Global and Integrated Approaches to Animal Health and Food Safety

March 31, 2026

Moderated by: Michelle Sayles, Diamond Pet Foods and Chair of the Animal and Pet Food Safety PDG

Organized by the Animal and Pet Food Safety PDG

Sponsored by the IAFP Foundation

International Association for Food Protection

Webinar Housekeeping

- It is important to note that all opinions and statements are those of the individual making the presentation and not necessarily the opinion or view of IAFP.

- All attendees are muted. Questions should be submitted to the presenters during the presentation via the Q&A section on your screen. Questions will be answered at the end of the presentations.

- This webinar is being recorded and will be available for access by IAFP members within one week.

Introduction/Comments

Todays Speakers:

Heather Tate, FDA
Valentina Trinetta, Kansas State University
Fabio Sossai Possebon, São Paulo State University (UNESP - Botucatu, Brazil)
Ansen Pond, Pilgrim

How U.S. monitoring of antimicrobial use and resistance informs policy and protects animal & human health

DEPARTMENT OF HEALTH & HUMAN SERVICES·USA

FDA U.S. FOOD & DRUG ADMINISTRATION

Heather Tate, PhD MS

FDA Center for Veterinary Medicine

Epidemiologist, NARMS (FDA–CDC–USDA)

Why AMR Matters for Food Safety

Agricultural use of antimicrobials creates selective pressure that promotes resistant bacteria

Resistant zoonotic enteric bacteria can move between animals, contaminated foods, environments, and people

AMR can compromise the effectiveness of medically important antimicrobials used to treat human infections

CVM Plan for Supporting Antimicrobial Stewardship in Veterinary Settings (Phase 3, FY 2024-2028)

01

Align antimicrobial use with stewardship principles

02

Foster stewardship in veterinary settings

03

Enhance monitoring of AMR and antimicrobial use in animals

*Antimicrobial stewardship helps to preserve the effectiveness of antimicrobial drugs and slows the development of resistance

How AMR monitoring supports stewardship

AMR monitoring detects emerging resistance hazards allowing veterinarians to adjust prescribing

AMR data inform FDA decisions about veterinary antimicrobial approvals or post-approval label changes or policies

Monitoring can be used to measure the effects of stewardship interventions

One Health AMR data reveal how antimicrobial resistance circulates in animals, humans, and the environment

National Antimicrobial Resistance Monitoring System (NARMS)

National system tracking AMR in zoonotic enteric bacteria

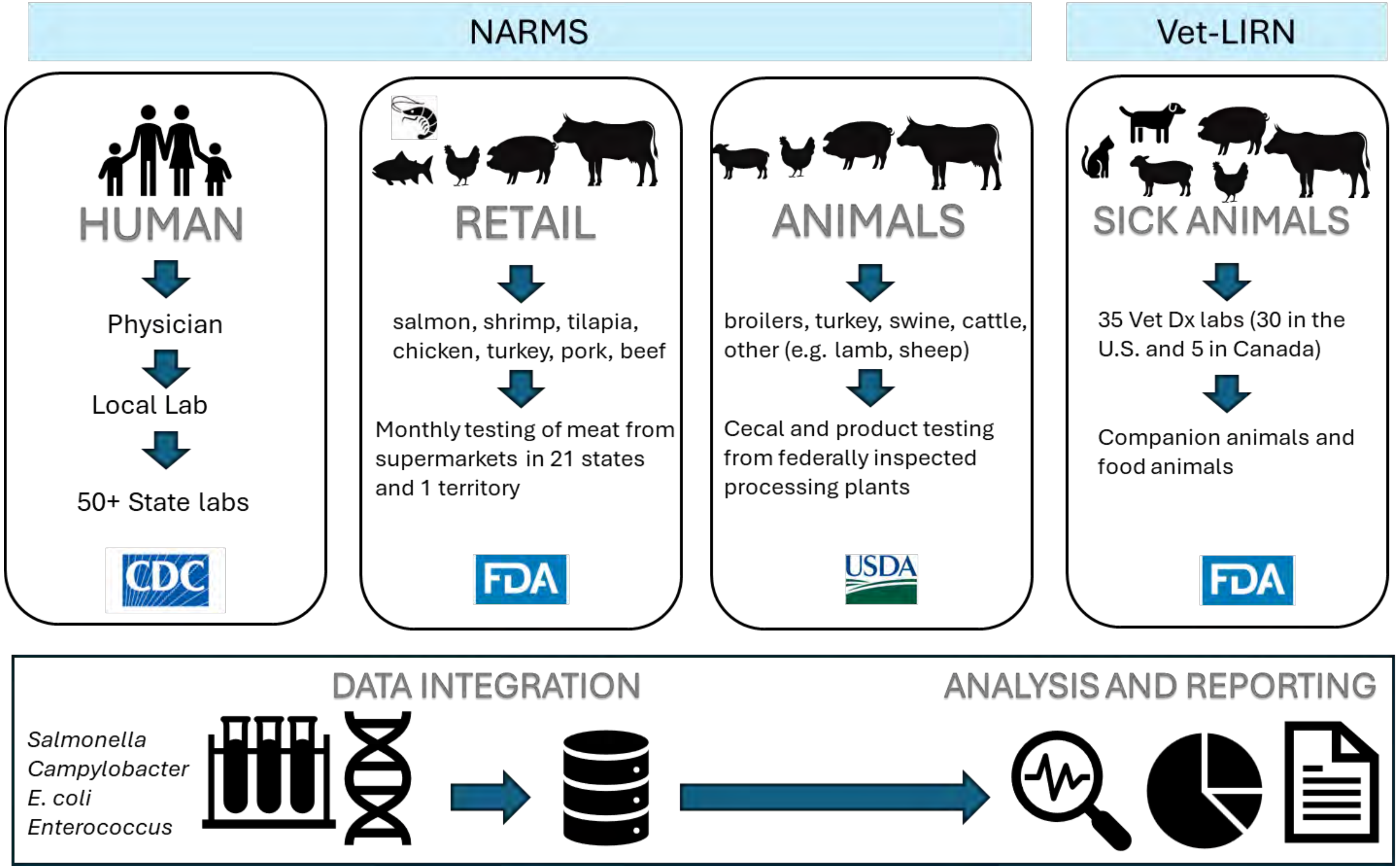
Core organisms: *Salmonella*, *Campylobacter*, *E. coli*, *Enterococcus*

Uses antimicrobial susceptibility testing + genomics to detect and characterize resistance

NARMS data assist with outbreak detection and prioritization

NARMS data inform risk and policy

One Health Framework



NARMS

Vet-LIRN

HUMAN

Physician

Local Lab

50+ State labs

CDC

RETAIL

salmon, shrimp, tilapia, chicken, turkey, pork, beef

Monthly testing of meat from supermarkets in 21 states and 1 territory

FDA

ANIMALS

broilers, turkey, swine, cattle, other (e.g. lamb, sheep)

Cecal and product testing from federally inspected processing plants

USDA

SICK ANIMALS

35 Vet Dx labs (30 in the U.S. and 5 in Canada)

Companion animals and food animals

FDA

DATA INTEGRATION

ANALYSIS AND REPORTING

Salmonella
Campylobacter
E. coli
Enterococcus

Veterinary Laboratory Investigation and Response Network (Vet-LIRN)

Established

2010 - Partnership between FDA CVM and VDLs

Geographic Coverage

48 veterinary diagnostic laboratories across North America

Mission & Priorities

Addresses a broad range of CVM's priorities

courtesy of Dr. Olgica Ceric

Vet-LIRN Main Priorities

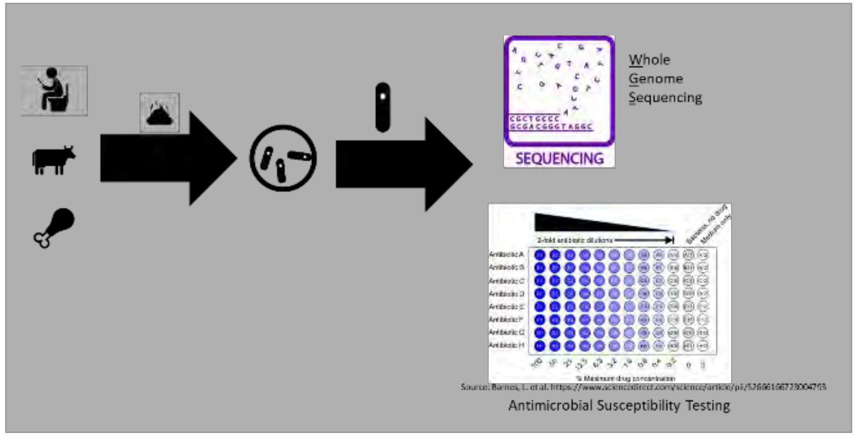
- Rapid Emergency Response
  - Respond to health threats like contaminated pet food, feed, drugs
  - Collect samples from ill animals; tests not available in FDA labs
  - Provide rapid preliminary food testing data
  - Support regulatory actions and recalls

- Proactive Research & Preparation
  - Proficiency exercises ensure preparedness
  - Develop and validate new tests
  - Monitor antimicrobial resistance
  - Advance veterinary medicine and public health

courtesy of Dr. Olgica Ceric

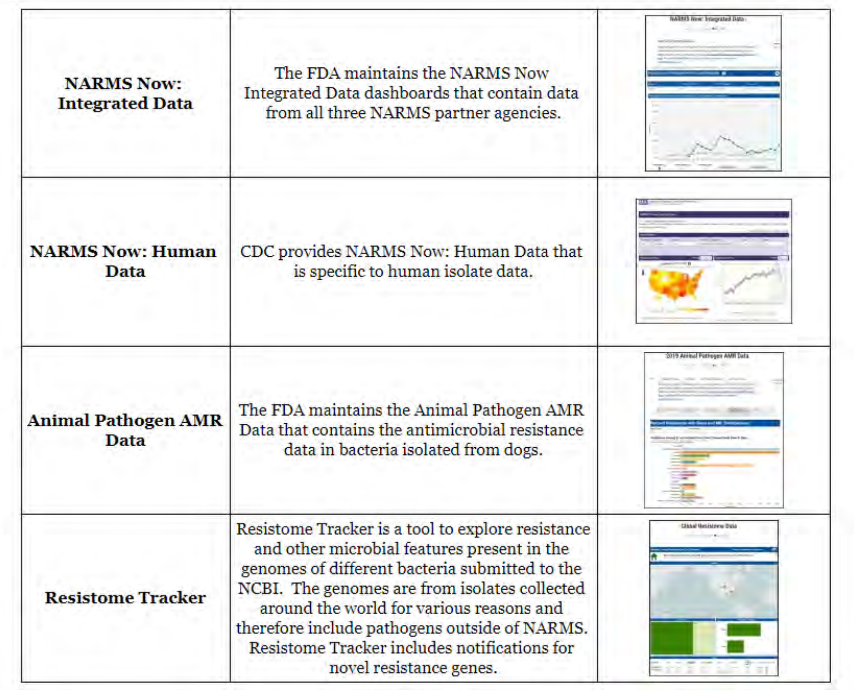
Tools: AST + Whole Genome Sequencing (WGS) + Open Data

- Antimicrobial susceptibility testing (AST) tracks phenotypes (MICs)
- WGS identifies resistance genes/mutations and relatedness
- Trend monitoring: detect unusual or concerning patterns earlier
- Open Data access points: NCBI Pathogen Detection, NARMS Now, Animal Pathogen AMR Data, Resistome Tracker



Source: Barnes, L. et al. https://www.sciencedirect.com/science/article/pii/S2666166723004793

Antimicrobial Susceptibility Testing



NARMS Now: Integrated Data	The FDA maintains the NARMS Now Integrated Data dashboards that contain data from all three NARMS partner agencies.	
NARMS Now: Human Data	CDC provides NARMS Now: Human Data that is specific to human isolate data.	
Animal Pathogen AMR Data	The FDA maintains the Animal Pathogen AMR Data that contains the antimicrobial resistance data in bacteria isolated from dogs.	
Resistome Tracker	Resistome Tracker is a tool to explore resistance and other microbial features present in the genomes of different bacteria submitted to the NCBI. The genomes are from isolates collected around the world for various reasons and therefore include pathogens outside of NARMS. Resistome Tracker includes notifications for novel resistance genes.	

Antimicrobial Drug Use Data Monitoring

Why collect data on use?

- Monitor trends
- Inform national, regional, or local policies and interventions
- Evaluate effectiveness of policy changes or stewardship efforts
- Understand drivers of resistance in veterinary and agricultural settings

Example challenges

- Diversity of animal health record sources
- Lack of coordinated infrastructure or database repository
- Lack of standardized metrics, numerators and denominators
- Data confidentiality concerns
- Data access issues and fees

courtesy of
Dr. Katherine Huebner

FDA Efforts to Support AMU Data Collection

2015

Joint FDA/USDA/CDC public meeting to **discuss AMU metrics**

2016

Funded 2 cooperative agreements to pilot data collection methodologies in **food animals**

2020

Funded 2 cooperative agreements to pilot AMU data collection methodologies in **companion animals**

2022

Reagan Udall Foundation/FDA Collaboration – Report and public meeting on **feasibility of public private partnership** for collecting AMU data

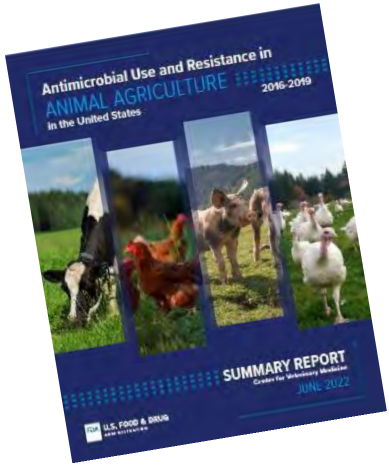
FDA publishes summary report entitled *"AMU and AMR in Animal Agriculture in the US"*

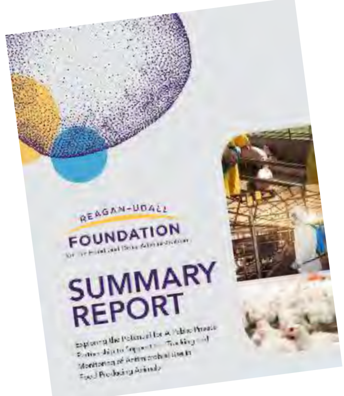
2023

Reagan Udall Foundation/FDA Collaboration – Second report published on **potential data collection framework**

2024

Announced **new AMU data collection funding opportunity** awarded **3 new** Cooperative agreements.


Antimicrobial Use and Resistance in
ANIMAL AGRICULTURE
in the United States
2016-2019
SUMMARY REPORT
Center for Veterinary Medicine
JUNE 2022
U.S. FOOD & DRUG


REAGAN-UDALL
FOUNDATION
SUMMARY
REPORT


REAGAN-UDALL
FOUNDATION
SUMMARY
REPORT
AUGUST 2023

courtesy of
Dr. Katherine Huebner

Timeline of FDA Judicious Use Policies and Guidance for Industry

1997

ELU-prohibition on the use of glycopeptides and fluoroquinolones in food animals

2005*

Withdrawal of the approval of fluoroquinolones for use in poultry

2016*

ELU-restrictions on third-generation cephalosporins

2017

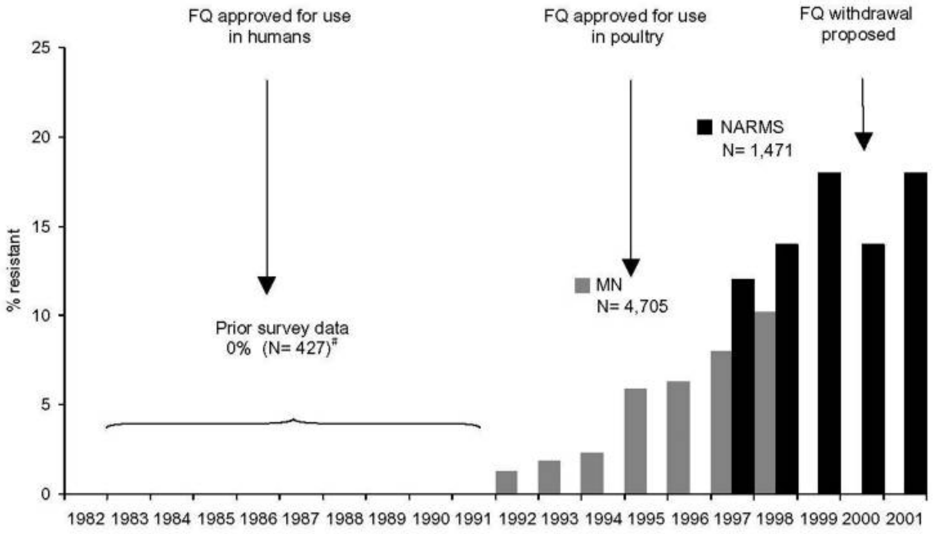
GFI #213 eliminates production uses of medically important antibiotics used in feed/water of food-producing animals and brings their use under veterinary oversight

2026

GFI #273 provides recommendation for drug sponsors to establish durations of use for medically important antimicrobials given in or on the feed of food producing animals

Approval of Fluoroquinolones for Poultry Withdrawn in 2005

Fluoroquinolones (FQ) had been available in human medicine since 1986. In 1995 and 1996, CVM approved the use of the fluoroquinolones, sarafloxacin and enrofloxacin in poultry.

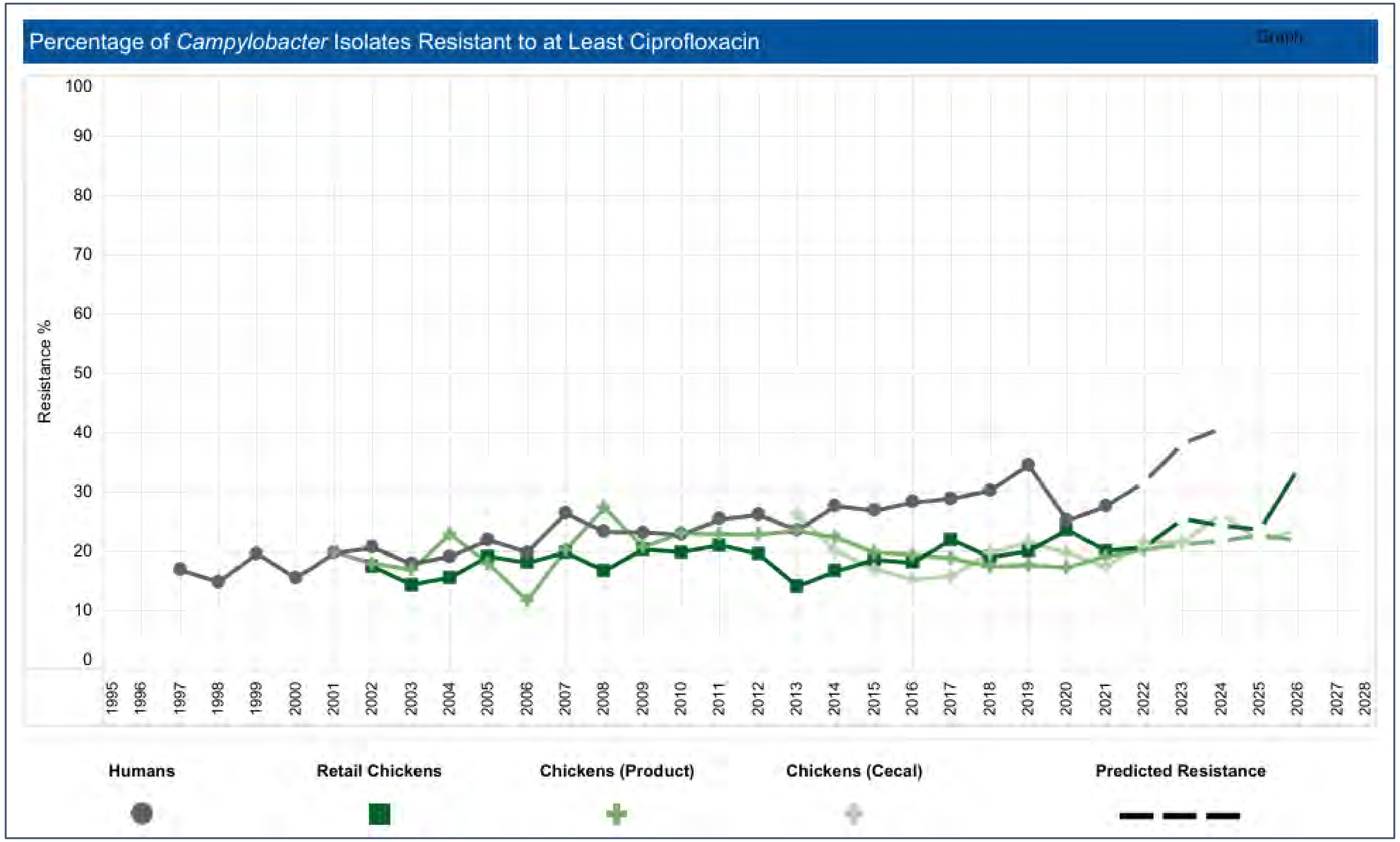


Prior to 1990, various county surveys showed no FQ^r *Campylobacter* in humans, however, by 1999, NARMS found that 18% of *Campylobacter* were FQ^r.

Gupta A., et al. Antimicrobial Resistance among *Campylobacter* Strains, United States, 1997-2001, Emerg Infect Dis. 2004 Jun; 10(6):1102-1109

FDA used human and animal data from NARMS to develop a quantitative risk assessment model that said 153,580 person were infected with FQ^r *Campylobacter* in 1999 as a result of chicken consumption

Fluoroquinolone-resistant *C. jejuni* continues to increase in humans but has not increased in chickens



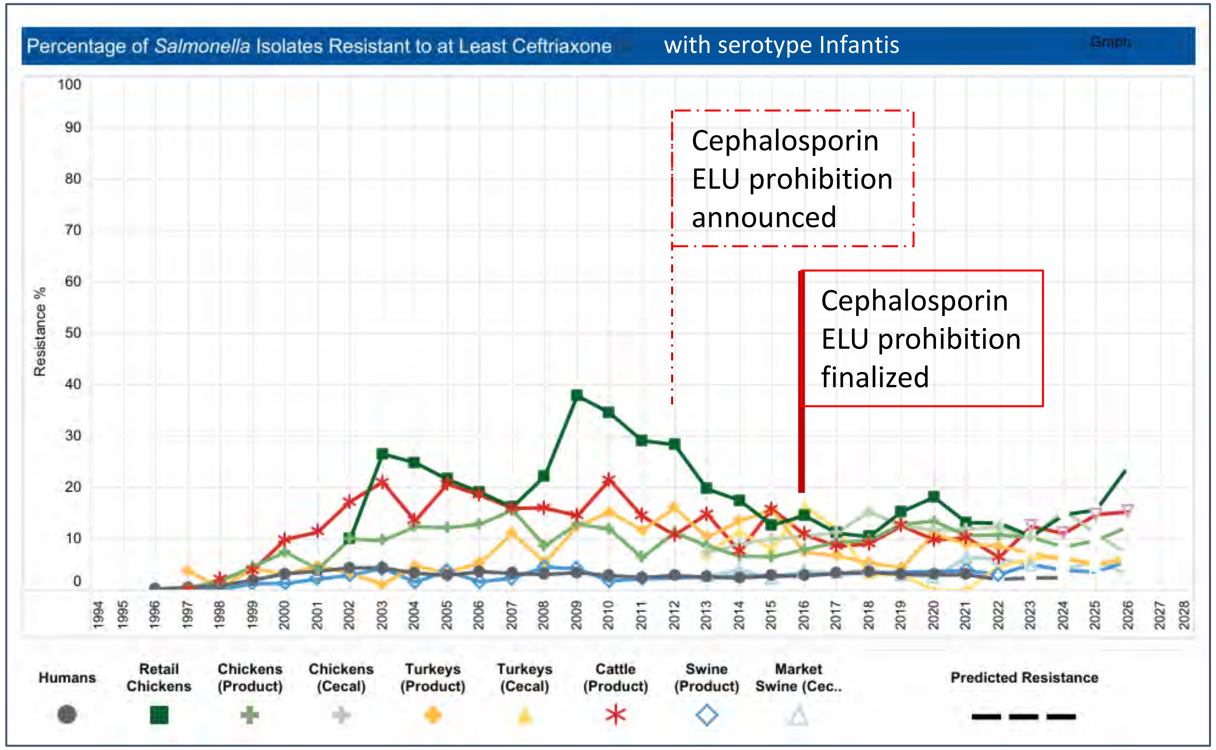
Percentage of *Campylobacter* Isolates Resistant to at Least Ciprofloxacin

Cephalosporin extra label use prohibition (ELU) effective April 5, 2012

FDA prohibits unapproved uses of 3rd gen. cephalosporins in cattle, swine, chickens and turkeys. Specifically, the prohibited uses include:

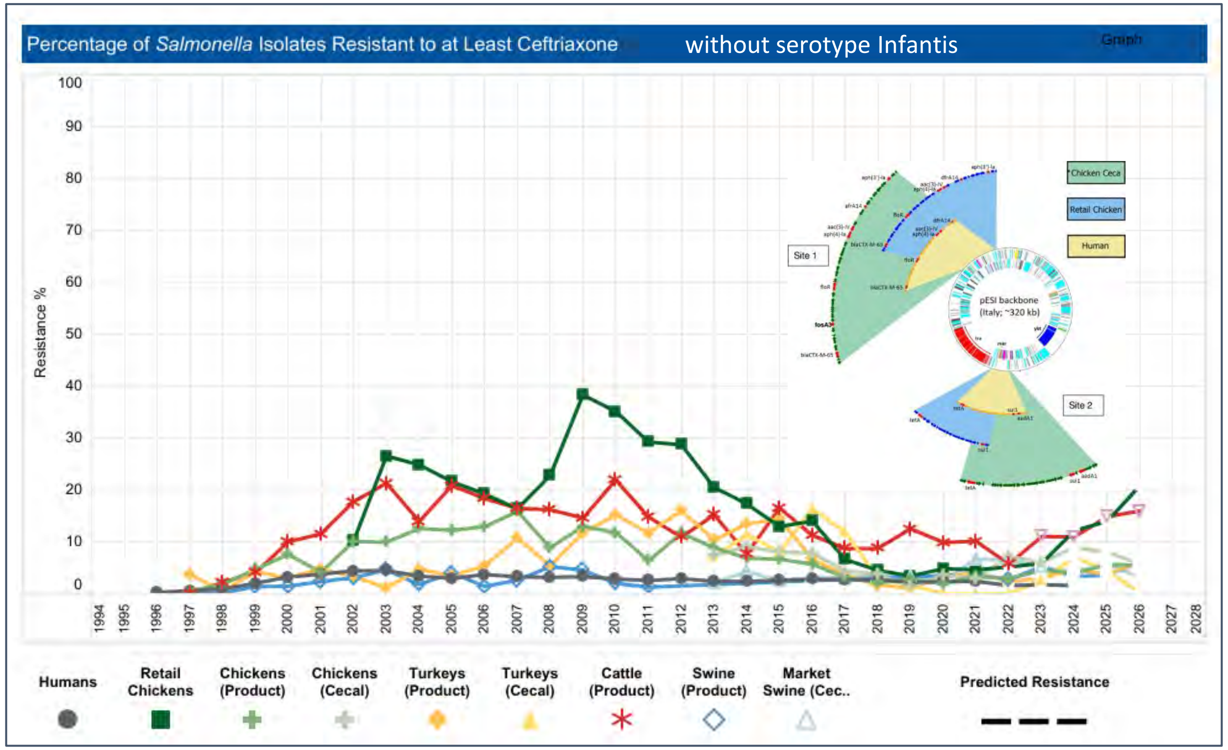
- using cephalosporin drugs at unapproved dose levels, frequencies, durations, or routes of administration;
- using cephalosporin drugs in cattle, swine, chickens or turkeys that are not approved for use in that species (e.g., cephalosporin drugs intended for humans or companion animals);
- using cephalosporin drugs for disease prevention.

NARMS data showed increasing cephalosporin-resistance early on. Prior ELU hatchery studies showed the poultry industry was injecting ceftiofur *in ovo*. Resistance has since declined but is also influenced by circulating strains.


Percentage of *Salmonella* Isolates Resistant to at Least Ceftriaxone with serotype Infantis

Cephalosporin ELU prohibition announced

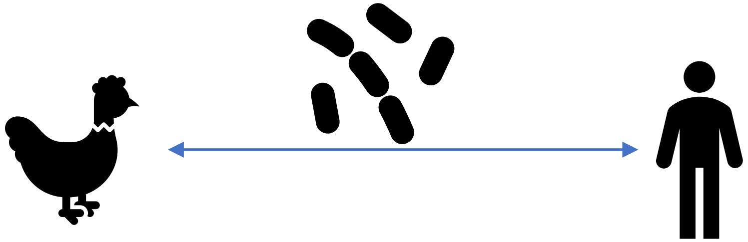
Cephalosporin ELU prohibition finalized


Percentage of *Salmonella* Isolates Resistant to at Least Ceftriaxone without serotype Infantis

Other Priority Trend Signals NARMS Tracks

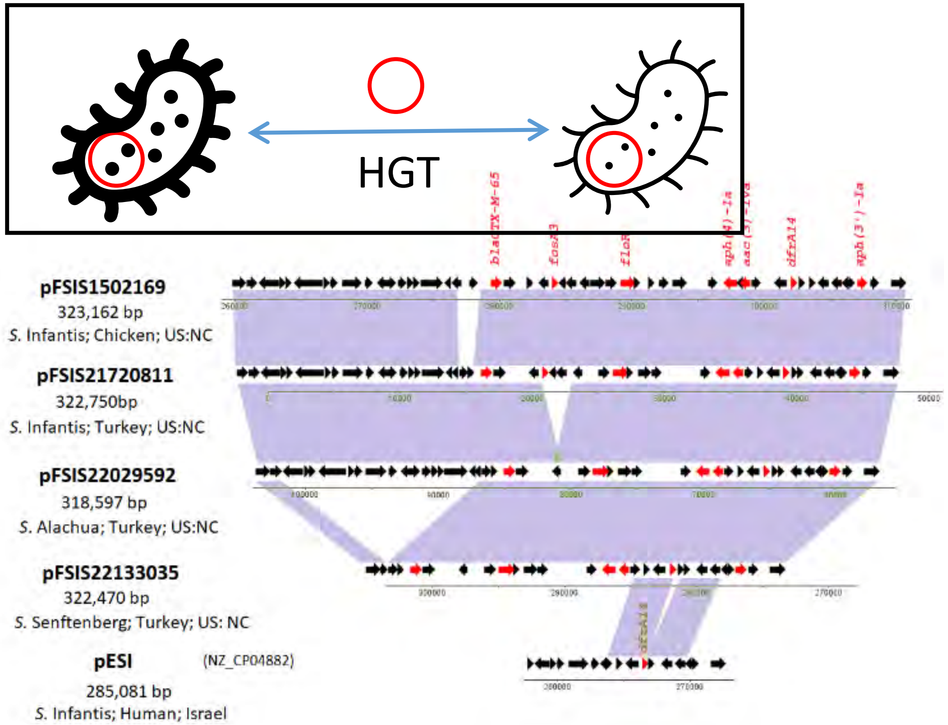
- *Campylobacter*: macrolide and carbapenem resistance
- *Salmonella*: macrolide, carbapenem, colistin resistance and emerging mechanisms
- Commensal/indicator organisms: early warning for resistance gene spread
- Genomic clustering helps identify emerging clones and routes of dissemination

Plasmid and Mobile Genetic Element Tracking



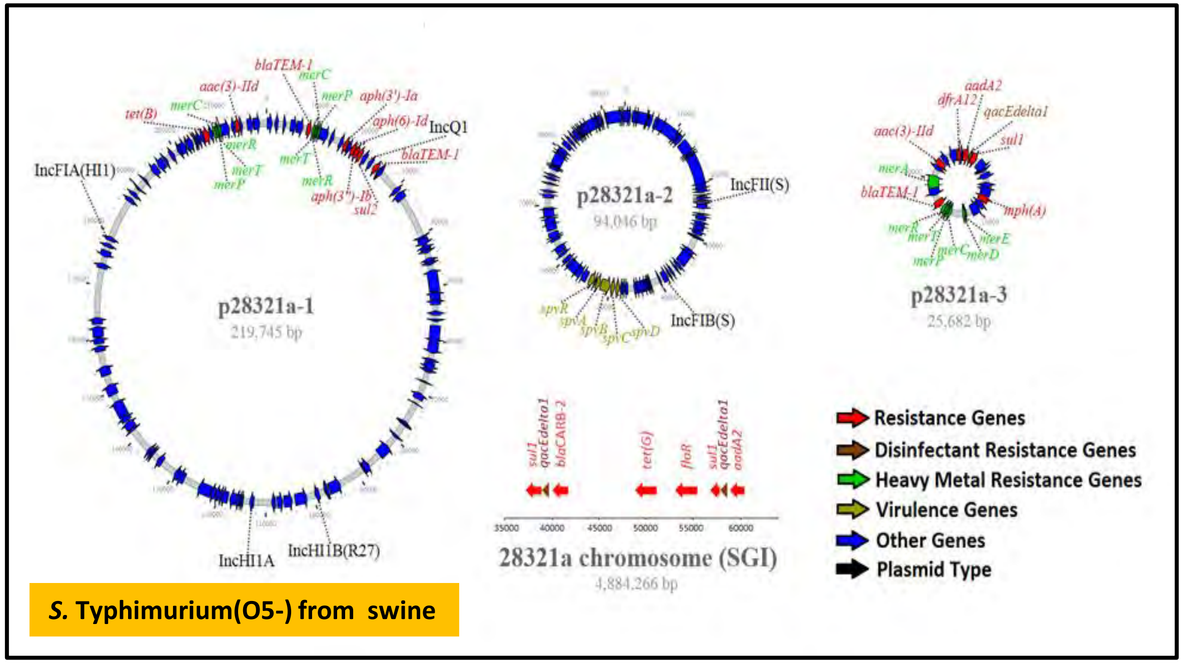
Before: Tracking spread of AMR bacteria between sources

After: Tracking spread of AMR determinants between bacteria



The spread of pESI-mediated extended-spectrum cephalosporin resistance in Salmonella serovars-Infantis, Senftenberg, and Alachua isolated from food animal sources in the United States. Li C et al. 2024.

After: Characterizing resistance plasmids and co-selection factors



Zhao, S., et al. Comparative Genomic Analysis of Four Hundred Fifty Salmonella Strains Isolated from Diseased Animals. Genes 2020, 11(9), 1025. http://dx.doi.org/10.3390/genes11091025

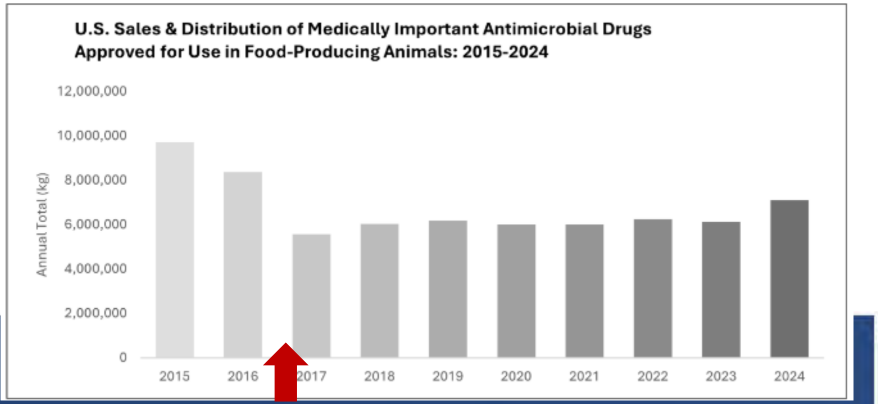
With Greater Genetic Resolution Comes

Better understanding of indirect drivers of AMR (e.g., heavy metals, biocides, etc.)

Information on broader stewardship strategies beyond antimicrobial policies

Insights into risk-stratified AMR surveillance based on other bacterial factors (e.g., virulence)

Investigate AMR After GFI #213 Implemented


U.S. Sales & Distribution of Medically Important Antimicrobial Drugs Approved for Use in Food-Producing Animals: 2015-2024

Antimicrobial Resistance Trends Dashboard

Observed mean Log_2MIC with segmented regression lines and confidence bands — by animal source and lag period


Antimicrobial: GEN

Organism: Escherichia coli

AMU/AMR Monitoring: Supporting Antimicrobial Stewardship

Help to preserve efficacy of medically important antimicrobials

Informs risk assessments for antimicrobial drug approvals and post-approval monitoring

Supports evidence-based decision-making for veterinarians and animal health stakeholders

Enables evaluation of stewardship interventions over time

Thank You

Heather.Tate@fda.hhs.gov

Acknowledgments:

Beilei.Ge@fda.hhs.gov
Olgica.Ceric@fda.hhs.gov - VetLIRN
Katherine.Huebner@fda.hhs.gov - AMU

Pilot AMU Cooperative Agreements (Completed)

Swine and Poultry

- **Mindwalk Consulting Group (Grant number 5U01FD005878)**
- 2016 – 2023
- Project Title: Antibiotic Use Data Collection in U.S. Poultry and Swine
- COMPLETED 2023

Cattle

- **Kansas State University (Grant number 5U01FD005868)**
- 2016 – 2022
- Project Title: Characterization of Antimicrobial Use in Beef Feedlots and Dairies
- COMPLETED 2022

Companion Animals

- **University of Minnesota (Grant number 5U01FD007061)**
- 2020- 2025
- Project Title: Representative, scalable, and sustainable surveillance methodologies to track companion animal antimicrobial use
- COMPLETED 2025

Companion Animals

- **North Carolina State University (Raleigh) (Grant number 5U01FD007057)**
  - 2020-2025
  - Project Title: Automated Data Collection on Antimicrobial Use in Dogs and Cats in a Tertiary Hospital and Private Practices
  - COMPLETED 2025

Program Objectives for RFA-FD-24-031

Cooperative Agreement for Long Term Data Collection on Antimicrobial Use in Animals

Building upon prior antimicrobial use data collection efforts, including exploration of a potential framework for establishing public-private partnership to collect and analyze antimicrobial use data, the purpose of the funded studies is to:

1. Gather, summarize, and report information about antimicrobial use in domestic animals from diverse veterinary or animal production sectors; and
2. Contribute to and support long-term data collection efforts that are under development within the United States, including potential public-private partnership frameworks and national data repositories or dashboards intended to securely store, analyze, and report antimicrobial use data.

FY2024 Cooperative Agreements (2024-2029)

Poultry

- **Mindwalk Consulting Group (Grant number 1U01FD008419)**
- Project Title: Antimicrobial Use Data Collection in the U.S. Poultry Production System

Dairy Cattle

- **Cornell University (Grant number 1U01FD008421)**
- Project Title: A System Approach to Animal-Level Antimicrobial Use Monitoring in Dairy Cattle

Livestock, Poultry, Minor Species

- **Kansas State University (1U01FD008416)**
- Project Title: Bridging Critical Data Gaps in Veterinary Medicine Via Artificial Intelligence and Advanced Large Language Models to Procure Real-Time Antibiotic Use Data in Livestock, Poultry and Companion Animals

FY25 Cooperative Agreements (2025-2030)

University of Minnesota (Grant number 1U01FD008646-01)

- Project Title: Advancing Antimicrobial Use Measurement in U.S. Companion Animal Practice
- Proposes to advance AMU measurement in U.S. companion animal practice through the Companion Animal Veterinary Surveillance Network (CAVSNET), a public-private partnership that compiles veterinary data from 1300 US clinics and 55 million animals into a standardized common data model. This project extends a previous grant to create a 10-year initiative that will provide yearly national estimates of AMU prevalence, generate condition-specific use data, and address measurement gaps through NLP and point-prevalence surveys for dogs, cats, and horses.

Cornell University (Grant number 1U01FD008648-01)

- Project Title: Artificial Intelligence and Dashboard Tools to Collect, Anonymize, and Summarize Companion Animal Antimicrobial Use Data
- Proposes to develop an artificial intelligence-powered data extraction and analysis pipeline for sustainable companion animal antimicrobial use (AMU) surveillance. This work would create a large language model to extract AMU data from veterinary electronic health records across multiple systems, paired with an interactive dashboard to streamline analysis and generate standardized reports, ultimately enabling national trend identification while maintaining data privacy and security.

Biomass Dashboard

Measurement of antimicrobial sales adjusted by animal weight and population

FDA (2024) Biomass-Adjusted Antimicrobial Sales and Distribution Data in Food Producing Animals: Interactive Summary

Biosecurity Practices and Their Impact on Pathogen Persistence in Animal Production Systems

VALENTINA TRINETTA – *KANSAS STATE UNIVERSITY*

FABIO SOSSAI POSSEBON – *UNESP – BOTUCATU, BRAZIL*

Why This Matters

Foodborne illness and recalls continue to impact public health and industry

Many recurring events are driven by persistent environmental contamination

Standard sanitation alone is often insufficient to eliminate established populations

Persistence turns sporadic contamination into ongoing risk

What are Biosecurity Practices?

- Prevents pathogen introduction, amplification, and spread
- Applied across all stages of animal production systems
- Integrates:
  - Hygiene and sanitation
  - Movement and access control
  - Environmental and facility management
- Critical to limiting pathogen persistence

Pathogen Persistence in Animal Production Systems

- Pathogens can persist for extended periods in production environments

- Persistence is driven by the formation of environmental reservoirs (niches)

- Influenced by:
  - Environmental conditions
  - Effectiveness of biosecurity practices

- Represents a continuous risk of contamination and transmission

Bacterial Persistence Across Animal Production Systems

ELSEVIER

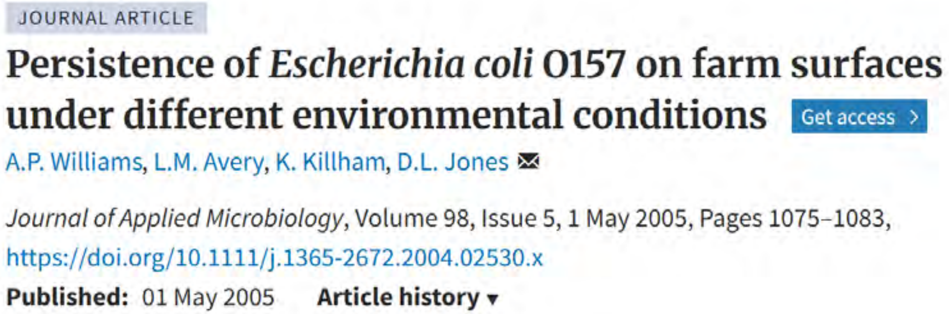
Poultry Science

Volume 102, Issue 12, December 2023, 103086

Symposium Articles

Controlling *Salmonella*: strategies for feed, the farm, and the processing plant

Tomi Obe * ✉, Timothy Boltz †, Mike Kogut ‡, Steven C. Ricke §, Lasheda A. Brooks #, Ken Macklin †, Ashley Peterson ‖



JOURNAL ARTICLE

Persistence of *Escherichia coli* O157 on farm surfaces under different environmental conditions

Get access ›

A.P. Williams, L.M. Avery, K. Killham, D.L. Jones ✉

Journal of Applied Microbiology, Volume 98, Issue 5, 1 May 2005, Pages 1075–1083, https://doi.org/10.1111/j.1365-2672.2004.02530.x

Published: 01 May 2005 **Article history** ▾

Feed and Transport as Pathways for Viral Persistence

Infectious Dose of African Swine Fever Virus When Consumed Naturally in Liquid or Feed

Megan C. Niederwerder, Ana M.M. Stoian, Raymond R.R. Rowland, Steve S. Dritz,
Vlad Petrovan, Laura A. Constance, Jordan T. Gebhardt, Matthew Olcha,
Cassandra K. Jones, Jason C. Woodworth, Ying Fang, Jia Liang, Trevor J. Hefley

Received: 6 May 2021 | Revised: 11 October 2021 | Accepted: 11 October 2021
DOI: 10.1111/tbed.14354

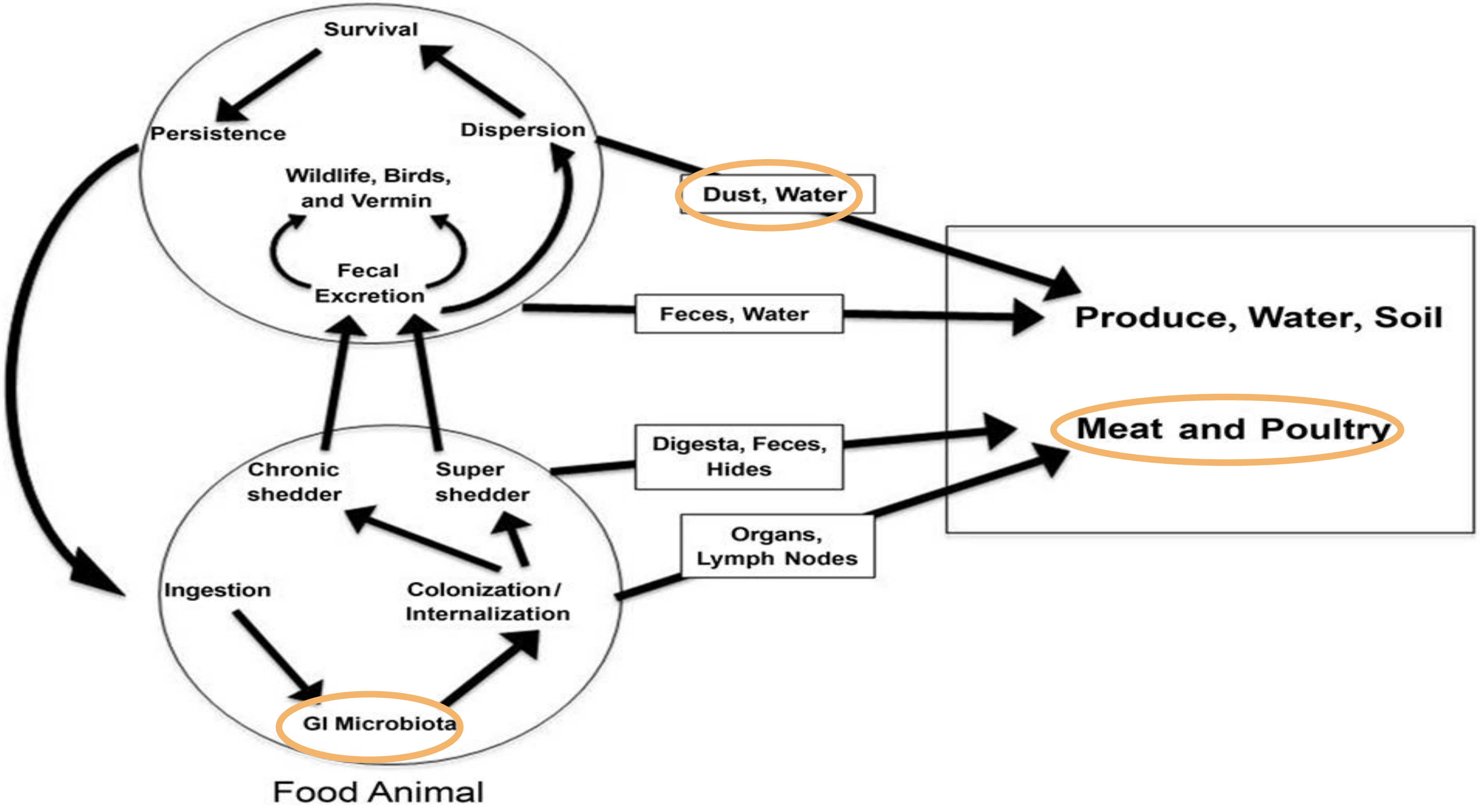
Transboundary and Emerging Diseases WILEY

SPECIAL ISSUE ARTICLE

Feed or feed transport as a potential route for a porcine epidemic diarrhoea outbreak in a 10,000-sow breeding herd in Mexico

Jorge Garrido-Mantilla[1] | Alicia Lara[2] | Ezequiel Guardado[1] | Jose Lopez[2] |
Joel Nerem[1] | Gustavo Pizarro[1] | Jean Paul Cano[1]

Persistence and transmission pathways in animal production systems



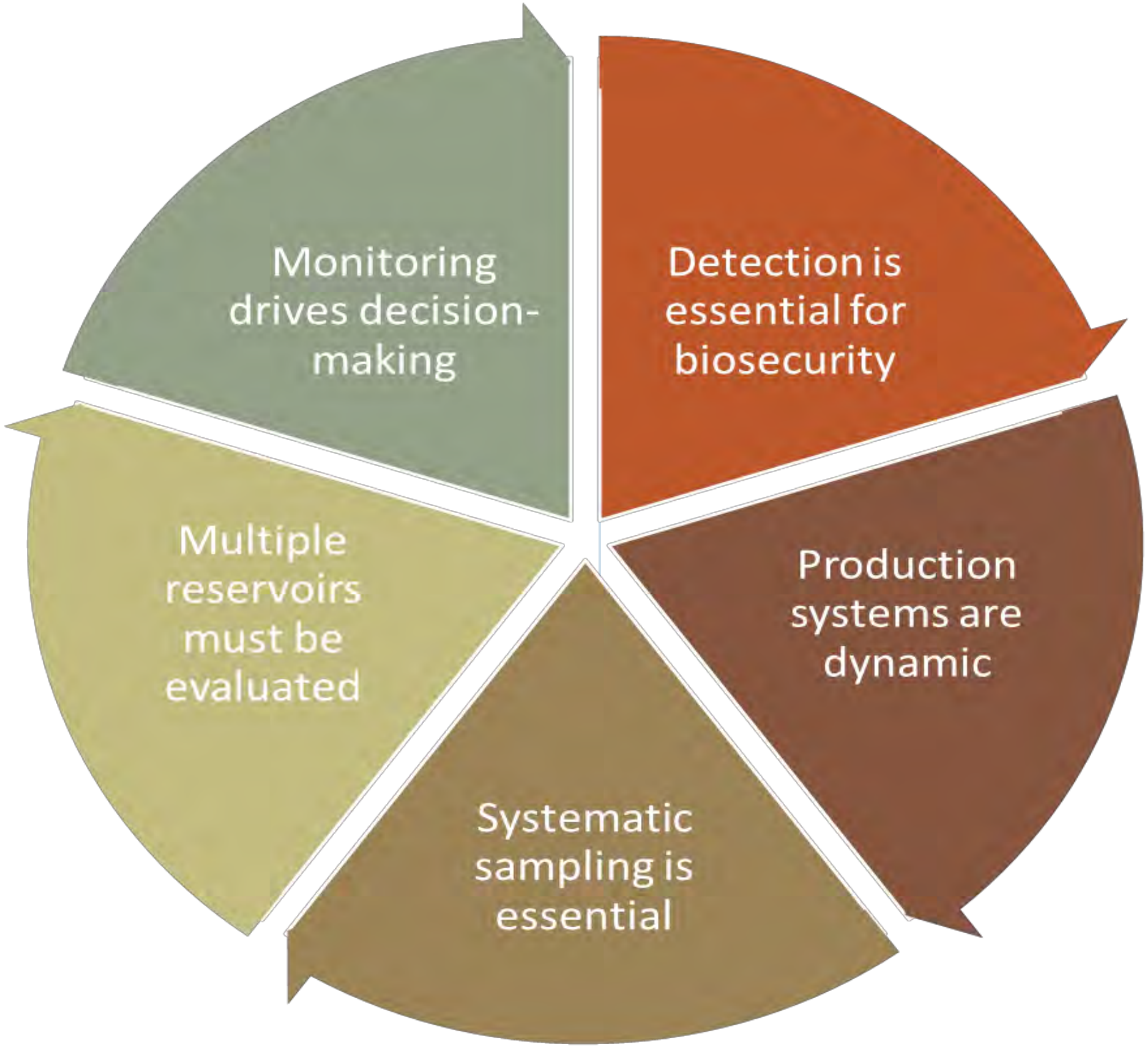
Picture adapted from Berry ED, Wells JE. 2016. Reducing foodborne pathogen persistence and transmission in animal production environments: challenges and opportunities. Microbiol Spectrum 4(4):PFS-00062014. doi:10.1128/microbiolspec.PFS-0006-2014.

Mechanisms Driving Pathogen Persistence

- Environmental niches – hard to clean areas
- Organic Matter Protection – reduce cleaning and sanitation efficacy
- Biofilm formation – physical protection
- Stress adaptation – increased survival

Niu, H., Gu, J. & Zhang, Y. Bacterial persisters: molecular mechanisms and therapeutic development. *Sig Transduct Target Ther* **9**, 174 (2024). https://doi.org/10.1038/s41392-024-01866-5

Why is monitoring essential?



Detection is essential for biosecurity

Production systems are dynamic

Systematic sampling is essential

Multiple reservoirs must be evaluated

Monitoring drives decision-making

Sampling Strategy in Production Systems

Sampling across high-risk point in the production system

Sample types include:

- Environmental samples
- Feed samples
- Animal-associated samples

A comprehensive approach to understand contamination patterns

Case study: understanding *Salmonella* risk in swine production systems

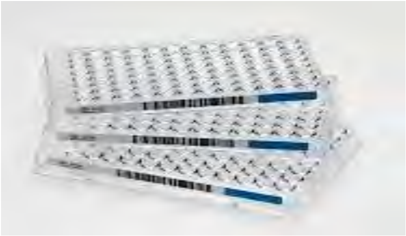
Pork Check Off

Sampling Design & Methods

Selection of 10 major swine production areas across the United States

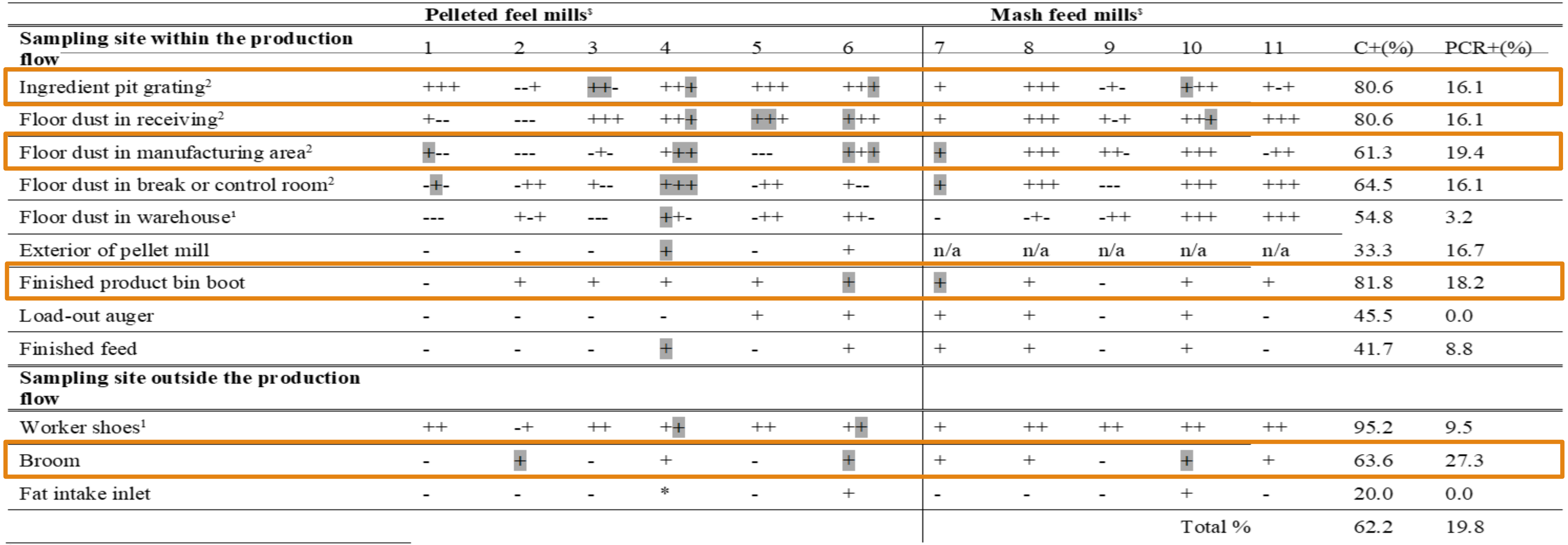
Identification of 12 sampling sites

Isolation and identification of *Salmonella* and characterization isolates



A total of 383 environmental and feed samples were collected: 65 (17%) were *Salmonella* PCR+

Salmonella culture positive (C+) and PCR positive (PCR+) samples in feed mill facilities selected in this study.



	Pelleted feel mills$						Mash feed mills$						
Sampling site within the production flow	1	2	3	4	5	6	7	8	9	10	11	C+(%)	PCR+(%)
Ingredient pit grating[2]	+++	--+	++-	+++	+++	+++	+	+++	-+-	+++	+-+	80.6	16.1
Floor dust in receiving[2]	+--	---	+++	+++	+++	+++	+	+++	+-+	+++	+++	80.6	16.1
Floor dust in manufacturing area[2]	+--	---	-+-	+++	---	+++	+	+++	++-	+++	-++	61.3	19.4
Floor dust in break or control room[2]	-+-	-++	+--	+++	-++	+--	+	+++	---	+++	+++	64.5	16.1
Floor dust in warehouse[1]	---	+-+	---	++-	-++	++-	-	-+-	-++	+++	+++	54.8	3.2
Exterior of pellet mill	-	-	-	+	-	+	n/a	n/a	n/a	n/a	n/a	33.3	16.7
Finished product bin boot	-	+	+	+	+	+	+	+	-	+	+	81.8	18.2
Load-out auger	-	-	-	-	+	+	+	+	-	+	-	45.5	0.0
Finished feed	-	-	-	+	-	+	+	+	-	+	-	41.7	8.8
Sampling site outside the production flow													
Worker shoes[1]	++	-+	++	++	++	++	+	++	++	++	++	95.2	9.5
Broom	-	+	-	+	-	+	+	+	-	+	+	63.6	27.3
Fat intake inlet	-	-	-	*	-	+	-	-	-	+	-	20.0	0.0
										Total %		62.2	19.8

$ mills name and location were substituted by number to protect collaborators privacy

[1] Left and right shoes swabbed

[2] Sites swabbed in three different location using a 10 cm x 10 cm template

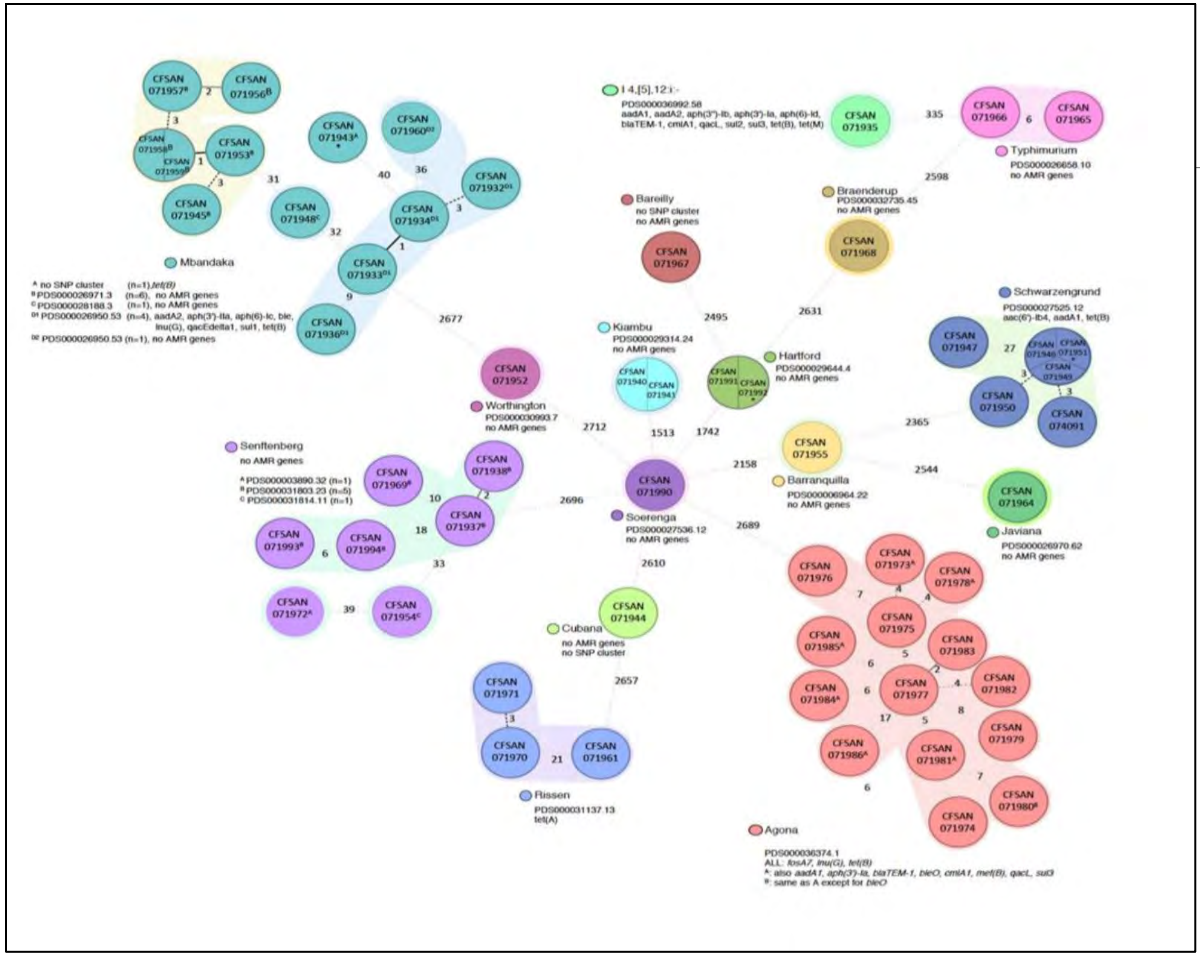
*Site could not be sampled

n/a: Site not present in mash facilities

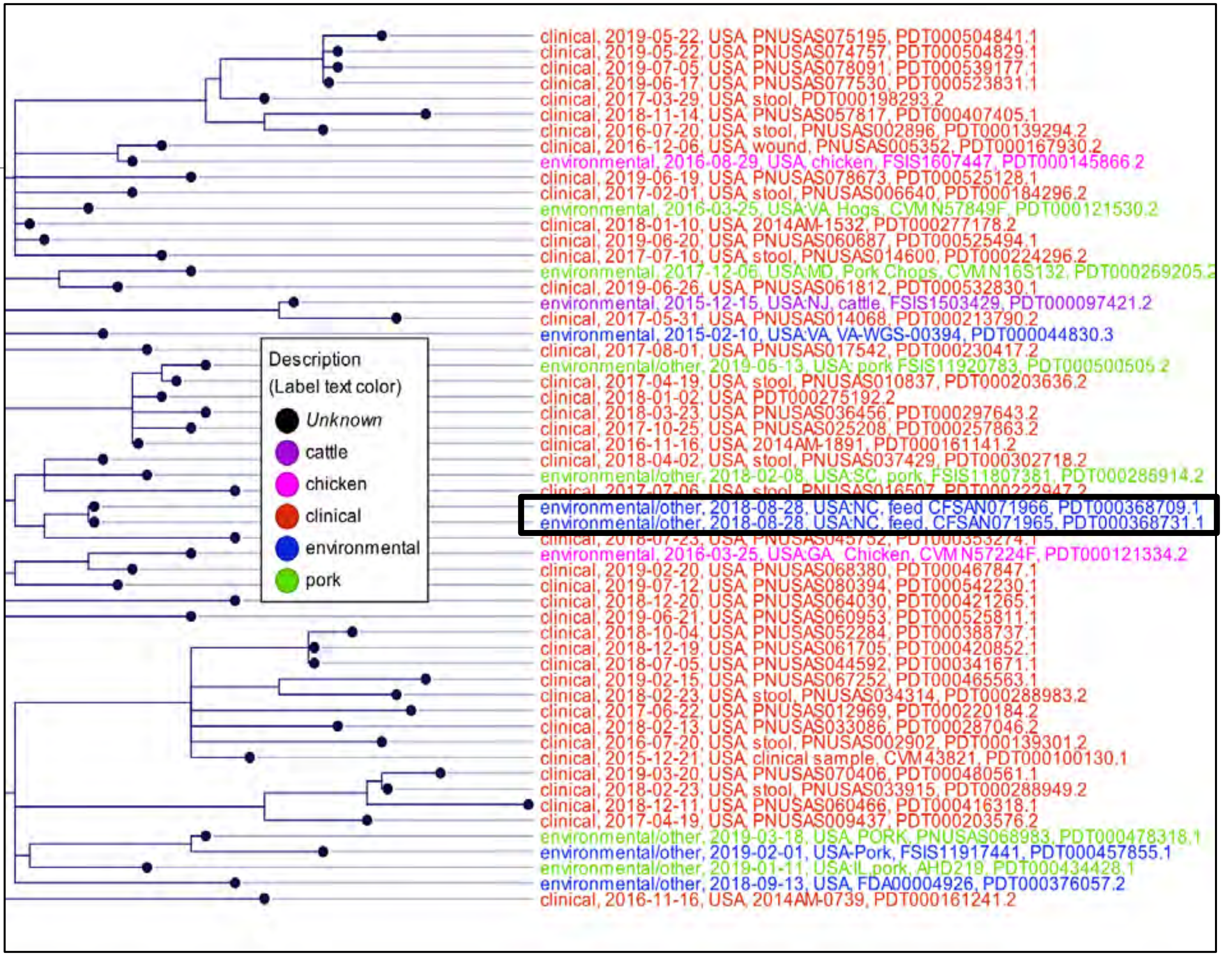
The % of PP and CP at the end of each row were calucalted for sample sites

Magossi G., Lambertini E., Noll L., Bai J., Jones C., Nagaraja T., Phebus R., Woodworth J., Trinetta V. (2020). Potential risk factors affecting *Salmonella* spp. and *E. coli* occurrence in Midwestern U.S. swine feed mills. *Journal of Applied Microbiology.*

Feed mill *Salmonella* isolates cluster with human clinical cases



Minimum spanning tree (MST) for *Salmonella enterica* isolates from US feed mills



Example of phylogenetic tree for SNP cluster PDS000027525.16

Trinetta, V., Magossi, G., Allard, M. W., Tallent, S. M., Brown, E. W., & Lomonaco, S. (2020). Characterization of *Salmonella enterica* isolates from selected U.S. swine feed mills by whole-genome sequencing. *Foodborne Pathogens and Disease, 17*(2), 126–136.

Antibiotic and metal resistance in *Salmonella* isolates from swine feed mills

AMR prevalence

51% carried antimicrobial resistance genes

58% resistant to ≥1 antibiotic

Most frequent: tetracycline, sulfisoxazole, fosfomycin

Genotype–phenotype agreement

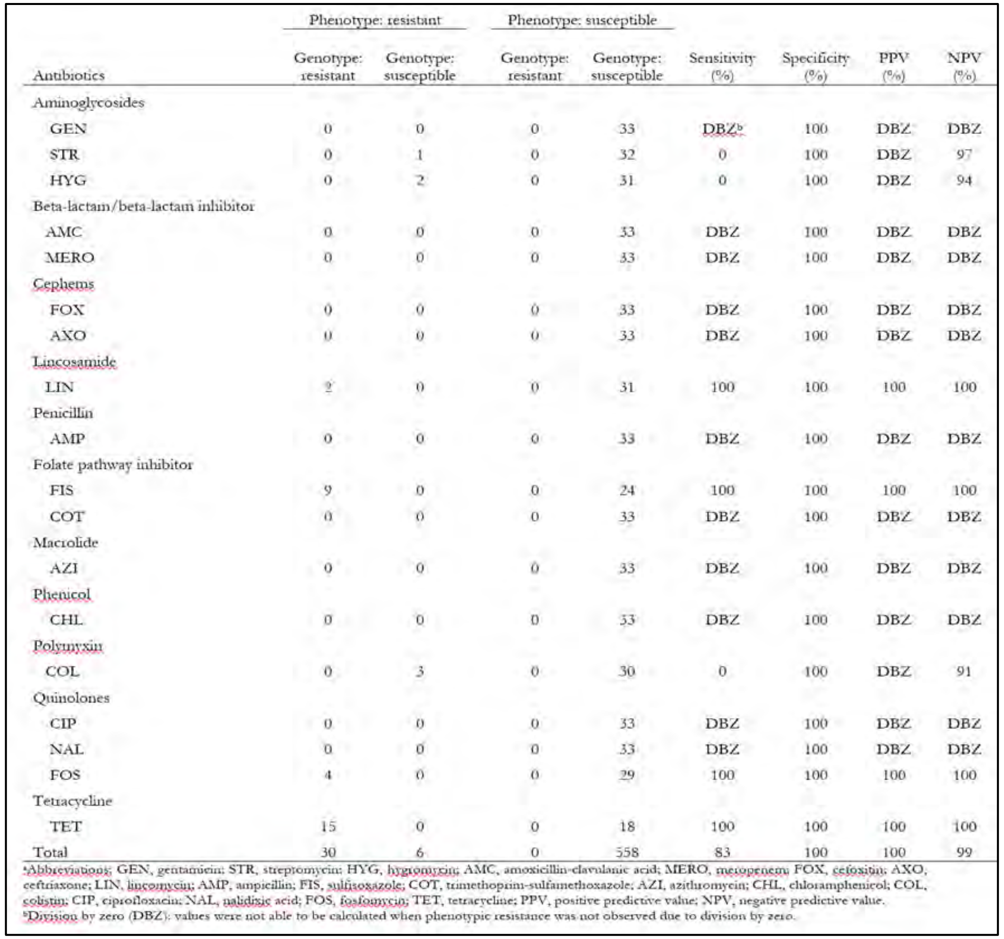
99% concordance between phenotypic resistance and AMR genes

Metal resistance & co-selection

Metal resistance genes (Cu, Hg, Ag) detected in all isolates

52% carried both metal and antibiotic resistance genes

Metal exposure may contribute to co-selection of antimicrobial resistance in feed mill environments



	Phenotype: resistant		Phenotype: susceptible					
Antibiotics	Genotype: resistant	Genotype: susceptible	Genotype: resistant	Genotype: susceptible	Sensitivity (%)	Specificity (%)	PPV (%)	NPV (%)
Aminoglycosides								
GEN	0	0	0	33	DBZ[b]	100	DBZ	DBZ
STR	0	1	0	32	0	100	DBZ	97
HYG	0	2	0	31	0	100	DBZ	94
Beta-lactam/beta-lactam inhibitor								
AMC	0	0	0	33	DBZ	100	DBZ	DBZ
MERO	0	0	0	33	DBZ	100	DBZ	DBZ
Cephems								
FOX	0	0	0	33	DBZ	100	DBZ	DBZ
AXO	0	0	0	33	DBZ	100	DBZ	DBZ
Lincosamide								
LIN	2	0	0	31	100	100	100	100
Penicillin								
AMP	0	0	0	33	DBZ	100	DBZ	DBZ
Folate pathway inhibitor								
FIS	9	0	0	24	100	100	100	100
COT	0	0	0	33	DBZ	100	DBZ	DBZ
Macrolide								
AZI	0	0	0	33	DBZ	100	DBZ	DBZ
Phenicol								
CHL	0	0	0	33	DBZ	100	DBZ	DBZ
Polymyxin								
COL	0	3	0	30	0	100	DBZ	91
Quinolones								
CIP	0	0	0	33	DBZ	100	DBZ	DBZ
NAL	0	0	0	33	DBZ	100	DBZ	DBZ
FOS	4	0	0	29	100	100	100	100
Tetracycline								
TET	15	0	0	18	100	100	100	100
Total	30	6	0	558	83	100	100	99

[a] Abbreviations: GEN, gentamicin; STR, streptomycin; HYG, hygromycin; AMC, amoxicillin-clavulanic acid; MERO, meropenem; FOX, cefoxitin; AXO, ceftriaxone; LIN, lincomycin; AMP, ampicillin; FIS, sulfisoxazole; COT, trimethoprim-sulfamethoxazole; AZI, azithromycin; CHL, chloramphenicol; COL, colistin; CIP, ciprofloxacin; NAL, nalidixic acid; FOS, fosfomycin; TET, tetracycline; PPV, positive predictive value; NPV, negative predictive value.

[b] Division by zero (DBZ): values were not able to be calculated when phenotypic resistance was not observed due to division by zero.

Schwan, C. L., Bastos, L. M., Young, S., Domesle, K., Ge, B., Hsu, C.-H., Li, C., Strain, E., Vipham, J., Jones, C., Amachawadi, R., Nagaraja, T. G., & Trinetta, V. (2023). Genotypic and phenotypic characterization of antimicrobial and heavy metal tolerance in *Salmonella enterica* and *Escherichia coli* isolates from swine feed mills. *Journal of Food Protection, 86*(8), 100113.

Conclusions

- *Salmonella* isolates from feed mills clustered with strains from feed ingredients, pork products, pet food, and human clinical samples.
- The serotypes detected have pathogenic potential for both animals and humans, indicating potential public health relevance.
- Genotypic and phenotypic AMR data showed strong agreement, and several isolates displayed multidrug resistance and heavy-metal co-resistance.

MAJOR OUTCOME: Feed mill environments may represent an under-estimated entry route for *Salmonella* into the animal production system and ultimately the human food chain.

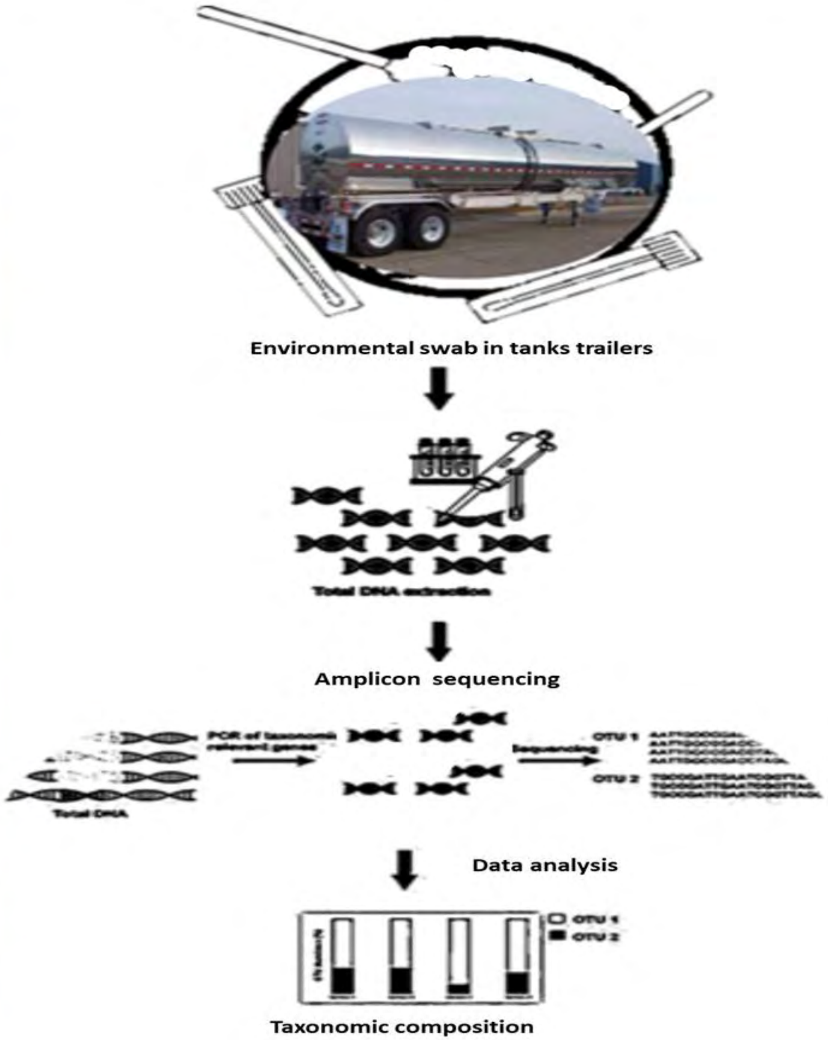
Understanding the full microbial ecology is essential to explain pathogen persistence and transmission

> Foodborne Pathog Dis. 2025 Nov 17. doi: 10.1177/15353141251393831. Online ahead of print.

Genomic Characterization of Resident Bacteria from Selected Swine Feed Mills in the Midwest Region of the United States

Savannah C Stewart [1], Beilei Ge [2], Shenia Young [2], Kelly Domesle [2], Chih-Hao Hsu [2], Cassandra Jones [3], Valentina Trinetta [1]

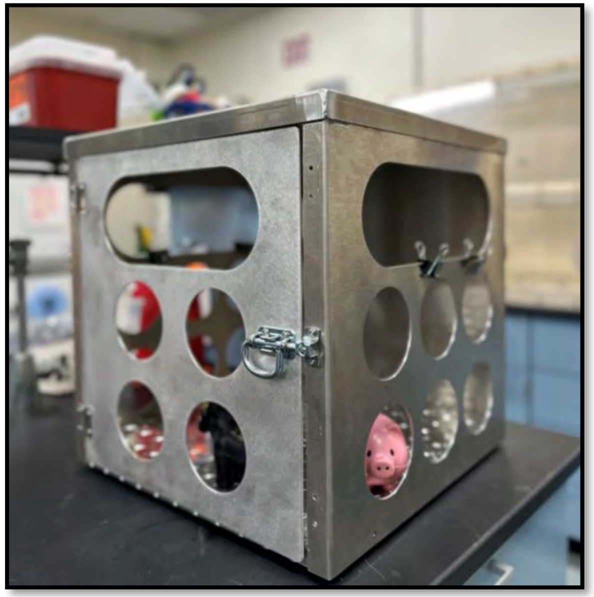
Impact of cleaning and sanitizing on microbial contamination in rendered fat tanker trucks



Ivers, C., Abou Elias, C. L., Yucel, U., Sayles, M., Jones, C., & Trinetta, V. (2025). The influence of cleaning and sanitizing on *Enterobacteriaceae*, coliforms, and *Escherichia coli* presence in rendered fat transportation tankers used for the pet food industry. *Food Protection Trends, 45*(6), 423–430

Modeling the impact of weather on disinfection strategies in swine transportation trailers

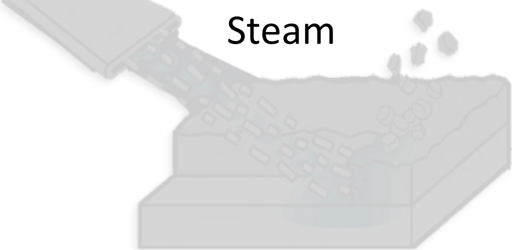
Experimental model



Strategies evaluated

Cleaning methods
Scraping
Compressed air
Vacuum

Disinfection strategies
Hydrogen peroxide
Sodium hypochlorite
Quaternary ammonia
Chlorine dioxide
Dry CO_2
Steam



Validation in swine transportation trailers

fmvz - unesp
Faculdade de Medicina Veterinária e Zootecnia
Campus de Botucatu

SOAP
INSPEÇÃO DE ALIMENTOS

IBTEC
Instituto de Biotecnologia - UNESP

FAPESP

CAPES
PrInt

Epidemiological characterization of the conventional and antibiotic-free poultry production in antibiotic resistance perspective using a One Health approach

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Biotechnology Institute - IBTEC and
Department of Animal Production and Preventive Veterinary Medicine – School of Veterinary Medicine and Animal Science
São Paulo State University (UNESP) - Botucatu/SP
Brazil

Objective

Compare Conventional and Antibiotic Free systems

- Microbiome
- Resistome
- “Conventional Microbiology” and Metagenomic approach

Methodology

Selection of farms

- Two companies – Conventional (150k birds/day) and Antibiotic Free production (20k birds/day)
- Summer and winter for two years

Sample Collection

- Sampling of poultry. poultry products. and production environments in both systems

Laboratory analyses

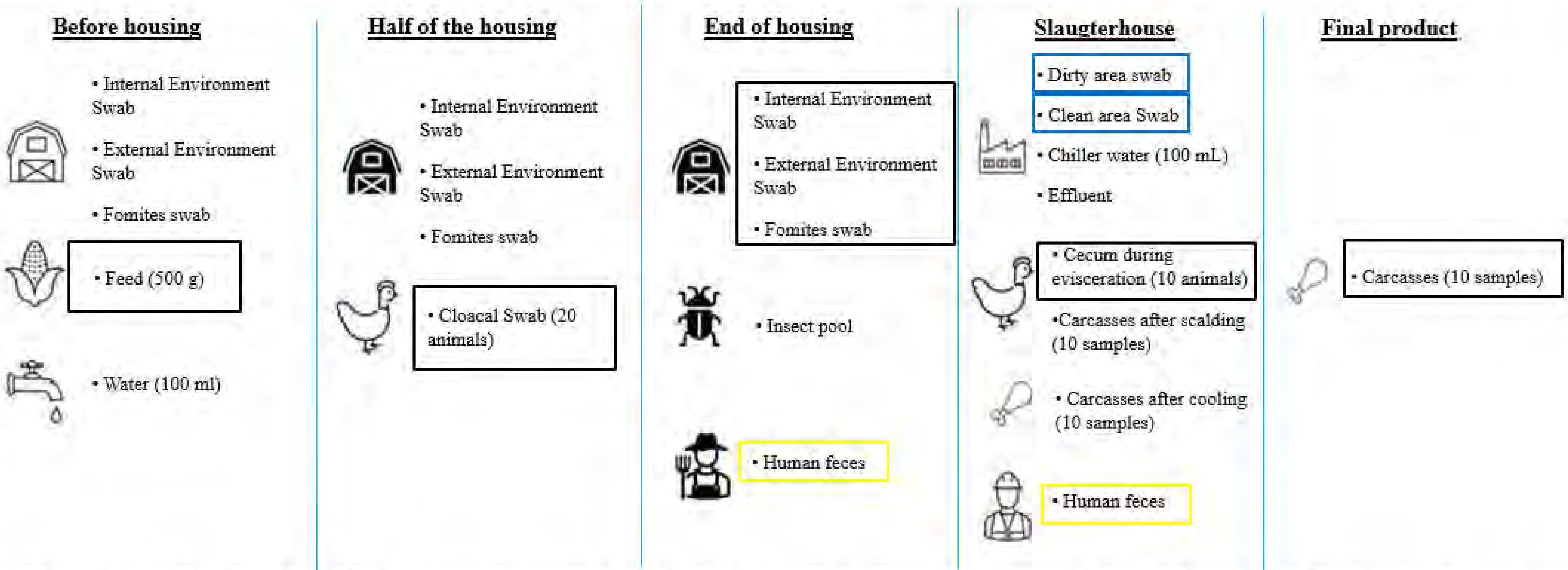
- Isolation and molecular confirmation of *Salmonella* spp.
- Isolation and molecular confirmation of *E. coli*;
- Isolation and molecular confirmation of *Enterococcus* spp.

Phenotypical resistance profile of isolates

DNA sequencing

- Shotgun (metagenomics) and isolates sequencing

Experimental Design – For each Batch:



Before housing

- Internal Environment Swab
- External Environment Swab
- Fomites swab
- Feed (500 g)
- Water (100 ml)

Half of the housing

- Internal Environment Swab
- External Environment Swab
- Fomites swab
- Cloacal Swab (20 animals)

End of housing

- Internal Environment Swab
- External Environment Swab
- Fomites swab
- Insect pool
- Human feces

Slaugterhouse

- Dirty area swab
- Clean area Swab
- Chiller water (100 mL)
- Effluent
- Cecum during evisceration (10 animals)
- Carcasses after scalding (10 samples)
- Carcasses after cooling (10 samples)
- Human feces

Final product

- Carcasses (10 samples)

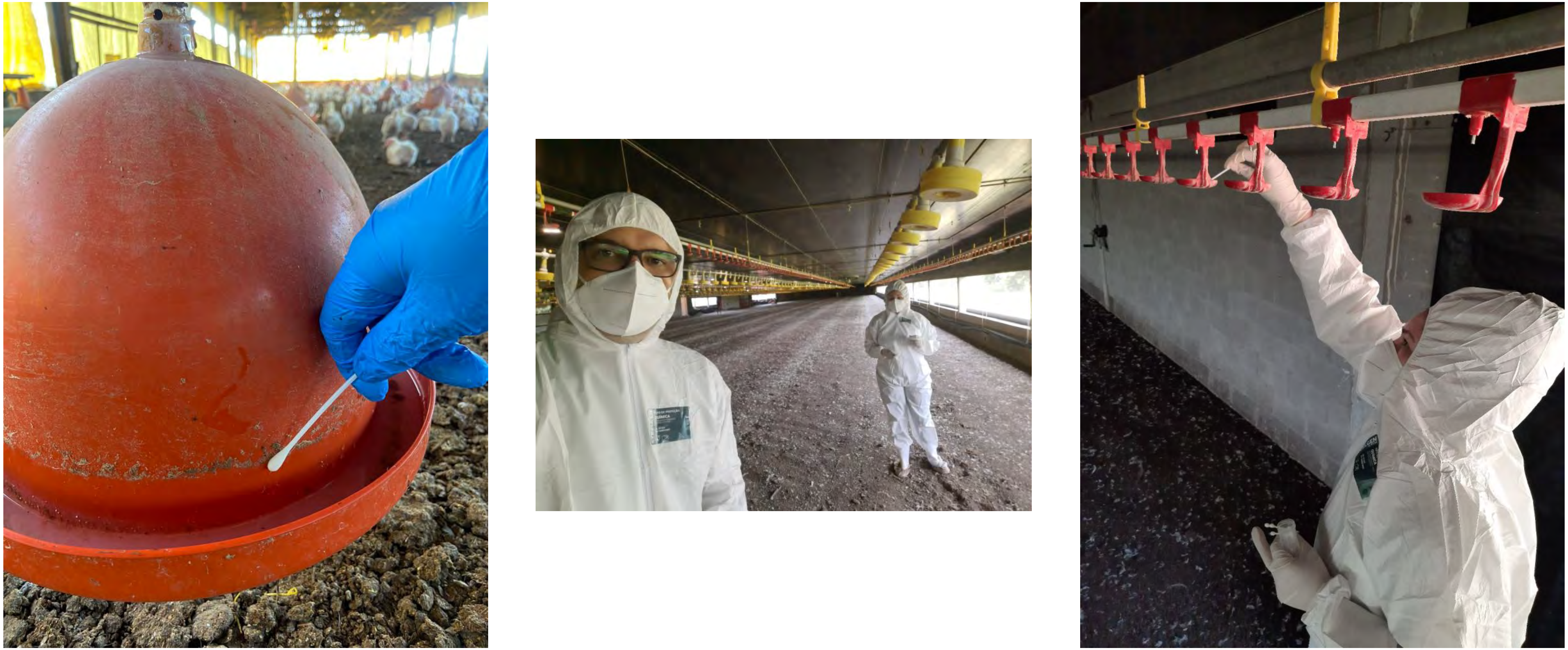
Each item indicates a sample to be collected for conventional microbiological analysis (except for human feces samples). Items indicated in the black rectangles will constitute a sample for shotgun sequencing with each batch. Items indicated in the blue rectangles will constitute a sample for shotgun sequencing evaluation collected twice a year (dry season and rainy season) at each slaughterhouse. Human feces samples (indicated in yellow rectangles) will be collected from one collaborator on each rural property and two collaborators at each slaughterhouse

Experimental Design

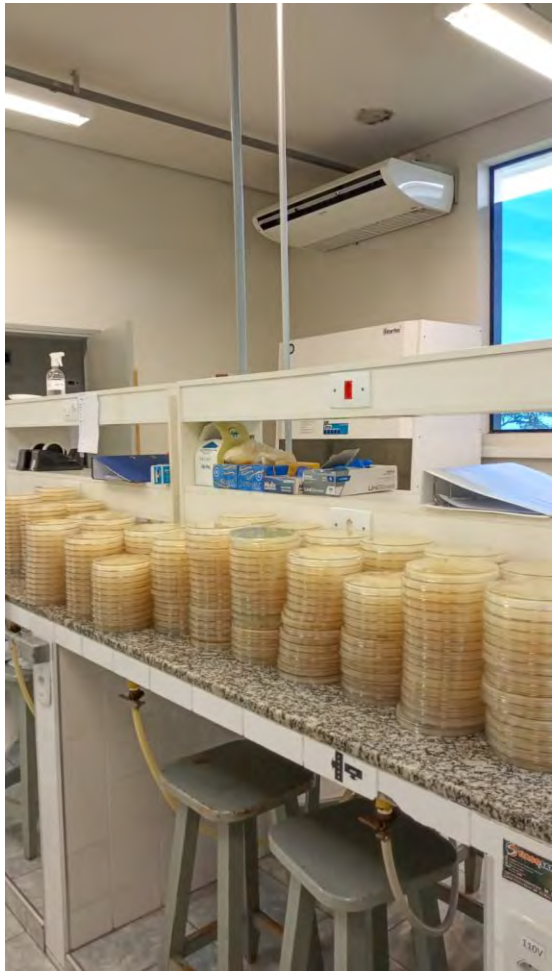
- 8 farms
  - 4 conventional breeding process
  - 4 antibiotic free breeding process
- 2 visits each year
  - Winter
  - Summer
- 2 years of project

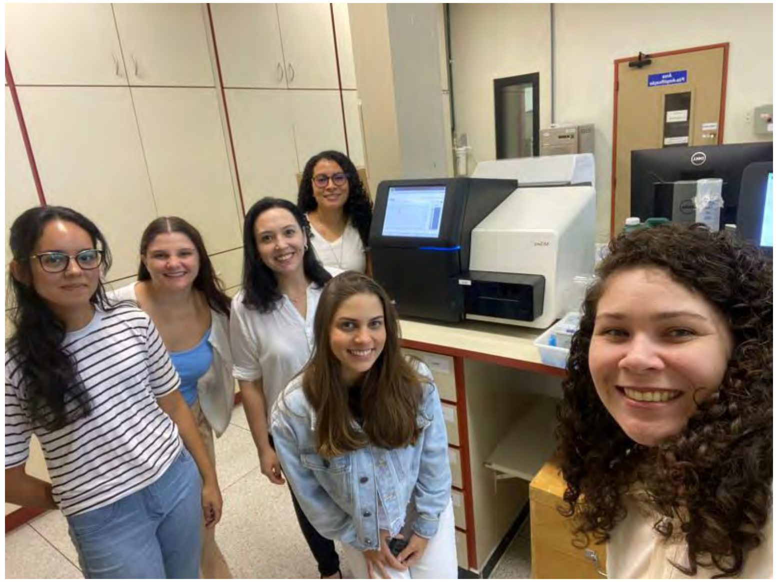
Total of 32 visits

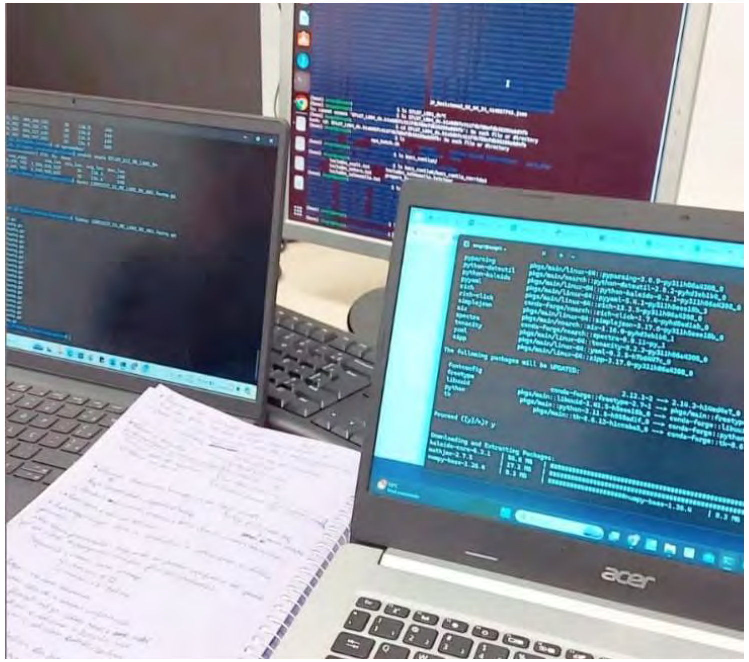
	Samples per Batch		Total of samples in project	
Sampling Time	**Conventional Microbiology**	**Metagenomic Sequencing**	**Conventional Microbiology**	**Metagenomic Sequencing**
Before Housing	5	-	160	-
Half of Housing	13	1	416	32
End of Housing	4	1	128	40*
Slaughterhouse	33	1	1056	44
Carcass	10	1	320	32
Total			2080	148




STEELGEN
TIPO DE PROTEÇÃO:
QUÍMICA







Phenotypical profile of antimicrobial resistance for *Salmonella* isolates in conventional and antibiotic free broiler production systems

System	Sampling Point	CTX	AMO	CAZ	AMP	NAL	TET	CIP	GEN	IMP	TRI	NOR	CLO
Conventional	Before Chick Placement (n= 1)	100.0	100.0	100.0	100.0	100.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0
	Mid-Production (n = 81)	96.3	97.5	95.1	96.3	82.7	69.1	38.3	32.1	28.4	17.3	14.8	21.0
	End of Production (n=14)	100.0	100.0	100.0	100.0	42.9	50.0	78.6	64.3	57.1	42.9	28.6	21.4
	Slaughterhouse (n= 216)	96.8	94.9	95.4	93.5	66.7	56.9	46.8	39.4	38.4	17.6	15.7	9.3
Antibiotic free	Before Chick Placement (n= 3)	100.0	33.3	66.7	66.7	33.3	0.0	33.3	33.3	100.0	0.0	0.0	0.0
	Mid-Production (n = 16)	93.8	81.3	75.0	68.8	25.0	18.8	81.3	68.8	75.0	37.5	25.0	12.5
	End of Production (n=3)	66.7	66.7	66.7	66.7	33.3	0.0	66.7	66.7	66.7	33.3	33.3	33.3
	Slaughterhouse (n= 15)	100.0	100.0	100.0	100.0	26.7	6.7	93.3	100.0	93.3	40.0	20.0	20.0

Phenotypical profile of antimicrobial resistance for *E. coli* isolates in conventional and antibiotic free broiler production systems

System	Sampling Point	AMP	NAL	AMO	TET	CIP	CLO	CTX	TRI	CAZ	NOR	GEN	IMP
Conventional	Before Chick Placement (n= 37)	100.00	83.78	97.30	70.27	62.16	56.76	64.86	56.76	54.05	48.65	35.14	24.32
	Mid-Production (n = 172)	96.51	98.26	99.42	91.28	96.51	82.56	87.21	75.00	83.72	80.23	57.56	29.07
	End of Production (n=61)	93.44	95.08	90.16	90.16	91.80	72.13	78.69	81.97	75.41	70.49	31.15	6.56
	Slaughterhouse (n= 536)	91.42	91.04	90.11	81.34	79.48	67.35	60.82	64.55	55.41	53.36	33.58	17.72
Antibiotic Free	Before Chick Placement (n= 48)	89.6	60.4	87.5	58.3	60.4	39.6	50.0	50.0	45.8	39.6	27.1	16.7
	Mid-Production (n = 191)	81.7	74.3	83.2	69.1	67.0	37.2	54.5	42.4	48.7	40.8	40.3	11.0
	End of Production (n=66)	83.3	66.7	75.8	59.1	63.6	45.5	53.0	39.4	50.0	28.8	24.2	22.7
	Slaughterhouse (n= 563)	77.8	70.5	76.4	59.7	52.4	30.6	40.7	42.3	33.6	22.9	24.5	18.7

Metagenomic Insights into the Microbiota and Resistome of Broiler Feed: Assessing the Impact of Conventional vs. Antibiotic-Free Production Systems

Emanoelli Aparecida Rodrigues dos Santos[1]; Patrícia Regina Lopes Melo[1]; Evelyn Cristine Silva[1,2]; Leonardo Ereno Tadielo[3], Beilei Ge[5]; Kelly Domesle[5]; Ryan McDonald[5]; Chi-Hao Hsu[5]; João Pessoa Araújo Junior[2]; Fábio Sossai Possebon[1,2]; Juliano Gonçalves Pereira[1], Valentina Trinetta[4]

[1]São Paulo State University (UNESP), Botucatu Campus, School of Veterinary Medicine and Animal Science, Rubião Jr District, SN, Botucatu, São Paulo, Brazil

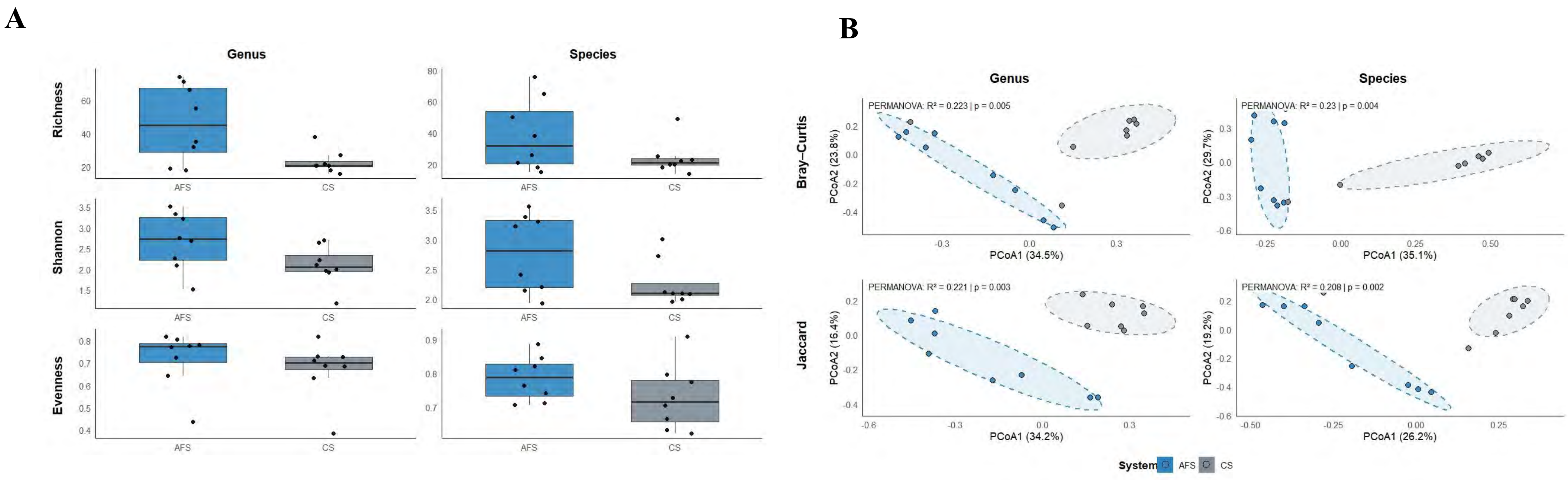
[2]São Paulo State University (UNESP), Botucatu Campus, Institute of Biotechnology – IBTEC, Botucatu, São Paulo, Brazil

[3]Department of Veterinary Medicine, Federal University of Paraná (UFPR), Curitiba, PR, Brazil

[4]Department of Food, Nutrition, Health and Dietetics, Kansas State University, United States

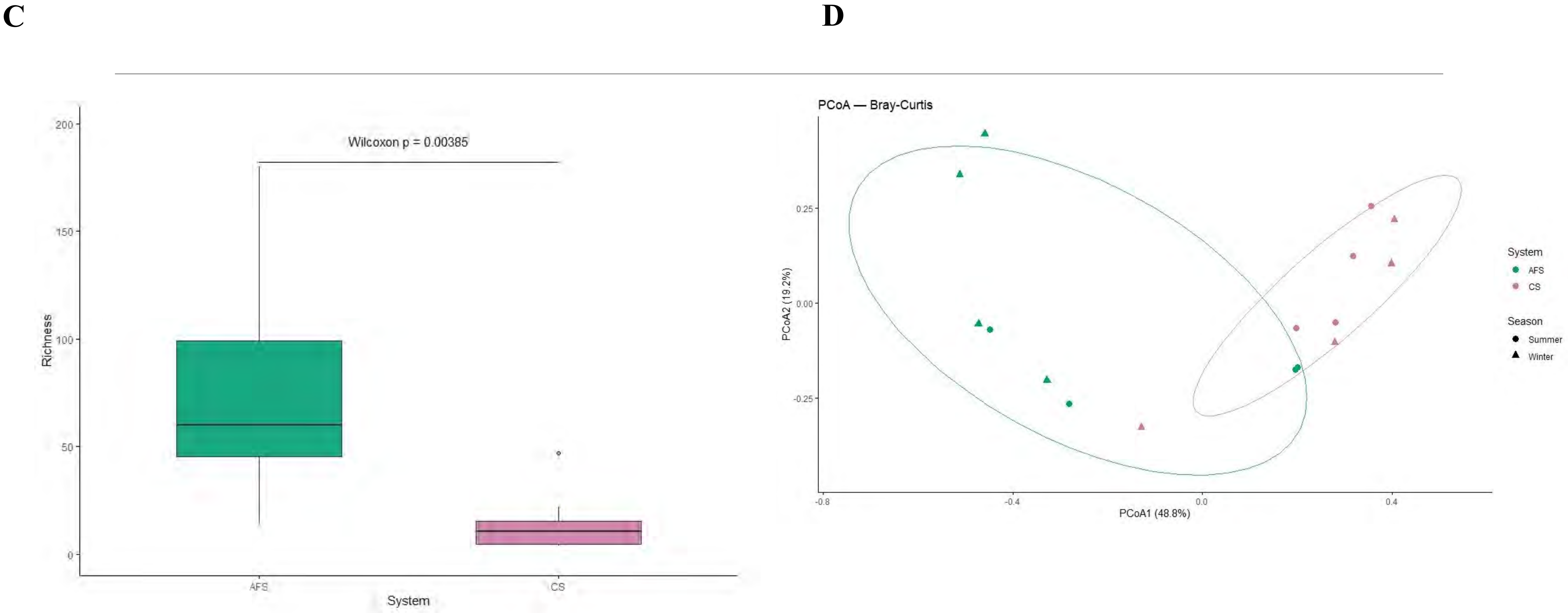
[5]Center for Veterinary Medicine, U.S. Food and Drug Administration (FDA), Laurel, Maryland, United States

Taxonomic composition of feed microbiota across production systems



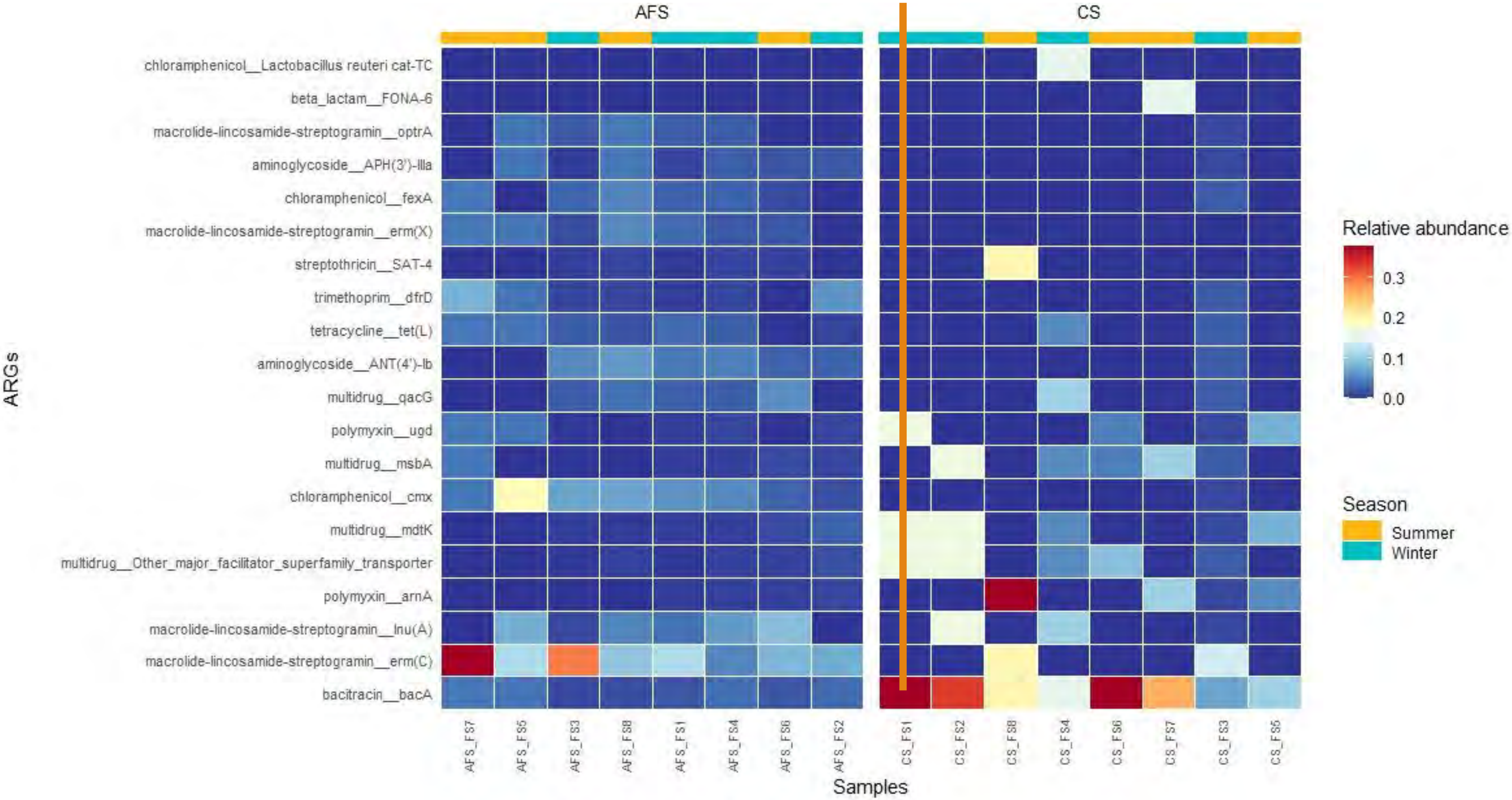
(A) α-diversity at genus and species levels computed from sample-wise relative abundances: richness, Shannon diversity, and Pielou’s evenness. (B) β-diversity ordinations (PCoA) based on Bray–Curtis and Jaccard dissimilarities computed on sample-wise proportions. Ellipses depict 68% t-distribution confidence regions per system, axis labels report the percentage of variance explained by each coordinate.

Patterns of antibiotic resistance

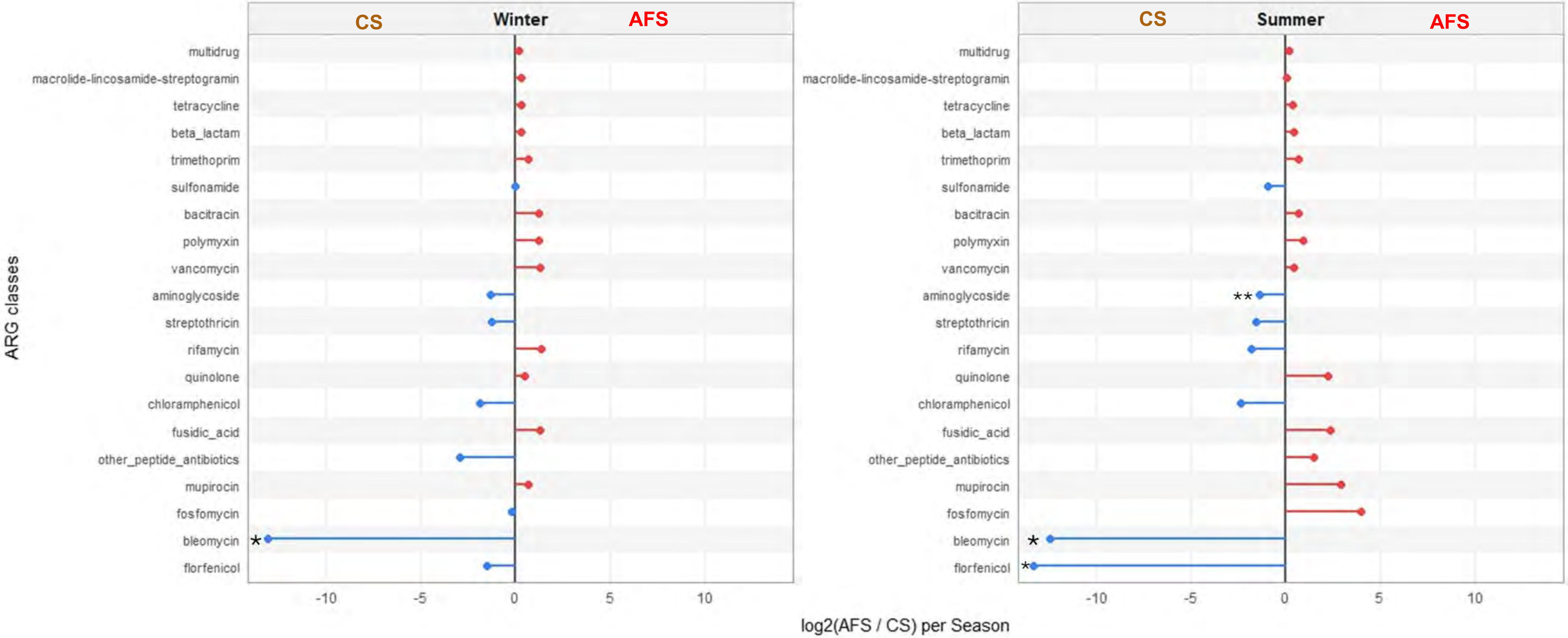


(C) Alpha-diversity (Richness) of ARGs in conventional (CS) and Antibiotic Free (AFS) systems (D) Beta-diversity (Bray-Curtis) of ARGs in conventional (CS) and Antibiotic Free (AFS) systems

Figure 1. Relative abundance of antimicrobial resistance genes (ARGs) across **broiler feed samples** by production system and season.



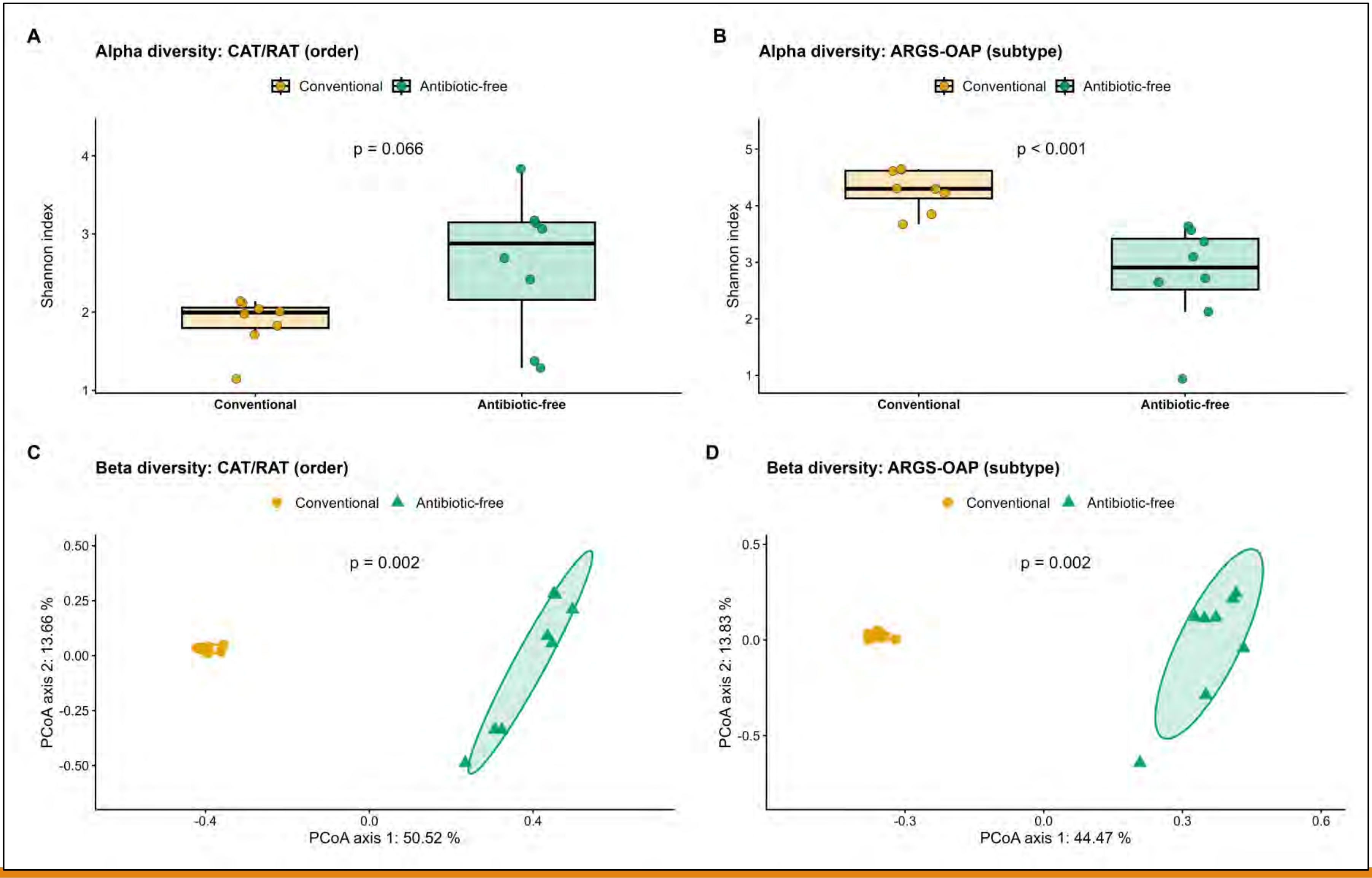
Detection and Circulation of ARGs in the Broiler Production System – All sampling points



Seasonal differential profiles and the overlap of ARGs between conventional and antibiotic-free systems.

Log₂ fold change (log₂[AFS/CS]) of ARG classes per season. Positive values indicate higher abundance in AFS, while negative values indicate enrichment in CS. Asterisks mark significant differences between systems (Wilcoxon rank-sum test; FDR-adjusted $p < 0.05$).

Diversity analysis in treated effluents of conventional and antibiotic free broiler production systems, for microbiome and resistome



Final considerations

- Some microbiota characteristics can remain resilient throughout food processing steps.

- Production systems significantly impact both the microbiome and the resistome.

- Metagenomic analysis is a powerful tool for evaluating microbial ecology across the food processing chain.

- Biosecurity is fundamental to food safety (e.g., GMP, HACCP).

Thank you!

vtrinetta@ksu.edu

fabio.possebon@unesp.br

The APPI Model for Industry Accountability

March 31st, 2026

Ansen Pond, Ph.D.
Head of Protein Conversion and Pet Food Ingredients

NARA

NORTH AMERICAN RENDERERS ASSOCIATION

FPRF

FATS AND PROTEINS RESEARCH FOUNDATION

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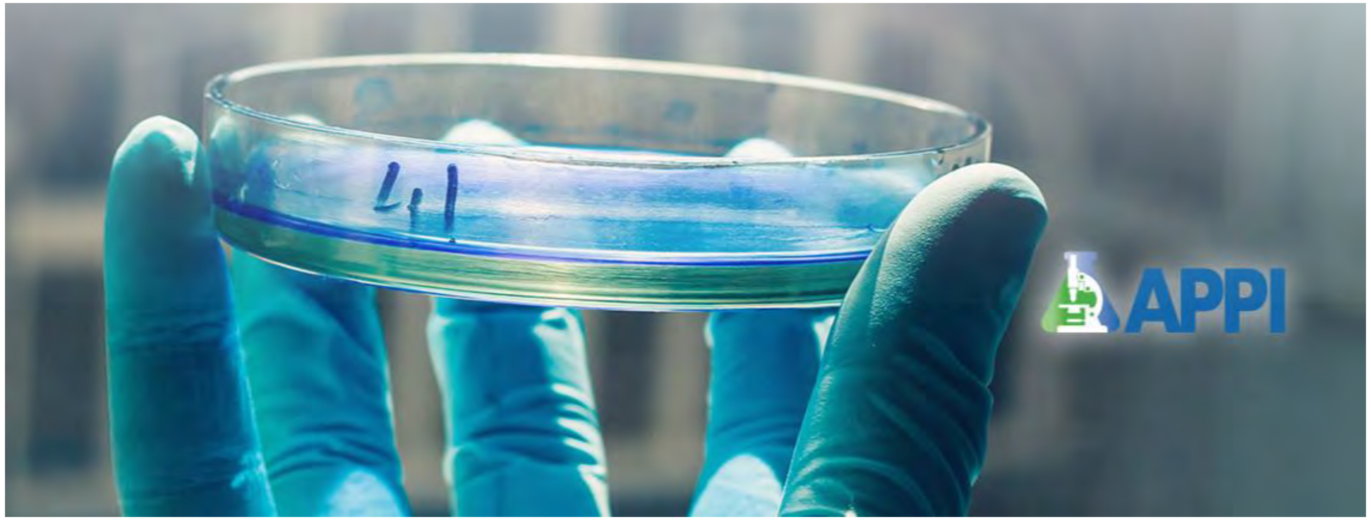
THE ANIMAL PROTEIN PRODUCERS INDUSTRY

APPI Toolbox for Members



Education

Biological Testing

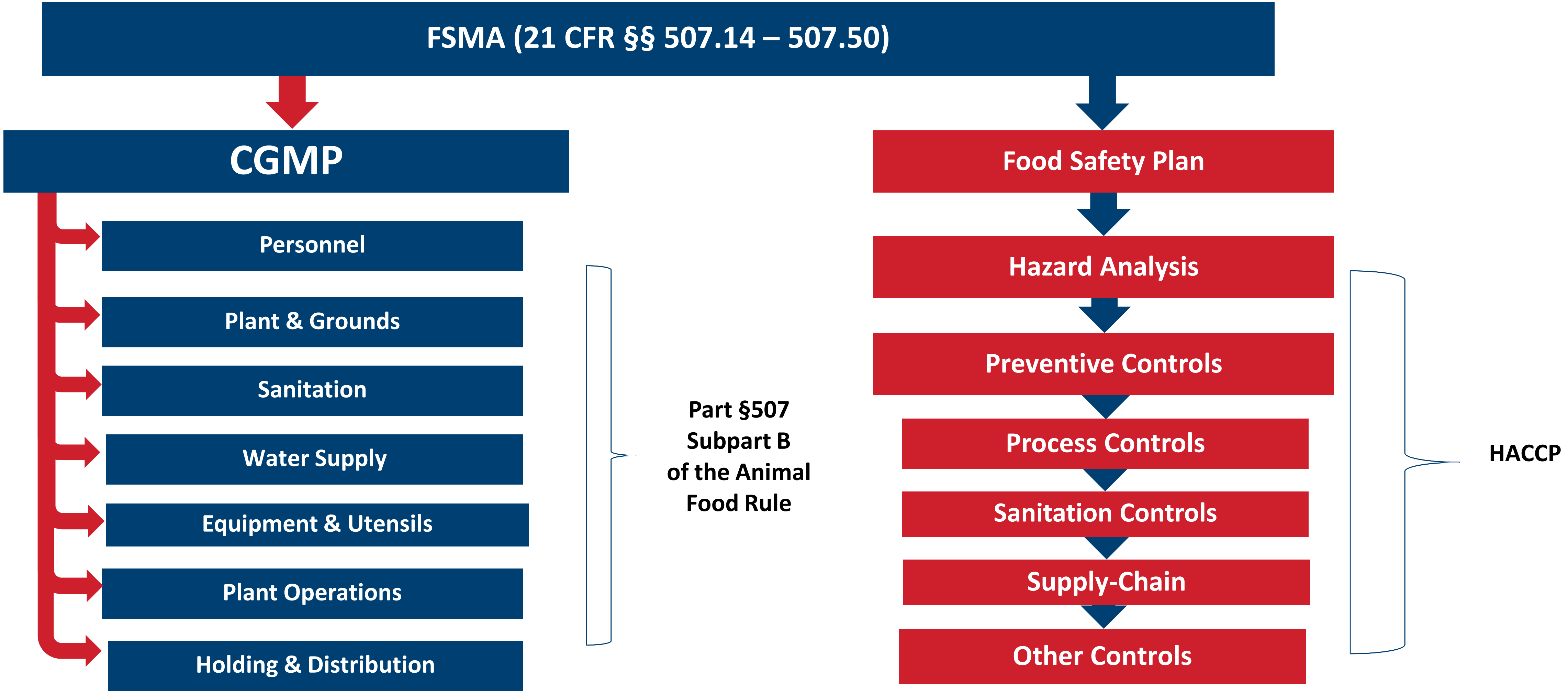
Certification

Research

APPI Educational Programs

- Annual Code of Practice (Sept. 2025)
- Educational Videos
  - Salmonella
  - Sample Collection
  - Foreign Material Control
- Tools to Promote Thinking
  - Plant Signage
  - Infographics

APPI Code of Practice



FSMA (21 CFR §§ 507.14 – 507.50)

CGMP

- Personnel
- Plant & Grounds
- Sanitation
- Water Supply
- Equipment & Utensils
- Plant Operations
- Holding & Distribution

Part §507
Subpart B
of the Animal
Food Rule

Food Safety Plan

Hazard Analysis

Preventive Controls

Process Controls

Sanitation Controls

Supply-Chain

Other Controls

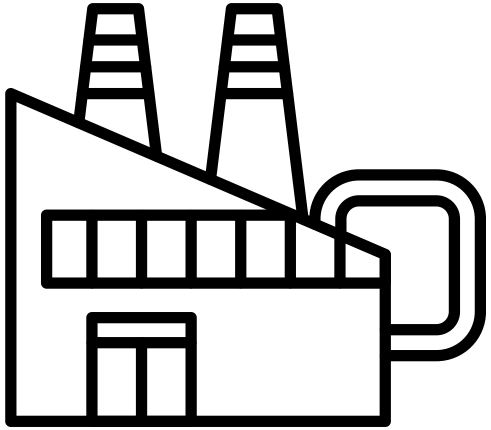
HACCP

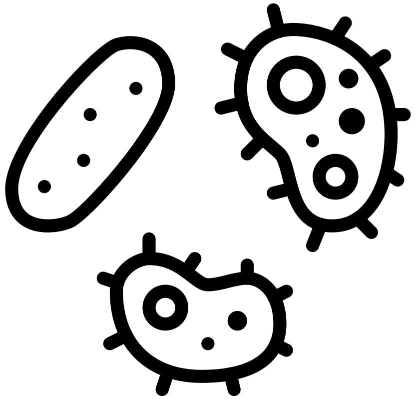
APPI Biological Testing Programs

In Process Product Testing

Finished Product Testing

Environmental Testing





Clostridium perfringens

Enterobacteriaceae

Salmonella

APPI Certification

2025 Audit Process

- Annual onsite audits
  - Plant evaluation
  - Equipment evaluation
  - CGMP standards
  - Food safety plan standards
- Grading system 0-100%
- Certificate

APPI Certification

2026 Audit Process

- Overhaul of audit system
- Unannounced audits
- Audit export standards (Similar to APHIS)
- Review of testing results

APPI Historical Research

- Targeted food safety research and education
- Spent >$1.2M on Salmonella research over the past 15 years
- Partnership with Clemson (ACREC)
- Targeted research
  - Texas Tech University
  - Texas A&M University
  - Colorado State University
  - Kansas State University

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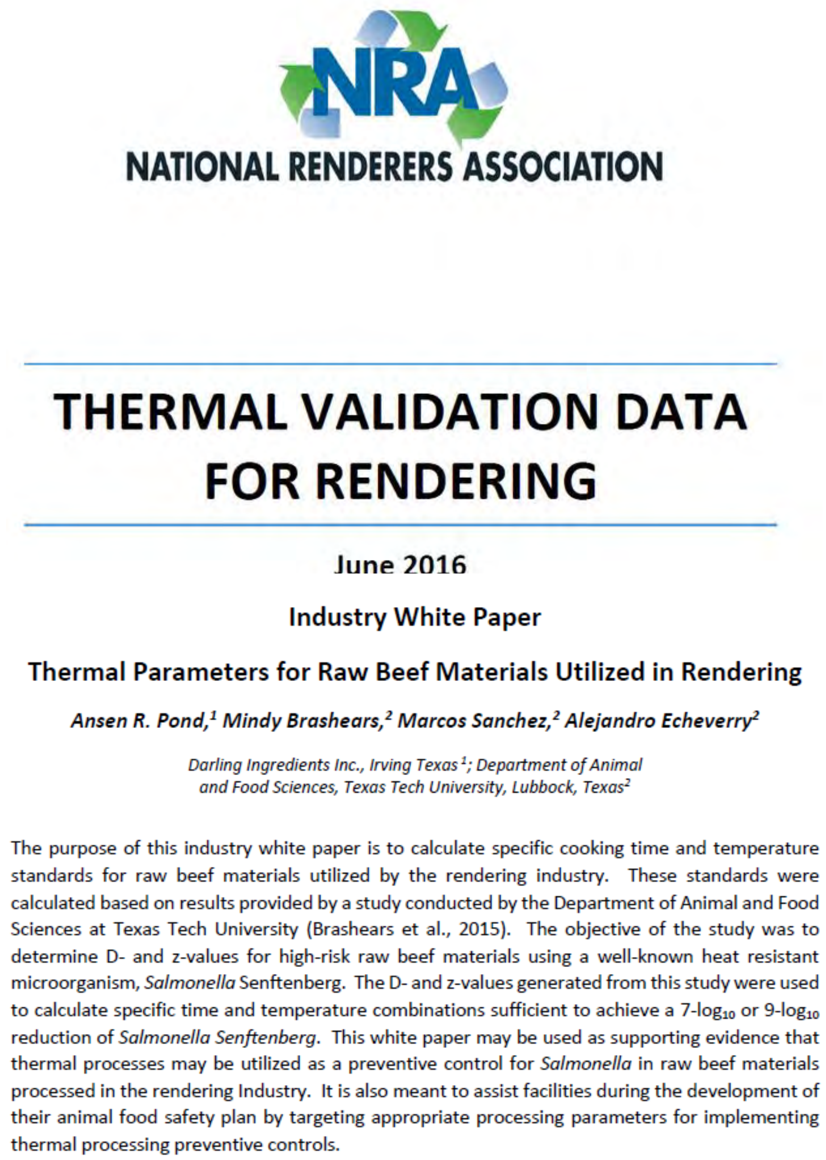
APPI Historical Research



NATIONAL RENDERERS ASSOCIATION

THERMAL VALIDATION DATA FOR RENDERING

June 2016

Industry White Paper

Thermal Parameters for Raw Beef Materials Utilized in Rendering

Ansen R. Pond,[1] Mindy Brashears,[2] Marcos Sanchez,[2] Alejandro Echeverry[2]

Darling Ingredients Inc., Irving Texas [1]; Department of Animal and Food Sciences, Texas Tech University, Lubbock, Texas[2]

The purpose of this industry white paper is to calculate specific cooking time and temperature standards for raw beef materials utilized by the rendering industry. These standards were calculated based on results provided by a study conducted by the Department of Animal and Food Sciences at Texas Tech University (Brashears et al., 2015). The objective of the study was to determine D- and z-values for high-risk raw beef materials using a well-known heat resistant microorganism, *Salmonella* Senftenberg. The D- and z-values generated from this study were used to calculate specific time and temperature combinations sufficient to achieve a 7-$\log_{10}$ or 9-$\log_{10}$ reduction of *Salmonella Senftenberg*. This white paper may be used as supporting evidence that thermal processes may be utilized as a preventive control for *Salmonella* in raw beef materials processed in the rendering Industry. It is also meant to assist facilities during the development of their animal food safety plan by targeting appropriate processing parameters for implementing thermal processing preventive controls.

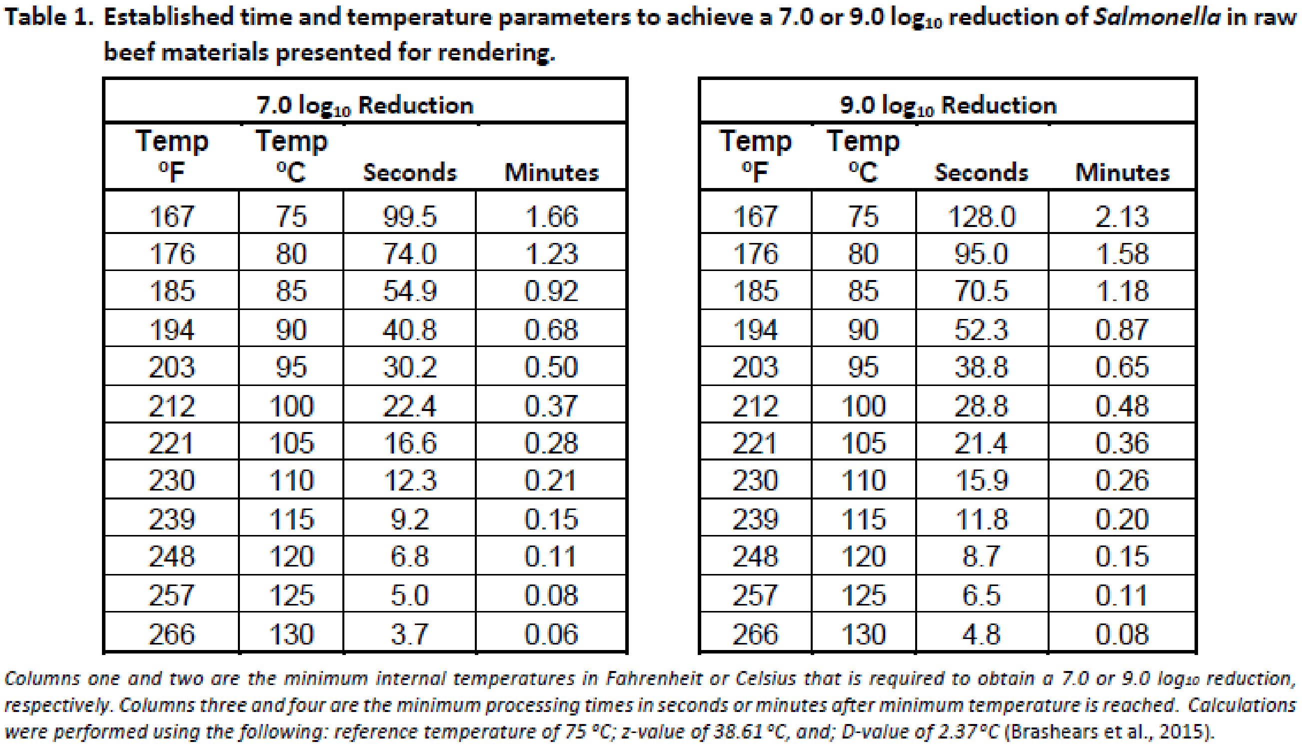


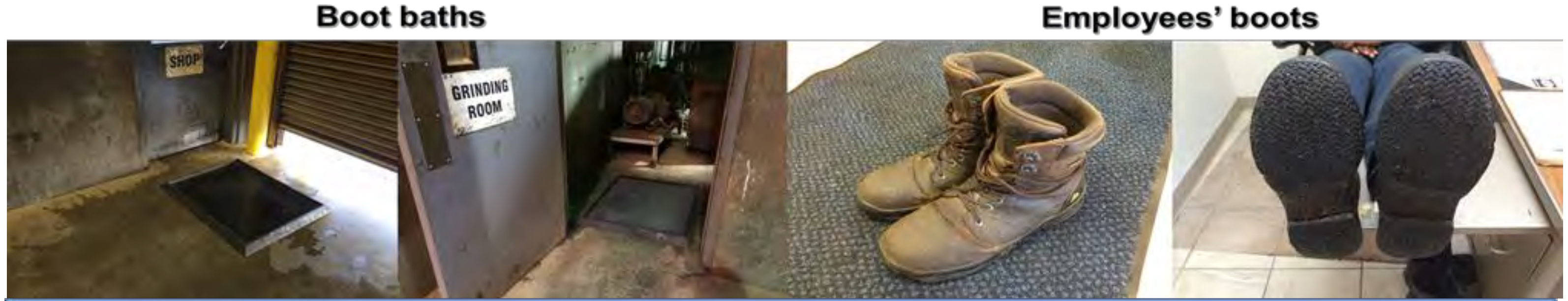
Table 1. Established time and temperature parameters to achieve a 7.0 or 9.0 $\log_{10}$ reduction of *Salmonella* in raw beef materials presented for rendering.

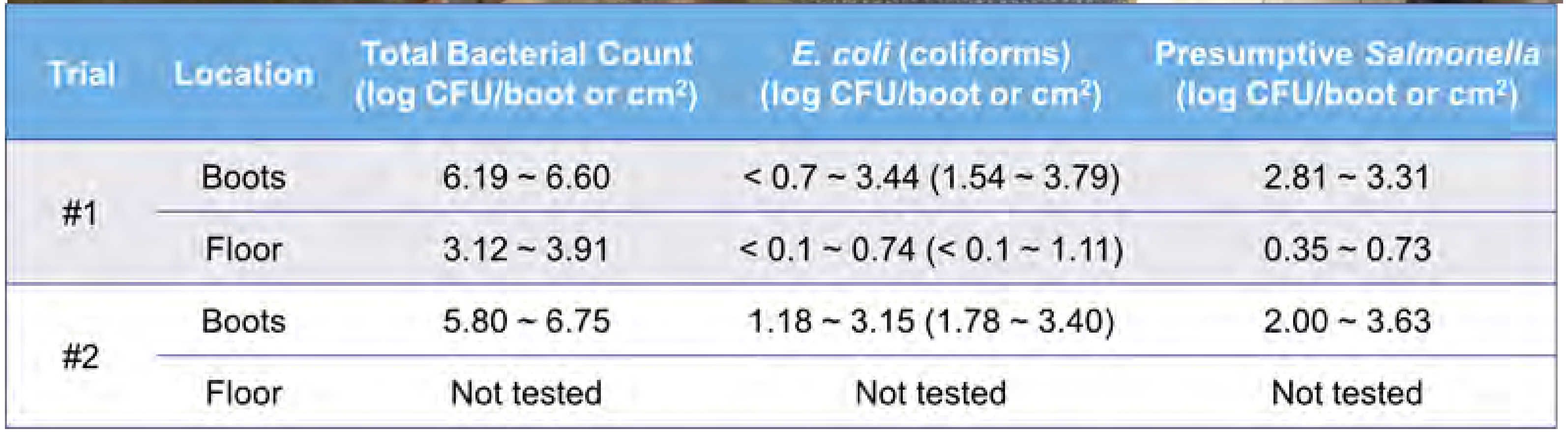
7.0 $\log_{10}$ Reduction				9.0 $\log_{10}$ Reduction			
Temp °F	Temp °C	Seconds	Minutes	Temp °F	Temp °C	Seconds	Minutes
167	75	99.5	1.66	167	75	128.0	2.13
176	80	74.0	1.23	176	80	95.0	1.58
185	85	54.9	0.92	185	85	70.5	1.18
194	90	40.8	0.68	194	90	52.3	0.87
203	95	30.2	0.50	203	95	38.8	0.65
212	100	22.4	0.37	212	100	28.8	0.48
221	105	16.6	0.28	221	105	21.4	0.36
230	110	12.3	0.21	230	110	15.9	0.26
239	115	9.2	0.15	239	115	11.8	0.20
248	120	6.8	0.11	248	120	8.7	0.15
257	125	5.0	0.08	257	125	6.5	0.11
266	130	3.7	0.06	266	130	4.8	0.08

Columns one and two are the minimum internal temperatures in Fahrenheit or Celsius that is required to obtain a 7.0 or 9.0 $\log_{10}$ reduction, respectively. Columns three and four are the minimum processing times in seconds or minutes after minimum temperature is reached. Calculations were performed using the following: reference temperature of 75 °C; z-value of 38.61 °C, and; D-value of 2.37 °C (Brashears et al., 2015).

APPI Historical Research

Isolated Salmonella-specific Bacteriophages





Trial	Location	Total Bacterial Count (log CFU/boot or cm^2)	*E. coli* (coliforms) (log CFU/boot or cm^2)	Presumptive *Salmonella* (log CFU/boot or cm^2)
#1	Boots	6.19 ~ 6.60	< 0.7 ~ 3.44 (1.54 ~ 3.79)	2.81 ~ 3.31
	Floor	3.12 ~ 3.91	< 0.1 ~ 0.74 (< 0.1 ~ 1.11)	0.35 ~ 0.73
#2	Boots	5.80 ~ 6.75	1.18 ~ 3.15 (1.78 ~ 3.40)	2.00 ~ 3.63
	Floor	Not tested	Not tested	Not tested

New APPI Partnership

PET FOOD ALLIANCE
Rendering | Innovation | Research

FOOD SAFETY

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Thank You!

Contact Information

Ansen Pond, Ph.D.

Phone: +1 (806) 674-3717

ansen.pond@pilgrims.com

Questions?

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