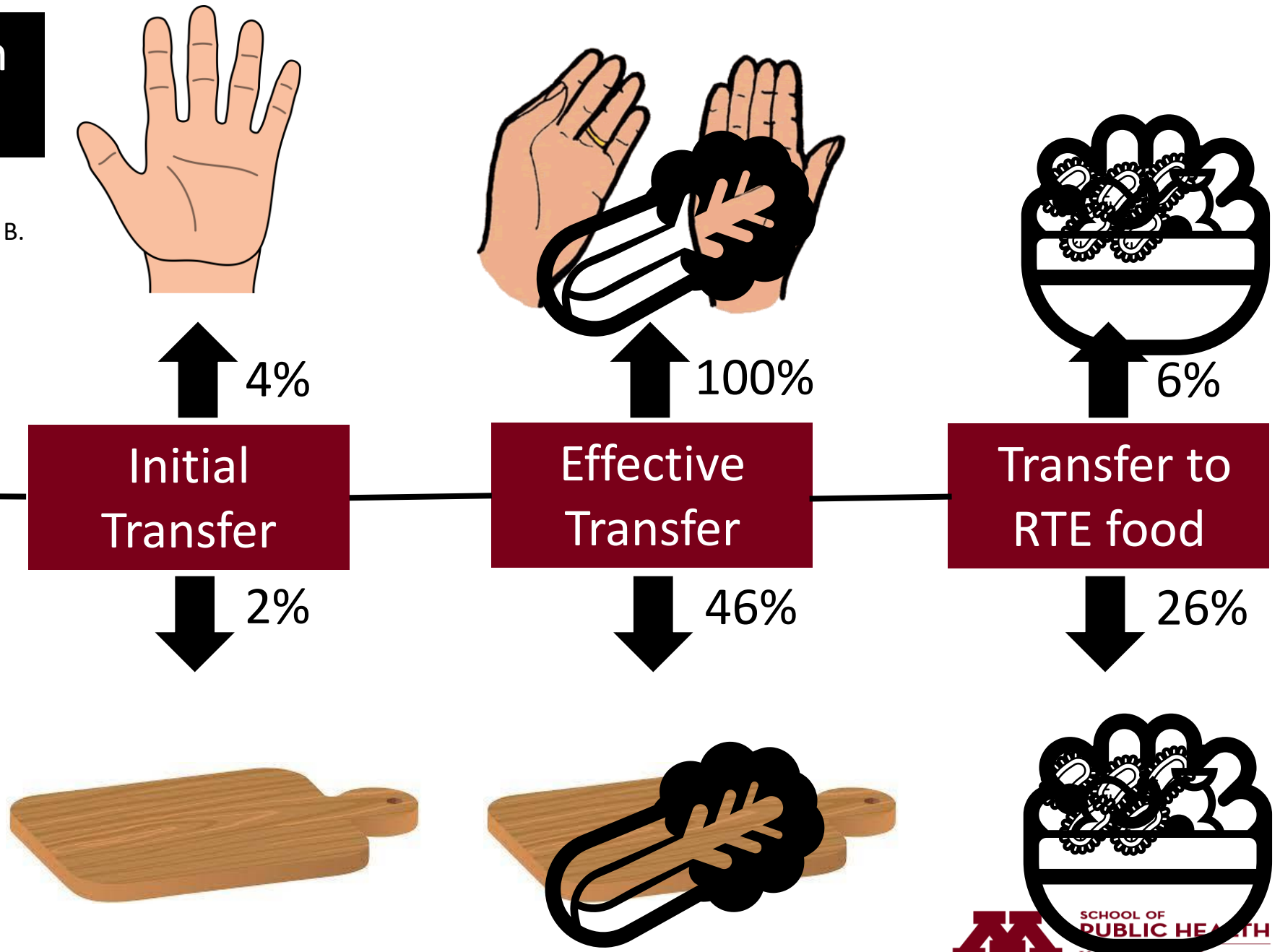
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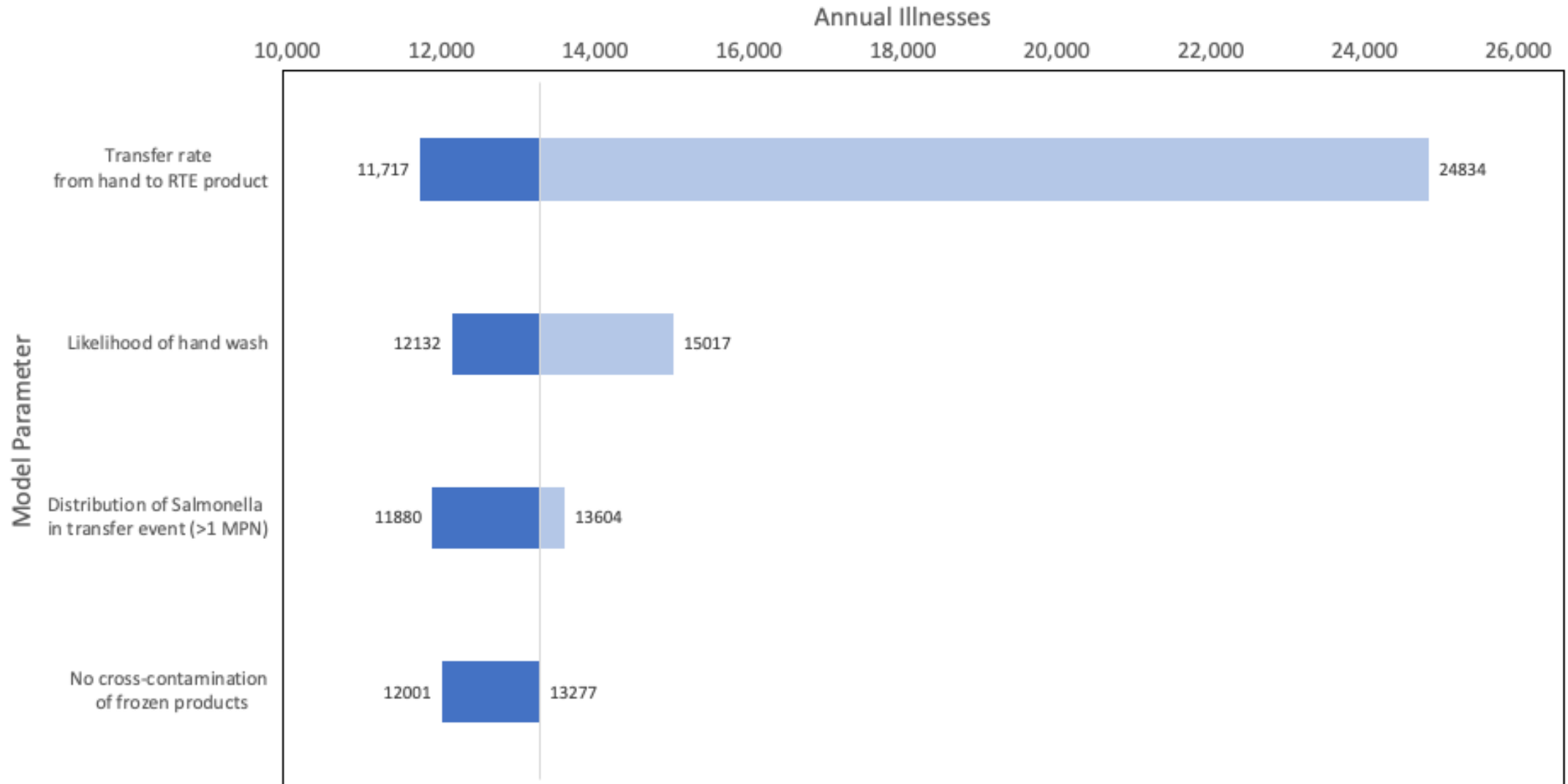


Ground pork model estimates for cross-contamination scenarios at baseline

Cross-contamination Scenario	Annual Illnesses (90% CI)	Increase from Baseline (%)*
Unwashed Hands n = 1,528,676	11,400 (6983, 17240)	7.65
Unwashed Board n = 780,265	11,041 (6764, 16698)	4.26
Unwashed Hands or Board n = 2,308,941	11,851 (7263, 17993)	11.9

*Compared to 10,590 annual illnesses at baseline without cross-contamination incorporated

Tornado diagram illustrating sensitivity analysis of cross-contamination model



Research Highlights

Consumption Model	Baseline	Removal of lots >10 MPN/g (% decrease)	Removal of lots >1 MPN/g (% decrease)	After Cross-contamination (% increase)
Ground Beef	8,980	7,759 (13.6)	5,686 (36.7)	15,310 (70.5)
Ground Pork	10,590	-	5,632 (46.8)	11,851 (11.9)

- >90% annual illnesses attributable to high virulence NTS serotypes
- Significant illness reduction at each pathogen concentration threshold
- Cross-contamination effectively managed after removal of highly contaminated production lots

Impacts for Industry

- Most ground pork is contaminated at low concentrations and majority of *Salmonella* serotypes not highly virulent.
- Human illnesses are driven by high levels of contamination and highly virulent *Salmonella* serotypes.
- **To reduce *Salmonella* illnesses due to consumption of pork, identify and remove products**
 - contaminated above threshold of 1MPN/g
 - contaminated with virulent *Salmonella* serotypes

Data Gaps to Improve Risk Assessment Models

- Dose-response relationships for *Salmonella* strains
- Levels of detection for testing
- Ground pork cooking practices and preferences
- Cross-contamination coefficients
- Product transportation conditions (time and temperature)

