Meat Foundation

# RESEARCH UPDATE

October 2025

## Current Research Projects

### Understanding *Salmonella* ecology and internal colonization in market hogs, University of Wisconsin-Madison, University of Arkansas

This study will use barcoded *Salmonella* to inoculated market hogs orally, intranasally, and at various locations intradermally to explore *Salmonella* ecology and internal colonization in market hogs. The findings are intended to address the following research questions: How quickly does *Salmonella* contaminate lymph nodes, tonsils, liver, spleen, cecal contents, and feces of market hogs?; and Does inoculation method (oral vs. intradermal) impact frequency and concentration of *Salmonella* recovered from inoculated market hogs?

*Funded in part by the Pork Checkoff.*

### Survival of African swine fever in pork and processed pork products, Canadian Food Inspection Service, Agriculture and Agri-Food Canada

African Swine Fever (ASF) is a contagious, haemorrhagic viral disease of pigs that is currently spreading westwards throughout Europe and eastwards into China, with significant economic losses along its path. While strict regulatory guidelines are in place to prevent the spread of this virus, little is known about the effectiveness of current meat processing methods in inactivating ASF. In addition, the matrix effect of individual meat products and ingredients on ASF survival is not well documented. This project aims to explore the survival of ASF in different meat products from ASF infected pigs as well as investigate the effect of different ingredients, cooking temperature, storage time and high pressure processing on ASF inactivation in different meat model systems.

*Funded in part by the Pork Checkoff under an ASF Partnership and administered by the Foundation.*

### Creating Alternative Support for Lethality and Stabilization for Heat Treated and Fully Cooked Meat and Poultry Products, University of Wisconsin, HansonTech

Nearly all meat processors in the United States utilize USDA, FSIS Appendix A and B to ensure adequate thermal lethality and stabilization is achieved for partially and fully cooked products. Through the development and release of updated versions in 2017 and 2021, and the realization that a host of potential food safety vulnerabilities exist, the widespread usefulness and in-plant practical application of these guidance documents has become a significant concern and practical challenge to implement. The primary objective of this study is to develop a scientific-based, regulatory-supported, and industry-useful thermal processing and cooling resource (*e.g.* cooking and cooling food safety handbook) for validating pathogen destruction and control, and regulatory compliance for partially and fully cooked meat products that can be used in conjunction with or in lieu of USDA, FSIS Appendix A & B.

*Funded in part by the Beef Checkoff.*

### Carbon Accounting for Genetic Progress in Pork, Kearney (formerly Context Network)

The project intends to demonstrate the market readiness for value creation to occur utilizing credible accounting for genetic progress within pork systems. The demonstration will advance the infrastructure and market research needs that inform future scalability for the industry to use this approach. Findings will enable pork packers and processors to leverage these innovations to manage their environmental footprint and business goals by incentivizing productivity and efficiency.

*Funded in part by PIC.*

**Effect of minimally processed animal protein within the Dietary Guidelines for Americans on biomarkers for cognitive decline, South Dakota State University**

Investigators will leverage an ongoing well-designed, randomized, controlled, crossover, feeding study following USDA Dietary Guidelines for Americans to establish the role of lean animal protein in cognitive health promotion. A minimally processed lean meat incorporated diet will be compared with an isocaloric lacto-ovo-vegetarian control. It is expected the addition of animal protein will enhance nutrient adequacy and reduce markers associated with cognitive decline and neurodegenerative diseases.

**Characterizing *Salmonella* Isolates from Ground Beef in the United States, Texas Tech University, Kansas State University, University of Georgia, USDA-ARS, Meat Animal Research Center, Food Safety Net Services**

It is hypothesized that *Salmonella* serotypes and presence of highly pathogenic *Salmonella* (HPS) in ground beef will vary by geographic location and season depending on the facility. Samples obtained from a separate study will be analyzed to determine the *Salmonella* serotype(s) present in each positive sample and the presence of HPS associated with U.S. ground beef.

*Funded in part by the Beef Industry Food Safety Council.*

**Revealing mechanisms for internal *Salmonella* colonization and persistence in porcine lymphoid and fat tissue, USDA-ARS-NADC - Food Safety and Enteric Pathogens Research Unit**

Swine can become persistently infected with *Salmonella*, shedding little to no bacteria in the feces, until subjected to a stressful event, which increases fecal shedding. A clear understanding of the mechanisms of *Salmonella* persistence in porcine immune cells is needed to developing targeted intervention strategies to significantly reduce *Salmonella* carriage in swine and the risk of contamination of products and the environment. The overall hypothesis is that *Salmonella* resides in myeloid-lineage cells in porcine lymphoid tissues and fat, and subsequently modulates the cellular state to limit bacterial clearance. The objectives of this project are to identify the cell types harboring *Salmonella* in pig lymphoid and adipose tissue at various stages of colonization; characterize the cellular response; and identify mechanisms of intracellular colonization.

*Funded in part by the Pork Checkoff.*

***Salmonella* deep serotyping and microbial community profiling though swine production and processing, USDA-ARS-MARC, University of Georgia, Texas Tech University**

This study will investigate the implementation of effective interventions at the most appropriate points in swine production, as well as deepen the understanding of *Salmonella* serotype diversity and complexity at all stages of production. This study will use archived samples of swine finishing barns as well samples collected under currently funded work, for CRISPR-SeroSeq and microbiome analysis to gain a deeper understanding of the microbiome and *Salmonella* serotype ecology from farm to fork.

*Funded in part by the Pork Checkoff.*

## Research Funded By the Beef Checkoff and Administered by the Foundation

**Historical analysis of *Salmonella* using pre-existing data: trends in outbreaks, genomics, and geographic factors, University of Georgia**

Emerging pathogen monitoring programs, such as wastewater monitoring for COVID-19, have gained critical focus as a possible way to predict the next outbreak and assist in development of management tools before the first wave of illnesses hits. These approaches can be extended to beef-related *Salmonella* outbreaks by leveraging the wealth of surveillance data that is collected into the NCBI Pathogen Detection Isolates Browser. This study will develop a framework for understanding where, why, and how certain *Salmonella* strains emerge to cause outbreaks. A short-list of warning signs and monitoring recommendations will be developed to predict the next outbreak before it happens.

### From Trim to Table: Tracking *Salmonella* Dynamics, Including Levels and Survival, from Beef Trim to Ground Product, Kansas State University and Cargill

This research will conduct an inoculation study to evaluate the influence of *Salmonella* levels in beef trim (including lymph nodes) on *Salmonella* levels in ground beef, providing valuable insights for managing *Salmonella* in final product. *Salmonella* survival will be assessed during standard industry storage periods to further understand its persistence and potential risks in products intended for commerce.

### Improving and validating the THERM model for predicting growth of *Staphylococcus aureus* in raw meat products during temperature abuse and come-up-time (CUT) deviations, University of Wisconsin – Madison

The current Temperature History Evaluation for Raw Meats (THERM) model, originally intended for use by small and very small processors who lacked refrigeration in their raw processing areas and now widely used at all levels of the meat processing industry to estimate pathogen growth in raw materials, may overestimate pathogen growth when following USDA temperature recommendations. This study will refine product categories and determine the growth of *Staphylococcus aureus* in uncured model meat products with varying pH levels and temperatures which represent come-up-time ranges where *S. aureus* may grow. A validated predictive model will be developed using a variety of different meat products and formulations.

### Reliability and repeatability of digital PCR and VAE assays for the enumeration of *Salmonella* in beef samples, Florida State University and U.S. Meat Animal Research Center USDA-ARS

This study intends to optimize digital PCR (dPCR) and varying amplification efficiency (VAE) assay workflows for the detection and quantification of *Salmonella* load in beef samples. The reliability and repeatability of dPCR and VAE assays will be validated and their applicability will be compared with an AOAC performance-tested method. The application of a partition-based digital PCR approach will enable highly reliable and repeatable detection and quantification of *Salmonella* load in contaminated beef samples. The VAE assay will enable simple estimation of *Salmonella* levels in beef samples.

### Rapid identification of ground beef and beef trim samples exceeding a *Salmonella* threshold level, Kansas State University and Cargill

The study will determine the impact of the *Salmonella* inoculation method on various *Salmonella* quantification and limit of detection (LOD) methods. Additionally, the study will determine the reliability and repeatability of various *Salmonella* quantification and LOD methods for the identification of non-intact beef samples harboring *Salmonella* equal to or above a threshold. Findings will address beef industry concerns regarding specific methods.

### Effect of organic acid components on the inhibition of *Clostridium perfringens* during extended cooling of uncured meat products and the inhibition of *Listeria monocytogenes* during extended refrigerated storage, University of Wisconsin-Madison Food Research Institute

This research will compare the relative efficacy and synergistic effect of the active components (lactate, propionate, acetate/diacetate) found in clean label growth inhibitors (such as cultured sugar and vinegar-based products) on the inhibition of *Clostridium perfringens* in a model-uncured beef system, with primary focus on extending Phase 1 cooling (120 to 80°F). It will also validate inhibition of *Listeria monocytogenes* during extended refrigerated storage of a model deli meat system formulated with organic acid salts used to control *C. perfringens*.

**Assessing *Salmonella* status (prevalence, load, pathogenicity, and serotype complexity) through beef processing, University of Georgia, and University of Wisconsin-Madison**

This study will integrate four advanced laboratory techniques, e.g. PiLOT, CRISPR-SeroSeq, to improve understanding of *Salmonella* dynamics in beef processing. Specifically, these data and techniques will enable (1) identifying steps in the processing chain which change the *Salmonella* communities either by load or loss or gain of subtypes (serotype, pathogenicity), or both and (2) describing which *Salmonella* subtypes (serotype, pathogenicity) are selected for, or which are lost, during processing steps. Findings will help build the research foundation needed for food safety protocols to produce integrated data sets. This data can then be applied to ensure that proposed regulatory frameworks meaningfully improve beef safety.

**Targeting Foodborne Pathogens in the Beef Industry through an Integrated Analysis of the Beef Processing System, Texas Tech University, University of Nebraska, US MARC, and Auburn University**

This research will take a comprehensive approach to targeting *Salmonella* and Shiga Toxin Producing *E. coli* (STEC) conducted through optimization of sampling techniques, microbial detection and microbial quantification methods combined with microbiome and metagenomic analysis to enable mitigation strategies and validation techniques to impact pathogen presence in beef products.

## Recently Completed Research

**A surveillance of *Salmonella* in the lymph nodes of sows and boars, Kansas State University, Texas Tech University**

This study provides nationwide surveillance data associated with *Salmonella* contamination in cull hog lymph nodes (LN) and tonsils across multiple seasons and regions of the United States. Cull hog processors can use these data to determine risk and identify appropriate mitigation strategies designed for control of *Salmonella* contamination in LNs. Further research is necessary to determine the repeatability of data trends.

**Understanding the impact of the farm and lairage environments on *Salmonella* contamination in market hogs, University of Wisconsin-Madison, Kansas State University, Texas Tech University, USDA-ARS**

This study represents a comprehensive evaluation of *Salmonella* transmission and carriage in market hogs from their farm environments, through transportation and abattoir lairage, and to internal contamination in lymph nodes. The data provide additional evidence that market hogs are routinely exposed to *Salmonella*; however, when evaluated as single variables, *Salmonella* prevalence associated with the farm, transportation trailer, and lairage environments does not effectively predict *Salmonella* contamination in market hog mesenteric lymph nodes.

*Funded in part by the National Pork Checkoff.*

## Recently Completed Research Funded by the Beef Checkoff and Administered by the Foundation

**Analysis of beef *Salmonella* outbreaks using the USMARC SNP analysis pipeline, U.S. Meat Animal Research Center USDA-ARS**

Using the pipeline developed in a previously funded project, genomes from past *Salmonella* outbreaks were analyzed to characterize the genomic variation between sequenced isolates related to the outbreak. The main observation of the analysis was presence or absence of insertion or deletion events involving bacteriophage and plasmid sequences between outbreak strains confirming that the USMARC pipeline developed is useful to determine relatedness between *Salmonella* foodborne outbreak strains. This tool offers a clearer and more complete view of isolate relationships for outbreak traceback and provides a practical solution for industry members to conduct internal genomic data analyses without submitting sensitive data to public databases.