Beef Safety Breakout: Salmonella Risk Assessment & Lymph Node Research

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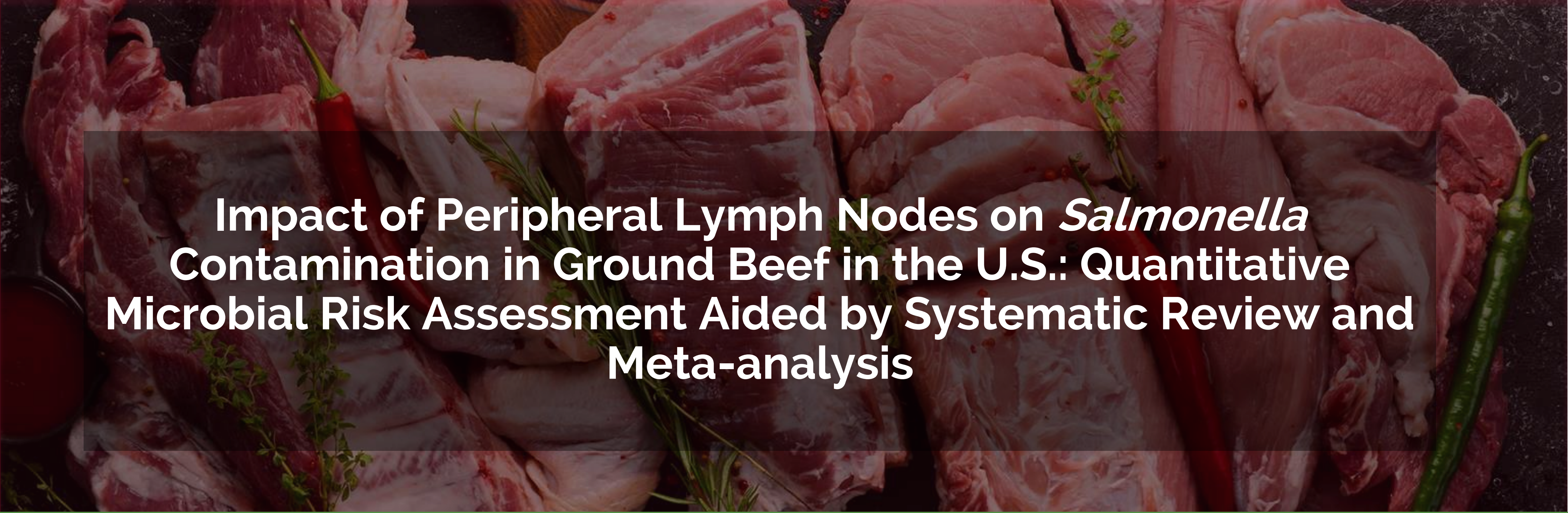

Impact of Peripheral Lymph Nodes on *Salmonella* Contamination in Ground Beef in the U.S.: Quantitative Microbial Risk Assessment Aided by Systematic Review and Meta-analysis

Ilhami Okur[1], Dayna M. Harhay[2], John W. Schmidt[2], Terrance M. Arthur[2], Annette M. O'Connor[3], Xiang Yang[5] , Omar A. Oyarzabal[4], Bing Wang[1]

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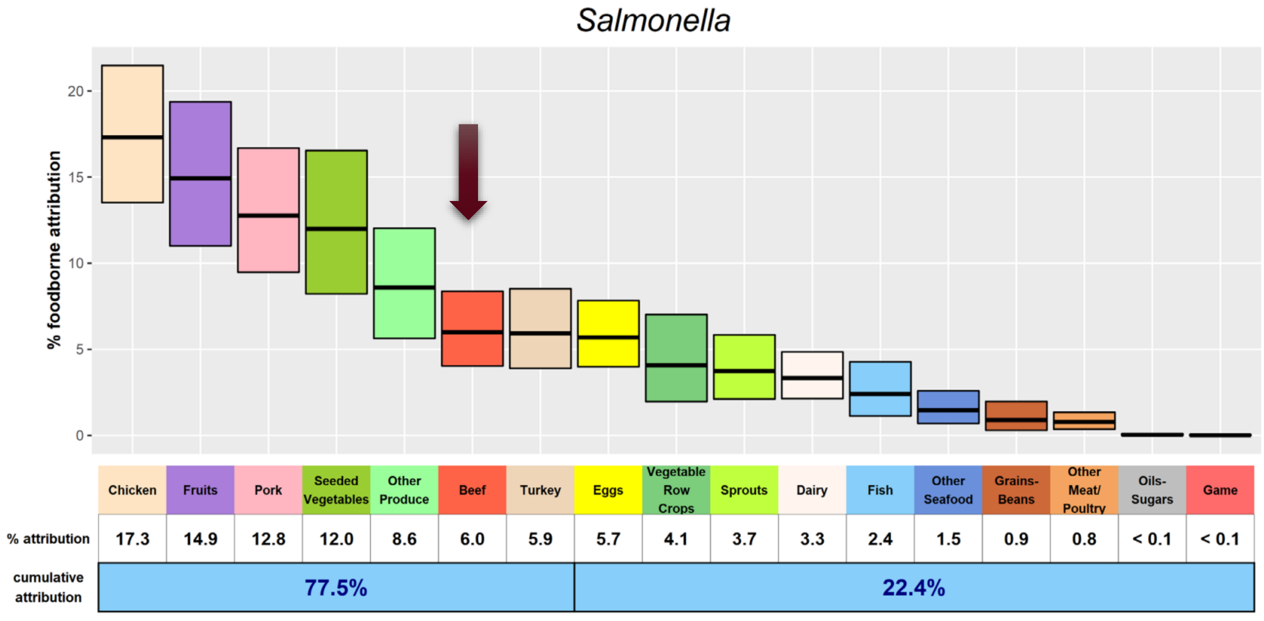
Salmonellosis in the U.S.

- Salmonellosis in the U.S.:
    - Among the top 5 foodborne pathogens causing illness, hospitalizations, and deaths
    - 1.35 million illnesses, more than 26,000 hospitalizations, 420 deaths yearly
    - Total annual costs attributable to *Salmonella*: $4.1 billion
- Source attribution (IFSAC 2020)
    - A wide variety of foods
    - Beef among the 7 highest contributing food commodities
    - Beef contribution: 6%



	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%									

Health Risks of Ground Beef

- Not all beef products of equal risk
  - CDC, *Salmonella* outbreaks linked to beef, 2012 – 2019 (Canning *et al.* 2023)

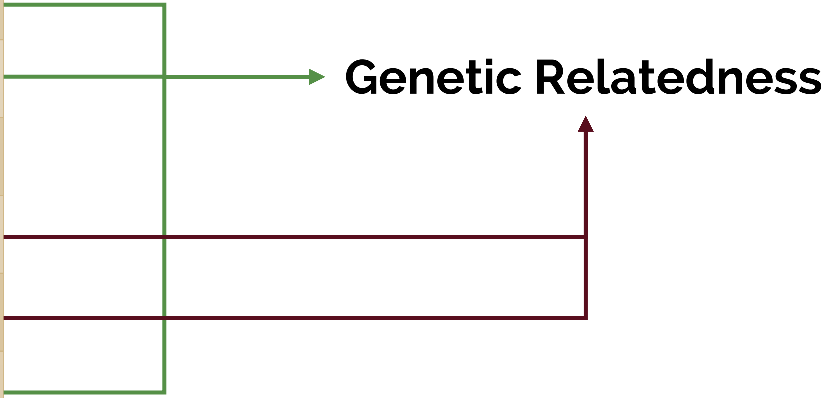
	Beef (Total)	Ground Beef
Outbreaks	27	12 (44%)
Illnesses	1103	800 (73%)
Deaths	2	2 (100%)

- Outbreaks associated with ground beef have not decreased
  - Illnesses since 2016 as many as during previous 36 years
- Urgent needs in interventions at production, at slaughter and processing, and during preparation

Salmonella in Ground Beef

- Main sources: hide and peripheral lymph nodes (Koohmaraie *et al*. 2012)

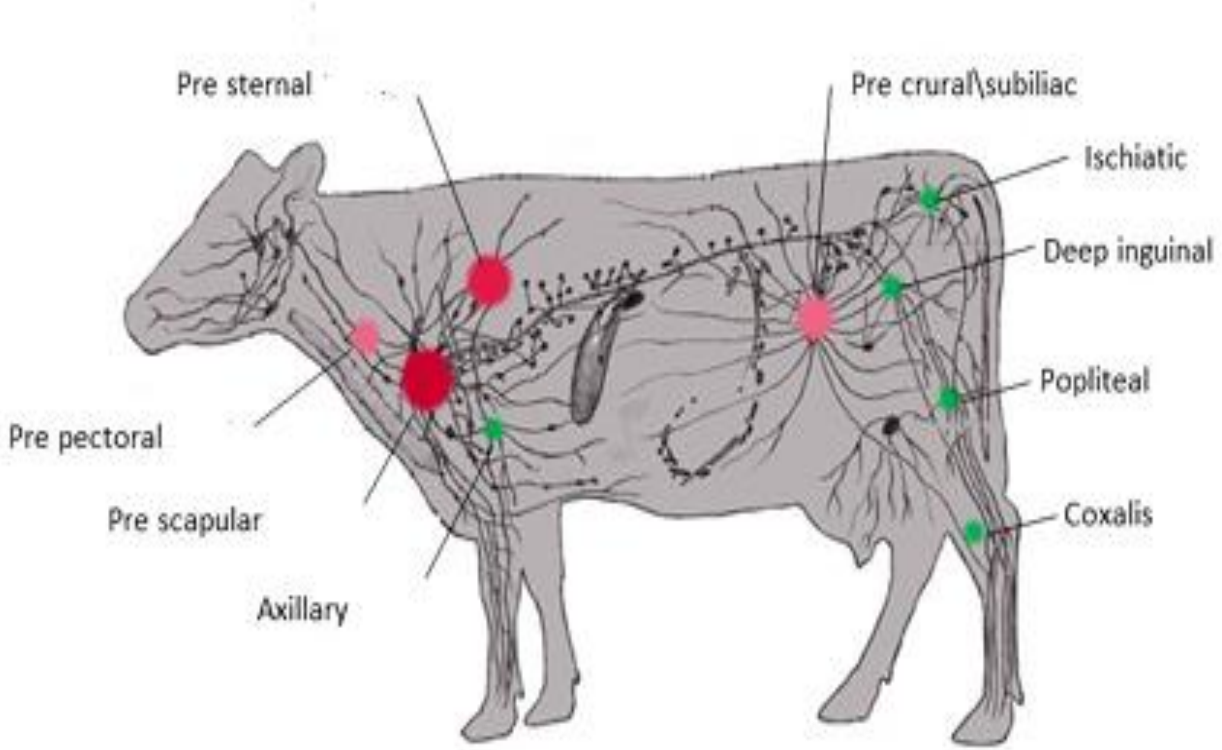
Samples	Prevalence
Hide	96%
Carcasses before interventions	47%
Carcasses after interventions	0%
Peripheral lymph nodes	18%
Trim	7%
Ground beef	2%



- Minimize the hide-to-carcass transfer and inclusion of lymph nodes

Salmonella in Peripheral Lymph Nodes

- Important part of immune system, filters for foreign particles
- Mesenteric lymph nodes vs PLNs.
- PLNs can harbor pathogens, including *Salmonella*.
- Important contamination source of *Salmonella* in ground beef.



Goal and Specific Objectives

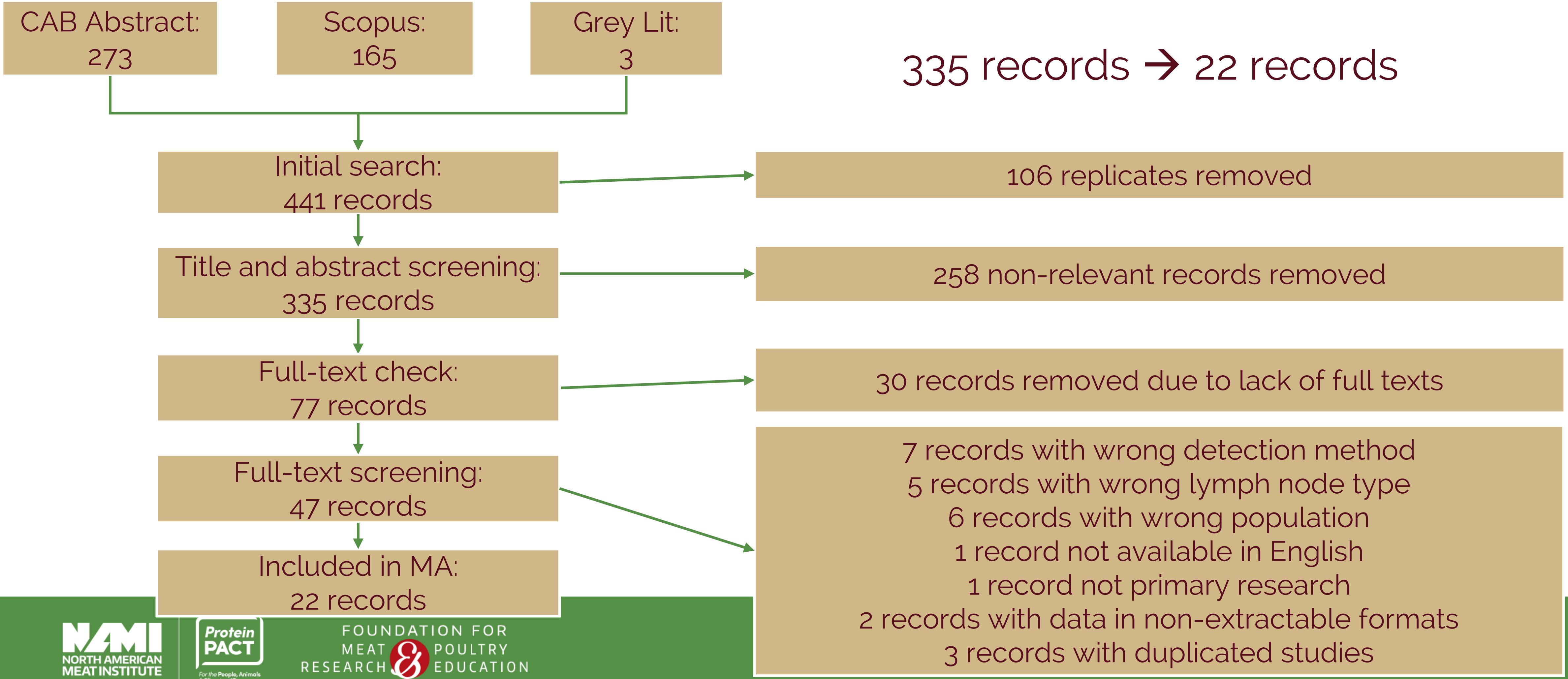
- **Risk management goal:** Determine the contribution of endogenous extra-intestinal sources of *Salmonella* (i.e., lymph nodes) to reduce foodborne infections caused by *Salmonella*.
- **Objective 1.** Characterize the distribution of both prevalence and concentration of *Salmonella enterica* in bovine PLNs by lymph node type, production source, region, and season.
- **Objective 2.** Assess the relative contribution of PLNs to the public risks imposed by the consumption of ground beef, and identify critical control points in the slaughter-to-table continuum in reducing human salmonellosis associated with the consumption of ground beef in the US.

Obj. 1 Distribution of *Salmonella* in PLNs

- **Method:** Systematic review and meta-analysis
- **Review question:** "*What are the prevalence and levels of* Salmonella *in PLNs of beef and dairy cattle*?"
- **Searching strategy and eligibility determination**
  - CoCoPop: *Salmonella*, PLNs, beef and dairy cattle, in the U.S.
  - Electronic databases (Scopus and CAB Abstracts) and grey literature
  - Stepwise screening
  - Quality assessment: appraisal tool for prevalence studies with modified questions
- **Data synthesis → Obj. 2**
  - Random-effects meta-analysis using 'metaphor' in R

Flowchart of Systematic Review

335 records → 22 records



CAB Abstract:
273

Scopus:
165

Grey Lit:
3

Initial search:
441 records

106 replicates removed

Title and abstract screening:
335 records

258 non-relevant records removed

Full-text check:
77 records

30 records removed due to lack of full texts

Full-text screening:
47 records

7 records with wrong detection method
5 records with wrong lymph node type
6 records with wrong population
1 record not available in English
1 record not primary research
2 records with data in non-extractable formats
3 records with duplicated studies

Included in MA:
22 records

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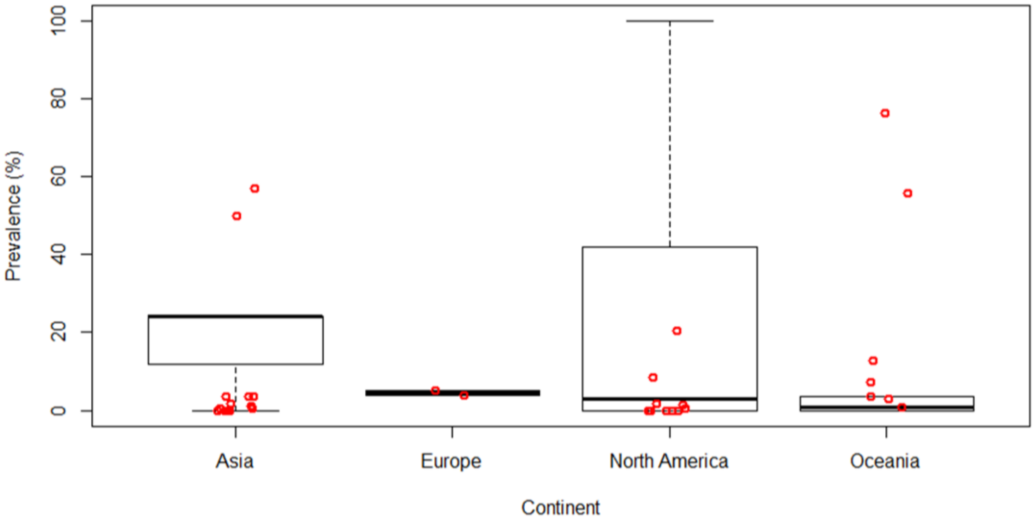
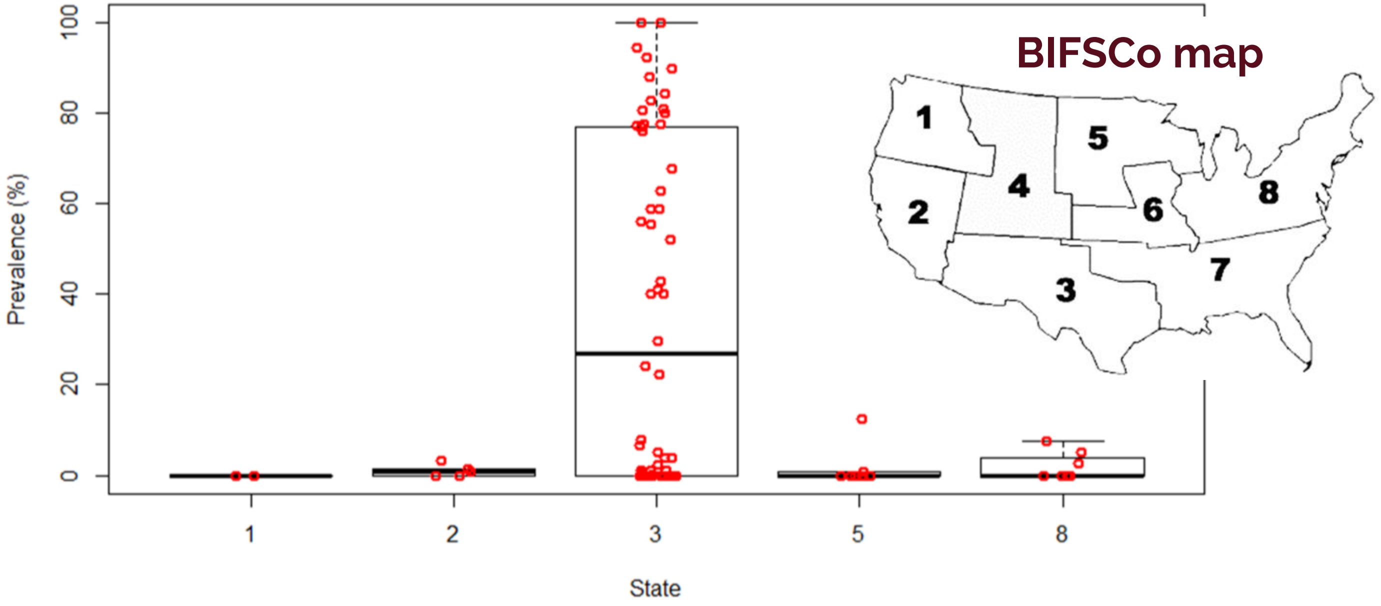
Overall Prevalence in PLNs

Study #	Sample Size	Prevalence [95% CI]	I^2	P-value, Heterogeneity
22	17,073	13% [9%, 18%]	97.7	<0.0001



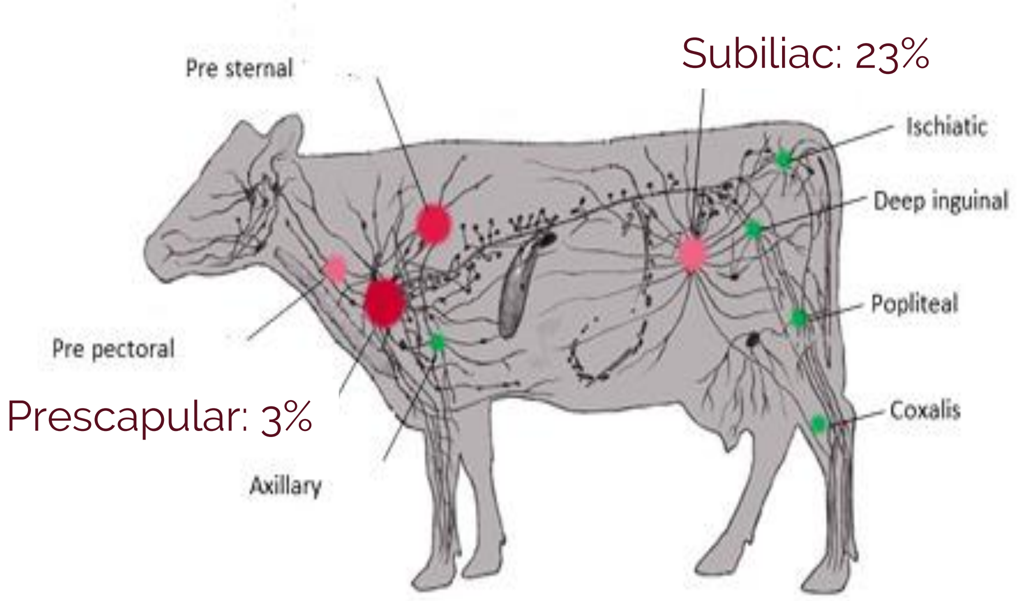


Majority of studies (14/22, 63.6%) were in the U.S., showing a prevalence of 16% (12%,23%).

Prevalence by LN Type and Season

LN Type	Study #	Sample Size	Prevalence %
Subiliac	10	7019	23 (13, 33)
Iliofemoral	2	184	34 (0, 100)
Retropharyngeal	1	28	4 (0, 15)
Prescapular	1	240	3 (0, 10)
Prefemoral	1	240	2 (0, 2)
Unspecified	4	6073	7 (1, 15)

Season	Study #	Sample Size	Prevalence %
Cool	7	5827	3 (1, 6)
Warm	10	5717	11 (5, 18)



Subiliac: 23%

Prescapular: 3%

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Serotype and Antibiotic Resistance

Serotype	Study #	Sample Size	Serotype %
S. Enteritidis	1	283	25%
S. Cerro	6	806	17%
S. Montevideo	6	869	17%
S. Reading	2	347	16%
S. Anatum	7	887	15%
S. Mbandaka	4	726	14%
S. Typhimurium	6	383	13%
S. Muenchen	4	780	10%
S. Kentucky	4	787	9%
S. Lille	2	12	8%
S. Brandenburg	2	148	6%
S. Give	2	38	5%
S. Infantis	2	345	1%

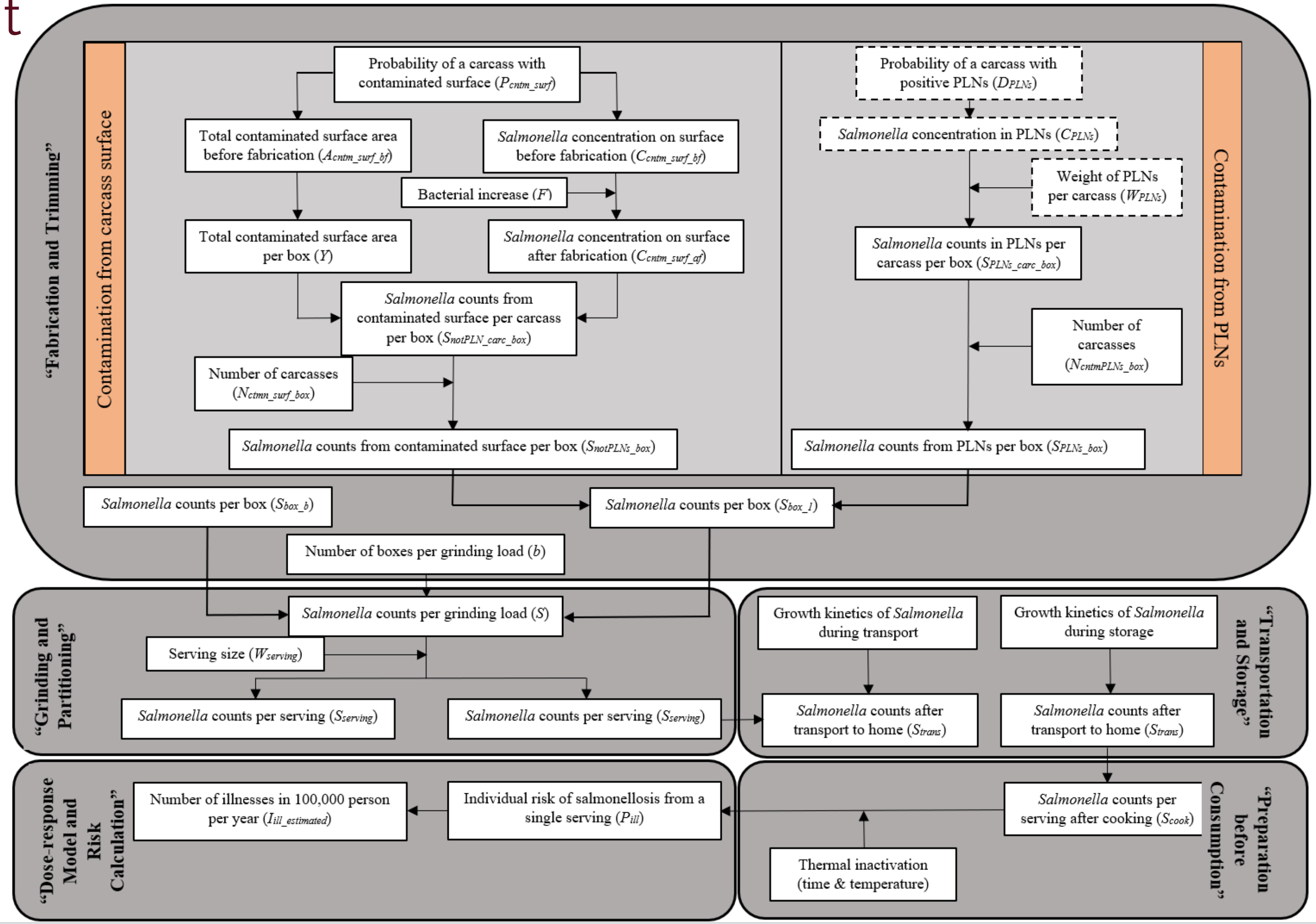
Antibiotics	Study #	Sample Size	Resistance %
Neomycin	1	5	60%
Multi-drug resistance	3	290	37%
Tetracycline	3	290	36%
Streptomycin	3	290	35%
Chloramphenicol	3	290	33%
Ampicillin	3	290	25%
Sulfa-trimethoprim	2	23	24%
Cefoxitin	3	290	19%
Ceftiofur	3	290	18%
Gentamycin	3	56	17%
Ceftriaxone	3	290	16%
Kanamycin	2	51	10%
Sulfioxazile	1	266	9%

Lack of Data on Concentration

- Only three studies (vs 22 reporting prevalence data).
- Diverse reporting styles: tabular vs graphical, on gram or LN basis.
- The *Salmonella* concentration of overall studies was found as 1.5 log cfu/g (95%CI: 0.5, 2.8 log cfu/g) according to 838 sample size.
- Not enough data for a stratified analysis.

Obj. 2 Impact of PLNs

- Quantitative microbial risk assessment
  - Modular Process Risk Model
- Slaughter to table
  - Fabrication and trimming
  - Grinding and partitioning
  - Transport and storage
  - Cooking
- Dose-response model
- Risk characterization
  - # of illnesses / 100,000 population



“Fabrication and Trimming”

Contamination from carcass surface

Probability of a carcass with contaminated surface (P_{cntm_surf})

Total contaminated surface area before fabrication ($A_{cntm\_surf\_bf}$)

Salmonella concentration on surface before fabrication ($C_{cntm\_surf\_bf}$)

Bacterial increase (F)

Total contaminated surface area per box (Y)

Salmonella concentration on surface after fabrication ($C_{cntm\_surf\_af}$)

Salmonella counts from contaminated surface per carcass per box ($S_{notPLN\_carc\_box}$)

Number of carcasses ($N_{ctmn\_surf\_box}$)

Salmonella counts from contaminated surface per box ($S_{notPLNs\_box}$)

Contamination from PLNs

Probability of a carcass with positive PLNs (D_{PLNs})

Salmonella concentration in PLNs (C_{PLNs})

Weight of PLNs per carcass (W_{PLNs})

Salmonella counts in PLNs per carcass per box ($S_{PLNs\_carc\_box}$)

Number of carcasses ($N_{cntmPLNs\_box}$)

Salmonella counts from PLNs per box (S_{PLNs_box})

Salmonella counts per box (S_{box_b})

Salmonella counts per box (S_{box_1})

Number of boxes per grinding load (b)

“Grinding and Partitioning”

Salmonella counts per grinding load (S)

Serving size ($W_{serving}$)

Salmonella counts per serving ($S_{serving}$)

Salmonella counts per serving ($S_{serving}$)

“Transportation and Storage”

Growth kinetics of *Salmonella* during transport

Growth kinetics of *Salmonella* during storage

Salmonella counts after transport to home (S_{trans})

Salmonella counts after transport to home (S_{trans})

“Preparation before Consumption”

Salmonella counts per serving after cooking (S_{cook})

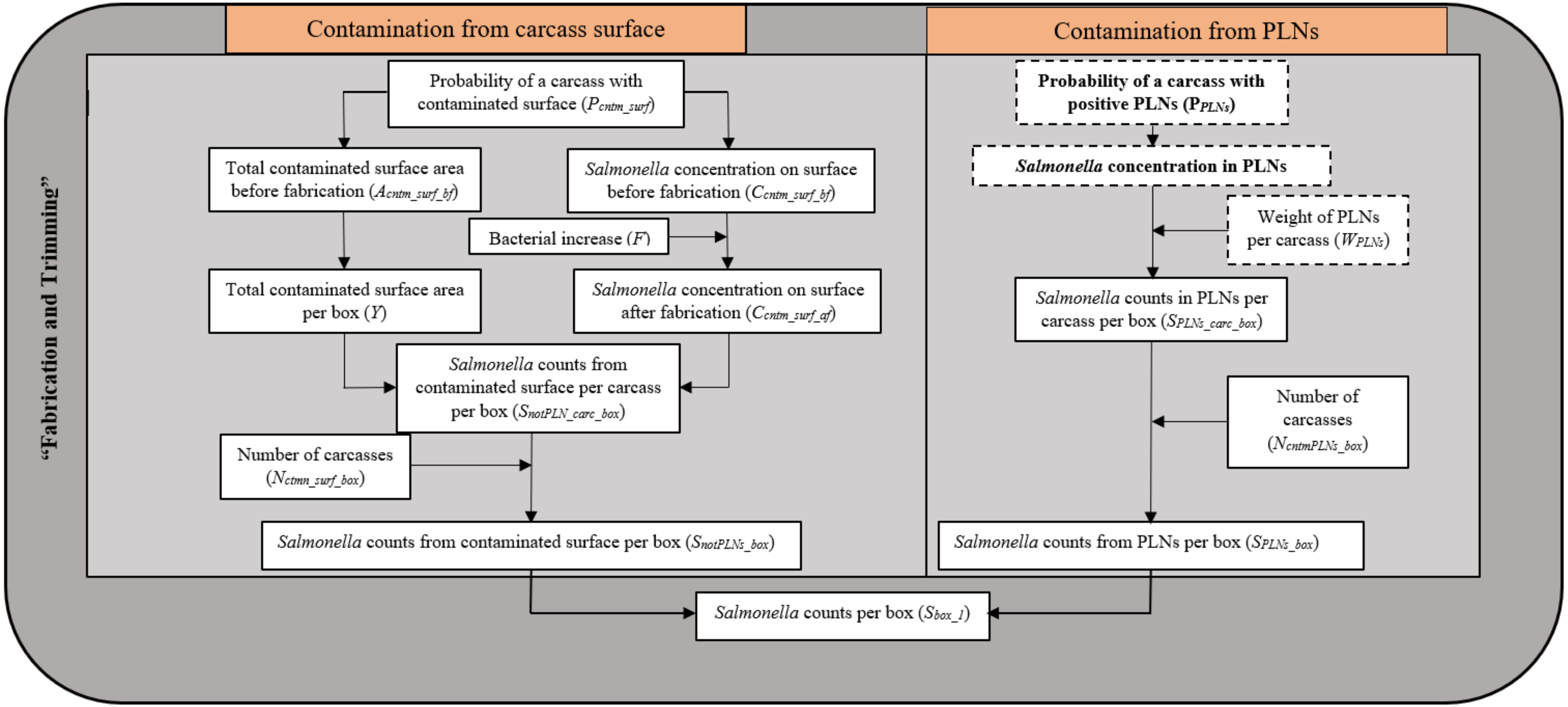
Thermal inactivation (time & temperature)

“Dose-response Model and Risk Calculation”

Individual risk of salmonellosis from a single serving (P_{ill})

Number of illnesses in 100,000 person per year ($I_{ill\_estimated}$)

Module – Fabrication & Trimming



“Fabrication and Trimming”

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Number of carcasses ($N_{ctmn\_surf\_box}$)

Salmonella counts from contaminated surface per box ($S_{notPLNs\_box}$)

Contamination from PLNs

Probability of a carcass with positive PLNs (P_{PLNs})

***Salmonella* concentration in PLNs**

Weight of PLNs per carcass (W_{PLNs})

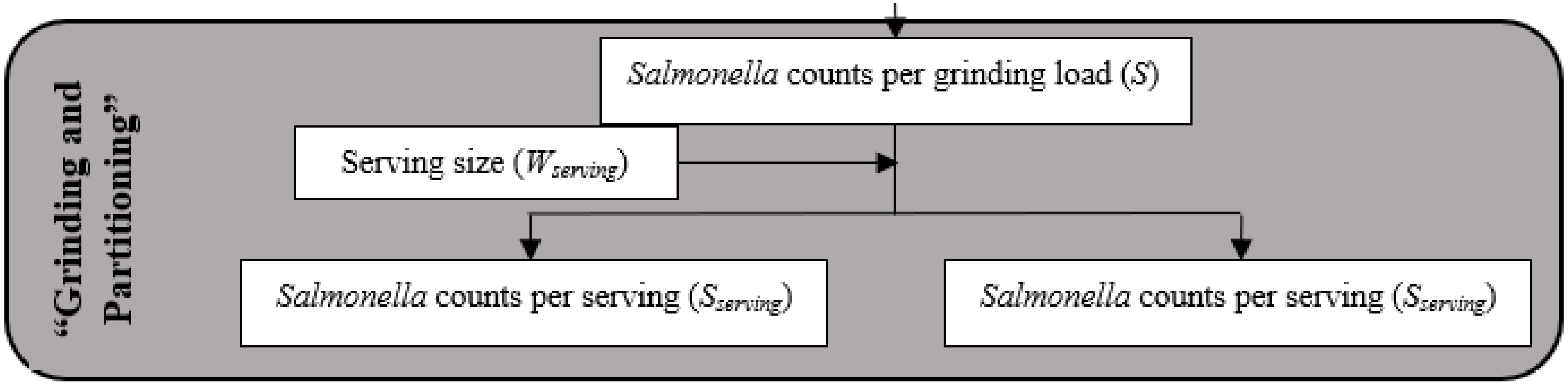
Salmonella counts in PLNs per carcass per box ($S_{PLNs\_carc\_box}$)

Number of carcasses ($N_{cntmPLNs\_box}$)

Salmonella counts from PLNs per box (S_{PLNs_box})

Salmonella counts per box (S_{box_1})

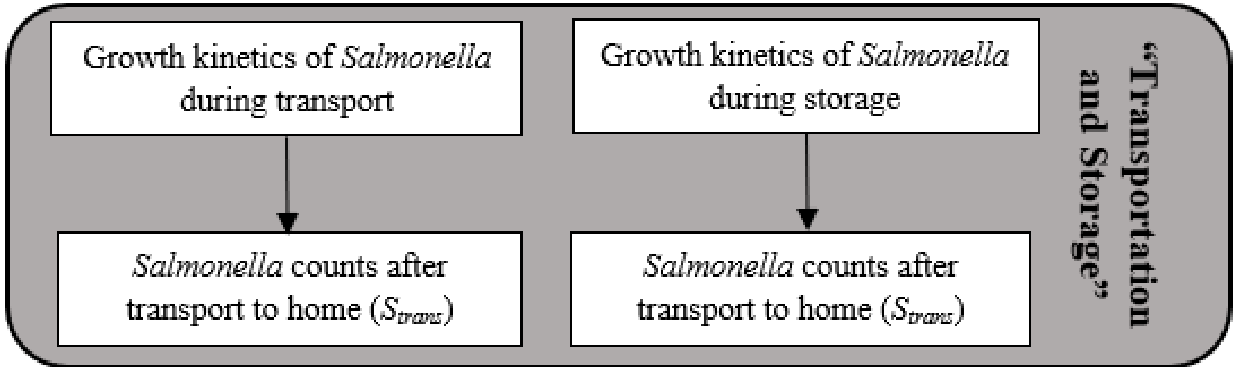
Module – Grinding & Portioning



Assumptions

- *Salmonella* population remained constant due to qualified control of the cold temperature during processing.
- The distribution of *Salmonella* in ground beef is homogeneously distributed.

Modules – Transport, Storage & Cooking



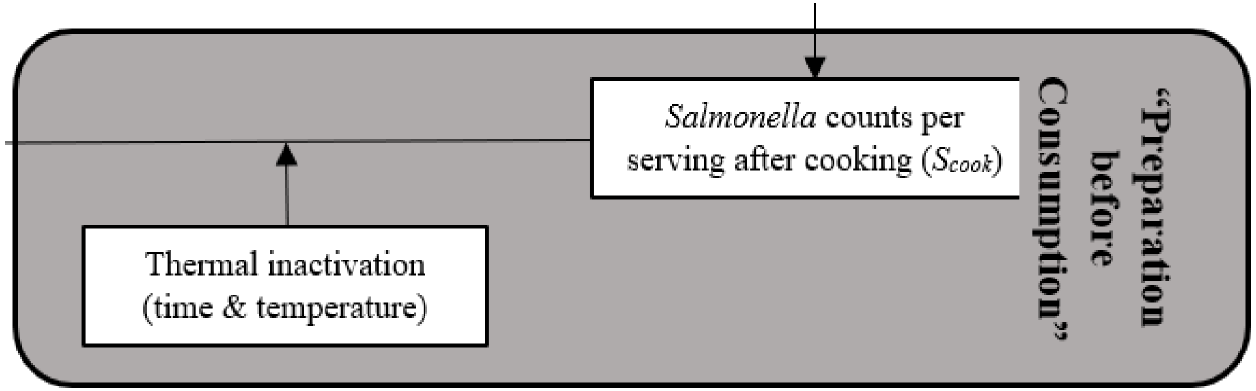
Growth kinetics of *Salmonella* during transport

Salmonella counts after transport to home (S_{trans})

Growth kinetics of *Salmonella* during storage

Salmonella counts after transport to home (S_{trans})

"Transportation and Storage"



Salmonella counts per serving after cooking (S_{cook})

Thermal inactivation (time & temperature)

"Preparation before Consumption"

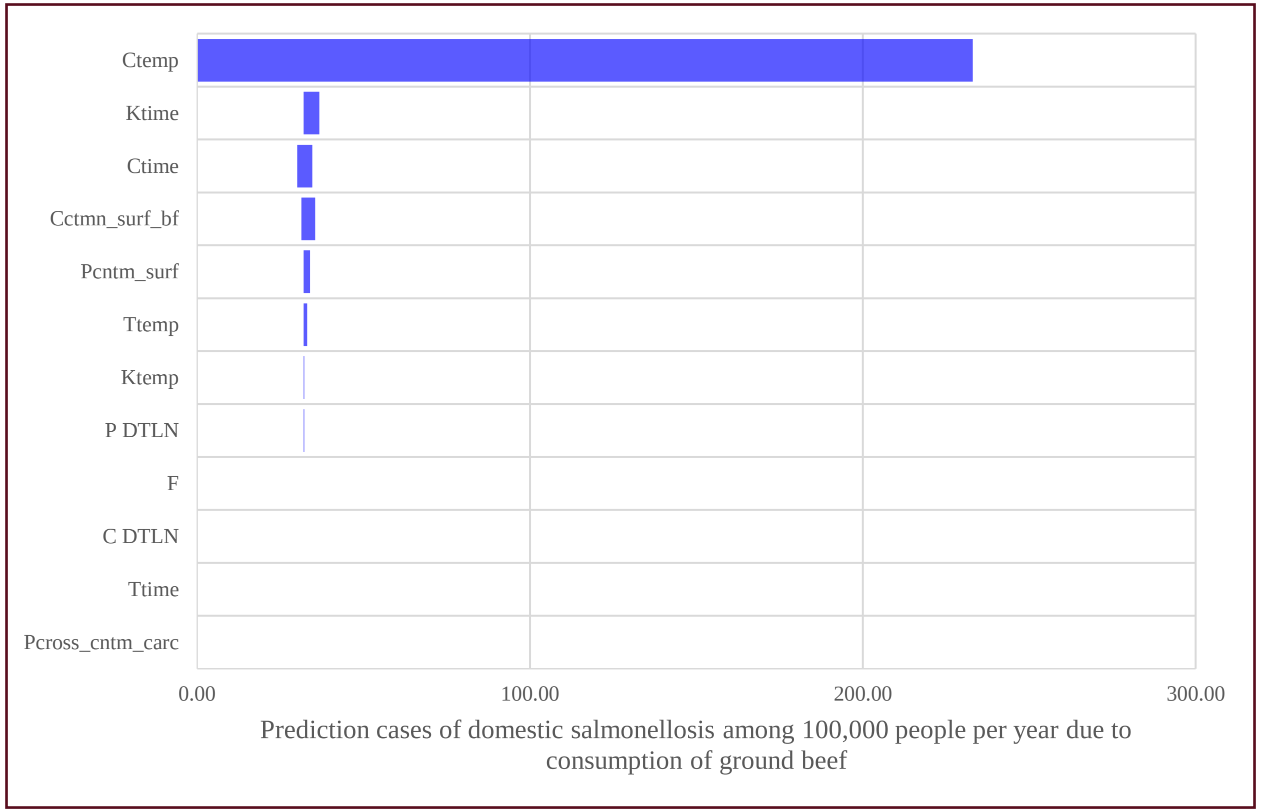
- *Salmonella* population remained constant due to qualified control of the cold temperature during
  - Transport from plant to retail
  - Storage at retail

- No effect of cross-contamination
  - Ground beef is generally cooked without cutting or washing steps

Baseline Risk Estimate

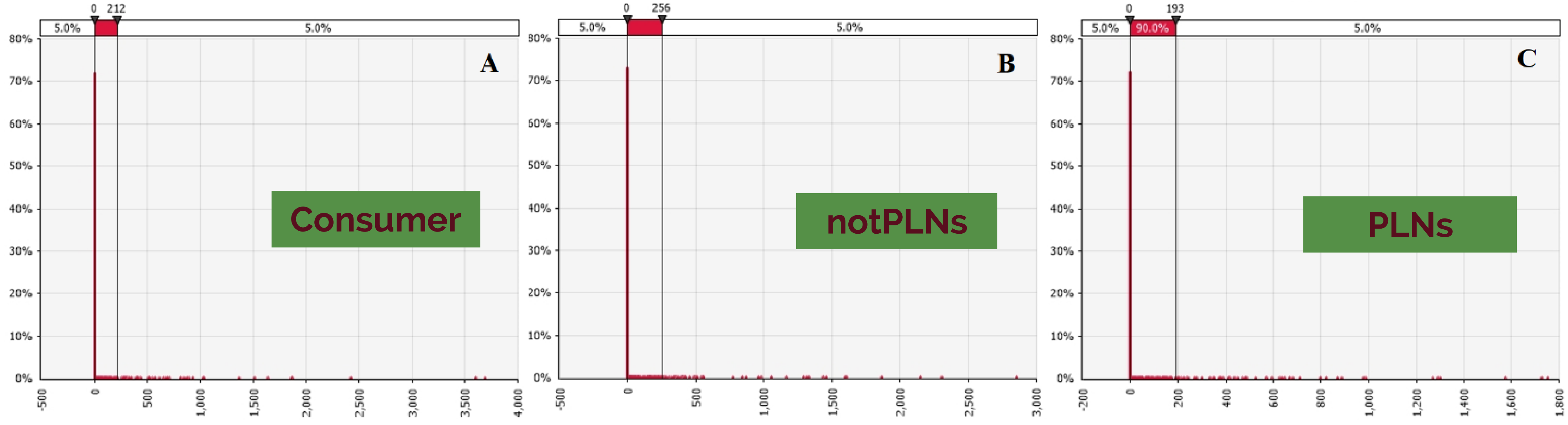
- Population risk of the predicted number of salmonellosis cases among 100,000 persons in U.S. because of consumption of ground beef was estimated as 45.0 cases (90% CI: 22.9-67.2).
    - Highly skewed to the right with the 25th percentile, median, and 75th percentile values of 0, 0, and 0, resulting in a great difference between median and mean values.
- Model validation: Back calculation from CDC estimate, 1.35 million cases and 6% attributable to beef → 24 / 100,000.

Influential Factors



- Sensitivity analysis
- Top factors: Cooking Temperature and time, Storage time
- Surface contam > PLNs

Impact of PLNs and Other Sources



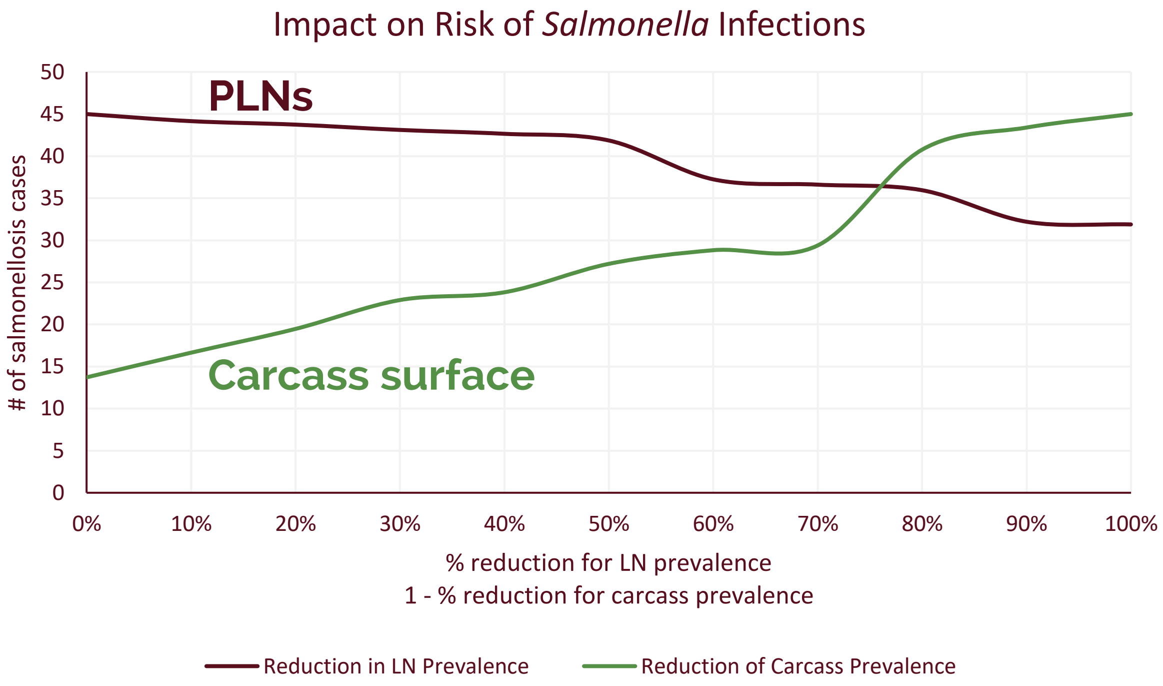
Ranges: 0-4000 for consumer 0-3000 for notPLNs 0-1800 for PLNs

The frequency distributions of the predicted average number of human salmonellosis cases due to the variation of input variables grouped by different sources of contamination

Impact of PLNs and Carcass Surface

Based on our model,

- ~30% of salmonellosis cases related to ground beef can be attributable to the contamination in PLNs.
- 0.5 log ↓ in PLNs → 20% ↓ in cases.
- 0.5 log ↓ on carcass surface → 40% ↓ in cases.



Take Home Messages

- Detection of *Salmonella* in bovine PLNs is not uncommon.
- Reduction of *Salmonella* in PLNs can be associated with noticeable reduction in salmonellosis cases posed by ground beef consumption.
- Interventions to control *Salmonella* on carcass surface may be more effective.
- More factors need to assessed, such as costs, technology, and feasibility.
- Model improvement: more concentration data, data allowing for differentiation in virulence.

Acknowledgements

- This study was supported by a grant from the Beef Checkoff administered by the Foundation for Meat and Poultry Research and Education
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Salmonella control in beef production risk-based methods and virulence

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Salmonella serovars exhibit different "virulence"

Hospitalization %

S. Dublin ≈ 67%

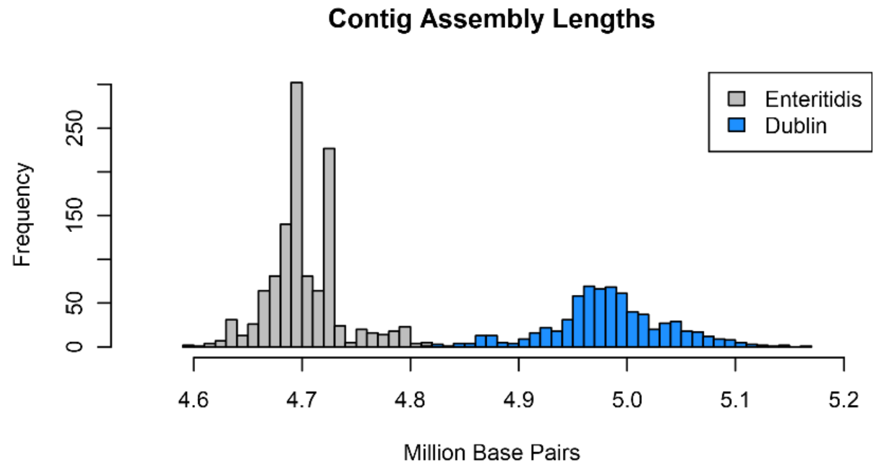
S. Enteritidis ≈ 21%

Mortality %

S. Dublin ≈ 3.0%

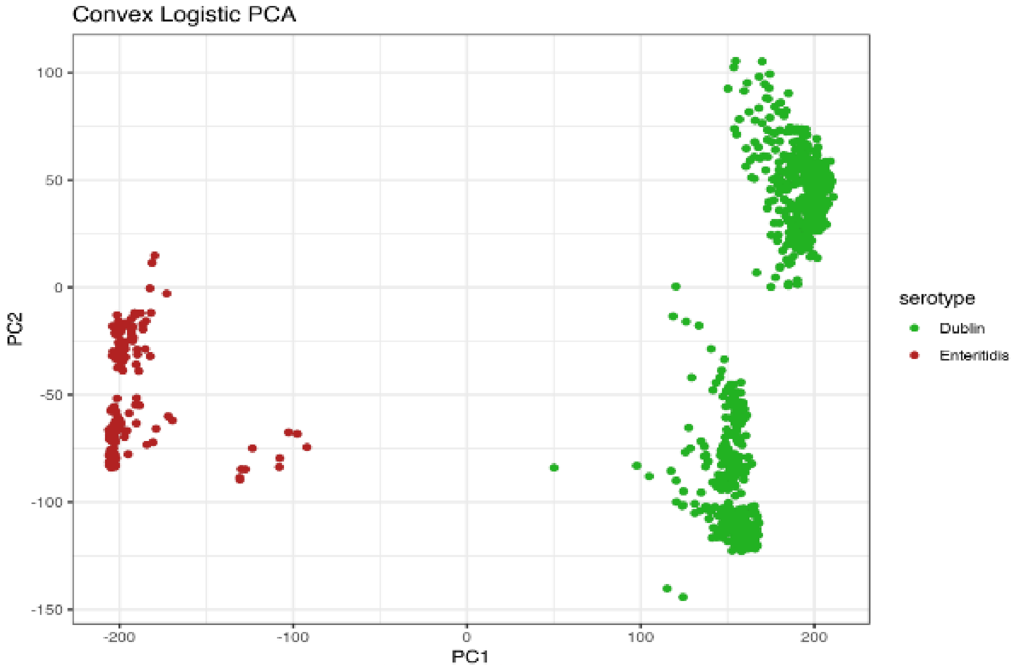
S. Enteritidis ≈ 0.6%

Jones et al, 2008 [*https://doi.org/10.1086/588823*](https://doi.org/10.1086/588823)



Between and within serovar variation in genome composition

Pangenome PCA S. Dublin vs Enteriditis



Fenske et al, 2019 [*https://doi.org/10.1093/gbe/evz158*](https://doi.org/10.1093/gbe/evz158)

Virulence Factors (VF) - Genes that facilitate pathogenesis. Mechanisms not fully understood. Interactions even less.

Why don’t we just target top serovars in reported foodborne illnesses?

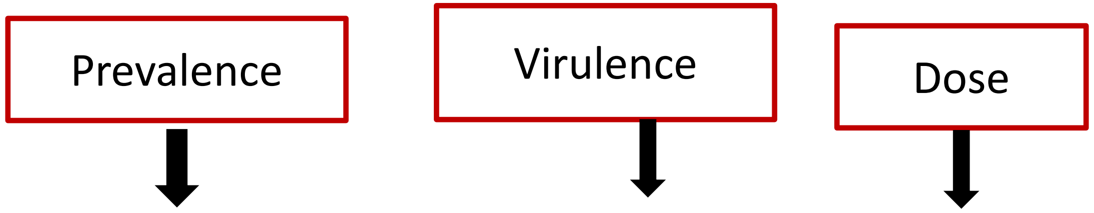
“Foodborne illness surveillance and monitoring systems **only detect a fraction of all cases** that occur, and **most reported cases do not have a known source**. Also, infrequent large events can have a marked effect on the case count in a given year. This adds **statistical “noise” to the numerical signal needed to detect temporal changes in foodborne salmonellosis trends and its main food sources.”**

NACMCF (2023) Response to Questions Posed by the Food Safety and Inspection Service: Enhancing Salmonella Control in Poultry Products
https://www.fsis.usda.gov/sites/default/files/media_file/documents/NACMCF%20Salmonella-Poultry17Mar2023.pdf

Ebel et al (2017)

- 4% confidence detect 10% ↓ ill **1 yr**
- <53% chance detecting 30% ↓ ill sustained **4 years**

https://www.sciencedirect.com/science/article/abs/pii/S2352352217301354



$$\text{Illnesses}_{NTS} \approx \#\text{ servings} \times \text{Proportion}_{NTS} \times \mathbf{Prob(ill|Exposed)}$$

Takeaways:

- Detecting risk trends takes time

- Prevalence and load matters

… can we use risk-based methods to achieve greatest public health gains?

Grouping isolates/serovars by virulence (Patent pending)

Results using the beef foodborne pathway shown here,
upcoming work incorporating other food sources

Collect sequence data from US surveillance programs 2013-2020

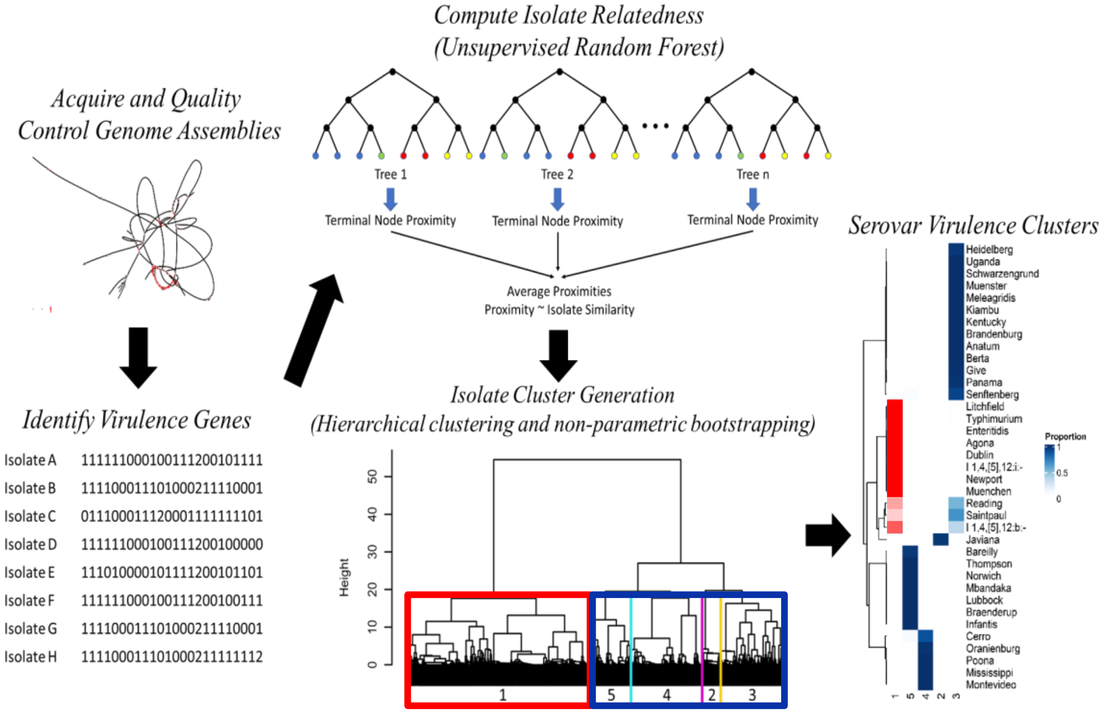
- (*n* = 12,337)
- 37 serovars (*n* ≥ 50 isolates with WGS data)
- Human (FoodNet and NORS): *n* = 6,751
- Bovine/beef (FSIS regulatory samples, NARMS FDA): *n* = 5,586

Group isolates based on genetics

- Using machine learning (random forest followed by hierarchical clustering)
- 182 virulence loci as grouping factors

Validate grouping with human disease outcomes

- Human cases from FoodNet (n=55,525)
  - Hospitalization
  - Invasive disease
  - Mortality
  - Frequency in exposure relative to incidence of disease



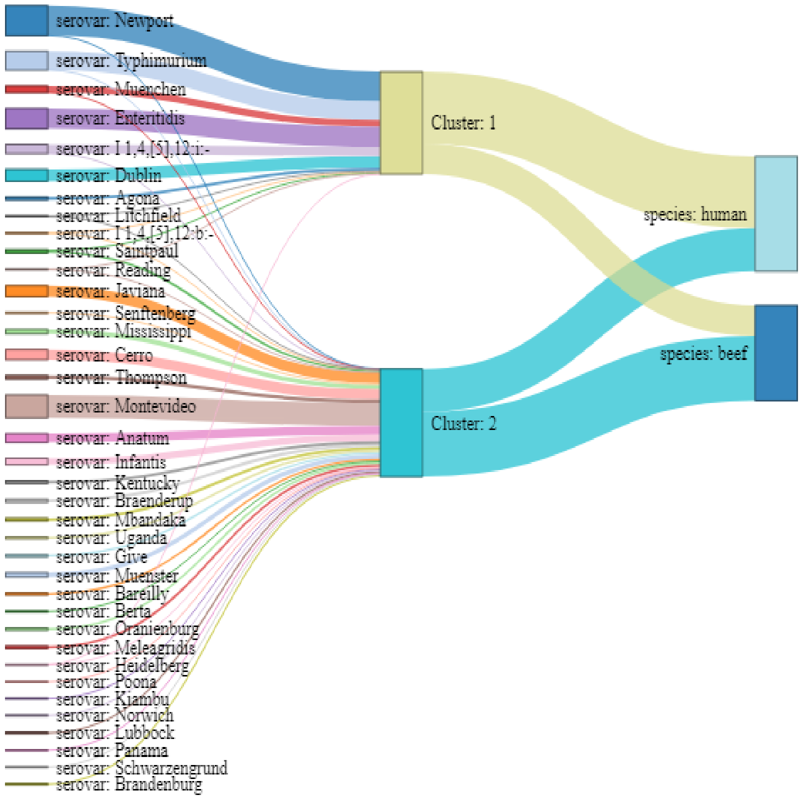
Isolate A	1111110001001112001011111
Isolate B	1111000111010002111110001
Isolate C	0111000111200011111111101
Isolate D	1111110001001112001000000
Isolate E	1110100001011112001011101
Isolate F	1111110001001112001001111
Isolate G	1111000111010002111110001
Isolate H	1111000111010002111111112

Pouzou J, Fenske G, Pouillot R, Costard S, Taylor D, Zagmutt F. I3S2022 conference, St Malo, France. https://www.i3s2022.com/content.php?PAGE=11

Higher (HV) and Lower Virulence (LV) groups

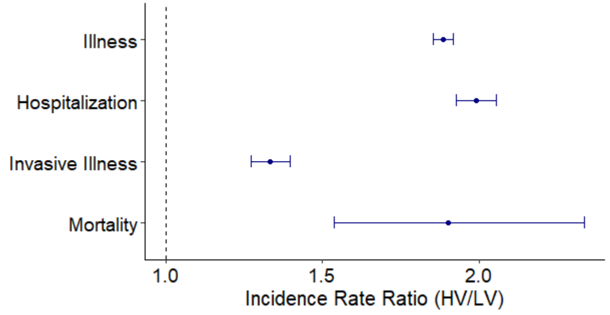
- Epi validation resulted in HV and LV groups, allocated isolates to serovar using majority rule
- Most often implicated in foodborne outbreaks of any cause AND
- In beef-associated outbreaks ***but not most common in beef***

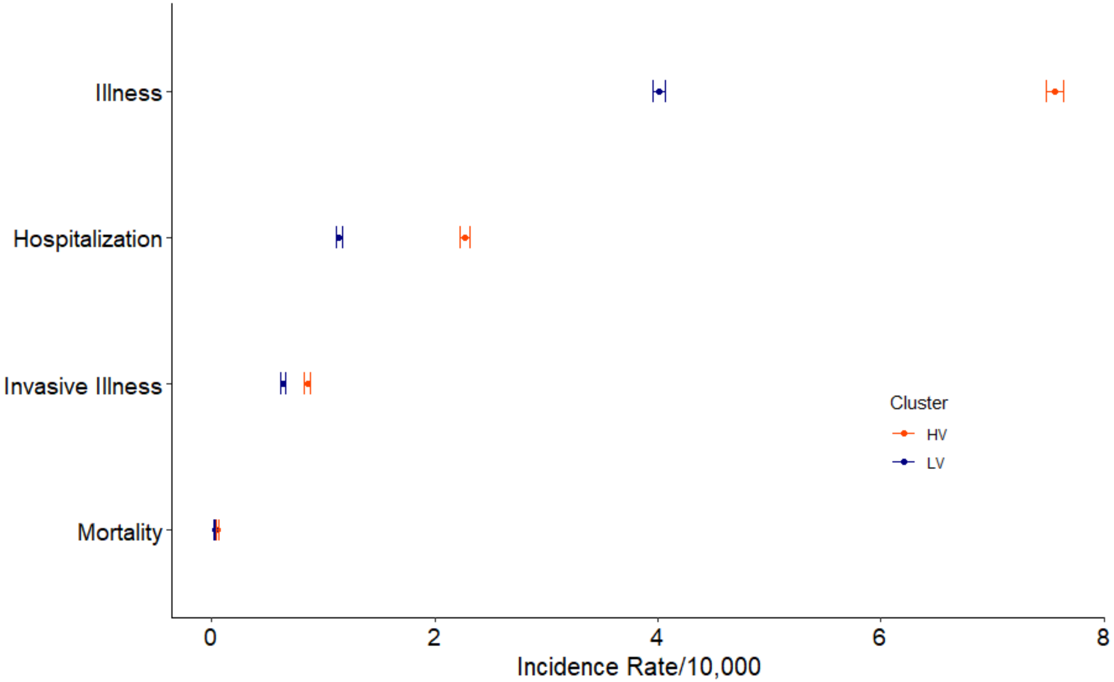
Relative appearance in beef (HV/LV): 0.44 (0.37 – 0.53)

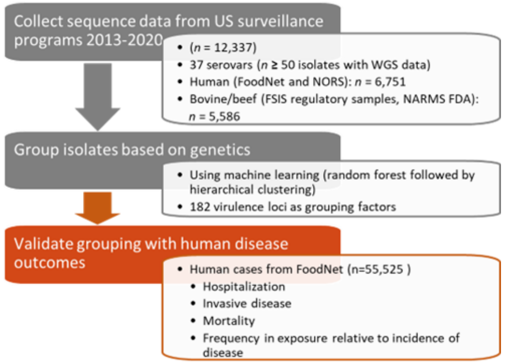


Higher virulence

Typhimurium
Enteritidis
I 1,4,(5),12:i:-
Newport
Muenchen
Paratyphi B
Dublin
Minority groups of St. Paul and Reading
Agona
Litchfield



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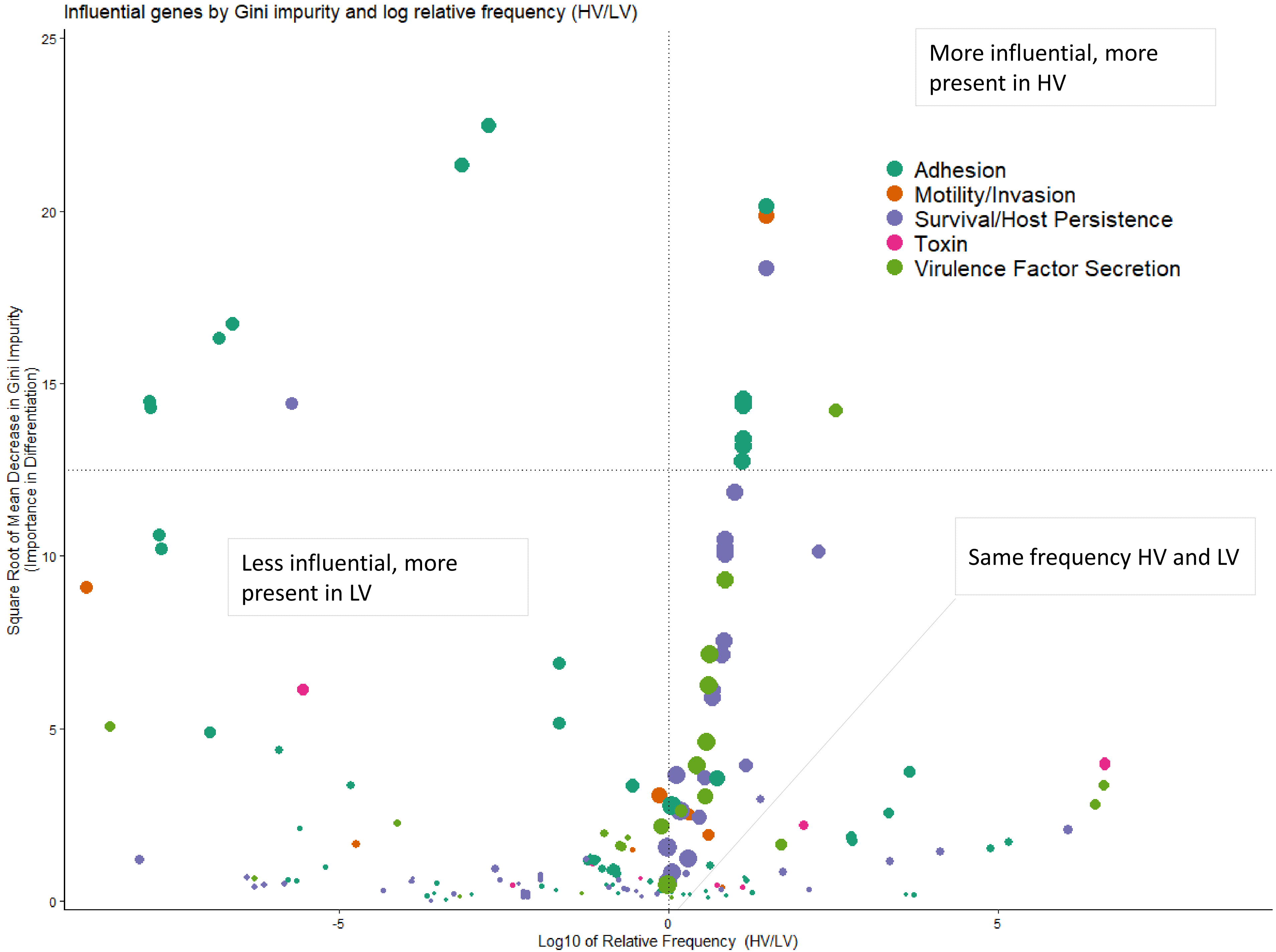
Gavin J. Fenske, Jane G. Pouzou, Régis Pouillot, Daniel D. Taylor, Solenne Costard, Francisco J. Zagmutt
medRxiv 2022.12.13.22283417; doi: https://doi.org/10.1101/2022.12.13.22283417

More influential

Size proportional to # of isolates carrying VF

Mechanism categories derived from VFDB/BV-BRC

Takeaway: no single gene or category explain virulence differences



More influential, more present in HV

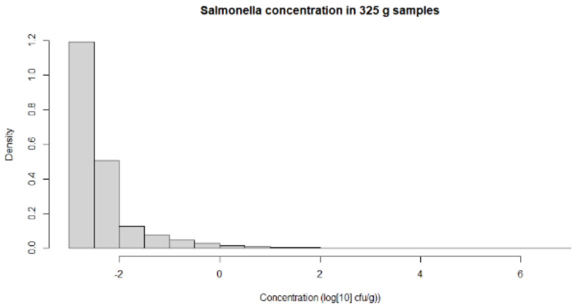
Less influential, more present in LV

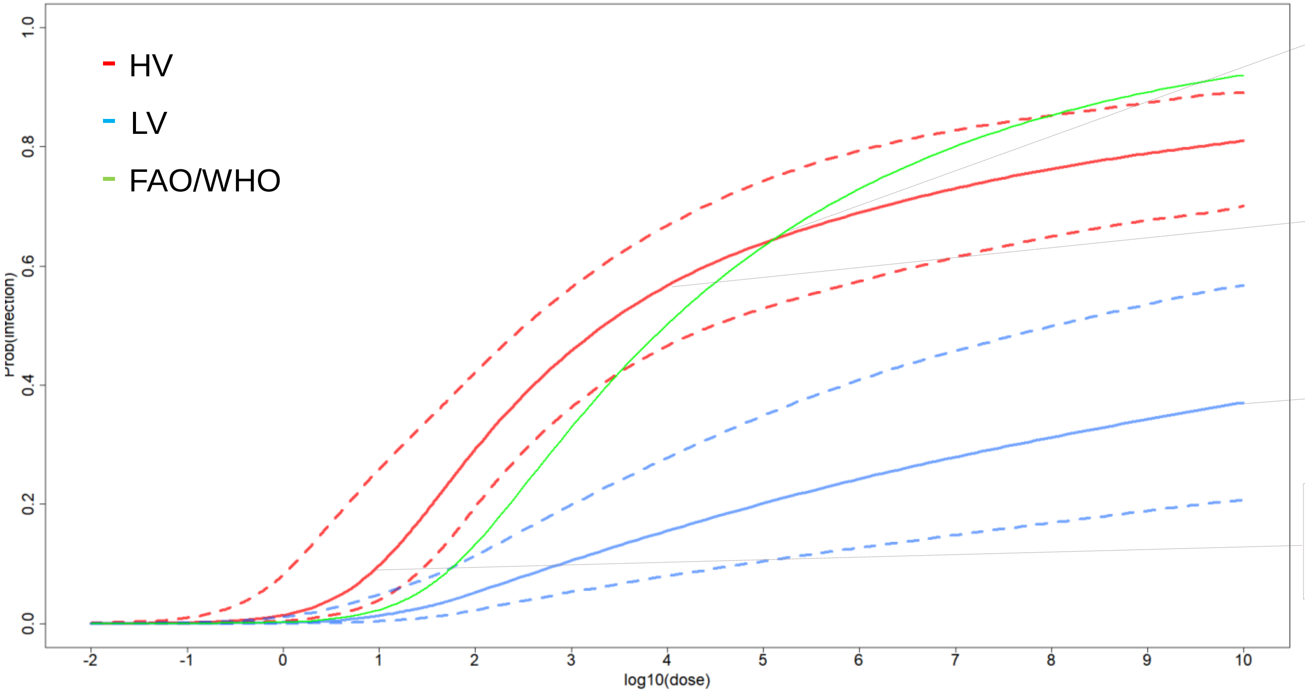
Same frequency HV and LV

Connecting load to illnesses, by virulence

CFU/g (MT43)
96.7% of samples 0 CFU/g

93.8% mean -5.8 CFU/g
6.1% mean -2.1 CFU/g





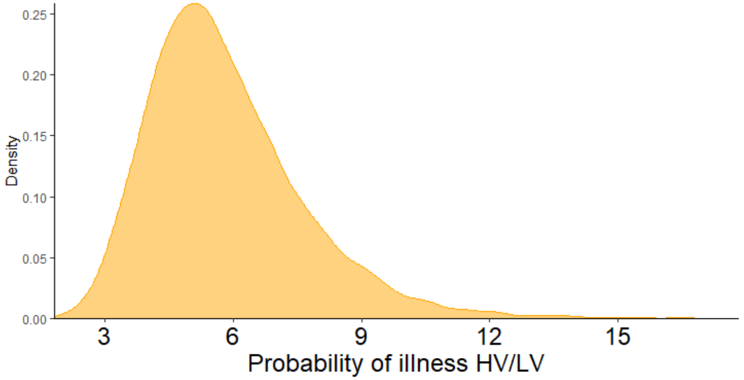
HV steeper than FAO/WHO< Log10(5) cells, shallower after.
LV much lower throughout range!

HV -> average of 10,000 *Salmonella* cells roughly 57% chance infection

LV -> average of 10^{10} *Salmonella* cells roughly 37% chance of infection

10 cells, >**7 times greater** infection probability for HV

Prob. Illness HV/LV beef serving (after attenuation)



Takeaway: P(ILL) NOT the same as 2.5 ratio from surveillance once integrating Dose/uncertainty.

	Higher virulence	**Lower virulence**
Proportion in outbreaks	0.68 [0.43; 0.87]	0.27 [0.09; 0.50]*
Proportion in beef	0.28 [0.18, 0.39]	0.63 [0.51; 0.75]
RR	**RR_{HV}: 2.5 [1.4; 3.9]**	**RR_{LV}: 0.43 [0.14; 0.83]**

*rows don't add up to 1, excluding serovars not assigned to a group

Modeling salmonella interventions and illness reduction

Quantitative microbial risk assessment using empirical prevalence and load combined with virulence-specific DR to (ground beef in US as model case)

- Outcomes: reduction of illnesses vs baseline, diversion of positive products
- Scenarios combine:

Testing and diversion frequency:
<0.5% (FSIS),
10%, 25%, 75%, 100%

OR

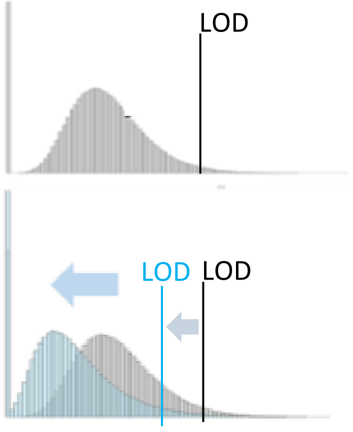
% reduction in prevalence:
25%, 50%

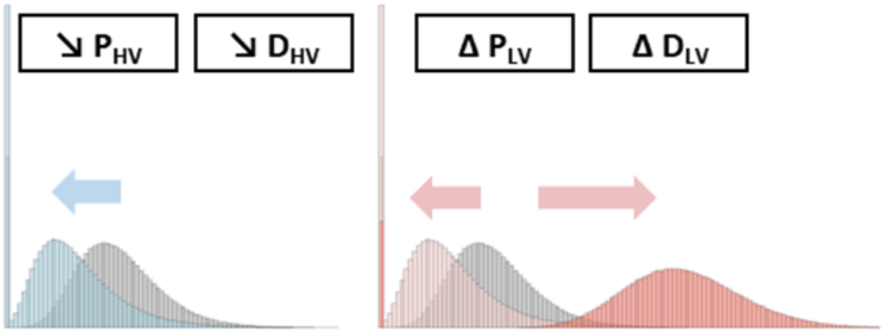
AND

Log CFU reduction:
-0.5, -1, -2

Quantitative limits on bacterial load:
LOD=1 CFU/sample
LOD=10

Differential targeting - LV LOD vs HV LOD:
Same LOD
LOD for HV only



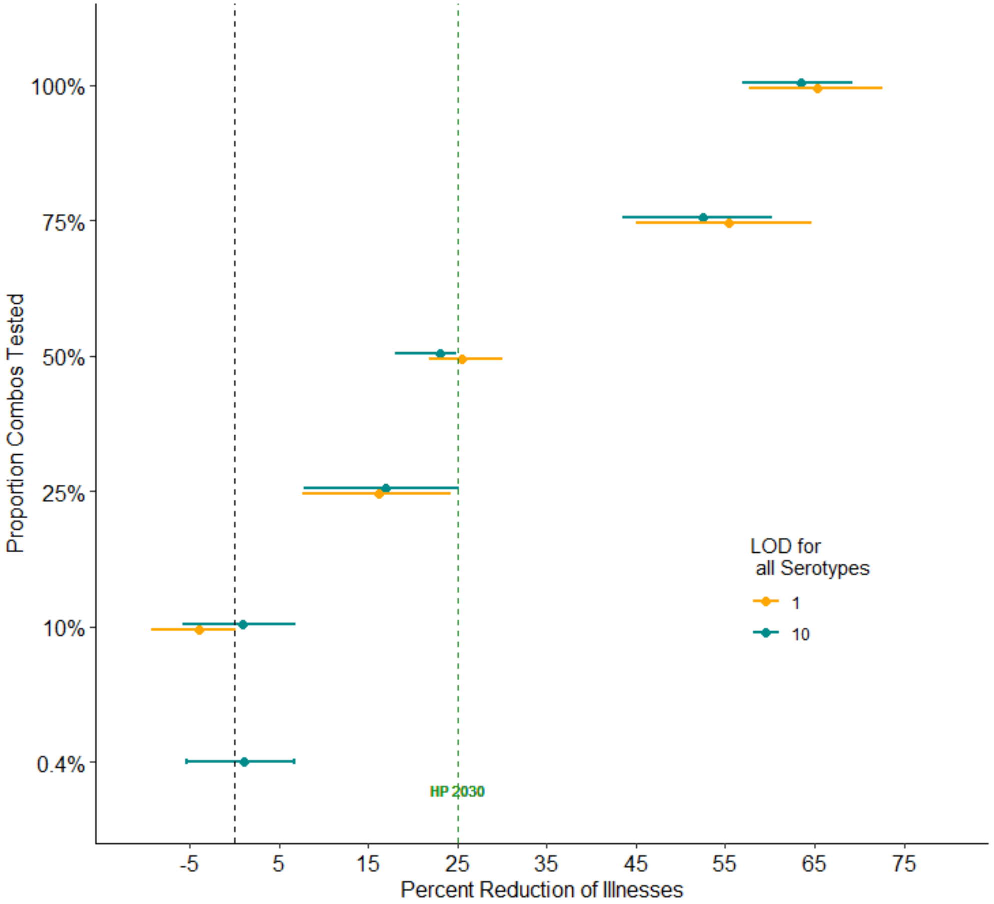


Test and diversion scenarios

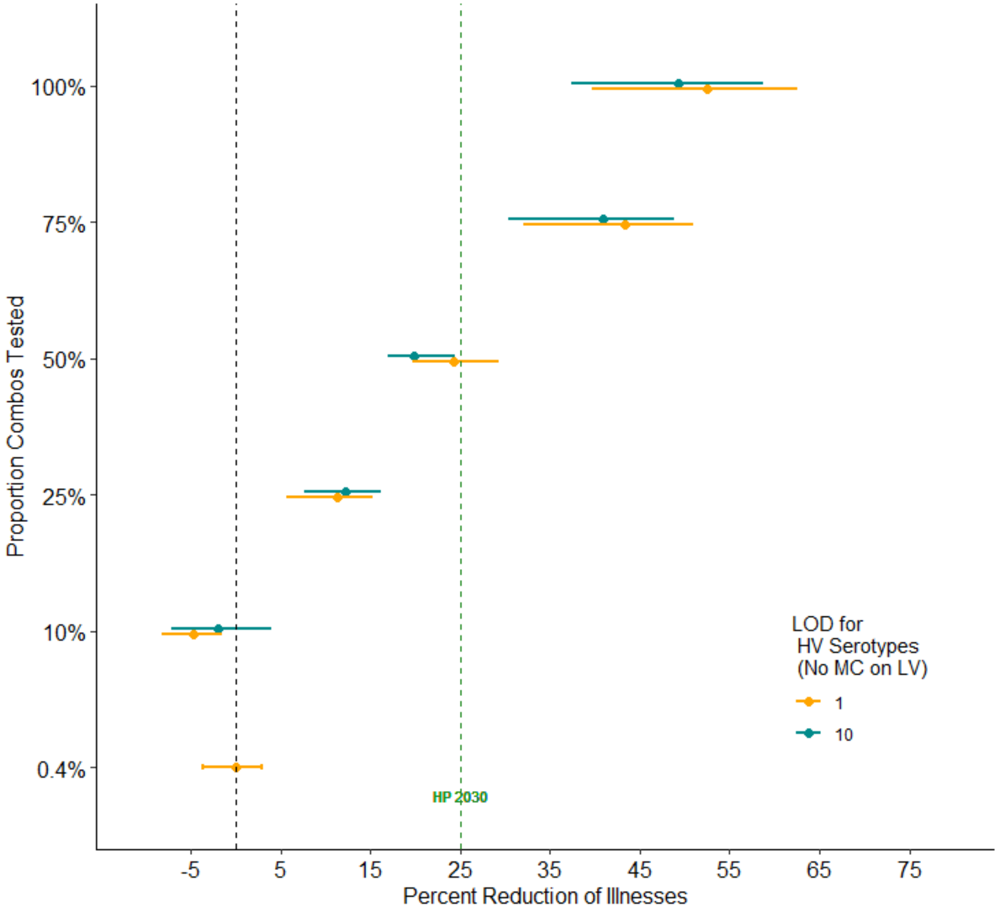
Targeting levels, HV/LV, sampling proportions

Baseline: any *Salmonella* sp. positive diverted (stricter than current FSIS MC)

Same MC for all serovars

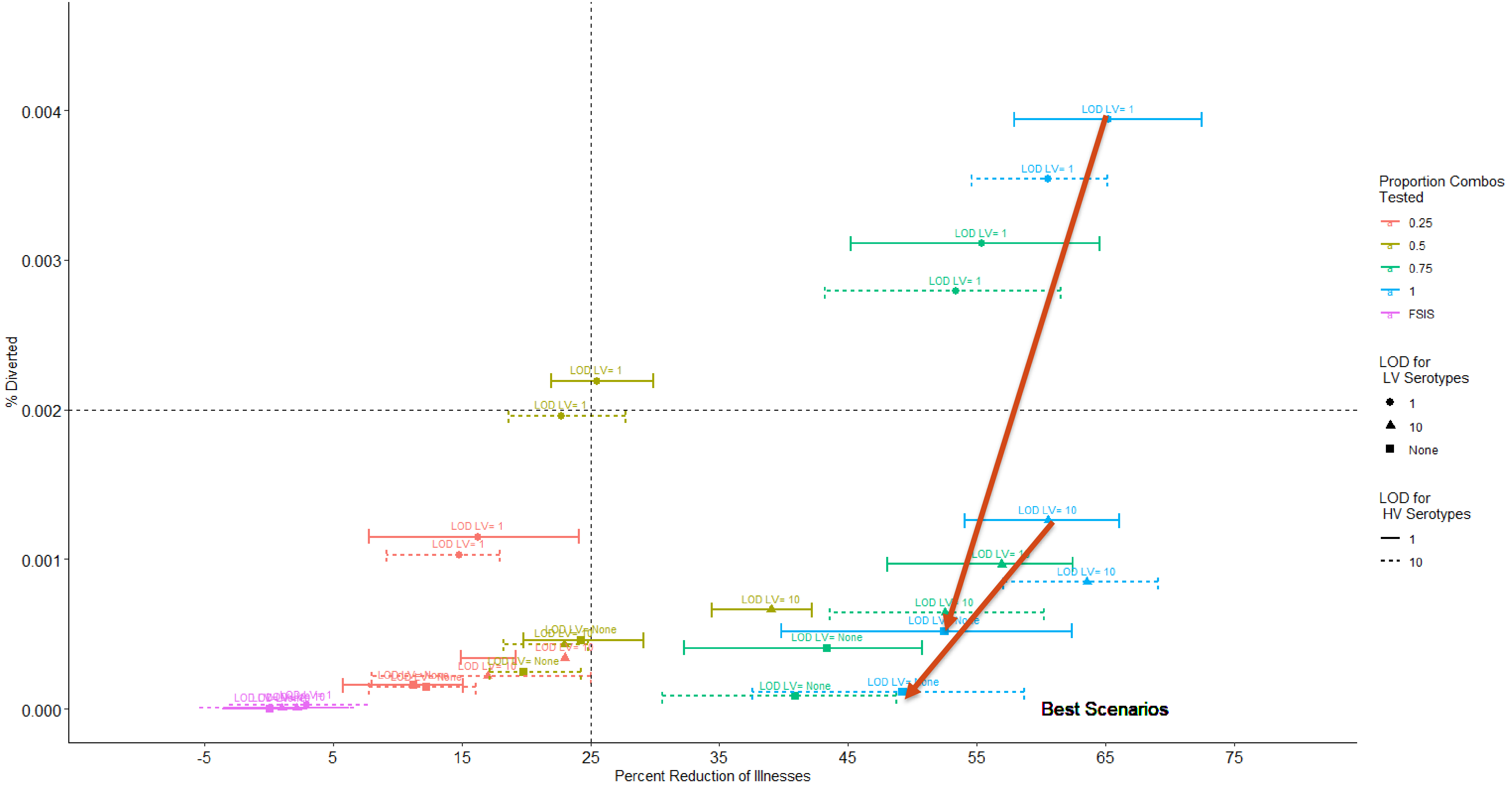


MC only HV serovars



Illness reduction vs diversions

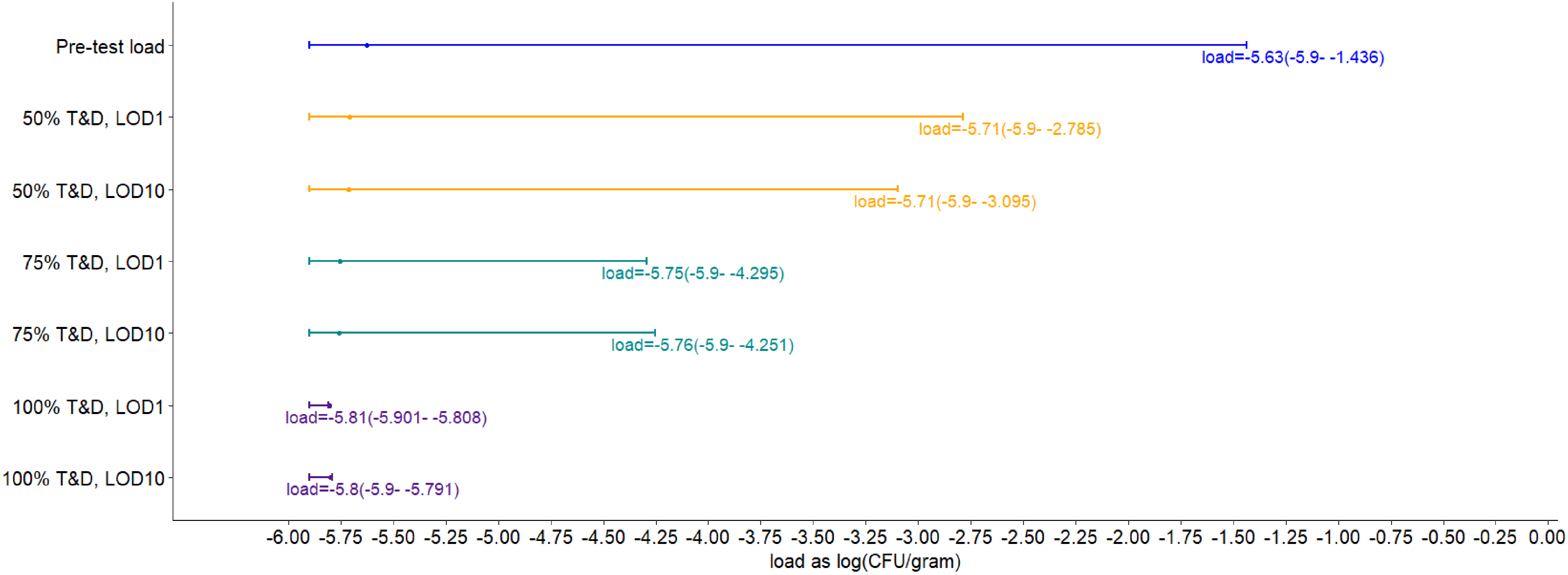
Takeaway: targeting HV equivalent risk reduction with less diversions



Effect of test and diversion on salmonella load

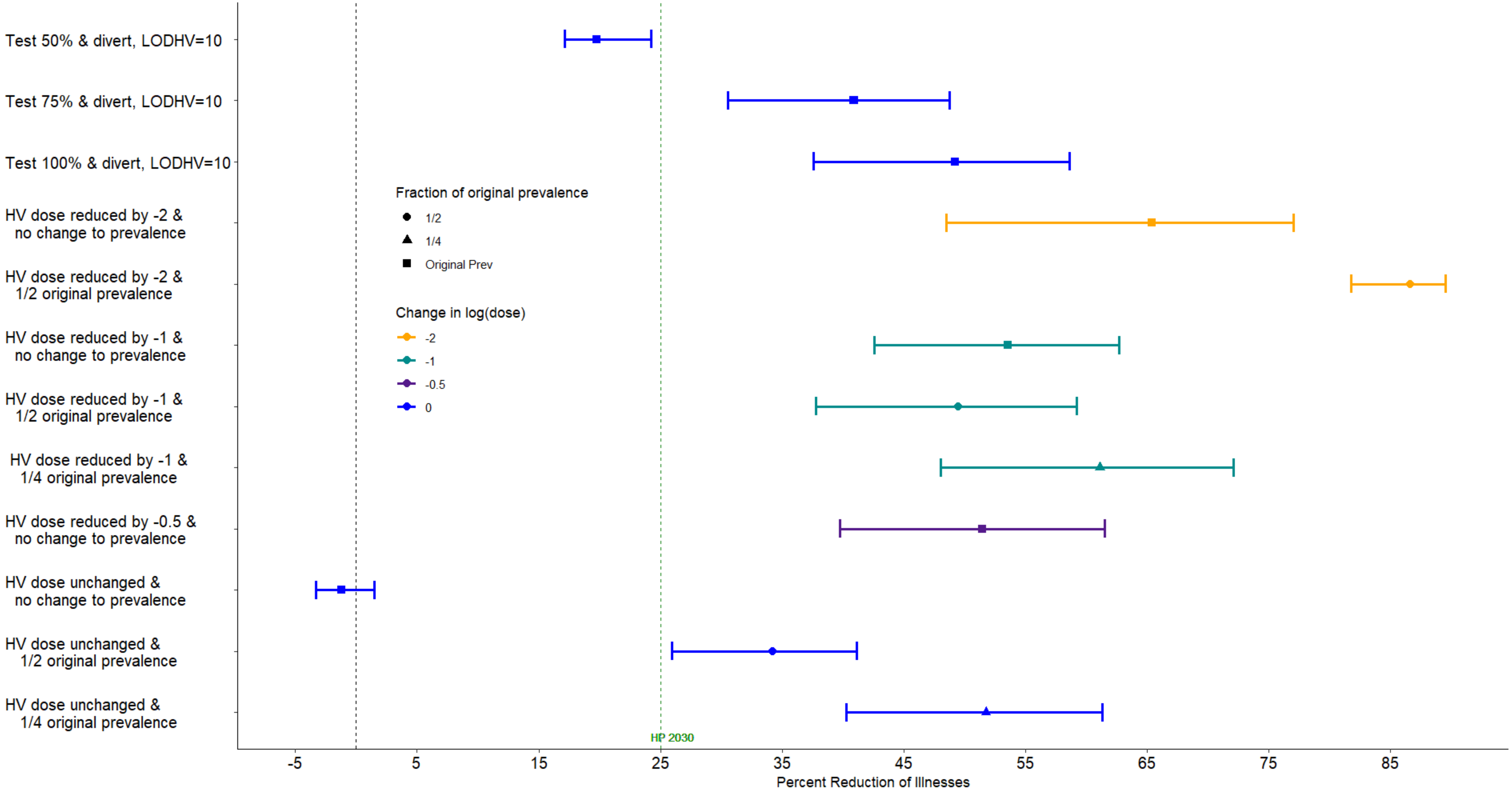
Test and diversion can achieve > 25% illness reduction, but diversions may not be feasible for all processors

Can we achieve similar/better risk reduction by lowering prevalence and/or load via other methods?



Prevalence/load reduction scenarios

Takeaway: equivalent results to test/divert by targeting prevalence/load



Conclusions/practical applications

- Genomic identification of highest-risk serovars is feasible, faster than waiting to see changes in public health surveillance data

- Test and diversion works at higher testing proportions, but other strategies reducing prevalence/load can also result in significant public health gains

Targeting highest risk sources and adapting programs to evolving risks (emerging, seasonal, source-based) can be more cost-effective while achieving significant PH gains

- Diagnostic tests that can be quickly deployed to identify emergent threats will be important, but also **data sharing efforts** to best detect and manage risks

Predicting and devising **optimal plans at individual plant level might provide** highest salmonellosis prevention while being cost-effective

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  Dr. Dan Taylor
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  Dr. Solenne Costard
Collaborator: Dr. Gavin Fenske

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- FoodNet Data: The findings and conclusions in this report are those of the author(s) and do not necessarily represent the official position of the Centers for Disease Control and Prevention.

Beef Safety- *Salmonella* Outbreaks and Risk Assessment

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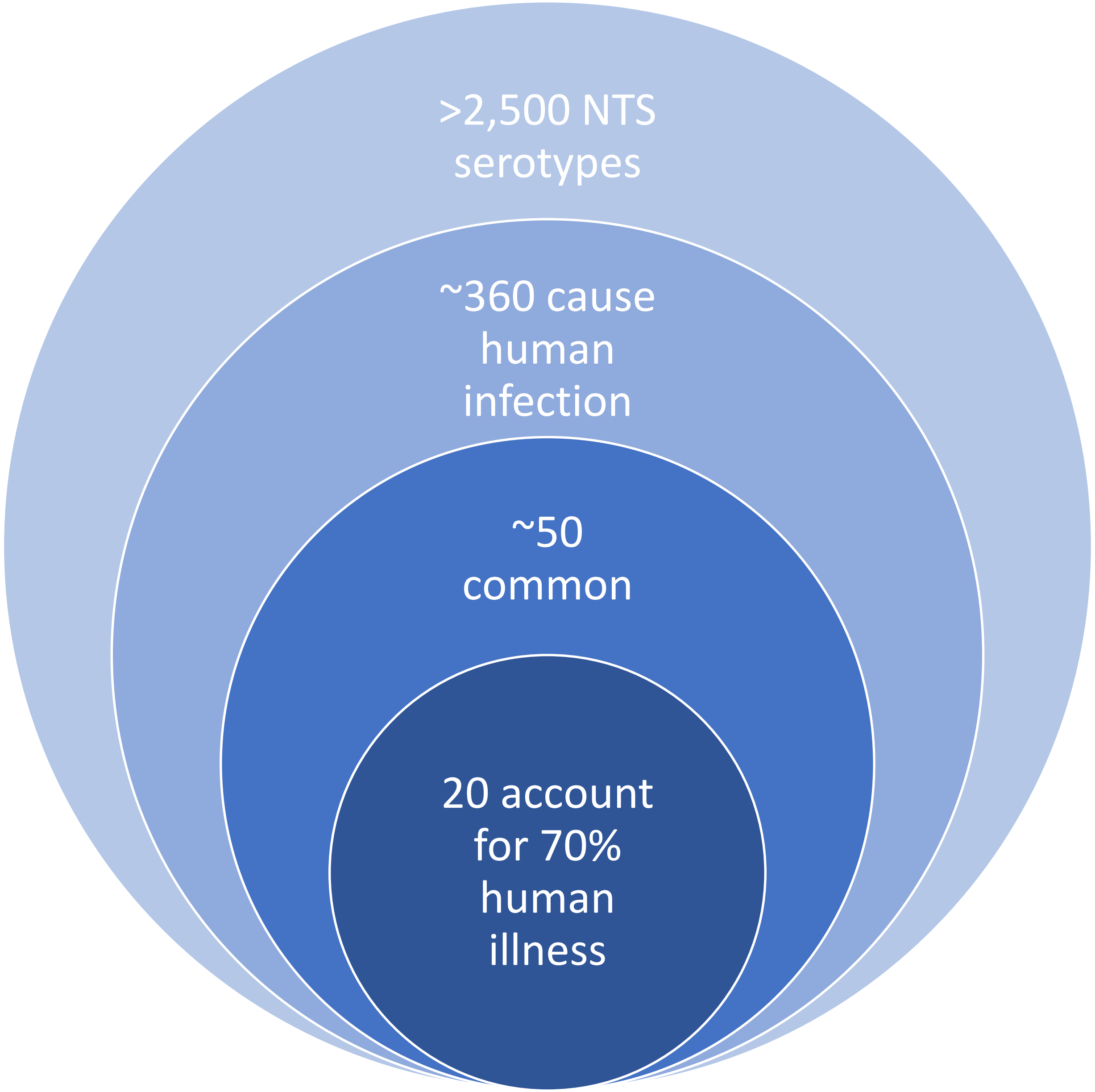
UMN School of Public Health

MINNESOTA INTEGRATED
FOOD SAFETY CENTER OF EXCELLENCE
UNIVERSITY OF MINNESOTA • MINNESOTA DEPARTMENT OF HEALTH

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



>2,500 NTS serotypes

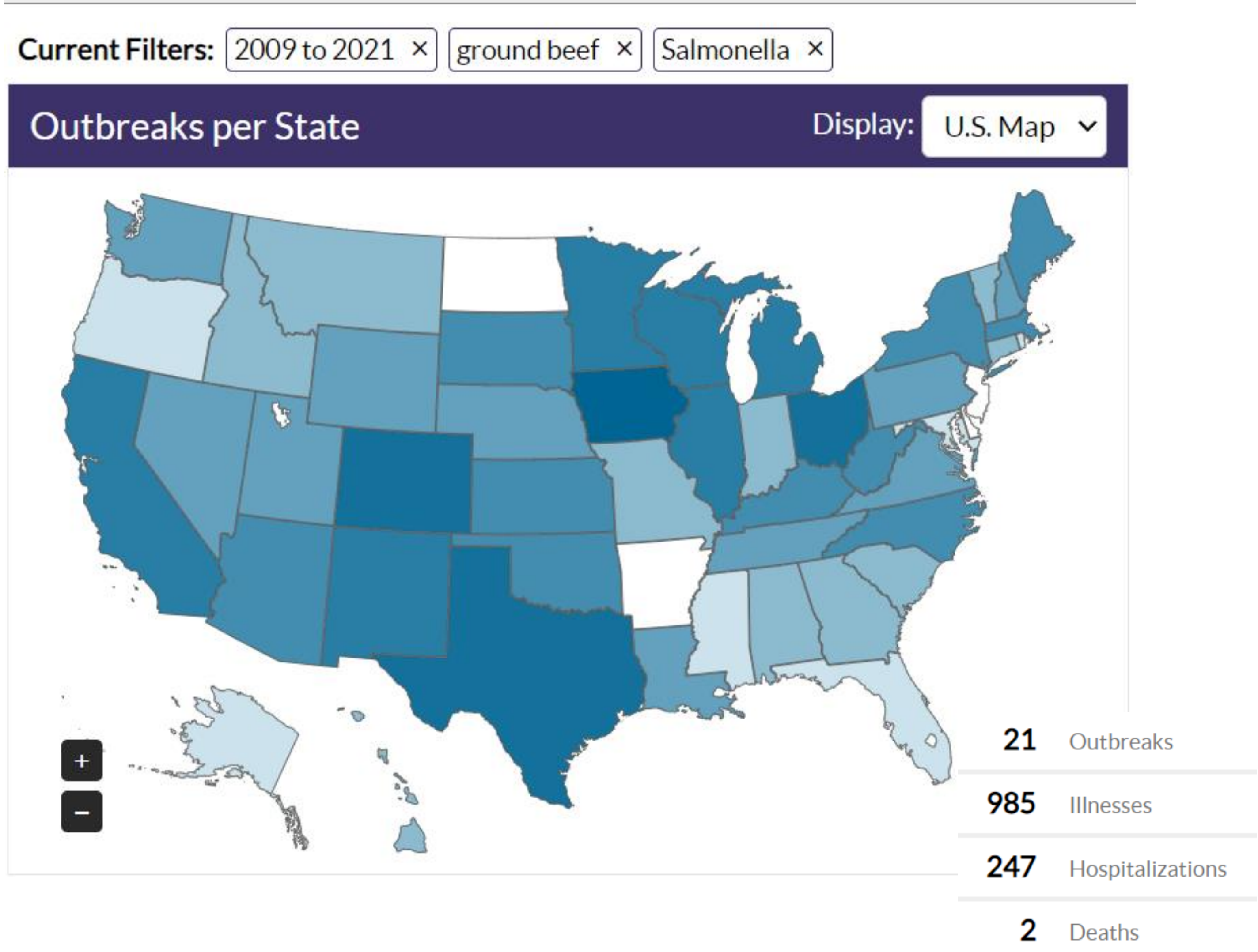
~360 cause human infection

~50 common

20 account for 70% human illness

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



Current Filters: 2009 to 2021 × ground beef × Salmonella ×

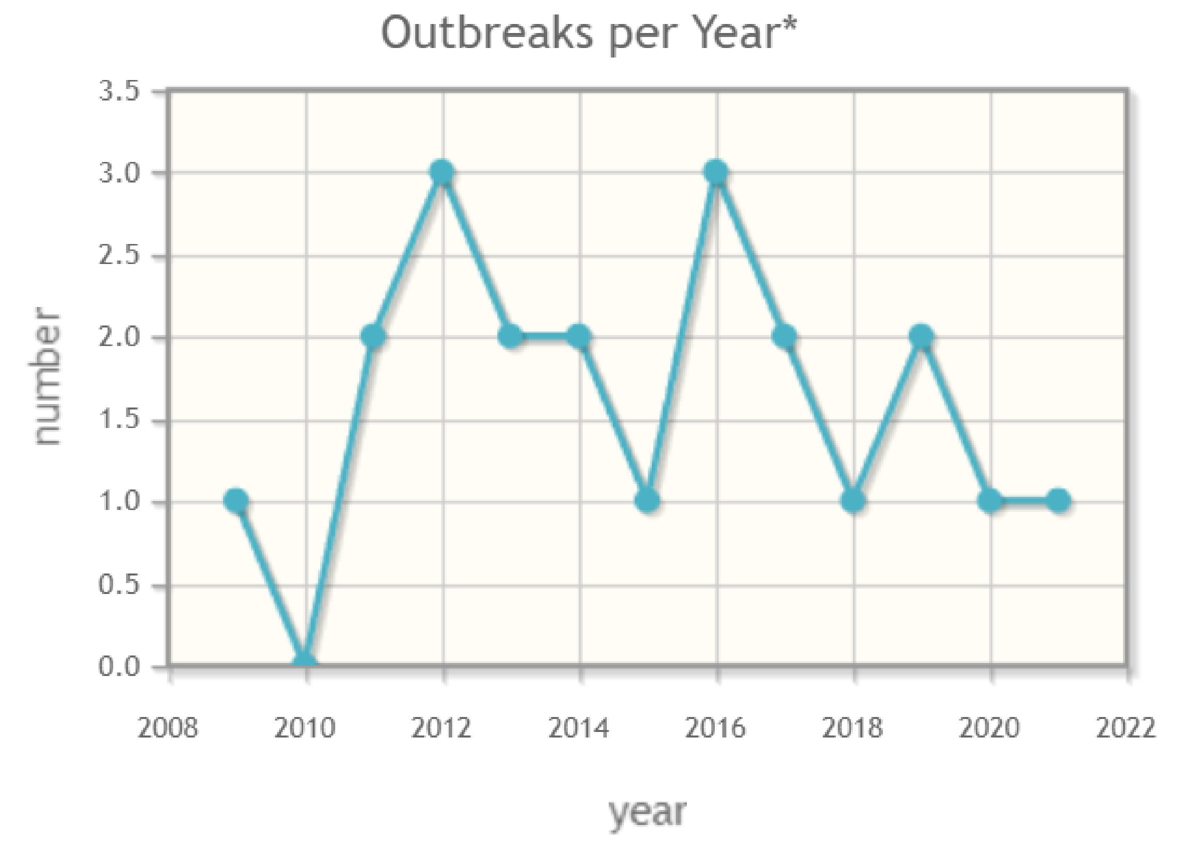
Outbreaks per State

Display: U.S. Map

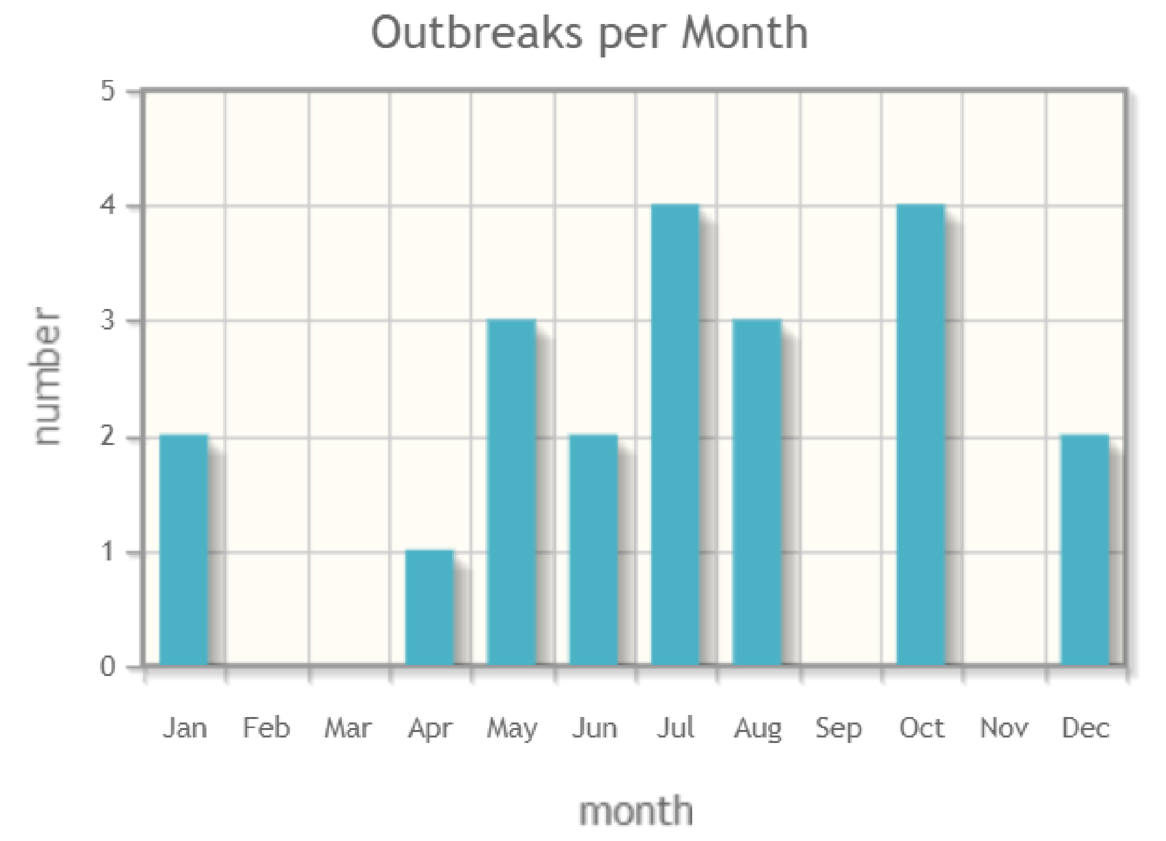
21	Outbreaks
985	Illnesses
247	Hospitalizations
2	Deaths

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

Salmonella Outbreaks Associated with Ground Beef, US, 2009-2021



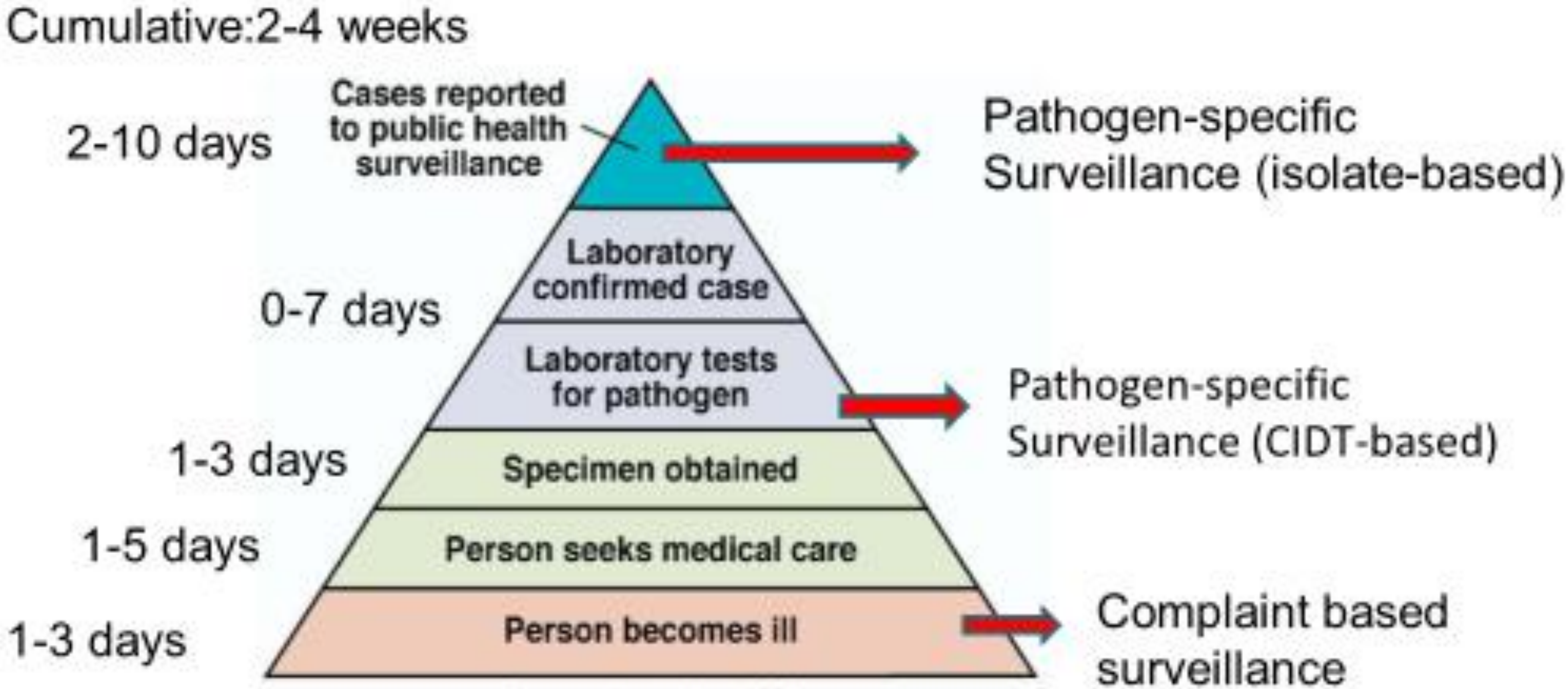
Outbreaks per Year*



Outbreaks per Month

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

Primary Sources for Outbreak Detection



Cumulative:2-4 weeks

2-10 days

Cases reported to public health surveillance

Pathogen-specific Surveillance (isolate-based)

Laboratory confirmed case

0-7 days

Laboratory tests for pathogen

Pathogen-specific Surveillance (CIDT-based)

1-3 days

Specimen obtained

1-5 days

Person seeks medical care

1-3 days

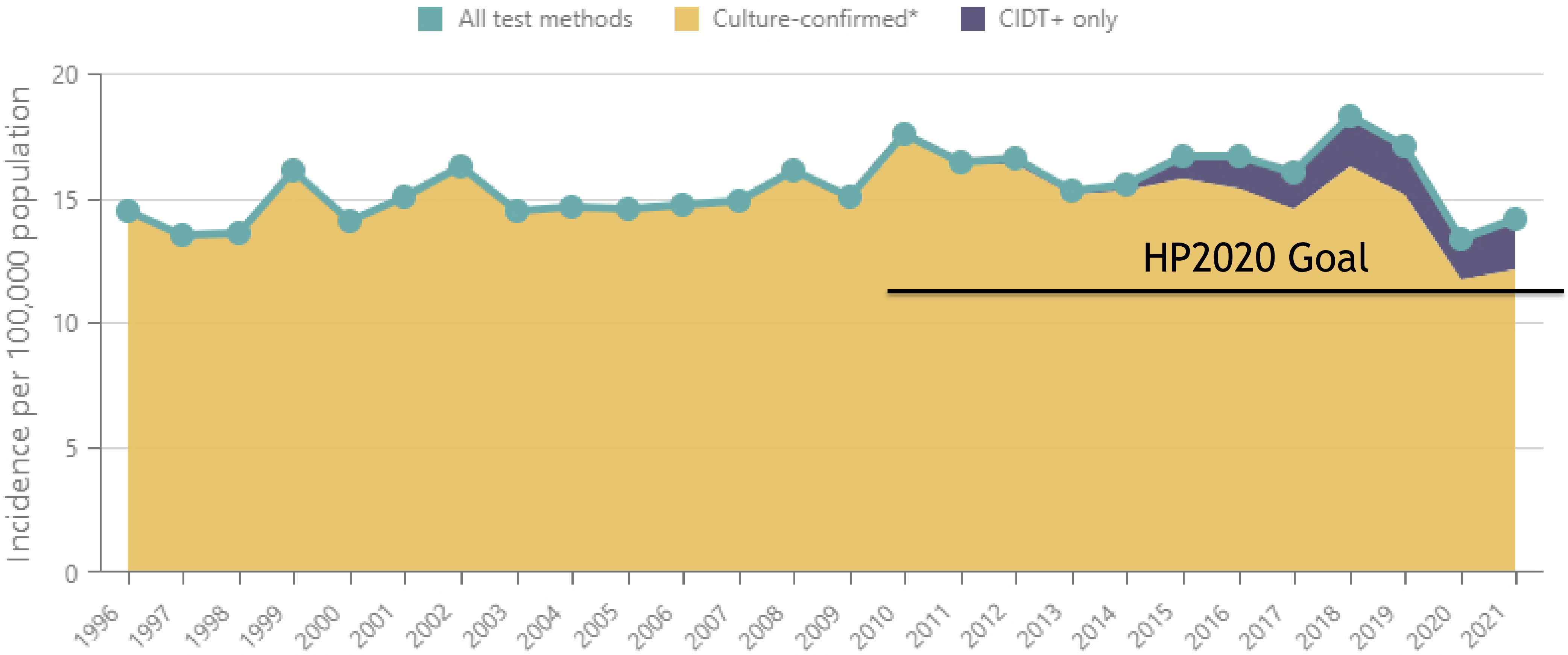
Person becomes ill

Complaint based surveillance

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

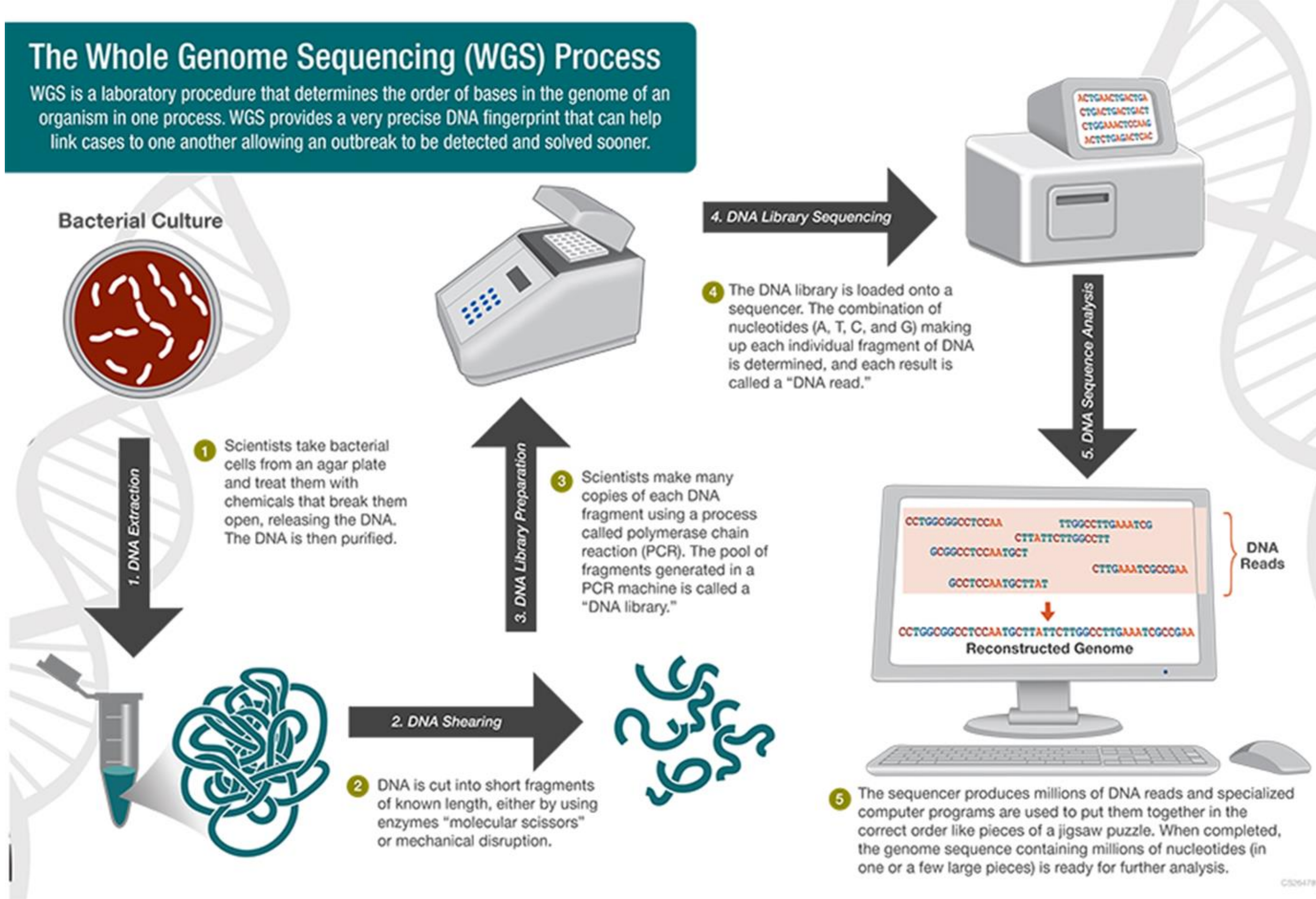
Salmonella infections by year; 1996-2021

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



https://www.cdc.gov/foodnet

Whole genome sequencing improves the detection and investigation of foodborne outbreaks



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.

① Scientists take bacterial cells from an agar plate and treat them with chemicals that break them open, releasing the DNA. The DNA is then purified.

② DNA is cut into short fragments of known length, either by using enzymes "molecular scissors" or mechanical disruption.

③ Scientists make many copies of each DNA fragment using a process called polymerase chain reaction (PCR). The pool of fragments generated in a PCR machine is called a "DNA library."

④ The DNA library is loaded onto a sequencer. The combination of nucleotides (A, T, C, and G) making up each individual fragment of DNA is determined, and each result is called a "DNA read."

⑤ The sequencer produces millions of DNA reads and specialized computer programs are used to put them together in the correct order like pieces of a jigsaw puzzle. When completed, the genome sequence containing millions of nucleotides (in one or a few large pieces) is ready for further analysis.

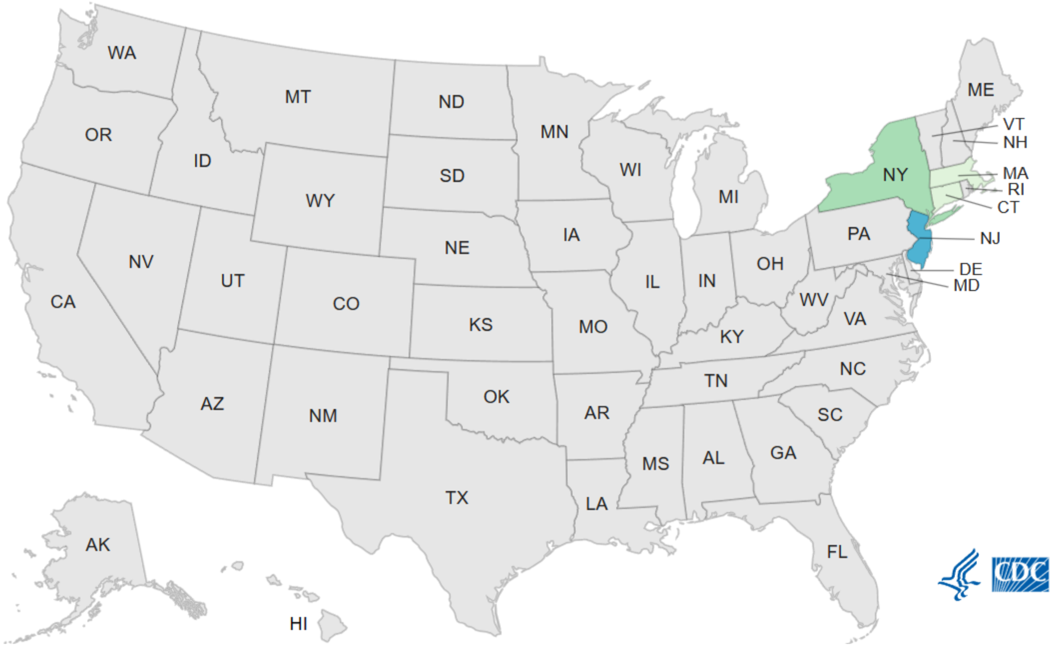
- 🟩 Before using whole genome sequencing (WGS) (Sept 2012-Aug 2013)
- 🟩 Year 1 of WGS (Sept 2013-Aug 2014)
- 🟩 Year 2 of WGS (Sept 2014-Aug 2015)

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

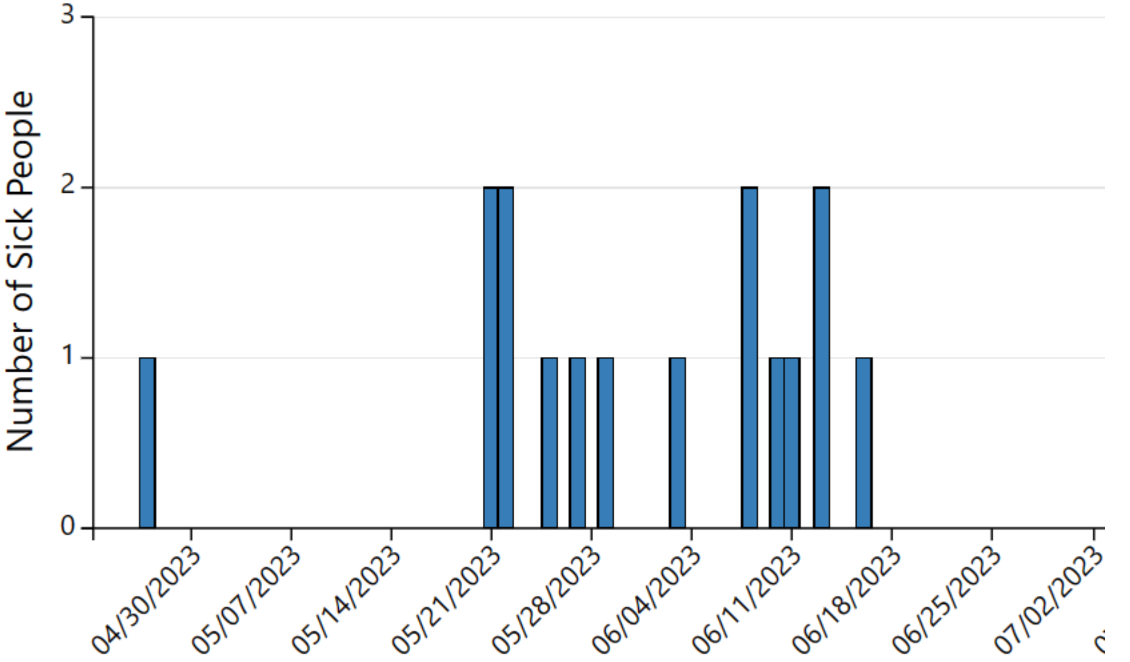
August 2002

Salmonella Outbreak Linked to Ground Beef



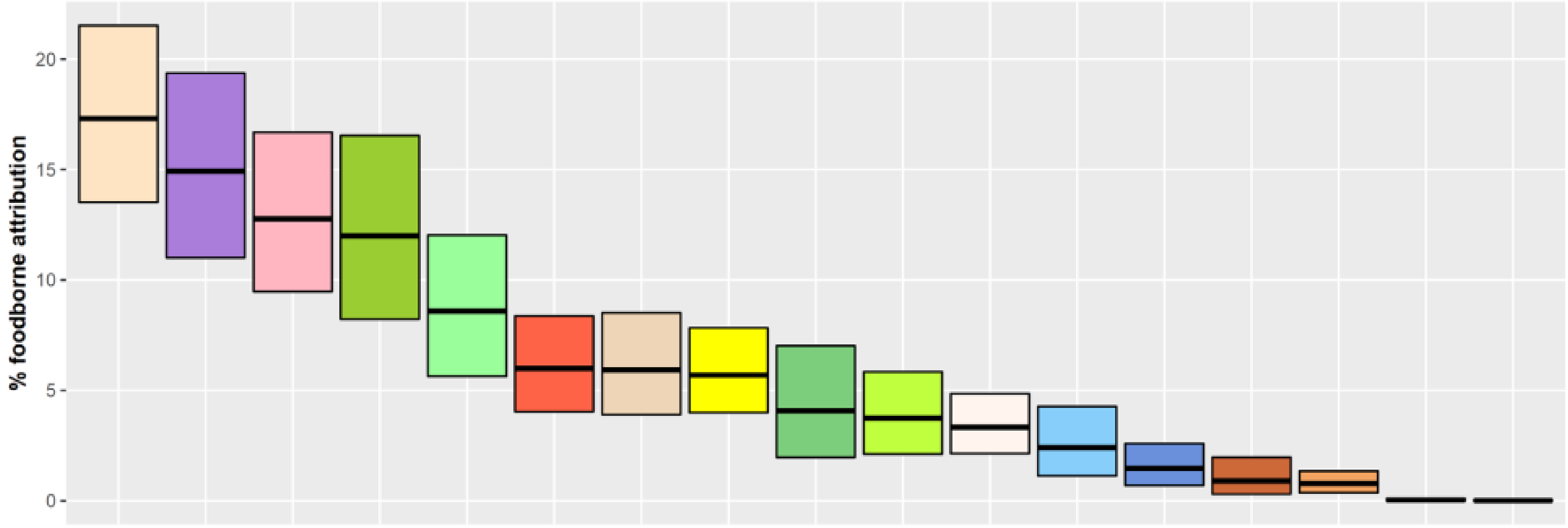
Salmonella Outbreak Linked to Ground Beef

- 16 ill
- Age 0 to 97 years,19% under 5 years
- 56% female
- 14 interviewed, 9 (64%) ate ground beef, all named same grocery store chain.
- Routine FSIS ground beef surveillance sample in March 2023 was closely related to bacteria from sick people's samples.



https://www.cdc.gov/salmonella/i45-10-21

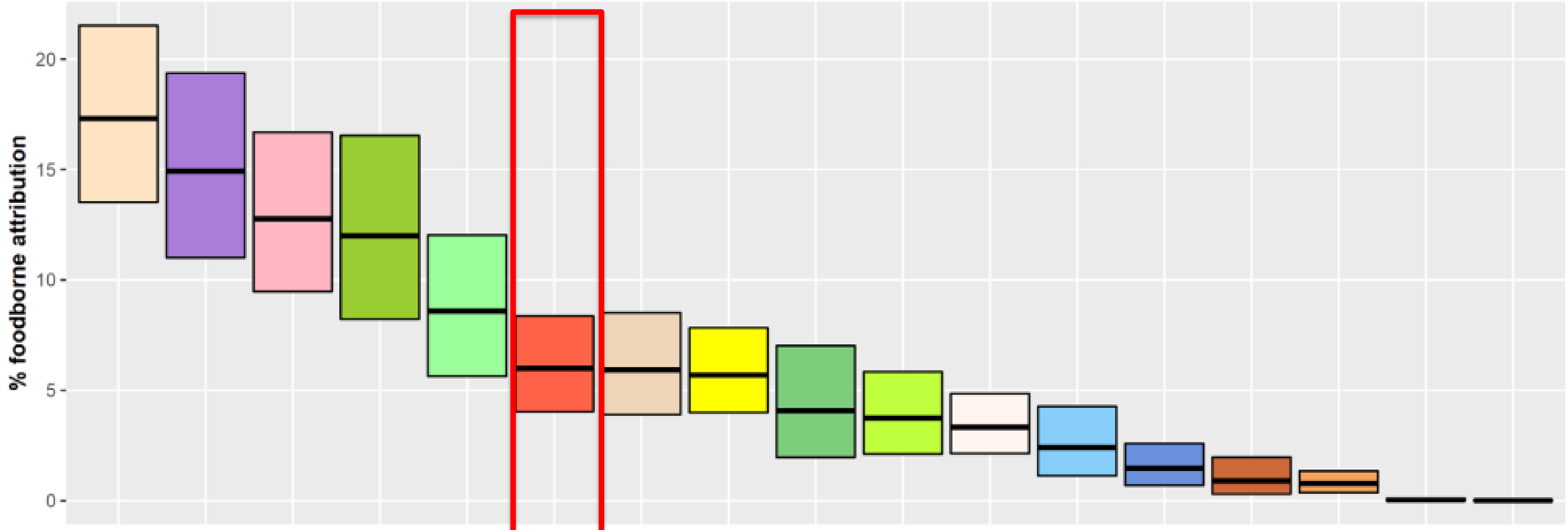
Salmonella Attribution to Food Categories, 2020



	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%									

https://www.cdc.gov/foodsafety/ifsac/pdf/P19-2020-report-TriAgency-508.pdf

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
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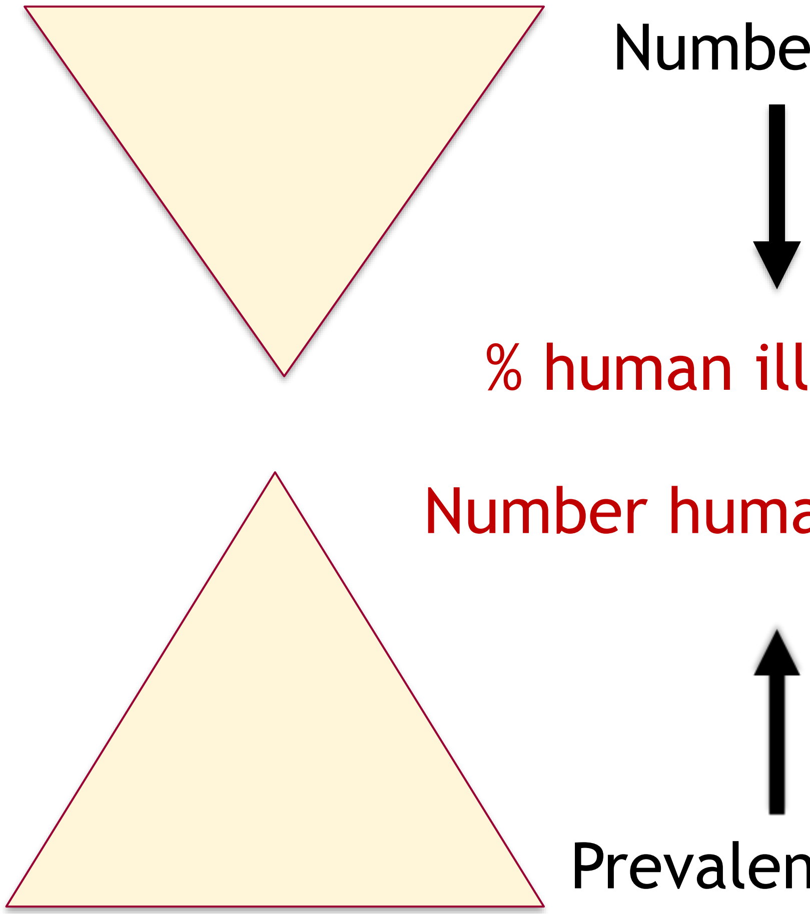
cumulative attribution	77.5%							22.4%									

https://www.cdc.gov/foodsafety/ifsac/pdf/P19-2020-report-TriAgency-508.pdf

Risk Assessment Models



Top-down models:

Number of human illnesses

Attribution estimates

% human illnesses due to ground beef

Number human illnesses due to ground beef

Preparation and consumption scenarios

Prevalence of *Salmonella* in ground beef

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%**

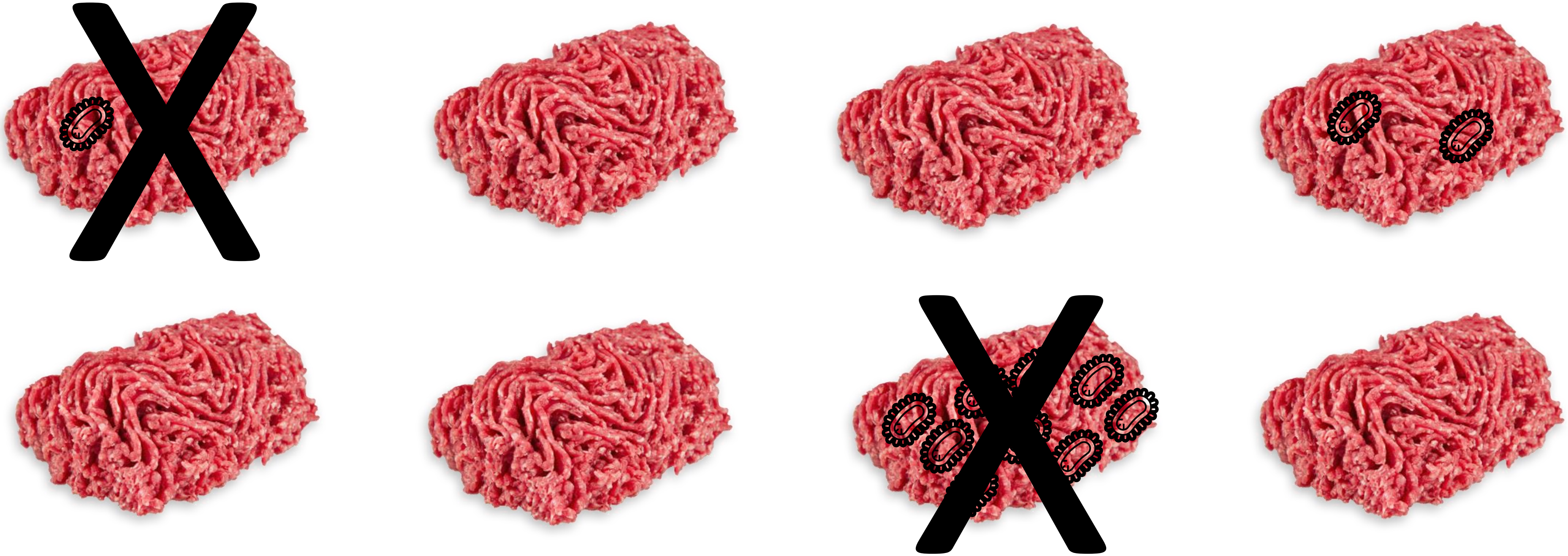
https://www.fsis.usda.gov/science-data/data-sets-visualizations/microbiology/microbiological-testing-program-rte-meat-and-7

Limitations in Prevalence-Based Performance Standards

Prevalence: 3/8 = 37.5%

Limitations in Prevalence-Based Performance Standards

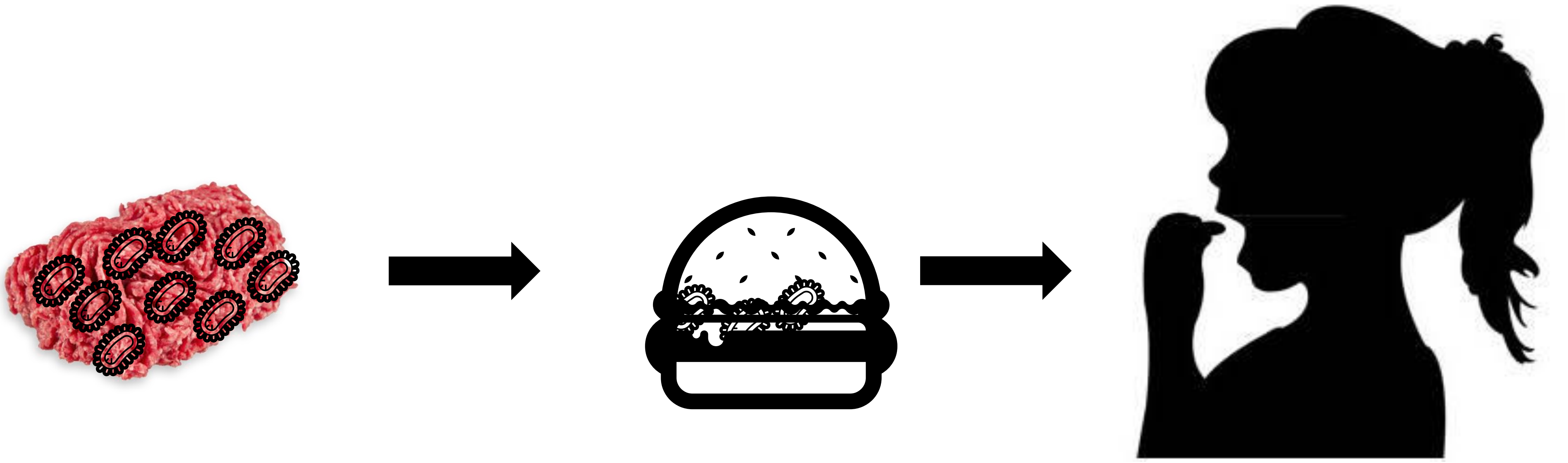
Prevalence: 1/6 = 16.7%



Limitations in Prevalence-Based Performance Standards

Prevalence: 1/6 = 16.7%

Limitations in Prevalence-Based Performance Standards



Ground Beef Risk Assessment

- Estimate annual reductions in *Salmonella* infections when highly contaminated ground beef lots were diverted from consumption.
- Estimate contribution of high and low-virulent and multi-drug resistant (MDR) serotypes on the total number of illnesses and burden of disease.
- Prioritize risk-based pathogen mitigation strategies.

FSIS Enumeration Data

1060 *Salmonella* enumerated samples (2010-2020)

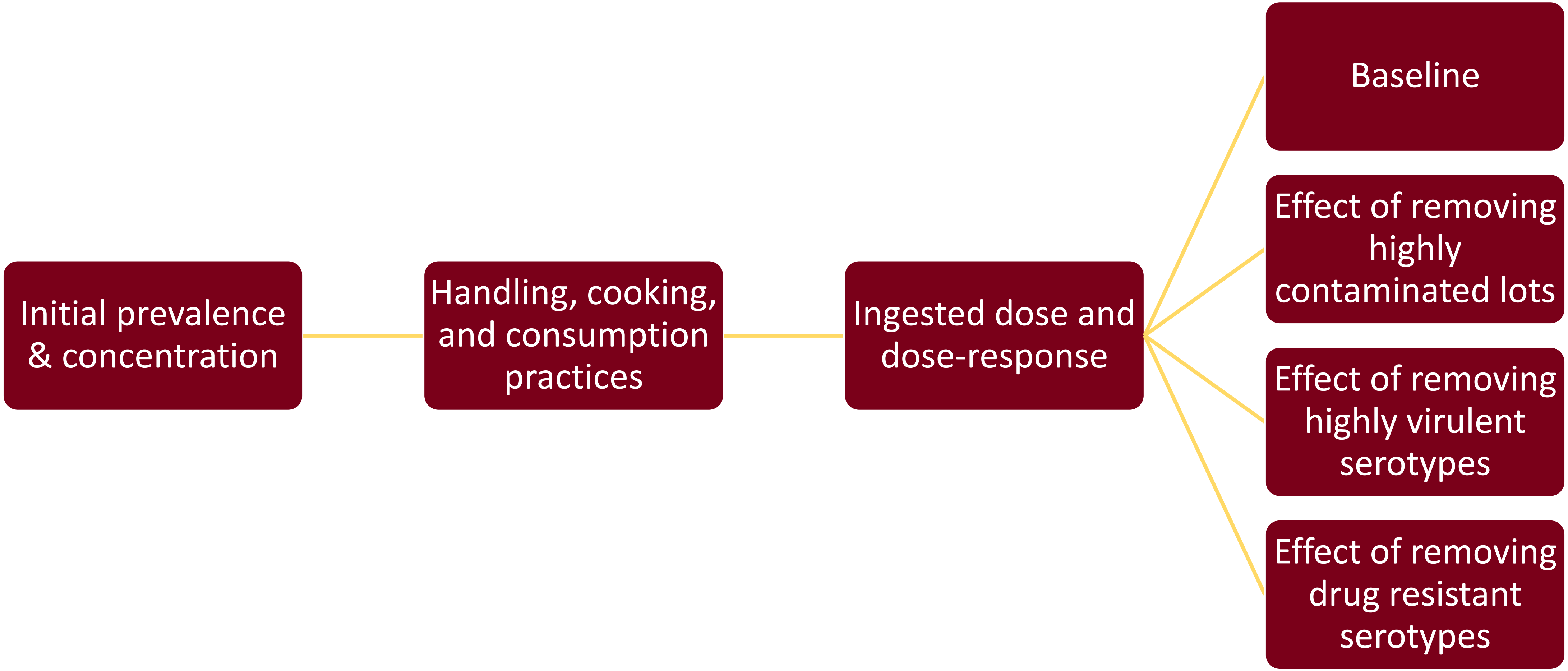
- *Salmonella* prevalence in models varied from 1.43 – 1.47%
- 13.7% met high virulence criteria
- 15.9% MDR

Very low *Salmonella* prevalence in production lots sampled

- >1 MPN/g = 2.4% production lots
- >10 MPN/g = 0.4% production lots

Average concentration = 0.017 MPN/g (4.07 MPN/g)

Risk Assessment Process - Ground Beef



Initial prevalence & concentration

Handling, cooking, and consumption practices

Ingested dose and dose-response

Baseline

Effect of removing highly contaminated lots

Effect of removing highly virulent serotypes

Effect of removing drug resistant serotypes

High Virulence Criteria

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

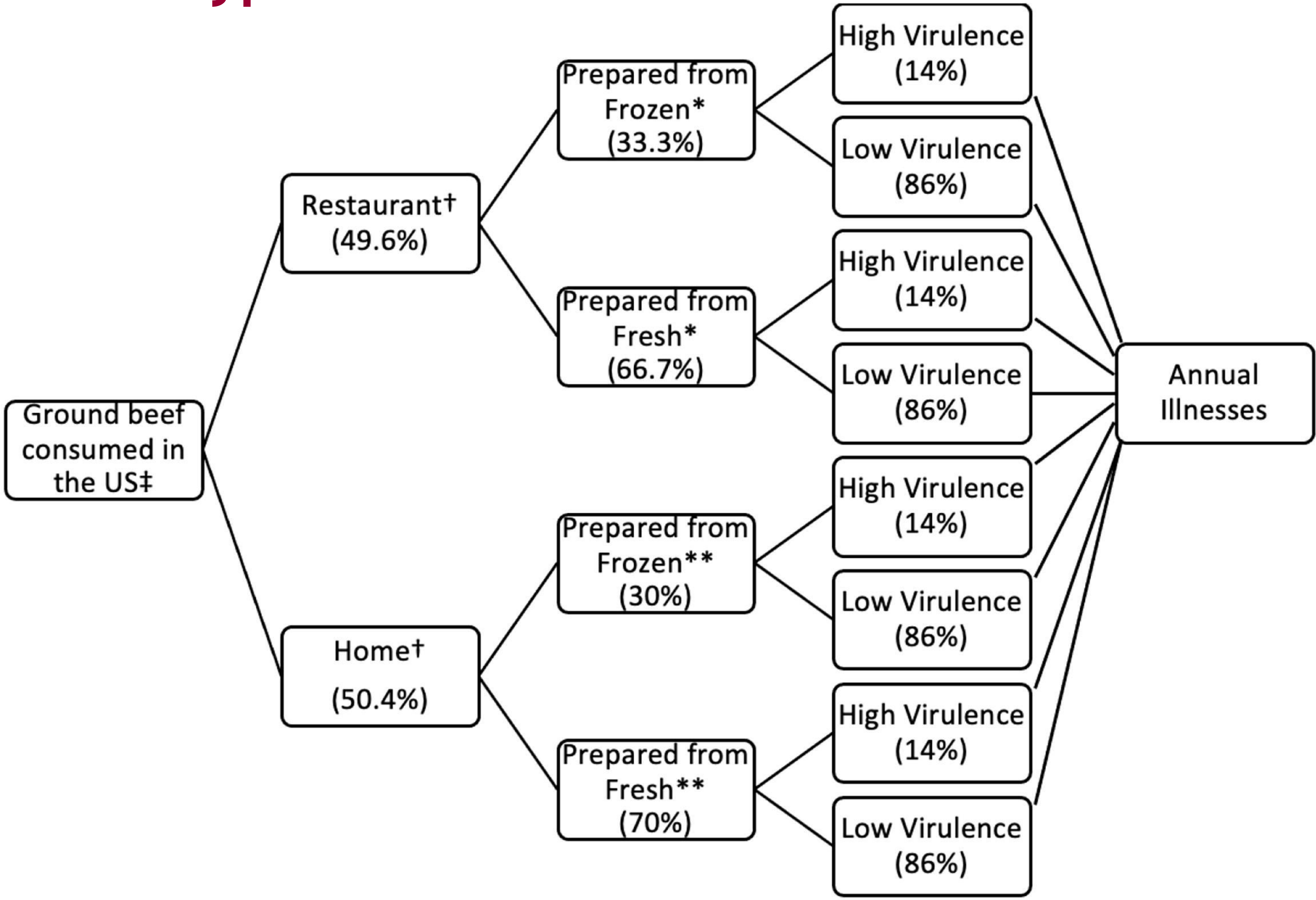
OR

- 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

Consumption Scenarios and Proportion of High- and Low-Virulence Serotypes



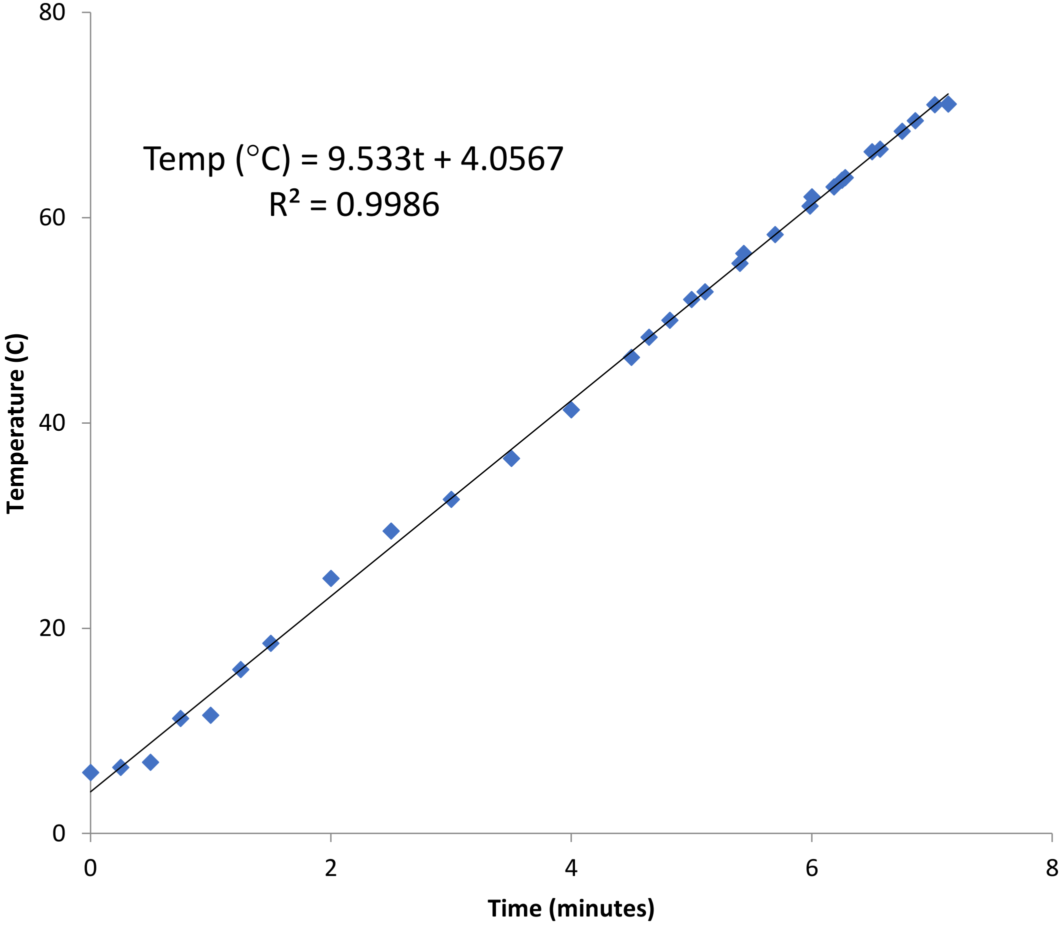


Figure 1. Linear Thermal Profile for Thawed or Fresh Products

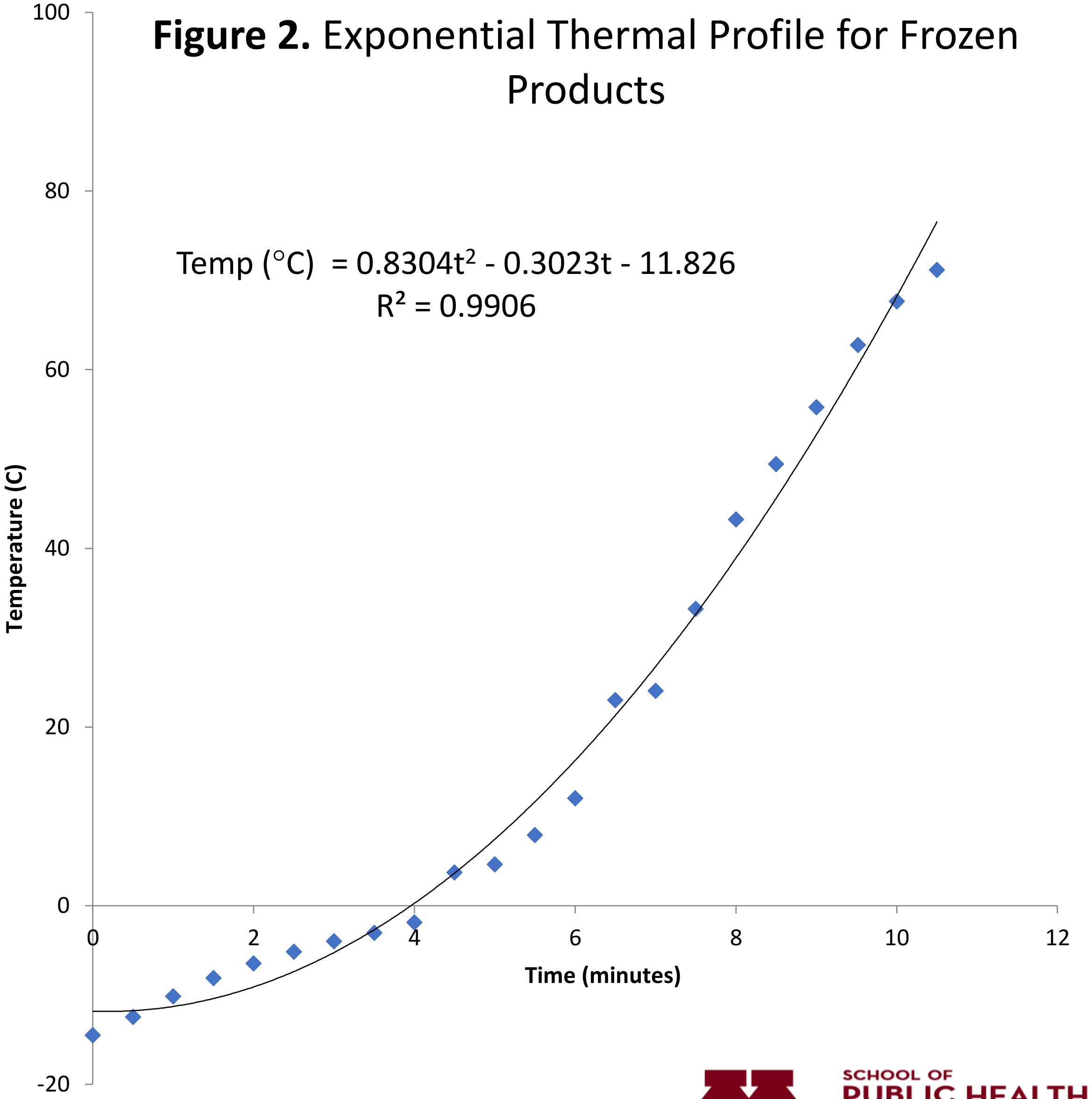
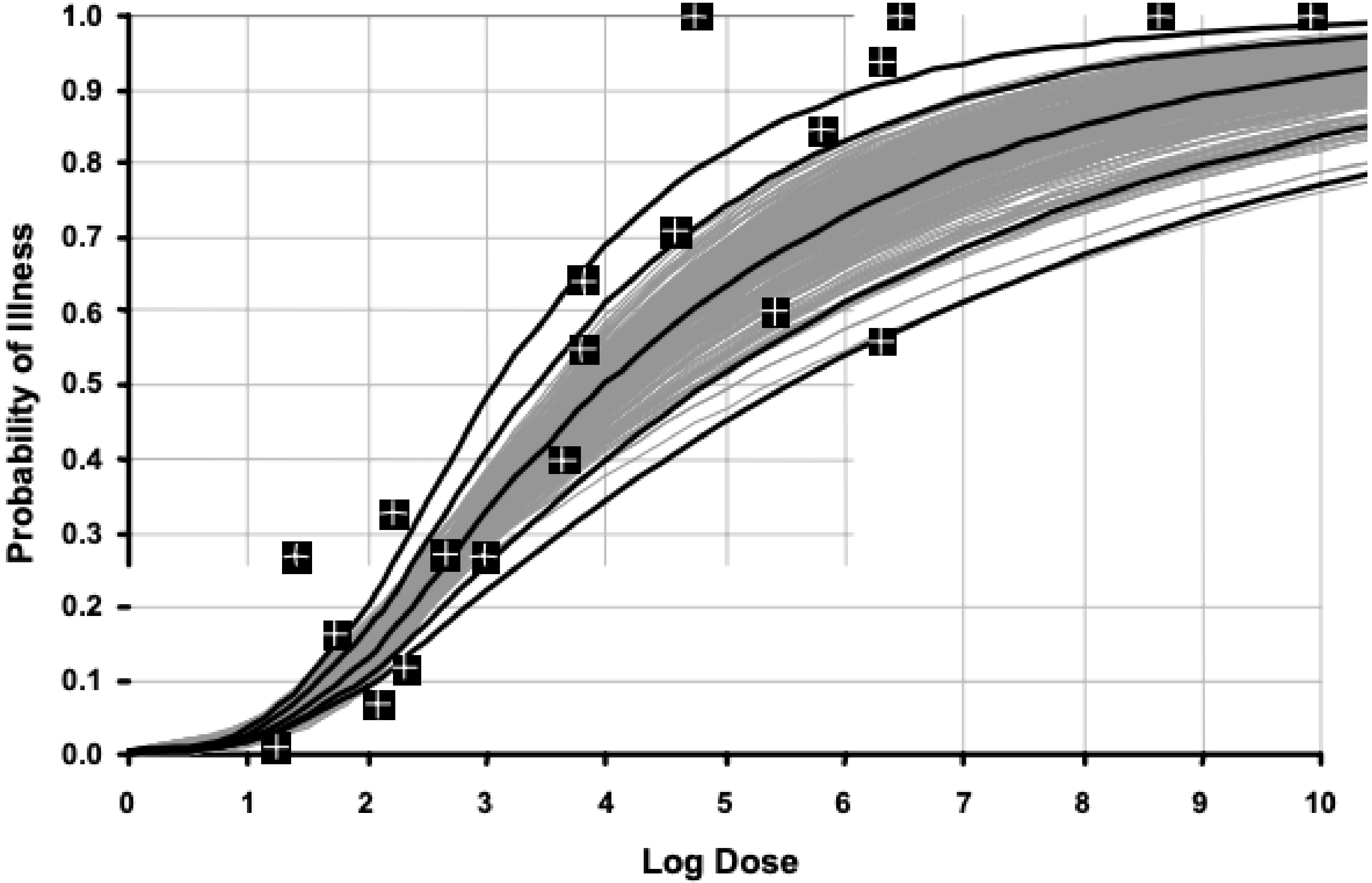


Figure 2. Exponential Thermal Profile for Frozen Products

High Virulence NTS *Salmonella* Dose-Response



Source data: World Health Organization, Food and Agriculture Organization of the United Nations, 2002

Results

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

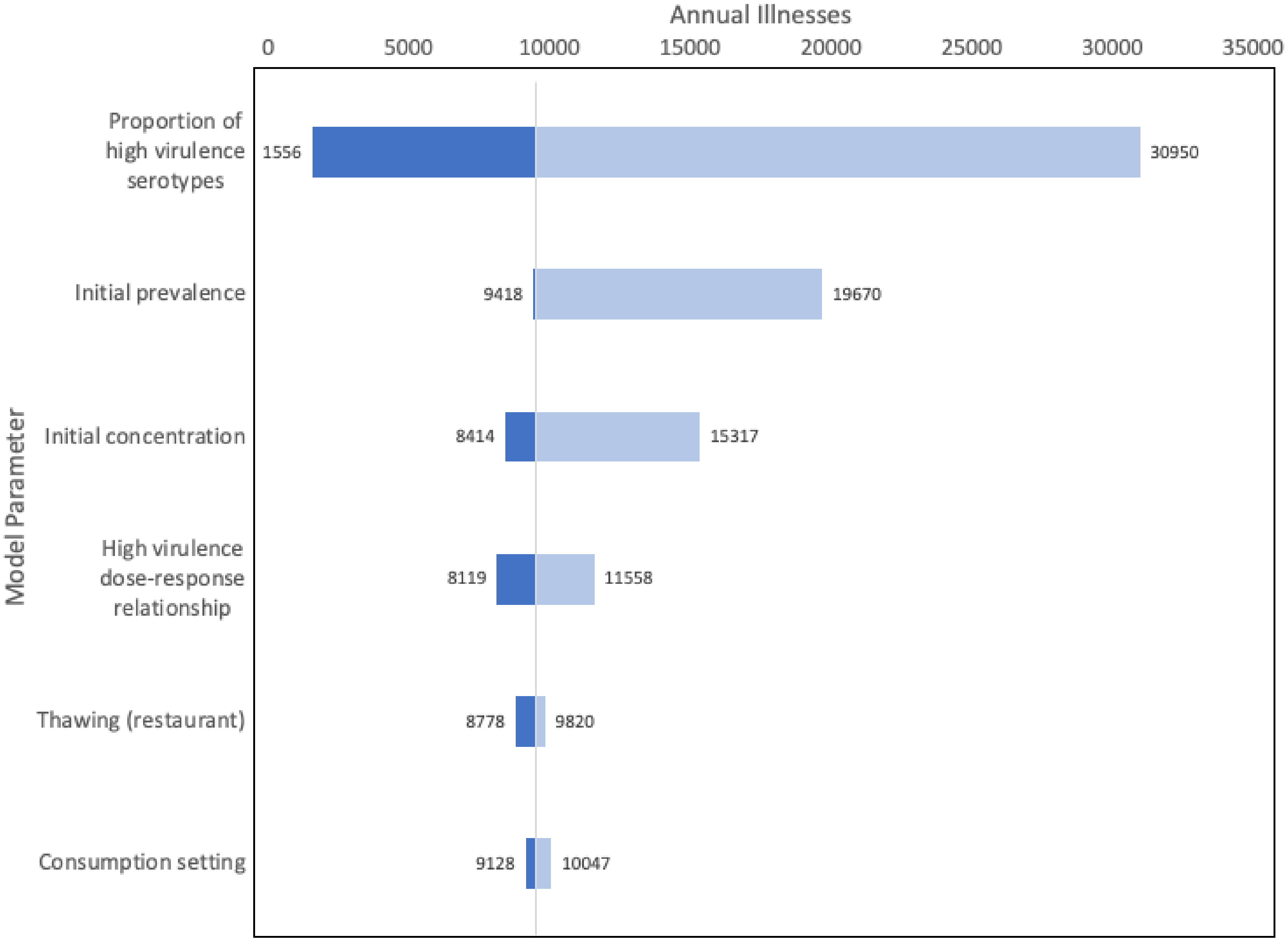
Model	Annual Illnesses*	Reduction from Baseline (%)
Baseline	8,980	-
>10 MPN/g removed	7,759	13.6
>1 MPN/g removed	5,686	36.7
Highly virulent lots removed	300	96.7

*Unadjusted for under-reporting

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

	Annual Illnesses by Virulence Profile		
Consumption Scenario	High-virulence (90% CI)	Low-virulence (90% CI)	Total
Home, Fresh (n = 3.2×10^9)	3360 (2360, 4480)	116 (43, 1020)	3476 (2403, 5500)
Home, Frozen (n = 1.6×10^9)	2690 (1900, 3590)	93 (35, 819)	2783 (1935, 4409)
Restaurant, Fresh (n = 3.5×10^9)	1250 (882, 1670)	43 (16, 379)	1293 (898, 2049)
Restaurant, Frozen (n = 1.5×10^9)	1380 (968, 1840)	48 (18, 417)	1428 (986, 2257)
Total	8680 (6110, 11580)	300 (112, 2635)	**8980 (6222, 14215)**

Tornado diagram illustrating sensitivity analysis of ground beef baseline model



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UNIVERSITY OF MINNESOTA

MDR *Salmonella* Removal

Removal of MDR *Salmonella:*

- 21% decrease in Years of Life Disabled
- 56% decrease in Years of Life Lost

- **45% reduction in Disability Adjusted Life Years**

Project Highlights:

~9,000 annual cases of salmonellosis attributable to ground beef

Removing >1 MPN/g resulted in a 36.7% reduction in illnesses

Removing >10 MPN/g resulted in a 13.6% reduction in illnesses

Removing MDR *Salmonella* reduces burden of disease by 45%

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

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 beef 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 ground beef, identify and remove products**
  - contaminated above threshold of 1MPN/g
  - contaminated with virulent *Salmonella* serotypes, MDR *Salmonella*

Data Gaps to Improve Risk Assessment Models

- Dose-response relationships for *Salmonella* strains
- AMR-specific burden of disease estimates
- Levels of detection for testing
- Cross-contamination coefficients

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