National Program 101 Food Animal Production

National Program Annual Report: FY2021

NP 101 Mission Statement:

Conduct research to improve food animal production efficiency, industry sustainability, animal welfare, product quality and nutritional value while safeguarding animal genetic resources.

Introduction

Food animals contribute substantially to the U.S. economy. The United States gross domestic product was estimated at $23.17 trillion (US-BEA, Sept. 2021) with Animal Production and Aquaculture accounting for $199 billion or ~0.85% of US GDP (US BEA. Sep 2021). According to the National Agricultural Statistics Service, 2017 Census of Agriculture, which is the most recent census, 39.4 million cattle and calves were sold contributing $77 billion (0.4%), 9.5 million milk cows contributed $36 billion (0.2%), 235 million pigs contributed $26.3 billion (0.14%), 5.4 million sheep and goats contributed $1 billion (0.005%, includes meat, wool and milk), and poultry contributed $49.2 billion (0.25%, includes turkeys, broilers and eggs). The livestock figures include animal product sales, but do not include sales associated with allied industries, like animal feeds, farm supplies, genetic companies and germplasm sales, and animal health related sales. Along with the direct economic contribution, food animals convert plant materials into animal products that are excellent sources of high biological value protein and contain nutrients like vitamin B12 that are essential for human health. Ruminant food animals (cattle and sheep) convert forages (e.g., grasses, alfalfa) that are not suitable for human consumption into nutritious human food products, utilizing lands that are also unsuitable or less suitable for human edible crop production. In addition, pigs and poultry convert plant energy and protein products and co-products into protein- and vitamin-rich meat and egg products. The nutrient density of food animal products plays a vital role in the diets of people around the world, providing valuable sources of high-quality protein, fatty acids, vitamins, and minerals.

The vast contributions of ARS scientists to enhancements in food animal efficiency have helped ensure international food security and directly impacted human health by reducing the real cost of nutritionally valuable animal products, making animal products more available, especially to those populations most in need. While the contributions to improved human health are clear, food animal production sectors have challenges to address. Recent reports draw attention to the potential negative impact of food animal production on the environment, including food animal contribution(s) to greenhouse gas generation, feed and manure derived nitrogen and phosphorus runoff resulting in algal blooms, degradation of wildlife habitat, and the contribution of animal waste to the prevalence of pathogenic and antibiotic resistant microorganisms in the environment. Animal production sectors also face the perception that technologies that improve the efficiency of animal production simultaneously compromise the health and well-being of food animals. In addition, regulations are redefining how food animals are raised within some areas of the United States, creating new challenges to food safety (greater bacterial concerns in floor-raised vs. caged hen housing), animal care and well-being (aggression and an associated increase in injury risk for group-housed breeding swine and laying hens), and changes in the ability to control disease in food animal populations because of restrictions on use of antibiotics that are considered medically important to humans). These current and emerging challenges require attention and focus to maintain sustainable food animal production sectors.

Research focusing on livestock production efficiency has far-reaching impacts, as efficiency is an all-encompassing term in food animal production. Efficiency improvements involve both animal feed and non-feed resource utilization. Key drivers and focal areas include:

- capture and effective use of nutrients from traditional and emerging feedstocks;
- enhanced gut and rumen function and the associated improvements in animal health and well-being;
- evaluation and optimization of production, reproduction, and product quality traits;
- discovery, verification, and adoption of new technology;
- enhanced analytical capabilities and statistical modeling to use 'big' data and bioinformatics;
- expanding knowledge of animal and microorganism genomes and phenomes to identify key genes, pathways, and associations that improve selection response and offer gene editing targets; and
- focused efforts to monitor individual animal needs, identify optimal housing, and understand the myriad of environmental factors that influence stress, health, and behavior of food animals.

All with goals focused on offering solutions that ameliorate concerns for animals produced for food.

Improved efficiency directly reduces waste production and greenhouse gas emissions, decreases the impact on the land, water, and air resources while also continuing to provide food resources that are wholesome, safe, nutritious, and affordable. These outcomes are key to providing food to an expanding human population and offering sustainable profitability to the producer. Addressing efficiency, now more than ever, requires multi-disciplinary approaches applied to complex biological systems, application of technology that enhances research outcomes, the transfer of information to decision makers, and the adoption of scientifically proven best practices by livestock producers. Excellent scientists working with partners and stakeholders underpin the ARS-driven collaborative research efforts that provide solutions to known challenges and discover new science and technologies that support efficient and profitable food animal production.

Studies within this program that identify indicators of animal stress and methods to alleviate stress in the production environment will ensure that as production efficiency improves, so will animal well-being in those production systems. Individual and collective scientific advancement of genetic and genomic selection methods, animal nutrition, physiology and reproduction, and animal health will improve the conversion of feed resources into usable food animal products while concurrently reducing the volume of waste products generated. As an example, milk production per cow increased 11% and total milk production increased 14% in the United States within the past 10 years with only a 2% increase in U.S. herd size (USDA, NASS, 2011 – 2020 data). These findings underpin the application of science-based knowledge at the farm level. In addition, science-based animal waste management strategies provide for the beneficial return of animal waste nutrients to the environment, in support of plant production and improved soil health. The study of microorganisms is an essential focus of this project. Understanding their roles in food animal health and production will advance pathogen reduction strategies that influence human, animal and environmental health and also contribute to ongoing efforts to reduce greenhouse gas emissions from food animal production systems.

Future Directions

As the existing 5-year Food Animal Production projects near their completion in 2022, the scientific advances made through these projects have and will continue to drive and expand research opportunities in the next 5-year cycle. A progressive National Program in Food Animal Production will build on successes and address the animal and associated non-animal influencers in the face of existing and emerging challenges. Advances in science have allowed greater depth of knowledge of biological function than ever before and ARS scientists continue to be scientific leaders in discovery and application of these findings to food animal production. Artificial intelligence, autonomous monitoring and measurement capabilities, and advances in bioinformatic analysis capabilities will underpin future research and hasten delivery of solutions to food animal industries and consumers.

Program staffing, funding, and collaborations

During FY 2021, National Program 101 (NP 101) had 87 full-time scientist positions working at 15 locations across the United States on twenty-seven appropriated research projects. In fiscal year 2021, appropriated funding for NP101 was $58 million; and total funding was approximately $60 million including extramural awards. Technology transfer included seven Material Transfer Agreements.

In 2021, NP 101 scientists participated in international research collaborations with scientists in:

Australia, Austria, Belgium, Brazil, Canada, Denmark, Ethiopia, France, Germany, India, Ireland, Israel, Italy, Malawi, Mexico, Mongolia, Netherlands, New Zealand, Nigeria, Poland, Russia, Scotland, South Africa, Spain, Sweden, Uganda, United Kingdom.

In 2021, NP101 scientists participated in academic research collaborations with:

- Nearly every U.S. Land-Grant College and University
- Private Agricultural Universities

Outreach Activities

Students working with ARS Scientists and Scientist Academic Outreach

Undergraduates	Graduates	Post-Docs	Scientist Advisors	Mentors	Adjunct Professors/Other
14	28	6	14	14	13

ARS Animal Production Program: Student-Related Outreach Activities

	Presentation to Schools	Student Tours/Visits to ARS Locations
Number of Activities	6	5
Number of Students	190	12

Animal Production Program General Outreach to Stakeholders and the Public

Name of Activity	Number of Activities	Number of Participants
Presentation to Local/Community Groups	1	18
Training/Demonstration	8	44
Webinars	1	1
Presentation to Practitioner/Industry/Producer	6	2856
Workshops	3	214
Stakeholder Meetings	7	464
Laboratory Review	1	4
Teaching (Courses)	1	2
Stem Events	2	1100

New scientists in NP 101 2021:

Dr. Tyson Fuller, Postdoctoral Researcher, joined the Cell Wall Biology and Utilization Research Unit at the U.S. Dairy Forage Research Center, Madison, Wisconsin.

Dr. Kouassi Kpodo, Research Physiologist, joined the Animal Biosciences and Biotechnology Laboratory, Beltsville, Maryland.

Dr. Bryan Neville, Research Animal Scientist, joined the Nutrition, Growth and Physiology Research Unit at the U.S. Meat Animal Research Center, Clay Center, Nebraska.

Dr. Bethany Redel, Research Physiologist, joined the Plant Genetics Research Unit, Columbia, Missouri. Dr. Redel's efforts will focus on the application of gene editing technology to expand and enhance efforts in genetic and genomic technology applications in food animal production.

The following scientists retired in 2021:

Dr. Gary Bennett, Supervisory Research Geneticist, Genetics and Animal Breeding Research Unit, U.S. Meat Animal Research Center, Clay Center, Nebraska. Dr. Bennett's distinguished research career spanned 36 years, and his groundbreaking efforts in Beef Cattle Genetics and Genomics are recognized world-wide.

Dr. James Neel, Research Animal Scientist, Grazinglands Research Laboratory, El Reno, Oklahoma. Dr. Neel's research included herbage energy and nitrogen balance, and development systems for pasture-based beef production and silvo-pastoral grazing.

The distinguished record of these scientists is recognized world-wide and they will be missed at NP 101.

The following scientists in NP 101 received prominent awards in 2021:

Drs. Derek Bickhart, Benjamin Rosen, Timothy Smith, and Curt Van Tassell were recognized by Nature Genetics for previous ground-breaking published research on de novo assembly of complex genomes. Their work, domestic goat genome ARS1, was recognized in a Nature Genetics 20-year celebration of the Human Genome Sequence, Milestone 16 – Genomes Go Platinum.

Dr. John Dunn received the American Association of Avian Pathologists P.P. Levine Award for 2020 as the senior author of the best paper published in the journal Avian Diseases

Dr. Jay Johnson received the 2021 ASAS Midwest Section, Outstanding Young Researcher Award from the American Society of Animal Science.

Dr. Brittney Keel received the 2021 ARS Early Career Scientist of the Year Award for applying machine learning and novel mathematical modeling to complex livestock genomic analyses.

Dr. Gary A. Rohrer received the 2021 Area Senior Research Scientists of the Year Award for his leadership and development of genomic technologies which resulted in improvements in pork production and animal well-being.

Major Accomplishments in 2021

This section summarizes significant research results for Fiscal Year 2021. Within each section, selected accomplishments of individual research projects in NP 101 are presented. The accomplishments are highlighted here due to their significance and alignment to action plan components and anticipated products. They are a subset of accomplishments within the program. To see all the accomplishments for each project within the program, please visit the USDA ARS National Program 101 website:

https://www.ars.usda.gov/research/project-reports-by-program/?npCode=101

Many of the projects are the result of significant domestic and international collaborations with both industry and academia. These collaborations provide extraordinary opportunities to leverage funding and scientific expertise for USDA - ARS research and allow scientists to tackle larger problems that could not be addressed without such collaborations. Improved food animal production efficiencies decrease the real cost of animal products, making the products more available to people worldwide, and decreasing the environmental footprint of animal production.

Accomplishments are listed below that correspond to each of the Components and Problem Statements of the *Action Plan National Program 101 Food Animal Production 2018 – 2022*. Following each accomplishment, the corresponding anticipated product from the NP 101 Action plan is indicated.

Component 1: Improving Production and Production Efficiencies while Enhancing Animal Well-Being across Diverse Food Animal Production Systems

Problem Statement 1A: Improving the Efficiency of Growth and Nutrient Utilization

Leveraging "taste" for targeted grazing

The American West sagebrush ecosystem supports agricultural economies, rural communities, and more than 350 native plant and wildlife species, but also faces serious threats from human-altered fire regimes and invasive plant species. ARS researchers in Dubois, Idaho, partnered with University of Idaho researchers and developed a method to identify sheep that can or cannot taste bitter flavors. They also developed a method to quantify genes affecting sheep's ability to taste bitter-flavored compounds. Using these genetic markers in sheep selection and an evidence-based grazing approach will lead to the development of sheep with rangeland grazing patterns that foster resilient, robust, and sustainable sagebrush ecosystems.

Anticipated product: Management strategies and programs for improving grazing-land health and sustainability and conservation/return of natural ecosystem services.

Problem Statement 1B: Improving Reproductive Efficiency

Isolation and transcriptome analysis of turkey sperm storage tubules

Female avian species have specialized sperm storage tubules that store spermatozoa for 2 to 15 weeks without compromising sperm's capacity for fertilization. Identifying the molecular and physiological mechanisms that allow sperm storage tubules to maintain sperm fertility would create opportunities for applying these mechanisms to commercial system protocols and significantly improve the fertility of stored poultry sperm. ARS scientists in Beltsville, Maryland, were the first to isolate sperm storage tubules using laser capture microdissection. Characterization and pathway analysis of 745 differentially expressed genes revealed mechanisms associated with the fertility duration and cholesterol and lipid metabolism associated with sperm protection. These results give ARS scientists promising avenues for developing protocols for semen storage and use that exploit the sperm preservation capabilities of sperm storage tubules.

Anticipated product: Successful and efficient cryopreservation technologies and methods available for all livestock and poultry species.

Breeding for carcass traits does not reduce reproductive performance

Breeding for production traits in beef cattle can also reduce reproductive functions. ARS researchers in Clay Center, Nebraska, previously reported that newly identified genetic markers associated with desirable tenderness in beef steers may also be associated with an undesirable delayed calving date, which reduces reproductive ability in heifers. ARS researchers used genetic information and genomic markers from pedigree-related steers to generate a genome-enhanced breeding value for tenderness in breeding heifers. They did not find detrimental associations between production and reproductive function and observed that previous associations between production and reproduction can be overcome using marker-assisted, genomic approaches combined with quantitative genetic analyses. Cow-calf producers can apply these genetic markers to improve tenderness in progeny without concern for unintended negative impacts on reproductive function in the breeding herd.

Anticipated product: Strategies that break the antagonistic relationship between production and reproductive efficiency, allowing both to be simultaneously improved.

Reproductive failure in breeding female pigs (gilt) influenced by brain proteins

In the United States, around 40 percent of gilts (young female pigs retained for breeding) are culled annually due to reproductive failure. This is a loss of around 2.4 million gilts and results in industry losses of more than $50 million. ARS scientists in Clay Center, Nebraska, examined how cells in the brain are involved in controlling reproduction in replacement females (gilts) during development and maturation. They found that certain cells express two types of proteins, called kisspeptin and neurokinin B, and that these cells are uniquely organized in the pig brain to control the secretion of reproductive hormones. This is the first report of localization of these proteins in pigs, and this foundational knowledge will be critical for developing new strategies and technologies to better manage reproduction and increase fertility in gilts.

Anticipated product: Identification of critical control points limiting improvements in reproductive rate in food animals including physiological and management factors.

Problem Statement 1C: Enhancing Animal Well-Being and Reducing Stress

Characterization of metal tolerance in a pork outbreak-associated *Salmonella* strain

High levels of copper and zinc are frequently included in young pig diets as alternatives to antimicrobials to reduce pathogens and increase animal growth. However, the continuous use of copper or zinc may promote metal tolerance in bacterial pathogens. ARS researchers in Ames, Iowa, found that a *Salmonella* strain associated with a 2015 U.S. human outbreak linked to pork had increased genetic tolerance to copper, arsenic, and antimony. Furthermore, ARS researchers found that metal tolerance in this *Salmonella* strain can be transferred to other bacterial isolates and increase their metal tolerance; therefore, using elevated levels of zinc and copper in nursery swine diets may eventually result in pathogen strains more resistant to metals and not reduce colonization in pigs over the long term. This research provides information to veterinarians, swine producers, and microbiologists that certain *Salmonella* strains in U.S. pig populations have increased tolerance to copper used in animal production. The presence of metal tolerance genes in bacterial populations may limit the effectiveness of metals used to control disease.

Anticipated product: Identification of alternatives to antibiotics for improving growth performance in livestock.

Rapid eye temperature measurement to evaluate animal health

Rapid temperature measurement using forehead thermometers has become normal practice for humans, but current practices in cattle rely on obtaining rectal temperatures which is time-consuming. ARS scientists in Lubbock, Texas, and university collaborators studied infrared ocular thermography, measuring the temperature of the eye, to detect fever in cattle. Results indicate that infrared ocular thermography can detect fever in cattle in less than 30 seconds and that eye temperature is highly correlated with rectal temperature. Adopting this rapid method for detecting fever in cattle allows high-throughput measurement in production facilities that will improve cattle management and sickness identification practices, improve cattle well-being and productivity, and reduce production costs.

Anticipated product: Improved precision animal management/production systems to better identify compromised animal well-being for individual and groups of animals in conventional production systems.

Component 2: Understanding, Improving, and Effectively Using Animal Genetic and Genomic Resources

Problem Statement 2A: Develop Bioinformatic and other Required Capacities for Research in Genomics and Metagenomics.

Development of a high-throughput means of assessing microbial virus-host associations

Bacteriophages are viruses that infect bacteria and they offer distinct opportunities for therapeutics and prophylactics in human medicine and agriculture. Previous sequencing and classical microbial isolation approaches missed candidate viruses and required intense manual labor. ARS researchers in Madison, Wisconsin, in collaboration with industry partner Phase Genomics, developed a new, automated high-throughput sequence-based method that offers much greater accuracy and reliability in selecting candidate viruses. The method, *ProxiPhage*, developed by Phase Genomics, provides discriminatory power to place a viral genome within a specific bacterial cell, resulting in direct evidence of integration. These findings have also allowed discovery of new viral genomes, several of which may be manipulated for phage-therapy applications that can reduce microbe pathogenicity, such as transferring antimicrobial resistance genes and plasmids with virulence genes into pathogenic microbes. Several clinical research studies have applied this methodology to identify benign microbial hosts that indirectly enable the proliferation of these detrimental alleles to pathogens.

Anticipated product: Enhanced metagenomic characterization and analysis of the gut microbiome to develop better understanding of the relationship between the microbiome and the health, productivity, and environmental impact of food animals.

Farm Genotype-Tissue Expression (FarmGTEx) Consortium and the Cattle Gene Atlas

Understanding the regulation of livestock gene expression underpins the study of biological mechanisms that contribute to economically important traits and animal improvement through selective breeding. FarmGTEx is an international collaboration focused on the development of a comprehensive atlas of tissue-specific gene expression and genetic regulation in farm animals. Co-led by ARS scientists in Beltsville, Maryland, and researchers at the University of Edinburgh, Scotland and 20 other universities and institutes around the world, FarmGTEx built a Cattle Gene Atlas using approximately 12,000 publicly available RNA-sequence datasets that represented more than 100 tissues and cell types from more than 40 cattle breeds. The atlas describes the landscape of RNA expression in the genome and across tissues and identifies variation in gene expression and protein isoform variants for 24 major tissues and 43 economically important traits in cattle. This data portal allows researchers to query gene expression, alternative splicing, and DNA regions associated with economically important traits in an easy, uniform way. FarmGTEx serves as the primary international reference source for cattle genomics, breeding, adaptive evolution, comparative genomics, and veterinary medicine. This research directly addresses the collective quest to enhance efficiency in cattle production and contributes to improvements in the environment, sustainable systems, and consumer expectations of beef and dairy products.

Anticipated product: Better integration of expertise, infrastructure, and genetic and genomic technologies within ARS and with industry and academic partners to facilitate development of comprehensive bioinformatic, metagenomic, and phenotypic databases tools, and technologies to exploit shared resources.

A new method to screen the gastrointestinal microbiome of livestock

The microbiome is the combined genetic material of all microorganisms—such as bacteria, fungi, protozoa, and viruses—that live in a particular environment. ARS scientists in Madison, Wisconsin, and Beltsville, Maryland, led research conducted by an interdisciplinary team of international researchers from four countries and two private United States companies to develop new methods for microbiome screening to identify the organisms present. Using the latest high accuracy, long-read DNA sequencing technologies, microbial strains could be resolved down to single nucleotide variants. More than 44 bacterial genomes were assembled into single, continuous chromosome genomes, which is the greatest number ever achieved in a single sequenced sample; more than 400 viral- and 250 plasmid-host associations were identified. These discoveries represent the highest resolution image of genomic DNA in a gastrointestinal sample, furthering the interpretation of microbiome sequencing discoveries and the future identification of 'high-value' organisms influencing animal efficiency and health.

Anticipated product: Enhanced metagenomic characterization and analysis of the gut microbiome to develop better understanding of the relationship between the microbiome and the health, productivity, and environmental impact of food animals.

Genome assembly of closely related microbes in metagenomic DNA samples

A metagenome is the recovery and sequencing of all genetic material in an environmental sample. Metagenomic assembly is hampered by the presence of multiple bacteria that are closely related in a genome sequence, but can represent different strains, species, or subspecies. Improper assembly reduces the accuracy of linking antibiotic resistance genes to a specific strain or species, and accuracy is essential when potential pathogenic microbes are present along with closely related non-pathogenic organisms. ARS researchers in Clay Center, Nebraska, and university collaborators developed a method to separately assemble genomes from mixed genomic material, even within the same species, while simultaneously providing links to antibiotic resistance genes that reside in the bacteria but that are not integrated into the bacterial chromosome. This new method offers great promise in clinical microbiology and livestock production sectors by enabling sequence-based tracking of strain-level genomes more efficiently and effectively than previous methods. This new method also improves the ability to determine if antibiotic resistance genes are associated with known human or animal pathogens; it also can reduce diagnostic costs and wait times.

Anticipated product: Enhanced metagenomic characterization and analysis of the gut microbiome to develop better understanding of the relationship between the microbiome and the health, productivity, and environmental impact of food animals.

Problem Statement 2B: Characterize Functional Genomic Pathways and their Interactions.

Relationships between rumen physiology and liver abscesses in beef cattle

Beef cattle liver abscesses cost the beef industry approximately $64 million annually. Liver abscesses are caused by bacteria transported from the rumen that subsequently colonize the liver.

ARS scientists in Clay Center, Nebraska, and University of Nebraska-Lincoln collaborators studied genetic variations and gene expression in the cattle rumen and variation in bacterial communities attached to the rumen in cattle with liver abscesses. More than 200 genes, including many genes involved in inflammation and protein translation pathways, were differentially expressed in affected cattle. In addition, the bacterial communities attached to the rumen were different than communities in cattle without liver abscesses. Researchers identified associations between differentially expressed genes and the bacterial species attached to the rumen and wrote the first published study on these relationships. These findings indicate that measuring changes in gene expression may be an effective biomarker for identifying the development of liver abscesses in feedlot cattle and for developing treatments. This groundbreaking discovery will allow additional study of the factors contributing to liver abscess development, provide effective identification of animals susceptible to liver abscesses, and reduce the negative impacts of abscesses on production efficiency and animal welfare.

Anticipated product: Gene targets for the development of additional strategies to beneficially manipulate the environment of the food animal to improve economic traits.

Problem Statement 2C: Preserve, Characterize and Curate Food Animal Genetic Resources.

Germplasm Preservation and Application

Realization of ongoing efforts to establish and utilize resources within the National Animal Germplasm Program (NAGP) collection comes from application in the field, at the producer level. ARS scientists in Fort Collins, Colorado, evaluated germplasm for key genes and genomic information and expanded the size of the banked genetic resource base across livestock industries. Brangus breeders, following identification of the causative mutation for white eye disease, used a single sire's negative genotype and ancestry pathways to trace genetic dispersion within the breed. Knowledge of the gene banked ancestor's negative genotype eliminated the need for expensive, comprehensive gene testing on over 150,000 cattle, saving the industry breeders over $1.5 million. Germplasm preservation also allowed the nation's largest seller of beef bulls (>3,900 annually) to reintroduce 1980s-1990s genetic resources through embryo transfer, allowing the breeder to 'go back' in time and resurrect lines that can offer additional genetic variation, foster innovative genetic selection, and expand opportunities to match genetic resources more closely with environments they best serve. Collaborations with Purdue University and the Livestock Conservancy leveraged ARS Innovation Funds to import, store, and utilize semen from the Large Black breed, resulting in expansion of genetic diversity in U.S. Large Black populations and establish resources for future research to identify key alleles that influence phenotypes.

Anticipated product: A publicly available database providing germplasm sample, phenotypic, and genomic information to industry and the research community.

Problem Statement 2D: Develop and Implement Genetic Improvement Programs using Genomic Tools.

Discovery of an undesirable genetic factor in Jersey cattle

Jersey calves are sometimes born with a congenital condition called Jersey Neuropathy with Splayed Forelimbs (JNS); affected calves are unable to stand on splayed forelimbs and display neurological symptoms. JNS was reported to the American Jersey Cattle Association in Columbus, Ohio, by Jersey breeders. ARS researchers in Beltsville, Maryland, used pedigree and genetic analyses to identify the genetic basis for JNS and the identity of a common ancestor born in 1995. Scientists then tracked inheritance of the JNS defect and the Council on Dairy Cattle Breeding first reported results in December 2020. In January 2021, the American Jersey Cattle Association updated its comprehensive mating program, JerseyMate^{TM}, to include JNS genotype results. Industry will soon have access to ARS software and testing methods that will assist producers as they make mating decisions to reduce the estimated 6 percent frequency of JNS carrier animals in the Jersey breed. Genetic testing and avoiding carrier-to-carrier matings can prevent the birth of about 300 affected calves annually.

Anticipated product: Development of DNA-based diagnostics to provide genotypic information for use in centralized genetic evaluation and improvement systems particularly for novel traits.

Problem Statement 2E: Improved Techniques for Genetic Modification and Genetic Engineering of Food Animals.

none

Component 3: Measuring and Enhancing Product Quality and Enhancing the Healthfulness of Meat Animal Products

Problem Statement 3A: Systems to Improve Product Quality and Reduce Variation in Meat Animal Products.

Muscle metabolism intermediates influence beef flavor development

Beef flavor is the most important factor in determining consumer eating satisfaction of beef products. The role of beef processing strategies and cooking in flavor development has been the subject of extensive research. However, little attention has been paid to the role of inherent animal-to-animal variation in muscle metabolism in the development of beef flavor. ARS scientists in Clay Center, Nebraska, determined that variation in muscle metabolites is associated with both positive and negative flavor attributes in beef strip loin steaks. These findings provide a greater understanding of the mechanisms responsible for variation in beef flavor. Furthermore, these results offer the beef industry genetic selection strategies to improve overall beef flavor and consistency to increase consumer satisfaction and demand, which could add millions of dollars in revenue to the U.S. beef industry.

Anticipated product: Better understanding of the biological mechanisms that control and influence meat product quality, color stability and consistency.

Problem Statement 3B: Improving the Healthfulness and Nutritional Value of Meat Products from Traditional and Non-Traditional Production Systems.

None

NP101 Projects contributing accomplishments to this report:

PROJECT NO.	PROJECT TITLE	CITY	STATE
3040-31430-006-000D	Strategies to Optimize Meat Quality and Composition of Red Meat Animals	Clay Center	NE
5030-31000-006-000D	Reducing Production Losses due to Oxidative Stress and Bacterial Pathogens in Swine	Ames	IA
8042-31000-110-000D	Development of New Technologies and Methods to Enhance the Fertility, Utilization, and Long-Term Storage of Poultry and Swine Germplasm	Beltsville	MD
3040-31000-097-00D	Improve Nutrient Management and Efficiency of Beef Cattle and Swine	Clay Center	NE
3040-31000-095-000D	Improving Lifetime Productivity in Swine	Clay Center	NE
5090-31000-026-000D	Investigating Microbial, Digestive, and Animal Factors to Increase Dairy Cow Performance and Nutrient Use Efficiency	Madison	WI
8042-31000-002-000D	Improving Dairy Animals by Increasing Accuracy of Genomic Prediction, Evaluating New Traits, and Redefining Selection Goals	Beltsville	MD
2056-31610-006-000D	Enhancing Sheep Enterprises and Developing Rangeland Management Strategies to Improve Rangeland Health and Conserve Ecology	Dubois	ID
3096-32000-008-000D	Nutritional Intervention and Management Strategies to Reduce Stress and Improve Health and Well-being in Cattle and Swine	Lubbock	TX
5090-31000-026-000D	Investigating Microbial, Digestive, and Animal Factors to Increase Dairy Cow Performance and Nutrient Use Efficiency	Madison	WI
8042-31000-001-000D	Alternatives to Antibiotics: Developing Novel Strategies to Improve Animal Welfare and Production Efficiency in Swine and Dairy	Beltsville	MD
3040-31000-100-00D	Developing a Systems Biology Approach to Enhance Efficiency and Sustainability of Beef and Lamb Production	Clay Center	NE
3040-31000-096-00D	Applying Developmental Programming to Improve Production Efficiency in Beef Cattle	Clay Center	NE
8042-31000-001-000D	Enhancing Genetic Merit of Ruminants Through Improved Genome Assembly, Annotation, and Selection	Beltsville	MD
3012-31000-006-00D	National Animal Germplasm Program	Fort Collins	CO