

# **National Program 101 Food Animal Production**

## **National Program Annual Report: FY2019**

### **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 \$19.39 trillion. According to the National Agricultural Statistics Service, 2017 Census of Agriculture, 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 broilers and eggs), totaling \$190 billion, which was 1% of gross domestic product. This figure includes animal product sales, and does not include sales associated with allied industries, like animal feeds, farm supplies, breeding companies, and animal health related sales. Along with this 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. Some food animals (cattle and sheep) convert forages (e.g., grasses, alfalfa) that are unsuitable for human consumption, which are grown on marginal lands that are also unsuitable for human edible crop production, into human food products. However, even pigs and poultry convert high energy, protein and nutrient poor plant foods 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 as valuable sources of high quality protein, fatty acids, vitamins and minerals.

Despite these clear contributions, food animal production also has some real challenges. Recent reports draw attention to the potential negative impact of food animal production on the environment, including livestock contribution to greenhouse gas generation, contributions of livestock manure and feed production for livestock to nitrogen and phosphorus contamination of water resulting in algal blooms, degradation of wildlife habitat by livestock, and the contribution of animal wastes to the prevalence of pathogenic and antibiotic resistant microorganisms in the environment. In addition, retrospective diet survey studies (asking people what they remember of what and how much they ate) suggest negative human health outcomes from over-consumption of animal products in the human diet, including incidence of cancer and heart disease. Even though the most recent evidence suggests that the benefits of animal products in the human diet outweigh much of the detrimental effects on human health, particularly in developing countries, these two concerns have been incorporated into the concept of a “sustainable human diet”, which recommends a diet low in animal products. Proponents suggest

that if this “sustainable human” diet were adopted, it would address both livestock induced problems, environmental footprint and human health concerns, simultaneously. Proponents also argue that government should play a role in fostering the broad adoption of this diet. However, the likely effects of such a diet on the livestock industry and the rural economy, and for vast areas of the United States that are unsuitable for anything but raising ruminant livestock, have not been addressed.

Along with environmental concerns, there is a perception that technologies that improve the efficiency of animal production also compromise the health and well-being of food animals. Cages for egg-laying hens reduce bacterial contamination of eggs compared to eggs laid on the floor in group housing. Gestation crates for pregnant sows ensure that each sow is protected from negative interactions with herd-mates, and helps ensure that each sow receives individual attention regarding health problems and needed dietary adjustments. In addition, although use of antibiotics for growth promotion has been banned in the United States by FDA since 2017, some in the international human health arena, e.g. *WHO guidelines on use of medically important antimicrobials in food-producing animals*, have suggested that antibiotics used in human medicine should not be used for disease prevention in food animals. Should the ability to use antibiotics for disease treatment and prevention be restricted, the potential effects on animal well-being would be strongly negative.

Thus, research is needed to improve livestock production efficiency, which would reduce the feed and other environmental resources that are needed for livestock production. Better methods are needed to ensure that raising livestock does not contribute unnecessarily to environmental degradation and contamination. Viable alternatives to antimicrobials in food animal production are also needed, to replace the production efficiencies that these compounds once offered to livestock production. Antimicrobial alternatives research would have two goals: (1) restore the growth improvement that was once available through the use of antimicrobials and (2) reduce disease incidence, to reduce the need for preventive use of antibiotics.

Given the health benefits of food animal products, dramatic improvements in production efficiencies developed by ARS scientists will help ensure international food security and directly impact human health by reducing the real cost of nutritionally valuable animal products, making animal products more available to those populations most in need. 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. Improvements in food animal production efficiencies will reduce food animal wastes. Reductions in the numbers of breeding animals to maintain production reduce the livestock waste environmental footprint. Ongoing improvements in food animal nutrition and other production efficiencies reduce grain requirements and manure production, and science-based animal waste management strategies provide for the beneficial return of animal waste nutrients to the environment. Improvements in production efficiency will reduce microbial pathogen contamination of the environment and greenhouse gas emissions from livestock production systems and ensure that livestock production remains environmentally sustainable.

## **Some standout science**

The Agricultural Research Service provides solutions for agricultural producers, and by extension improvements in the efficiency of food production for consumers within the United States and beyond. The accomplishments provided below are presented in these terms, describing the impact of the accomplishment on the livestock production system and/or consumers. However, ARS scientists also contribute to the human scientific endeavor, and their contributions to science are often not presented, in favor of describing accomplishments in terms of “real world impact”. In this section, A couple of the accomplishments included below are presented in terms of their contribution to science.

The accomplishment entitled “Application of an interspecies cross to improve the efficiency of genome sequencing and assembly” is not only a highly impactful accomplishment for cattle production, it is also a highly impactful accomplishment within genome science. The concept of mating two divergent breeds, e.g. Highland breed cattle and Yak, to produce a hybrid offspring for sequencing and using sequence from both parents as well as the offspring to generate two separate genome sequences from the single hybrid offspring is entirely opposite of the genome sequencing strategy that has been used for genome sequencing for decades. The new strategy produced genome sequences for Highland cattle and Yak in a single experiment that was better than the current human genome in several characteristics, despite nearly two decades of effort on the human genome. Application of this strategy to general genome sequencing promises to rapidly improve genome sequences of many species, and so this accomplishment is likely to have a huge impact on genome science. This breakthrough was made possible by improvements in sequencing technologies, including the generation of both long and short read sequences. Still, our scientists had to realize that a strategy nearly opposite to that used by most scientists might work better, and risk trying it. The freedom within ARS to take scientific risk, with the potential promise of a huge reward, is one of the reasons why this effort was successful and is a strong argument for continued ARS intramurally funded research.

In the accomplishment entitled “DNA sequences of the rumen microbial community and development of a software tool to identify candidate bacterial hosts for viruses in the rumen”, ARS scientists took a conceptually simple straightforward approach to the rumen microbiome, sequence everything and see what is there. As in the accomplishment described above, recent improvements in long and short read sequencing were a component in the success of this work, but the simple concept belies the complexity of the analysis needed to be successful. Many scientists would criticize this type of experiment as a “fishing expedition”, but this is only a legitimate criticism if one fails to “catch anything”. In this case, scientists “caught” the existence of bacterial viruses within the rumen and were able to link the viruses to their microbial hosts. This contributes to microbiome science in that it is likely that bacterial viruses are a component of all microbiomes. It also suggests a way in which the microbiome may be manipulated, either by using viruses to alter bacterial content of the microbiome directly, or by using viruses as vectors to introduce genes into various microbes within the microbiome. Here again, part of the success of this experiment was the freedom within ARS to try something that required long term investment without certainty of the outcome. The contribution of bacterial viruses to microbiome

function, and to the ability to manipulate the microbiome, was an unexpected result that currently impacts microbiome science, and could have a huge impact on being able to beneficially control microbiomes in general.

### **Some future directions**

Animal genomics is a major emphasis of the Food Animal Production National Program. Much of our work up to now has been focused on exploiting the additive genetic component of traits in various livestock species using sophisticated genomic technologies. The best example of this in livestock is dairy cattle, where the structure of the industry in the United States, along with relatively high individual animal value and long generation intervals, have combined to make genomic selection very successful. Research to add useful traits to dairy selection indices, and fully implement additive genomic selection in other livestock species will continue to be a focus going forward. But we will also need to go beyond additive genetic selection to incorporate interactions between environmental characteristics and the additive genetic component, to be able to best fit animals to their environment. Some work in this area has already been done, but much more is needed. In addition, we also need to go beyond the additive genetic component of inheritance and include components like epigenetics and heterosis in our selection methods. Fifty percent of beef cattle, and nearly all swine and poultry in the United States, are crossbred animals. Crossbreeding is done to take advantage of heterosis, which is the improvement in a trait that results from dominant effects of some gene alleles on other gene alleles at various genetic loci. It should be possible to optimize heterosis using genomic technologies, and research is needed to explore this possibility.

It has been typical of livestock research to consider the animal as a single individual, interacting with its environment, and controlled by its individual genome. However, it has always been true that individual animals exist as a collection of organisms consisting of the individual and its microbiome, and it is only recently that we have technologies that can address this fact. We have ongoing research in all livestock species to measure the effect of the microbiome on the function of the individual, and its consequences for health and production efficiency. This report describes two accomplishments in this area, one for the microbiome of the rumen in cattle and one for the mycobiome (fungal) in weaned piglets. In the future, scientists will begin to manipulate the microbiome in beneficial ways, to increase feed efficiency, reduce pathogens, and reduce environmental impacts of livestock. Methane production by cattle falls into this last category. Methane is entirely a product of the cattle microbiome, and not only represents a potent greenhouse gas, it also represents wasted feed energy. Although it is likely to be challenging, our future goal will be to reduce cattle methane production to zero, adjusting the microbiome so that the feed energy that is currently lost to methane production will be incorporated into energy in the cow, without decreasing feed intake or growth rates of cattle.

Raising livestock is labor intensive. The production systems in which many of our food animal species are raised continue to grow larger, because the fixed costs of an operation are more economically distributed over larger numbers of animals. Expanding animal numbers and labor expense can combine to reduce the ability to optimally manage every animal. To make the production system work, farmers manage for the average animal, or manage so that a high

percentage of the animals can produce optimally. The former results in reduced production of animals needing more resources, and the latter results in significant overapplication of resources to underperforming animals. Improvements in electronic technologies over the last 40 years are now beginning to make it feasible to monitor and manage individual animals to reduce these inefficiencies. To make this a reality, new sensors, data infrastructure, and decision support tools are needed. Data handling capabilities have been increasing by 10-fold every 5 years over the last 4 decades and will likely continue at this rate, so what is not feasible now may be easy in 20 years. To take full advantage of these changes, research is needed now to develop the individual precision livestock methods that will lead to the greatest improvements in livestock management.

### **Program staffing, funding, and collaborations**

During FY 2019, National Program 101 (NP 101) had 75 full-time scientist positions working at 14 locations across the United States on twenty-six appropriated research projects. In fiscal year 2019, appropriated funding for NP101 was \$51 million; and total funding was \$54 million including extramural awards. Three new inventions were disclosed and 1 patent awarded. Additional technology transfer included eight Material Transfer Agreements.

### **In 2019 NP 101 scientists participated in research collaborations with scientists in:**

Australia, Austria, Brazil, Canada, Chile, China, Denmark, France, India, Ireland, Israel, Italy, Malawi, Mexico, Mongolia, Netherlands, New Zealand, Nigeria, South Africa, Spain, Sweden, Switzerland, Uganda and United Kingdom.

### **Outreach Activities:**

#### **Students working with ARS Scientists and Scientist Academic Outreach**

Undergraduates	Graduates	Post-Docs	Scientist Advisors	Mentors	Adjunct Professors/Other
27	56	13	35	20	32

#### **ARS Animal Production Program: Student-Related Outreach Activities**

	Presentation to Schools	Science Fair Participation	Student Tours/Visits to ARS Locations
Number of Activities	3	3	31
Number of Students	52	110	900

#### **Animal Production Program General Outreach to Stakeholders and the Public**

Name of Activity	Number of Activities	Number of Participants
Field Day	1	550
Tours	14	157
Presentation to Local/Community Groups	5	527

Training/Demonstration	5	98
Webinars	1	354
Presentation to Other Scientists	7	2045
Presentation to Practitioner/Industry/Producer	5	176
Workshops	1	50
Stakeholder Meetings	3	124
Laboratory Review	1	4

**New scientists in NP 101 2019:**

**Dr. Ahmed Al-Khudhair**, Post-Doctoral Fellow, joined Animal Genomics and Improvement Lab, Beltsville, Maryland.

**Dr. Mahesh Neupani**, Post-Doctoral Fellow, joined Animal Genomics and Improvement Lab, Beltsville, Maryland.

**Dr. Juan Nani**, Post-Doctoral Fellow, joined Animal Genomics and Improvement Lab, Beltsville, Maryland.

**Dr. Tom Murphy**, Research Geneticist, joined US Meat Animal Research Center, Clay Center, Nebraska.

**The following scientists retired in 2019:**

**Dr. Chadwick Chase**, Research Animal Scientist, Nutrition and Environmental Management Research Unit, Clay Center, Nebraska.

**Dr. Susan Eicher**, Research Physiologist (Animals), Livestock Behavior Research, West Lafayette, Indiana

**Dr. Mark Petersen**, Research Leader and Range Livestock Nutritionist, Fort Keogh Livestock and Range Research Laboratory, Miles City, Montana.

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

**The following scientists accepted new positions outside of ARS:**

**Dr. Tami Brown-Brandl**, Agricultural Engineer, U.S. Meat Animal Research Center, Clay Center, Nebraska, accepted a position with the University of Nebraska.

**Dr. Kristin Hales**, Research Animal Scientist, U.S. Meat Animal Research Center, Clay Center, Nebraska, accepted a position with Texas Tech University.

The distinguished record of these scientists is recognized world-wide and it is hoped that productive collaborations will continue with ARS scientists.

### **The following scientists in NP 101 received prominent awards in 2019:**

**Dr. Terrance Arthur**, received the Technology Transfer Award from the Federal Laboratory Consortium in recognition of outstanding efforts in transferring federally developed technology into commercial usage.

**Dr. Jeff Carroll**, received the Distinguished Service Award from the American Society of Animal Science for outstanding service to the livestock industry.

**Dr. Anthony Capuco**, had an entire lactation symposium titled “The Lactation Biology Symposium” held in his honor at the 2019 American Dairy Science Association Annual Meeting.

**Dr. Kristin Hales**, received the Mid-West American Society of Animal Science Outstanding Young Researcher award.

**Dr. Nicole Sanchez**, received the 2019 Outstanding Young Alumni Award by the Texas A&M University’s Department of Animal Science.

**Dr. Steven Shackelford**, received the American Society of Animal Science Meats Research Award for Outstanding Career in Meat Research and contributions to the industry.

**Dr. Paul VanRaden**, received the Zinpro Award for excellence in Dairy Science from the American Dairy Science Association.

**Dr. Tommy Wheeler**, received the Technology Transfer Award from the Federal Laboratory Consortium in recognition of outstanding efforts in transferring federally developed technology into commercial usage.

### **Major Accomplishments in 2019**

This section summarizes significant research results for Fiscal Year 2019 that addressed specific components and anticipated products of the 2018– 2022 Action Plan for the Food Animal Production National Program. Within each section, selected accomplishments of individual research projects in NP 101 are presented. These 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 NP101 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**

#### **Characterization of the porcine mycobiome (fungus).**

For young piglets, the transition from milk to solid feed (weaning) is a period of stress, dietary changes, and a predisposition to gastrointestinal problems including diarrhea, which affects their growth and welfare. The microbial organisms found in the gastrointestinal tract of animals is recognized as a critical component of host health and gut function. To understand the role of fungal microorganisms in gut health during this period, ARS scientists at Beltsville, Maryland, performed the first in-depth analysis of fungal microorganisms present in the gastrointestinal tract of piglets during the period between birth and transition to post-weaning life. Results demonstrated a dramatic increase in fungal populations at the time of weaning, with a dominance of the fungus, *Kazachstania slooffiae*. This increase in the fungal microorganisms in piglets has not been previously reported and suggests that milk may suppress fungi in the gut until weaning. Furthermore, the consequences of the dramatic onset of fungal microorganisms in the gut after weaning is not known, but the trajectory of fungal development could influence future immune competence. Thus, further research could be helpful in producing future interventions and dietary modifications to enhance piglet performance, reduce disease and increase the productivity of the swine herd.

**Anticipated product: Comprehensive characterization of digestive system microflora in livestock species, including the organisms present and their prevalence, and identification of those species that are correlated with improved performance, nutrient utilization efficiency, and reduced environmental impact.**

#### **A new equation to improve estimates of feed metabolizable energy in beef cattle.**

It is important to know the metabolizable energy of feed in order to accurately determine the feed requirements of animals, to ensure that diets adequately meet the energy needs of animals for optimal growth. Measuring metabolizable energy in ruminants is time consuming and expensive and requires the measurement of energy in the feed, feces, urine, and released methane, the last being technically difficult to measure. Developing mathematical relationships between digestible and metabolizable energy allows for the prediction of metabolizable energy and reduces the cost associated with getting estimates. Historically, a constant of 0.82 has been used; however, recent literature suggests that the relationship between digestible and metabolizable energy is variable depending on the type of diet used and is typically greater than



0.90 when high-concentrate diets are fed. ARS scientists at Clay Center, Nebraska, developed and evaluated a new equation for estimating metabolizable energy from digestible energy on 234 beef cattle from several studies. Results indicated that the historical 0.82 constant normally used corresponded to diets with digestible energy of 2.2 megacalories per kg, and the constant rises to 0.91 at 3.78 megacalories per kilogram of digestible energy, and then levels off at greater DE concentrations. These data indicate that the relationship between digestible energy and metabolizable energy is not static, especially in high-concentrate diets. The use of the 0.82 constant for high digestible energy diets underestimates the metabolizable energy of these diets, potentially leading to over-feeding of energy in the diet. Use of the equation is expected to more correctly predict metabolizable energy in high energy diets, reducing feed levels needed for adequate metabolizable energy and saving feed costs.

**Anticipated product: Precision feeding systems for livestock and poultry that optimize nutrient availability to the animal while minimizing nutrient losses to the environment.**

#### **Problem Statement 1B: Improving Reproductive Efficiency**

**Blood vessel size and dilation of blood vessels supplying the boar testes are heritable.**

The blood vessels outside of each testis, known as the pampiniform plexus, provides blood to the testis, and acts to maintain appropriate testicular temperature for efficient sperm production. When these vessels are abnormally enlarged or contain lesions, a condition known as varicocele, blood flow and heat exchange are impaired. This condition occurs in humans and contributes greatly to infertility, however in swine, less is known about this condition. An ARS scientist at Clay Center, Nebraska, along with University of Nebraska researchers, using ultrasonography, measured the right and left pampiniform plexus vessel area and determined the presence of varicocele in a large population of young boars. They further derived the degree to which vessel area and varicocele is an inherited trait. Pampiniform plexus vessel size was highly heritable while the presence of varicocele was moderately heritable. These data suggest that the incidence of testicular blood vessel enlargement in boars exists and may influence fertility of individual boars. Results also suggest that the size of the pampiniform plexus could be influenced by selection, thereby potentially improving fertility characteristics of breeding boars, which would lead to improved economic and animal production efficiencies for pork producers.

**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**

**Development of a model to predict illness using swine feeding behavior.**

Recognizing sick pigs in a modern production environment takes animal husbandry experience combined with diligence in observing the animals. Thus, properly assessing pig health is a skilled, labor-intensive activity, and these skills are harder and harder to find. As a possible solution, automated measurement of feeding patterns of pigs were investigated for

utility in identifying sick animals within a herd. Feeding behavior is dependent on many factors including breed, temperature, humidity, gender, and time of day, but feeding is also a good proxy for an animal's health. As an animal gets sick, feed consumption often drops off, even before diagnostic symptoms appear, like fever or difficulty breathing. Machine learning is a type of artificial intelligence that can change and adapt when exposed to new data. ARS scientists at Clay Center, Nebraska, and collaborators at South Dakota State University, used an electronic system to monitor the feeding behavior of pigs during the grow-finishing phase and applied machine learning tools to predict swine feeding behavior based on temperature and time of day. Large deviations between predicted and observed feeding behavior prior to an outbreak of pneumonia demonstrated the potential for this technology to be used in automated early detection of a disease outbreak and/or other stressful events. Future work is expected to lead to the development of software tools that will allow swine producers to utilize real-time feeding behavior data as an early predictor of illness and stress events at the individual animal level, improving both animal well-being and productivity and freeing up labor for other activities. This is an excellent example of the potential benefits of continuous monitoring of livestock for beneficial outcomes in animal health and production.

**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.**

#### **Determination of the thermal preferences of sows.**

Heat stress in pigs reduces welfare, feed intake and growth rates, but there are no current ambient temperature recommendations for gestating sows. Swine temperature threshold recommendations provided by the *Guide for the Care and Use of Agricultural Animals in Research and Teaching* (AgGuide) are based on data that are over 30 years old and likely do not represent the thermal preferences of modern commercial swine, which grow faster and are larger. ARS scientist in West Lafayette, Indiana, performed a study to determine what temperatures sows at three reproductive stages (open, mid-gestation, late-gestation) preferred. In order to determine thermal preference, we designed and constructed two temperature gradients in which sows could choose the temperature at which they wanted to spend the most time. Using these gradients, it was determined that sows preferred temperatures ranging from 13 to 16°C, with late-pregnant sows preferring temperatures at the lower end of the range compared to non-pregnant and mid-pregnant sows. These data indicate that current recommendations for pregnant sows should be updated to reflect the genetic and metabolic improvements of modern swine.

**Anticipated product: Enhanced understanding of genetic, physiological, immunological, microbial and behavioral responses of food animals to management and environmental stressors.**

#### **The use of non-linear measures of heart rate variability may be useful to assess pain in swine.**

The measurement of pain is essential to assess the welfare of animals in various production environments. If pain can be accurately assessed, then management procedures or

production environments that minimize pain can be developed and employed. However, pain is difficult to assess in livestock, because animals are evolutionarily adapted to hide outward signs of pain. ARS researchers in West Lafayette, Indiana, investigated several novel methods of heart rate variability analysis when pigs were subjected to castration. Two measures of heart rate variability were specifically enlightening to distinguish pain from the mere stress of handling. These results are expected to provide researchers with a more advanced procedure to determine which procedures are less painful. An objective method of pain assessment in pigs will be useful in the development of methods that decrease pain and increase animal welfare.

**Anticipated product: Objective, science-based criteria for assessment of animal stress and well-being in production systems in response to various management techniques.**

## **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.**

#### **Application of an interspecies cross to improve the efficiency of genome sequencing and assembly.**

The genome sequence can be used to enhance genetic selection, and perform comprehensive gene expression and protein measurements, but the quality of the genome sequence is directly related to its utility for these purposes. The importance of the quality of the genome sequence is reflected in the fact that the first draft of the human genome was published in 2001, and there have been 38 versions (improvements) of the sequence in the 18 years since first publication. A new method for assembling genetic sequencing data into more complete genomes has been pioneered by ARS researchers in Clay Center, Nebraska, and Beltsville, Maryland, in collaboration with the National Institutes of Health, University of Nebraska, and University of Kentucky. Using the new process, an individual animal resulting from the mating of a Highland breed bull and a yak cow was used to create reference-quality assemblies of the Highland breed of cattle and the yak in a single experiment. By applying the new technique, called “trio binning” to an interspecies hybrid that maximized the difference between maternal and paternal chromosome sequences, the researchers created individual sequences for both the yak and cattle. The sequences were of equal or better quality than any currently existing mammalian genome assembly (including that of human). The technique to generate two complete high-quality genome sequences from a single individual in a single experiment will rapidly bring the genome sequences of livestock species up to a quality that is equivalent to or surpasses that of the current human genome, which took 18 years to accomplish. This will improve genomic selection and gene and protein measurement technologies for livestock species.

**Anticipated Product: Improved annotation of genome sequence assemblies for food animals, including participation in the Functional Annotation of Animal Genomes consortium (FAANG-this international consortium strives to understand how gene expression is controlled in different tissues, under**

**different conditions. Results generated will provide DNA regions where changes in sequence are likely to affect gene transcription, and therefore cause changes in production traits).**

### **DNA sequences of the rumen microbial community and development of a software tool to identify candidate bacterial hosts for viruses in the rumen.**

It is said that one does not feed a cow, one feeds the rumen of a cow, and the microorganisms that eat the feed in the rumen then feed the cow. Thus, this relationship is extremely important to the efficiency of feed usage by the cow, and we are still learning important details of the complex microbial community within the rumen. Using cutting edge software and the latest DNA sequencing methods, ARS scientists in Madison, Wisconsin, in collaboration with scientists at Clay Center, Nebraska, and Beltsville, Maryland, were able to assemble 103 independent genome sequences from the bacteria and archaea microorganisms in the cattle rumen. Additionally, a total of 188 novel bacteria-virus interactions were identified from this dataset, representing the first high resolution exploration of the activity of bacterial viruses in the rumen of cattle. Finally, the new assembly methods pioneered by ARS scientists allowed identification of 94 antimicrobial-resistance genes within the genomes of rumen bacteria. The complete genomes of microorganisms within the rumen provide a catalog of metabolic enzymes that could potentially degrade feed that can be exploited to improve feed efficiency. Also, based on the viral-bacterial host results, there is the potential to design custom viral vectors with exogenous metabolic genes to modify rumen bacteria to manipulate feed usage and increase production. Finally, this study identified more antibiotic resistance genes in the rumen microbiota than previously detected and will be of use in ongoing efforts to document the effects of antibiotics in animal feed.

**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.**

### **SowPro90, a high-density genotyping platform for swine containing functional variants.**

High-density genotyping methods in swine rely on evenly-spaced single base changes (SNP) within the genome sequence that are chosen to provide the optimum measure of differences between animals. These genetic variants are assigned effects based on data and analyses (i.e., training) collected from ancestors of the population in which one would like to select. However, these SNPs typically do not directly cause differences in traits, so their utility in genomic selection is confined to the population used for training. To create a more useful genotyping method, several thousand SNP predicted to significantly and directly alter the proteins coded by the genes were identified, increasing the likelihood that the variants cause changes in traits. ARS scientists at Clay Center, Nebraska, in collaboration with University of Nebraska scientists, created a genotyping product for swine that contains >90,000 SNP, targeting over 4,000 genes and containing 676 loss of function variants (predicted to truncate or eliminate the resulting protein produced by the gene). Gene targets were further selected from genome-

wide association studies of reproductive traits and disease resistance to further enhance the utility of the genotyping platform. This genotyping product provides swine producers with a powerful new tool for genetic marker informed selection based on functional variants for critically important traits of high pork industry priority.

**Anticipated product: Development of comprehensive intensive and extensive phenomic and analytical tools to relate genomic and phenotypic data for development of improved genome based estimates of genetic merit including well-characterized and deeply phenotyped ARS, field and other research food animal populations.**

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

**First global map of gene regulatory elements in cattle and definition of their coordinated activities.**

Traits like feed efficiency are partially controlled by how much a gene is expressed, and both increased and decreased expression of a particular gene can have profound effects on a trait. There are several techniques that can determine regions of DNA that control gene expression in a given tissue, and this information is essential for being able to predict the effects of DNA changes on traits in livestock. Using state-of-the-art technologies to detect regions of DNA sequence that affect expression of genes, ARS scientists in Beltsville, Maryland, discovered DNA regions that affect gene expression in rumen epithelial primary cells and rumen tissues during a maturation process in which the cells and tissues transitioned to greater capability to absorb nutrients. Because these tissues absorb nutrients from the rumen during the digestion and fermentation of feed, changes in gene expression within these tissues during maturation likely affect feed efficiency. This information is needed to predict how changes in DNA sequence might affect gene function and economically important traits, such as feed efficiency. This mapping of regions affecting the cattle genome will be used by researchers worldwide to enhance genomic selection in beef and dairy cattle.

**Anticipated product: Information relating the function and regulation of individual genes and their interaction with environmental and epigenetic effects contributing to economically important traits in food animals.**

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

**Developed genetic and reproductive technologies for under-served pig and sheep producers.**

Rare breeds of livestock are typically raised by producers who are often under-served and minorities. The nexus of producer expertise, appropriateness of technology, and potential biological differences limit ARS capacity to collect germplasm and employ genetic techniques needed to maintain genetic diversity. To assist producers and this important segment of the animal industry, ARS scientists in Fort Collins, Colorado, sponsored workshops for sheep and

Large Black pig producers. Sheep workshops focused on transferring basic information on reproduction and the implementation of non-surgical artificial insemination. The Large Black pig workshop, supported by ARS Innovation Funds, addressed reproductive technologies and breeding plans to enhance the breed's genetic diversity. In preparation for this workshop, collaborative research with Purdue University evaluated artificial insemination. This research showed insignificant differences in ovulation time in Large Black pigs demonstrating to Large Black pig producers the feasibility of artificial insemination. Our research also suggests the breed has sufficient genetic diversity so as not to be an impediment to production. To transfer this knowledge, a blueprint for breeders was developed cooperatively with stakeholders and distributed to this under-served producer group.

**Anticipated product: A broad spectrum of genetic diversity in the form of viable and well documented livestock and poultry germplasm conserved.**

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

**National genomic evaluations for crossbred dairy cattle.**

Some dairy producers turned to crossbreeding to increase genetic diversity and reverse the decrease in reproductive fertility that was associated with selection for increased milk production in purebred dairy cows. However, current genomic evaluations are for purebred Holstein and other dairy breeds. For these producers, genomic evaluations were needed that could account for the crossbreeding within their herds. Although producers had spent more than \$1 million to genotype more than 50,000 crossbred animals, they had no tools to test and select their whole herds based on genomic evaluation. In collaboration with the Council on Dairy Cattle Breeding (CDCB) and Sao Paulo State University, ARS researchers in Beltsville, Maryland, developed genomic evaluations for crossbred dairy cattle based on animals' breed composition for the five dairy cattle breeds routinely evaluated (Holstein, Jersey, Brown Swiss, Ayrshire, and Guernsey). The new evaluation methodology was adopted by CDCB, and national genomic evaluations for crossbreds were released to the dairy industry for the first time in April 2019. Those evaluations will aid commercial producers in managing their breeding programs and selecting tens of thousands of replacement heifers each year.

**Anticipated product: Genetic prediction tools for traits in food animals related to health, production efficiencies, adaptability, and functionality in varied domestic and international production systems.**

**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.**

##### **Increases in pork carcass weight will improve tenderness of pork loin chops.**

Historical trends indicate the size of U.S. hogs is likely to continue to increase, thus, ARS scientists at Clay Center, Nebraska, collaborated with the University of Illinois and Kansas State University to determine the effect of increased carcass weights on pork quality. Results indicated that the heaviest group of carcasses weighed 36% more than the industry average and given current increasing weight trends, represents the expected average carcass weight by 2050. The increased carcass weight resulted in slower rates of loin muscle chilling when carcasses are cooled after slaughter. This, in turn, resulted in loin chops that retained more moisture during cooking and were more tender and juicy. Carcass weight had minimal effect on other pork quality traits including lean color and marbling. These results show that continued improvement in production efficiency through selection for growth in pigs resulting in heavier market weights will improve eating quality of pork chops.

**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:

<b>PROJECT NO.</b>	<b>PROJECT TITLE</b>	<b>CITY</b>	<b>STATE</b>
3012-31000-006-00D	National Animal Germplasm Program	Fort Collins	CO
3040-31000-095-00D	Improving Lifetime Productivity in Swine	Clay Center	NE
3040-31000-097-00D	Improve Nutrient Management and Efficiency of Beef Cattle and Swine	Clay Center	NE
3040-31000-099-00D	Identifying Genomic Solutions to Improve Efficiency of Swine Production	Clay Center	NE
3040-31000-100-00D	Developing a Systems Biology Approach to Enhance Efficiency and Sustainability of Beef and Lamb Production	Clay Center	NE
3040-31430-006-00D	Strategies to Optimize Meat Quality and Composition of Red Meat Animals	Clay Center	NE
5020-32000-013-00D	Protecting the Welfare of Food Producing Animals	West Lafayette	IN
5090-31000-026-00D	Investigating Microbial, Digestive, and Animal Factors to Increase Dairy Cow Performance and Nutrient Use Efficiency	Madison	WI
8042-31310-078-00D	Improving Feed Efficiency and Environmental Sustainability of Dairy Cattle through Genomics and Novel Technologies	Beltsville	MD
8042-31000-002-00D	Improving Dairy Animals by Increasing Accuracy of Genomic Prediction, Evaluating New Traits, and Redefining Selection Goals	Beltsville	MD
8042-31440-001-00D	Alternatives to Antibiotics: Developing Novel Strategies to Improve Animal Welfare and Production Efficiency in Swine and Dairy	Beltsville	MD