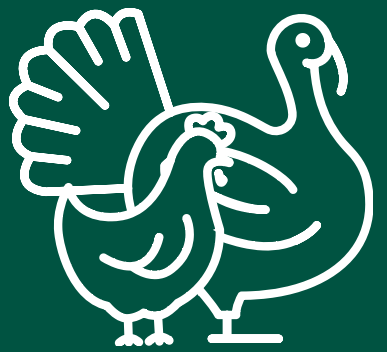
National Advisory Committee on Microbiological Criteria for Foods (NACMCF)

Enhancing *Salmonella* Control in Poultry Products Subcommittee Meeting

April 25, 2022
12:00 – 3:00 PM Eastern Time



Version 4/25/22, 7:35 am ET

Agenda

- Call to order
- Roll call/introductions
- Review of charge
- “Public Health” Work Group: Q1, Q4
- “Microbial Criteria” Work Group: Q2, Q3, Q5
- Break
- “Lab Technology” Work Group: Q6, Q7, Q8
- Timeline for completion and adoption
- Adjourn

Review of Charge and Milestones

FSIS is seeking guidance to develop risk management strategies to reduce salmonellosis associated with poultry.

Questions to address, by subcommittee working groups:

- Public health impact assessment
  - Q1 Impact of controlling specific serotypes in poultry to reduce salmonellosis
  - Q4 Use of foodborne illness surveillance data to identify specific problematic serotypes and ongoing monitoring for changes in prevalence of various serotypes to reassess interventions
- Establishing microbial criteria
  - Q2 Pre-harvest (Live birds on farms)
  - Q3 Poultry carcasses, parts, comminuted products prior to and after interventions
  - Q5 Use of APC as indicator of occurrence of *Salmonella*
- Laboratory technology
  - Q6 Rapid methods/technologies for quantification of *Salmonella*
  - Q7 Selective identification of serotypes/bias
  - Q8 Use of WGS (serotype, virulence, antimicrobial resistance) to develop criteria
- Research Gaps
  - Q9
- Plenary session for adoption November 2022

Public health impact assessment

Q 1 Francisco Zagmutt

Q4 Rob Tauxe

Q1. What type of approaches can be used to **assess the public health impact** (e.g., reduction in salmonellosis) by controlling specific serotypes or levels of *Salmonella* in poultry?

Two perspectives necessary to answer this question:

(1) How to ***predict*** the public health impact of hypothetical changes in *Salmonella* control strategies in poultry products ***prior to their implementation***, and

(2) How to ***assess*** the effectiveness of the standards in reducing salmonellosis ***once they are implemented***.

- The first *predictive* approach can be best addressed using **quantitative microbial risk assessment (QMRA)** methods
- The second *assessment* approach post implementation can be best addressed using **public health surveillance** available for salmonellosis

Will it work? QMRA to predict the public health impact of hypothetical changes in *Salmonella* control strategies in poultry products *prior to their implementation*

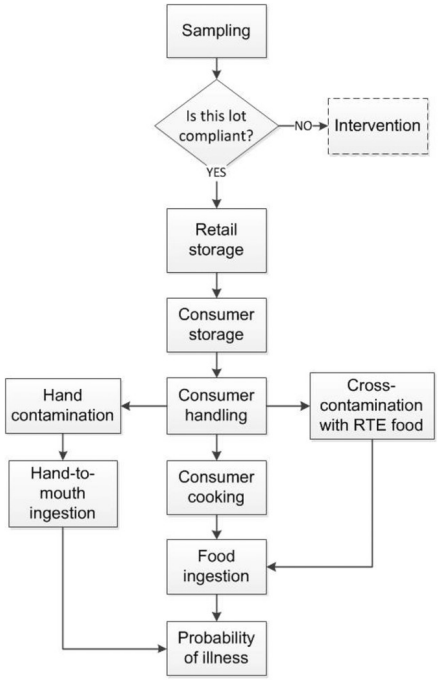
Summary of current content:

- The objective of microbiological criteria (MC), combined with hazard reduction intervention(s) when the MC is not met, is to control the extent of contamination of a target hazard in a food product, to reduce foodborne illnesses.
- **Three main MC** to be compared:
  - Current FSIS performance standards (prevalence-based)
  - Infectivity/virulence (targeting serotypes)
  - Exposure amounts (*Salmonella* levels in commodity)
  - Also, possible combinations such as different levels by serotype
- Existing QMRAs have addressed **some, but not all MC simultaneously** for *Salmonella* in different commodities. Some rely on strong assumptions. Uncertainty in some data affects precision.

Lambertini et al. Risk Anal. 2021 Aug;41(8):1376-1395. doi: 10.1111/risa.13635.

Types of QMRA approaches:

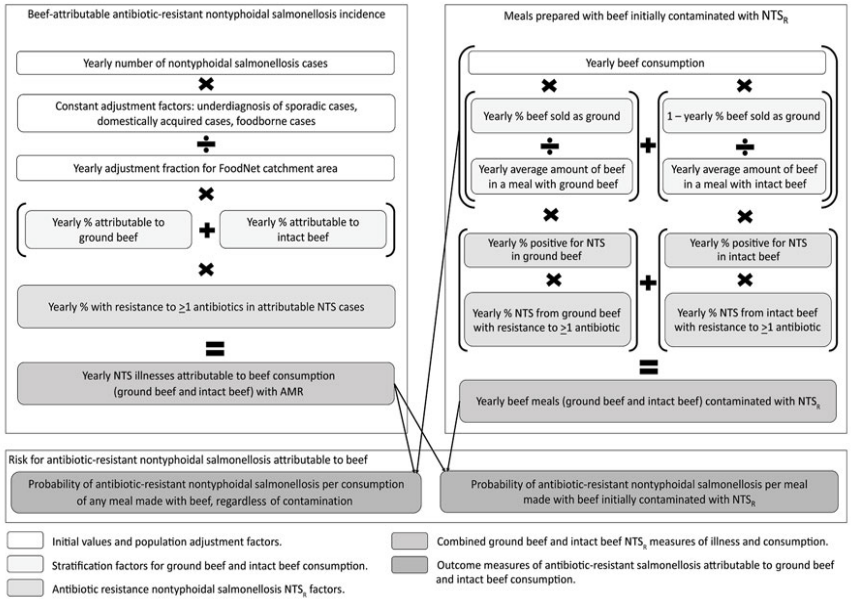
- ***Bottom-up* or *mechanistic*** QMRA approaches model the fate *Salmonella* on poultry products from a production stage (e.g. end of slaughter) through consumption and associated risk for consumers.
  - Pros: possibility to model more detailed control strategies, more intuitive
  - Cons: very data intensive, require dose-response by serotype, usually don't match surveillance illnesses
- ***Top-down or empirical***: use surveillance illnesses and prevalence to establish a linear dose-response relationship (e.g., current FSIS approach).
  - Pros: simplified structure requires less parameters, anchored to surveillance data
  - Cons: currently do not account for levels, serovars, lot-to-lot variability.
- Possible incorporation of alternative indicators such as ***indicator bacteria***: criteria such as International Commission on Microbiological Specifications for Foods (ICMSF)



Costard et al. Emerg Infect Dis. 2020;26(9):2108-2117. doi: 10.3201/eid2609.190922

Content in progress:

- Pro/cons of possible combinations of QMRA methodologies to address all MC parameters
- Discussion of data needs and possible data representativeness issues
- Brief discussion of targeting genes/clades vs serotypes in QMRA



Did it work? Using existing public health surveillance data to assess the effectiveness of MC in reducing salmonellosis *once they are implemented* *(see also Q4)*

Summary of current content:

- Measuring operational success of MC requires incorporating existing public health **surveillance data for salmonellosis** and adjusting for seasonal and cyclical fluctuations to ensure that the efficacy measurement is robust and unbiased.

- Although roughly 92% of reported salmonellosis is sporadic (not part of recognized outbreaks), successful control of *Salmonella* in poultry would be expected to reduce both outbreak-associated and sporadic cases.

- Current **attribution** of salmonellosis to different foods (sources) is primarily based on outbreak investigations. Emerging source attribution technologies based on Whole Genome Sequencing might allow for better estimation of success of the MC in poultry as it would also allow for attribution of sporadic salmonellosis cases.

Content in progress:

- Further discussion of emerging source attribution methods
- Limitations of measurements of success using surveillance data

Q4. Looking at foodborne **illness surveillance data**, how can data from outbreaks and sporadic cases and data on *Salmonella* serotypes in poultry products, be used to identify *Salmonella* serotypes of greatest concern in poultry products, that should be targets of control?

- With the changes in predominant serotypes isolates, how frequently should these data be reassessed? In other words, how frequently should priority *Salmonella* serotypes be reassessed?
- How will this information affect methodology and criteria that focus on specific *Salmonella* serotypes in poultry products?

Public Health Working Group: Q4

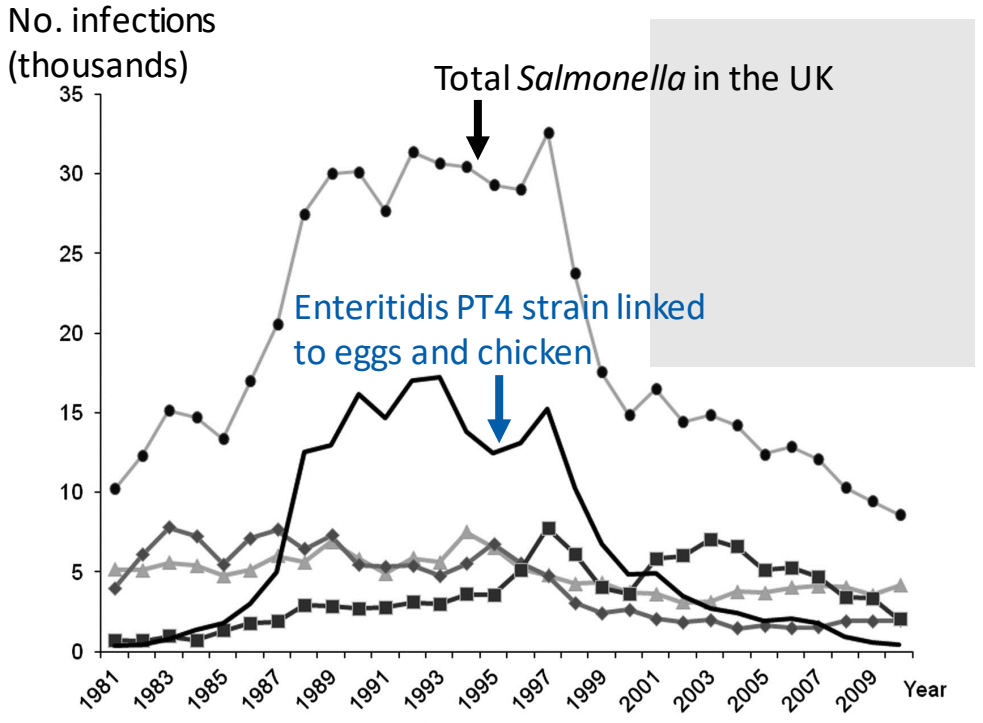
Data and approaches to identify *Salmonella* serotypes of concern in poultry

1. How might foodborne illness surveillance data on human illnesses, foodborne outbreaks, and data on *Salmonella* serotypes in poultry and poultry products be used to identify the Salmonella serotypes of greatest public health concern?
2. What time frame of data? Should only the most current data be used?
3. Going forward what methodology and criteria would focus on *Salmonella* serotypes most frequently associated with human illness and attributable to poultry products
4. How frequently should the list of priority *Salmonella* serotypes associated with poultry be revised, considering changes in their occurrence while still ensuring continuity in industry and regulatory testing?

Introductory Questions: Has targeted prevention been successful? What does success look like?

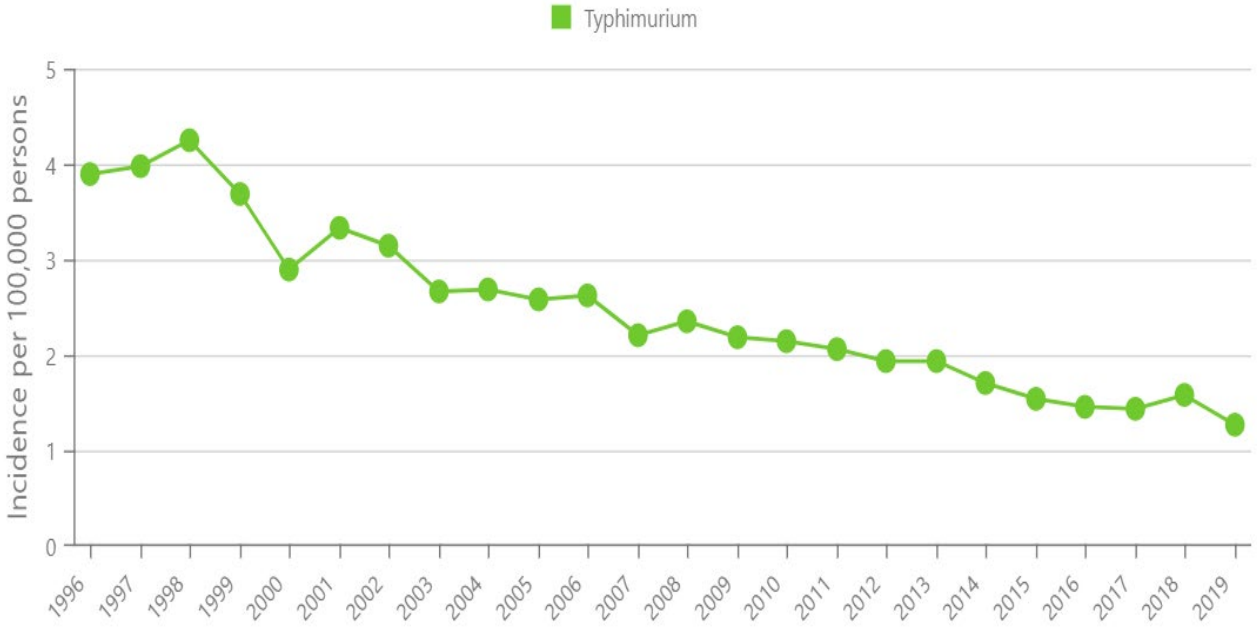
- In the 1990's, the UK had a major surge of S. Enteritidis (SE) infections reaching 21,500 in 1997 = 65% of all salmonellosis. One subtype (phage type 4) was linked to both eggs and chicken. With vaccination and other efforts targeting layer flocks and later broiler breeders, this fell by 87% to 2,900 SE infections in 2010. The specific PT4 strain most linked to poultry fell 97%, from ~18,000 to 459 infection cases.

- In Canada, 2016-2018, a surge in SE infections occurred, with many outbreaks linked to raw breaded processed poultry products (chicken nuggets, strips and tenders). New regulations required such products to be either cooked or tested and shown to be *Salmonella*-free. In two years, SE infections dropped by 55%: from 13 per 100,000 infection cases in 2017 to 5.8 per 100,000 in 2019. (CFIA Website)



O'Brien, 2013, CID 56:707-10

Decreases in two formerly common serotypes, 1996-2019 (U.S.)



***S*. Typhimurium** was #1 in 2007;
but #3 in 2019. Declined **67%**
from 3.90/100,000 in 1996
to 1.27/100,000 in 2019

***S*. Heidelberg** was #4 in 2000;
but #22 in 2019. Declined **90%**
from 0.80/100,000 in 1996
to 0.08/100,000 in 2019

From FoodNet Fast: cdc.gov/foodnetfast

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Q4 Part 1. How might foodborne illness surveillance data on human illnesses, foodborne outbreaks, and data on Salmonella serotypes in poultry and poultry products be used to **identify the *Salmonella* serotypes of greatest public health concern**?

Part 1a: What surveillance data are available?

- National *Salmonella* case reporting (usually including serotype)
- PulseNet (National subtyping network), now with DNA sequencing
- FoodNet (More detailed interviews in 10 sites, 15% of population)
- National Antimicrobial Resistance Monitoring System
  - 1 in 20 human cases, food samples, regulatory testing
- Reporting of foodborne and other outbreaks (National Outbreak Reporting System or NORS)
- *Salmonella* detected in chickens and in poultry product testing
  - NARMS samples, FSIS regulatory samples, testing in states, etc.

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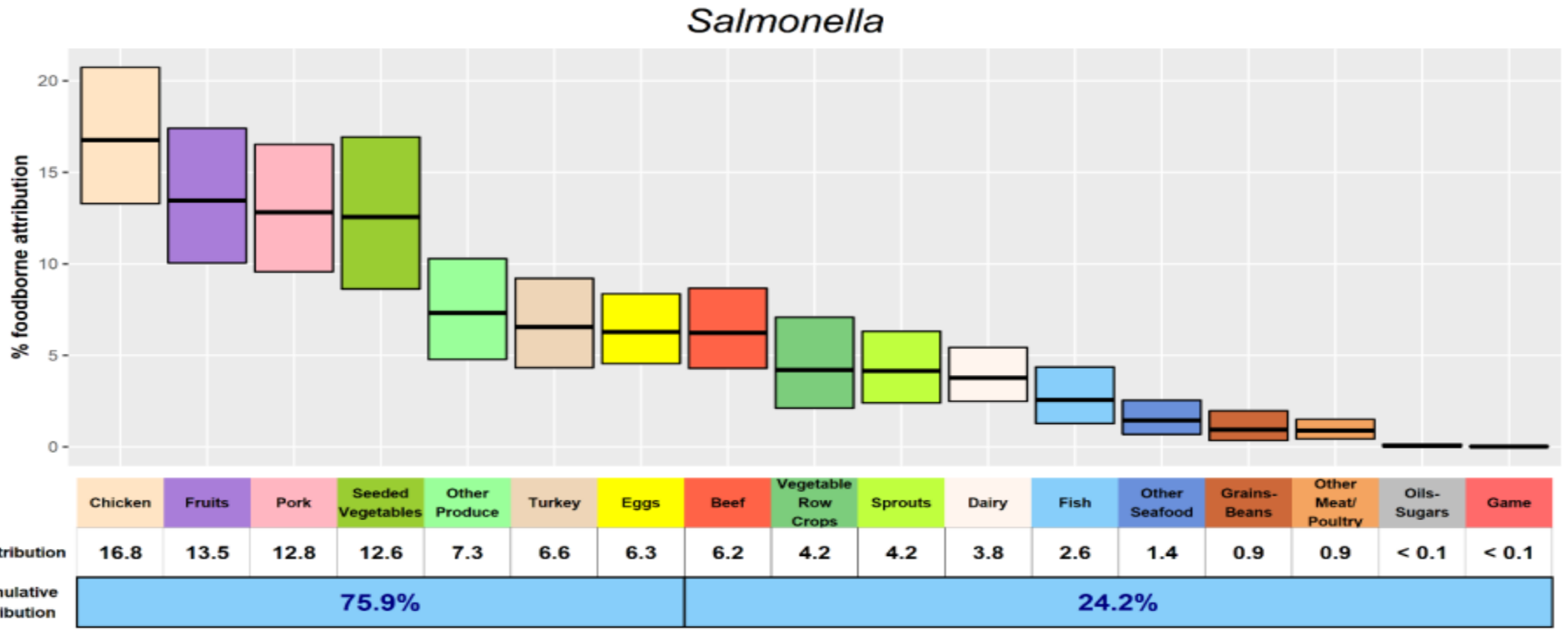
Q4 Parts 1b & 3. How might these data be used to identify the serotypes of greatest public health concern associated with poultry products, and what methods and criteria would focus on those serotypes most frequently associated with human illness and attributable to poultry products?

What fraction of human salmonellosis is related to poultry?

First model: Interagency Food Safety Analytics Consortium (IFSAC) model based on **foodborne outbreaks 1998-2019**, with most weight given to most recent 5 years:



2019:
Based on outbreak reports:
17% of outbreak-associated cases from chicken,
7% turkey,
slowly increasing each year.

Data for individual serotypes too sparse in general to analyze

No accounting for multi-food outbreaks, cross-contamination

Are outbreak sources the same as those for sporadic cases?

Second model: New IFSAC model based on **comparing sequences** of human (2014-2017) and non-human strains from a range of animal, food, and environmental sources.

Model trained on ~18,000 non-human isolates over last two decades to identify genetic subgroups associated with specific food sources, then compared to ~ 6,500 human isolates (2014-2017) with a Random Forest model. Travel-associated cases and outbreak-associated cases excluded. These are preliminary results.

Counting those with >50% probability attribution to one food source

All serotypes together: **49% were related to a poultry source** (46% chicken and 3% turkey)

By serotype, poultry-source attribution was:

86% of Enteritidis (O-group 9, was D)

66% of Typhimurium (O-group 4, was B)

62% of Heidelberg (O-group 4, was B)

55% of Infantis (O-group 7, was C1)

29% of I: 4,5,12:i:- (monophasic Tm) (O-group 4, was B)

These 5 serotypes (in 3 serogroups) account for a poultry association for 40% of food-attributable domestic sporadic salmonellosis (2014-2017 data)

If serotype criteria include :

- Common cause of human infections
- Present in poultry
- Transmitted through foods

These 5 meet those criteria

As both Typhimurium and Heidelberg are decreasing, model may need updating soon.

Thanks to Beau Bruce and Erica Rose at CDC

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Q4 Part 2. Should only the most current data (e.g., of foodborne illness surveillance case, outbreak or food/animal testing) be used?

Slow change occurs over years; we hope to see change accelerate.

To measure change, need a baseline from which to measure. It should be pre-pandemic (e.g., 2017-2019 baseline for HP2030)

For current status, ideally should use the most current data available (though may need to exclude 2020, 2021 because of pandemic perturbations:

- For case data and sequence-based data, should have sufficient data in last 3-5 years for statistical power to show change from baseline
- For outbreak data, which accumulate more slowly, will need to combine data over more years to see change

  E.g.: In IFSAC annual report based on outbreak data, give most weight to last 5 years, and then progressively discount over the preceding 17 years.

4 Q4 Part 4 How frequently should the priority *Salmonella* serotypes associated with poultry be revised considering changes in their occurrence while still ensuring continuity in industry and regulatory testing?

Yogi Berra *"It is hard to predict, especially about the future!"*

Ideal to repeat analyses every year with updated data

How soon would we expect to see impact?

Within 3-4 years? Rethink approach if nothing has changed by then

If a major decrease occurs in reported cases of a targeted serotype (> 25%?), then appropriate to consider adding an additional targeted serotype, chosen by same process, or even specific subtypes of particular concern.

Many practical considerations e.g. how quickly a testing process can be updated to include a new serotype, and how quickly new prevention/control strategies such as vaccines can be developed for additional serotypes

Prevention strategies will need to be modifiable, and a method for regular modification can be considered as part of the regulatory approach

Establishing microbial criteria

Q2: Stan Bailey

Q3: Jim Dickson

Q5: Stan Bailey

Q2. What microbiological criteria can be used with live birds (on-farm) as a means to encourage control of *Salmonella* **pre-harvest**?

- What, if any, qualitative microbiological criteria can be used to identify the presence of *Salmonella* in a flock at harvest?
- Can these indicators be used to target *Salmonella* serotypes that are most frequently associated with human illness?
- What industry data can be used to assess control?

Q2: Outline of presentation

- Current testing, and actions triggered by test results
- Context of existing pre-harvest control strategies (prevention and process control than a MC would verify)
- Examples of MC + control strategies in the U.S. and other countries: what has worked?

Microbial criteria to assess and inform preharvest control

What have we been testing?

- Filter paper under newborn chicks tested to assure free of salmonella
- Boot sock samples of broiler houses test for all Salmonella, including just before slaughter
- If positive for salmonella, depopulate flock, and compensate farmer with shared corporate and Federal financing until control is achieved and houses with biosecurity financed and built

Serotype-specific control strategy

- Only vaccines can target specific serotype of serogroup
- Almost all breeders currently vaccinate, but very few broilers

WG needs:

- *Invite expert (suggest Dr. Chuck Hofacre) to address the committee to detail current status of vaccines in chickens and to discuss types of vaccines and time to development and implementation. (→ reduction potential, time to develop/deploy new vaccines; see Q1/4)*
- *Latest 'other' on-farm interventions and studies which follow Salmonella from on-farm through processing.*

Q2. Salmonella Control in Scandinavian Production Systems Compared to Production Systems in the U.S.

Q2. Scientific principles of Swedish program

- If broilers are never exposed to *Salmonella* then they cannot become colonized and subsequently they will not be contaminated after processing.
- Primary method of control is eradication of *Salmonella*-positive breeders or broilers
- Control *Salmonella* on farm. No chemical treatments in the processing plant.

Q2. Potential US Intervention strategies
- with no eradication program -

- Control *Salmonella* in breeder flocks
  - feed, biosecurity, vaccination, competitive exclusion, moisture control
- Control *Salmonella* in broiler production
  - feed, biosecurity, competitive exclusion, moisture control

Best Management Practices for Control of Salmonella in U.S. Poultry Industry (1)

Breeders:

- Salmonella-free chicks
- Competitive exclusion treatments
- Vaccination program
- Biosecurity
  - Rodent and insect control program
  - Footbaths / movement of workers

Best Management Practices for Control of Salmonella in U.S. Poultry Industry (2)

Feed

- Attempt to control quality of ingredients
- Sufficient time in conditioner to give time/temperature/moisture for Salmonella kill
- Control post pelleting (processing) recontamination. Pay particular attention to cooling area

Best Management Practices for Control of Salmonella in U.S. Poultry Industry (3)

Hatchery:

- Enforce cleaning/sanitation program
- Control air movement in hatchery
- Institute chemical disinfection program in hatch cabinets during hatch period
- Do not reuse tray liners

Best Management Practices for Control of *Salmonella* in U.S. Poultry Industry (4)

Grow-out:

- Only *Salmonella*-free chicks
- Competitive exclusion treatments
- Moisture control (no leaking nipple drinkers)
- Proper working ventilation system (reduce stress on birds – litter amendments if necessary)
- Rodent and insect control program
- Limit movement of workers / visitors

Best Management Practices for Control of *Salmonella* in U.S. Poultry Industry (5)

Transport:

- Insist on proper feed and water withdrawal time
- Clean transport coops [more work needs to be done]
- To extent possible, limit time in transport cages

Q2. Conclusion so far & next steps

- *Salmonella* control will require careful attention to all aspects of production and processing, e.g. a series of integrated MCs
- On-farm controls needed to eliminate or keep levels of *Salmonella* low
- Transportation appears to increase both internal and external carriage of *Salmonella*
- Chemical treatments in plant can reduce *Salmonella* on chicken products as long as the level of *Salmonella* is not too high (see Q3)

- Work in progress by WG:

- Considering available control strategies, what (sufficiently low) contamination extent at pre-slaughter would be proof of preharvest process control (farm level, flock/batch level)? What is feasible?
- At which pre-harvest stages/processes can MC be useful?
- Answering sub-questions: 1, 2, 3

Q3. What microbiological criteria could be established for poultry carcasses, parts, and comminuted products prior to applying interventions and after interventions?

- Can quantitative assays be used and what key parameters should be considered in the choice?

- How could serotypes most frequently associated with human illness be considered in developing the microbiological criteria?

Q3: Outline of answer

- Can quantitative assays be used and what key parameters should be considered in the choice?
  - What information currently available supports a quantitative assay?
  - What are the limitations of the available information?
    - Seasonal variation
    - Geographic variation
  - What are the alternatives to quantitative information?
  - USDA FSIS scientists will review their study with the working group

Q3: Outline of answer

- How could serotypes most frequently associated with human illness be considered in developing the microbiological criteria?
  - What are the relevant serotypes?
  - Are there methods available to detect specific serotypes within a processing timeframe?
  - Where should the testing occur?
  - What is the relevance of finding different serotypes in production versus in the product?

Q3. Conclusion so far & next steps

- The working group will review the available information regarding quantitative methods
- The working group will suggest a protocol for verifying that a specific quantitative method is reasonable and appropriate for assessing the *Salmonella* status
- The working group may come forward with recommendations for quantitative methods for assessing the *Salmonella* status

Q5. There is a documented correlation between a reduction in the quantity of APC between carcasses and finished products and the occurrence of *Salmonella* in finished products for beef, pork, and poultry.

How might this information be used to set microbiological criteria to assess process (pathogen) control in poultry?

Q5: Outline of answer

- USDA FSIS scientists will review their findings with the working group
- The working group will determine if there is additional supporting documentation

Q5. Conclusion so far & next steps

- After USDA FSIS's presentation (within the next 4 weeks), the working group will complete the review of supporting data
- WG will provide decision support guidance that can be used to assess whether a specific quantitative method is effective and appropriate for assessing *Salmonella* status (e.g., how much correlation is informative enough)
- WG will provide a review of different quantitative measures as potential process control indicators, and their effectiveness in predicting *Salmonella* presence/levels or other relevant factors.
- Discuss options for inclusion into combined MC (*Salmonella* + other indicators).

Laboratory technology

Q6: Wendy McMahon

Q7: Wendy McMahon

Q8: Haley Oliver and Randy Worobo

Q6. What rapid methods and technologies are available for the quantification of Salmonella? How should FSIS make the best use of these methods?

Rapid methods for *Salmonella* quantification (enumeration):

- MPN not operationally friendly (USDA MLG Chapter 4.11 and Appendix 2.05) and requires high level of resources (time, disposables)
- New protocols, culture-dependent and -independent quantification methods, have been reported, developed, and adopted in different laboratory settings
- Some of the methods are considered alternative or, in some cases, complementary to the traditional culture-based methods
- Examples of methods in the market with validation (Hygiena and bioMerieux) along with some methods still in development or to be validated (BioRad and 3M) are presented in a table (next slide)
- Considering literature review for research based methods

Rapid methods for *Salmonella* quantification (enumeration)

	USDA MLG	Hygiena	BMX	BioRad		3M
		BAX	GeneUP	iQ-Check Salmonella	dd-Check Salmonella	MDS- (info in May)
Technology/ platform	MPN	RT PCR estimate from CT at shortened enrichment time point (4-8h)	qPCR quant (no enrich) Concentrate Salmonella pre-enrichment; count from CT	qPCR	ddPCR	
Time to result	Screening result Day 2	6-8h	4h	4.5-5 hr	5.5-6 hr	
LOD	Dependent on # tubes and sample volume	LOD1 (1 cfu/mL or g)	10 cells	10 CFU/g	1 CFU/ sample size	
Range of quantification	Dependent on # tubes and sample volume (see MPN tables/calculators)	Dynamic range 1-10,000 cfu/ml or 1-1000 cfu/g depending	Up to 7 log			
Approvals	Standard Methods (USDA MLG)	RI 081201, OMA submission in progress	AOAC RI #	N/A	N/A	N/A
Applicable matrices approved	MLG Chapter 4.11 *Salmonella*	2021 – comminuted chicken (325g) and Turkey (325g) 2022 – poultry rinsates (30ml)	5 matrices	Ground Turkey	Ground Poultry, poultry rinses,	
References	Appendix 2.05 Most Probable Number Procedure and Tables 6/29/14	User guide AOAC RI #	User guide AOAC RI #	User guide	User guide	

Q7. Are there particular approaches that would result in selective identification of the serotypes of public health concern?

- Is there strain selection bias introduced by laboratory methods? And if so, what strategies can be used to mitigate this bias?

Outline of answer

- Review of literature on:
  - Current confirmation methods require only a selected number of isolates that are serotyped
  - Enrichment conditions show a shift in populations (CRISPR)
  - Present published examples – last 5-10y
  - Evidence of bias from literature
  - Factors influencing potential bias
    - Phenotypic and biochemical bias from culture methods
    - Temperature, Time, Formulation of enrichment
- Serotypes of interest
  - Reference responses to earlier questions here (Typhimurium, Enteriditis, Infantis) CDC human illness, predominant serotypes in human and chicken
- Possible ways to mitigate bias -
  - Current ARS study with HPS (Highly Pathogenic *Salmonella*) developing an assay
  - Can we learn from other industries (beef from N Shariat)
    - clinical
    - animal/vet
- What type of research is needed
  - Incubation conditions (time, temperature, media formulation, detection)
    - May recommend having more than one enrichment, for example
  - Feed into Q9

Q8. How should pathogen characteristics derived from whole genome sequencing (e.g., serotype, virulence, antimicrobial resistance) be considered in the development of microbiological criteria?

Lab Technology Work Group: Q8

Q8. How should pathogen characteristics derived from whole genome sequencing (e.g., serotype, virulence, antimicrobial resistance) be considered in the development of microbiological criteria?

- Recent WGS-based advancements in *Salmonella* characterization and current use case
  - Greatest value of WGS is at the convergence of serotype, epidemiological, and phenotypic data to differentiate *Salmonella* with high public health relevance from *Salmonella* of limited public health relevance.
  - WGS can be used to differentiate hypo- and hypervirulent serovars and clades
  - WGS identifies/differentiates polyphyletic serovars

- Current limits to WGS sequencing to characterize pathogen virulence
  - Always a function of the quality of the database
  - WGS alone cannot predict virulence (e.g., no agreed upon gene presence/absence profile)

Q8. Research needs

- A risk assessment that assesses public health impacts of different risk-based *Salmonella* control strategies
  - Reduction in *Salmonella* levels in food?
  - Targeted reduction in specific serotypes or subtypes?
  - Combination?

Q/A

Next Steps: Timeline for Completion

- WG Virtual meetings (minimum every 2 weeks through July)
  - Update text after each meeting
- **Late June/Early July 2022**: **Subcommittee meeting;** reports from each work group
- **Late August/early Sept 2022**: **Subcommittee meeting;** reports from each working group
- September 30, 2022: "Final" draft document due
  - Subcommittee review/revisions; finalize references
- October 15, 2022: Draft to Full Committee and FSIS comments/revisions
- October 21, 2022: Comments returned by Full Committee and FSIS Final revisions
- October 31, 2022: Final document sent to Full Committee and FSIS for review
- **November 15, 2022: Plenary NACMCF Meeting; Vote for adoption**

Resources for WGs

- To invite speakers: each WG should contact NACMCF with name/contact (cc co-chairs)
- Digitop (and training sessions)
- Reference management
- Resources in Teams: article PDFs, recordings of talks