Interagency for Food Safety Analytics Collaboration (IFSAC)



History of IFSAC

- IFSAC established in 2011 by:
 - Centers for Disease Control and Prevention (CDC)
 - U.S. Food and Drug Administration (FDA)
 - United States Department of Agriculture's Food Safety and Inspection Service (FSIS)
- Charter established in 2016
- Guided by Strategic Plans and Priority Setting Plans



Introduction

- Shared vision amongst CDC, FDA, and FSIS to improve foodborne illness source attribution
- Brought leaders, scientists, and analysts from the 3 agencies together to create, implement, and complete projects
- Projects designed to complement one another to ensure maximum utility and efficiency
- IFSAC identified four priority pathogens as the initial focus of projects:
 - 1. <u>Salmonella</u>
 - 2. <u>E. coli 0157:H7</u>
 - 3. Listeria monocytogenes (Lm)
 - 4. <u>Campylobacter</u>



IFSAC's Purpose and Goals

- Three federal agencies working together to:
 - Analyze and interpret human surveillance and food contamination data;
 - Share data and methods; and
 - Monitor progress toward the goal of preventing foodborne illness
- Major goals:
 - Identify, plan, and conduct food safety and foodborne illness analytic projects recognized as high priority by all three agencies
 - Improve coordination of federal food safety analytic efforts; and
 - Address cross-cutting priorities for food safety data collection, analysis, and use



Importance of IFSAC

- Accomplishments build on each other and allow pursuit of new, ever-more challenging objectives and projects
- Project outputs are supported by all three agencies and can be used to implement and promote harmonized approach to attribution estimation



IFSAC Structure

Steering

Committee (SC)

- Provides oversight of analytic projects and ensure projects are coordinated and managed effectively
- Composed of 2 representatives from each agency

Technical Workgroup (TWG)

- Provides the analytic expertise to develop and execute IFSAC projects
- Workgroup composed of 2 points of contact from each agency

Communication Workgroup (CWG)

- Advise SC and TWG on development and implementation of communication materials
- Composed of 1-2 representatives from each agency





- Steering Committee (SC) identifies top priorities
- Technical Workgroup (TWG) develops analytic project plans to address priorities
 - Plans include deliverables, timeline, and milestones
 - Projects typically conclude with an internal final report and/or other publicfacing deliverable (published manuscript, presentation at conferences/meetings, etc.)
- SC tracks all projects and provides input on analyses
- All public documents and web pages undergo formal clearance by all 3 agencies



Strategic Priorities for 2024 – 2028

- Explore additional data sources and alternative methods to better estimate the sources of foodborne illnesses caused by *Campylobacter* and harmonize estimates across different approaches and data sources
- Expand our list of priority pathogens to include non-O157 Shiga toxinproducing *Escherichia coli* (STEC) and provide source attribution estimates in IFSAC's annual Foodborne Illness Source Attribution reports
- Consider incorporating data on non-foodborne sources of priority pathogens, such as animal and environmental sources, into IFSAC's annual Foodborne Illness Source Attribution estimates to better refine and contextualize foodborne illness source attribution estimates
- Finalize existing analyses and disseminate findings to multiple audiences



Foodborne Illness Source Attribution Estimates for *Salmonella*, *E. coli* 0157, and *Listeria monocytogenes* —United States, 2021







Selected IFSAC Completed Projects

- **Shared Needs**: Developed a shared understanding and statement of needs for foodborne illness source attribution.
- New Food Categorization Scheme: Improved food categorization scheme for attributing outbreaks and related illness to food.
- Sporadic and Outbreak Comparison: Compared characteristics of sporadic and outbreak-associated foodborne illness.
- Improved Outbreak Analyses: Improved analyses of outbreak data used to assign implicated foods to food categories.
- **Harmonized Estimates**: Developed a method for food source attribution for four bacteria (*Salmonella*, *E. coli* O157:H7, *Listeria monocytogenes* [*Lm*], and *Campylobacter*) using outbreak data.





Selected Current Projects

- **Change Over Time**: Determining possible statistical modeling approaches to evaluate temporal changes in attribution estimates.
- **Campylobacter Comparative Review**: Scoping review of available literature to characterize the current understanding of the attribution of *Campylobacter* infections to foods
- Whole Genome Sequencing (WGS) for Salmonella Enteritidis (SE) Attribution: Develop a model to estimate the percentage of SE human illnesses from each food category.
- Campylobacter attribution: Evaluating the use of case-control data, WGS data, and a combination of the two for improving Campylobacter attribution methods.



Campylobacter Comparative Review Project Overview

Purposes

- Contextualize IFSAC estimates
- Identify alternative estimates
- Inform future studies

Two scales of attribution estimates of interest

- Proportion foodborne
- Proportion to specific commodities (particularly dairy and chicken)

Variation across regions

• Want to be able to compare U.S. findings to international findings

Variation across study type

• Want to examine differences in estimates by methods/data



Campylobacter Comparative Review Steps in Scoping Review

Search	Relevance Screening	Full Text Review	Data Extraction	Synthesis and Analysis
 Develop search criteria Pre-test search criteria Verification strategy 	 Remove duplicates Define first level eligibility criteria (i.e., attribution study) Reviewers apply first level eligibility criteria to titles and abstracts 	 Define second level eligibility criteria (i.e., includes extractable data) Reviewers confirm eligibility to first AND second level criteria 	 Define variables for extraction by study type Extract data and populate database Second reviewer confirms extraction 	 Summarize findings Descriptive statistics Visual display



Campylobacter Comparative Review Project Status and Next Steps

Phase 1

Search Time Period: 2010-2018

1,400 studies identified through initial searches

1378 studies assessed for fulltext eligibility through abstract review

1229 studies excluded

149 studies for full text review

77

Final number of studies identified for data extraction after full text review



Phase 2

Search Time Period: 2018-2024

Estimate the Percentage of Human *Salmonella* Illnesses From Unknown Source

- Develop a random forest model using whole genome multi-locus sequence typing (wgMLST) calls to predict the source of isolates
- Apply model to human isolate with unknown source to estimate likely source



Salmonella Isolates From Known Single Source Foods

- 18,661 isolates, all assigned to single source foods
- Trained model accuracy >80%





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Isolates Were From Many Categories

- >18,600 isolates, all assigned to single categories
 - About 1/3 from chicken reservoir
- Trained model accuracy >80%

	Chicken	5531	119	71	25	41	3	10	17	1	5	0	2	2	4	2	
	Turkey	159	2016	64	10	21	0	13	3	0	1	0	1	0	0	0	
	Pork	83	91	1686	20	109	13	3	12	4	0	1	1	1	1	1	
	Vegetables-	50	19	45	1966	51	78	14	71	46	6	21	7	5	10	1	
	Beef-	93	54	134	46	1303	8	10	18	4	0	3	2	5	3	0	
	Fish-	13	12	24	109	13	741	5	40	29	3	41	4	12	0	1	
/ed	Egg-	99	2	8	2	4	0	256	5	3	4	0	1	0	0	0	Proportion of Observed
ser	Nuts/seeds-	34	12	12	139	31	38	4	615	33	3	15	1	3	6	1	0.75 0.50
ö	Fruit	21	3	10	102	13	49	2	28	434	2	24	3	3	4	0	0.25
(Other Poultry-	40	11	6	12	4	3	21	4	0	100	0	0	3	1	0	
	Shellfish-	10	6	13	62	8	147	3	14	29	0	253	5	1	5	1	
(Grains/beans-	16	7	7	27	6	4	3	12	3	2	4	76	1	1	1	
	Other Meat-	13	4	9	21	15	20	2	13	7	6	7	0	77	2	0	
	Dairy	10	1	12	27	31	3	2	8	10	0	3	1	4	46	1	
	Game	24	10	6	16	2	1	0	4	0	3	1	2	0	1	8	
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CENTERS FOR DISEASE" CONTROL AND PREVENTION																	

Source Attribution for Domestic Infections

- 44% of domestic infections assigned as unknown reservoir
- Among those with known reservoirs, this model predicts that among domestic infections
 - 46% from chicken reservoir
 - 27% from vegetable reservoir



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Campylobacter Attribution Using Sporadic Case Data Obtained From State and Local Investigations

- Improve methods for *Campylobacter* attribution
 - We are exploring the use of case-control data, WGS data, and a combination of the two
 - >New methods will require new data streams
- We will identify the best approach based on science **and** whether the data can be sustainably collected over time



WGS *Campylobacter* Attribution Ratio Preliminary Results

Several exposures linked to previous outbreaks or illness were associated with an increased odds of being a case

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Differences Between Salmonella and Campylobacter (Inputs)

Counts and distribution of available NCBI isolates

	<i>Salmonella</i> (Project 25)	<i>Campylobacter</i> (Project 30)
Number of isolates	18,661	25,579
Genes (loci) present in >1%	8,143	2,902
Food categories	15	7
Chicken proportion	31%	71%

Food category distribution of available NCBI isolates





Using WGS and Case Control



IFSAC Collaborations

- Centers of Excellence (COE) outbreak bias and uncertainty
- Develop a shared understanding and statements of need for foodborne illness source attribution with the Interagency Risk Assessment Consortium (IRAC)



IFSAC's Work Supports Agency Efforts

- Support FDA's effort to implement the Food Safety Modernization Act (FSMA)
- Support FDA's pathogen prioritization efforts through preliminary analyses of foodborne outbreaks for food source attribution (Risk Prioritization)
- Support USDA FSIS' *Salmonella* Framework



IFSAC Publications



- Annual Reports on Foodborne Illness Source Attribution Estimates
- Recency-Weighted Statistical Modeling Approach to Attribute Illnesses Caused by 4 Pathogens to Food Sources Using Outbreak Data, United States
- An Updated Scheme for Categorizing Foods Implicated in Foodborne Disease Outbreaks: A Tri-Agency Collaboration





Contact us at IFSAC@FDA.HHS.gov



