

National Program 101 Food Animal Production National Program Annual Report: FY2011

Introduction

The USDA-ARS National Program for Food Animal Production had a productive and dynamic year in 2011. Notable highlights include the retrospective scientific review for NP101. The program review went very well with NP101 receiving excellent marks for research programming and accomplishment in the core areas of priority for the food animal industries. Other highlights of note included hosting a very successful national stakeholder meeting which brought stakeholders and the NP101 research community together to prioritize the scope and direction of research in NP101 and to discuss current and future areas of impact for the food animal industries. These efforts are documented online at:

http://www.ars.usda.gov/research/programs/programs.htm?NP_CODE=101

Included on this site are the *Retrospective Review Panel Executive Summary*; the *2011 Workshop Program and Summary*; and the *FY2013-FY2018 Action Plan* for NP101 which will direct the next 5 years of research in NP101 starting October 1, 2012.

Food animal products fill a vital role in the diets of people around the world as valuable sources of high quality protein, fatty acids and minerals. The dramatic improvements in production efficiencies developed and harvested by ARS scientists help ensure international food security and directly impact human health and obesity by reducing the real cost of nutritionally valuable meat animal products, making animal products more available to those populations most in need. Ongoing improvements in production efficiencies also continually lessen the environmental impact of meat animal production by reducing grain and forage requirements and lessening the amount of manure produced. These improvements have dramatically reduced the amount of green house gas emissions produced by livestock and will continue to have impact.

The scientific accomplishments of the USDA Agriculture Research Service and National Program 101 are truly remarkable and were again well documented in 2011. NP 101 scientists continue to make inroads toward a better understanding of food animal production challenges relating to genomic discovery science and application, growth and production efficiency, lifetime productivity, animal well-being, environmental adaptation, product quality, reduction of feed and energy inputs, enhancements in energy retention, and reduction of environmental impact. Application of technologies developed or enhanced by NP 101 scientists promise to continue to address the high priority issues for consumers while enhancing the profitability and competitiveness of food animal producers across the USA in today's very competitive global agriculture community.

During 2011, 91 full-time scientists working at 17 locations across the US were actively engaged in 32 research projects in the program. Research projects in NP 101 were approved through the ARS Office of Scientific Quality Review in 2007, making this the fourth year of implementation of these five-year project efforts. The gross fiscal year 2011 funding for NP101 was \$ 49,680,000.

Personnel in NP 101

New additions to the NP 101 team in 2011 are:

David Parker, U.S. Meat Animal Research Center, Clay Center, Nebraska

The following scientist retired from the ranks in NP 101:

John Nienaber, U.S. Meat Animal Research Center, Clay Center, Nebraska

The distinguished record of service of **John Nienaber** is recognized world-wide and he will be missed in NP101.

The following scientists in NP 101 received prominent awards in 2011:

Eduardo Casas, Ames, Iowa, (formally in Clay Center, Nebraska) received the *Bouffault International Animal Agriculture Award* for distinguished service to animal agriculture from the American Society of Animal Science.

Hans Cheng, East Lansing, Michigan received the *2011 Embrex Fundamental Research Award* given by the Poultry Science Association.

Larry V. Cundiff, (retired), Clay Center, NE, received the *Morrison Award* from the American Society of Animal Sciences. The Morrison Award is ASAS' most prestigious award.

Gary J. Hausman, Athens, GA, was selected as an *ASAS Fellow* by the American Society of Animal Science.

David "Andy" King, Clay Center, NE, received the *American Meat Science Association Achievement Award* for outstanding research and service to the livestock and meat industries.

Mike MacNeil, Miles City, Montana received the *Pioneer Award* from the Beef Improvement Federation.

Mike MacNeil, Miles City, Montana received the *Rockefeller Prentice Award* in Breeding and Genetics from the American Society of Animal Science.

H. Duane Norman, Beltsville, Maryland received the *Distinguished Service Award* from the American Dairy Science Association.

H. Duane Norman, Beltsville, Maryland received the *Distinguished Service Award* from the Northeast American Dairy Science Association – American Society of Animal Science.

H. Duane Norman, Beltsville, Maryland was named the *World Dairy Expo's Industry Person of the Year*.

Paul Van Raden, Beltsville, Maryland received the *Journal of Dairy Science Most Cited Award* from the American Dairy Science Association.

Gary Rohrer, Tim Smith, Ralph Wiedmann and Dan Nonneman, Clay Center, NE and **Curt Van Tassell**, Beltsville, MD led an international consortium to develop a 50K Porcine beadchip which was selected as an *Excellence in Technology Transfer Award* for the Mid-continent region of the Federal Laboratory Consortium.

The quality and impact of NP 101 research was further evidenced in 2010 by following:

- Over 150 refereed journal articles published
- Over 100 invited presentations at national and international symposia
- Application for one new patent
- Fourteen new cooperative research and development agreements with stakeholders
- Thirty two new scientific technologies developed relating to genomics and other research, and
- Administration or development of 13 web sites for academia or stakeholders

In 2010 NP 101 scientists participated in research collaborations with scientists in: Australia, Brazil, Canada, China, Denmark, France, Germany, Ghana, India, Iraq, Ireland, Israel, Italy, Kazakhstan, Kenya, Mexico, Netherlands, New Zealand, Pakistan, Romania, Russia, Scotland, South Africa, Spain, Sweden, Switzerland, Tunisia, Turkey and United Kingdom.

Accomplishments in 2011

This section summarizes significant and high impact research results which address specific components of the FY 2008 – 20012 action plan for the Food Animal Production National Program. Each section summarizes accomplishments of individual research projects in NP101. Many of the programs summarized for FY 2011 include 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 to ensure international food security by rapidly disseminating technology which enhances the productivity and efficiency of meat and milk production. Improved production efficiencies decrease the real cost of food and animal products and make these products more available to people worldwide.

Five new lethal recessive defects that reduce dairy cow fertility

Lethal recessive defects that cause embryo loss are difficult to detect without genomic data even with very large sets of phenotypic and pedigree data because of too few observations per estimated mating interaction. Based on genomic testing, ARS scientists in Beltsville, MD developed a method to discover lethal defects by detecting the absence of haplotypes (a set of single nucleotide polymorphisms associated on a single chromosome) that had high population frequency but were never homozygous in the population. Haplotype testing revealed 5 new (3 in Holsteins, 1 in Jerseys, and 1 in Brown Swiss) as well as 2 previously known defects, consistent with the presence of a lethal recessive. The carrier genotypes exist in the three populations at levels from 2.7% to more than 20% indicating that there is opportunity to significantly improve conception rates and reproductive efficiency in dairy cattle, which is a very high industry priority. This research was the first ever documented in human or animal genomics to utilize deep Mendelian sampling of commercial data for biological discovery, and a combined use of high density genotyping, haplotyping, resequencing, and low density validation genotyping technologies in the analysis. Once animals have been genotyped, dairy farmers can now avoid mating carrier animals, increasing profitability, and reducing those defects in the population. The

results of this research are already being incorporated by the dairy industry to inform breeding programs and improve reproductive performance.

Copy number variation explored in dairy cattle

Copy number variation (CNV) is a form of genetic variation in mammalian genomes due to varying numbers of specific alleles in an individual due to deletions or duplications of genetic material. Copy number variations (CNVs) are gains and losses of genomic sequence between two individuals of a species. While not yet well understood, CNV has been estimated to account for 100 to 1000 times more variation in a population than point mutations. CNVs also impact a higher percentage of genomic sequence and have potentially greater effects, including the changing of gene structure and dosage, altering gene regulation and exposing recessive alleles. Early work in humans through genome-wide association studies have associated CNVs with diseases such as intellectual disability, autism, schizophrenia, neuroblastoma, Crohn's disease, and severe early-onset obesity. Research by ARS scientists in Beltsville, Maryland, indicates that CNV variation may be associated with animal performance for many traits relating to health and production. In dairy cattle ARS scientists have identified 682 candidate copy number variations (CNV) regions, which represent ~4.60% of the genome. Many CNV regions (~56%) overlap with cattle genes (1,263), which are significantly enriched for immunity, lactation, reproduction, and nutrition. ARS scientists also reported an initial analysis of CNV in cattle selected for resistance or susceptibility to intestinal nematodes and identified 20 CNV in total. Further analyses indicated that annotated cattle genes within these variable regions are particularly enriched for immune function. These results provide a valuable foundation for future studies of gene variants underlying economically important health and production traits.

Potential major cause of reproductive failure in beef cattle found

Feed and care for unproductive cows that fail to achieve pregnancy is a major cost in beef production. A test capable of identifying young cows with low likelihood to conceive and produce a live calf would have a substantial impact on the efficiency of beef production. During a study to identify genes producing variation in reproductive efficiency, ARS researchers at Clay Center, Nebraska, discovered that as many as 30% of cows that had low success achieving pregnancy appeared to carry portions of the male-specific Y chromosome. Since only bulls are expected to have the Y chromosome, this research suggests transmission of Y chromosome to female offspring (via a chromosomal crossover event) may be a significant contributor to reproductive failures. This discovery will now be used to develop a test that identifies beef heifers and cows which should not be used for breeding. A robust test for Y chromosome in beef cattle breeding herds that improves reproductive efficiency will lead to improved reproductive efficiency and lower production costs that will increase economic returns to producers, lower beef prices, and enhance beef exports.

Genetic variation determined that is associated with important diseases of beef cattle

Respiratory disease, foot rot, and pinkeye are high impact diseases of beef cattle that increase the cost of production and reduce animal well-being. New DNA technology makes it possible to identify genes in cattle associated with susceptibility or resistance to these diseases. ARS researchers in Clay Center, Nebraska, used this technology to identify areas on six different chromosomes associated with the occurrence of these common and expensive diseases of cattle. This discovery will allow development of specific DNA tests targeting susceptibility to these diseases and determine whether DNA-based selection can reduce the incidence of these diseases in beef cattle. Breeding for reduced susceptibility to common diseases would enhance animal well-being and production efficiencies, while reducing the

need for antibiotic use in beef cattle and improving the profitability and competitiveness of the beef industry.

Rapid chilling of pork carcasses reduces the tenderness of pork loin chops

Very rapid chilling of pork carcasses has been widely adopted by the pork industry as a means to improve throughput, food safety, and color attributes of pork products. However, decreased tenderness has been identified as a source of consumer dissatisfaction with pork products. ARS scientists at Clay Center, Nebraska, have demonstrated that pork loins produced in plants using rapid chilling systems are significantly less tender and subject to much larger variations of tenderness than those produced in plants using conventional chilling systems. This research identified very rapid chilling as a large contributor to pork tenderness variation. These results led the National Pork Board and industry to initiate a cohesive research collaboration led by ARS to find solutions to this problem.

Sows which were not previously housed beside one another make better group mates

The largest single challenge of keeping sows in groups is aggression. Increased aggression increases the incidence of injury, increases costs and reduces production efficiencies and profitability for producers. Sows typically fight to varying degrees when mixed but there is little information on the effects of pre-exposure prior to mixing. The swine industry is challenged to address these issues as more sows are being housed in groups rather than individual stalls in commercial production facilities. ARS researchers in West Lafayette, Indiana, studied a method of introducing sows intended to decrease aggression. This method relies on 'pre-exposure' in which sows are housed side by side but prevented from fighting with each other. Contrary to expectation, the study found that pre-exposure prior to mixing sows together in a group caused the sows to fight more, not less, when group housed. It appears that the inability of the sows to resolve aggressive dominance interactions prior to mixing, but after side by side association, actually promotes more aggressive behavior when the sows are placed in groups, thus future work should use a different approach to resolve aggression prior to mixing.

Prediction model developed for feedlot cattle susceptibility to heat stress

Annual losses associated with heat stress in the beef industry average \$369 million. In an extreme heat stress event losses to an individual livestock producer can be devastating. Currently, management strategies to combat heat stress such as shade, sprinkle cooling, and dietary changes have not been fully employed primarily due to cost and system maintenance. Animal heat stress is a result of the combination of three different components: environmental conditions, animal susceptibility, and management. ARS researchers at Clay Center, Nebraska, developed a model to predict individual animal susceptibility to heat stress. The model summarize the effects of animal color, sex, species, temperament, hair thickness, previous exposure to hot conditions, age, condition score, previous cases of pneumonia, previous other related health issues, and current health status into a single value of susceptibility to heat stress. The validated model accurately predicts heat stress susceptibility, allowing producers to group animals by susceptibility to heat stress. When current management strategies are applied to susceptible animals, producers can provide appropriate care for each animal in the feedlot, improving welfare, maximize animal performance, and increase profitability by decreasing financial losses.

Assessing transportation stress in beef cattle

Transporting livestock in confined trailers has long been considered stressful on the animals, even in the absence of conclusive evidence. With ever-rising welfare concern from consumers, producers must be

able to assure that animal well-being is not overlooked. Therefore, ARS scientists from Lubbock, Texas, and Texas AgriLife Research, teamed up to evaluate the effects of transportation on feed intake, feeding behavior, and productivity of weaned calves. While considerable variation in post-weaning feeding behavior in cattle was found, this study found that the decrease in body weight following transportation is primarily due to feed and water withdrawal. Finally, these studies indicate that cattle are most stressed during handling and loading, rather than during transportation itself. Thus, contrary to popular opinion, transportation in and of itself does not appear to negatively impact the health, productivity, and overall well-being of yearling cattle even for relatively extended transportation times. This information is valuable for the development of policies or regulations related to the humane transportation of livestock.

Increased ewe prolificacy for sheep producers

A high priority and focus of the sheep industry is to increase the number of lambs weaned per ewe exposed for breeding. The use of Romanov crossbred ewes is increasing in the United States because the Romanov breed is the most prolific breed available. It was hypothesized that Romanov crossbred sheep may differ in reproductive performance when produced using Romanov rams or Romanov ewes because Romanov ewes produce much larger litters than ewes of other breeds. Therefore, the relative performance of Romanov crossbred ewes sired by Romanov rams compared to those born to Romanov ewes is an important industry issue. ARS researchers at Clay Center, Nebraska, determined that Romanov crossbred ewes produced by either method were similar in their high levels of productivity – there was no significant maternal dam effect. Consequently, producers can mate Romanov rams to ewes of locally-adapted breeds to lower the cost of producing Romanov crossbreds and still realize improved fecundity and reproductive performance of the resulting Romanov crossbred ewe. This practical information will further increase use of Romanov superior genetics, resulting in greater productivity and profitability for sheep producers.

A defective gene causes a novel stress syndrome in pigs

A defect within a gene, mutated in human muscular dystrophies, causes a novel stress syndrome in pigs. The stress syndrome can result in death of affected pigs after handling or transportation. ARS researchers at Clay Center, Nebraska, using sophisticated genetic and physiological techniques, determined that a defective gene called dystrophin leads to elevated blood enzymes, heart arrhythmias and dramatically reduced levels of the protein in heart and skeletal muscles. The researchers' findings are consistent with observations of genetic mutations in humans with milder forms of muscular dystrophy associated with muscle weakness and heart failure. This research will assist pork producers to eliminate this defect from their herds improving production efficiencies, pork quality, and the competitiveness and profitability of the pork industry. Pigs with this defect can also now be used as valuable biomedical models for human muscular dystrophy research.

Genetic analysis of boars for better sperm survival after cryopreservation

Discovery of genetic markers for boars with superior sperm cryosurvival would allow boar semen distributors to predict which boars will best produce litters from frozen/thawed semen. ARS researchers at Clay Center, Nebraska and Beltsville, Maryland, estimated genetic parameters from 920 ejaculates collected over seven years from 254 boars representing a four breed composite that were frozen and then thawed for the determination of sperm viability and motility. The likelihood of a genetic cause for motion parameters was high for the percentages of motile and viable sperm in both fresh and frozen/thawed sperm samples. Sperm freezability is an ideal candidate for marker assisted selection or selection for favorable alleles and freezability could be improved through genetic selection without

negative impact on production traits. This work was presented at the 7th International Conference on Boar Semen Preservation in August 2011.

The degree of embryonic death from cold egg storage has a genetic component

Storing eggs for up to 10 days in a cold room prior to incubation is a common practice in the broiler industry but often has a negative impact on embryo survival. An ARS scientist in Beltsville, Maryland, investigated the impact of cold storage on the embryo survival of eggs from two different hen lines. While nearly identical before cold storage, the embryonic cell numbers, embryo diameters, and percentage of viable cells differed between the two lines after cold storage. Of interest is that 22% of the embryos from one line died after the onset of blood formation, whereas 45% of the embryos from the other line died at the same point. This suggests that the mechanism signaling the onset of blood vessel formation in these two hen lines are differentially impacted by egg storage time.

Official national genomic evaluations developed for dairy cattle with genotypes based on a low-density marker panel

Due to the recent increase in availability of a low-density marker panel at a low cost, the number of animals with genomic information has increased greatly, which provides an opportunity to improve the accuracy of genetic evaluations. Methods developed by ARS scientists in Beltsville, Maryland, were used to combine genomic information from low-density genotypes with previous higher density information were implemented for national genetic evaluations of yield and fitness traits of Holsteins, Jerseys, and Brown Swiss and made official in December 2010. The availability of genomic evaluations for animals with low-density genotypes has increased the accuracy of their estimated genetic merit compared with their traditional evaluations. For young animals with low-density genotypes, gain in accuracy over parent average was about 80% of the gain realized with higher density genotypes. Low density genotypes also provide a low cost alternative to traditional parentage verification.

Diet affects chicken body fat

Excess fat production by the modern broiler chicken is problematic. The consumer has health concerns about the link between cardiovascular disease and dietary fat. Consequently, producers would like to produce leaner meat with a lower fat content. Historically, shifts in metabolism have resulted in dietary fat being merely shunted to replace that from other feed ingredients. ARS researchers in Starkville, Mississippi, designed studies to determine if dietary protein elicited changes in intermediary metabolism and if changes resulted from alterations in the expression of genes coding for certain regulatory proteins. We have found that altering feeding regimens and dietary crude protein in the broiler will cause permanent changes in fat synthesis and storage, such that dietary fat will not be shunted to body fat stores. Although increasing dietary protein decreased fat synthesis by the broiler, the expression of genes regulating fat synthesis did not accompany this decrease unless the diet contained a very high level of protein. Modest increases in dietary protein will decrease lipid synthesis without affecting gene expression. Knowing exact dietary protein levels for effective growth would be a savings to the poultry industry because protein is the most costly dietary component in broiler diets.

Characterized residual feed intake (RFI) in lactating dairy cattle

RFI is used to select beef cattle that are more efficient at conversion of feed to gain and produce less methane (a greenhouse gas) during digestion. ARS scientists found that RFI is heritable in dairy cattle and repeatable within cows over multiple lactations. Consistent with beef cattle, low-RFI (efficient) cows consumed 17% less feed than high-RFI (inefficient) cows, with no differences in energy-corrected

milk yield or body weight. Relative to inefficient cows, efficient cows spent less time feeding and ate at a slower rate, which are thought to reduce energy expenditure, contribute to increases in digestibility of feed, and ultimately increase the efficiency of feed conversion to milk. The results suggest that RFI is a trait to consider for multi-trait genetic selection of dairy cattle to reduce feed costs and the environmental impacts of dairy production.

Commercial genotyping tools for cattle

ARS' continued leadership in development of the commercial genotyping tools (BovineSNP50, BovineHD, Bovine3K-Illumina, and BOS1-Affymetrix) has had a major impact on livestock research and the dairy Artificial Insemination (AI) industry. Awareness of the success in genotype tool development and application to genomic research in cattle fueled development of an additional SNP beadchip (BovineLD-Illumina). ARS scientists co-lead development of this product, and its impact on the industry is anticipated to be high as it replaces the Bovine3K assay in the marketplace. ARS has also developed the first sequence based genotyping tool (BovineExome-Agilent) for high-resolution genetic characterization. Because this product is not commercially available yet, its impact remains unknown. The BovineSNP50 assay continues to be the global de facto standard for cattle genomics research and genetic prediction use with sales having surpassed 700,000 samples.

Genetic basis for Weaver Syndrome in dairy

ARS Scientists in Beltsville, MD identified a 4.82 million base pair fragment of genome on Chromosome 4 coding for the late onset degenerative neuro-muscular disease in dairy cattle called Weaver syndrome. This refined mapping of the locus better identifies animals which carry this autosomal recessive disease. The methodologies used to better map Weaver have also led to creation of our first genomics unified schema database: where phenotype, genotype, DNA genome sequence, and gene annotation information are combined to better analyze large complex data sets. These results will be used to provide a new diagnostic test that is more reliable than the previous single-marker test used by the industry for screening animals since 1995.

Developed a better model to describe adaptation of forage systems to climate change

ARS researchers developed a technique utilizing Monte Carlo simulation to evaluate forage systems. The goal of the method is to develop sample distributions under varying environmental conditions and produce probability expectations of forage for system success or failure. Conventional methods (such as Analysis of Variance or regression analysis) to evaluate forage performance require numerous trials to evaluate whether one forage system is "better" than another. The modeling technique utilized by the study is much more efficient than conventional techniques, produces a more-robust dataset and permits the development of probabilities for determining the success or failure of forage and/or management systems. This research greatly reduces the financial and time resources needed to evaluate forage systems and is capable of handling much more complex systems. Data produced from this technique and analyses are directly useful to farmers, researchers and policy makers. The technique would be extremely useful in translating results from genomic analysis to real-world agriculture.

Improved chicken genome sequence assembly

An ARS scientist in East Lansing, MI, in collaboration with other scientists at Washington University School of Medicine in St. Louis, Michigan State University, and Wageningen University in The Netherlands developed a new assembly of the chicken genome. This assembly is more accurate and contains less duplication compared to the previous version. This assembly and the accompanying

genetic map are powerful tools for helping scientists around the world understand chicken biology including agronomically important traits such as production and disease resistance.

More digestible corn silage for ruminants

Corn silage is a major feed resource for livestock, but fiber digestibility of the stover fraction is poor. A corn mutant with reduced ferulate cross linking, an inhibitor of fiber digestion, was fed to lactating dairy cows by ARS researchers at Madison, Wisconsin, as part of a typical mixed ingredient diet. Cows fed the mutant corn silage ate more feed, did less sorting of their feed to avoid fiber, digested more fiber, and produced more milk. Because corn is a type of grass, if the gene responsible for cross linking can be isolated from this corn mutant, then the digestibility of all grass forages, not just corn silage, can be improved genetically.

New laboratory procedures allow more accurate evaluation of dietary proteins fed to dairy cattle

The amount of protein escaping microbial breakdown in the rumen (“bypass protein”) determines much of the value of feeds for dairy cows. Thus far, no laboratory test has proven reliable to measure bypass protein in dairy feeds. A new procedure developed by ARS scientists in Madison, Wisconsin, was applied to a number of feed proteins commonly fed to dairy cows. The new technique gave more rapid rates of protein degradation and yielded values for bypass protein that were similar to measurements made in living dairy cows. The method was applied to assess the value of protein concentrates (soybean meals, canola meals) and samples of tropical grasses collected in several grazing studies. This research indicated that tests used throughout the world to measure bypass protein from the rumen consistently overestimate protein escape. The new ARS technique will allow nutritionists to more accurately measure bypass protein allowing improved evaluation of feeds which will lead to the formulation of diets that are more efficiently utilized by dairy cattle.

Terminal-sire breed evaluation for sheep for lamb survival

Sheep producers throughout the U.S. claim that fitness traits of lambs, specifically survivability, have decreased as mature body size and growth rates have increased during the last 20 to 30 years. To address this issue, ARS research scientists in Dubois, ID determined whether breed of sire affected the survival of crossbred lambs from birth to market age. Breeds such as Columbia, USMARC-Composite, Suffolk, and Texel rams, which are terminal-sire breeds used to sire high-value market lambs, were mated with Rambouillet ewes, which have superior maternal abilities, and the traits of birth weight, survival, growth, feed efficiency, carcass composition, and meat quality of the crossbred lambs were evaluated. Breed of sire did not affect the survival of crossbred lambs, but breed of sire affected the other traits that were measured. Based on this information from this research, sheep producers can use any of the sire breeds that were evaluated to produce high-value market lambs, without reducing lamb survival from birth to market age.

Prototype systems for national cattle evaluation

National cattle evaluation provides information for use in making genetic improvement in efficiency of beef production. To date, there have been essentially no systems for evaluation of sustained reproductive success, and feed intake and feed efficiency. ARS researchers in Miles City, Montana, developed prototype systems as components of the national cattle evaluation systems for Hereford and Angus cattle. Tens of thousands of cattle producers will use these systems to evaluate hundreds of thousands of animals. This technology provides the opportunity for permanent and cumulative

improvement in the evaluated traits potentially leading to reduced cost of production and environmental impact.

Predicting breed composition of crossbred beef cattle

The breed composition of crossbred beef cattle is often unknown, yet such knowledge would be useful to aid management decisions. ARS scientists at Clay Center, Nebraska, accurately estimated breed composition of crossbred cattle using BovineSNP50 genotype markers and allele frequencies estimated from a sample of bulls of 16 breeds. The use of genetic markers could accurately determine if a specific breed contributed 0, 25, 50, or 75% to the genetic makeup of an individual animal. Determination of breed composition is important for verification of product brand and source. This methodology is being applied by the Animal and Plant Inspection Service in disease trace back cases.

Genetic markers associated with pork tenderness made available to producers

Genetic markers residing in the calpastatin gene (developed by ARS) have been shown to be predictive of aged pork tenderness in multiple commercial populations of pigs. Based on the results of several validation studies completed by ARS scientists in Clay Center, Nebraska, the best performing markers were transferred to a commercial genotyping company to add to the list of markers producers can now genotype in their populations. The utilization of these markers will result in improved tenderness and more consistent pork products.

Replacing antibiotics in young swine feed with natural alternatives

Antibiotics have been fed at sub-therapeutic levels as health, growth and efficiency promoters for more than 50 years and much of the swine produced in U.S. receives antibiotics in their feed at some point during the production process. However, because of concerns over antibiotic resistance, alternatives to antibiotics are a high priority for U.S. swine producers. ARS researchers in Clay Center, Nebraska, determined that feeding a natural antimicrobial agent called lysozyme to young pigs consuming a liquid diet was as effective as antibiotics in increasing growth performance, improving gastrointestinal health, and decreasing pathogen shedding in feces this natural antimicrobial agent is a suitable alternative to antibiotics for young pigs consuming manufactured liquid diets. The identification of suitable alternatives to antibiotics will enable the swine industry to effectively transition away from dietary antibiotic use.

Fitting nutrition to cattle genetics

Establishing the growth pattern and the proportion of mature weight at puberty of cows is important in developing management and nutrition programs targeted to increase the efficiency of beef production. Few data sets that track skeletal and body weight from birth through maturity are available. Even fewer data sets are available that compare diverse genetic types of cattle. ARS researchers in Clay Center, Nebraska, assembled the data sets that allowed comparisons of growth patterns across diverse genetic types of cows. This research described the proportion of mature weight and skeletal size cows reach at puberty, and that the proportion differs with genetic type. Knowing how growth rate changes as a cow ages, and the target weight required for successful reproductive performance allows for the development of nutrient management programs that fit the genetics of the cow.

Chromium in the diet of beef cattle for better performance and health

Even with the use of antibiotics and other medications, sub-optimal health and poor growth performance of cattle in U.S. feedlots continue to be a significant economic drain for producers. Economically

feasible alternative management practices that improve health and performance are greatly needed. One method that is showing promise is the inclusion of chromium, a mineral known to be involved in the metabolism of carbohydrates, fats, and protein in cattle diets. Scientists from Lubbock, Texas, teamed with scientists from Texas Tech University for a cattle study that showed that adding chromium to the diet of cattle when they first come into a feedlot not only enhances their immune response following an acute infection, but also improves growth performance. The study also suggests that chromium may speed the recovery of stressed and/or sick cattle, thus reducing the production costs. Improving the health of animals within our livestock production systems will also reduce potential health risks for consumers.

A novel endophyte-infected tall fescue improves pasture and steer productivity

Ergot alkaloids, produced by an endophyte (*Neotyphodium coenophialum*) which infects most tall fescue and imparts tolerances to the plant to environmental stresses, are causal agents of “fescue toxicosis” in cattle. Fescue toxicosis substantially reduces animal production and well being and costs producers nearly one billion dollars annually. ARS animal scientists at Lexington, Kentucky, partnering with University of Kentucky researchers, evaluated a late maturing tall fescue genotype, bred to improve seedling vigor and adapted to the northern half of the transition zone of the eastern half of the United States. This novel endophyte-infected variety will soon be commercially available to producers and is the first novel endophyte-infected tall fescue specifically developed/adapted to the northern part of the transition zone. Ultimately, the new variety is expected to improve sustainability of forage-based enterprises and attendant benefits to rural communities and the environment offered by forage.

Sexual maturity varies widely between Brahman cattle and other breeds

Brahman cattle, which are a *Bos indicus* breed, reach sexual maturity at older ages than do *Bos taurus* breeds such as Angus and Romosinuano. Brahman-crossed cattle; however, experience heterosis or hybrid vigor for heifer and cow fertility traits, especially in subtropical and tropical production systems. The growth endocrine axis, primarily growth hormone (GH) and insulin-like growth factor (IGF) have been shown to influence reproductive processes. This endocrine axis has been intensively studied for its role in growth, lactation, and adiposity in domestic animals. Research conducted by ARS scientists in Brooksville, Florida, evaluated population genetic characteristics of single nucleotide polymorphism (SNP) genotypes within genes of the GH and IGF axis in straightbred and crossbred Angus, Brahman, and Romosinuano heifers and tested the association(s) of these genotypes with measures of reproduction. Three SNP useful (informative) SNP were identified among straightbreds. Two SNP significantly influenced traits indicative of 1st-calf heifer rebreeding (i.e., calving interval, days to calving, and pregnancy rate). Heifers that had two copies of one of these haplotypes had a 9.2% advantage over heifers with no copies for the 3 traits. The third SNP genotype interacted with pedigree suggesting that predominately *Bos taurus* heifers had a 16% reduction in calving interval and days to calving relative to predominately *Bos indicus* heifers. Results of this study provide support for two positional candidate genes associated with 1st-calf heifer re-breeding traits. Identifying genes associated with reproductive traits is important to more efficient cattle production.