United States Department of Agriculture

Research, Education & Economics

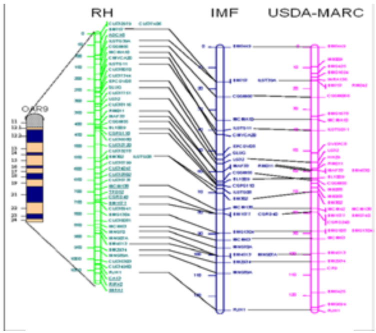
Agricultural Research Service

Office of National Programs

December 2010

National Program in Food Animal Production (101)

Retrospective Accomplishment Report



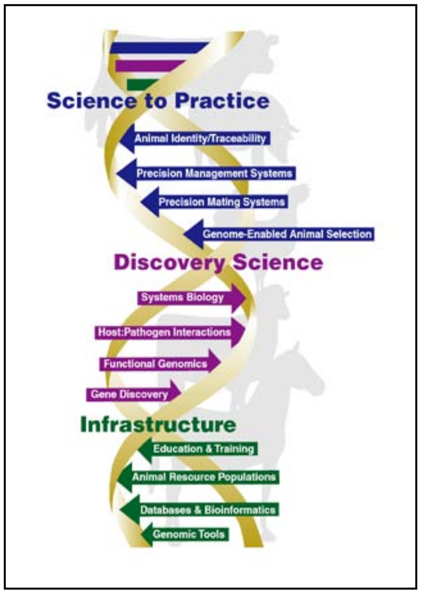


Table of Contents

Background and General Information

Introduction

Food animal production and product consumption is increasing significantly around the world as consumers seek higher quality and more nutrient dense sources of protein, iron and other vital nutrients. This trend will continue as the world's population continues to grow and as animal production systems increase efficiencies across varied environments and production systems. Animal production systems fit a unique and valuable niche in the global food production equation by utilizing feeds and forages not appropriate for human consumption. Animal production will continue to serve in this vital role in human nutrition and in environmentally sustainable food production systems across the globe.

The United States has historically been a leading source of quality animal products and has led the world in technological development and adoption. These advances have enabled the United States to develop one of the most efficient animal production systems on earth and U.S. Department of Agriculture Agricultural Research Service (USDA/ARS) has been a vital part of that achievement. However, agriculture is being relied on to provide for a growing world population more now than at any other time in modern history. Pressure to feed a projected nine billion people by 2050 make the role of the USDA/ARS critically important and underscores the importance of this retrospective review of National Program 101 (NP101) and the subsequent 5 years programming planning process. To remain competitive in the face of extraordinary growth in animal production systems around the world, the animal industries in the United States must continue to focus on increasing production efficiencies through the development and adoption of scientific technologies. The application of new tools in genomics, metagenomics, reproductive physiology, nutrition, and molecular biology in concert with animal health and in support of traditional husbandry, animal welfare and ecosystem services will continue to improve the long tradition of global economic competitiveness and sustainability of U.S. food animal production.

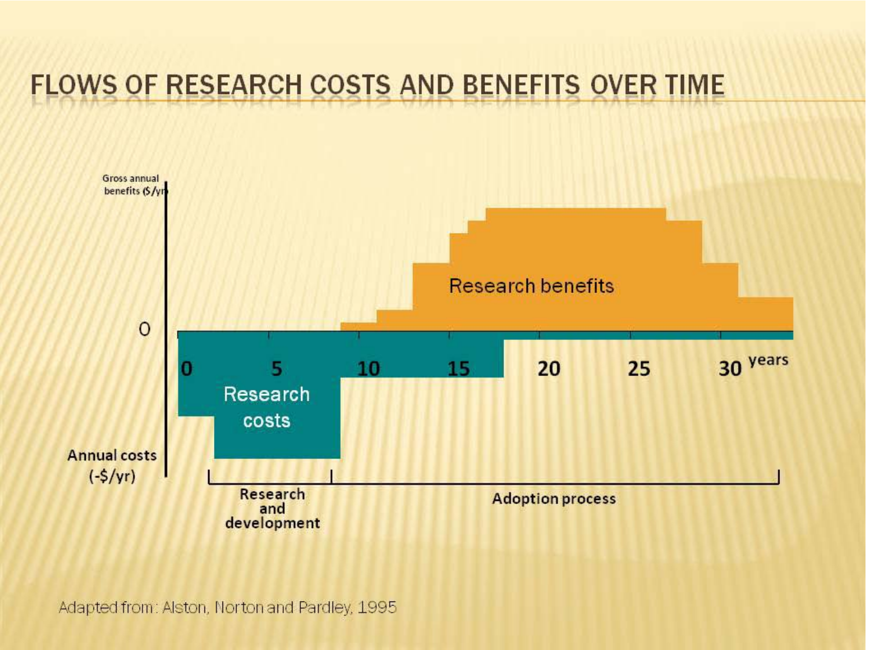
US systems of agricultural animal management and production face formidable challenges. One of the most exacting challenges is successful adaptation to the accelerating demands of society that impact animal productivity and product quality. The demands placed on the national system of food animal production by a rapidly changing world, for example increasing population, rising obesity, demands for better nutrition and lower costs, can only be met by technologies that optimally harness the inherent genetic potential of animal and plant germplasm in concert with certified industry and food marketing practices. Production systems that successfully identify, preserve, and harness that genetic potential will maximize profits, secure supply, increase market competitiveness, sustain small and mid-sized producers, and maintain genetic diversity and consumer confidence.

Unfortunately, the USDA-ARS or NP101 does not have the resources or scope to address all valid researchable priorities for the livestock production industries in the US or internationally, so consequently must concentrate in areas where maximum impact is possible. While these limitations may restrict the overall scope of the research in NP101, the current priorities and focus of the research in NP101 have produced extraordinary results for the livestock industries in the US and internationally in specific areas of focus. ARS research in NP101 directly impacts production livestock agriculture across species and around the world in genetics, reproduction, nutrition, animal well-being and product quality.

According to the USDA-Economic Research Service, agricultural research has historically produced remarkable rates of societal return on investment with estimates ranging from 20% to 60% for annually. In other words, for every $1 invested in agricultural research approximately $5 to as much as $15 is returned to the economy in present value terms. A specific focus on industry priorities has allowed NP101 to produce returns estimated to be well within this range and the current advancement of genomic technologies will increase the impact of the program even further. Much of the current research in NP101 is just beginning to engage genomic technologies and the opportunities they provide to accelerate scientific discovery.

It is important to consider that the value of applied and translational research is not typically maximized without prior basic research to set the foundation and identify scientific priority and opportunity. Both are critical to deliver the ultimate promise and value of the research. There can be little truly valuable applied research without strong basic research and basic research is of no value if the technologies developed are never applied successfully in the field. Basic discovery science is often more difficult, longer term and with additional inherent risk than applied or translational research. However, basic discovery science provides the opportunity to realize extraordinary scientific benefit, ultimately through applied and translational research, by providing the foundation and vehicle for scientific discovery and eventual application. That is one of the primary tenets of USDA/ARS and NP101 research and will continue to underpin the research programs. The following graphics illustrate these points.

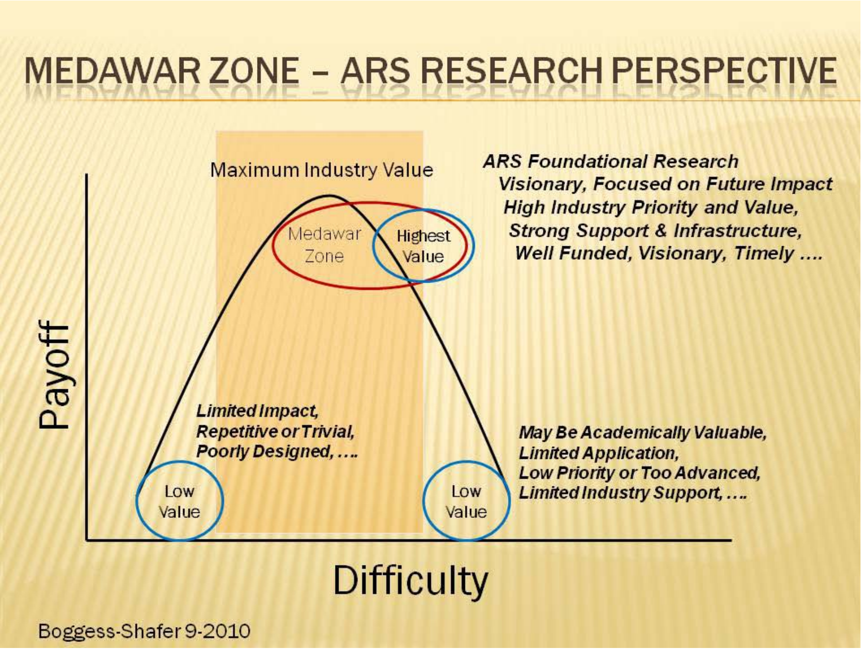
Figure 1. Flow of resources, research benefits and research costs for public research.



Adapted from: Alston, Norton and Pardley, 1995

This graphic developed by Alston et al., 1995, illustrates the flows of resources, research benefits, and research costs for public research in agriculture. It shows clearly the challenge of basic discovery science in that while the benefit is often extraordinary, as reflected in the estimated value of the return on investment for public research of 20 to 60% annually, the benefits are typically not realized for many years. This dichotomy – the time between discovery and application – jeopardizes the long term support and commitment required to realize maximum benefit, unless the funding entities and stakeholders clearly understand the critical need for long term sustained support and investment in basic discovery science.

Figure 2. Optimizing the focus and timing of basic discovery science.



This illustration adapted from Loehe illustrates the principal of the the **Medawar Zone** where the area of scientific discovery is most likely to produce maximum benefit. Research that is trivial, repetitive or overly simple are unlikely to produce novel or significant results. Research that is too ambitious, purely academic or not adequately developed scientifically may not succeed at all, may be rejected by the research community at large or may be irrelevant. The challenge for USDA/ARS and NP101 is to focus scientific discovery in the Medawar Zone or the area where maximum societal value is realized by the research, and to avoid trivial repetitive research as well as research that may be academically valuable but is poorly timed or has no ultimate scientific utility or value to industry stakeholders. This challenge again underscores the need for long term sustained funding, strong visionary leadership and stakeholder commitment to ensure the value and impact of research in NP101.

Finally, research in NP101 continues to increase in scientific complexity as the most valuable and impactful challenges to the livestock industries are addressed. Challenges characterized as having maximum industry priority and value are well represented in Figure 2 at the top of the Medawar Zone and in the case of the USDA/ARS and NP101 to the right of the Medawar Zone peak as scientific discovery progresses over time. These challenges are not simple. They require strong research programs with visionary and long term commitment, multidisciplinary collaborations, strong leadership and strong industry stakeholder support. These challenges now typify much of the research undertaken by scientists in NP101. New models for research program development and implementation in NP101 are being developed across USDA/ARS program, Land Grant Universities and industry collaborators to best address the complex challenges facing the research community in NP101. An example of the level of complexity for scientific discovery is illustrated in Figure 3.

Figure 3. Scientific complexity of a production trait: Sow Lifetime Productivity

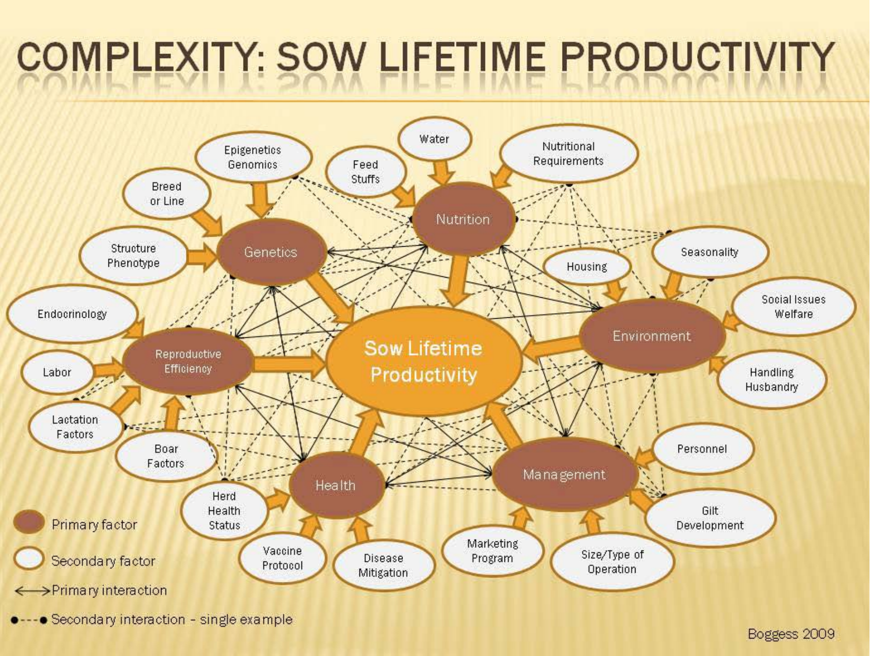


Figure 3 illustrates the complexity of the production trait sow lifetime productivity and includes primary and secondary factors as well as primary interactions. For a research program to make a significant impact on lifetime productivity of sows in the pork industry each of these factors must be considered and accounted for in a research program. Significant scientific progress can only be reached through collaborative visionary research that is focused on impact while accounting for all relevant factors as shown in this Figure 3.

The USDA/ARS has the national capability and demonstrated performance to lead U.S. food animal research and technology development to enhance the sustainable and economically viable production of food animal products in the United States. USDA/ARS and partners conduct a food animal research program that has contributed significantly to national growth and global competitiveness of the U.S. production industries. A strong USDA commitment to food animal production research, technology development, and technology transfer through ARS and the National Institute for Food and Agriculture (NIFA) in cooperation with university and private research programs, and linked to State and regional agricultural extension programs, is critical to energize industry development, improve production efficiency, and assure quality and wholesomeness of food animal products.

The Agricultural Research Service (ARS) is the intramural research agency for the U.S. Department of Agriculture (USDA), and is one of four agencies that make up the Research, Education, and Economics mission area of the department. The ARS budget is allocated to research conducted in 22 national program areas. Research is conducted in 108 laboratories by ~2,200 full-time scientists within a total workforce of ~8,000 ARS employees. The ARS national program addressing animal production is NP 101 – Food Animal Production. NP 101 involves research conducted at 20 U.S. locations by 102 full-time scientists and has an appropriated budget of approximately $46.5 million per annum.

The vision for National Program 101 – Food Animal Production is *“to furnish scientific information about biotechnologies and management practices that ensure an abundant supply of competitively priced animal products”*. The overall mission is to: 1) safeguard and utilize animal genetic resources, associated genetic and genomic databases, and bioinformatic tools;

2) develop a basic understanding of the physiology of livestock and poultry; and 3) develop information, tools, and technologies that can be used to improve animal production systems, all to ensure an abundant, safe, and inexpensive supply of animal products produced in a healthy, competitive, and sustainable animal agriculture sector of the U.S. economy. This National Program mission follows from the USDA/ARS Strategic Plan (see http://www.ars.usda.gov/aboutus/docs.htm?docid=1766) which, in turn, is directed towards achieving goals mandated by the USDA Research, Education, and Economics Mission Area Strategic Plan and the USDA Strategic Plan (see http://www.usda.gov/ocfo/usdasp/usdasp.htm).

The products of research conducted in this national program contribute toward broader goals associated with four specific Performance Measures from the ARS Strategic Plan for 2007 - 2012.

Goal 1: Enhance Economic Opportunities for Agricultural Producers.

Performance Measure 1.2.1: Provide producers with scientific information and technology that increase production efficiency, develop improved germplasm, safeguard the environment, improve animal well-being, and reduce production risks and product losses. Target: Specific information and technology will be available to food animal producers for evaluating animal productivity and wellbeing, increasing efficiency, and decreasing environmental impact through improved management models and reproduction methods.

Performance Measure 1.2.2: Develop needed information on the relationships between nutrients, reproduction, growth, and conversion to and marketability of animal products. Target: Information will be available to producers for more efficiently converting improved knowledge about the interactions of reproduction, growth, and nutrient intake to increase marketability of food animals.

Performance Measure 1.2.3: Identify genes responsible for economically important traits, including animal product quality, efficiency of nutrient utilization, and environmental adaptability. Target: Better understanding will be available of how genes are responsible for economically important traits in food animals, such as nutrient utilization and environmental adaptability.

Performance Measure 1.2.4: Maintain, characterize, and use genetic resources to optimize and safeguard genetic diversity and promote viable, vigorous animal production systems. Target: The diversity of food animal germplasm will be maintained and optimized to invigorate production systems.

Linkages with Other ARS National Programs

Research projects in the Food Animal Production National Program are strongly inter-linked to activities in a number of other ARS national programs which either directly or indirectly impact animal agriculture. These programs include NP 103 (Animal Health); NP 104 (Veterinary, Medical, and Urban Entomology); NP 106 (Aquaculture); NP 215 (Rangelands, Pastures, and Forages); NP 206 (Manure and Byproduct Utilization); and NP 108 (Food Safety).

Linkages with USDA-NIFA National Programs

Research projects in this ARS national program are also coordinated with research, education, and extension programs administered by USDA's National Institute for Food and Agriculture (NIFA). This process was facilitated by co-hosting of a Joint USDA-ARS/NIFA Stakeholder Planning Workshop for the national program area of Animal Production and Well-Being held in April 2006. The activities of the ARS NP 101 research program are directly inter-linked with activities in the NIFA national program areas of: 1) Genetic Improvement of Animals and Animal Genomes; 2) Reproductive Performance of Animals; 3) Nutrient Utilization of Animals; 4) Animal Physiological Processes; 5) Environmental Stress in Animals; 6) Animal Management Systems; 7) Improved Animal Products (Before Harvest); and 8) Animal Health and Protection. These programs are all coordinated with the goals and funded research programs affecting animal production within the AFRI Competitive Grants Program of NIFA.

Planning and Coordination for NP 101

USDA/ARS established national programs for organizing and communicating its research programs with customers, stakeholders and partners in 1996. A national program on food animal production was established at that time to provide leadership in research for the U.S. animal production industries. The ARS Food Animal Production National Program Team held a National Program Planning Workshop to establish program direction and implementation of the plan. An Action Plan was written which provided the basis for individual prospectus and project plan development, peer panel review and the authority for the research conducted in the national program.

The first *Joint ARS-CSREES (NIFA) Food Animal Production National Program Stakeholder Planning Workshop* was held on April 10-12, 2006 in Kansas City, Missouri. See (http://www.ars.usda.gov/research/programs/programs.htm?np_code=101&docid=12556) for more information.

The expected outcomes of the workshop were:

- ✓ Identification of a list of the research needs of the livestock and poultry industries.
- ✓ Prioritization of the research needs for the USDA’s animal production and well-being research programs.
- ✓ Communication to increase support and strengthen the integration of USDA’s research, technology transfer, and extension programs in animal production and well-being.
- ✓ Enhanced working dialogue among USDA’s partners, professional organizations, the livestock industries, and USDA national program leaders and scientists to help solve priority problems in American animal agriculture.

The primary goal of this meeting was to establish the new USDA Animal Production and Well-Being research action plan, which guided USDA projects over the next 5 years. Review of output from the workshop indicated that the USDA/ARS Food Animal National Program was generally on target. There was a sense of urgency detected in customer presentations for information to solve problems with over-arching themes or contexts such as reducing costs of inputs, increasing production efficiency, improving animal health, developing and protecting domestic genetic resources, increasing environmental compatibility and sustainability, and improving product quality. It was recommended that the National Program 101 Action Plan incorporate food animal research holistically involving production system efficiencies, and, integrate biological and social sciences to focus on environmental stewardship, animal well-being, and economic viability in food animal production.

The NP 101 Action Plan was subsequently drafted by writing teams composed of ARS scientists and members of the USDA/ARS National Program Staff (NPS). The writing teams combined input from the workshop, their own knowledge of the subject matter area, and input from other ARS scientists and their cooperators to identify the key priority needs that could be addressed by ARS research in the coming five year period. These needs were aggregated into Problem Areas for each National Program Research Component. After a public comment period, the draft Action Plan was revised, edited, and completed in 2006. See http://www.ars.usda.gov/SP2UserFiles/Program/101/2007-2012ActionPlan/101ActionPlan2007-2012FINAL.pdf for more information.

Once the Action Plan was completed, ARS project teams each developed a project prospectus containing objectives of specific research from the framework of the Action Plan. Project Plans were then written by project teams of scientists after NPS approval of their project prospectus. Project Plans included statements of the anticipated products or information to be generated by the project, how they contributed to solving the larger National Program Problem Areas, and time lines and milestones for measuring progress toward achieving the project goals. All project plans were then evaluated for scientific quality by external peer review panels. The project peer reviews were administered by the ARS Office of Scientific Quality Review (OSQR). Project Plans were revised in response to review panel recommendations, and were then approved for implementation. Project plans were approved for the period of October 2007 to September 2012.

The progress achieved in attaining the Action Plan goals is now being assessed by an external retrospective assessment panel. This program assessment is in preparation for the beginning of the next five-year national program cycle (October 2012-September 2017). **The next cycle, which will begin with a national program stakeholder workshop in March 2011, will be driven by a new action plan that will incorporate information from this assessment process.**

Day-to-day coordination of the ARS national program in food animal production is the task of the National Program Leaders who comprise the NP101 Leadership Team. The national program is also coordinated with other ARS National Programs previously listed and with activities of other agencies. For example, discussions and analyses of the Interagency Working Group on Domestic Animal Genomics coordinate and align NP 101 research with efforts in other agencies across the Federal government. This interagency working group includes representatives from the USDA (ARS and NIFA), National Science Foundation, National Institutes of Health, Department of Commerce, Department of Energy, Food and Drug Administration, U.S. Agency for International Development, Office of Science and Technology Policy, National Oceanic and Atmospheric Administration, and the Office of Management and Budget.

In addition to ongoing planning and coordination during the NP 101 program cycle, USDA/ARS National Program Staff and Area Offices organized and conducted various information gathering efforts focused on specific research issues relevant to the needs of U.S. food animal production industries. Most of these workshops also involved coordinating and integrating ARS NP 101 efforts with those of cooperating agencies, and with university and industry partners.

How This Report Was Constructed and What It Reflects

In this report, information about NP 101 achievements and their impact is organized according to National Program Research Components and their constituent Problem Areas, described in the current National Program Action Plan. The report first outlines the individual NP 101 Research Components. This is followed by a section for each of the components. The actual language from the current Action Plan is given to outline the **committed goals, planned approaches, expected outcomes, and engaged USDA/ARS locations** for each of the Problem Areas within each Component. These are followed by **selected accomplishments** achieved under the current Action Plan and include the **impact and/or potential anticipated**

benefits of those achievements on solving the problems and meeting the high priority needs identified by customer/stakeholders in the NP 101 action plan.

The purpose and intent of this document is to illustrate the direction and impact of NP 101 to develop a more accurate vision and strategy for NP101 going forward. This is a critically important task for the USDA/ARS. The following excerpts from remarks made by USDA Undersecretary of Research, Education and Economics, U.S. Department of Agriculture, Dr. Cathie Wotecki underscore the importance and challenge of agriculture research, of leveraging resources and expertise and of the importance and role of the USDA/ARS. They were provided to the Association of Public and Land Grant Universities Annual Meeting in Dallas, Texas on November 15, 2010.

> "Today, there is also growing recognition that agriculture and natural resources are at the crossroads of the world's most critical problems: sustainable food production, providing clean and abundant water, responding to climate change, renewable energy, and improving human health. Climate change, land use changes, population growth, and emerging pests and diseases are placing intense pressure on the world's food and agricultural system and threaten the future availability of sufficient food supplies. At the same time, 87% of America's surface-derived drinking water comes from America's farms, ranges and forests. The challenges facing agriculture, natural resources and conservation are immense, and need to be faced with the most robust research enterprise we can muster….
>
> Our new compact must reflect that we have at USDA and in our partner institutions many of the world's best scientists. This rich and deep talent base is capable of addressing almost any problem we can put before it. But instead of focusing on myriad problems at once, we should be figuring out how those many problems relate to our most urgent issues and tackle the root causes, not manage the symptoms.
>
> Our new compact must reflect that we have at USDA, and in the researchers we support, unbounded passion and enthusiasm for all facets of agricultural and natural resource research. But instead of trying to grow as many narrow, single-issue or single-focus research programs as we can, we should identify who are the best minds – whether they are within USDA, or in programs we fund outside USDA – and make sure we recruit, retain, and reward those researchers for their work.
>
> Putting this new compact in place will require us to:
>
> - Articulate the scope and capacity of USDA's scientific agencies and programs and of our university partners, and identify critical roadblocks and knowledge gaps that constrain rapid progress in the agricultural, conservation, economic, and social sciences.
> - Identify and prioritize agriculture's most urgent problems that require the combined support of USDA, other federal agencies, and the States.

- Provide guidelines for investments in agricultural research, education and extension, so that limited resources are allocated effectively to realize the greatest public benefits.
- Cultivate public awareness of the diversity and benefits of our research and information, whether in large-scale production agriculture or small family farms; by Native American communities; by organic farmers; by backyard gardeners; by foresters, livestock producers, farmers' markets, and consumers.
- Chart a course that includes a broader base of the contributors to and beneficiaries of agricultural science to plan and work together in a transparent and inclusive process, to advance our knowledge.

We need to craft a compact firmly rooted in the 21st century. We need to address both the direction of science and the structure and functions within the system, keeping in mind the sweeping changes in the scientific landscape itself. This compact will call for enhanced science capacity through a more formal, coordinated and leveraged science organization. It will integrate planning of science across USDA, its partners and beneficiaries of science. It will enhance education and create opportunities for the next generations of scientists. It will foster an appreciation of food and agricultural science, and will identify improved processes for engaging traditional and nontraditional stakeholders throughout the realm of research, education, and outreach activities. It will recognize that conservation is a principal that affects all working lands -- farm, range, or forest.

Lastly, and very importantly, it will call for aggressive partnering with the states and with other Federal science agencies and for increasing the recognition of USDA's research role in the broader science community. USDA science needs to recommit to a true partnership with the states – and with the private sector – a partnership that is focused, that leverages the strengths and resources of all its partners, and that recognizes that each partner brings site-specific, experience based, or culture-specific expertise to the table. And it needs to concentrate on select priorities at a large scale to produce valued outcomes. But most importantly, this partnership ultimately must be informed by the philosophy that our success in science has to be matched by impact in society.

A 21st century research compact will be built on three important components: competitive, peer reviewed research grant making; coordinated and interwoven with a strong federal intramural research program; and leveraged against the incredible infrastructure, expertise, and intellectual capacity of our state partners supported, in part, through state and federal funds. It is important to acknowledge the vital role that the

> capacity building funds have played and should continue to play in providing for the infrastructure for site-specific agriculture research.
>
> While competitive grants are central to our strategy, the federal government has a unique responsibility in this new compact: intramural research capacity also needs to be sustained to undergird and complement competitively funded extramural research. Our intramural research will emphasize:
>
> - Research that directly addresses the scientific needs of USDA program delivery agencies whose characteristics may appear arcane outside of government.
> - Research that builds on unique or confidential data sources, collections, or special infrastructure unavailable outside of USDA.
> - Research that provides coordination for a national perspective or framework, setting a single standard for use by others, and;
> - Research addressing questions with payoffs in the short term or requiring immediate response to a health, safety, or policy challenges.
>
> Our state partners need to be fully vested co-creators and signatories to this compact. The success of the American agriculture to date can be attributed in large part to how well the relationship between the states, the LGUs, and the federal government has worked in the past 150 years. "

These remarks clearly illustrate the priority and direction for the USDA/ARS and should help guide the evaluation of the past research for ARS in NP101 and provide guidance for recommendations for future research program development.

The content of this report is derived primarily from annual reports from individual NP 101 scientists who were asked to summarize their project's major accomplishments in terms of impact, and key references documenting those accomplishments. Consequently, this report does **not** include **all** accomplishments achieved in the national program but, rather, only those **selected** by ARS and the National Program Leader who authored this report. As a result, the scope of this report is not all inclusive, but encompasses a subset of the total spectrum of NP 101 accomplishments, chosen to illustrate **impactful stakeholder achievements at the national program level**.

Program Components and Associated Problem Statements

Research Component 1: Genetic Improvement - Understanding, Improving, and Effectively Using Animal Genetic and Genomic Resources

- Problem Statement 1A: Develop Genome-Enabling Tools and Reagents.
- Problem Statement 1B: Identify Functional Genes and Their Interactions.
- Problem Statement 1C: Preserve and Curate Livestock and Poultry Genetic Resources.

- Problem Statement 1D: Develop and Implement Genome-Enabled Genetic Improvement Programs.

Research Component 2: Enhancing Animal Adaptation, Well-Being and Efficiency in Diverse Production Systems

- Problem Statement 2A: Enhance Animal Well-Being and Reduce Stress in Livestock and Poultry Production Systems.
- Problem Statement 2B: Reducing Reproductive Losses.
- Problem Statement 2C: Improving Efficiency of Nutrient Utilization and Conversion to Animal Products.
-

Research Component 3: Measuring and Enhancing Product Quality

- Problem Statement 3A: Developing Systems for Reducing Variation in Product Quality and Yield.
- Problem Statement 3B: Characterization of Products from Non-Conventional Production Systems.

The details of each highlighted accomplishment are documented selectively to illustrate the overall variety of products and knowledge generated by this National Program. In the report text, selected accomplishments found in the narrative are cross-referenced, by numerical citation [e.g., "(1)"], to supporting information presented in **Appendix 1 – Selected Support Information and Documentation For Accomplishments and Impact of NP101 Research.** Appendix 1 is organized according to the individual NP 101 specific areas of research that best exemplify the scope and direction of the research in NP101.

NP 101 encompasses 32 appropriated research projects. The titles of the individual projects, objectives, funding levels, scientific staffing and scientific collaborators are listed in **Appendix 2 - Listing of Individual Appropriated CRIS Projects by Geographic Location**, which is organized according to the geographical location of the research unit. Each project is coded to reflect the National Program Action Plan components to which it contributes.

Appendix 3 – Annual Report Information (2006-2010), provides an aggregated copy of the introduction of the annual reports of the national program for fiscal years 2006-2010. Full copies of the reports are available on the ARS website http://www.ars.usda.gov/research/programs/), but this information has been condensed to provide an overview of new scientists, awards and recognitions, and additional activities associated with the national programs not reflected by any other section of this report.

National Program 101 – Food Animal Production – Action Plan (2007-2012)

National Program 101 (NP101) strives to closely align research with industry priorities and specifically in researchable areas that positively impact production efficiencies through improved reproduction, growth, efficiency, health and animal well-being. Livestock industry stakeholder and producer support is vital to program development and direction for NP101 research programs and was critical to the current Action Plan. Addressing industry priorities are even more critical when considering the economic and structural challenges facing the industry such as increasing grain and input costs, increased regulation, growing foreign competition, increased reliance on export markets and increasing pressure on social responsibility and animal well-being. That direction from the livestock industries is exemplified in the following accomplishment summaries.

ARS research has been on the front edge of scientific discovery and application in many areas. ARS research in genomics has produced impactful and economically valuable results for all the food animal species and has received national and international recognition. Genomic science and the development of genomic tools and technologies will continue to be a high priority for NP101 and will provide opportunity to accelerate scientific discovery in all research disciplines. ARS research in reproduction continues to focus on basic physiology and has contributed significantly to the body of knowledge regarding factors critical to increasing reproductive efficiencies. ARS research in growth biology and feed efficiency is a growing priority for NP101 and is a high priority for the livestock industries. ARS research in animal adaptation, stress management and animal well-being has also set the standard for research accomplishment and will continue to be a priority for NP101.

The following sections provide a summary of these accomplishments and their impact and value to the livestock industries. It is important to consider that some accomplishments were significantly impactful in their reporting year, but were improved upon by research in subsequent reporting years. Some of these selected accomplishments are included in this report as a sequential point of reference. It is also important to consider that this summary includes specific impactful accomplishments for NP101 but does not systematically represent the contributions of an individual research program or ARS laboratory. Accomplishments are grouped by area of discipline and by farm animal species in longer sections, but are not in any priority order or other classification within a section. Finally, many accomplishments fit into 2 or more categories (such as genomics and reproduction), but are listed only once in this summary in the section best related to the objectives of the original research project.

Linkages:

1. USDA/ARS National Programs: 103 Animal Health; 106 Aquaculture; USDA/ARS National Animal Germplasm Repository.
2. Other Associated Agencies and Departments: USDA National Institute of Food and Agriculture; U.S. Colleges of Agriculture and State Experiment Stations.
3. Private Sector: National Beef Cattlemen's Association, National Pork Board, American Sheep Industries, American Livestock Breeds Conservancy, US Beef Breeds Council, National Swine Registry, National Association of Animal Breeders, U.S. Livestock Producers, Allied Genetic and Production Industries.

NP101 Locations: Beaver, WV; Beltsville, MD; Booneville, AR; Brooksville, FL; Clay Center, NE; Dubois, ID; East Lansing, MI; El Reno, OK; Fort Collins, CO; Lexington, KY; Lubbock, TX; Madison, WI; Miles City, MT; Starkville, MS; and West Lafayette, IN.

Research Component 1: Genetic Improvement - Understanding, Improving, and Effectively Using Animal Genetic and Genomic Resources

To meet preferences and needs of consumers for animal products while effectively utilizing the natural resource base, livestock and poultry are produced in a wide array of environments and management systems. Insufficient quantitative and genomic characterization of existing genetic resources compromises efficiency of production across climactic zones of the U.S., limiting optimal use of feed resources and response to disease threats. Losses in production efficiency from genotype by environment interactions and gene by gene interactions must be better understood to respond to these challenges and increase profitability. Existing genetic resources provide producers with numerous options that can be tailored to meet current and future demands. However, several of these resources are at risk of being lost, even before they are adequately characterized. Germplasm conservation efforts require a wide range of information and analytical tools.

Genetic improvement of livestock and poultry populations is a key strategy for increasing efficient production in an ethically responsible manner. The rate of improvement, however, is hindered by lack of data on some economically important traits, inadequate understanding of quantitative and molecular genetic controls of component traits and interrelationships among traits, less than optimal methods for evaluating candidates for selection, and inefficient strategies to incorporate genomic data in to breeding programs. This includes the ability to move novel forms (alleles) of genes between populations.

Comprehensive knowledge of the genome and its interactions with environmental factors is required to fully understand the biological basis of all animal and poultry science disciples. Acquiring new knowledge in a “systems biology framework”, pertaining to animal adaptation and well-being, reproductive efficiency, nutrient utilization and conversion to animal products, and product quality, will be significantly enhanced with appropriate genomic tools and reagents. Continued public involvement in the construction of these resources is critical to ensure development of economically feasible management tools for livestock producers and to provide all researchers access to these tools and reagents to spur forward technology development for transfer to industry as quickly as possible.

Problem Statement 1A: Develop Genome-Enabling Tools and Reagents.

Significant public resources have been devoted to developing genomic and bioinformatic infrastructure for the important livestock and poultry species over the past two decades. These efforts have culminated in significant improvement in the genomic information on these species available in the public domain, yet, considerable work remains to bring the poultry (chicken and turkey), and livestock (bovine, porcine, ovine, caprine, and equine) genomes to a level of information content necessary for optimal “mining” through functional genomic and proteomic approaches. ARS remains committed to devoting the necessary resources to fill these research gaps.

Research Needs:

ARS research will contribute to the development of annotated genome sequence assemblies of the chicken, bovine, and porcine genomes (minimum 7-fold coverage). These annotated genome assemblies will also be highly valuable for informing the physical maps of the ovine, caprine, turkey, and equine genomes through comparative genomic approaches. Haplotype maps of the chicken, bovine, and porcine genomes are required to speed fine mapping of quantitative trait loci (QTL) and evaluate the potential for whole genome selection for complex quantitative traits. A full and comprehensive array of full-length cDNAs is required for functionally important tissues under differing environmental conditions and developmental stages to ascertain alternative splicing of genes and to fully explore gene function and regulation. Further development of gene expression tools to a commercially available level are required to fully facilitate functional genomic and genetical genomics approaches. ARS should further develop resource populations for these species that provide an optimal framework for mining genomic information. Furthermore, work is needed in the development and study of specialized cell lines from food animals that can be used to study gene expression through the use of tools such as RNA interference and targeted gene transfer. Fundamental research is needed to further develop methodology for transfer of genes within and across species. Finally, significant gaps exist in the minimum bioinformatic infrastructure required to facilitate rapid access to and visualization of livestock and poultry genomic and proteomic data by the research community on a routine basis.

Anticipated Products:

- ✓ Annotated genome sequence assemblies of the chicken, bovine, and porcine genomes.
- ✓ Densely populated haplotype maps of the chicken, bovine, and porcine genomes.
- ✓ Improved physical and genetic linkage maps of the ovine, caprine, equine, and turkey genomes.
- ✓ Full-length cDNA libraries and gene expression tools spanning important tissues, environments, and developmental stages for the important livestock and poultry species.
- ✓ Well-characterized and deeply phenotyped resource populations of dairy cattle, beef cattle, swine, and sheep.
- ✓ Specialized cell lines enabling the study of gene expression.
- ✓ Improved techniques and methodologies for intra- and inter-species gene transfer.
- ✓ Improved bioinformatic tools for rapid, routine access to and visualization of genomic information.

Potential Benefits:

The completion of these genome-enabling tools and reagents is the foundation upon which continued genetic and managemental improvement of livestock and poultry systems relies. These tools will be used to develop new genetic selection methodologies, identify the functional role and interactions of gene products in the interactome of the animal, and ultimately to develop “precision genetic management systems” for livestock and poultry. These tools will not only be used for traditional animal production research applications (reproduction, growth and development, nutrient intake and utilization, product quality), but will also be used to decrease the environmental footprint of animal production, improve animal health, well-being and resistance to disease, and enhance food safety.

Problem Statement 1B: Identify Functional Genes and Their Interactions.

The development of initial genetic linkage maps for the livestock and poultry species quickly led to whole genome scans for the detection of chromosomal regions (Quantitative Trait Loci, QTL) harboring genes contributing to the variation observed in economically important production traits. A large pool of QTL have now been identified for a variety of traits including growth rate, components of reproductive efficiency, and product yield and quality attributes; yet only a relative few of these QTL have been elucidated to the genic (Quantitative Trait Nucleotide, QTN) level. Additionally, QTL have yet to be identified in a significant way for complex traits that have been more difficult to describe in genetic models. Such traits include efficiency of nutrient utilization, reproductive capacity and longevity, various animal behaviors, and genetic resistance to stress and disease.

Research Needs:

Post-sequencing genomic architectures will be used to fine map existing QTL for livestock and poultry production traits in chickens, dairy and beef cattle, and swine. Considerable research effort is required to develop and validate the measurement of relevant phenotypes for components contributing to the complex traits of efficiency of nutrient utilization, reproductive capacity and longevity, animal well-being and resistance to stress, and product quality. Identification of QTL for these traits is a high priority which will eventually lead to the identity of genes impacting these traits and how they may be regulated genetically, epigenetically, and environmentally.

Anticipated Products:

- ✓ Valid standardized phenotyping systems for determination of genetic and phenotypic variation in efficiency of nutrient utilization, reproductive capacity and longevity, animal well-being and stress resistance, and product quality.
- ✓ Identification of QTL for efficiency of nutrient utilization in livestock and poultry.
- ✓ Information relating the function and regulation of individual genes contributing to economically relevant traits in livestock and poultry.
- ✓ Development of DNA-based diagnostics to provide genotypic information for use in centralized genetic evaluation and improvement systems.
- ✓ Further contribution to the annotation of the genome sequence of livestock and poultry species.

Potential Benefits:

Information generated from the research conducted in this area will form the basis for inclusion of genotypic data in national genetic evaluation programs. Functional genomics data will serve as the cornerstone for enablement of systems biology research. Development of a more complete understanding of the biological systems underpinning livestock and poultry performance will ultimately lead to a precision livestock and poultry production management framework. Production of animal products will become more energy efficient, have lessened environmental impact, and be from animals with enhanced wellbeing and welfare. Ultimately, the impact of this research work will be to enhance profitability and economic competitiveness of U.S. livestock and poultry producers.

Problem Statement 1C: Preserve and Curate Livestock and Poultry Genetic Resources.

Maintenance of genetic diversity in populations of livestock and poultry is critical to the long-term competitiveness of animal agriculture. Considering the trends of the past several decades toward increased consolidation and integration of production, along with employment of breeding systems that accumulate inbreeding within breeds and lines, this need has risen to highest priority. Furthermore, due to increased concentration of livestock and poultry, and continued increase in the easy and rapid movement of animals, the need exists to be able to respond to repopulation of animal and poultry systems in the event of a widespread disease outbreak or other catastrophe that would threaten the genetic resource base of animal agriculture.

Research Needs:

Selection of specific germplasm to be preserved requires phenotypic and genetic characterization for a wide variety of phenotypic characteristics measured within the appropriate production environments and systems. Genetic diversity characterization of individuals within breeds and lines should be performed using a suite of tools, including carefully designed genomic evaluations using appropriate high-throughput DNA marker systems (eg. single nucleotide polymorphism (SNP) panels). Such a process will allow minimization of redundancy while insuring complete coverage of germplasm diversity. Considerable gaps exist in the ability to preserve gametes and embryos of the various livestock and poultry species, with the need for improved cryopreservation technologies being most critical in poultry. The need exists to select, catalog, and curate DNA and other tissue-based collections of germplasm for both research and germplasm conservation purposes. Finally, the bioinformatics platform (Germplasm Resources Information Network, GRIN) interfacing the database of the nation's livestock and poultry genetic resources held in the National Animal Germplasm Program should be further developed to make information quickly and readily accessible, as well as become effectively linked to other such resources around the world.

Anticipated Products:

- ✓ A broad spectrum of genetic diversity in the form of viable and well documented livestock and poultry germplasm conserved.
- ✓ Genomic diversity in conserved populations ensured via the use of molecular technologies in selection of individuals to be preserved.
- ✓ Successful and efficient cryopreservation technologies and methods available for all livestock and poultry species.
- ✓ DNA and other tissue banks in place for research and genetic resource preservation purposes for livestock and poultry species.
- ✓ High-quality, comprehensive characterization, evaluation, and Genebank curatorial data made readily accessible, either from a transformed, upgraded, well-maintained GRIN, from databases housed at GRIN as the primary site, or at sites linked to GRIN.

Potential Benefits:

Careful strategic planning for and successful implementation of genetic resource management projects will provide industry users with a more dependable and more diverse source of high quality livestock and poultry genetic resources. In particular, vulnerable or threatened genetic resources will be better preserved and more secure. The National Animal Germplasm Program will be a repository of the alleles being elucidated in the post-genome sequencing era so that they may be available for long-term use by the animal agriculture industry in responding to the needs of the future. Readily available access to comprehensive and curated germplasm characterization information will allow strategic use of livestock and poultry genetic resources in fulfilling the demands for animal products in the future.

Problem Statement 1D: Develop and Implement Genome-Enabled Genetic Improvement Programs.

Application of quantitative genetics theory to populations of livestock and poultry has resulted in significant directed genetic change in particular components of performance, primarily from the use of field data recorded in both public and private national schema. Much of this improvement was facilitated by the maturation of statistical methodology coupled with increased scope and power of computing platforms that could be applied to large-scale pedigreed phenotypic data sets. Genetic evaluation and improvement programs are now poised to jump to new plateaus with elucidation of genetic parameters and interrelationships among traits, development of objective multi-trait breeding goals, and the availability of genomic resources for characterization at the individual gene and gene sets level. Additionally, the focus of genetic improvement programs is now shifting from production-driven to animal well-being and functionality-driven strategies.

Research Needs:

The suite of traits included in genetic evaluation programs of livestock and poultry is in need of expansion beyond the traditional production traits. Specifically, research to describe genetic parameters for a suite of economically important traits including efficiency of nutrient utilization, reproductive capacity and longevity, animal behavior, and resistance to stress is needed. These parameters include direct and maternal breed and heterosis effects, heritabilities, and genetic, phenotypic, and environmental correlations. As new traits continue to be defined and added to the genetic evaluation pipeline(s), continued work to define breeding objectives incorporating information from multiple traits under specific production-marketing environments is warranted. Work in functional genomics and proteomics will yield new diagnostics and genetic evaluation tools regarding specific genes and gene complexes. This new molecular information must be incorporated in to genetic evaluation and prediction frameworks in order to maximize genetic improvement. Additionally, new approaches to holistically use molecular information from the entire genome at the haplotype map level, must be investigated and validated to determine if and how they can be employed in genetic selection and mating programs. The complexity of the new types of information becoming available for genetic evaluation and improvement will require significant advances in statistical methodology and software to effectively put such data to practical seed stock industry use.

Anticipated Products:

- ✓ Genetic prediction for a suite of new traits in livestock and poultry related to adaptability and functionality in production-marketing environments.
- ✓ Enhancement of genetic evaluation and breeding system design for economically important production traits in livestock.
- ✓ Validation of new whole-genome selection methods for genetic improvement programs.
- ✓ Development of technologies allowing producers to identify genetic inputs fitting breeding objectives defined within their specific production-marketing environment.
- ✓ Statistical tools and methodology for incorporating molecular genetic data into genetic evaluation and prediction programs, resulting in “genome-enabled” genetic improvement.

Potential Benefits:

Enhancement of genetic improvement programs by adding traits which enable producers to better match genetic potential to the production resource base and consumer and societal demands will lead to a more profitable and sustainable animal agriculture. Genomic-level information will allow complex traits previously excluded from genetic improvement to be evaluated, these traits include many of the most important to enterprise profitability. Identification of elite genetic seed stock at younger ages with higher levels of inherent accuracy will allow the rate of genetic change to accelerate to previously unattainable levels. Much of the value of previous public research investments in animal genomics will be realized through “genome-enabled” genetic improvement programs resulting from this research.

Selected Accomplishments for Genetic Improvement

This section includes selected accomplishments that demonstrate stakeholder impact for NP101 for the current action plan. Each accomplishment is cross referenced with specific sections in Appendix 2 listing relevant references. However, many of the accomplishments listed to not have a specific corresponding reference or journal article because the research in many instances is just being completed. In addition, Appendix 2 includes many more references than can be linked to the accomplishment list and further demonstrates the scope of the research in NP101. Accomplishments including a cross reference including "M" are listed in the "Miscellaneous" section of Appendix 2.

Conserve, Characterize and Utilize Genetic Resources

National Animal Germplasm Program (NAGP) – FY2010 Collection Summary (1). This section summarizes the NAGP increases and impact over the past 5 years. The national collection of animal genetic resources held by ARS, ended FY10 with 599,112 germplasm and tissue samples from 13,638 individual animals of agronomically important animal species. Over the past five years the collection has grown linearly and increased in size by 163%. To date the collection contains samples from 32 different species, 143 breeds, and 181 specialized lines across all life forms in the collection. The collection is the largest national repository in the world and is at least twice as large as any of the European gene bank collections. This repository serves a vital role in protecting and preserving economically valuable germplasm and genetic diversity for the livestock industries.

Table 1. Summary of Animal Numbers and Germplasm and Tissue Inventory by Species, Breed within Species, and Line within Breed and Species.

Common Name	Species	Breeds	Lines	Number of Individuals	Units of Germplasm	Contribution to Inventory
Aquatic Freshwater Fish	13	0	24	690	20,444	3.35%
Aquatic Invertebrates	3	0	3	213	7,198	1.18%
Aquatic Marine Fish	6	0	0	15	823	0.13%
Beef Cattle	2	47	7	2,867	123,261	20.18%
Bison	1	0	1	73	1,565	0.26%
Chicken	1	11	100	1,411	6,502	1.06%
Dairy Cattle	1	12	1	4,997	175,847	28.78%
Elk	1	0	0	4	340	0.06%
Goat	1	14	0	392	9,536	1.56%
Pig	1	21	30	1,238	196,288	32.13%
Screwworm	1	0	10	10	19,350	3.17%
Sheep	1	38	5	1,728	49,779	8.15%
Total:	32	143	181	13,638	610,933	100%

National Animal Germplasm Program enhances genetic security and improves germplasm storage technologies (1). Research projects were conducted by ARS to ensure the long term viability of the germplasm collection. Beef semen has been cryopreserved since the 1950's but the viability of samples in long term storage has not been scientifically evaluated. Preliminary results indicate that storage time has not significantly affected fertility. Additional research was conducted to improve the efficiency of mating procedures with cryopreserved germplasm involving a non-surgical procedure for artificially inseminating sheep. The procedure is effective with fresh ram semen (55% conception rates) however cryopreserved semen typically produces significantly lower conception rates and therefore requires additional exploration for methods or technologies to overcome this limitation. In addition, 1,194 samples from 263 animals left the repository for animal generation, germplasm evaluation, or DNA studies. One example of the value of germplasm storage was demonstrated through a genetic distancing study (a study of genetic divergence between species) involving US sheep breeds and five breeds from Kazakhstan. It was determined that the Kazakh breeds were clustered and separate from US breeds, with the exception of the Karakul breed. This research is important to the identification of genetic variation in the sheep industry for economically important traits and to protect as much diversity as possible in the National Animal Germplasm Program. This research program has ongoing international collaborations with Canada, Brazil, and Tunisia to facilitate germplasm storage and to develop cooperative data base management protocols.

Germplasm storage and evaluation technologies ensure that genetic diversity is preserved (1). Significant progress was made by ARS in the areas of sperm physiology during hypothermic storage to develop more efficient hypothermic storage methods for poultry, swine and fish sperm. High-performance liquid chromatography was used to characterize the lipid fraction of freshly collected spermatozoa and to classify the proportion of phospholipid to cholesterol. Lipids, which are essential for poultry sperm functions are disrupted during cryogenic storage and are partly responsible for the low fertility rates of frozen and then thawed semen. This baseline data provides the foundation necessary for delineating the effect of hypothermic storage on poultry sperm, and is critical for developing reliable methods for poultry semen storage to improve production efficiencies through increased genetic progress and improved fertility and to ensure long-term germplasm preservation for the poultry industry.

Securing Holstein germplasm – expanding collections in France, the Netherlands, and the US (1). Globally, Holstein is the predominant dairy cattle breed but has been shown to have a relatively small effective population size (< 36 animals). This analysis determined how well the Holstein breed is secured and the diversity represented in each of the three countries' gene banks. Working with scientists from France and the Netherlands ARS scientists coordinated information and analyses for the US Holstein collection, suggested analytical approaches, interpreted the results, and co-authored a proceedings paper. This project concluded that, among the three gene banks, the US collection was the largest in terms of number of bulls represented, and had the lowest genetic relationships (more variation) when compared to the French and Dutch collections. Using the effective number of foundation sires to compare gene bank collections to each country's set of active bulls it was determined that the US collection with 784 foundation bulls, exceeding our current population of active bulls with 115 foundation bulls. Given these results, we can state that the US collection is the largest and most diverse collection among the three countries and includes significantly more diversity than the current U.S. Holstein breed population and that the gene bank has secured the Holstein breed for future use by industry.

Worldwide and genome-wide assessment of poultry biodiversity indicates large loss of alleles in commercial lines (1). Following decades of intense selection primarily for meat or egg production, and competition that has reduced the poultry industry to a few multi-national firms, the question has arisen as to whether sufficient genetic diversity exists to address future needs (nutritive value, emerging diseases, etc). To survey extant biodiversity of commercial poultry, an extensive collection of commercial pure lines, experimental chickens, and standard breeds were assembled (2,580 unique individuals), genotyped with 3,072 genetic markers equally spaced throughout the chicken genome, and analyzed for loss of alleles by the ARS scientists. Results revealed that individual commercial breeding lines have lost 70% or more genetic diversity of which only 25% can be recovered by combining all stocks of commercial poultry. However, modern agricultural practices do not appear to be the primary source of this allele loss as the majority of the alleles were lost prior to the formation of the current industry. These results emphasize the need for concerted national and international efforts to preserve chicken biodiversity to ensure adaptability and development opportunity for emerging challenges or genetic opportunities for the poultry industry.

Determining germplasm collection requirements for chickens (1). Knowing the quantity of germplasm necessary to reconstitute a population is one requirement for gene banks to use in setting goals for germplasm collections. The Food and Agricultural Organization of the United Nations (FAO) has recommended that to secure a chicken breed at 150% of reconstitution needs, gene banks must have a minimum 2,454 straws (0.5 ml) of semen to capture the scope of the inherent genetic variation. In FY2007 scientists at the National Animal Germplasm Program in Fort Collins evaluated inseminating hens intramagnally vs intravaginally and found the intramagnal procedure was significantly better in regard to fertility rates. Additionally, econometric procedures were used to evaluate the maximum efficiency and duration by which fertile eggs could be obtained from a single insemination. These results showed that maximum efficiency occurred at day 8 and maximum fertility occurred at day 17. These findings significantly impact the development of germplasm collections for chickens. By using intramagnal insemination, rather than intravaginal insemination the number of units of germplasm required to secure a breed can be reduced from 2,454 to 386. The impact of this finding is that collections of germplasm from chicken breeds can be secured more rapidly at a lower cost of collection and a lower storage cost. In addition the results have been adopted by FAO in their gene banking literature.

Embryonic death due to cold egg storage in poultry (1). Cold egg storage is a common practice prior to incubation in the broiler industry to prevent spoilage. However, cold storage longer than 10 days is typically associated with an increase in early embryo mortality. ARS scientists in collaboration with scientists from Aviagen, Ltd. found that after prolonged egg storage at 16 C, embryonic deaths within the broiler lines examined varied and occurred at different stages of development. The time of embryonic death from a broiler line with lower overall fertility was predominately before the onset of blood formation. In contrast, embryonic death in a broiler line with higher fertility was after the onset of blood formation. Further research is needed to investigate the cell and molecular mechanisms regulating the onset of embryonic blood formation, and the impact of cool egg storage on these mechanisms, to determine if this specific stage of embryonic development is associated with the biological basis of early embryonic mortality in broilers. This research will lead to improved fertility and reproduction rates for broiler improving production efficiencies for the poultry industry.

Sperm surface carbohydrate improves the fertility of turkey sperm (1). ARS scientists previously have shown that carbohydrates essential for poultry sperm function (sperm/egg recognition, sperm energetics and sperm motility) are lost during cold storage, and that this loss is partly responsible for the low fertility rates of stored poultry semen. This basic information served as the foundation for a strategy to improve the fertility of stored poultry semen by supplying exogenous carbohydrates in the semen extender. ARS research first demonstrated that turkey sperm can bind the carbohydrates in a time- and dose-dependent manner, followed by selection of the optimal dose that substantially improved the fertility of stored semen from

40% to 80%. While commercial breeders require fertility rates of 96-98% to maintain economic profitability, the results here provide significant progress towards the goal of using stored semen instead of freshly-collected semen for artificial insemination of turkeys which will improve production efficiencies for the poultry industry by increasing genetic progress and lowering costs of production.

Oviduct tissue type, presence of sperm, and genetic line affect gene expression in turkey hens (1). Turkey sperm maintained in the hen's sperm storage tubules (SST) are capable of fertilization for up to ten weeks after a single insemination; whereas the fertility rates of turkey semen stored in vitro decline dramatically after six to eight hours of storage. The genetic basis of SST sperm storage activity is unknown. ARS scientists found that differences exist between lines of turkeys with respect to expression of avidin and avidin-related proteins, and that these differences correlated with the known fertility of the turkey lines. Moreover, the presence of sperm in the oviduct increased avidin mRNA expression in the SST. These results improve the understanding of turkey fertility. The recent availability of the turkey genome sequence provides an opportunity to build on these results for a more thorough investigation of the genetic basis of sperm storage in the turkey hen which should lead to improved semen storage techniques for the turkey industry.

Comparing sheep DNA from Brazil and the US (1). Understanding the genetic distinctness of U.S. sheep breeds in relation to those in other countries can impact conservation strategies and breeding programs. Using genotypes generated in our respective countries, ARS and Brazilian scientists explored methods to combine and analyze genetic differences of sheep breeds found in the US and Brazil. This approach successfully determined genetic distances and illustrated how breeds are grouped together based upon physiological function (meat vs wool/hair production). Importantly, this study also showed that the Brazilian and U.S. hair breeds are substantially different from one another suggesting different and distinct histories of origin. As a result, U.S. breeders interested in Brazilian breeds (and vice versa) could expect substantial hybrid vigor by importing and crossing these breeds; potentially enhanced genetic performance for traits such as heat tolerance, and disease and parasite resistance; and that countries can leverage information generated independently and use that information to enhance germplasm conservation programs. Exploiting these differences may provide sheep producers in the U.S. with opportunities to increase genetic value and improve production efficiencies.

Efficient use of cryopreserved boar semen (1). Germplasm collected and stored in a gene bank will become a limited resource as it is used over time. To address this issue, an evaluation of the optimal insemination dose (1.0, 0.75, 0.5, and 0.25 billion sperm) for boar semen was performed. ARS scientists co-designed, cryopreserved boar samples, performed pre-freeze and post-thaw analysis of the semen samples, provided input into statistical analysis and prepared an abstract with university collaborators. The experiment found no statistical differences in pregnancy rate for each of the respective doses. However, the 0.25 treatment had numerically fewer pregnant sows. To ascertain the dose most appropriate to use if semen is limited, the total number of fetuses per sow inseminated was multiplied by the number of potential doses available if only one billion motile sperm cells existed. The results suggest that the optimal dose of semen to utilize per insemination was between 0.50 and 0.75 billion motile sperm cells. Such information significantly aids the National Animal Germplasm Program in planning germplasm collections and assures that effective use of stored germplasm can be made when needed. For industry, these results suggest that inseminating sows with one or two billion cells may exceed what is needed to create a pregnancy with optimal litter size and illustrates the need for additional research to address these issues for the commercial swine industry.

Science to Industry: Conserve, Characterize and Utilize Genetic Resources

National Program 101 is leading a very productive effort to conserve and characterize genetic resources for the livestock industries. Primary focus has been on germplasm preservation through the National Animal Germplasm Program and in basic science to develop better techniques and technologies to store and preserve avian germplasm. These programs have been very successful and are closely coordinated with industry stakeholders, breed representatives and external experts worldwide. The animal germplasm collection administered by ARS and NP101 is the largest and most diverse of its kind in the world and continues steady annual growth. NP101 scientific efforts to address the challenges associated with avian semen and germplasm preservation are recognized worldwide and continue to produce promising results. Collaborative efforts are underway to better understand the longevity of semen and germplasm storage and to develop alternative germplasm storage technologies featuring stem cell lines and related technologies. Additional focus is being directed at analyzing the genetic diversity of germplasm collections to ensure that maximum genetic variation is captured in existing collections and that target priority areas can be identified for future expansion of germplasm collections.

Genetic Improvement and Selective Breeding for Economically Important Traits

Beef

Test for Osteopetrosis for the beef industry (8). Osteopetrosis is a rare inherited disorder that makes bones increase in both size (mass) and fragility and is an emerging genetic disease in the Red Angus breed resulting in stillborn calves. Research was conducted by ARS to map the Osteopetrosis disease mutation locus using genotypes developed from Red Angus DNA samples using the Bovine SNP50 beadchip, also developed by ARS. This project was then used to develop a commercial diagnostic test for Osteopetrosis in collaboration with the University of Illinois, University of Nebraska, and the Red Angus Association of America. This research led to the identification of the mutation and a commercial DNA test was produced that identifies carriers of the defect in the Red Angus breed. This test is enabling beef producers to prevent the occurrence of the disease and to systematically eliminate this deleterious mutation from the Red Angus breed.

Across-Breed EPD Adjustment Factors (2). Beef cattle breed associations produce expected progeny differences (EPDs) as a measure of the genetic merit of individual animals for economically relevant traits. However, association EPDs are not directly comparable among different breeds. To address this challenge, across-breed EPD adjustment factors were calculated by ARS scientists for 16 breeds for growth traits (birth, weaning, and yearling weights and maternal milk) and for 8 breeds for carcass traits (ribeye area, backfat depth, and marbling) using data from the USMARC Germplasm Evaluation program and conventional EPDs from breed associations. These adjustment factors were presented and released at the Beef Improvement Federation meeting to a North American audience, followed by publication on various industry websites and in the popular press. This research allows producers to more accurately apply industry genetic resources and thereby more rapidly improve production of lean beef and meat quality.

Genetic evaluation of sustained reproductive success in beef cattle (8). Genetic improvement of reproductive performance has been hampered by lack of systems for use in conducting national cattle evaluation. In collaboration with the American Hereford Association, ARS scientists developed a system based on ages when females fail to maintain an annual calving interval, using survival analysis techniques. This system was adopted by the American Hereford Association to develop a genetic evaluation of reproductive performance for Hereford cattle breeders. Breeders of Hereford seedstock now have a tool to use for genetic selection to improve reproductive efficiency which will significantly improve genetic progress for the Hereford breed.

Using genomics to enhance national beef cattle evaluation (2). Genomic companies produce products that may be predictive of economically relevant traits. When these products are used independent of national cattle evaluation, producers making selection decisions can be misinformed. In collaboration with the American Angus Association, ARS scientists developed the necessary information to incorporate carcass merit genomic information into systems of national cattle evaluation (marker assisted). Breeders of Angus seedstock now have access to EPDs that incorporate both conventional quantitative genetic evaluations and genomic marker information which will accelerate genetic progress for carcass merit in the Angus breed.

Genetic factors influence bovine respiratory disease (12). Genetic, environmental and economic factors influencing the incidence of bovine respiratory disease (BRD) in feedlot calves were characterized by ARS scientists in nine breeds (Angus, Braunvieh, Charolais, Gelbvieh, Hereford, Limousin, Pinzgauer, Red Poll, and Simmental) and three composite types (MARC I, MARC II, and MARC III) over a 15 yr period. Epidemiological patterns for BRD infection were described. Few differences among breeds for BRD incidence were detected, however Herefords were generally more susceptible than the composite types. Estimates of heritability for resistance to BRD were low to moderate suggesting resistance to BRD could be improved over time from genetic selection programs. Phenotypic, environmental, and genetic correlations of carcass and palatability traits with BRD were low or negligible; inferring that selection to reduce BRD would have an insignificant effect on those traits. Significant economic loss associated with BRD infection in a feedlot was estimated at $13.90 per animal in 2007. This research may lead to genetic selection programs that improve resistance to BRD.

Heritability of follicle size and genetic correlation with fertility in beef cattle (2). Sustained reproductive success is the most important determinant of beef industry profitability. However, a lack of identified highly heritable traits that are closely correlated with fertility limits opportunity for genetic improvement of reproductive success. Previous research had identified size of the ovulatory follicle as being temporally associated with conception and/or establishment of pregnancy. However, there has been no previous attempt to estimate the degree to which genetic effects control variation in follicle size or the magnitude of its relationship with pregnancy rate. ARS scientists estimated the heritability of follicle size to assess its usefulness as an indicator trait associated with reproductive success in beef cattle. Results indicate the heritability of the size of the ovulatory follicle is greater than the heritability of pregnancy rate. However, because of the low genetic correlation of follicle size with pregnancy rate the use of follicle size as an indicator trait for fertility is limited.

Identification of quantitative trait loci for infectious bovine keratoconjunctivitis (12). Infectious bovine keratoconjunctivitis, also known as pinkeye, is one of the most economically important diseases in cattle. ARS scientists identified two putative quantitative trait loci for this trait, one on bovine chromosome 1 and the other on bovine chromosome 20. A gene known to be involved in pathogen resistance has been located under the quantitative trait loci on chromosome 1. These findings should motivate future studies with the objective of identifying the genetic base of pinkeye resistance. Resistance to pinkeye would improve production efficiencies for beef producers by lessening the incidence of pinkeye and would also enhance animal well-being.

Identification of a genomic marker linked with pre- and post-natal growth in beef cattle (8). A single nucleotide polymorphism in the osteopontin gene on bovine chromosome 6 was found by ARS scientists to be associated with birth weight, weaning weight, and yearling weight, but not twinning or ovulation rate, in a large multi-generation, cross-bred cattle population. Frequency of the minor allele in this cattle population was estimated to be 5.2%, and the estimated phenotypic difference between alleles was 1.14 kg for birth weight and 5.16 kg for 205-day weaning weight. This polymorphism is a probable functional mutation candidate that successfully tracks functional alleles affecting growth. Marker-assisted selection for the favorable genotype could have a beneficial effect on growth in cattle positively impacting production efficiencies for beef producers.

Slick hair gene localized to bovine chromosome 20 (5). The slick hair coat phenotype has been observed in tropical breeds of Bos taurus cattle and has been found to be beneficial for heat tolerance with body temperatures often 0.5 degrees Celsius lower for slick-haired animals compared to their normal-haired half-sibs on hot days. ARS scientists conducted a genome scan to map the slick hair gene in Senepol-derived cattle. The gene was localized with high certainty to a specific region of bovine chromosome 20 bound by two very tightly linked microsatellite markers. The mapping of the slick hair locus is the first step towards the eventual identification of the causative mutation that would constitute the definitive test for the slick hair coat phenotype. The results will facilitate efforts towards introgression of this gene into important temperate Bos taurus breeds (such as Angus and Charolais) to enhance their adaptation to tropical environments.

Dairy

Genetic prediction in dairy cattle improved using genomic and phenotypic information (2). Previously developed genomic predictions were transitioned from a research project to a production system, and the United States became the first country to replace official traditional genetic evaluations with genomic evaluations based on direct examination of DNA in January 2009. Numerous changes were made to the USDA genetic evaluation program to enable efficient management of genomic information, incorporate it in official USDA evaluations, and distribute those evaluations to stakeholders. Artificial-insemination and breed organizations now can use an online query to designate animals to be genotyped, determine if the animal has already been nominated, and check the reason a genotype was rejected. Four commercial laboratories provide genotypes that are stored in the USDA national dairy database, and the most recent international evaluations are combined with genomic and traditional data into a single evaluation that includes all available information. The evaluation system is continuing to be streamlined to provide genomic evaluations that meet industry needs with available resources. The programs and edited genotypes were also used to compute Canadian national evaluations in August 2009; USDA and Canadian researchers cooperated in developing international evaluation methods to combine genomic information from both countries. This research led to the development of a web site (http://aipl.arsusda.gov/) to catalog and manage the genetic evaluations for 20 million dairy cattle and goats for yield (milk, fat, protein, and component percentages) and fitness (mastitis resistance, longevity, conformation, and reproduction) traits and economic indexes as well as supporting documentation. This website is utilized by dairy industries worldwide, including producers, breed registry societies, artificial-insemination organizations, milk-recording associations, and dairy records processing centers, as well industry and university researchers. The availability of genetic evaluations and supporting documentation on the web site allows earlier access to estimates of genetic merit, which significantly increases genetic progress for economically important traits that contribute to production efficiency. These increases lessen the real costs associated with dairy production making dairy products more available to those most in need and reduce the production of green house gases.

First national genetic evaluations of U.S. dairy cattle including crossbreds implemented (2). Because of increased interest in crossbreeding by dairy producers worldwide, evaluations were developed and implemented to estimate the genetic merit of 19 million U.S. dairy cattle regardless of breed by ARS scientists. For the first time, genetic evaluations for crossbreds based on information from both parents were made available to dairy producers for use in making breeding decisions. Because evaluations are available for more animals, evaluation accuracy for purebred relatives was increased as well. A primary benefit of multi-breed evaluations is that genetic differences among breeds can be measured and used to improve production efficiency and health of dairy populations.

Genomic predictions of genetic merit for dairy cattle (2). Genotypes derived from DNA of 5,285 Holstein bulls and 75 Holstein cows were used in estimating genetic effects for nearly 40,000 single-nucleotide polymorphisms. Based on those effects, genomic predictions for yield (milk, fat, and protein), somatic cell score (indicator for mastitis resistance), productive life (longevity), daughter pregnancy rate (cow fertility), calving ease, final score (conformation), and net merit (a genetic-economic index) were developed. Two different evaluations were developed to predict the genetic merit of an animal's daughters and sons separately. Genomic predictions for genotyped bulls and cows were distributed in April and July 2008 to owners and to organizations. These predictions significantly improved the accuracy of genetic evaluations in Holsteins which will accelerate genetic progress for economically important traits in the Holatein breed.

Conception rate evaluation for the dairy industry (2). Declining fertility in the U.S. dairy herd has been a concern of the dairy industry for many years, and the increased use of estrous synchronization as part of reproductive management programs has intensified the importance of conception rate as a fertility trait. ARS scientists developed and implemented national genetic evaluations for heifer and cow conception rate for both bulls and cows, and the two new traits were included in genetic estimates for longevity. Genetic evaluations for conception rate will improve reproductive efficiency for the dairy industry providing a valuable selection tool to address a significant economic priority. Genetic evaluations for fertility traits also enhance animal well-being and welfare as well as provide an improved understanding of relationships between yield and functional traits. The availability of conception rate evaluations also allows international comparisons that can enhance exports of semen, embryos, and animals and positively impacts the economic value of the U.S. dairy industry.

Combining genomic information from low- and high-density marker sets (2). Recent advances in technology for detection of genetic markers have made genotyping dairy cows affordable for the commercial dairy industry. However, genotypes are based on various marker densities and contain different amounts of genomic information. ARS scientists developed and implemented computing software to determine (impute) missing genomic information based on haplotypes (closely linked genetic markers that tend to be inherited together) and to handle genotypes from detection chips of various marker densities. The initial application was to impute genotypes of dams from their genotyped progeny. These new algorithms for haplotyping and imputation allow multiple marker sets to be included in the same genetic evaluation. For young Holsteins genotyped with approximately 3,000 markers, the gain in accuracy of estimated net genetic-economic merit was almost 80% of the gain from genotyping 43,000 markers; simulated imputation of genotypes for 500,000 markers from 50,000 markers increased accuracy by 1.4%. Including a combination of marker densities for genotypes in genetic evaluations can improve evaluation accuracy at lower costs for dairy producers increasing genetic progress for economically important traits.

Genetic-economic indexes for lifetime merit of dairy cattle (2). Since 2006, feed costs have dramatically risen, which affected the emphasis that should be placed on a number of traits in national dairy indexes (net merit, cheese merit, and fluid merit). ARS scientists updated key economic values as well as milk utilization statistics, and recent changes in premiums paid for somatic cell score. Compared with indexes developed in 2006, less weight now is placed on fat and protein yields and calving ability (an index that includes calving ease and stillbirth), and more emphasis is placed on longevity, mastitis resistance, udder and leg traits, body size (favoring smaller cows), and cow fertility. The revised indexes should improve accuracy of selection of animals to be parents of the next generation of U.S. dairy cattle. The increase in genetic progress from use of the revised indexes is estimated to produce $6 million for the dairy industry annually for the dairy industry.

Sheep

Evaluation of hair breeds of sheep (11). Two important goals of the sheep industry are to increase reproductive rate and to decrease costs of labor. Hair breeds of sheep evolved to express “easy-care” attributes and are widely perceived to perform well with minimum labor requirements due to hardiness, parasite tolerance, and shedding of hair/wool. To investigate these issues, ARS scientists mated rams of two wool breeds (Dorset, Rambouillet) and three hair breeds (Dorper, Katahdin, and White Dorper) with Romanov ewes and the resulting crossbred daughters were evaluated for productivity in both high- and low-input production systems. The relative performance of the five types of crossbred ewes was similar in both production systems, with White Dorper x Romanov crossbred ewes being the most productive in each system. These results documented that prolific sheep and low inputs can be successfully combined to increase efficiency, production and profitability for sheep producers.

High prolificacy and lamb survival in a low-input system (11). Sheep producers are reluctant to use prolific breeds in low-input, pasture-lambing production systems because of the perception that such breeds require more labor during lambing and that the increased prolificacy will be entirely offset by lower lamb survival. Easy-care sheep that achieve high prolificacy and high lamb survival while lambing on pasture are needed to improve efficiency of production, increase profitability, and address the issue of animal well-being. ARS scientists established that Romanov crossbred ewes can successfully raise triplets on pasture without labor or supplemental feed. Therefore, progressive sheep producers can use appropriate breed resources to increase profitability by marketing more lambs per ewe and reducing use of labor and harvested feed.

Terminal-sire breed evaluation for sheep (11). Sheep producers throughout the U.S. claim that fitness, specifically survivability, of terminal-sire breeds of sheep has decreased as mature body size and growth rates have increased. Scientists from ARS, Virginia Polytechnic Institute and State University, and The Ohio State University completed the initial analyses of data from a three-year study that was conducted to characterize Columbia-, USMARC Composite III-, Suffolk-, and Texel-sired crossbred lambs (Rambouillet ewes) for traits of survival, growth, feed efficiency, carcass composition, meat quality, and pelt characteristics. The results of these analyses indicate that breed of sire did not affect the survivability of crossbred lambs from birth to harvest, but breed of sire affected feed efficiency, residual gain, and estimated profit. Based on these and other data from the study, ARS scientists and their collaborators have initiated the development of a white-faced, three-breed, terminal-sire composite genetic line to provide the sheep industry with an alternative terminal-sire genetic line. This composite will provide competitive growth, carcass merit and efficiencies and should have superior fitness to conventional terminal sires in the breeding flock.

Evaluation of maternal genetics for sheep (11). In a multiyear study, ARS scientists are comparing Polypay, Rambouillet, and ¼ Romanov ewes mated in a terminal-sire crossbreeding system to quantify the performance of the breed types in extensive management environments. In traditional extensive management environments, triplet litters have been reduced to twins, and the excess lambs have been sold at very low prices. One component of this study was aimed at assessing the ability of ewes to produce and raise triplet lambs. Initial data analyses indicate that ewes that produced twins raised approximately 87% of their lambs (1.74 lambs weaned), and ewes that produced triplets raised approximately 62% of their lambs (1.86 lambs weaned). The per-lamb average weaning weight of twin lambs was approximately 2 kg greater than that of triplet lambs, indicating that no significant improvement in total weight of lambs weaned was achieved by ewes raising triplets. Based on these early data, the study has been expanded to better determine when, between birth and weaning, the lambs are lost and whether body weight of the ewes affects lamb survival to weaning.

High fertility during spring breeding of Romanov crossbred ewes (11). Most breeds of sheep are far more fertile during fall breeding than spring breeding, resulting in the vast majority of lambs being born in the spring due primarily to environmental photoperiod. The seasonal production of lambs adversely affects product availability for consumers and this situation is a major obstacle for the U.S. sheep industry. To address this problem, producers have traditionally used crossbred ewes of Dorset, Finnsheep and Rambouillet breeding to achieve fertility rates averaging from 60 to 70% when breeding in the late spring. ARS scientists documented that Romanov crossbred ewes realized fertility rates of 87 to 89% when exposed during May, regardless of the remaining breed composition (Dorper, Dorset, Katahdin, Rambouillet, and White Dorper). Commercial producers can now better overcome the seasonal constraint of fertility rate by use of Romanov crossbred ewes improving production and reproductive efficiencies as well as providing additional higher value marketing opportunities.

Science to Industry: Genetic Improvement and Selective Breeding for Economically Important Traits

National Program 101 is a world leader in areas associated with genetic improvement programs. Historically, ARS and NP101 have been relied on to evaluate germplasm options for producers as well quantify genetic by environmental interactions to help producers identify best genetic and management programs for unique production systems. NP101 has continued this traditional role, but has also progressed to assist industry with the addition of genomic information in traditional genetic evaluation programs. ARS and NP101 was the first institution worldwide to offer genetic predictions for industry which combined direct DNA sampling for genomic information with conventional phenotypic data in the Holstein dairy breed. This work, and the functioning model, is now being copied worldwide by numerous other animal breeds. The impact of the research has been profound and far-reaching.

NP101 continues to lead the animal breeding community as leaders in the development of genetic parameters for genetic/genomic evaluation and prediction systems for cattle. These parameters are the statistical building blocks for development of genetic evaluation programs for all animal species and are critical components. This NP101 role has become even more important as new traits are identified and as the utility and impact of genomic information increases.

In the genomic arena, NP101 scientists have been instrumental in the discovery and development of genomic resources for application in all disciplines relating to food animal production and product quality as well innumity and disease resistance. NP101 research has also developed specific genetic tests to fight genetic diseases such as Osteopetrosis in the Red Angus cattle breed. This is a valuable role for NP101 which provides immediate industry support and creates simple and effective diagnostic tools for use in industry.

Scientists in NP101 continue to serve as a critically valuable expert resource for genomic and genetic programs across ARS through support and collaborate of related areas of research where techniques and technologies developed in NP101 are relevant. NP101 scientists are also leaders in the development and implementation of bioinformatic tools and techniques to enable the manipulation and evaluation of large genomic data sets which is necessary to produce the ultimate impact for producers.

Genomic Resources

General Accomplishments

Commercial genotyping tool (BovineSNP50, Illumina) - impact on livestock research and the dairy AI industry (5). Awareness of the success in the development and application of beadchips to genomic research in cattle fueled development of additional SNP beadchips for cattle. ARS led the development of a low (3K) and a high density (777K) product, and their impact on the industry is anticipated to be high as testing of different genetic improvement paradigms begins using cheaper SNP chips. The BovineSNP50 assay, developed by ARS remains the global de facto standard for cattle genomics research and genetic prediction use with sales having surpassed 500,000 samples. ARS received the USDA Secretary's Honor Award for Excellence by implementing genome selection in dairy cattle. Adoption of these technologies has had a tremendous impact on the dairy industry and has resulted in significantly improved genetic prediction accuracies and enhanced genetic progress.

Genome wide association using sample pooling (5). Whole genome association (WGA) studies based on high-density genotyping arrays are a powerful but expensive tool for dissecting genetic variation underlying a trait. For traits with low heritability large required sample sizes lead to costs in the millions of dollars per trait. A strategy to reduce these costs is to pool the DNA of many animals and genotype the pools, but the power of this approach has not been tested using genetic arrays currently available for cattle genotyping. ARS demonstrated that DNA pooling is effective with a 50,000 marker commercial cattle genotyping array, and extended it to show that some tissues can be pooled before DNA extraction to further reduce cost. A tissue pooling approach reduces the cost of WGA as much as three orders of magnitude. This technique makes it possible to evaluate more traits with higher accuracy at much lower costs significantly improving genetic progress for the dairy industry.

Bovine genome tools being used to develop whole genome selection methods and

further genome annotation in dairy and beef cattle (5). A research consortium including two ARS labs, an industry biotech company, a dairy industry organization representing all AI studs, and an industry pharmaceutical company has been formed to investigate the utility of genome selection in improving genetic gain, reducing costs of genetic testing in dairy cattle, and detecting quantitative trait loci (QTL). Resources were assembled to develop a 60,000 single nucleotide polymorphism (SNP) "chip" for genotyping and material to extract DNA from over 600 Angus, 2,500 Holstein, 250 Brown Swiss and 750 Jersey cattle. This project was only made possible because of the new availability of genome sequence information that quickly allowed identification of new SNP markers on a dense and genome-wide scale. In a second project, ARS scientists are developing a “gene atlas” of the bovine genome. Total RNA from 98 tissues derived from the cow used to develop the bovine genome sequence and one of her offspring has been isolated. Ultimately, this project will generate 100 million tags of sequence data that will be mapped back to the genome assembly. This information will assist in annotating most of the bovine transcriptome and will provide a robust framework of gene expression similarities and differences between various bovine tissues to help guide annotation.

Whole genome single nucleotide polymorphism assay development for estimating genetic merit (5). A research consortium led by ARS, the University of Missouri, Illumina, Inc., National Association of Animal Breeders (a trade group representing cattle artificial insemination organizations in N.A.), INRA (France), and Merial, Inc. developed, tested, and commercialized a genome-wide bovine single nucleotide polymorphism (SNP) beadchip that assays the allele content at approximately 58,000 genome locations. Genotypes for over 10,000 cattle were generated on this SNP chip. These genotypes were used to develop a whole genome selection (WGS) algorithm that produced genome enhanced predictions of genetic merit for three major dairy breeds. Over 3,000 genomic DNA samples were extracted from semen to support this work. The initial success of WGS to enhance selection in Holsteins led to release of unofficial genome enhanced genetic predictions in April 2008. Genome enhanced evaluations are now provided quarterly to the NAAB. These tools represent a portion of the initial development of significant technologies from the bovine genome sequence and will positively impact genetic progress and improve production efficiencies for beef and dairy producers.

Partial-genome evaluation to partition individual additive genetic effects into polygenic and genotypic components (5). Numerous progeny are needed to accurately predict an individual animal’s breeding value in traditional evaluation of polygenic effects informed by phenotype and pedigree records. Accuracy of non-parent breeding value predictions can be increased by including genotypes of informative single nucleotide polymorphisms (SNP) in the genetic evaluation. ARS scientists applied partial-genome evaluation procedures to feedlot intake and gain records of 1100 crossbred steers. This research determined that including genotypes of the 96 most informative SNP for each trait would increase non-parent accuracy by the equivalent of 5 to 20 progeny for intake, gain and efficiency traits. More accurate breeding value predictions enabled by partial-genome evaluations should significantly accelerate genetic improvement for these economically important traits in the beef industry.

Metabolic and gene expression-related changes in response to Vitamin E treatment in bovine cells (8). ARS scientists discovered that Vitamin E - alpha-tocopherol is more than a simple fat-soluble antioxidant. Through integrated global gene expression information and knowledge of cell regulation, it was determined that the action of alpha-tocopherol is mediated by specific receptors in the cell nucleus, such as estrogen and androgen. This work provided evidence that alpha-tocopherol may interact with receptors or gene transcription factors that control a myriad of cell functions and ultimately affect production efficiency in dairy cattle.

Knowledge gained from this research may be used to develop effective interventions that enhance nutrient uptake and use by livestock.

Discovery of microRNA expression in cattle and swine (5, 10). MicroRNA genes are a recently discovered form of genetic regulation with enormous impact on a variety of traits including growth, development, and tissue homeostasis. ARS scientists performed the first survey of microRNA in cattle and swine muscle, and identified similarities and differences between reports from human and mouse muscle microRNA expression profiles. The small RNA fraction containing putative microRNAs was isolated, cloned and sequenced to identify regulatory molecules. The first experimentally verified cattle microRNA sequences were deposited in the public database, and comparisons with published data from other species were made to identify potential ruminant-specific molecules. These results have significant impact on understanding the biology of ruminant muscle and address the general problem of annotation and subsequent analysis of the bovine genome sequence. Further elucidation of the bovine and porcine genome is a critical ongoing industry need and will require additional effort to provide maximum economic value from the sequences for the meat animal production industries.

Copy number variation (CNV) and segmental duplication regions of the bovine genome (14). A copy number variant (CNV) is a segment of DNA in which differences in base pairs or even genes exist between two or more genomes. The segment may range from one kilobase to several megabases in size. Animals ordinarily have two copies of each autosomal region, one per chromosome. CNVs may either be inherited or caused by mutation. CNVs can be caused by genomic rearrangements such as deletions, duplications, inversions, and translocations and are a surprising and important source of genetic variation not associated with traditional genetic theory. ARS research has identified over 200 candidate CNV regions (CNVRs) in total and 177 within known chromosomes, which harbor, or are adjacent to, gains or losses in genetic material. These 177 high-confidence CNVRs cover 28.1 mega bases or ~1.07% of the genome. Multiple gene families, have gone through ruminant lineage-specific gene amplification. ARS detected and confirmed marked differences in CNV frequencies across diverse breeds, indicating that some cattle CNVs are likely to arise independently in breeds and contribute to breed differences. Regions with varying copy number span about 400 known genes for specific biological functions, such as immunity, lactation, reproduction, and rumination. These results provide a valuable resource beyond microsatellites and single nucleotide polymorphisms to explore the full dimension of genetic variability for future cattle genomic research and will lead to significant genetic tools for the beef industry. These tools will increase genetic progress for traits of economic value, illuminate variability in phenotypic trait expression, explain complex production and behavioral traits, and improve disease resistance and treatment strategies.

ARS genomics research support. ARS provides scientific, computing, technical, and bioinformatic support for various projects that incorporate next-generation sequencing applications. ARS efforts have been highlighted by other researchers through the discovery of differential gene expression studies from corn smut, SNP discovery in catfish, metagenomic studies of the bovine rumen, gene expression studies for cattle, and genome sequence for water buffalo, cattle, and varroa mites. ARS also generated and analyzed the world's largest resource of DNA sequence information for cattle (>550 billion bases) representing more than 19 breeds and containing the locations of more than 48 million high-quality SNP that form the basis for the vast diversity present in cattle. These differences will lead to the development of numerous specific genetic tools for industry.

Beef

Integrated genetic map developed to aid in assembly and annotation of the bovine genome sequence (5). Through an internationally funded effort, the Baylor College of Medicine Human Genome Sequencing Center led the effort in generating sequences and assembling the bovine genome sequence. ARS scientists contributed to this effort by constructing an integrated genetic map comprised of approximately 17,000 markers using several genetic linkage and radiation hybrid maps from around the world. This integrated map was used in the bovine genome sequencing project to serve as the scaffold for assigning sequence contigs to chromosomal positions. In addition, over 1,500 full-length cDNA sequences were generated and annotated. These accomplishments will greatly accelerate the discovery of DNA markers suitable for marker-assisted selection and fine mapping of genes for economically important traits in cattle.

Construction of a Gene Atlas for cattle (5). Genome research in cattle is hampered by the lack of data on the expression of genes in normal tissues. ARS scientists collected in-depth data on gene expression of 95 normal cattle tissues and created an interactive database permitting a genome-level view of expression across tissues, tissue types, and tissue functions (immune tissues, neurological tissues, etc). The bovine Gene Atlas had substantial impact in research of cattle physiology, genetics, and genomics by providing a control for gene expression patterns to contrast against expression in various physiological states or genetic backgrounds, and facilitated further annotation of the bovine genome sequence. Further elucidation of the bovine genome is a critical ongoing industry need and will require additional effort to provide maximum economic value from the genome for the beef industry.

Bovine genome resources (5). The release of the bovine genome sequence assembly by the International Bovine Genome Sequencing Consortium facilitated the development of highly applied genomic tools for use in beef and dairy cattle research programs. ARS scientists provided principal leadership for the bovine community in this area. Results of these efforts include: 1) A genotyping platform was produced through Reduced Representation Libraries for use in genome-wide assessment of association of genotype with production phenotypes. “Next generation” sequence technology was implemented through Illumina Inc. to handle the sequencing of the libraries and identification of the single nucleotide polymorphisms, leading to the generation and validation of over 75,000 novel bovine SNP markers with minor allele frequencies. This work created the DNA marker resources for generation of a “50K SNP chip” that was made commercially available in 2007. 2) Developed an integrated genome map for cattle in cooperation with international collaborators. Several genetic and physical mapping resources were integrated into one map with over 20,000 markers and 300,000 large clones, providing an important resource for assembling and evaluating the genomic sequence, identifying quantitative trait loci, and supporting functional genomics. 3) Deposited over 500 full length gene sequences in the GenBank public database. Partial gene sequence and comparative information were used to identify clones containing complete genes. Genes containing clones were fully sequenced and 100 of these sequences were used by the international bovine genome annotation committee to assist in the annotation of the bovine genome sequence. Collectively these genomic resources will allow exploitation of the bovine sequence for genome-enabled animal improvement and precision animal management applications.

Breeding programs to identify genetic tools for industry (5, 8). Crossbred progeny representing the seven most widely used breeds in the US beef industry underwent extensive performance recording by ARS scientists for feed intake, carcass and tenderness traits in steers, and reproductive traits in females. Crossbred cows born in 1999 and 2000 were individually fed to determine maintenance requirements and continue to be evaluated for longevity (productive herd life), reproductive and maternal traits. Additional traits evaluated include vaccination response, treatment and diagnostic records, lung lesions at slaughter, and blood counts on entering the feedlot to support research on genomics of disease resistance. Genotypes for over 54,000 single nucleotide polymorphism (SNP) markers on the BovineSNP50 assay were obtained on steer and heifer calves, their crossbred sires and purebred grandsires. Genotype and phenotype data from this population, combined with that from similar populations in Canada and Australia will contribute to determining associations of genetic markers with traits important to cattle production. The associations can be used to develop robust DNA tests to guide breeding and management decisions by cattle breeders, ranchers and feeders.

Using data from the previous study, ARS scientists examined BovineSNP50 genotypes and weights at birth, weaning and one year of age of over 2500 crossbred cattle. Hundreds of strong associations between markers and growth were estimated with a high degree of confidence. Thousands of weaker associations for growth were also identified. These results are a critical step in developing additional tools that can be widely used by the cattle industry to improve growth and birth weights. As part of this study, the researchers also examined relative differences between weaning and yearling weights and birth weight, because undesirable increases in birth weight and calving difficulty can occur as a correlated response to selection for desirable increases in weaning weight and postweaning growth of beef calves. They determined that several single nucleotide polymorphisms (SNP), located throughout the genome, were associated with postnatal growth but not birth weight. These SNP may now be tested to determine their utility for selection to increase growth without affecting birth weight. A few other SNP, associated with large effects on birth weight and postnatal growth, may be considered in selection and mating decisions to manage both birth weight and growth. These discoveries will lead to the development of advanced genetic tools for the beef industry that will improve growth and production without increasing birth weight and dystocia which would increase calf mortality and decrease reproductive efficiencies.

Feedlot data were examined for growth and composition traits of beef cattle. ARS scientists used the BovineSNP50 on 1,800 crossbred steers measured for weight gain, meat tenderness, marbling, carcass weight and fatness. Hundreds of strong associations between genetic markers and specific phenotypic expression were estimated with a high degree of confidence, and these markers were often located on chromosomes previously identified as affecting growth. Thousands of weaker associations between markers and growth were identified with less confidence. These results will be useful in developing additional tools that can be widely used by the cattle industry to increase genetic progress for growth, carcass quality and fat content.

Genetic mechanisms associated with improved feed efficiency in cattle (8). Because feed efficiency is a time consuming and expensive trait to measure, genetic markers of feed efficiency in cattle could greatly enhance selection for this trait. However, measuring and improving feed efficiency is a very high priority for the beef industry because of the impact of feed costs on profitability. A study was completed in growing steers to identify changes in liver gene expression associated with increased feed conversion efficiency during feed restriction and compensatory weight gain. Several pathways were up regulated during improved feed efficiency included electron transporter activity in the mitochondria. Mitochondrial complex genes will be targets of further characterization because these genes have been associated with increased feed efficiency in poultry and cattle, and with quantitative trait loci for feed efficiency in cattle. These results will lead to definition of markers to improve selection for feed efficiency in cattle and industry tools that are much less expensive than measuring feed efficiency directly.

Relationships between genotype and phenotype in beef cattle (2). Scientists from ARS and North Carolina State University conducted studies examining the accuracy of imputed genotypes, changes in allele frequency resulting from selection, and conducted a genome-wide scan for regions having greater than expected heterozygosity. Using a segment of the Line 1 Hereford population genotyped with a high density (high cost) single nucleotide polymorphism (SNP) chip, genotypes of the remainder of the Line 1 population were imputed from a low density (low cost) SNP chip with greater than 80% accuracy. The close pedigree relationship among members of the Line 1 population makes this a more stringent test of imputation than using a pedigreed population that is less closely interrelated. Using a novel approach based on selection applied, four quantitative trait loci affecting growth to a year of age were identified. It also appears there are specific regions of the genome where heterozygosity is maintained in Line 1 in excess of levels expected except under an over-dominance model of inheritance. These results will lead to the development of low cost genomic tools for producers that will significantly impact genetic progress and improve production efficiencies.

DNA markers associated with respiratory disease in cattle (12). Previously, ARS scientists had established that bovine chromosome 20 is the site of genetic variation affecting a range of infectious disease-related phenotypes, using new high-density genotyping arrays. ARS has now examined the annotated genome of cattle in the area of this variation and identified two functional candidate genes with known roles in immune function. Previously discovered DNA sequence markers not present in the initial arrays, but predicted to lie in this area of the genome, were tested for association with disease traits in order to provide supporting data for the original study, and identify markers with better predictive merit for disease resistance. Seven markers in the two genes displayed association, providing potential markers for selecting animals with superior response to disease challenge in beef cattle. Effective genetic resistance to disease would significantly improve production efficiencies for the beef industry and improve animal well-being.

Specific genetic differences may identify cattle with superior fertility (8). Fertility of the cowherd is important to the profitability of beef production. Use of traditional selection techniques is slow, usually requiring several generations to produce significant changes within a herd. However, use of specific genetic differences among cattle can accelerate the selection of cattle that are more fertile on toxic tall fescue. Scientists from ARS and the University of Arkansas identified genetic differences in certain regions of two genes, prolactin and heat shock protein 70, and determined the association of these differences with fertility in Bos indicus beef cows. Differences in these two genes were associated with significant differences in calving rate of beef cows. These results provide information that suggests identification of cows with specific genotypes can assist beef producers in selection of cows that may have increased fertility. Improved fertility and reproductive efficiencies in Bos indicus beef breeds would increase production efficiencies for beef producers.

Dairy

Genetic merit in dairy cattle increased through genome selection and analysis (5). The results of ARS development of the commercial genotyping tool (BovineSNP50, Illumina) continue to have a major impact on livestock research. The dairy artificial insemination industry capitalized on substantial gains in accuracies of predicted genetic value early in an animal's life and predictions of genetic merit enhanced by genome-wide SNP genotypic data from the

BovineSNP50 have been implemented into the genetic evaluations of the Holstein, Jersey and Brown Swiss breeds. As a result, increased genetic gain will be an immediate impact of this technology as superior animals are more readily identified and more intense selection pressure applied to produce the next generations of dairy animals. Applications of commercial genotyping technologies developed by ARS scientists were used in numerous related applications including rumen metagenomic and soybean SNP discovery. These technologies were also used internationally in collaborative projects in Kenya to evaluate nematode resistance in sheep and in Pakistan to sequence indigenous dairy breeds and water buffalo. ARS scientists cooperated with the University of Maryland in research to identify a more precise marker order and complete coverage of the bovine genome, critical for cattle genome research. This research will further improve accuracies of genome enhanced predictions of genetic merit and identification of causal genetic variation underlying phenotypic differences in traits of economic importance. Increased genetic progress improves production efficiencies for dairy producers decreasing relative production costs.

Variation in an immune-related gene and milk production traits. Understanding differences among individual animals in their susceptibility to stresses to the immune system is important for identifying superior (or inferior) animals for milk production. Two polymorphisms in an immune-related gene called tumor necrosis factor alpha (TNF-alpha) were identified in cattle by ARS scientists and shown to be related to an increase in TNF-alpha protein expression in the blood and various measures of milk production. These results may reflect an increased efficiency of the mammary gland tissue to recover after injury, or improved aspects of immune function in certain individuals. The knowledge gained from this work can be applied to identifying mechanisms underlying differences in milk production efficiency of dairy cattle, and used in the development of selection criteria for improved mammary gland function and health.

Nutritional regulation of the transcriptome of cattle (8). Butyrate is a normal byproduct of carbohydrate fermentation produced by microbes present in the rumen and is a critical energy source for the cow. Two molecular technologies (next-generation sequencing and chromatin immunoprecipitation) were combined by ARS scientists to map key protein targets encoded in the bovine genome that are responsive to butyrate. In addition, microarray technology was used to identify a specific type of genetic material, called microRNAs, as targets of butyrate action. The microRNAs function in the regulation of gene expression. This research provides systematic and novel insights into relationships between nutrition and regulation of gene expression in cattle by showing microRNA involvement in butyrate response and will lead to nutritional strategies to improve dairy cattle production efficiencies.

Salmonella dublin infectivity and immune response in neonatal dairy calves (M-1). Salmonella dublin persists as a cause of morbidity and mortality of neonatal dairy calves and can be perpetuated on a dairy to become a potential pathogen for humans. Although body temperature increases within 48 hours in experimental models, little enteric disease is evident as with other Salmonella types. ARS scientists found that microbial analysis and immune communication genes showed quick progression to lung tissues within 48 hours of an oral infection. A supplement of a yeast extract plus ascorbic acid (vitamin C) increased the number of immune cells in lung tissues and Salmonella dublin infection increased cell infiltration into the lungs. No changes caused by the supplement or by the Salmonella dublin challenges were detected in white blood cells, mesenteric lymph nodes, or spleen cells. Weight gain increased with supplement feeding, except with the challenge when gain was similar to the non-supplemented calves. This information shows that lungs are a likely tissue for prevention or intervention for calves that are at high risk for Salmonella dublin infection and that yeast extract plus ascorbic acid is effective in immune modulation in lung tissues.

Poultry

Turkey genome assembly completed using a novel combination of sequencing and computational technologies (6). Scientists from ARS, Virginia Tech's Bioinformatics Institute and the University of Maryland's Center for Bioinformatics and Computational Biology completed the genomic map of turkey which will serve as the cornerstone for the development of sophisticated genomic technologies for the turkey industry. The information gleaned from this project will help breeders develop improved commercial turkey lines for producers and consumers. The turkey genome assembly was further strengthened when physical, comparative and genetic maps built by researchers from Michigan State University and the University of Minnesota were used to match DNA sequences to the turkey chromosomes. At completion, the original partnership expanded to include 68 scientists affiliated with 28 national and international research institutions. This project illustrates the rapid pace of genomic sequencing technology improvements. The turkey genome was sequenced in less than a year at a fraction of the cost of the chicken or bovine genomes and provides a valuable tool for the turkey industry to improve production and performance and decrease production costs.

Selection for body weight in chickens affects genes controlling growth and metabolism (6). Increased body size in commercial chicken and turkey lines has been accompanied by unintended changes in correlated traits such as increases in voluntary food intake and energy storage. Poultry breeders have intensively selected meat-type birds over many generations with specific emphasis on increasing growth rate (body weight) and meat production. Scientists at ARS and Virginia Polytechnic Institute and State University determined the levels of expression for genes involved in the regulation of fat metabolism, growth, and energy balance. Significant differences were observed for the expression of genes encoding lipogenic enzymes, AMP-activated protein kinase subunits and IGF system components in liver, brain and breast muscle tissue. These results indicate some of the potential impact of genetic selection for body weight on genes regulating growth and metabolism in chickens and this information will be useful for developing genetic selection strategies for commercial lines of poultry.

Restriction feeding management of female broiler breeder candidates affects gene expression (6). Broiler breeders in the poultry industry are feed restricted to reduce the occurrence of reproductive problems associated with obesity. Skip-a-day feed restriction programs are commonly used in preference to everyday programs even though there is a potential for excess fat accumulation by using the skip-a-day regimen. A project was conducted by ARS scientists to determine the effects of certain management regimens and metabolism of the broiler breeder candidate. The regimens were: 1) restricted amount of feed given to candidates on a daily basis (every day feeding) and 2) the daily feed allocation given on a two-fold basis but only given every other day (skip-a-day). Skip-a-day feeding increased the expression of certain genes implicated in the regulation of lipid metabolism. An increase in hepatic lipid accompanied the increase in gene expression, which could be deleterious to the long-term health of the birds. These results show the potentially significant impact of feeding regimens on gene expression in breeder pullets.

Chicken genome sequence enables DNA fingerprinting of commercial and experimental chicken lines (6). The availability of the chicken genome sequence offers opportunity to understand complex biological questions such as how genetic variation influences economically important traits. As a prelude to this advancement, ARS scientists evaluated a large number of chicken lines including birds from 36 elite commercial lines. By scoring 3,072 SNP markers on

2,580 different chickens, it was possible to screen the genome for unique or common alleles among the various chicken lines. These results are valuable to scientists and poultry breeding companies as it helps determine what genes are under genetic selection for economically important traits in industry broiler and layer lines. In addition, it is now possible to “trace back” poultry products to individual companies and lines through DNA fingerprinting using these markers. Additional aspects of this project are developing a linkage disequilibrium map of the chicken genome (haplotype map) to allow evaluation of whole-genome selection methodology. This is the first comprehensive genetic profile of virtually an entire commodity group. This research provides substantial contributions to poultry breeding and food safety and will lead to increased genetic progress for economically valuable traits in poultry..

DNA fingerprinting of unique chicken lines (6). For over seventy years, ARS has developed and maintained forty unique genetic lines of chickens, which serve ARS scientists and other institutes and universities by providing germplasm for critical research needs. Selected chicken lines were DNA fingerprinted with 3K and 60K genetic marker panels. Efforts were made to explore and analyze this unique data to improve and enhance the general understanding of the genetic variability between and within the chicken lines with respect to the underlying mechanisms that confer disease resistance. The findings will enhance the power of scientists to solve problems facing the poultry industry, especially with respect to infectious diseases and animal welfare issues which will improve the production efficiency of the poultry industry.

Targets in the chicken genome for a viral oncogene (12). Marek’s disease, a T cell lymphoma of chickens caused by a pathogenic virus, costs the poultry industry approximately $1 billion worldwide annually in losses and control measures. Thus, understanding how the Marek’s disease virus leads to disease is of both scientific and commercial interest. Meq is the putative cancer-causing viral protein and leads to aberrant expression of chicken proteins. Using molecular biology techniques and high-throughput sequencing, ARS research identified several target candidate genes in the chicken genome that Meq might affect. This information may help develop more effective vaccines or improve genetic resistance, both of which would reduce costs and improve animal welfare in the poultry industry.

Fine-mapping of genes conferring genetic resistance to Marek’s disease (MD) (12). MD is an avian herpes virus-induced disease, which continues to pose a significant threat to the poultry industry. Although MD has been tenuously controlled by vaccines since the 1970s, the importance of host genetic resistance to MD is widely recognized. A chicken population was developed by ARS scientists from highly inbred chicken lines, which differ in genetic resistance to MD. Chickens from this population were challenged with the causative virus and examined for MD incidence. DNA samples from 254 chickens were comprehensively analyzed for sequence variations throughout the entire chicken genome. Preliminary analyses of the data identified 172 genetic markers located on four chromosomes, some of which agreed with previous reports while others are new. The identified genetic markers will be very useful in two ways: to search for causal genes responsible for disease resistance and to accelerate genetic improvement of chickens in selection and breeding programs.

Marek’s disease virus evolves to higher virulence in poultry with limited genetic variation (12). Marek’s disease (MD), a serious problem for the poultry industry caused by the pathogenic Marek’s disease virus (MDV), is primarily controlled by vaccines. However, MD is now increasing in impact as the MDV continues to evolve to higher virulence. Most studies addressing the evolution of MDV virulence have concentrated on the virus while largely ignoring the hosts’ influence. The host system, called the major histocompatibility complex (MHC), represents a highly variable system designed to defend a species from extinction from the fast paced evolution of a parasite. In natural chicken populations, there are hundreds of different MHC haplotypes that oscillate or rotate in response to pathogen evolution providing protection and resistance. A haplotype is a specific and preserved combination of alleles (DNA sequences) at different places (loci) on the chromosome that are transmitted together. A haplotype may be one locus, several loci, or an entire chromosome and in this case represents the MHC. Commercial poultry breeding has limited the number of MHC haplotypes to six or less which restricts the ability of the poultry line to adapt to the disease challenge – the proper MHC haplotype does not exist. ARS research shows that MDV can evolve to higher virulence in birds with a single MHC haplotype. Based on this research ARS recommends that producers rotate the placement of MHC haplotypes by rotating genetic lines, similar to the simple method of crop rotation used to control pests in the field. This simple production practice should prevent the increase in virulence in MDV and to reduce the chronic problem of MD for producers resulting in substantial savings to the poultry industry and increased performance and production efficiencies.

RNA interference to inhibit viral disease in chickens (12). Modern vaccines have reduced productivity loss to viral diseases, however, many viral diseases continue to decrease animal productivity and welfare. Additional tools to complement vaccine control methods could aid in further reducing the negative effects of viral disease. Recently, a system known as RNA interference or RNAi has been developed that reduces the expression of specific genes. ARS scientists adapted this technology to reduce the severity of viral infections in chickens by targeting virus genes. The feasibility of this approach was shown in live birds where Marek's disease virus replication and pathogenesis has been reduced. This method has the potential to inhibit any infectious disease and may offer a valuable tool to control viral disease in the poultry industry.

Host chicken genetics - effect on vaccine efficacy (12). Vaccines have proven to be the most effective and economical method to combat infectious diseases in humans as well as in livestock. Efforts to improve vaccine protective efficiency have continued and expanded. Host genetics differences were investigated by ARS scientists for the influence on Marek's disease (MD) vaccine efficacy using unique genetic lines of chickens. ARS data suggests that host genetics play an important role influencing MD vaccine protection efficiency. Continuous analyses of ARS research data further suggest that different genetic lines of chickens respond to the same vaccine with variable protective efficiency. These results will be utilized to develop methods to target vaccine development to specific genetic lines in poultry, possibly improving health, production efficiencies and animal well-being.

Genetic markers to accelerate, enhance, and improve precision in poultry breeding (6). Genomic selection, which involves the use of a dense genetic marker panel to predict breeding values, is an exciting method that has great potential for accelerating the breeding of commercial chickens to meet growing consumer demands. Using two elite broiler (meat-type) and three layer (egg-type) commercial lines, ARS scientists led an international consortium to select birds over multiple generations based on predictions from 60K genetic markers. To date, genomic selection has been shown to be superior for the vast majority of the traits selected, including body weight and breast yield, compared to birds selected in parallel using current state-of-the-art quantitative breeding methods. This research strongly suggests that genomic selection is an improved breeding method. If costs for genetic testing continue to decrease, poultry breeders should be able to significantly increase genetic progress using genomic selection and increase genetic progress for economically important traits.

Swine

Genomic technologies developed for the pork industry – production, fertility and carcass quality (7). ARS scientists contributed 115,572 novel genetic markers which were combined with other publicly available markers to produce a high density porcine genomic assay for use in genome selection programs and research for the swine industry. ARS scientists also contributed DNA samples for preliminary assessment of the assay (SNP chip). This technology has now been adopted worldwide for use in genomic research and breeding programs in the swine industry. Similar research identified 18 genes and various other regions for associations with female reproductive performance. This research validated several known genes involved in signaling or synthesis of reproductive hormones additional results indicate that genes affecting energy metabolism are also significant, especially for reproductive performance traits. In related work, predictive DNA markers for pork quality near the calpastatin gene were evaluated for pork tenderness. Five markers were identified that were consistently associated with shear force tenderness across four different populations of industry-relevant pigs. These SNPs are highly predictive of pork tenderness in industry populations and will enable the swine industry to improve product tenderness increasing consumer demand for pork products.

Mapping the porcine genome (7). The swine linkage map is based on over 3400 markers, developed by ARS scientists. The Swine Genome Sequencing Consortium assembled 172 large fragments, from over 260,000 pieces, covering approximately 98% of the pig genome into a BAC physical map. Several computational methods were utilized to create thousands of links between the linkage and physical maps. Furthermore, comparing the porcine physical map to the human genome, the continuity and local ordering of segments of the porcine genome were improved. Some pig chromosomes are well mapped with few gaps remaining, while others consist of many fragments. The map is publicly accessible on the internet (http://pre.ensembl.org/Sus_scrofa/index.html). This physical map is providing a framework for the generation and assembly of the pig genome sequence. Furthermore, the map is immediately useful to the pig research community to direct maker development, identify genes and fine map quantitative trait loci.

Development of a panel of DNA markers for parentage and animal identification in swine (7). The swine industry required a panel of single nucleotide polymorphism (SNP) markers for parentage and animal identification to reduce the cost and improve the reliability of these DNA tests. Highly informative genetic markers developed by ARS were selected and tested in a large group of pigs selected from the industry by the National Swine Registry to represent purebred Duroc, Hampshire, Landrace and Yorkshire germplasm populations. Sixty markers that were sufficient for these industry applications remained in the final panel. These markers were then grouped together so that the information could be obtained in an economical manner. This panel has been provided to the U.S. swine industry and will improve genetic progress for economically important traits by providing more accurate relationships between animals.

Quantitative trait loci (QTL) affecting first parity female reproductive performance in commercial swine (10). Currently, over 20% of females retained for breeding in commercial production fail to produce two litters largely due to poor reproductive performance. The identification of genetic markers capable of predicting a gilt’s future reproductive performance in commercial herds would help eliminate many of these poor performing animals before they enter the breeding herd. Genotypic data were collected by ARS scientists on 700 boars contributed by industry partners using the Porcine 60K BeadChip. Phenotypic data on each of the boars’ daughters were available and their deviations from contemporary group means were used as phenotypes for each boar. In addition, similar data were available for 123 boars used in the USMARC commercial population. Two significant QTL were detected for number born dead, nine suggestive QTL were detected for number born alive, and two suggestive QTL were detected for weaning-to-estrus interval by ARS scientists. These findings will be used to develop tools for the pork industry to improve reproductive efficiency.

Reproductive and production traits in a Landrace-Duroc-Yorkshire population (10). Heparanase (HPSE) and Hyaluronidase (HYAL) 1 and 2 have been shown to be biologically relevant in ovarian and placental activity. Therefore, a study was conducted by ARS scientists to determine if polymorphisms within these genes were associated with reproduction and production events in a Landrace-Duroc-Yorkshire population of pigs. Both age at puberty and weaning-to-estrus interval were associated with a genetic marker for HYAL2. Birth weights and litter size components were associated with genetic markers for HPSE, HYAL1, and HYAL2. The identified genetic markers for HPSE, HYAL1, and HYAL2 will be further examined for use in marker-assisted selection protocols for breeding females to determine potential fertility, litter size capabilities, and(or) piglet survivability prior to introduction into the breeding system.

Adipose secretory genes revealed by gene expression studies in swine (10). ARS used microarray and real time RT-PCR technology to demonstrate the expression of numerous genes that encode secreted and non secreted regulatory proteins in porcine adipose tissue from growing pigs. Furthermore, this is the first report of expression of five secretory genes in adipose tissue of any kind. Many of these genes are cytokines and include interleukin- 8, interleukin-1beta, brain derived neurotrophic factor, and Insulin-like growth factor binding protein-7. Gene expression of insulin-like growth factor binding proteins (IGFBPs), hormones, growth factors, neuropeptide Y (NPY) receptors (NPYRs) and other receptors in OSQ and MSQ changed little with age in growing pigs. Distinct patterns of relative gene expression were evident within NPYR and IGFBP family members in adipose tissue from growing pigs. Relative gene expression levels of NPY2R, NPY4R and angiopoietin 2 (ANG-2) distinguished OSQ and MSQ depots in growing pigs. We demonstrated, for the first time, the expression of IGFBP-5, NPY1R, NPY2R, NPY, connective tissue growth factor (CTGF), and ciliary neurotrophic factor (CNTF) genes in pig adipose tissue. Furthermore, adipose tissue CTGF gene expression was upregulated while NPY and NPY2R gene expression were significantly down regulated by age. These studies demonstrate that expression of neuropeptides and neurotrophic factors in pig adipose tissue may be involved in regulation of leptin secretion,This information is vital to the development of novel methods to promote maximal growth and enhance onset of puberty and subsequent reproductive function in the pig. Furthermore, expression of cytokine secretory factors indicates that adipose tissue may mediate the influence of health and well-being on the onset of puberty. Furthermore, the relative expression of 13 non-secreted regulatory genes distinguished OSQ and MSQ depots in growing pigs. The expression of several such genes were influenced by age including an increase in CCND3, HSF1 and PTGR1 expression in MSQ and a decrease in UCP2 and REA (prohibitin -2) expression in OSQ. Negative associations between expression of some regulatory factors and leptin gene expression indicated that local leptin may decrease or antagonize adipogenesis.

Specific Breeding Aids

A cell culture model to study heat stress (4). Controlling production losses enable cattle producers to increase production efficiency of their herds by ensuring that the metabolic costs for maintenance of health are minimized. Heat stress is common in dairy cattle during summer months and often decreases milk production and reproductive performance. Heat stress can also exacerbate the detrimental effects of infectious and metabolic diseases. An immortalized cell line from a specific cell type present in the mammary gland of cattle was developed and used to demonstrate significant changes in cell form and structure in response to a temperature increase as small as 2.5°C and as brief as 1 hour. This development will allow the more efficient study of cellular and molecular changes during heat stress without the use of live animals and expensive environmentally-controlled chambers.

Feeder-cell-independent culture of the ARS-PICM-19 pig liver stem cell line (4). The ARS-PICM-19 pig liver stem cell line that is normally dependent on a layer of mouse fibroblast “feeder-cells” was adapted to growth without the feeder cells. ARS scientists established the feeder-independent cell culture of ARS-PICM-19, designated PICM-19FF (feeder-free), and validated its maintenance of key liver functions. The PICM-19FF cells were found to retain their normal liver cell morphology and functions. The creation of the PICM-19FF cell line will simplify the genetic analysis of the cells when used as an in vitro model of pig liver function and will simplify the use of the cells for future projects of agricultural interest including the metabolic engineering of pigs, and of biomedical interest, for example use as the biological component of an artificial liver device. ARS scientists also successfully created new bovine cell lines from umbilical cord tissue, allantoic fluid, and fetal skin tissue. The cell lines will be useful for animal cloning, or for the creation of bovine induced pluripotent stem cell (iPSC) lines.

Triple-acting staphylolytic peptidoglycan hydrolase fusion proteins are refractory to resistance development (4). Staphylococcus aureus is a notorious pathogen that has a very high rate of antimicrobial resistance development. It is believed that no bacterium can resist three simultaneous, uniquely-acting, antimicrobial agents. To develop such antimicrobials ARS fused the staphylococcal phage K endolysin LysK, to the staphylolytic bacteriocin, lysostaphin. These two proteins together harbor three unique, synergistic peptidoglycan hydrolase enzymatic domains. The resultant triple-acting fusion protein maintains all three enzymatic activities in the final fusion. When S. aureus cultures are exposed repeatedly (>10X) to sublethal doses of this triple fusion, there is no resistance observed, despite significant resistance observed in cultures exposed to either LysK or lysostaphin alone. S. aureus naturally resides topically on humans and animals including the nasal nares. The triple-acting staphylolytic peptidoglycan hydrolase fusions described above perform with greater efficacy than either of the parental lysins in eradicating S. aureus in a rat model of nasal colonization. We predict these triple fusion antimicrobials will be refractory to resistance development in animal models of staphylococcal infection which may potentially result in the development of a new class of antimicrobials for the livestock industries.

Protein fusions developed to combat mastitis in dairy cattle (4). Streptococcus aureus is a notorious pathogen causing chronic bovine mastitis in dairy cattle. The unique ability of S. aureus to hide in mammary cells provides a high level of protection to the pathogen from both the host immune defenses and conventional antibiotics, preventing elimination. This usually results in the culling of between 8% and 15% of the US dairy herd annually due to chronic infection. To combat this significant economic threat to the dairy industry, ARS scientists have developed a fusion of 2 proteins capable of carrying a lysostaphin enzyme across the plasma membrane of mammary epithelial cells and kill intracellular S. aureus. This technology is not limited to just mammary epithelial cells and may have novel antimicrobial application in many other areas. Now in field trials, this work will potentially produce tremendous saving for the dairy industry. This research program has ongoing international collaborations with Pakistan, Russia, Switzerland, the United Kingdom and Spain to develop related technologies in dairy cattle and other ruminant species. These collaborations provide extraordinary opportunities to leverage funding and scientific expertise for this research. They also help in the effort to ensure international food security by rapidly disseminating technology which enhances the productivity and efficiency of meat and milk production.

Bioinformatics and Statistical Analysis Tools

Bioinformatics pipelines to analyze metagenomic datasets (13). The rumen microbial community has profound effects on the health and ability of the cow to digest and extract nutrients from its feed. ARS initiated several studies to examine changes in the rumen microbial population in response to dietary changes, developmental changes, and disease states (e.g., parasitic infection) using next-generation sequencing technology. Limitations of this approach include the extensive data sets that are generated from this technology, statistical analysis of the data, and biological interpretation of the results. To facilitate these studies, we have successfully developed bioinformatics pipelines to improve our efficiency and ability to analyze large, metagenomic datasets. These tools increase the speed and efficiency of scientific discovery facilitating the development of better and more timely technologies for the dairy industry.

A statistical method for estimating the degree to which DNA tests are able to predict economically important traits (13). A method to estimate the proportion of genetic variation in economically important traits accounted for by the DNA test, which in turn determines the degree to which a DNA test can improve the accuracy of evaluations of genetic merit. Previous approaches to estimating this proportion were widely recognized as overstating the effect of the test and, consequently, were not widely used. The method developed by ARS scientists provides accurate estimates and is able to use DNA tests results in the form that DNA testing companies are currently providing them – molecular breeding values.
The estimator can be computed using software that is commonly used by animal breeders. This method provides a basis for potential customers of DNA tests to evaluate the utility of DNA testing technology and compare alternative DNA testing products.

Science to Industry: Genomic Resources

A primary research effort in National Program 101 is the development of genomic resources for the livestock industries. These efforts have been extraordinarily productive and NP101 continues to be a world leader in many of these areas. NP101 collaborated and provided significant contribution and leadership in the sequencing efforts of the genomes for beef, chicken and swine as well as other species of industry and scientific interest. In 2010, NP101 scientists led the successful effort to sequence the turkey genome. Work is currently underway by several NP101 teams to further refine and annotate the sequences for each of the food animal species. Further efforts are being made to address genetic variation not tied directly to the original genome sequences such as copy number variation. Additional research is being undertaken to better understand the epigenetic effects associated with food animal production traits and relationship between genetic/genomic merit and widely varying environmental effects.

A particular impactful research development in NP101 was the Bovine 50K SNP bead chip. This technology was instrumental to the NP101 effort to develop and implement the first genetic evaluation system in the world that combines genomic and phenotypic data – for the Holstein breed in the U.S. This technology has now been copied and developed for multiple species and populations around the world, much of which is also being led by ARS and NP101 scientists.

NP101 scientists are applying these and other tools, along with sequence information, to develop an impressive record of genomic discovery and application for traits of economic importance as well as for traits of basic scientific relevance and importance. NP101 scientists are developing and implementing much larger SNP bead chips and are exploring technologies which facilitate individual genome sequencing of animals with significant impact in relevant populations.

Related current research focused on the functional genomics of growth, reproduction, development, carcass quality and immune function is producing extraordinary results. Understanding the genomic basis for these traits is providing impactful tools for the livestock industries and is rapidly advancing the scientific body of knowledge relating to genomic function.

Additional research focused on the direct physical manipulation of the genome and of specific cells in ongoing in NP101 to develop technologies and techniques that will enable further exploitation of cellular and genetic resources. Current research is focused on the development of pluripotent stem cells in cattle and in techniques to develop alternative antimicrobials that are resistant or refractory to the development of pathogen resistance. Research to develop immortal cell lines and related technologies is also ongoing for use in research and for the development of new technologies relating to germplasm preservation, basic genomic function and numerous other functions. These "next generation" technologies offer significant potential future value for the food animal industries.

Research Component 2: Enhancing Animal Adaptation, Well-Being and Efficiency in Diverse Production Systems

Livestock and poultry production are considered value-adding industries to various agricultural input commodities as well as land resources considered marginal for crop production. Production systems operate in a wide range of physical and marketing environments from a highly diverse natural resource base. Proper matching of animal genotype and management system to the production-marketing environment is critical for sustainable and profitable production. This requires a comprehensive understanding of factors affecting animal adaptability and functionality, well-being, and efficiency. The development of scientific measures of stress and well-being and an enhanced ability to interpret such measures is crucial to the evaluation of current animal agriculture management practices and development of improved alternatives. Stress caused by social, nutritional, and environmental factors and their interactions need to be understood to limit negative impacts on care, production efficiency and well-being. Society is now demanding that scientific standards for documenting animal welfare within industry production systems become a critical control point in quality assurance programs.

The major cost contributing to unit cost of production in the livestock industry is the maintenance of the breeding herd or flock. Two limiting factors hinder reducing this cost: 1) reproductive rate per breeding female, and 2) the relatively high energy cost required for maintenance of the breeding herd. Furthermore, longevity of breeding females is an important contributor to lowering cost of production (i.e. increased longevity is desirable due to the high cost of producing replacements), yet, in several of the livestock industries the average age of breeding females has been declining in recent years, reflecting a loss of longevity.

Successful and efficient reproduction is essential to food and fiber production from livestock and poultry. Numerous environmental factors compromise reproductive success and contribute to decreased breeding longevity. Seasonal infertility in swine and reduced conception rates in cattle breeding programs are particular areas of concern. Sub-optimal embryonic, fetal, and neonatal development and survival significantly contribute to reduced reproductive efficiency in several of the species. Feeding and nutritional regulation of cells and organs jointly affect every aspect of livestock and poultry production. Animal industries are challenged to efficiently produce livestock products and to balance growth, feed consumption, and management of waste products. Given that upwards of 60% of total energy costs in the livestock and poultry industries are in feed inputs, it is imperative that solutions be found to allow improved efficiency of nutrient utilization for conversion to animal and poultry products.

Problem Statement 2A: Enhance Animal Well-Being and Reduce Stress in Livestock and Poultry Production Systems.

Recent food industry trends reflect a growing concern in the American public regarding animal welfare in food production systems. These concerns have resulted in a new set of supply system requirements from a number of major animal product customers for certification of specific animal care, production, and transport guidelines. It is unlikely that this trend will diminish in the near-term future. The livestock and poultry industries need to have clear and interpretable scientific criteria developed to allow proper assessment of animal well-being to meet these consumer demands in the marketplace. These criteria must be developed and validated within standard industry production systems. Development of such criteria will require a much improved understanding of stress physiology and animal ethology. The ultimate goal is to identify means for enhancing animal well-being through identification of improved production management practices that are profitable and sustainable for producers.

Research Needs:

Research is needed to further develop and refine scientific criteria for measuring animal welfare within production systems by comprehensively utilizing endocrine and immunological biomarkers in combination with animal behavioral and production performance data. A more complete understanding of the physiological, immunological, and behavioral responses of livestock and poultry to various stressors is needed to allow strategies to be developed to reduce production risk and losses. Specific research data are needed to address preweaning piglet losses, gastric ulceration, aggression, and sow welfare in swine production systems. Improvement of production systems to reduce neonatal calf morbidity and cow lameness is needed in dairy production systems while stress imposed by weaning, transportation, and co-mingling as well as from heat stress and fescue toxicosis are areas of needed focus in commercial beef production systems. Housing related issues encompass the primary need areas of poultry production including delineation of appropriate space, thermal, and lighting requirements, and a better understanding of feather pecking and aggression in birds. Research is also needed to consider the impacts and alternatives to beak trimming as well as to reduce lameness in laying hens and broilers. Forage and secondary metabolite induced equine conditions, including laminitis and fescue toxicosis, are not well documented or understood. A more complete understanding of the relationship between various animal temperaments, innate and adaptive immunity, and productivity is needed for all livestock and poultry species.

Anticipated Products:

✓ Scientific criteria for the assessment of animal welfare in livestock and poultry production systems.

✓ Enhanced understanding of physiological and behavioral response of livestock and poultry to environmental stressors.

✓ Improved management practices and production system designs that maintain or enhance productivity while improving animal well-being targeted to specific priority animal welfare issues.

✓ Identification of means to increase longevity of breeding animals.

Potential Benefits:

Animal stress and well-being research will benefit animals, producers, and ultimately consumers, by ultimately identifying means for reducing animal healthcare costs and improving food production efficiencies. Achievement of these economic and societal goals will help maintain and increase demand for livestock and poultry products in domestic markets and become more competitive in world markets, particularly in light of rapidly changing requirements for animal production practices in the international sector.

Problem Statement 2B: Reducing Reproductive Losses.

Increasing reproductive rate has been a goal of livestock and poultry research for the last several decades but has been largely unrealized in ruminants while only modest gains have been achieved in non-ruminants. Reproductive capacity and longevity is a complex trait and is affected by a number of environmental factors including temperature, humidity, photoperiod, and plane of nutrition. Managing the production environment for optimum reproductive efficiency requires an understanding of basic neuro-endocrine regulatory mechanisms, gonadal and uterine function, and development of the conceptus. These systems may be further altered by other environmental factors including social interactions among animals, handling by humans, housing, and transportation. Prepubertal development, seasonally reduced gamete production, postpartum anestrus, and aging all represent periods of reproductive inefficiency in livestock and poultry. Opportunities exist to optimize economic returns by determining how to combine genetic and nutritional resources in a manner that reduces the duration of these periods of reproductive quiescence. Delays in establishing pregnancy increase cost and reduce output of food animal systems. Maximum production efficiency requires every fertilized egg to result in birth of a healthy offspring that survives and grows during the neonatal period. Factors contributing to embryonic and fetal losses and/or inappropriate development in domestic livestock are only partially understood. Incidence of embryonic and fetal mortality has been estimated to be 20 to 40% in livestock species and 10 to 14% in poultry. Collectively, significant improvement of reproductive efficiency will require a true “systems biology” approach to be successful.

Research Needs:

Data to elucidate the impacts of environmental stressors on successful gamete production, fertilization, and pregnancy resulting in live births are needed for all livestock and poultry species. Research to address the observed decline in conception rate per service in dairy cattle as well as research to identify the physiology underlying seasonal infertility in swine should be conducted. Data to address how to reduce the prevalence of small litter sizes in swine are needed as well as research to better predict male fertility at early ages. Research to identify contributing factors and underlying physiology responsible for embryonic and neonatal losses in swine, cattle, and sheep is warranted. Physiological factors underlying lowered longevity of breeding females must be elucidated to address this issue in cattle and swine. Research to better understand the relationship of fescue pasture systems with cattle, small ruminant, and equine reproductive function is needed in the transition zone of the U.S. Finally, maternal epigenetic and behavioral effects on neonatal survival should be investigated.

Anticipated Products:

- ✓ Identification of critical control points limiting improvements in reproductive rate in livestock and poultry.
- ✓ Data to facilitate appropriate matching of management and production resources with genetic potential of breeding animals with the goal of increasing reproductive rate.
- ✓ Improved management practices and systems for improved reproductive success across production systems and environments.
- ✓ Identification of physiological means for reducing seasonal infertility in swine.
- ✓ Recommended production practices and management alternatives for increasing non-return rate in dairy cattle.
- ✓ Strategies based on physiological data for increasing longevity of breeding females in livestock systems.

Potential Benefits:

Increasing reproductive capacity and longevity of the nation’s breeding herds of livestock and poultry will lead to a more stable and profitable animal agriculture primarily by reducing production risks and losses. By spreading overhead costs associated with maintenance of breeding herds and flocks over more output per individual, production efficiency and profitability should be concurrently increased. Optimization of management and human and natural resources with genetic potential of breeding animals has the greatest potential payoff in animal production systems in this arena.

Problem Statement 2C: Improving Efficiency of Nutrient Utilization and Conversion to Animal Products.

The single largest cost of livestock and poultry production lies in feed inputs. Enhancement of nutrient utilization, therefore, is one of the major pathways toward improvement of production efficiency. A number of research priority areas exist in this area, including:

1) Livestock and poultry improvement programs continue to rapidly change genetic merit for production, particularly for rate of growth and yield of meat, milk, and eggs. Specific nutrient requirements and feeding systems must be determined and validated to allow the realization of these higher levels of genetic potential while minimizing nutrient losses to the environment. A comprehensive understanding of the metabolic or physiological functions that limit production potential is required to achieve this goal. As the genomes of livestock and poultry species are annotated, opportunities are increased for using functional genomics to develop an understanding of the regulation of genes and gene complexes by specific nutrients.

2) A major controlling factor of growth and development across species is feed intake. Feed costs represent the primary economic input into livestock and poultry production systems. Metabolic and sensory factors affect short-term feeding behavior. Long-term feeding behavior is controlled by the animal in its attempt to achieve a defined equilibrium within its environment. Understanding mechanisms involved in regulating feeding behavior and appetite should lead to more efficient production of livestock and poultry.

3) Ruminants rely on diverse microflora to digest feeds while monogastrics also host microbial populations in their gut that can influence efficiency of nutrient use. However, past research in microbiology of the rumen and other gut environments has barely scratched the surface of understanding the composition, function, and dynamics of these communities. Mathematical tools and new technologies emanating from the genomics revolution (i.e. metagenomics) provide exciting opportunities to delve deeper in to this area. Enhanced understanding of rumen microbiology also may provide insight in to applications to the area of bioenergy production.

4) Ethanol and biofuel production is rapidly increasing in the U.S., with current estimates predicting that over 20% of corn supplies will be used for ethanol production by 2010. This shift in the availability of feedstuffs for livestock and poultry production, along with the concurrent increase in byproducts from biofuel production, will require attention to the development of nutritional regimens under lower energy diet systems.

5) A substantial portion of the livestock production in the U.S. relies on forage based systems. In recent years, there has also been a growing trend toward development of pasture-based dairy and beef production systems. Effective utilization of forages by livestock suffers from a lack of adequate understanding of rumen digestion of forages in mixed diets, an incomplete understanding of the characteristics of forage plants that alter nutrient digestibility, inability to deal with toxicosis problems from some forages, and inadequate methodology for evaluating feed characteristics and digestibility.

Research Needs:

Research to utilize the chicken, cattle, and swine annotated genome sequences to develop an understanding of the regulation of genes and gene complexes by nutrients needs to be undertaken. Developing an understanding of metabolic syndromes in cattle through this approach is also warranted. Work to better understand feed intake in poultry and cattle should be conducted including identification of genes and gene products affecting feed intake and how they may be regulated by specific nutrients. Knowledge gaps exist in how feed efficiency may be altered in beef cattle, particularly in understanding genetic effects. Means of increasing the efficiency of nitrogen utilization are lacking and need further development in cattle and swine. Metagenomics, community fingerprinting, and PCR-based population assessments to characterize the rumen and other gut microbial ecosystems is warranted. Gaps exist in the ability to optimally utilize forage-based systems for dairy and beef production including an incomplete understanding of: 1) plant characteristics and factors limiting digestibility; 2) digestive physiology; 3) transformation of nutrients and factors affecting the partitioning of nutrients into end products from digestive fermentation; 4) animal physiological response to fescue toxicosis; 5) methodology for describing the relevant characteristics of forages including digestibility, physically effective fiber, starch, non-fiber carbohydrates; and 6) year-round forage-beef finished systems. Finally, critical research is needed to determine the nutrient requirements of genetically-enhanced livestock and poultry in combination with genetically-enhanced feedstuffs. This includes research to address the changing composition of production diets due to the increase in the biofuels sector of the U.S. economy.

Anticipated Products:

- ✓ Precision feeding systems for livestock and poultry that optimize nutrient availability to the animal while minimizing nutrient losses to the environment.
- ✓ Updated and current nutrient requirement tables for enhanced feedstuffs and increased genetic potential for production of animals and poultry.
- ✓ Optimization of lower energy diets in poultry and swine.
- ✓ Development of refined methodology allowing precise nutrient evaluation of forages.
- ✓ A demographic picture of the rumen and other gut environments.
- ✓ A “gene atlas” for feed intake, animal metabolism, and effects of various feed nutrients.
- ✓ Nutritional and production-management strategies for reducing the incidence of metabolic imbalance in cattle.
- ✓ Strategies to reduce the negative effects of fescue toxicosis in grazing livestock.
- ✓ Determination of the degree of genetic control of feed efficiency in cattle.
- ✓ Optimized year-round forage-based finished beef systems.

Potential Benefits:

Research in this area will allow the development of precision management livestock and poultry systems that make optimal use of nutrient inputs in both intensive and extensive production environments. Better understanding of genetic regulation will lead to the development of nutritional modulators that increase efficiency of nutrient use. Improved nutrient utilization will allow improved use of natural resources and will lower the environmental footprint of animal agriculture. Development of forage-based and other less-conventional production systems opens up new value-added market opportunities for midsized and small livestock producers. Improved understanding of the digestive environment will lead to applications to enhance gut fermentation, including potential applications to other processes including bioenergy production.

Selected Accomplishments for Animal Adaptation, Well Being and Efficiency

This section includes selected accomplishments that demonstrate stakeholder impact for NP101 for the current action plan. Each accomplishment is cross referenced with specific sections in Appendix 2 listing relevant references. However, many of the accomplishments listed to not have a specific corresponding reference or journal article because the research in many instances is just being completed. In addition, Appendix 2 includes many more references than can be linked to the accomplishment list and further demonstrates the scope of the research in NP101. Accomplishments including a cross reference including "M" are listed in the "Miscellaneous" section of Appendix 2.

Well-Being and Immune Response

Beef

Yeast products for feedlot cattle (15). As with other livestock production systems, there is an increasing concern over the potential link between feeding low levels of antibiotics in cattle feedlots and the incidence of antibiotic-resistant bacteria that affect human health. In an effort to identify potential alternatives to antibiotics, ARS scientists in cooperation with scientists from Texas Tech University and Lesaffre Feed Additives, Milwaukee, Wisconsin, evaluated the effect of feeding the cell wall of yeast to feedlot cattle that are at a higher risk for becoming sick. The researchers demonstrated that supplementing the diet of incoming feedlot cattle with yeast (Saccharomyces cerevisiae) and/or its cell wall not only improved the health of the cattle, but also improved their ability to combat exposure to the toxin from E. coli bacteria. Additionally, inclusion of this yeast altered the population of bacteria species within the intestine in a manner that suggested that the yeast may have caused an increase in beneficial bacteria. Identifying alternatives to low levels of antibiotics for inclusion in livestock feeds is an essential step towards securing the sustainability of livestock production in the U.S.

Respiration rate used as an indicator to determine heat stress in feedlot cattle (14). ARS scientists used respiration rate as an indicator to determine risk factors for heat stress in feedlot heifers. It was determined that at temperatures above 25ºC, dark-hided animals were 25% more heat stressed than light-colored animals; a history of pneumonia increased stress level by 10.5%; each level of fatness increased stress level by approximately 10%; and excitable animals had a 3.2% higher stress level than calm animals. Not only did the stress level increase with these risk factors, but average daily gain was reduced. The results of this study have not only revealed heat-stress risk factors of breed (color), condition score (fatness), temperament, and health history (treated or not treated for pneumonia), but also have shown the effectiveness of using respiration rate as an indicator of heat stress. These results will be developed into intervention strategies for beef producers to better manage heat stress and improve feedlot performance.

Intervention strategies to predict and prevent heat stress losses in cattle feedlots (15). Animal susceptibility to heat stress is difficult to determine visually. Animal performance can be reduced and well being compromised during periods of hot weather. Impacts of excessive heat load are varied, ranging from little or no effect to death of vulnerable animals during an extreme heat event. During a severe event, producers can lose 5% of their animals in a single day with resulting losses can exceed $1,000,000 to a single producer. A knowledge-based inference system with 11 animal characteristics has been developed based on previous research findings. This model summarized the risk factors into a single susceptibility number. Currently, data is being summarized to validate the model based on cattle feedlot data. An additional heat stress prediction model has been developed to summarize weather factors into a single index value. The model was used to develop a feedlot cattle heat stress website through a collaborative project with National Oceanic and Atmospheric Administration (NOAA) and National Weather Service (NWS). The website's primary feature is a seven-day graphical forecast of cattle heat stress. Additionally, helpful information is included such as impacts of heat stress, cattle and environmental risk factors, guides to recognizing heat stress, and actions to take for minimizing heat stress. The model continues to be evaluated to ensure accurate predictions of stress level. These tools help beef producers determine when intervention strategies are needed to prevent excessive heat stress to ensure animal comfort and welfare and prevent production losses.

Cattle temperament and production (14). Scientists from ARS, Texas A&M AgriLife and Mississippi State University investigated the influence of cattle temperament on various production parameters and stress responses to determine if an animal's temperament influenced its ability to handle management practices such as being transported, or its ability to cope with a bacterial infection. These studies have clearly indicated that calm and temperamental cattle have distinct physiological and immunological responses. Temperamental cattle seem to be more resistant to a toxin produced by E. coli bacteria, displaying less sign of clinical illness and recovering more rapidly. While handling temperamental cattle in production systems poses various challenges, there are clearly beneficial characteristics of these animals that could possibly be exploited to improve disease resistance and the associated morbidity and mortality that are significant economic burdens for the beef industry. This research will undoubtedly lead to a better understanding of variations in beef cattle production and will be essential information needed to develop alternative management practices to improve livestock production, health, and overall well-being.

Romosinuano cattle are more heat tolerant than Angus (14). Heat tolerance is an important attribute for the productivity of cattle in subtropical and tropical regions of the world. Typically Brahman or Bos indicus and their crosses are featured in these regions primarily for their heat tolerance capability. However, the Romosinuano a tropically adapted Bos taurus breed was evaluated for heat tolerance as a possible alternative source of germplasm in subtropical and tropical production environments. To increase understanding of heat tolerance in Romosinuano and heat sensitivity in Angus, scientists from ARS and the University of Missouri evaluated the physiological response in purebred steers of each breed while housed in environmentally controlled chambers. Steers were evaluated under thermoneutral conditions for 18 days followed by heat stress for 14 days. During thermoneutral, Angus steers maintained higher rectal temperature, respiration rate, and sweating rate compared to Romosinuano steers. During heat stress, although steers of both breeds increased in rectal temperature, respiration rate, and sweating rate, Angus steers maintained significantly higher levels than Romosinuano steers. This study clearly shows that Romosinuano are more heat tolerant compared to Angus. Elucidation of those mechanism(s) responsible for heat tolerance or those that maintain core body temperature will require further comparative studies.

Immune response in cattle is characterized (14). Understanding how stressors impact the immune system of cattle is important to maintain animal well being and productivity. The acute phase response is a component of the innate body defense that is characterized by varied reactions of the body to infection, inflammation, disease, or trauma. Characteristic reactions include fever; shifts in liver synthesis from normal products to acute phase proteins; increase in circulating white blood cells; and changes in behavior. The acute phase response is stimulated by the release from macrophages and monocytes of the pro-inflammatory cytokines at the site of inflammation or infection. Scientists from ARS, the University of Missouri and the University of Florida examined the immune response in cattle to a challenge of bacterial lipopolysaccharide (LPS). This study was designed to characterize the circulating patterns of six cytokines and four acute phase proteins in response to an LPS challenge. Results indicated that LPS increased concentrations of cortisol, four of six cytokines, and one of four acute phase proteins studied. Likewise, rectal temperature and respiration rate were increased by LPS. These new baseline results are being used in other studies to compare differences in the acute protein immune response due to breed and heat tolerance.

Intramuscular fat and immune response in beef cattle (14). Scientists from ARS and Mississippi State University demonstrated that the amount of intramuscular fat, fat located between muscles, may affect the immune response of cattle. In this study, researchers evaluated the ability of Angus heifers that had been genetically selected for high and low levels of intramuscular fat to combat the unfavorable effects of a toxin produced from E. coli bacteria. The study revealed that heifers lacking the genetic markers for intramuscular fat deposition had an altered immune response compared to those heifers that had a greater number of genetic markers. Further research is needed to determine the link between the amount of intramuscular fat and an animal's ability to mount an immune response.

Dairy

Novel methods to measure stress in livestock are developed (15). Cow lameness is one of the biggest challenges faced by the dairy industry and contributes to animal stress and decreased production efficiencies. ARS scientists compared cows housed on rubber mats to cows housed on concrete floors and found that cows on rubber mats had a greater ability to fight disease. Molecular markers of pain signaling taken from white blood cells were lower for the concrete-housed cows. These data imply that inflammation was occurring in the concrete-housed cows leading to increased lameness and stress. These data are useful for producers to determine the potential benefits of investing in rubber flooring that may extend beyond the reduction of incidence of lameness.

Molasses consumption is a reliable measure of social stress in dairy calves (15). Obtaining non-invasive measures of stress is a challenge to researchers who wish to evaluate housing and management procedures. ARS scientists established a mixing and isolation model and showed that stressed calves would voluntarily consume more molasses compared to non-stressed controls. This model can be used by researchers in the design and evaluation of novel agricultural housing methods and procedures.

Bedding material for calf hutches can affect well-being (15). Heat stress effects on calves begin before birth, but housing after birth can also affect well-being during heat episodes. To assess housing effects on the heat stress, health, and fly loads of calves, bedding material of the hutch (straw, sand, or wood shavings) and flooring of the outdoor area of hutches (dirt or rubber mats) were examined during later summer months. Immature fly populations (larvae and pupae) were greatest for straw; however fly counts on the inside of the hutch were least with straw bedding. The calves that had rubber mats in the exercise area had reduced growth rates compared to those with the uncovered dirt. ARS and Purdue researches determined that during a mild summer, straw, sand, or wood shavings were all acceptable hutch bedding, but fly larvae may need control measures in straw-bedded hutches and rubber mats are not a good addition for calves during summer months. These results can be used by producers to optimize their calf housing using bedding choices that are most available and economical for them.

Molecular mechanisms of improved milk production and immune function in dairy cows (14). Heat stress contributes to nutrient loss of dairy cattle through energy spent on non-productive processes to maintain proper body temperatures. Controlling these losses enables dairy producers to increase the production efficiency of their herds by reducing metabolic costs for maintenance and health. In collaboration with the University of Florida, dairy cows were provided cooling (sprinklers and fans) for the ~45-day period prior to calving known as the dry period, or no cooling during the dry period. The cows that were not cooled experienced heat stress. Relative to heat-stressed cows, cooled cows showed improvements in their transition into milking and exhibited gene expression changes in the signaling pathway for the hormone prolactin, which supports milk yield. In addition, improvements in the function of the immune system were observed in cooled cows. Cooling exclusively during the dry period is a promising management strategy to improve the cow's transition into milking, although additional study on its effects on the incidence of diseases related to calving are needed to confirm the practical application of these findings.

Poultry

Feed additive is successful in inducing molt without feed restriction (15). Induced molting by food withdrawal is a routine husbandry practice in the poultry industry, which may cause stress in birds and affect their well-being. ARS scientists discovered that including melengestrol acetate into the diets of laying hens allows for an induced molt, without food deprivation. These results show that this compound could be used as a welfare-friendly alternative for molting. The results also provide evidence that it is valuable to further examine if low energy fed birds are experiencing hunger. These results are useful to producers in addressing society and industry demands for an alternative to traditional induced molt practices.

Cannibalism can be reduced with genetic selection and infra-red beak trimming (15). Beak trimming in layer hens functions to reduce and/or inhibit undesirable behaviors**.** Beak trimming in the poultry industry typically involves the removal of 33 to 50% of the upper and lower mandibles using a heated blade that both cuts and cauterizes the beak tissue. There is a considerable body of morphological, neurophysiological, behavioral, and production research demonstrating the emergence of several markers of acute pain, chronic pain or both (e.g., persistent lethargy and guarding behaviors, reduced feed intake, and development of neuromas) as a result of beak trimming. ARS scientists have shown that: 1) genetic selection of kind, gentle birds is a suitable approach for controlling cannibalism in poultry, and 2) infrared beak treatment causes less beak re-growth and fewer bill morphological changes compared to hot blade cutting. These results will aid producers and scientists in managing layers most efficiently by reducing beak trimming associated damage and losses due to cannibalism before non-cannibalistic egg-laying strains are commercially available.

Infrared beak trimming improves hen welfare (15). Beak trimming, using a hot blade, is a common practice in the poultry industry that is often criticized as inhumane. ARS scientists investigated an alternative method of beak trimming which uses an infrared laser, similar to those used in biomedical procedures. They used both treatments and studied 60 production hens from 5 to 35 weeks of age. Hens which were beak-trimmed using the infrared laser method showed an improvement in performance and a reduction in stress levels. These results suggest that the infrared beak treatment provides a more welfare friendly means of beak trimming, allowing birds to display more efficient feeding behavior with less morphological abnormalities of the beak stumps. This study provides scientific evidence to support the use of infrared beak-trimming by producers and addresses the welfare concern of the current practice.

Genetic variation in heat stress responses in laying hens (14). Heat stress is a major problem experienced by poultry during high-temperature conditions. The ability to manage the detrimental effects can be attributed to many factors, including genetics. ARS scientists studied two different genetic lines of poultry to determine their ability to cope with heat. The two strains tested differed in their ability to cope with heat, with one strain showing more panting and behavioral modifications aimed at reducing their heat load. The data suggest that heat stress has detrimental effects on the physiology of laying hens; however, differences were observed in the heat stress response due to the genetic basis of variation. This study provides scientific evidence to support the use of genetic selection to combat heat stress. These results provide evidence that will be valuable for determining interventions for laying hens under heat stress conditions.

Genetic selection in layer hens reduces social stress (14). Social stress is a major problem in the poultry industry. Layer hens respond to social interaction affected by many factors, including genetics. ARS scientists studied three stains of layer hens to determine their ability to cope with social stress, resulting from large group size plus high density. The hens selected for high group productivity and survivability exhibit an altered regulation of their neuroendocrine homeostasis in response to social stress. The data suggest that genetic selection improves hens' behavioral adaptation to domestic environments. These results provide scientific evidence that genetic selection is a useful tool to address the welfare concern of social stress in the modern egg production industry.

Bill searing improves duck welfare (14). Bill trimming is a routine husbandry procedure used by the duck industry to prevent or control feather pulling and to minimize injury. It typically involves the removal of the tip of the both the upper and lower mandibles by cutting with hot-blade cautery (TRIM) or by searing (SEAR) the tip. Bill trimming may cause scar tissues, neruromas, and pain in ducks as those found in the beak trimmed chickens. ARS scientists showed that: 1) trauma-induced pathological changes are dependent on the type of bill trimming methods used and 2) in Pekin ducks, SEAR caused fewer morphological changes than TRIM, which suggests that SEAR may causes fewer effects on bird welfare compared to TRIM. These results will aid duck producers in managing ducks most efficiently and to decrease losses due to cannibalism.

Biomarkers for evaluating welfare in poultry (14). Social stress resulting from aggression and cannibalism is one of the major stressors in the poultry industry. Selective breeding of chickens for kinder and gentler domestic behavior could provide an alternative approach to address these problems and improve chicken welfare. However, biomarkers to be used for the selection are severely lacking. ARS scientists showed that neurotransmitters (dopamine and serotonin), stress hormones (epinephrine, norepinephrine, and corticosterone), and lymphocytes (T- and B-cells, and IgG) are useful indicators for evaluating chicken welfare. These results will aid producers and scientists in selection of chickens with greater resistance to stress.

Visual imprinting improves welfare in broiler chickens (14). Broilers are kept in large groups in a single house. Some of them self-restrict themselves within a small area of the house, causing them difficulty to get to feed and water, which affects chicken health and increases mortality. One contributing factor may be a deficit in spatial skills arising from the absence of essential environmental factors during routine rearing. ARS scientists illustrated that 1) the development and function of the central nervous system can be further induced in chicks by early imprinting and 2) imprinting improves chicks' spatial skills. This result provides a new approach for the controlling of physical damage and reducing mortality in broiler chickens by visual imprinting at an earlier age.

Swine

Lairage beneficial to pigs during transport (15). ARS scientists showed that use of a clean lairage (temporary housing) environment and maintained social structure for a period of 8 hours was beneficial to pigs during transport. Lairage in a known clean environment had benefits of diminished stress and immune stimulation, even 2 weeks after transport. Measures of behavior on the truck, during the lairage, and after the transport showed effects of increased transport stress in continuously transported pigs. Rehydration during the lairage was beneficial and access to feed improved intestinal microbial population stability, potentially altering the ability of the pig to use the nutrients that it eats. These results will aid producers and scientists in managing transported swine more efficiently while simultaneously decreasing losses due to animal stress.

Heart rate variability frequency provides a measure of positive and negative stress (14). The causal neurophysiological processes that mediate behavioral and physiological reactivity to an environment have largely been ignored. Heart rate variability analysis is a clinical diagnostic tool used to assess affective states (stressful and pleasant) in humans, but its application is very limited in farm animals. ARS scientists conducted an experiment to define the low frequency and high frequency components of heart rate in swine using pharmacologic blockade. They successfully defined both the low and high frequency bands which are measures of negative and positive states, respectively. This will allow future research to use heart rate variability analysis in assessing the welfare state of swine.

Understanding aggression when sows are mixed in indoor and outdoor housing systems (15). ARS scientists identified important behavioral sequences when unacquainted sows meet in limited and unlimited space. Unacquainted sows fight when introduced to each other but their detailed behavior during introduction has not been studied to determine whether escalation of their behavior into aggression can be predicted from behavioral sequences. The study found that certain behaviors such as nose-to-nose contact decrease subsequent risk of aggression, whereas others, such as ignoring social contact, increase subsequent risk of aggression, particularly in indoor pens. Indoors, sows engage in steadily escalating aggressive behaviors over time and display more pushes, knocks, and bites than sows being mixed outdoors in more space. However, outdoor sows are quicker to initiate high intensity aggression without the steady escalation seen indoors. Although biting occurs more quickly outdoors, the total number of bites delivered and the number of bites per interaction are lower than seen indoors. These differences in strategy are most likely due to the amount of space in the different situations. Indoors, sows cannot get away from each other after a fight has taken place, and therefore before engaging in a fight, they probably use low intensity interactions to obtain information about their chances of winning a fight. Outdoors, the space available for escape means that a loss can be immediately followed by withdrawal and avoidance. Aggression at mixing is a major issue for the U.S. swine industry as it moves towards group housing of sows. These results improve the understanding of what causes aggression to escalate and will help in the design of methods and facilities that will promote ‘positive’ behaviors before mixing, thereby reducing the aggression.

Antimicrobial alternatives for young pigs (15). There is an increasing demand and interest in alternatives to feeding low levels of antibiotics in livestock production systems due to concerns over increased incidences of antibiotic-resistant pathogens. In fact, there has been a recent call for voluntary elimination of the use of low level antibiotics in livestock production in the U.S. A collaborative study by ARS scientists demonstrated that feeding a diet that contained 10% citrus pulp for 13 days eliminated the presence of E. coli in the feces of pigs. Supplementation of citrus pulp could potentially be used to enhance growth in weaned pigs by suppressing chronic and acute pathogenic challenges without the use of low levels of antibiotics. Identifying alternatives to antibiotics for inclusion in livestock feeds is an essential step towards securing the sustainability of livestock production in the U.S if subclinical uses of feed grade antimicrobials is eliminated.

Removing the human element when measuring stress (15). ARS scientists evaluated stress conditions in livestock with the objective to measure stress more accurately and develop strategies and interventions to target and reduce stress in food animals. For example, obtaining a true measure of stress hormones from pigs is difficult because traditional blood sampling involves restraint of the animal. A novel penning system allows blood samples to be taken automatically. Levels of hormones such as cortisol and norepinephrine were significantly lower than those in blood obtained using a traditional restraint method. The development of automatic blood sampling will enable ARS to investigate real effects of environmental stressors rather than artifacts influenced by collection method.

Understanding the neurochemistry of aggression in pigs (14). Aggression among pigs is common especially when pigs are mixed, or if they have to compete for resources. It can impact the pigs' health and welfare and may reduce profitability for the producer. Ractopamine, a β-adrenoreceptor agonist, is fed to finishing pigs to improve growth performance and leanness. By mimicking catecholamines, ractopamine increases arousal but may also have other impacts. ARS scientists found that feeding ractopamine increased activity and led pigs, especially females, to engage in more, higher intensity aggression. Physiological measures showed that ractopamine-fed females had greater plasma catecholamine concentrations, lowered serotonin concentration in the blood and in parts of the brain. The expression of receptors essential for aggression inhibition was also suppressed in the brain of female pigs. By linking behavior of pigs with neurophysiological profiling, scientists have elucidated potential mechanisms related to aggression. This understanding is an essential component to help improve swine productivity and welfare.

Exercise of sows enhances bone health and sow productivity (15). A high percentage of sows are culled from the herd due to lameness. ARS scientists exercised sows to determine if the lack of exercise due to stall housing caused bone, cartilage or muscle injury. They found that sows who were exercised during gestation had stronger bones and lost fewer pigs. Thus producers which group house sows may find it beneficial to increase separation between feed and water, and to increase the number of times sows are fed. This will increase sow movement and may decrease sow lameness. However, we found no effect of exercise on cartilage health or lameness. Thus researchers still need to concentrate future efforts on decreasing the occurrence of lameness in the sow herd.

Prenatal stress alters sexual morphology and stress response (14). Prenatal stress, the stress imposed on a pregnant dam that may influence her subsequent offspring, has been shown to have profound effects on behavior and physiology of many species, including monkeys, rats, guinea pigs, goats, humans and swine. ARS scientists found that swine, exposed to pre-natal stress, can have alterations in sexual morphology and hypothalamic-pituitary-adrenal function; but with little effect on growth or immune function. This project has shown that prenatal stress in swine is likely caused not by cortisol alone but by other factors as well. These findings will aid scientists in understanding the implications of prenatal stress and it identifies possible mechanisms of action.

Refining piglet processing (15). One to three days after being born, piglets on commercial farms undergo various routine processing procedures to safeguard later welfare. These procedures have come under scrutiny from the animal welfare lobby as they inflict a degree of pain and distress when carried out. Alternative methods have been developed to reduce the impact of single procedures on the piglet. However, ARS scientists found quite clear distinctions between techniques. Processing techniques that can be carried out quickly and with minimal tissue damage are least stressful for the piglet. Alternative techniques such as teeth grinding, hot-iron tail-docking and oral dosing of iron, which might be expected to have some well-being advantages over teeth clipping, cold tail-docking and iron injecting respectively, were found to be disadvantageous primarily because of the amount of extra time needed to carry the procedure out. However, the alternative method of tagging for identification purposes, rather than ear-notching, did appear to improve piglet well-being, by being both a quicker technique and by greatly reducing tissue damage. Producers should ensure that procedures are carried out as quickly and as accurately as possible.

Decreasing pig aggression through diet (15). Aggression is a major problem for swine production as it negatively impacts the pigs' health and welfare. The neurotransmitter serotonin is essential for aggression control and is synthesized from the amino acid tryptophan. ARS scientists found that feeding a high tryptophan diet raised the concentration of tryptophan in blood at both 3 and 6 months of age. The high tryptophan diet also reduced behavioral activity, decreased the number of fights and overall aggressiveness when fed to the 3-month-old gilts, but not when fed to the 6-month-old gilts. These results are likely mediated by activation of the serotonergic system in the brain. Inclusion of higher levels of tryptophan in commercial diets could improve swine welfare by reducing aggression.

Yeast product and vitamin C modulate piglet and calf innate immunity (15). Some management practices may cause animals to become stressed and have a decreased abilty to combat disease. Thus methods to enhance immunity during times of stress are beneficial. ARS scientists found that yeast extracts and vitamin C act synergistically to improve calf and piglet growth; and to enhance well-being and the immune function of calves and piglets 3 to 4 weeks post-transport. This product has also been shown to be beneficial in reducing the incidence of respiratory disease. The product is now on the market and producers can use it to enhance immune function when livestock are expected to be stress.

Science to Industry: Well-being and Immune Response

Society's perspective of animal production continues to evolve. Consumers now are much more interested in the "way" animal are cared for and managed than at any other time in history. NP101 scientists are leading efforts to ensure animal health and well-being in modern production systems that are efficiently addressing the increasing global demand for animal products. This is a critical and expanding role for NP101. Current research is focused on the basic physiology of animal stress and adaptation, as well as management, housing and environmental factors relating to animal well-being. Specific research is producing a significantly improved understanding of how animals react to, and adapt to, stressors relating to housing, handling and transportation. Additional research is targeted at better understanding how animals adapt to environmental stressors such as heat stress in feedlots and in sub-tropical production environments common in the Southern U.S.. This research has led to numerous industry tools and technologies which are improving the production efficiencies of producers while protecting and enhancing the well-being of the animals in their care. Specifically, NP101 research has developed improved methods for de-beaking hens and castrating piglets, developed better flooring options for dairy cows and has developed a heat index-heat stress monitoring and computer based alert system for feedlot producers. NP101 research has also led to a better understanding of physical factors such as pen sizes and stocking density and transportation and lairage practices on stress and well-being as well as environmental factors such as ventilation rates and temperature variation.

Nutrient Utilization, Growth and Efficiency

General Accomplishments

Microbial diversity in the bovine rumen (13). Scientists at ARS and the J Craig Venter Institute completed a survey of the diversity of microbial populations in the rumen of cows fed forage diets and established guidelines for conducting future research examining the rumen micro-biome. The observed bacterial diversity was between 3181 to 7483 species-level taxonic units, the largest number observed for a ruminant species. This diversity was dominated by Bacteroidales, Bacteroidetes, Clostridiales, unknown bacteria taxa (group of organisms). There was a considerable difference in microbial diversity between cows from which the samples came. The fungal community was sequenced to saturation and also resulted in identification of a novel unknown fungal group. Raw extrusa should be suitable for future studies on rumen microbial diversity. These findings shed light on the incredible microbiological diversity in the rumen and identify ways to improve production efficiencies and mediate environmental effects through manipulation of the rumen microbiome.

Unique bacterial communities in the rumen (13). Performance differences in cows fed the same diet have been suggested to be due in part to a specificity of the ruminal bacterial community for the host cow, but this has not been demonstrated experimentally. ARS scientists used molecular markers to characterize changes in bacterial community composition in pairs of cows following nearly complete (~95%) exchange of ruminal contents. Ruminal pH and organic acid concentrations in rumens generally returned to their pre-exchange profiles within one day, while the bacterial community returned to its pre-exchange composition over a longer time scale (generally 2 to 9 weeks). The data suggest that cows harbor specific communities adapted to the individual host, and will vary in their response to microbial inoculants (probiotics) intended to beneficially alter ruminal microbial populations. These results will help researchers as they seek to improve the efficiency of dairy cattle diets and minimize the output of greenhouse gases by dairy cattle.

Determination of relative population sizes of classical ruminal bacterial species (13). Previous studies have not systematically quantified populations of individual bacterial species in the rumen. ARS scientists determined the percentage of 16S ribosomal RNA gene copy number contributed by 13 different bacterial species, two bacterial genera, and the domain Archaea, in several different cows, using a novel adaptation of a real-time PCR method originally developed for eukaryotic gene expression. The genus Prevotella was shown to account for nearly half the ruminal bacterial population, although classical Prevotella species make up only a small fraction of the group. Overall, the 13 most commonly studied ruminal bacterial species comprise only 5 to 7 per cent of the total bacterial 16S rRNA gene copy number, indicating that the vast majority of ruminal bacteria are likely to represent uncharacterized species. These results indicate that large-scale application of metagenomics for characterization of the rumen microflora is needed to address this large pool of uncharacterized species.

Modifying rumen fermentation with plant metabolites (13). A principle theory in rumen microbiology is that the activities of the rumen microbes can be optimized like any other fermentation. This concept has been applied in a number of ways, and antimicrobial feed additives are one of the most successful. Bacteria produce most commercially available antimicrobial feed additives (i.e. antibiotics), but plants also make antimicrobial compounds. ARS scientists demonstrated that hops (Humulus lupulus L.) decreased ammonia production by mixed rumen bacteria and inhibited pure cultures of ruminal hyper ammonia producing bacteria. Hops extracts revealed that the active compound was β-lupulone, and the mechanism of action was bioenergetic uncoupling of the cell membrane. Like many membrane-active antimicrobials, the activity was enhanced at low pH values. Results indicate that plant-based feed additives could be beneficial in improving ruminal efficiency through decreased ammonia production and may serve as alternatives to bacterial products in modifying the rumen ecology. This accomplishment has attracted attention by feed industry representatives and is currently being considered for a Cooperative Research and Development Agreement.

Influence of fiber composition on corn silage digestibility (10). Corn silage is a major feed resource for livestock, but fiber digestibility of the stover fraction is poor. A corn mutant with reduced inhibition of fiber digestion was fed to lambs (silage) by ARS scientists to measure feed intake and digestibility response. Lambs fed the mutant corn silage were less selective against fiber in the feed they consumed and digested more fiber. Future research will focus on the isolation of the gene responsible which will then have the potential to improve the digestibility of all forages used for livestock, increasing their value and utility and improving nutritional efficiency in ruminant species.

Value of amino nitrogen sources in ruminant nutrition (6). The ability of most ruminal bacteria to use ammonia as a nitrogen source for growth is a highly advantageous characteristic of ruminal fermentation, but non-fiber carbohydrate (NFC) degrading bacteria typically grow faster and more efficiently if amino nitrogen sources (ruminally degraded protein, peptide or amino acids) are also available. ARS Scientists showed the potential impacts of amino nitrogen on the efficiency of NFC bacterial growth include: 1) carbon sparing and an increased availability of carbohydrate to generate energy, 2) an increase in growth rate and a concomitant decrease in the fraction of energy used to maintain the cells, and 3) a decrease in energy loses (energy spilling). The effect of amino nitrogen sources on bacteria was incorporated into a model of ruminal fermentation that will improve the prediction accuracy of nutrient availability for ruminant species.

Coumarate-3-hydroxylase (C3H) down-regulation alters lignin composition and improves forage digestibility (10). The lignin component of the plant cell wall limits the utilization of polysaccharides by dairy and beef cattle. Down-regulation of the gene for C3H in alfalfa results in lignin that is derived from 65% of a lignin monomer, p-coumaryl alcohol, that is normally only minor (~1-2%). The compositional and structural changes result in improved digestibility of the plant cell wall. In collaboration with the Noble Foundation who produced transgenic plants, ARS scientists performed detailed structural and compositional analysis, and involved the industry in field trials for digestibility. C3H-down-regulation provides a new approach to improving digestibility of forages. A 10% improvement in cell-wall digestibility of forages by dairy cows in the U.S. is estimated to annually produce $350 million in increased milk sales and meat production concomitantly with 2.8 million tons less manure solids and 2 million tons less in grain supplements.

Gut hormone pathway in cattle (6). Glucagon-like peptide 2 (GLP-2) is a hormone released from specialized cells in the gut. Previous research in rodents and pigs showed that GLP-2 treatment promotes growth and reduces loss of cells lining the intestinal tract. In addition, it enhances nutrient absorption and barrier function of the intestinal lining. The gene and protein expression of members of the GLP-2 pathway were evaluated in 9 regions of the bovine gut at different stages of development and lactation by ARS scientists. In addition, the correlation of expression of the hormone and its receptor with markers for cell growth, cell death, nutrient transporters, enzyme activity, and blood flow were evaluated. Our findings support a functional role of GLP-2 in cattle and suggest that GLP-2 therapy may be useful to improve intestinal function and nutrient absorption in ruminant species. This research contributes to basic knowledge of the ruminant intestinal tract and suggests that GLP-2 treatment is a possible means to improve gut function and healing after injury or infection in cattle. These finding may lead to selection or intervention strategies that will improve production efficiencies in cattle.

Kinetic characterization of how bromocryptine (a model ergopeptine alkaloid) inhibits uptake of uridine by polarized bovine epithelia (12). In ruminants, microbial-derived nucleic acids are a major source of N and are absorbed as nucleosides by small intestinal epithelia and reabsorbed by renal epithelia. Although the biochemical activities of 2 nucleoside transport systems have been described for cattle, nothing is known about their sensitivity to ergot alkaloids (apparent causative agents of fescue toxicosis). ARS scientists in collaboration with the University of Kentucky used an in vitro bovine epithelial cell culture model (Madin-Darby Bovine Kidney [MdBK] cells), delineated the sensitivity of the ENT2 equilibrative nucleoside transporter to inhibition of uridine uptake by bromocryptine; demonstrated that the IC_{50} curve for inhibition of uridine uptake by ENT2-activity was essentially identical to that observed for ergovaline (alkaloid of endophyte-infected tall fescue and suspect causative agent of fescue toxicosis); identified the mode of bromocrytpine inhibition of uridine uptake by ENT2 as a "mixed" mode of inhibition, suggesting that ergopeptines inhibit through both competition with uridine for binding and an allosteric mechanism.; documented that D2 receptor protein is expressed by MDBK cells and highly sensitive to forskolin-stimulated production of cAMP. This accomplishment provides basic discovery data that will be useful in enhancing current prediction models and future improvements in the efficiency of nitrogen utilization in beef cattle, especially in regards to ergot alkaloid contaminated forage (e.g., endophyte-infected tall fescue).

Influence of ruminal and post-ruminal starch digestion on basal expression of nucleoside transporter mRNA in beef steers consuming forage (6, 12). In ruminants, microbial-derived nucleic acids are a major source of N and are absorbed as nucleosides by small intestinal epithelia. Although the biochemical activities of 2 nucleoside transport systems have been described for cattle, little is known regarding the regulation of their gene expression. ARS scientists in collaboration with the University of Kentucky demonstrated (in vivo) the differential expression of concentrative and equilibrative nucleoside transporters within the various segments of the small intestine and a positive relationship between expression of nucleoside transporters within the small intestine and luminal supply of nucleosides and glucose. This accomplishment provides basic discovery data that can be used to enhance current prediction models and future improvements in the efficiency of nitrogen utilization in beef cattle.

Beef

Tropically adapted beef breeds suited for Southern US cattle herds (6). To improve the overall value of calves from Southern USA cow herds, tropically adapted Bos indicus and Bos taurus breeds were evaluated by ARS scientists to determine the impact of tropical adapted breed type on dry matter intake and digestibility of low- and high-quality forage diets with and without protein supplementation. In one experiment, with Boran, Brahman, Tuli, and Gelvieh sired steers, breed of sire had no effect on diet digestibility. However, Boran-sired steers had lower dry matter intake of the low-quality diet than the other breed types used. In a second experiment, dry matter intake of the low-quality diet was increased when supplemental protein was fed. Steers with 25% Senpol or Tuli breeding had greater dry matter intake than steers with 25% Brahman breeding or purebred Romosinuano steers. We confirmed that previously developed concepts in conventional U.S. breeds describing the interaction of low quality forage diets and protein supplementation are applicable also to these breed types. Alternative sources of tropical adaptation germplasm in beef cattle can be incorporated into cow herds that generate stocker calves. The resulting prodigy could enter existing production systems without changing management strategies while increasing heterosis and improving growth and efficiencies for beef producers.

Forage intake by beef cattle (11). Hardware and software to classify ingestive events and estimate intake in grazing beef cattle was developed by ARS scientists and has the capacity to record and classify grazing events for up to 5 hours. This system is first to solve the previously intractable problem of estimating forage intake directly. The estimates demonstrate a high degree of precision and are relatively inexpensive to make providing an accurate technology for forage research in cattle based on grazed forage sonsumption.

Ethanol extract of tall fescue seed for induction of fescue toxicosis in Holstein steers (12). Tall fescue toxicosis caused by ergot alkaloids produced by the endophyte Neotyphodium coenophialum results in health and production issues in animals grazing the infected fescue, resulting in negative economic effects for producers. The decrease in productivity caused by fescue toxicosis has been estimated to cost producers more than $600 million per year. Most research examining the effects of fescue alkaloids on animal performance uses ground seed added to a basal diet to mimic grazing infected pasture. As one of the symptoms of fescue toxicosis is a reduction in feed intake, alteration of alkaloid intake level can occur using this methodology. A more precise method may be to dose animals with an extract containing the alkaloids found in toxic fescue. University of Kentucky and ARS scientists measured physiological indicators of fescue toxicosis following ruminal dosing of Holstein steers with an ethanol extract and showed that the ethanol extract of tall fescue seed can induce the symptoms of fescue toxicosis. Animals exhibited reduced intake, lowered heart rates, increased core temperatures, in addition to other symptoms. This research demonstrates the validity of an extract model for further research in the field of fescue toxicosis. This model should provide a more precise and repeatable method for inducing fescue toxicosis and subsequent nutritional and physiological studies on the mechanisms of the intoxication.

Hemodynamics in the caudal artery of beef heifers fed different ergot alkaloid concentrations (12). Fescue toxicosis, induced by consumption of ergot alkaloids (ergovaline) produced in endophyte-infected tall fescue, is a syndrome that costs cattle, horse, and small ruminant producers nearly a billion dollars a year in lost production. Although the syndrome was identified approximately 30 years ago, the lack of sensitive tools for measuring in vivo (real time) effects of the intoxication have hindered definition of the threshold level of exposure for induction of fescue toxicosis and also, the development of fully successful mitigation protocols for the syndrome. Recently, ARS scientists validated the use of Doppler ultrasonography for tracking fescue toxicosis induced vascular dysfunction (a primary functional deficit in intoxicated animals) in cattle on endophyte-infected tall fescue. Caudal artery area and blood flow rates were reduced in heifers receiving endophyte-infected tall fescue seed and these reductions were related to dose and length of exposure. These data demonstrate the usefulness of Doppler ultrasound technology as a tool for the real time study of fescue toxicosis and form the beginnings of a database that will be useful in determining the threshold level of intoxication.

Separation and quantification of ergot alkaloids in forage animal vein tissue to study endophyte toxicity (12). Ergot alkaloid related toxicosis (fescue toxicity) has been documented in forage animals for over 30 years. However, analytical methods for measuring these compounds have typically been limited in sensitivity making them unsuitable for tracking alkaloid levels in tissues of animals exposed to these alkaloids in their feedstuffs. ARS scientists in collaboration with Eastern Kentucky University developed a high performance liquid chromatography/mass spectrometry method for the detection and quantification of 8 ergot alkaloids (lysergic acid, ergovaline, alpha-ergocryptine, ergocornine, ergonovine, ergotamine, ergocristine, bromocryptine) from vascular tissue exposed in vitro to the alkaloids. This procedure provides the ability to now study the in vitro bioaccumulation of each of these alkaloids in vascular tissue. Recent efforts by ARS scientists using this technology have shown that ergovaline but not lysergic acid (two ergot alkaloids in tall fescue) is bioaccumulated in vascular tissue. Providing evidence that ergovaline is the primary vascular toxicant in animals afflicted by fescue toxicosis. Further, this method will be useful in helping to determine the needed time to clear an animal of the tall fescue toxicants.

Comparing feed efficiency across groups of cattle (6). Approaches currently used to identify efficient cattle allow for cattle to be ranked within study or experiment; however, these approaches do not lend themselves to comparing the feed efficiency of cattle across populations. The inability to compare efficiency measurements across studies reduces the ability to identify superior animals for genetic selection, and makes identifying common physiological differences that result in improved feed efficiency difficult. ARS scientists demonstrated that using robust biological systems models such as the Decision Evaluator for the Cattle Industry developed by ARS, provides a method to compare data across studies and provides more accurate estimates of feed efficiency in small data sets.

Evaluation of the effects of early versus normal weaning in beef cattle (6). Scientists from ARS and the University of Florida conducted a study to evaluate the effect of early weaning beef calves (90 days) compared to normal weaning (250 days of age). Previous research indicated that early weaning prior to shipment can reduce transportation stress and can increase subsequent performance in the feedlot. These data suggest that coincident weaning and transport stresses may compromise the immune system of calves, thus hindering subsequent performance and health. This study was conducted to determine if the innate immune response of early weaned calves differed from normal weaned calves in response to an immune challenge. Eighteen Brahman x Angus calves were fitted with an indwelling jugular catheters and blood samples for 10 hours to determine serum concentrations of stress hormones, pro-inflammatory cytokines and acute phase proteins. Based upon these data, the innate immune system of early weaned calves appears to be less naïve than that of normal weaned calves, therefore making them more effective at recognizing and eliminating endotoxin from their body. These data suggest that an altered innate immune system may be responsible for the improved feedlot performance previously reported in early weaned calves.

Providing glucose to the small intestine does not decrease amino acid metabolism (6). Improving the efficiency that nitrogen is converted to animal products improves feed efficiency and decreases nutrient release into the environment. Catabolism of amino acids at the small intestine represents one of the major events in the metabolism of protein that leads to inefficiency. Research conducted by ARS reported that providing glucose, a readily available energy source, to the small intestine did not improve the net appearance of amino acids into circulation. These finds suggest that amino acid catabolism by the small intestine is not solely driven by energy metabolism, and occurs to support other metabolic requirements.

Effect of µ-calpain deficiency on skeletal muscle development (6). Protein turnover requires proteolytic enzymes to degrade skeletal muscle proteins and the calpain system has been identified as a potential candidate protein turnover enzyme. ARS scientists reported that the proteases m-calpain and caspase 3/7 are up-regulated in skeletal muscle to compensate for the lack of µ-calpain. However at 30 weeks of age, muscle from mice lacking µ-calpain had cellular changes that indicated a potential for increased protein synthesis and skeletal muscle growth. These findings improve our understanding of µ-calpain function, including interactions with other proteases, which will contribute the development of approaches for promoting the preservation and(or) restoration of skeletal muscle mass.

Viral effects on growth hormones in beef cattle (6, M2). Scientists have known for many years that sick animals don't grow to their full potential. Scientists from ARS and Mississippi State University demonstrated that even a relatively mild infectious bovine rhinotracheitis viral challenge in beef steers alters the growth hormones in these animals. In fact, the study revealed alterations in the hormones that control growth, even in the absence of detectable increases in the blood of chemical messengers that are associated with regulation of the immune system. Therefore, it appears that even a mild viral infection can have significant impact on the potential growth and performance of cattle decreasing profitability.

Brahman influenced cattle have lower residual feed intake than Angus (6). Feed efficiency is one of the more important economic traits in beef cattle production. Brahman (Bos indicus) influenced cattle are important for cow-calf production in warmer climates such as the Gulf Coast region of the U.S., but the calves are purported to be less productive or efficient during growing and finishing. Scientists at ARS and the University of Florida evaluated the feed efficiency of Brahman:Angus crossbred cattle ranging in Brahman influence from 0 to 100 percent during a 70 day feeding test. Brahman cattle were more efficient than Angus when residual feed intake (RFI) was the criterion for efficiency but were less efficient by the feed conversion ratio (FCR) criterion. As the proportion Brahman increased, the trends for efficiency (RFI) or inefficiency (FCR) were linearly affected. The reasons for the discrepancy will require further research but may relate to a lower rate of growth in the cattle as the proportion of Brahman increased.

Beef cattle production efficiency improved through heifer development (6). Reducing cost of production hinges on maintaining high rates of reproductive success while reducing the use of harvested feeds. Traditional heifer development systems attempt to maximize pregnancy rates, but not necessarily optimize profit or sustainability. ARS scientists found that heifers developed to lower target weights than those traditionally recommended by industry consumed 27% less feed over winter and had improved efficiency throughout the post weaning period and subsequent grazing season in Northern climates. This strategy is estimated to reduce costs of developing each replacement female by more than $31.

In related research ARS scientists have undertaken efforts to; identify significant markers and genetic relationships in the beef cattle genome sequence focusing on energy utilization and carcass quality; develop a genetic analysis of longevity using survival statistics; and develop evidence that nutritional influences on replacement heifers may begin in utero and continue throughout life.

Dairy

Diet and management impacts on nutrient losses from dairy farms (6, M3). Two integrated feed-manure management trials and a survey of dairy feed practices were conducted by ARS to examine relationships between dairy diets, milk production, manure nutrient excretions and environmental risks. On Wisconsin dairy farms, approximately 20-35% of feed crude protein and phosphorus is secreted into milk and the remaining is excreted in manure. The amount and form of nitrogen and phosphorus losses to the environment were highly influenced by what was fed to dairy cows, and other management practices. For example, feeding dietary protein above recommended levels increased excretions of nitrogen in manure, and subsequent ammonia nitrogen loss from barns and field after manure land application. Unnecessary dietary phosphorus supplements dramatically increased total and water-soluble phosphorus concentrations in manure, and runoff from soil surfaces after manure application. Recommendations to use total mixed rations, balancing rations at least four times per year, and milking thrice daily results in highest milk yields and highest levels of feed nitrogen and phosphorus transformed into milk. Dietary options and practices are now available that satisfy the nutritional requirements of high-producing dairy cows, and also produce manure less susceptible to environmental contamination.

Nutrient use assessment tool developed for the dairy industry (6, M3). Nutrient use efficiency can be broadly defined as the relative amount of feed, fertilizer and/or manure nutrients inputs that are incorporated into milk, crops/pasture or other outputs. Relatively little information has historically been available on nutrient use efficiency for commercial dairy farms, or on how it can be measured and evaluated for impacts on profitability and environmental performance. Scientists at ARS and the University of Wisconsin-Madison developed tools that can be used to provide snap-shot assessments of feed, fertilizer, and manure use on dairy farms in various settings. These tools and an associated web site now enable dairy producers to optimize production inputs and manage nutrient to optimize efficiency for the dairy and the accompanying crop lands. These tools not only improve producer competitiveness and profitability but limit environmental risk and pollution potential.

New dairy ration development tools developed (11). Inaccurate analyses of carbohydrates in dairy rations lead to inefficiencies and additional feed costs. Digestible carbohydrates in animal feeds provide critical nutritional energy, but can also lead to health issues if not properly balanced in the diet. ARS scientists collaborated with industry to develop a nutritional definition for dietary carbohydrates to represent the true nutritional value in a dairy ration. This definition will increase conformity of feed evaluation, improve interpretation of research results, allow standardization of feeding recommendations for different species and increase the nutritional information available to nutritionists. In a related project, ARS developed a carbohydrate assay that increased ease of handling of samples, increased accuracy and shortened the assay time. The assay is still being validated, but has already been adopted by some commercial feed analysis and research. The assay will improve the accuracy of ration fed dairy cows and all livestock. Improving the accuracy of carbohydrate nutrition in dairy cattle rations lowers production costs and protects the health and welfare of the animals in the industry.

Changes in moisture of feeds can have substantial impact on the amount & composition of rations fed to dairy cows. Typical dairy rations contain whole-plant silages that are stored in open bunker silos. Changes in dryness of the crop harvested, & rain/snow events can change silage moisture from day to day. When moisture increases, dry matter of the feed (containing the nutrients) is replaced by water. This changes the relative proportions of ingredients, resulting in rations with imbalanced nutrient ratios leading to a loss in production of as much as 1.5 lbs milk per cow daily. ARS scientists calibrated a Near-Infrared real time sensor to accurately predict moisture in silages. The technology can be used to adjust rations routinely and account for daily deviations in moisture associated with rain/snow events, drying and storage, etc. The technology improves cow performance & reduces health problems & excretion of excess nutrients associated with poorly balanced rations.

Measuring the quantity of feed protein passing through rumen in dairy cows (11). There are no reliable laboratory methods to measure the amount of feed protein moving undigested through the rumen, which determines much of the value of feed protein for dairy cows. ARS scientists developed an improved technique to measure dietary protein escape from the rumen by incubating rumen microbes with specific proteins being tested in the presence of chemicals that prevent microbial uptake of protein digestion products. Because the microbes cannot use the undigested products, there is a direct relationship between the microbes and how fast protein is being degraded. Previously, no accounting was made of the formation of peptides (small protein fragments produced during protein breakdown). This research involved adapting a new chemical assay that measured peptides, as well as the other protein degradation products, and evaluating whether this new assay yields improved results. The method was applied to several kinds of soybean meal, one of the most important protein supplements fed to dairy cows. Overall, accounting for peptide formation reduced the variation, increased the observed protein degradation rate by 28%, and yielded estimates of protein escape for soybean meal that were similar to measurements made in living dairy cattle. These results were more reliable than those obtained using one of the most widely applied assays for evaluating proteins fed to dairy cows. This research indicated that the new laboratory based diagnostic method provides significantly faster, less expensive and more accurate estimates of protein escaping the rumen for common feedstuffs.

Canopy structure and nutritive value influence pasture utilization (11). Forage availability is generally considered the primary criteria influencing intake and performance of grazing dairy cattle. However, when carefully controlled by rotational grazing, forage availability often exceeds the cow’s daily requirement, and intake may be affected by other factors. A study of four diverse cool-season grasses by ARS scientists demonstrated that canopy height and proportion of the leaf fraction relative to the poorer quality stem fraction often governed herbage consumption. Cows consumed more forage as both canopy height and the proportion of the leaf fraction increased. When grasses had similar canopy structure, pasture utilization was positively correlated with herbage nutritive value. The results provide guidelines for the selection and management of cool-season grasses in rotational grazing systems for dairy cattle.

Rumen-protected methionine allows cows to produce more milk on less protein (6). Dietary protein supplies lactating cows with amino acids to make the protein in milk and body tissues. About half of the amino acids are essential, meaning they cannot be made by the cow but must be supplemented and are absorbed in the intestine. Methionine, often the most limiting essential amino acid, is available in rumen-protected form allowing absorption at the intestine. A new, cheaper type of protected methionine has just become commercially available. This compound is a chemically modified derivative of methionine that can resist microbial attack in the rumen and is converted to methionine in the cow’s body after absorption. Lactating dairy cows fed a 15.6% protein diet were given no methionine, methionine protected with a physical coating, or the new chemically protected form of methionine. None of the diets influenced feed intake or actual milk production. However, feeding the chemically protected form of methionine increased yield of energy-corrected milk and milk protein concentration. Moreover, cows tended to yield more fat and protein on either methionine source versus low or high protein diets without methionine. Feeding 16.8% protein without methionine elevated urinary nitrogen excretion and reduced nitrogen efficiency from nearly 35% to about 30%. Results with either methionine source were similar, indicating that the less expensive chemically protected form was as effective as the physically protected methionine. This research indicates that protein efficiency is increased and the potential for nitrogen pollution on U.S. dairy farms is reduced by an inexpensive supplement of rumen-protected methionine.

Poultry

Use of distillers dried grains by broiler chickens (7). A possible alternative feed ingredient for broilers is distillers dried grains (DDGs). The goal of this work was to determine if lower energy diets formulated with DDGs could be utilized by broilers produced in the U.S. which have been typically selected based on growth attained with much higher energy diets. ARS scientists tested the possibility that diets formulated with DDGs could cause birds to perform differently from those fed traditional diets based on a corn-soybean composition. Measurements of metabolism including rate-limiting enzymes in the regulation of growth and metabolism as well as indirect measurements of body composition indicated that there were some beneficial characteristics of feeding DDGs. DDGs could be fed in high quantities to augment the known effect of protein on reducing fat accumulation in broiler carcasses. In particular, results indicated that DDGs fed as part of broiler starter rations improved apparent bone strength during the finisher period. This work clearly demonstrated that the modern broiler can achieve acceptable performance on diets containing high levels of DDGs. Thus, feeding DDGs represents a viable and economical option for replacing a significant portion of the corn used in feed formulations for broiler chickens.

Managing obesity in the female broiler breeder (7). Broiler breeders are adult birds and the parent stock responsible for producing the next generation of broilers used for meat production. These birds must be raised with strict feed restriction to reduce the incidences of reproductive and metabolic problems associated with the progressive development of obesity in adulthood. Skip-a-day feed restriction is commonly used in preference to an everyday limited-feeding program even though there is still a potential for excess fat accumulation by using the skip-a-day regimen. Scientists at ARS and the University of Arkansas determined the effects of certain feed management regimens on metabolism in the female broiler breeder. The feeding regimens tested were: 1) restricted amount of feed given to birds on a daily basis (everyday feeding) and 2) twice the daily feed allocation but only given every other day (skip-a-day). Skip-a-day feeding increased the expression of certain genes implicated in the regulation of fat production and metabolism. An increase in liver fat content accompanied an increase in fat regulating gene expression which could be deleterious to the long-term health and survival of these birds. This work identified potentially negative impacts of an alternate day restricted feeding regimen currently preferred by poultry producers. Protocols to provide limited feed on a daily basis lessen the degree of fat production and accumulation in female broiler breeder chickens and should promote healthier and more productive breeders.

Sheep

Real-time ultrasound of live sheep for estimating carcass measures, yield, and value (6). Real-time ultrasound of live sheep can be used to estimate carcass compositional traits and produce information that can then be used to make sheep breeding decisions, with the goal of improving carcass merit and quality of lamb muscle foods. Research to validate ultrasound as a predictive tool, using current ultrasound technologies and with diverse populations of U.S. sheep, was conducted by ARS scientists. This study found that real-time ultrasound of live sheep can provide reliable estimates of carcass measures and value, and there are biologic and economic incentives for increasing longissimus muscle area in market lambs. Ultrasound technicians can use the information to validate their procedures, and sheep producers can use the information to make sheep breeding decisions that will improve the value and marketability of their lambs improving production efficiencies and profitability.

Growth of stocker lambs on bermudagrass (6). Forage quality declines throughout the growing season and grazing animal performance reflects the lower nutrition during the mid to late growing season. For animals grazing on warm-season forages, such as bermudagrass, animal performance is also negatively impacted by heat stress, and stocker performance on warm-season forages often does not approach the genetic potentials of the livestock. ARS scientists showed that Katahdin (a tropically adapted hair breed of sheep) or Katahdin crosses were generally superior to purebred Suffolk lambs (a temperate climate breed) in gains on bermudagrass forages during summer grazing trials. Protein supplementation had little benefit on stocker gain in Katahdin, Suffolk, or reciprocal-cross lambs. There was an indication of hybrid vigor for average daily gain in lambs only when they were not supplemented with protein, suggesting that protein supplementation may narrow the performance gap between purebred and crossbred lambs. This research demonstrated that tropically adapted breeds are superior for summer grazing, however, further research is needed to optimize supplementation strategies for summer grazing as forage quality declines.

Swine

Neonatal piglet growth rate affects body composition (8). During the preweaning period, a significant number of piglets born at normal weight exhibit poor growth and other signs of a failure to thrive. However, whether slower growth rate is accompanied by changes in the content of total body fat, lean (non-fat and non-bone tissue), and water (body composition) in normal birth weight piglets is not known. ARS scientists utilized a technology, Quantitative Magnetic Resonance, which measures fat, lean, and water content in live piglets, to evaluate changes in body composition of 235 piglets from birth to weaning (postnatal day one to 23). Though measurements revealed a wide range in body composition and growth rates, body composition was more closely related to body weight, the measure of growth rate, than to postnatal age or birth weight. This research demonstrated that the body composition of a slower growing normal birth weight piglet is different than an age-matched faster growing piglet. It also suggested that factors other than birth weight have a greater influence on piglet growth rate and body composition during the preweaning period. These results provide valuable insight into the growth and development of neonatal pigs and provide direction for further research to further determine the biology of growth in market hogs.

A biological marker associated with impaired growth rate in piglets (8). Biological markers predictive of growth rate are needed to identify poor postnatal performance prior to weaning in normal birth weight pigs. This would allow the producer to administer earlier treatments that improve piglet growth, health, and well-being. ARS scientists collected blood samples from normal birth weight baby pigs within a day after birth and the growth rate of each piglet was followed until weaning. A relationship between the quantity of a predominant blood protein (alpha-1 acid glycoprotein) and the rate of postnatal growth was found; piglets with a lower concentration of the blood protein after birth had a faster growth rate. This research pinpointed a protein that can be investigated further for its potential use as a readily available and simple diagnostic tool to identify slow growing normal weight vulnerable pigs immediately following birth. Identifying these “at risk” pigs and developing intervention strategies may enable producers to decrease pre-weaning mortality and improve reproductive efficiency and growth in production herds.

Piglet growth rate alters genes in tissues important for normal metabolism (8). Prior to weaning, piglets of normal birth weight may exhibit different growth rates that can make some pigs underperform and become economically inefficient to the producer. Measureable biological markers have not been identified that predict which piglet will become an underperforming hog. To identify genes that may serve as early markers for divergence in growth rate, researchers at ARS delineated the gene level for factors regulating the immune system, hormones, or metabolism in fat, skeletal muscle, and liver tissue obtained from fast or slow growing piglets within litters prior to weaning. No common gene was found to differ across all three tissues between fast and slow growing piglets; however within each distinct tissue several genes were found whose level correlated with fast or slow growth. This study has identified potential changes in genes that function in metabolism, hormone or immune processes that can be investigated further to determine if they have a role in piglet growth.

Science to Industry: Nutrient Utilization, Growth and Efficiency

A high priority and the focus of substantial research in NP101 is in the areas of growth, physiology and nutrient utilization. Nutrient utilization has "re-emerged" as a very high industry priority over the past few years as demand for feed grains has increased production costs for many livestock producers. Consequently nutrition, growth biology and physiology, and basic endocrine function are all areas of priority and focus for NP101 research. Current research is focused on potentially high impact areas of research including physiological growth and development, evaluation of nutritional requirements, feeding and feed mixing technologies, evaluation of alternative ingredients, forage evaluation and forage utilization efficiencies and rumen-gut microbiology. NP101 scientists have helped develop numerous significant technologies and techniques for industry that continue to improve production efficiencies for producers. NP101 research has led to a much better understanding of the physiology of nutrient utilization and will lead to the additional development of tools for industry. NP101 research has also led to a tremendous increase in the level of understanding for the basic biology and physiology of animal growth and development in numerous areas. Research in these areas continues to provide steady incremental improvements for industry which is the result of long term sustained funding and research efforts in NP101. This continued basic research is critical to the future development of applied technologies that will continue to improve nutrient utilization, growth and production for the food animal industries.

Reproduction and Reproductive Efficiency

Beef

Cows with higher calf production potential (5). Increased embryo and fetal mortality resulting from crowding in the uterus can be associated with greater than twin pregnancies. Research conducted by ARS found that selecting for increased ovulation rate can be used to increase the number of calves within a pregnancy thus increasing the annual production potential of a cow. However, capacity of the uterus to successfully support the growth of more than two calves may be limiting suggesting the need to include uterine capacity in a selection index for increased birth rate. These findings demonstrate that selection for increased birth rate in beef cattle can be used as a tool for developing cattle with higher production potential.

Advances in reproductive efficiency lead to improved technologies for use in the beef industry (5). Research by ARS scientists demonstrated that yearling heifers with fewer uterine antral follicle counts have decreased heifer pregnancy rates. Antral follicles are small follicles that can be seen and counted with ultrasound. Each primordial follicle contains an immature egg that can potentially develop in the future. Identifying heifers with greater antral follicle counts offers a strategy to increase fertility and pregnancy rates of yearling heifers. Additional research by ARS scientists has demonstrated that the size of the ovulatory follicle is related to the probability that a cow will successfully become pregnant and have a calf. Breeding herd reproductive rates are one of the key factors determining the success and profitability of a commercial beef enterprise. At breeding, the ovulatory follicle has a diameter range from 12 to 30 mm. Fertility was demonstrated to be greatest for cows with ovulatory follicles ranging from 14 to 18 mm in diameter. Cows with follicles greater than 21 mm, did not conceive. Screening cows for ovulatory follicle size prior to breeding is a potential tool to allow producers to evaluate the fertility of individual cows if efficient production level diagnostic technologies can be developed. Decisions then can be made to cull non-fertile cows significantly improving reproductive efficiency and profitability.

Toxic compounds in tall fescue influence bull semen (3). Decreased performance of one bull will affect the pregnancy rate of 20 to 25 cows. Tall fescue has been implicated in reduced fertility of bulls, however, minimal actual research exists determining the negative effects of toxic tall fescue on bull reproductive performance. Less is known of how alkaloids found in toxic fescue have their effects on sperm cells. Scientists from the University of Arkansas and ARS investigated the specific pathways involved in how toxic compounds found in tall fescue reduce bovine sperm motility. Most of these toxic compounds are fat solubles, suggesting that they may easily move across sperm membranes to directly interact within the sperm cell. Beef producers should minimize the use of toxic fescue during the breeding season to optimize pregnancy rates of the cowherd. Use of nontoxic forage diets or grain supplementation during the breeding season will alleviate the detrimental effects of toxic fescue on sperm motility.

Genes associated with return to estrous in beef (5). Being late in returning to estrous after calving compromises the ability of a cow to rebreed early in the breeding season after calving. This failure impacts both the chance that she will get rebred at all and the weaning weight of her subsequent calf, if she does get rebred. Scientists at ARS and Washington State University compared gene expression profiles in anterior pituitary glands collected from anestrous and cycling postpartum beef cows. Surprisingly few genes identified have been associated with reproductive function. Gastrin-releasing peptide exhibited the largest fold increase in expression, and IGFPB-3 was expressed at greater levels in samples from different stages of the estrus cycle than in anestrous cow samples. Expression of versican was decreased in samples from the different stages of the cycle when compared to anestrous cow samples. Results identify numerous genes that may be involved in the transition from anestrous to cycling status, providing novel insight into mechanisms regulating reproductive function.

Early embryonic mortality in beef cattle (4). Fertilization from a single insemination is known to approach 100% in beef cattle. However, subsequent pregnancy rates are only approximately 60%. Scientists from ARS and University of Missouri used reciprocal embryo transfer to ascertain contributions of oocyte competence and maternal environment to pregnancy success in beef cows nursing calves. Increased ovulatory follicle size directly increased pregnancy rate by increasing fertilization rate, and indirectly increased pregnancy rate by: 1) increasing serum estrogen concentration at breeding through increased fertilization rate, increased progesterone during the early luteal phase, and increased pregnancy establishment, and 2) increased progesterone during the early luteal phase through increased embryo viability, increased embryonic developmental stage, and increased pregnancy establishment. However, increased follicle size also had direct negative effects on embryonic developmental stage and pregnancy establishment. The negative effects of ovulatory follicle size on pregnancy success appear to be mediated by oocyte competence and positive effects through improved maternal uterine environment. These results aid in understanding the complex interplay of factors ultimately affecting production efficiency through the timely establishment of viable pregnancies.

Blood progesterone concentration decreases as a cow ages (5). Replacing cows that are no longer reproductively sound is one of the major costs that effect production efficiency. In cattle, progesterone is required to maintain pregnancy. ARS scientists have shown that blood progesterone levels decrease as cows age. The decrease in blood progesterone occurs both at breeding as well as during pregnancy. These findings indentify one biological mechanism that can cause a decrease in fertility as the cow ages, which may lead to tools to effectively predict fertility in aging beef cows.

Poultry

Early programming of metabolism in the broiler chick (4). The first week after emerging from the egg is a critically important time for the broiler chick as it transitions from relying on nutrition derived from the egg to utilizing nutrients obtained from feed. How well the chick adapts metabolically to this transition determines not only its initial survival, but also how well it will perform during the remainder of the production cycle. To relate changes in the functioning of individual genes and gene products with the physiological adaptations that occur in response to the initiation of feed consumption, scientists from ARS and the University of Maryland utilized gene expression analyses surveying the entire chicken genome to evaluate unique gene functions that control metabolic activity in key tissues including liver, muscle, intestine and brain. These analyses revealed that a variety of genes involved in regulating the production and metabolism of fatty acids, cholesterol, carbohydrate and protein were coordinately activated or inactivated in different tissues with the onset of feed consumption during the first week of life outside of the egg. Providing feed to chicks immediately after hatching was found to be a key factor controlling gene activity. The impact of this work is to better define the genetic basis for programming the level of metabolic activity in newly hatched broiler chicks. Such information can be used to develop specific nutrition and management practices, applied at hatch or shortly thereafter, that will have lasting and beneficial effects on the level of performance.

Novel semen extender developed for turkey semen (3). Optimization of semen storage methods would greatly improve the efficiency of commercial turkey production. Traditional semen storage methods do not promote the high fertility rates required by the producers during the entire period of egg production. Previous ARS research has shown that turkey sperm are damaged by lipid peroxidation during semen storage. ARS scientists developed a method for preventing the loss of lipid from the plasma membrane during semen storage and have demonstrated that turkey sperm are able to incorporate supplemental phosphatidylcholine from the semen extender. Additional results have shown that the fertility rates of semen stored for 24h in the presence of exogenous phosphatidylcholine are higher than control semen stored without phosphatidylcholine. This research has demonstrated that supplemental phosphatidylcholine appears to counteract the damaging effects of lipid peroxidation during in vitro storage by providing exogenous phospholipids for incorporation into the turkey sperm plasma membrane. These results are being used by the poultry industry to design new semen extenders that lead to greater fertility in artificial insemination programs.

Sperm storage is not useful as a selection trait in breeder hens (3). ARS scientists investigated the biological basis of sustained fertility in broiler and turkey hens, specifically, the hen’s capacity to store sperm in the oviductal sperm storage tubules (SST). The objective of this study was to determine if sustained fertility in different strains of broiler hens is a function of the average number of SSTs in a given strain. No statistical differences were observed in SST numbers in the 4 strains of broilers examined or in turkey hens before and after the onset of egg production. The mean numbers of SST for broilers and turkeys were 4,893 and 30,566, respectively. It was conclude that any differences between the fertility of the four broiler breeder strains examined cannot be explained by differences in SST numbers. However, differences in the duration of fertility between broilers and turkeys are, in part, related to their respective numbers of number of SST. Poultry geneticists cannot rely on numbers of SST in different strains of breeders as a selection trait for sustained fertility in their breeder hens. These results effectively answer one specific question regarding poultry fertility enabling subsequent research efforts to be refocused.

Sheep

Analysis reveals primary factors affecting lamb survivability in range sheep production systems (5). Poor lamb survivability reduces ewe productivity and flock profitability, and survivability may be enhanced through genetic and management approaches. Scientists at ARS and the Virginia Polytechnic Institute and State University evaluated genetic and environmental factors that affect lamb survival from birth to weaning. Data from more than 20,000 Polypay lambs were used for this survival analysis. The greatest risk of death was associated with lambs born to young ewes, lambs born to litters larger than two, or lambs with low birth weights. Heritability estimates for lamb survivability were low; thus, direct selection for this trait is likely to have only limited benefit. However, because larger lambs at birth are more likely to survive, and because birth weight is heritable, selecting for larger lambs at birth may improve survivability.

Increasing lifetime productivity of breeding ewes (5). Lifetime productivity of ewes that first lamb as yearlings is greater than it is for ewes that first lamb later in life. In 2010, ARS scientists completed the third year of a five-year study to better understand factors that affect the likelihood that a ewe will lamb as a yearling. The data for the first three years indicate that body weights and ages did not affect the average date that ewes were first detected in estrus (typically assumed to be age at puberty) or the percentages of ewes that lambed as yearlings. Based on these data, the scientists have expanded the study to determine the expected progeny differences for ability to lamb as a yearling. The results of this study should provide the information needed to develop breeding and management programs that will increase the number of ewes that lamb as yearlings and increase the lifetime productivity of ewes.

Reducing difficult births in sheep (5). Slow or difficult births (dystocia) that require assistance can reduce the survivability of lambs and reduce overall flock production. The use of terminal-sire breeds or genetic lines, which are selected for size, growth potential, and carcass merit, may increase lamb birth weights enough to increase the incidence and severity of dystocia. ARS scientists developed methods for identifying the lamb or lambs within a litter that cause or contribute to dystocia. These methods have been used to initiate a long-term study to quantify the incidence of dystocia and determine whether breeding programs can be developed to minimize dystocia and its effects on lamb survival and human labor requirements during lambing. Initial data analyses indicate that 92.5% of ewes give birth to lambs without any need for assistance; 5.8% of the ewes need assistance because of lamb malpresentations (e.g., breech, feet back, head back); approximately 1.2% need assistance with lambs that were considerably heavier than the average for the breed type; approximately 0.3% require Caesarian sections; and approximately 0.2% need assistance because of inadequate cervical dilation. Data from this study are being used to determine whether a white-faced, three-breed, terminal-sire composite, which is being developed by ARS, increases the incidence of dystocia-related morbidity and mortality in ewes and lambs.

Swine

New Protocol Improves Fertility of Frozen-thawed Boar Semen (3). Use of cryopreserved semen in swine has been hampered by the poor performance of frozen-thawed semen which results in farrowing rates of 55% and 8 piglets/litter, which is 20-30 percentage lower and 2-3 fewer pigs per litter than expected with non-frozen semen. In order to obtain better fertility with cryopreserved boar semen, ARS developed a new protocol where females' time of ovulation was manipulated, and a single insemination of thawed boar semen was timed to have fertile sperm at the site of fertilization 0-4 hours before the expected time of ovulation. With our protocol litter size was about 96% of that using non-frozen semen; while the farrowing rate

(80%) was equal to that using nonfrozen semen in conjunction with standard industry breeding procedures. These results show that, with proper treatment of recipient females, frozen-thawed boar semen can be used by swine producers to obtain fertility that is comparable to non-frozen semen.

Reproductive research in swine improves reproductive performance (5). ARS scientists focused on several aspects of swine reproductive efficiency including; identification of the genetic control of puberty onset in boars; genetic influences related to uterine capacity; the placental role in regulating fetal growth and survival; and the relationship between fetal nerve myelination and survivability of post natal piglets. This research is leading to the development of intervention strategies and technologies that will improve litter size through improved placental efficiency and enhanced uterine capacity. Larger litter size will improve efficiency and profitability of the swine industry. This research will also improve nutritional strategies during late gestation focused on improving piglet brain stem myelination which will potentially decrease preweaning mortality of piglets. Improved reproductive efficiencies not only improve the efficiency and profitability of pork producer, but help reduce the relative cost of protein to consumers and help to ensure international food security.

Neonatal piglet energy stores vary by breed of the piglet (4). Preweaning piglet mortality reduces the profitability of swine production and occurs primarily in low birth weight piglets for conventional breeds in the US. However, despite decreased birth weights compared to European breed piglets, Meishan piglets have lower preweaning mortality rates. ARS scientists used reciprocal embryo transfer between Meishan and white crossbred gilts to examine the contributions of the breed of piglet and sow and their interactions on the development of neonatal piglets. Results indicate that at day 1 of age, there are significant piglet breed effects favoring Meishan compared to white crossbred piglets on stomach content weights; percentage of fat and nitrogen within the body composition; liver, bicep femoris, and longissimus dorsi glycogen concentrations; and serum albumin levels. Preweaning survival in Meishan piglets appears to correlate to improved energy storage and use during the neonatal period and suggests that focusing on neonatal piglet physiology regulating energy stores, appetite, and activity will identify and improve factors associated with piglet survival.

Metabolic measurements in the sow and relationship to post-weaning reproductive performance (5). Excessive weight loss during lactation is an indicator of tissue catabolism in exchange for maintaining metabolic output and can have adverse effects on reproductive parameters. Therefore, scientists at U.S. Meat Animal Research Center in Clay Center, Nebraska, established blood metabolic measurements and body condition measurements at periods of physiological changes due to parturition and lactation in the sow and investigated how these components related to post-weaning reproductive performance. First- and second-litter females that lost less body weight from late gestation through weaning had greater return to estrus than those females that had substantial body condition loss. First-litter females with less increase in plasma creatine phosphokinase activity and plasma L-Lactate levels (indicators of protein degradation) from late gestation through day 1 post-farrowing had improved return-to-estrus rates within a 14-day period following weaning. Post-weaning estrus rates from second-litter females were negatively associated with backfat thickness and plasma creatine levels. These data suggest that body weight, backfat thickness, and metabolic parameters contribute to the complex trait of post-weaning reproduction and by understanding these relationships producers could more effectively manage females to ensure improved return-to-estrus capabilities of animals.

Improved embryo survival in swine increases litter size and reduces mortality (4). The pork industry is challenged to improve the survivability of piglets prior to weaning, particularly in modern highly prolific genotypes. ARS research focused on growth-retarded piglets and examined alterations of physiological mechanisms/factors in vital metabolic tissues that modulate environmental stress responses during gestation and preweaning. Retarded fetal growth (runting) is often a result of uterine crowding and impeded placental development creating metabolic stress for the piglet. ARS research demonstrated that metabolic stress can induce the expression of cytokines in adipose tissue of neonatal pigs. Since stress in the neonatal pig contributes to high mortality rates, the present data suggest that cytokine production by the adipose tissue may have some role in neonatal survival and will be the focus of further research. Additional research was conducted to identify serum protein biomarkers in normal and runt piglets associated with poor growth performance. Stress related proteins and oxidative protein modifications were investigated in serum proteins at 1, 7, and 21 days of age. Newborn runt piglets had significantly less total protein per unit volume in serum compared to their one day old normal littermates. These data indicate that specific protein biomarkers associated with impaired growth are present at birth and may lead to intervention strategies to lessen the incidence of runt piglets. Concomitant with the establishment of the placenta at about gestational day 18 and complete by gestational day 50, is the initiation of the development of organs, liver, lung and muscle. The expression of fifteen factors regulating placental growth, placental tissue differentiation, placental transport, or response to poor placentation was examined at day 50 in the placental tissue of runt and control fetuses. Specific mRNA involved in the synthesis of an important nutrient transporter, nitric oxide, was significantly increased in whole placental tissue of runts. Compared to gestational day 37, mRNA was significantly decreased by gestational day 50 in control subjects, however, in runts the higher level of this specific mRNA was maintained. Considering insufficient nutrition is an important contributor to the retarded growth of runts and their organs, this finding highlights a potential nutrient transporter in the placenta whose functional role should be studied further.

Factors of the immune system regulate gene expression in the fat tissue of the neonatal piglet (4). Environmental (temperature) and biological (disease) stresses that impact the neonatal pig result in a mortality rate that sometimes approach 20%. Distinct hormone-like factors called cytokines are produced by the immune system and are released in response to stress. Consequently, cytokines are good indicators of stress in swine. Fat tissue also produces cytokines (adipokines), which are thought to play major roles in obesity and associated diseases including metabolic syndrome and insulin resistant diabetes in humans; thus, an understanding of the regulation of adipokines in swine could also be important for their health and well-being. This is relevant to the USDA priority of Childhood Nutrition and Health. ARS scientists were the first to investigate the role of two stress-induced cytokines, tumor necrosis factor alpha (TNF) and interleukin 6 (IL6), in regulating adipokines and genes that control fat metabolism between birth and weaning, a time when fat tissue is one of the fastest growing tissues in the piglet. Both cytokines altered the levels of distinct adipokines; however IL6 enhanced genes involved in fat metabolism and TNF inhibited genes involved in fat metabolism. These data indicate that cytokines released during stress could alter fat metabolism in the piglet during a critical survival period decreasing neonatal mortality.

A method for determining whether piglets receive adequate colostrum from the sow (5). Preweaning mortality of piglets represents a substantial loss to swine producers and one possible factor contributing to this loss is the failure of neonatal piglets to obtain sufficient colostrum from the sow, which can be caused by either failure of the piglet to nurse or failure of the sow to initiate lactation. An inexpensive and rapid method, the “immunocrit,” was developed and validated by ARS scientists to measure newborn piglet serum immunoglobulin G (IgG), which reflects whether a piglet has received adequate colostrum. Results indicated that immunocrit measurements are predictive of piglet mortality and litter average immunocrit indicated the ability of the sow to transmit IgG (via colostrum production). Low immunocrit values were primarily due to the failure of individual piglets to nurse and not due to failure of the sow to produce colostrum. Litter average immunocrit can be used to identify sows that fail to initiate colostrum production enabling selection for efficient IgG transfer (presumably efficient colostrum production) from sow to piglet. The immunocrit has been adopted by industry to monitor and manage newborn piglet colostrum intake.

Gromega and/or zinc supplementation on newborn piglet brain myelination (4). Low birth weight predisposes newborn piglets to mortality, and previous results indicated that low birth weight is associated with reduced myelination of the brain stem, which could impair coordination of movement of newborn piglets and increase susceptibility to crushing by the sow. With funding from the National Pork Board, ARS scientists performed an experiment to determine whether essential fatty acid supplementation (Gromega) and/or zinc supplementation would improve brain myelination of low birth weight piglets. Combined Gromega and zinc supplementation increased myelin basic protein in myelin membranes from the brain stem, but there was no effect on myelin lipids. There were also no effects of supplementation on preweaning mortality. These results suggest that combined Gromega and zinc supplementation can improve aspects of brain stem myelination, but further research is needed to determine whether supplementation improves preweaning mortality.

Science to Industry: Reproduction and Reproductive Efficiency

A high priority and the focus of substantial research in NP101 is in the areas of reproduction and reproductive efficiency. Historically, NP101 has focused on reproduction as a high industry priority and this research is ongoing. Reproduction and reproductive efficiency remains a high priority for NP101 and is a primary factor for improved production efficiencies and profitability for food animal producers. Research in NP101 is focused primarily on basic physiology and endocrinology. This research has led to extraordinary improvements in the scientific knowledge base for reproduction in the areas of male and female reproduction and embryo development. This research has also led to improved industry technologies for semen evaluation and preservation, and to improved technologies and techniques to manage the reproductive health and productivity of cows, ewes, sows and hens. Additional research has led to a better understanding of litter size and uterine function in swine. Ongoing research continues to focus on areas of priority and impact for the animal industries such as piglet mortality, improved maternal reproductive efficiencies in beef and dairy and improved semen storage technologies for poultry. This research will continue to produce incremental improvements in reproductive efficiencies for producers and will continue to add significantly to the scientific understanding of animal research as a result of long term sustained funding and research support in NP101.

Research Component 3: Measuring and Enhancing Product Quality

The primary goal of animal agriculture is to provide consistently uniform, high quality and nutritious foods to the consumer. Consumer demands, however, are not static and production systems must evolve to meet marketplace preferences. For example, as consumers demand foods lower in fat content, animal production systems respond with changes in breeding, nutrition, and management to deliver such products. A growing sector of the consuming public is demanding animal products from less intensive and non-conventional production systems including grazing dairy and beef finishing systems and organic animal production systems. Product consistency and quality from these systems is as yet relatively poorly characterized. American consumers have a wide array of readily available food products, resulting in stiff competition amongst the sectors of the food industry. New information is continually needed to provide food animal producers with the tools to continue to develop innovative products that meet processor and consumer needs.

Problem Statement 3A: Developing Systems for Reducing Variation in Product Quality and Yield.

Survey data at the processor, purveyor, and retail marketing sectors of the food industries continually point to lack of product consistency as a major concern in the beef, swine, and small ruminant industries. Many defects in quality are only noticed by the consumer, when it is unfortunately too late to take corrective action. Processors require non-invasive, non-destructive testing procedures to identify defects and measure product yield and quality characteristics. Objective measures and systems for determining product value characteristics should allow processors to more effectively communicate value differences to producers and give producers greater incentive to improve product quality and consistency. Such “value feedback” will facilitate the development of coordinated supply chains which effectively apply all available known tools to guarantee improved product quality and consistency.

Research Needs:

Continued research which attempts to better understand the biological basis for product quality attributes, including tenderness, flavor, juiciness and other important organoleptic properties of meat is needed across all muscle cuts in beef, pork, and lamb. Product variation introduced by various animal stressors has begun to be described and needs further attention. Research to develop techniques and instrumentation for the assessment of product yield and quality under commercial meat industry conditions is warranted.

Anticipated Products:

- ✓ Identification of supply chain critical control points which can be targeted for increasing product quality.
- ✓ Validated methodologies and instrumentation for on-line commercial industry use to determine product quality and yield.
- ✓ Profiling of factors contributing to product quality differences on a by-muscle group basis.

Potential Benefits:

Results of the research conducted in this area will facilitate the further development of value-based supply chains in the beef, swine, and small ruminant industries. Technology based on science to increase product quality and consistency will further reduce the risk experienced by livestock producers and will provide a means to enhance the profitability and sustainability of the U.S. livestock industry.

Problem Statement 3B: Characterization of Products from Non-Conventional Production Systems.

Increasing attention has been given in the past decade to the development of niche livestock and poultry markets based on more extensively managed production systems. While a variety of these systems exist in animal agriculture, a prevailing theme amongst them is a return to previously used animal husbandry systems that make extensive use of pasture-based forage systems and/or require certified organic production practices. While some research studies have been conducted to evaluate the characteristics of products from these systems, there is generally a lack of consensus in the research literature regarding the resulting comprehensive product nutritional profiles from them. Additionally, society is demanding information concerning the quality and safety of animal products derived from bioengineered animals, including clones produced by somatic cell nuclear transfer as well as recombinant DNA animals (i.e. transgenics).

Research Needs:

Data are needed that comprehensively characterize the product yield and quality attributes of meat, milk, and egg products from pasture-based and organic animal production systems. The most critical needs exist in the areas of grazing dairy systems and year-round grass-finished beef systems. These research data are needed across the diverse seasonal and regional production system parameters required to meet year-round supply chains. Data are needed on the characteristics of products derived from bioengineered animals (somatic cell nuclear transfer clones and their progeny, transgenic animals).

Anticipated Products:

- ✓ Scientific documentation of the nutritional value of products resulting from grass-finished beef systems and how these profiles may be affected by environmental (seasonal) and management factors in the production system.
- ✓ Identification of critical control points that define how production management systems should be operated to ensure the meeting of consumer preferences for these products.
- ✓ Scientific data to be used in the decision-making process regarding use of bioengineered animals in animal production systems.

Potential Benefits:

Research in this area will provide foundational scientific data upon which producers can develop and implement supply chains to meet consumer demands for these products on a regional basis. This will allow small and mid-sized land managers to contribute to new markets and thereby provide a sustainable and profitable return on their properties. Finally, data will be available upon which to make science-based decisions regarding the regulation of food animal products from bioengineered animals (clones and transgenics).

Selected Accomplishments for Product Quality, Composition and Characterization

This section includes selected accomplishments that demonstrate stakeholder impact for NP101 for the current action plan. Each accomplishment is cross referenced with specific sections in Appendix 2 listing relevant references. However, many of the accomplishments listed to not have a specific corresponding reference or journal article because the research in many instances is just being completed. In addition, Appendix 2 includes many more references than can be linked to the accomplishment list and further demonstrates the scope of the research in

NP101. Accomplishments including a cross reference including “M” are listed in the “Miscellaneous” section of Appendix 2.

Development and validation of marbling prediction for beef cattle (2). A primary determinant of beef carcass value is USDA quality grade, which is largely a function of the degree of marbling as estimated subjectively by USDA graders. Because marbling score determination is subjective, the grading system has been widely scrutinized due to perceived variation in application from plant-to-plant and among graders within plants. Therefore, USDA and the beef industry have sought development of instrumental methods to determine beef carcass marbling scores. ARS scientists collaborated with an instrument manufacturer to develop accurate methods for marbling score determination as an additional function of the U.S. Meat Animal Research Center (USMARC) beef carcass image analysis system. In collaboration with USDA Agricultural Marketing Service (AMS) scientists and meat grading coordinators, data was collected to develop standards for AMS approval of instruments for marbling score determination. Additionally, a series of cooperative studies were conducted to gain AMS approval for use of the USMARC beef carcass image analysis system for marbling determination. This technology has been widely adopted and it is expected to have an annual multi-million dollar impact on the beef industry. This technology should benefit both consumers and all sectors of the beef industry by improving the consistency and accuracy of grading and valuing beef.

Methods to measure and improve beef tenderness expanded for the beef industry (2). Previously, ARS scientists had developed a noninvasive method to predict tenderness of the ribeye muscle of U.S. Select and U.S. Choice beef carcasses based on visible and near infrared spectroscopy. Current research was expanded to demonstrate that this technology could also be used on the top sirloin and could logically be expanded to additional cuts. This technology should benefit both consumers and all sectors of the beef industry by identifying cuts of beef that are consistently tender and by providing the beef industry tools to improve overall beef tenderness and consistency. Additional research determined that injection marination could improve the tenderness of tip side steaks. The tip center steak had previously been identified as an economical menu alternative for foodservice outlets. However, tip center steaks have unacceptable tenderness characteristics. Restaurants can now feature tip side steaks as an alternative selection with acceptable tenderness levels improving customer satisfaction. Additional work demonstrated that previously identified genetic tenderness markers could partially mitigate the toughening effects of aggressive growth promotant strategies used by cattle producers. This work provides quantitative evidence of the value of genetic tenderness markers in commercial production systems.

Noninvasive tenderness prediction system of most major beef muscles (2). The U.S. beef industry and the Agricultural Marketing Service (AMS) have sought implementation of standards for tenderness claims. To this end, industry and AMS need instrumentation to noninvasively predict tenderness of meats. ARS scientists have developed a noninvasive method to predict tenderness of the ribeye muscle of beef carcasses based on visible and near infrared (VISNIR) spectroscopy. Further research showed that the existing system could also predict tenderness of other muscles of the carcass. These results suggest this technology could be utilized by virtually all segments of the industry to control variation in tenderness, which will greatly enhance the industry’s ability to manage tenderness in beef and should increase consumption of U.S. beef.

Genomic analysis of meat tenderness in beef cattle (1). Previous ARS research had determined that genetic variation in the calpastatin gene (CAST) makes a substantial contribution to variation in beef tenderness. Commercially available genetic markers in the gene have been successfully used for nearly ten years, but the marker system has limited utility in some breeds and populations. A thorough analysis of the CAST gene using new genomic technologies developed in part by ARS scientists identified 41 additional markers which were used to develop an improved test with wider applicability. In a test population of 556 animals, the improved test seperated animals into groups that differed by nearly twice the level of tenderness as groups based solely on the commercial markers, presenting the opportunity to make more rapid progress in genetic selection for increased meat tenderness. These advances in genomic technology for the beef industry will improve the health, welfare, efficiency and product quality of beef cattle improving beef producer competitiveness and profitability. This research program has ongoing international collaborations with Australia and France to further develop genomic technologies for the beef industry.

Fatty acid composition in beef (2). The fat content and composition of beef has received considerable interest in view of its implications for human health and meat quality characteristics. While unsaturated fats are beneficial when consumed in moderation, high levels of saturated fat are associated with increased serum low-density lipoprotein cholesterol concentrations and pose a risk factor for coronary heart disease. In addition, beef with the most desirable flavor has a higher percentage of monounsaturated fatty acids. ARS scientists discovered a QTL with large effects on the fatty acid composition of beef and preliminary results suggest the myostatin locus may be causative. The results guide future research to provide a clearer understanding of genetic mechanisms controlling palatability and healthfulness of beef and should ultimately lead to tools for producing beef of greater nutritional value to consumers.

Feeding of distillers grains has no detrimental effects on eating quality of beef (2). As corn prices increase and ethanol production increases, distillers grains are gaining widespread use in finishing cattle diets. The effects of various levels of distillers grains in cattle diets on eating quality of meat are largely unknown. ARS scientists evaluated the eating quality of meat from cattle fed 0, 15, 25, 40% distillers grains on an as-fed basis. There was no effect of any level of distillers grains on tenderness, juiciness, or beef flavor intensity. These results indicate cattle feeders can take advantage of the economic benefits of feeding distillers grains without detrimental effects on eating quality of beef.

Quantitative trait loci (QTL) affecting composition and healthfulness of beef identified (1). Consumers of beef desire a palatable and healthful product at a reasonable price and are increasingly concerned about relative levels of saturated and unsaturated fats in their diet. Genetically modifying lipid profiles can help cattle producers produce beef that more consistently meets consumer expectations. ARS scientists conducted a whole-genome scan in a Wagyu x Limousin population and identified seven QTL on five chromosomes involved in lipid metabolism, beef tenderness, and beef flavor. These QTL were independent of genes encoding major enzymes involved in fatty acid metabolism. The results guide future research to provide a richer understanding of genetic mechanisms controlling palatability and healthfulness of beef and may ultimately lead to tools for producing beef of greater value to consumers.

Body composition in broiler chickens (2). Noninvasive methods to determine body composition in livestock and poultry are needed to accurately assess the effects of feeding different nutritional regimens in a commercial setting. Studies were conducted by ARS scientists to assess the body composition of broiler chickens fed varying levels of protein in their diet. Quantitative Magnetic Resonance (QMR) measurements of total body fat, lean, and water content of the live chicken were compared with dual energy X-ray absorptiometry (DXA) and chemical analysis of the carcass. The results of this study demonstrated that, with proper calibration, both QMR and DXA can provide accurate measurements of the body composition of live chickens. The major advantage of the QMR method is that no anesthesia is required, thus facilitating the ease of single and repeated measurements. This new and accurate method provides a powerful new tool for the assessment of different nutritional and management practices on broiler composition and quality. Information obtained from this study will help to establish a data base to determine the relationship between dietary protein, body composition and gene expression in broiler chickens.

Identification and validation of SNPs in pig calpastatin that are predictive of pork tenderness (1). The quality and palatability of fresh retail pork is variable and tenderness is a key factor guiding consumer choices for pork. The ability to selectively breed for animals that are superior and consistent for meat quality traits would improve consumer acceptance and benefit the pork industry. A quantitative trait locus (QTL) region has been identified by ARS scientists for pork tenderness around the calpastatin gene. Three markers in the calpastatin gene were highly significantly associated with slice shear force, a measure of tenderness, in Duroc-Landrace and Duroc-Landrace-Large White populations. These results provide publicly available genetic markers associated with slice shear force that may be useful to the swine industry for marker assisted selection of animals with superior tenderness.

Noninvasive tenderness prediction system can accurately predict tenderness of pork loins (2). As the Agricultural Marketing Service has sought implementation of standards for tenderness claims, the pork industry has sought methods to control variation in tenderness. ARS scientists cooperated with the industry to determine if the ARS noninvasive tenderness prediction system developed for beef could be applied to pork. A series of trials were completed showing that pork loin tenderness could be predicted with the ARS noninvasive tenderness prediction system. Thus, under a trust agreement between ARS and the National Pork Board, ARS scientists conducted a large-scale test in four commercial packing plants. On-line classification of pork loins for tenderness based on visible and near infrared (VISNIR) spectroscopy using the USMARC noninvasive tenderness prediction was effective at identifying a class of loins that were more consistently tender.

Prediction of meat color stability in the retail case for beef and pork (2). Insufficient meat color stability results in huge economic losses to retailers when products don’t maintain their bright red color long enough and have to be discounted or diverted to ground product. ARS scientists have demonstrated that there is large animal and genetic variation in color stability with high correlations among muscles within an animal. In addition, ARS scientists have developed technology to predict meat color stability based on visible and near infrared spectroscopy that will allow industry to select beef and pork cuts with more stable color that are destined for retail markets. These findings will allow for genetic selection of animals with more stable meat color and will facilitate identification of meat cuts better suited to retail markets.

Genetic markers and quantitative trait loci (QTL) regions for pork quality and palatability (1). Numerous genetic marker associations for measures of pork eating qualities have been reported, but few have been independently evaluated in commercial pork products. The National Pork Board funded the Ohio State University to collect detailed pork quality data on over 900 pork loins collected at commercial abattoirs. ARS scientists genotyped each pork loin for over 200 single nucleotide polymorphisms (SNP) markers. SNP markers utilized were either located in QTL regions, candidate genes, or were previously associated with measures of pork quality. Several associations between SNP markers and pork quality were validated. These results will aid producers in determining which genetic markers to test in their herds to improve pork eating quality.

Science to Industry: Product Quality, Composition and Characterization

National Program 101 focuses in two primary areas for product quality and composition: genetic characterization and physical evaluation and improvement of meat products. NP101 scientists have been instrumental in the determination and evaluation of animal product composition and quality and have discovered numerous genomic relationships. NP101 research has led to a better understanding of numerous genetic and genomic factors relating to product tenderness and eating quality as well as composition traits relating to carcass lean and fat content. This research is ongoing. Significant additional research has been completed to characterize biological types of food animals for meat and carcass characterization.

Research related to biological type is continuing in NP101 to evaluate the effect of alternative feeding and management programs on carcass characteristics and nutritional value. This work is steadily expanding as the interest and consumer demand for products such as "grass fed beef" increases.

NP101 scientists have also been instrumental in developing techniques and technologies to improve carcass and meat quality through physical evaluation and manipulation of traits such as carcass lean percentage and tenderness. One high impact result of NP101 research was the development and subsequent industry adoption of a "near infrared" technology for evaluating carcass tenderness in beef cattle. This technology has proven to be very effective in conventional processing facilities and is now being adapted for the pork industry.

APPENDIX 1. SELECTED SUPPORT INFORMATION AND DOCUMENTATION FOR ACCOMPLISHMENTS AND IMPACT OF NP101 RESEARCH

Introduction

This appendix lists relevant research articles for National Program 101 (NP101) from 2006 through 2010. All references are grouped according to research focus to best illustrate the direction and the impact of research in NP101 for the meat animal industries. All accomplishments listed in the body of the report for the NP101 action plan are also cross referenced to their respective list of references below. While a logical grouping of all references was performed, many of the references in this appendix could also be logically listed in two or more sections. However, all references are listed only once. Readers are encouraged to review all sections of interest to best understand the scope and impact of individual research programs.

Research Component 1: Genetic Improvement

1. Germplasm preservation and resource management.

Blackburn, H.D., Silversides, F., Purdy, P.H. 2009. Inseminating Fresh Or Cryopreserved Semen For Maximum Efficiency: Implications For Gene Banks And Industry. Poultry Science 88:2192-2198.

Blackburn, H.D. 2009. Genebank Development for the Conservation of Livestock Genetic Resources in the United States of America. Livestock Science 120:196-203.

Blackburn, H.D., Gollin, D. 2009. Animal Genetic Resource Trade Flows: The Utilization of Newly Imported Breeds and the Gene Flow of Imported Animals in the United States of America. Livestock Science 120:240-247.

Blackburn, H.D. 2006. National animal germplasm program: challenges and opportunities for poultry genetic resources. Poultry Science. 85:210-215.

Blackburn, H.D. 2007. Integrating policies for the management of animal genetic resources with demand for livestock products and environmental sustainability. Animal Genetic Resources Information. 41:53-64.

Blackburn, H.D., Mezzadra, C. 2006. Policies for the management of animal genetic resources. 8th World Congress of Genetics Applied in Livestock Production. 33(2):1-7.

Gollin, D., Van Dusen, E., Blackburn, H.D. 2009. Animal Genetic Resource Trade Flows: Economic Assessment. Livestock Science 120:248-255.

Macneil, M.D., Cronin, M.A., Blackburn, H.D., Alexander, L.J. 2006. Genetic relationships among breeds of beef cattle in the united states that originated from the british isles, iberian penninsula, or west-central europe. World Congress of Genetics Applied in Livestock Production 32(2):1-4.

Moce, E., Purdy, P.H., Graham, J.K. 2009. Treating ram sperm with cholesterol-loaded cyclodextrins improves cryosurvival. Animal Reproduction Sciences 118:236-247.

Moore, D.T., Purdy, P.H., Blackburn, H.D. 2006. A Method for Cryopreserving Chicken Primordial Germ Cells. Poultry Science. 85:1784–1790.

Purdy, P.H., Moce, E., Stobart, R., Murdoch, W.J., Moss, G.E., Larson, B., Ramsey, S., Graham, J.K., Blackburn, H.D. 2009. The fertility of ram sperm held for 24 hours at 5 ºC prior to cryopreservation. Animal Reproduction Sciences 118:231-235.

Purdy, P.H., Song, Y., Silversides, F.G., Blackburn, H.D. 2009. Evaluation of Glycerol Removal Techniques, Cryoprotectants, and Insemination Methods for Cryopreserving Rooster Sperm with Implications for Breed and/or Line Regeneration. Poultry Science 88:2184-2191.

Purdy, P.H. 2008. Gene banking: A quality control perspective on collection, and analysis of samples for a national repository. Theriogenology. 10.1016/j.theriogenology.2008.06.012.

Purdy, P.H. 2006. Ubiquitination of boar sperm: what does this reveal about sperm physiology? Annual Meeting of the Society for the Study of Reproduction, Omaha, NE, July 29-August 1, 2006. p.189.

Spencer, K.W., Purdy, P.H., Blackburn, H.D., Spiller, S.F., Stewart, T.S., Knox, R.V. 2010. Effect of number of motile frozen-thawed boar sperm and number of fixed-time inseminations on fertility in estrous-synchronized gilts. Animal Reproduction Sciences 121:259-266.

Stewart, T., Gunsett, F., Welsh, C.S., Spiller, S.F., Purdy, P.H., Blackburn, H.D. 2006. Variation in sperm cell quality in cryopreserved boar semen. 8th World Congress of Genetics Applied in Livestock Production. 11(23):1-4.

Welsh, C.S., Stewart, T.S., Schwab, C., Blackburn, H.D. 2010. Pedigree Analysis Of Five U.S. Swine Breeds And The Implications For Genetic Conservation. Journal of Animal Science 88:1610–1618.

2. Genetic parameters, evaluation and prediction systems for cattle.

Al-Seaf, A., Keown, J.F., Van Vleck, L.D. 2007. Genetic parameters for yield traits of cows treated or not treated with bovine somatotropin. Journal of Dairy Science. 90:501-506.

Al-Seaf, A., Keown, J.F., Van Vleck, L.D. 2007. Impact of bovine somatotropin on ranking for genetic value of dairy sires for milk yield traits and somatic cell score. Genetics and Molecular Research. 6(1):79-93.

Appuhamy, A.D., Cassell, B.G., Cole, J.B. 2009. Phenotypic and Genetic Relationships of Common Health Disorders with Milk and Fat Yield Persistencies from Producer-Recorded Health Data and Test Day Yields. Journal of Dairy Science. 92(4):1785-1795.

Attalla, S.A., Seykora, A.J., Cole, J.B., Heins, B.J. 2010. Genetic Parameters of Milk ELISA scores for Johne's Disease. Journal of Dairy Science. 93(4):1729-1735.

Bohmanova, J., Misztal, I., Tsuruta, S., Norman, H.D., Lawlor, T.J. 2005. National genetic evaluation of milk yield for heat tolerance of United States Holsteins. International Bull Evaluation Service Bulletin 33:160-162.

Brown, M.A., Coleman, S.W., Lalman, D.L. 2005. Relationship of sire estimated progeny differences to milk yield in Brangus. Journal of Animal Science. 83:1194-1201.

Cole, J.B., Null, D.J. 2009. Genetic Evaluation of Lactation Persistency for Five Breeds of Dairy Cattle. Journal of Dairy Science. 92(5):2248-2258.

Cole, J.B., Van Raden, P.M., O'Connell, J.R., Van Tassell, C.P., Sonstegard, T.S., Schnabel, R.D., Taylor, J.F., Wiggans, G.R. 2009. Distribution and Location of Genetic Effects for Dairy Traits. Journal of Dairy Science. 92(6):2931-2946.

Cole, J.B., Van Raden, P.M. 2006. Genetic evaluation and best prediction of lactation persistency. Journal of Dairy Science. 89(7):2722-2728.

Cole, J.B., Wiggans, G.R., Van Raden, P.M. 2007. Genetic evaluation of stillbirth in United States Holsteins using a sire-maternal grandsire threshold model. Journal of Dairy Science. 90(5):2480-2488.

Dechow, C.D., Norman, H.D., Zwald, N.R., Cowan, C.M., Meland, O.M. 2008. Relationship between individual herd-heritability estimates and sire misidentification rate. Journal of Dairy Science. 91(4):1640-1647.

Degroot, B.J., Keown, J.F., Van Vleck, L.D., Kachman, S.D. 2007. Estimates of genetic parameters for Holstein cows for test-day yield traits with a random regression cubic spline model. Genetics and Molecular Research. 6(2):334-344.

De Vries, A., Cole, J.B. 2009. Profitable Dairy Cow Traits for Hot Climatic Conditions. In: Klopcic, M., Reents, R., Philipsson, J., and Kuipers, A., editors. Breeding for Robustness in Cattle. Wageningen, The Netherlands: Wageningen Academic Publishers. p. 227-248.

Hare, E., Norman, H.D., Wright, J.R. 2006. Trends in calving ages and calving intervals for dairy cattle breeds in the United States. Journal of Dairy Science. 89(1):365-370.

Kuhn, M.T., Hutchison, J.L. 2008. Prediction of dairy bull fertility from field data: Use of multiple services and identification and utilization of factors affecting bull fertility. Journal of Dairy Science. 91(6):2481-2492.

Kuhn, M.T., Hutchison, J.L., Norman, H.D. 2006. Dry period length to maximize production across adjacent lactations and lifetime production. Journal of Dairy Science. 89(5):1713-1722.

Kuhn, M.T., Hutchison, J.L., Norman, H.D. 2006. Effects of length of dry period on yields of milk fat and protein, fertility and milk somatic cell score in the subsequent lactation of dairy cows. Journal of Dairy Research. 73(2):154-162.

MacNeil, M.D., Northcutt, S.L. 2008. National cattle evaluation system for combined analysis of carcass characteristics and indicator traits recorded using ultrasound in Angus cattle. Journal of Animal Science 86: 2518-2524.

Mark, T., Fikse, W.F., Sullivan, P.G., Van Raden, P.M. 2007. Prediction of Correlations and International Breeding Values for Missing Traits. Journal of Dairy Science. 90(10):4805-4813.

Martinez, G.E., Koch, R.M., Cundiff, L.V., Gregory, K.E., Kachman, S.D., Van Vleck, L.D. 2005. Genetic parameters for stayability, stayability at calving and stayability at weaning to specified ages for Hereford cows. Journal of Animal Science 83:2033-2042.

MacNeil, M.D., Leesburg, V.L., Mott, T.B. 2007. Validating the breeding value for maternal preweaning gain in beef cattle with measured milk production. South African Journal of Animal Science 36(Issue 5 Supple. 1):1-5.

MacNeil, M.D., Matjuda, E. 2007. Breeding objectives for Angus and Charolais specialized sire lines for use in the emerging sector of South African beef production. South African Journal of Animal Science 37(1):1-10.

Miller, R.H., Kuhn, M.T., Norman, H.D., Wright, J.R. 2008. Death Losses for Lactating Cows in Herds Enrolled in Dairy Herd Improvement Test Plans. Journal of Dairy Science. 91(9):3710-3715.

Miller, R.H., Norman, H.D., Wright, J.R., Cole, J.B. 2008. Impact of Genetic Merit for Milk Somatic Cell Score of Sires and Maternal Grandsires on Herd Life of Their Daughters. Journal of Dairy Science. 92(5):2224-2228.

Norman, H.D., Wright, J.R., Miller, R.H. 2010. Response to alternative genetic-economic indices for Holsteins across 2 generations. Journal of Dairy Science. 93(6):2695-2702.

Norman, H.D., Hutchison, J.L., Wright, J.R., Kuhn, M.T., Lawlor, T.J. 2007. Selection on yield and fitness traits when culling Holsteins during the first three lactations. Journal of Dairy Science. 90(2):1008-1020.

Norman, H.D., Wright, J.R., Powell, R.L., Van Raden, P.M. 2005. Impact of maturity rate of daughters on genetic ranking of Holstein bulls. Journal of Dairy Science. 88(9):3337-3345.

Norman, H.D., Wright, J.R., Powell, R.L., Van Raden, P.M., Miglior, F., De Jong, G. Consistency of Maturity Rate for Milk Yield Across Countries and Generations. Journal of Dairy Science. 90(8):3937-3944.

Powell, R.L., Sanders, A.H., Norman, H.D. 2008. Investigation of country bias in international genetic evaluations using full-brother information. Journal of Dairy Science. 91(7):2885-2892.

Powell, R.L., Sanders, A.H., Norman, H.D. 2005. Impact of estimated genetic correlations on international evaluations to predict milk traits. Journal of Dairy Science. 88(10):3679-3687.

Riley, D.G., Coleman, S.W., Chase, C.C., Olson, T.A., Hammond, A.C. 2007. Genetic parameters for weight, hip height, and the ratio of weight to hip height from random regression analyses of brahman feedlot cattle. Journal of Animal Science.85:42-52.

Spangler, M.L., Sapp, R.L., Bertrand, J.K., MacNeil, M.D., Rekaya, R. 2008. Different Methods of Selecting Animals for Genotyping to Maximize the Amount of Genetic Information Known in the Population. Journal of Animal Science 86:2471-2479.

Van Vleck, L.D., Cundiff, L.V., Koch, R.M. 2007. Effect of competition on gain in feedlot bulls from Hereford selection lines. Journal of Animal Science. 85(7):1625-1633.

Van Raden, P.M., Van Tassell, C.P., Wiggans, G.R., Sonstegard, T.S., Schnabel, R.D., Taylor, J.F., Schenkel, F.S. 2009. Invited Review: Reliability of Genomic Predictions for North American Holstein Bulls. Journal of Dairy Science. 92(1):16-24.

Van Raden, P.M., Tooker, M.E., Cole, J.B., Wiggans, G.R., Megonigal Jr, J.H. 2007. Genetic Evaluations for Mixed-Breed Populations. Journal of Dairy Science. 90(5):2434-2441.

Wiggans, G.R., Cole, J.B., Thornton, L.L. 2008. Multiparity Evaluation of Calving Ease and Stillbirth with Separate Genetic Effects by Parity. Journal of Dairy Science. 91(8):3173-3178.

3. Genetic breed and line characterization for cattle.

Brenneman, R.A., Chase, C.C., Olson, T.A., Riley, D.G., Coleman, S.W. 2007. Genetic diversity among the angus, the american brahman, the senepol and the romosinuano cattle breeds. Animal Genetics. 38, 50-53.

Casas, E., Thallman, R.M., Kuehn, L.A., Cundiff, L.V. 2010. Postweaning Growth and Carcass Traits in Crossbred Cattle from Hereford, Angus, Brangus, Beefmaster, Bonsmara, and Romosinuano Maternal Grandsires. Journal of Animal Science. 88(1):102-108.

Casas, E., Cundiff, L.V. 2006. Postweaning growth and carcass traits in crossbred cattle from Hereford, Angus, Norwegian Red, Swedish Red and White, Friesian, and Wagyu maternal grandsires. Journal of Animal Science. 84:305-310.

Cundiff, L.V. and Franke, D.E. 2006. Growth and puberty characteristics of topcross females by tropically adapted sire breeds in temperate and subtropical regions of the United States. Proceedings 8th World Congress of Genetics Applied in Livestock Production. CD-ROM Communication No. 32-18. Belo Horizonte, Brazil.

Cushman, R.A., Allan, M.F., Thallman, R.M., Cundiff, L.V. 2007. Characterization of biological types of cattle (Cycle VII): Influence of postpartum interval and estrous cycle length on fertility. Journal of Animal Science. 85(9):2156-2162.

Elzo, M.A., Riley, D.G., Hansen, G.R., Johnson, D.D., Myer, R.O., Coleman, S.W., Chase, C.C., Wasdin, J.G., Driver, J.D. 2009. Effect of breed composition on phenotypic residual feed intake and growth in Angus, Brahman, and Angus x Brahman crossbred cattle. Journal of Animal Science 87:3877-3886.

Franke, D.E. and Cundiff, L.V. 2006. Reproduction and maternal performance of two-year-old topcross females by tropically adapted sire breeds in temperate and subtropical regions of the United States. Proceedings 8th World Congress of Genetics Applied in Livestock Production. CD-ROM Communication No. 32-6. Belo Horizonte, Brazil.

Jenkins, T.G., Ferrell, C.L. 2006. Matching beef genetics with production environment. In: Proceedings of the Beef Improvement Federation 38th Annual Research Symposium and Annual Meeting, April 18-21, 2006, Choctaw, Mississippi. p. 41-46.

Kuhn, M.T., Hutchison, J.L., Norman, H.D. 2007. Dry Period Length in US Jerseys: Characterization and Effects on Performance. Journal of Dairy Science. 90(4):2069-2081.

Macneil, M.D., Nkrumah, J.D., Woodward, B.W., and Northcutt, S. 2010. Genetic evaluation of Angus cattle for carcass marbling using ultrasound and genomic indicators. Journal of Animal Science 88:517-522.

MacNeil, M.D. 2009. Invited Review: Research contributions from 75 years of breeding Line 1 Hereford cattle at Miles City, Montana. Journal of Animal Science 87:2489-2501.

MacNeil, M.D., Cronin, M.A., Blackburn, H.D., Richards, C.M., Lockwood, D.R., Kantanen, J., Alexander, L.J. 2007. Genetic relationships between feral cattle from Chirikof Island, Alaska, and other breeds. Animal Genetics 38:193-197.

Phillips, W.A., Holloway, J.W., Warrington, B., Venuto, B.C. 2009. Stocker and feedlot performance of beef heifers sired by Braunvieh and Wagyu bulls from Angus-, Brahman-, Senepol- and Tuli-sired dams. Professional Animal Scientist. 25:809-814.

Phillips, W.A., Coleman, S.W., Riley, D.G., Chase, C.C., Mayeux, H.S. 2006. Stocker and feedlot performance and carcass characteristics of purebred Angus and Romosinuano steers. Professional Animal Scientist. 22:8-13.

Riley, D.G., Chase, C.C., Coleman, S.W., Olson, T.A. 2007. Evaluation of birth and weaning traits of romosinuano calves as purebreds and crosses with brahman and angus. Journal of Animal Science. 85:289-298.

Sanders, J.O., Key, K.L., Riley, D.G., Lunt, D.K. 2005. Evaluation of heterosis retention for cow productivity traits in bos indicus/bos taurus crosses. American Society of Animal Science Southern Section Meeting. Symposium on Tropically Adapted Breeds. Regional Project S-1013. Little Rock, AR., February 8, 2005. pp.196-203.

Phillips, W.A., Coleman, S.W., Riley, D.G., Chase, C.C., Mayeux, H.S. 2006. Stocker and feedlot performance and carcass characteristics of purebred Angus and Romosinuano steers. Professional Animal Scientist. 22:8-13.

Tshipuliso, N., Alexander, L.J., Geary, T.W., Snelling, W.M., Rule, D.C., Koltes, J.E., Mote, B.E., MacNeil, M.D. 2008. Mapping quantitative trait loci for fatty acid composition that segregate between Wagyu and Limousin. South African Journal of Science 38(2):126-130.

Wiggans, G.R., Thornton, L.L., Neitzel, R.R., Gengler, N. 2006. Genetic parameters and evaluation of rear legs (rear view) for Brown Swiss and Guernseys. Journal of Dairy Science. 89(12):4895-4900.

4. Stem cells, cell lines, cloning and transgenetic technologies.

Bauman, D.E., Mather, I.H., Wall, R.J., Lock, A.L. 2006. Major advances associated with the biosynthesis of milk. Journal of Dairy Science. 89:1235-1243

Becker, S.C., Don, S., Baker, J.R., Foster Frey, J.A., Pritchard, D.G., Donovan, D.M. 2009. LysK CHAP endopeptidase domain is required for lysis of live staphylococcal cells. FEMS Microbiology Letter. 294(1):52-60.

Becker, S., Donovan, D.M., Foster-Frye, J. 2008. The phage K lytic enzyme LysK and Lysostaphin act synergistically to kill MRSA. FEMS Microbiology Letter. 287(2):185-91.

Becker, S.C., Foster-Frey, J., Stodola, A.J., Anacker, D., Donovan, D.M., 2009. Differentially conserved staphylococcal SH3b_5 cell wall binding domains confer identical staphylolytic activity to a streptococcal prophage endolysin lytic domain. FEMS Immunology and Medical Microbiology. 443(1-2):32-41.

Chitko Mckown, C.G., Macneil, M.D. 2010. Development of Fibroblast Cell Lines From the Cow Used to Sequence the Bovine Genome. Animal Genetics. 41(4):445.

Donovan, D.M., Foster-Frye,J., 2008. LambdaSa2 prophage endolysin requires Cpl-7 binding domains and Amidase-5 domain for antimicrobial lysis of streptococci. FEMS Microbiology Letter. 287(1):22-23.

Donovan D.M., Foster-Frey J., Garrett W.M., Blomberg, L. 2008. Resolving the database sequence discrepancies for the Staphylococcus aureus bacteriophage phi11 amidase. Journal of Basic Microbiology. 48(1):48-52.

Donovan, D.M. 2007. Bacteriophage and peptidoglycan degrading enzymes with antimicrobial applications. Review Article. Recent Patents on Biotechnology. 1(2):113-122.

Donovan, D.M., Dong, S., Garrett, W.M., Rousseau, G.M., Moineau, S., Pritchard, D.G. 2006. Petidoglycan hydrolase fusions maintain parental specificities. Applied and Environmental Microbiology. 72:2988-2996.

Donovan, D.M., Foster Frey, J.A., Dong, S., Rousseau, G., Moineau, S., Pritchard, D.G. 2006. The cell lysis activity of the streptococcus agalactiae bacteriophage b30 endolysin relies on the chap endopeptidase domain. Applied Environmental Microbiology. 72:5108-5112.

Donovan, D.M., Kerr, D.E., Wall, R.J. 2005. Engineering disease resistant cattle. Transgenic Research. 14(5):563-567.

Filatova, L.Y., Becker, S.C., Donovan, D.M., Gladilin, A.K., Klyachko, N.L. 2010. LysK, the enzyme lysing Staphylococcus aureus cells: specific kinetic features and approaches towards stabilization. Biochimie. 92(5):507-13.

Hoopes, J.T., Stark, C.J., Kim, H.A., Sussman, D.J., Donovan, D.M., Nelson, D.C. 2009. A Novel Use of a Bacteriophage Lysin, PlyC, as a Disinfectant against Streptococcus equi. Applied and Environmental Microbiology. 75(5):1388-94.

Keefer, C.L., Pant, D., Blomberg, L., Talbot, N.C. 2006. Challenges and prospects for the establishment of embryonic stem cell lines of domesticated ungulates. Animal Reproduction Sciences. 98:147-168.

MacLea, K.S., Cheng, H.H. 2006. Cloning and expression of deoxyribonuclease II from chicken. Gene. 373:44-51.

Mao,W., Hunt, H.D., Cheng, H.H. 2010. Cloning and Functional Characterization of Chicken Stem Cell Antigen 2. Developmental and Comparative Immunology. 34(3):360-368.

Powell, A.M., Kerr, D.E., Guthrie, H.D., Wall, R.J. 2007. Lactation induction as a predictor of post-parturition transgene expression in bovine milk. Journal of Dairy Research. 74(2):247-254.

Talbot, N.C., Caperna, T.J., Blomberg, L., Graninger, P.G., Stodieck, L.S. 2010. The effects of space flight and microgravity on the growth and differentiation of PICM-19 pig liver stem cells. In Vitro Cellular and Developmental Biology - Animal. 46(6):502-15.

Talbot, N.C., Powell, A.M., Caperna, T.J., Garrett, W.M. 2010. Proteomic analysis of the major cellular proteins of bovine trophectoderm cell lines derived from IVP, parthenogenetic, and nuclear transfer embryos. Animal Reproduction Sciences. 120(1-4):187-202.

Talbot, N.C., Blomberg, L.A. 2008. The pursuit of ES cell lines of domesticated ungulates. Stem Cell Reviews. 4(3):235-254.

Talbot, N.C., Powell, A.M., Ocon, O.M., Caperna, T.J., Camp, M.J., Garrett, W.M., Ealy, A.D. 2008. Comparison of the interferon-tau expression from primary trophectoderm outgrowths derived from IVP, NT, and parthenogenote bovine blastocysts. Journal of Molecular Reproduction and Development. 75(2):299-308.

Talbot, N.C., Blomberg, L., Mahmood, A., Caperna, T.J., Garrett, W.M. 2007. Isolation and characterization of porcine visceral endoderm cell lines derived from in vivo 11-day blastocysts. In Vitro Cellular and Developmental Biology - Animals. 43(2):72-86.

Talbot, N.C., Powell, A.M., Camp, M.J., Ealy, A.D. 2007. Establishment of a bovine blastocyst-derived cell line collection for the comparative analysis of embryos created in vivo and by in vitro fertilization, somatic cell nuclear transfer, or parthenogenetic activation. In Vitro Cell Developmental Biology Animal. 43(2):59-71.

Talbot, N.C., Caperna, T.J., Powell, A.M., Ealy, A.D., Blomberg, L., Garrett, W.M. 2005. Isolation and characterization of a bovine visceral endoderm cell line derived from a parthenogenetic blastocyst. Vitro Cellular and Developmental Biology. 41:130-141.

Lawrence, J.L., Schrick, F., Hopkins, F.M., Welborn, M.G., Mccracken, M.D., Sonstegard, T.S., Wilson, T.J., Edwards, J. 2005. Fetal losses and pathologic findings of clones derived from serum-starved versus serum-fed bovine ovarian granulosa cells. Reproductive Biology. 5(2):171-184.

Van Hekken, D.L., Wall, R.J., Somkuti, G.A., Powell, A.M., Tunick, M.H., Tomasula, P.M. 2009. Fate of lysostaphin in milk from individual cows through pasteurization and cheesemaking. Journal of Dairy Science. 92:444-457.

Van Immerseel, F., Russell, J.B., Flythe, M.D., Gantois, I., Timbermont, L., Pasmans, F., Haesebrouck, F., Ducatelle, R. 2006. The use of organic acids to combat salmonella in poultry: a mechanistic explanation of the efficacy. Avian Pathology. 35:182-188.

Wall, R.J., Powell, A., Sohn, E.J., Foster-Frey, J., Bannerman, D.D., and Paape, M. 2009. Enhanced host immune recognition of mastitis causing Escherchia Coli in CD-14 transgenic mice. Animal Biotechnology. 20:1-14.

Wang, J., Kim, J., Donovan, D.M., Becker, K.G., Li, M.D. 2009. Significant modulation of mitochondrial electron transport system by nicotine in various rat brain regions. Mitochondrion. 9:186-195.

Willard, R.R., Shappell, N.W., Meekin, J.H., Talbot, N.C., Caperna, T.J. 2009. Cytochrome P450 expression erofile of the PICM-19H pig liver cell line: Potential application to rapid liver toxicity assays. In Vitro Cellular and Developmental Biology - Animals. 46(1):11-19.

Zhao, B., Wall, R.J., Yang, J. 2005. Transgenic expression of myostatin propeptide prevents diet-induced obesity and insulin resistance. Biochemical and Biophysical Research Communications. 337(1):248-255.

5. Genomic discovery, evaluation and technological development for ruminants.

Ashwell, M.S., Heyen, D.W., Sonstegard, T.S., Van Tassell, C.P., Ron, M., Weller, J.I., Lewin, H.A. 2005. Detection of quantitative trait loci influencing conformation traits and calving ease in holstein-friesian cattle. Journal of Dairy Science. 88(11):4111-4119.

Connor, E.E., Siferd, S., Elsasser, T.H., Clover, C.M., Van Tassell, C.P., Sonstegard, T.S., Fernandes, V., Capuco, A.V. 2008. Effects of increased milking frequency on gene expression in the bovine mammary gland. Biomed Central (BMC) Genomics. 9:362.

Connor, E.E., Ashwell, M.S., Schnabel, R., Williams, J.L. 2006. Comparative mapping of bovine chromosome 27 with human chromosome 8 near a dairy form QTL in cattle. Cytogenetics and Genome Research. 112:98-102.

Coutinho, L.L., Matukumalli, L.K., Sonstegard, T.S., Van Tassell, C.P., Gasbarre, L.C., Capuco, A.V., Smith, T.P. 2007. Discovery and profiling of bovine micrornas from immune related and embryonic tissues. Physiological Genomics. 29(1):35-43.

Elsik, C.G., Gibbs, R., Skow, L., Tellam, R., Weinstock, G., Worley, K., Kappes, S.M., Green, R.D., Alexander, L.J., Bennett, G.L., Carroll, J.A., Chitko Mckown, C.G., Hamernik, D.L., Harhay, G.P., Keele, J.W., Liu, G., Macneil, M.D., Matukumalli, L.K., Rijnkels, M., Roberts, A.J., Smith, T.P., Snelling, W.M., Stone, R.T., Waterman, R.C., White, S.N. 2009. The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. Science. 324:522-528.

Gasparin, G., Miyata, L.L., Coutinho, L.L., Martinez, M.L., Teodoro, R.L., Furlong, J., Machado, M.A., Silva, M.V., Campos, A.L., Sonstegard, T.S., Regitano, L.C. 2007. Mapping of quantitative trait loci controlling parasite resistance in a F2 experimental bovine population. Animal Genetics. 38(5):453-459.

Gibbs, R., Van Tassell, C.P., Weinstock, G.M., Green, R.D., Hamernik, D.L., Kappes, S.M., Liu, G., Matukumalli, L.K., Matukumalli, A., Sonstegard, T.S., Silva, M.V. 2009. Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. Science. 24:528-532.

Harhay, G.P., Sonstegard, T.S., Keele, J.W., Heaton, M.P., Clawson, M.L., Snelling, W.M., Wiedmann, R.T., Van Tassell, C.P., Smith, T.P. 2005. Characterization of 954 bovine full-CDS cDNA sequences. Biomed Central (BMC) Genomics 6:166 (11 pp).

Jiang, Z., Michal, J.J., Chen, J., Daniels, T.F., Kunej, T., Garcia, M.D., Gaskins, C.T., Busboom, J.R., Alexander, L.J., Wright, R.W., Macneil, M.D. 2009. Discovery of novel genetic networks associated with 19 economically important traits in beef cattle. International Journal of Biological Sciences 2009, 5: 528-542.

Li, C., Li, R.W. 2008. Butyrate Induced Cell Cycle Arrest in Bovine Cells through Targeting Gene Expression relevance to DNA Replication Apparatus. Gene Regulation and Systems Biology. 2:113-123.

Li, R.W., Meyer, M.J., Van Tassell, C.P., Sonstegard, T.S., Connor, E.E., Van Amburgh, M.E., Boisclair, Y.R., Capuco, A.V. 2006. Identification of estrogen responsive genes in the parenchyma and fat pad of the bovine mammary gland by microarray analysis. Physiological Genomics 27(1):42-53.

Liao, S.F., Alman, M.J., Vanzant, E.S., Miles, E.D., Harmon, D.L., Mcleod, K.R., Boling, J.A., Matthews, J.C. 2008. Basal Expression of Nucleoside Transporter mRNA Differs Among Small Intestinal Epithelia of Beef Steers and is Differentially Altered by Ruminal or Abomasal Infusion of Starch Hydrolysate. Journal of Dairy Science. 91(4):1570-84.

Liu, G., Li, R.W., Sonstegard, T.S., Matukumalli, L.K., Silva, M.V., Van Tassell, C.P. 2008. Characterization of a novel microdeletion polymorphism on BTA5 in cattle. Animal Genetics. 39(6):655-658.

Liu, G., Weirauch, M., Van Tassell, C.P., Li, R.W., Sonstegard, T.S., Matukumalli, L.K., Connor, E.E., Hanson, R.W., Yang, J. 2008. Identification of conserved regulatory elements in mammalian promoter regions: a case study using the PCK1 promoter. Genomics, Proteomics and Bioinformatics. 6(3-4):129-143.

Mariasegaram, H., Chase, C.C., Chaparro, J.X., Olson, T.A., Brenneman, R.A., Niedz, R.P. 2007. The Slick Hair Coat Locus Maps to Bovine Chromosome 20 in Senepol Derived Cattle. Animal Genetics. 38:54-59.

Marquez, G.C., Enns, R.M., Grosz, M.D., Alexander, L.J., MacNeil, M.D. 2009. Quantitative trait loci with effects on feed efficiency traits in Hereford x composite double backcross populations. Animal Genetics 40:986-988.

Matukumalli, L.K., Lawley, C.T., Schnabel, R.D., Taylor, J.F., Allan, M.F., Heaton, M.P., O'Connell, J., Moore, S.S., Smith, T.P., Sonstegard, T.S., Van Tassell, C.P. 2009. Development and Characterization of a High Density SNP Genotyping Assay for Cattle. PLoS One. 4(4):e5350. Available: http://dx.doi.org/10.1371/journal.pone.0005350.

Mccormack, B.L., Chase, C.C., Olson, T.A., Elsasser, T.H., Hammond, A.C., Welsh, Jr., T.H., Jiang, H., Randel, R.D., Okamura, C.A., Lucy, M.C. 2009. A Miniature Condition in Brahman Cattle is Associated with a Single Nucleotide Mutation Within the Growth Hormone Gene. Domestic Animal Endocrinology. 37(2):104-111.

Mckay, S.E., Schnabel, R.D., Murdoch, B.M., Matukumalli, L.K., Aerts, J., Coppieters, W., Crews, D., Neto, E.D., Gill, C.A., Gao, C., Mannen, H., Wang, Z., Van Tassell, C.P., Williams, J.L., Taylor, J.F., Moore, S.S. 2008. An assessment of population structure in eight breeds of cattle using a whole genome SNP panel. Journal of Animal Breeding and Genetics. 20(9):37.

Mckay, S.D., Schnabel, R.D., Murdoch, B.M., Matukumalli, L.K., Aerts, J., Coppieters, W., Crews, D., Neto, E.D., Gill, C.A., Gao, C., Mannen, H., Stothard, P., Wang, Z., Van Tassell, C.P., Williams, J.L., Taylor, J.F., Moore, S.S. 2007. Whole genome linkage disequilibrium maps in cattle. Journal of Animal Breeding and Genetics. 25(8):74.

Regitano, L.C., Ibelli, A.M., Gasparin, G., Miyata, M., Azevedo, A.L., Coutinho, L.L., Teodoro, R.L., Machado, M.A., Silva, M.V., Nakata, L.C., Zaros, L.G., Sonstegard, T.S., Silva, A.M., Alencar, M.M., Oliveira, M.C. 2008. On the search for markers of tick resistance in bovines. Developments in Biologicals. 132:225-230.

Schnabel, R.D., Sonstegard, T.S., Taylor, J.F., Ashwell, M.S. 2005. Whole genome scan to detect QTL for milk production, conformation and functional traits in two U.S. Holstein families. Animal Genetics. 36(5):408-416.

Snelling, W.M., Allan, M.F., Keele, J.W., Kuehn, L.A., Mcdaneld, T.G., Smith, T.P., Sonstegard, T.S., Thallman, R.M., Bennett, G.L. 2010. Genome-Wide Association Study of Growth in Crossbred Beef Cattle. Journal of Animal Science. 88(3):837-848.

Tellam, R.L., Lemay, D.G., Van Tassell, C.P., Lewin, H.A., Worley, K.C., Elsik, C.G. 2009. Unlocking the bovine genome. BioMed Central (BMC) Genetics. 24(10):193.

Villa-Angulo, R., Matukumalli, L.K., Gill, C.A., Choi, J., Van Tassell, C.P., Grefenstette, J.J. 2009. High-resolution haplotype block structure in the cattle genome. Journal of Animal Breeding and Genetics. 24(10):19.

Zimin, A.V., Delcher, A.L., Florea, L., Kelley, D.R., Schatz, M.C., Puiu, D., Hanrahan, F., Pertea, G., Van Tassell, C.P., Sonstegard, T.S., Marcais, G., Roberts, M., Subramanian, P., Yorke, J.A., Salzberg, S.L. 2009. A whole-genome assembly of the domestic cow, Bos taurus. Genome Biology. 10(4):R42.

6. Genomic discovery, evaluation and technological development for poultry.

Ben-Avraham, D., Blum, S., Granevitze, Z., Weigend, S., Cheng, H.H., Hillel, J. 2006. W-specific microsatellite loci detected by in silico analysis, map to chromosome Z of the chicken genome. Animal Genetics. 37:179-188.

Cogburn, L.A., Porter, T.E., Duclos, M.J., Simon, J., Burgess, S.C., Zhu, J., Cheng, H.H., Dodgson, J.B., Burnside, J. 2007. Functional genomics of the chicken - a model organism. Poultry Science. 86:2059-2094.

Granevitze, Z., Blum, S., Cheng, H.H., Vignal, A., Morisson, M., Ben-Ari, G., David, L., Feldman, M.W., Weigend, S., Hillel, J. 2007. Female-specific DNA sequences in the chicken genome. Journal of Heredity. 98:238-242.

Groenen, M.A., Wahlberg, P., Foglio, M., Cheng, H.H., Megens, H.J., Crooijmans, R.P., Besnier, F., Lathrop, M., Muir, W.M., Wong, G.K., Gut, I., Andersson, L. 2009. A High-Density SNP-Based Linkage Map of the Chicken Genome Reveals Sequence Features Correlated With Recombination Rate. Genome Research. 19(3):510-519.

Hillel, J., Granevitze, Z., Twito, T., Ben-Avraham, D., Blum, S., Lavi, U., David, L., Feldman, M.W., Cheng, H.H., Weigend, S. 2007. Molecular markers for the assessment of chicken biodiversity. World's Poultry Science Journal. 63(01):33-45.

Muir, W.M., Wong, G., Zhang, Y., Wang, J., Groenen, M., Crooijmans, R., Megens, H., Zhang, H., Okimoto, R., Vereijken, A., Jungerius, A., Albers, G., Taylor Lawley, C., Delany, M.E., Maceachern, S.A., Cheng, H.H. 2008. Genome-Wide Assessment of Worldwide Chicken SNP Genetic Diversity Indicates Significant Absence of Rare Alleles in Commercial Breeds. Proceedings of the National Academy of Sciences. 105(45):17312-17317.

Muir, W.M., Wong, G.K., Zhang, Y., Wang, J., Groenen, M.A., Crooijmans, R.P., Megens, H.J., Zhang, H.M., McKay, J.C., McLeod, S., Okimoto, R., Fulton, J.E., Settar, P., O'Sullivan, N.P., Vereijken, A., Jungerius-Rattink, A., Albers, G.A., Lawley, C.T., Delany, M.E., Cheng, H.H. 2008.

Review of the initial validation and characterization of a 3K chicken SNP array. World Poultry Science Journal. 64:219-225.

Proszkowiec-Weglarz, M., Richards, M.P, McMurtry, J.P. 2007. Molecular cloning, genomic organization, and expression of three chicken 5'-AMP-activated protein kinase gamma subunit genes. Poultry Science. 85(11):2031-2041.

Rosebrough, R.W., Russell, B.A., Poch, S.M., Richards, M.P. 2007. Using RT-PCR in a real time mode to determine expression of lipogenic genes in broilers. Comparative Biochemistry and Physiology. Part A. 147:215-222.

Yu, Y., Zhang, H.M., Byerly, M.S., Bacon, L.D., Porter, T.E., Liu, G.E., Song, J. 2009. Alternative Splicing Variants and DNA Methylation Status of BDNF in Inbred Chicken Lines. Brain Research. 1269(7):1-10.

Zhang, H.M., Bacon, L.D., Heidari, M., Muir, W.M., Groenen, M.A.M., Zhang, Y., Wong, G.K.S., Fulton, J.E., O'Sullivan, N.P., Albers, G.A.A., Vereijken, A.L.J., Rattink, A.P., Okimoto, R., McKay, J.C., McLeod, S., Cheng, H.H. 2007. Genetic variation at the tumour virus B locus in commercial and laboratory chicken populations assessed by a medium-throughput or a high-throughput assay. Avian Pathology. p. 283-291.

Zhou, H., Deeb, N., Clover, C.M., Ashwell, C.M., Lamont, S.J. 2006. Genome-wide linkage analysis to identify chromosomal regions affecting phenotypic traits in the chicken. I. Growth and average daily gain. Poultry Science. 85:1700-1711.

Zhou, H., Deeb, N., Evock-Clover, C.M., Mitchell, A.D., Ashwell, C.M., Lamont, S.J. 2007. Genome-wide linkage analysis to identify chromosomal regions affecting phenotypic traits in the chicken. III. Skeletal integrity Poultry Science. 86(2):255-266.

Zhou,H., Evock-Clover, C.M., McMurtry, J.P., Ashwell, C.M., Lamont, S.J. 2007. Genome-Wide linkage analysis to identify chromosomal regions affecting phenotypic traits in the chicken. IV. Metabolis traits. Poultry Science. 86:267-276.

7. Genomic discovery, evaluation and technological development for swine.

Alexander, L.J., Juneja, B., Shiroma, D., Nonneman, D.J., Snelling, W.M., Fahrenkrug, S.C. 2007. Comparative and physical mapping of 112 previously reported and 105 new porcine microsatellites. Animal Genetics 38:584-594.

Alexander, L.J., Juneja, B., Fahrenkrug, S. 2006. Isolation and radiation hybrid mapping of 213 porcine microsatellites. Animal Genetics 37(6):596-597.

Barb, C.R., Hausman, G.J., Lents, C.A., Lkhagvadorj, S., Qu, L., Cai, W., Couture, L., Wang, L., Rekaya, R., Nettleton, D. 2010. Gene expression in hypothalamus, liver and adipose tissues and food intake reponse to melanocortin-4 receptor (MC4R) agonist in pigs expressing MC4R mutations. Physiological Genomics. 41:254-268.

Bischoff, S.R., Tsai, S., Hardison, N., Motsinger-Reif, A.A., Freking, B.A., Nonneman, D.J., Rohrer, G.A., Piedrahita, J.A. 2009. Characterization of Conserved and Non-conserved Imprinted Genes in Swine. Biology of Reproduction. 81(5):906-920.

Bischoff, S.R., Tsai, S., Hardison, N.E., York, A.M., Freking, B.A., Nonneman, D.J., Rohrer, G.A., Piedrahita, J.A. 2008. Identification of SNPs and INDELS in swine transcribed sequences using short oligonucleotide microarrays. Biomed Central (BMC) Genomics 9:252.

Chen, K., Knorr, C., Bornemann-Kolatzki, K., Huang, L., Rohrer, G.A., Brenig, B. 2006. Characterization of the PGK2 associated microsatellite S0719 on SSC7 suitable for parentage and QTL diagnosis. Animal Biotechnology. 17:43-49

Erkens, T., Rohrer, G.A., Van Zeveren, A., Peelman, L.J. 2009. SNP Detection in the Porcine PPARGC1A Promoter Region and 3'UTR, and an Association Analysis in a Landrace-Duroc-Yorkshire Population. Czech Journal of Animal Science. 54(9):408-416.

Genini, S., Nguyen, T.T., Malek, M., Talbot, R., Gebert, S., Rohrer, G.A., Nonneman, D.J., Stranzinger, G., Vogeli, P. 2006. Radiation hybrid mapping of 18 positional and physiological candidate genes for arthrogryposis multiplex congenita on porcine chromosome 5. Animal Genetics. 37:239-244.

Germerodt, M., Beuermann, C., Rohrer, G.A., Snelling, W.M., Brenig, B., Knorr, C. 2008. Characterization and linkage mapping of 15 porcine STS markers to fine-map chromosomal regions associated with hernia inguinalis/scrotalis. Animal Genetics 39:671-672.

Holl, J.W., Rohrer, G.A., Brown Brandl, T.M. 2010. Estimates of Genetic Parameters Among Scale Activity Scores, Growth, and Fatness in Pigs. Journal of Animal Science. 88:455-459.

Holl, J.W., Rohrer, G.A., Shackelford, S.D., Wheeler, T.L., Koohmaraie, M. 2008. Estimates of genetic parameters for kyphosis in two crossbred swine populations. Journal of Animal Science. 86:1765-1769.

Humphary, S.J., Scott, C.E., Clark, R., Marron, B., Bender, C., Camm, N., Davis, J., Jenks, A., Noon, A., Patel, M., Sehra, H., Yang, F., Rogatcheva, M.B., Milan, D., Chardon, P., Rohrer, G.A., Nonneman, D.J., De Jong, P., Meyers, S.N., Archibald, A., Beever, J.E., Schook, L.B., Rogers, J. 2007. A high utility integrated map of the pig genome. Genome Biology. 8:R139.

Jacobs, K., Van Poucke, M., Mattheeuws, M., Chardon, P., Yerle, M., Rohrer, G.A., Van Zeveren, A., Peelman, L.J. 2002. Characterization of the porcine melanocortin 2 receptor gene (MC2R). Animal Genetics 33:415-421.

Jacobs, K., Rohrer, G.A., Van Poucke, M., Piumi, F., Yerle, M., Barthenschlager, H., Mattheeuws, M., Van Zeveren, A., Peelman, L. 2006. Porcine PPARGC1A (peroxisome proliferative activated receptor gamma coactivator 1a): coding sequence, genomic organization, polymorphisms and mapping. Cytogenetics and Genome Research. 112:106-113.

Miles, J.R., Blomberg, L.A., Krisher, R.L., Everts, R.E., Sonstegard, T.S., Van Tassell, C.P., Zuelke, K.A. 2008. Comparative transcriptome analysis of in vivo- and in vitro- produced porcine blastocysts by small amplified RNA-serial analysis of gene expression (SAR-SAGE). Molecular Reproduction and Development. 75:976-88.

Mousel, M.R., Nonneman, D.J., Rohrer, G.A. 2006. Rearranged gene order between pig and human in a quantitative trait loci region on SSC3. Animal Genetics. 37:403-406

Nonneman, D.J., Smith, T.P., Freking, B.A., Rohrer, G.A. 2005. Assignment of 12 genes to porcine chromosome 1q by linkage and radiation hybrid mapping. Anim. Genet. 36:532-533. 2005.

Ramos, A.M., Crooijmans, R.P.M.A., Affara, N.A., Amaral, A.J., Archibald, A.L., Beever, J.E., Bendixen, C., Churcher, C., Clark, R., Dehais, P., Hansen, M.S., Hedegaard, J., Hu, Z.L., Kerstens, H.H., Law, A.S., Megens, H.J., Milan, D., Nonneman, D.J., Rohrer, G.A., Rothschild, M.F., Smith, T.P.L., Schnabel, R.D., Van Tassell, C.P., Taylor, J.F., Wiedmann, R.T., Schook, L.B., Groenen, M.A.M. 2009. Design of a High Density SNP Genotyping Assay in the Pig Using SNPs Identified and Characterized by Next Generation Sequencing Technology. PLoS One 4(8):E6524. p. 1-13.

Rodriguez, K.F., Blomberg, L., Zuelke, K.A., Miles, J.R., Alexander, J.E., Farin, C.E. 2006. Identfication of mrnas associated with gonadotropin-induced maturation of murine cumulus oocyte complexes using serial analysis of gene expression (sage). Physiological Genomics. 27(3):318-327.

Rohrer, G.A., Freking, B.A., Nonneman, D.J. 2007. Single nucleotide polymorphisms for pig identification and parentage exclusion. Animal Genetics. 38:253-258.

Schook, L.B., Beever, J.E., Rogers, J., Humphray, S., Archibald, A., Chardon, P., Milan, D., Rohrer, G.A., Eversole, K. 2005. Swine Genome Sequencing Consortium (SGSC): A strategic roadmap for sequencing the pig genome. Comparative and Functional Genomics. 6:251-255.

Shimogiri, T., Kiuchi, S., Hiraiwa, H., Hayashi, T., Takano, Y., Yoshizane, M., Rohrer, G.A., Milan, D., Yasue, H. Assignment of 204 genes localized on hsa17 to a porcine rh (imprh) map to generatate a dense comparative map between pig and human/mouse. Cytogenetics and Genome Research. 112:114-120. 2006.

Tsai, S., Mir, B., Martin, A.C., Estrada, J.L., Bischoff, S.R., Hsieh, W., Cassady, J.P., Freking, B.A., Nonneman, D.J., Rohrer, G.A., Piedrahita, J. 2006. Detection of transcriptional difference of porcine imprinted genes using different microarray platforms. (BMC) Genomics. 7:328.

Wiedmann, R.T., Nonneman, D.J., Keele, J.W. 2006. Novel porcine repetitive elements. Biomed Central (BMC) Genomics. 7:304 (12 pp). Online. BMC Genomics doi:10.1186/1471-2164/7/304.

8. Functional genomics of reproduction, growth and development in ruminants.

Alexander, L.J., Geary, T.W., Snelling, W.M., MacNeil, M.D. 2007. Quantitative trait loci with additive effect on growth and carcass traits in a Wagyu-Limousin F*2 population. Animal Genetics 38:413-416.

Allan, M.F., Kuehn, L.A., Cushman, R.A., Snelling, W.M., Echternkamp, S.E., Thallman, R.M. 2009. Confirmation of quantitative trait loci using a low-density single nucleotide polymorphism map for twinning and ovulation rate on bovine chromosome 5. Journal of Animal Science. 87(1):46-56.

Allan, M.F., Thallman, R.M., Cushman, R.A., Echternkamp, S.E., White, S.N., Kuehn, L.A., Casas, E., Smith, T.P. 2007. Association of a single nucleotide polymorphism in spp1 with growth traits and twinning in a cattle population selected for twinning rate. Journal of Animal Science. 85(2):341-347.

Archibeque, S.L., Freetly, H.C., Ferrell, C.L. 2007. Net portal and hepatic flux of nutrients in growing wethers fed high-concentrate diets with oscillating protein concentrations. Journal of Animal Science. 85(4):997-1005.

Connor, E.E., Li, R.W., Baldwin, R.L., Li, C. 2009. Gene expression in the digestive tissues of ruminants and their relationships with feeding and digestive processes. Animal. 4(7):993-1007.

Connor, E.E., Kahl, S., Elsasser, T.H., Parker, J., Li, R.W., Van Tassell, C.P., Baldwin, R.L., Barao, S.M. 2009. Enhanced mitochondrial complex gene function and reduced liver size may mediate improved feed efficiency of beef cattle during compensatory growth. Functional and Integrative Genomics. 10(1):39-51.

Cronin, M.D., Macneil, M.D., Patton, J.C. 2006. Mitochondrial dna and microsatellite dna variation in domestic reindeer (rangifer tarandus tarandus) and relationships with wild caribou (r. t. granti, r. t. groenlandicus, r. t. caribou). Journal of Heredity 97:525-530. doi:10.1093/jhered/es1012.

Hart, E.J., Pinton, A., Powell, A., Wall, R., and King, W.A. 2008. Meiotic recombination in normal and clone bulls and their offspring. Cytogenetic and Genome Research. 120(1-2): 97-101.

Liu, G., Jiang, L., Tian, F., Zhu, B., Song, J. 2009. Calibration of mutation rates reveals diverse subfamily structure of galliform CR1 repeats. Genome Biology and Evolution. 2009:119-130.

Looper, M.L., Black, S.G., Reiter, S.T., Okimoto, R., Johnson, Z.B., Brown, M.A., Rosenkrans, C.F. 2010. Identification of polymorphisms in the enhancer region of the bovine prolactin gene and association with fertility in beef cows. Professional Animal Scientist. 26:103-108.

Macneil, M.D., Mott, T.B. 2006. Genetic analysis of gain from birth to weaning, milk production and udder conformation in line 1 Hereford cattle. Journal of Animal Science 84:1639-1645.

Meyers, S.N., McDaneld, T.G., Swist, S.L., Marron, B.M., Steffen, D.J., O'Toole, D., O'Connell, J.R., Beever, J.E., Sonstegard, T.S., Smith, T.P. 2010. A Deletion Mutation in Bovine SLC4A2 is Associated with Osteopetrosis in Red Angus Cattle. Biomed Central (BMC) Genomics. 11:337.

Rosenkrans, C., Banks, A., Reiter, S., Looper, M.L. 2010. Calving traits of crossbred Brahman cows are associated with heat shock protein 70 genetic polymorphisms. Animal Reproduction Sciences. 119:178-182.

Snelling, W.M., Allan, M.F., Keele, J.W., Kuehn, L.A., Mcdaneld, T.G., Smith, T.P., Sonstegard, T.S., Thallman, R.M., Bennett, G.L. 2010. Genome-Wide Association Study of Growth in Crossbred Beef Cattle. Journal of Animal Science. 88(3):837-848.

Van Raden, P.M., Miller, R.H. 2006. Effects of non-additive genetic interactions, inbreeding, and recessive defects on embryo and fetal loss by 70 days. Journal of Dairy Science. 89(7):2716-2121.

White, S.N., Casas, E., Allan, M.F., Keele, J.W., Snelling, W.M., Wheeler, T.L., Shackelford, S.D., Koohmaraie, M., Smith, T.P. 2007. Evaluation in beef cattle of six deoxyribonucleic acid markers developed for dairy traits reveals an osteopontin polymorphism associated with post-weaning growth. Journal of Animal Science. 85:1-10.

9. Functional genomics of reproduction, growth and development in poultry.

Atzmon, G., Ronin, Y.I., Korol, A., Yonash, N., Cheng, H.H., Hillel, J. 2006. QTLs associated with growth traits and abdominal fat weight and their interactions with gender and hatch in commercial meat-type chickens. Animal Genetics. 37(4):352-358.

Proszkowiec-Weglarz, M., Humphrey, B.D., Richards, M.P. 2006. Molecular cloning and expression of the chicken carbohydrate response element binding protein and Max-like protein X gene homologues. Molecular and Cellular Biochemistry. 312(1-2):167-184.

Richards, M.P., McMurtry, J.P. 2008. Expression of proglucagon and proglucagon-derived peptide hormone receptor genes in the chicken. General and Comparative Endocrinology. 156(2):323-338.

Rosebrough, R.W., Russell, B.A., Richards, M.P. 2008. Short term changes in the expression of lipogenic genes in broilers. Comparative Biochemistry and Physiology, Part A 149:389-395.

10. Functional genomics of reproduction, growth and development in swine.

Barb, C.R., Hausman, G.J., Rekaya, R. Gene expression in the brain-pituitary adipose tissue axis and luteinizing hormone secretion during pubertal development in the gilt. Reproduction. 62:33-44.

Blomberg, L., Garrett, W.M., Guillomot, M., Miles, J.R., Sonstegard, T.S., Van Tassell, C.P., Zuelke, K.A. 2006. Transcriptome profiling of the tubular porcine conceptus identifies the differential regulation of growth and developmentally associated genes. Molecular Reproduction and Development. 73(12):1491-1502.

Campbell, E.M., Nonneman, D.J., Kuehn, L.A., Rohrer, G.A. 2008. Genetic variation in the mannosidase 2B2 gene and its association with ovulation rate in pigs. Animal Genetics. 39:515-519.

Ford, J.J., McCoard, S.A., Wise, T.H., Lunstra, D.D., Rohrer, G.A. 2006. Genetic variation in sperm production. In: Ashworth, C.J., Kraeling, R.R., editors. Control of Pig Reproduction VII. Proceedings of the Seventh International Conference on Pig Reproduction, June 12-15, 2005, Kerkrade, The Netherlands. Society of Reproduction and Fertility Supplement 62:99-112.

Holl, J.W., Rohrer, G.A., Brown Brandl, T.M. 2010. Estimates of Genetic Parameters Among Scale Activity Scores, Growth, and Fatness in Pigs. Journal of Animal Science. 88:455-459.

Kim, J.G., Nonneman, D.J., Vallet, J.L., Wise, T.H., Rohrer, G.A. Sequence variation and evaluation of inhibin alpha-subunit and steroidogenic acute regulatory protein for reproductive traits in swine. Animal Genetics. 37:424-425. 2006.

Kim, J.G., Nonneman, D.J., Vallet, J.L., Wise, T.H., Rohrer, G.A. Sequence variation and evaluation of inhibin alpha-subunit and steroidogenic acute regulatory protein for reproductive traits in swine. Animal Genetics. 37:424-425. 2006.

Lkhagvadorj, S., Qu, L., Cai, W., Couture, L., Barb, C.R., Hausman, G.J., Netteton, D., Anderson, L., Deckers, J., Tuggle, C. 2010. Gene expression profiling of the short-term adaptive response to acute caloric restriction in liver and adipose tissues of pigs differing in feed efficiency. American Journal of Physiology. 298:R494-R507.

McDaneld, T.G., Smith, T.P., Doumit, M.E., Miles, J.R., Coutinho, L.L., Sonstegard, T.S., Matukumalli, L.K., Nonneman, D.J., Wiedmann, R.T. 2009. MicroRNA Transcriptome Profiles During Swine Skeletal Muscle Development. Biomed Central (BMC) Genomics. 10:77.

Miles, J.R., Vallet, J.L., Freking, B.A., Nonneman, D.J. 2009. Molecular Cloning and Characterization of Heparanase mRNA in Porcine Placenta Throughout Gestation. Reproduction, Fertility and Development. 21(6):757-772.

Miles, J.R., Blomberg, L.A., Krisher, R.L., Everts, R.E., Sonstegard, T.S., Van Tassell, C.P., Zuelke, K.A. 2008. Comparative transcriptome analysis of in vivo- and in vitro- produced porcine blastocysts by small amplified RNA-serial analysis of gene expression (SAR-SAGE). Molecular Reproduction and Development. 75:976-88.

Nonneman, D.J., Wise, T.H., Ford, J.J., Kuehn, L.A., Rohrer, G.A. 2006. Characterization of the aldo-keto reductase 1C gene cluster on pig chromosome 10: possible associations with reproductive traits. Biomed Central (BMC) Veterinary Research. 2:28. 2006.

Ramsay, T.G., Mitchell, A.D., Richards, M.P. 2007. Comparison of gene expression in lean contemporary and crossbred obese swine. Adipocytes 2(3/4):133-142.

Rempel, L.A., Nonneman, D.J., Wise, T.H., Erkens, T., Peelman, L.J., Rohrer, G.A. 2010. Association Analyses of Candidate Single Nucleotide Polymorphisms on Reproductive Traits in Swine. Journal of Animal Science. 88:1-15.

Rohrer, G.A., Wise, T.H., Ford, J.J. Deciphering the pig genome to understand gamete production. IN: Control of Pig Reproduction VII. C.J. Ashworth & R.R. Kraeling (Eds) Nottingham University Press. Proc. 7th Intl. Conference on Pig Reproduction, Society of Reprod. & Fertility, Suppl. 62:293-301. 2006.

11. Characterization of genetic and genomic variation in sheep.

Brown, M.A., Mayeux, H.S. 2006. Grazing performance of hair sheep. Sheep and Goat Research Journal. 20:60-65.

Casas, E., Freking, B.A., Leymaster, K.A. 2005. Evaluation of Dorset, Finnsheep, Romanov, Texel, and Montadale breeds of sheep: V. Reproduction of F1 ewes in spring mating seasons. Journal of Animal Science. 83:2743-2751.

Chitko Mckown, C.G., Leonard, J.C., Moscatello, D., Miller, L.C., Freking, B.A. 2008. Development of cell lines from the sheep used to construct the CHORI-243 ovine BAC library. Animal Biotechnology. 19(2):84-88.

Freking, B.A., Leymaster, K.A. 2006. Evaluation of the ovine callipyge locus: IV. Genotypic effects on reproductive traits. Journal of Animal Science. 84:311-316.

Hanford, K.J., Van Vleck, L.D., Snowder, G.D. 2006. Estimates of genetic parameters and genetic trend for reproduction, weight, and wool characteristics of polypay sheep. Livestock Production Science 102(1-2):72-82.

Leymaster, K.A., Shackelford, S.D., Wheeler, T.L., Koohmaraie, M. 2006. Breed effects on growth, carcass and meat quality traits of sheep. Proceedings of the British Society of Animal Science, New Developments in Sheepmeat Quality. p. 43-47.

Mousel, M.R., White, S.N., Hoesing, L.M. 2010. Association analysis of a CCR5 variant with ewe lifetime production in 3 breeds of sheep. Animal Genetics. 41(2):222-223.

Murphy, S.K., Nolan, C.M., Huang, Z., Kucera, K.S., Freking, B.A., Smith, T.P.L., Leymaster, K.A., Weidman, J.R., Jirtle, R.L. 2006. Callipyge mutation affects gene expression in cis: A potential role for chromatin structure. Genome Research. 16:340-346.

Phillips, W.A., Brown, M.A., Dolezal, G.H., Fitch, G.Q. 2006. Feedlot performance and carcass characteristics of crossbred lambs sired by Texel, Romanov, St. Croix, or Dorset rams from Polypay and St. Croix ewes. Sheep and Goat Research Journal. 20:12-17.

Sawalha, R.M., Snowder, G.D., Keown, J.F., Van Vleck, L.D. 2005. Genetic relationship between milk score and litter weight for Targhee, Columbia, Rambouillet and Polypay sheep. Journal of Animal Science 83:786-793.

Snowder, G.D. 2008. Genetic improvement of overall reproductive success in sheep: A review. Archivos Latinoamericanos De Produccion Animal. 16(1):32-40.

12. Functional genomics of immunology, disease and pathogen resistance.

Al-Seaf, A., Keown, J.F., Van Vleck, L.D. 2007. Estimates of correlations among yield traits and somatic cell score with different models to adjust for bovine somatotropin effects on Holstein dairy cows. Genetics and Molecular Research. 6(1):67-78.

Appuhamy, J., Cassell, B.G., Dechow, C.D., Cole, J.B. 2007. Phenotypic Relationships of Common Health Disorders in Dairy Cows to Lactation Persistency Estimated from Daily Milk Weights. Journal of Dairy Science. 90(9):4424-4434.

Arnaud, F., Caporale, M., Varela, M., Biek, R., Chessa, B., Alberti, A., Golder, M., Mura, M., Zhang, Y., Yu, L., Pereira, F., De Martini, J.C., Leymaster, K.A., Spencer, T.E., Palmarini, M. 2007. A paradigm for virus-host coevolution: Sequential counter-adaptations between endogenous and exogenous retroviruses. PLoS Pathogens Vol. 3(11):e170 doi:10.1371/journal.ppat.0030170.

Casas, E., Snowder, G.D. 2008. A putative quantitative trait locus on chromosome 20 associated with bovine pathogenic disease incidence. Journal of Animal Science. 86:2455-2460.

Casas, E., Stone, R.T. 2006. Putative quantitative trait loci associated with the probability of contracting infectious bovine keratoconjunctivitis. Journal of Animal Science. 84:3180-3184.

Chen, M., Payne, W.S., Dunn, J.R., Chang, S., Zhang, H.M., Hunt, H.D., Dodgson, J.B. 2009. Retroviral Delivery of RNA Interference Against Marek's Disease Virus In Vivo. Poultry Science. 88(7):1373-1380.

Cheng, H.H. 2008. Integrating genomics to understand the Marek's disease virus-chicken host-pathogen interaction. In: Gustafson, P., Stacey, G., Taylor, J., editors. Genomics of Disease. Stadler Genetics Symposium. New York, NY: Springer. p. 115-126.

Cheng, H., Niikura, M., Kim, T., Mao, W., MacLea, K., Hunt, H., Dodgson, J., Burnside, J., Morgan, R., Ouyang, M., Lamont, S., Dekkers, J., Fulton, J., Soller, M., Muir, W. 2008. Using integrative genomics to elucidate genetic resistance to Marek's disease in chicken. 2009. In: Pinard M-H, Gay, C., Pastoret, P-P, Dodet, B., editors. Integrative Genomics for Disease Resistance: Animal Genomics for Animal Health. Developments in Biologicals. Basel, Switzerland: Karger. p. 365-372.

Cheng, H.H. 2005. Integrated genomic approaches to understanding resistance to Marek's disease. In: Proceedings of the 3rd International Symposium on Genetics of Animal Health, July 13-15, 2005, Ames, Iowa. p. 24-33.

Cheng, H.H., Zhang, Y., Muir, W. 2007. Evidence for widespread epistatic interactions influencing Marek's disease virus viremia levels in chicken. Cytogenetics and Genome Research. 117:313-318.

Clawson, M.L., Heaton, M.P., Keele, J.W., Smith, T.P., Harhay, G.P., Richt, J., Laegreid, W.W. 2008. A sequencing strategy for identifying variation throughout the prion gene of BSE-affected cattle. BMC Research Notes [journal online]. 1:32. Available: http://www.biomedcentral.com/1756-0500/1/32.

Clawson, M.L., Heaton, M.P., Keele, J.W., Smith, T.P., Harhay, G.P., Laegreid, W.W. 2006. Prion gene haplotypes of U.S. cattle. BioMed Central (BMC) Genetics. 7:51.

Dennis, R., Zhang, H.M., Cheng, H.W. 2006. Effect of selection for resistance and susceptibility to viral diseases on concentrations of dopamine and immunological parameters in six-week-old chickens. Poultry Science. 85:2135-2140.

Evoniuk, J., Johnson, M., Borowicz, P., Caton, J.S., Vonnahme, K., Reynolds, J., Taylor, J.B., Stoltenow, C., Orourke, K.I., Redmer, D. 2008. Effects of Nutrition and Genotype on Prion Protein (PrPC) Gene Expression in the Fetal and Maternal Sheep Placenta. Placenta. 29(5):422-428.

Heaton, M.P., Keele, J.W., Harhay, G.P., Richt, J., Koohmaraie, M., Wheeler, T.L., Shackelford, S.D., Casas, E., King, D.A., Sonstegard, T.S., Van Tassell, C.P., Neibergs, H.L., Chase, C.C., Kalbfleisch, T.S., Smith, T.P., Clawson, M.L., Laegreid, W.W. 2008. Prevalence of the prion gene E211K variant in U.S. cattle. BioMed Central (BMC) Veterinary Research [journal online]. 4:25.

Heifetz, E.M., Fulton, J.E., O'Sullivan, N.P., Arthur, J.A., Cheng, H.H., Wang, J., Soller, M., Dekkers, J.C. 2009. Mapping QTL Affecting Resistance to Marek's Disease in an F6 Advanced Intercross Population of Commercial Layer Chickens. Biomed Central (BMC) Genomics. Available: http://www.biomedcentral.com/1471-2164/10/20.

Hunt, H.D., Goto, R.M., Foster, D.N., Bacon, L.D., Miller, M.M. 2006. At least one YMHCI molecule in the chicken is alloimmunogenic and dynamically expressed on spleen cells during development. Immunogenetics. 58(4):297-307.

Hunt, H.D., Kim, T., Niikura, M., Cheng, H.H., Parcells, M., Ewald, S., Osterrieder, K. 2006. Marek's disease virus immune escape mechanisms. American Association of Avian Pathologists. In: American Association of Avian Pathologists Symposium Program. Impact of Subclinical Immunosuppression on Poultry Production, July 2006, Honolulu, Hawaii. p. 61-66.

Kim, T., Hunt, H.D., Cheng, H.H. 2010. Marek's Disease Viruses Lacking Either R-LORF10 or LORF4 Have Altered Virulence in Chickens. Virus Genes. 40(3):410-420.

Kunkle, R.A., Miller, J.M., Alt, D.P., Cutlip, R.C., Cockett, N.E., Wang, S., Richt, J.A., Thomsen, B.V., Hall, S.M. 2006. Determination of sheep prion gene polymorphisms from paraffin-embedded tissue. Journal of Veterinary Diagnostic Investigation. 18(5):443-447.

Larue, R.S., Jonsson, S.R., Silverstein, K.A., Lajoie, M., Bertrand, D., El-Mabrouk, N., Hotzel, I., Andresdottir, V., Smith, T.P., Harris, R. 2008. The artiodactyl APOBEC3 innate immune repertoire shows evidence for amulti-functional domain organization that existed in the ancestor ofplacental mammals. BioMed Central (BMC) Molecular Biology. 9:104.

Mao, W., Niikura, M., Silva, R.F., Cheng, H.H. 2008. Quantitative evaluation of viral fitness due to a single nucleotide polymorphism in the Marek's disease virus UL41 gene via an in vitro competition assay. Journal of Virological Methods. 148:125-131.

McElroy, J.P., Dekkers, J.C., Fulton, J.E., O'Sullivan, N.P., Soller, M., Lipkin, E., Zhang, W., Koehler, K.J., Lamont, S.J., Cheng, H.H. 2005. Microsatellite markers associated with resistance to Marek's disease in commercial layer chickens. Poultry Science. 84:1678-1688.

Miller, L.C., Harhay, G.P., Lager, K.M., Smith, T.P., Neill, J.D. 2008. Effect of porcine reproductive and respiratory syndrome virus on porcine alveolar macrophage function as determined using serial analysis of gene expression (SAGE). Developments in Biologicals. 132:169-174.

Niikura, M., Dodgson, J.B., Cheng, H.H. 2006. Stability of Marek's disease virus 132bp repeats during serial in vitro passages. Archives of Virology. 151:1431-1438.

Niikura, M., Kim, T., Hunt, H.D., Burnside, J., Morgan, R., Dodgson, J., Cheng, H.H. 2007. Marek's disease virus up-regulates major histocompatibility complex class II cell surface expression in infected cells. Virology. 359(1): 212-219.

Sherman, M.A., Goto, R.M., Moore, R.E., Hunt, H.D., Lee, T.D., Miller, M.M. 2008. Mass Spectral Data for 64 Eluted Peptides and Structural Modeling Define Peptide Binding Preferences for Class I Alleles in Two Chicken MHC-B Haplotypes Associated with Opposite Responses to Marek's Disease. Immunogenetics. 60(9):485-555.

Snowder, G.D., Van Vleck, L.D., Cundiff, L.V., Bennett, G.L. 2006. Bovine respiratory disease in feedlot cattle: Environmental, genetic and economic factors. Journal of Animal Science 84(8):1999-2008.

Snowder, G.D., Van Vleck, L.D., Cundiff, L.V., Bennett, G.L., Koohmaraie, M., Dikeman, M.E. 2007. Bovine respiratory disease in feedlot cattle: Phenotypic, environmental, and genetic correlations with growth, carcass, and palatability traits. Journal of Animal Science. 85:1885-1892.

Tai, S.H., Niikura, M., Cheng, H.H., Kruger, J.M., Wise, A.G., Maes, R.K. 2010. Complete Genomic Sequence and an Infectious BAC Clone of Feline Herpesvirus-1 (FHV-1). Virology. 401(2):215-227.

Thallman, R.M., Kuehn, L.A., Allan, M.F., Bennett, G.L., Koohmaraie, M. 2008. Opportunities for collaborative phenotyping for disease resistance traits in a large beef cattle resource population. Developments in Biologicals. 132:327-330.

Van Eenennaam, A.L., Li, J., Thallman, R.M., Quaas, R.L., Dikeman, M.E., Gill, C., Franke, D.E., Thomas, M.G. 2007. Validation of commercial DNA tests for quantitative beef quality traits. Journal of Animal Science. 85:891-900.

Ylinen, L.M., Keckesova, Z., Webb, B.L., Gifford, R.J., Smith, T.P., Towers, G.J. 2006. Isolation of an active Lv1 gene from cattle indicates that tripartite motif protein-mediated innate immunity to retroviral infection is widespread among mammals. Journal of Virology. 80(15):7332-7338.

Yul, Y., Zhang, H.M., Tian, F., Bacon, L.D., Zhang, Y., Zhang, W., Song, J. 2008. Quantitative evaluation of DNA methylation patterns for ALVEs and TVB genes in a neoplastic disease susceptible and resistant chicken model. PLoS One. 3(3):e1731.

Yu, Y., Zhang, H., Tian, F., Zhang, W., Fang, H., Song, J. 2008. An Integrated Epigenetic and Genetic Analysis of DNA Methyltransferase Genes (DNMTs) in Tumor Resistant and Susceptible Chicken Lines. PLoS One. 3(7):1-13.

Zhang, H., Bacon, L.D., Fadly, A.M. 2008. Development of an Endogenous Virus-Free Line of Chickens Susceptible to All Subgroups of Avian Leukosis Virus. Avian Diseases. 52(3):412-418.

Zhang, W., Ding, J., Qu, Y., Hu, H., Lin, M., Datta, A., Larson, A., Liu, G., Li, B. 2008. Genomic expression analysis by single-cell mRNA differential display of quiescent CD8 T cells from tumor-infiltrating lymphocytes obtained from in vivo liver tumours. Immunology. 127(1):83-90.

Zhang, H.M., Hunt, H.D., Kulkarni, G.B., Palmquist, D.E., Bacon, L.D. 2006. Lymphoid organ size varies among inbred lines 63, 72 and their thirteen recombinant congenic strains of chickens with the same major histocompatibility complex. Poultry Science. 85:844-853.

13. Bioinformatic tools for genomic and quantitative genetic evaluation in livestock.

Chen, K., Knorr, C., Bornemann-Kolatzki, K., Ren, J., Huang, L., Rohrer, G.A., Bertram, B. 2005. Targeted oligonucleotide-mediated microsatellite identification (tommi) from large-insert library clones. BMC Genetics 6:54.

Cole, J.B. 2007. Pypedal: A computer program for pedigree analysis. Computers and Electronics in Agriculture. 57:107-113.

Isler, B.J., Freking, B.A., Thallman, R.M., Heaton, M.P., Leymaster, K.A. 2006. Evaluation of associations between prion haplotypes and growth, carcass, and meat quality traits in a Dorset x Romanov sheep population. Journal of Animal Science. 84:783-788.

Liu, G., Van Tassell, C.P., Sonstegard, T.S., Matukumalli, L.K., Shade, L.L. 2006. Genomic divergences among cattle, dog, and human estimated from large-scale alignments of genomic sequences. Biomed Central (BMC) Genomics. 7(1):140.

Matukumalli, L.K., Grefenstette, J.J., Van Tassell, C.P., Choi, I., Cregan, P.B. 2006. Application of machine learning in SNP discovery. BMC Bioinformatics. 6(7):4.

Tsai, S., Mir, B., Martin, A.C., Estrada, J.L., Bischoff, S.R., Hsieh, W., Cassady, J.P., Freking, B.A., Nonneman, D.J., Rohrer, G.A., Piedrahita, J. 2006. Detection of transcriptional difference of porcine imprinted genes using different microarray platforms. (BMC) Genomics. 7:328.

Van Tassell, C.P., Smith, T.P., Matukumalli, L.K., Taylor, J.F., Schnabel, R.D., Lawley, C.T., Haudenschild, C., Moore, S.S., Warren, W.C., Sonstegard, T.S. 2008. SNP discovery and allele frequency estimation by deep sequencing of reduced representation libraries. Nature Methods. 5:247-252.

Van Vleck, L.D. 2007. Technical Note: Computing numerator relationships between any pair of animals. Genetics and Molecular Research. 6(3):685-690.

14. Statistical methodology for genomic and quantitative trait evaluation.

Bennett, G.L. 2008. Experimental selection for calving ease and postnatal growth in seven cattle populations. I. Changes in estimated breeding values. Journal of Animal Science. 86(9):2093-2102.

Bennett, G.L., Thallman, R.M., Snelling, W.M., Kuehn, L.A. 2008. Experimental selection for calving ease and postnatal growth in seven cattle populations. II. Phenotypic differences. Journal of Animal Science. 86(9):2103-2114.

Casas, E. 2004. The use of genomics to identify genes influencing economically important traits in beef cattle. Proceedings of the First Agrobiotechnology Congress, November 30 to December 4, 2004, Monterrey, Mexico. p. 56-74.

Casas, E., Thallman, R.M., Smith, T.P. 2004. The application of molecular genetics in a commercial environment to improve production and carcass composition in cattle. Advances in Animal Biotechnology and Their Applications in the National Livestock Industry, Symposium & Compendium Series Proceedings. October 13-15, 2004, Villarica, Chile. 10:53-70.

Caperna, T.J., Shannon, A., Garrett, W.M. 2008. A gel-based reference map of the porcine hepatocyte proteome. Domestic Animal Endocrinology. 35(1):142-156.

Chen, C., Kachman, S.D., Johnson, R.K., Newman, S., Van Vleck, L.D. 2008. Estimation of genetic parameters for average daily gain using models with competition effects. Journal of Animal Science. 86:2525-2530.

Chen, C., Johnson, R.K., Kachman, S.D., Van Vleck, L.D. 2006. Estimation of variance components due to competition effects for selected lines of swine. Proceedings 8th World Congress of Genetics Applied in Livestock Production. CD-ROM Communication No. 17-03. Belo Horizonte, Brazil.

Cole, J.B., Van Raden, P.M. 2010. Visualization of Results from Genomic Evaluations. Journal of Dairy Science. 93(6):2727-2740.

Cole, J.B., Null, D.J., Van Raden, P.M. 2009. Best Prediction of Yields for Long Lactations. Journal of Dairy Science. 92(4):1796-1810.

Cole, J.B., Wiggans, G.R., Van Raden, P.M., Miller, R.H. 2007. Stillbirth (co)variance components for a sire-maternal grandsire threshold model and development of a calving ability index for sire selection. Journal of Dairy Science. 90(5):2489-2496.

Dechow, C.D., Norman, H.D. 2007. Within-herd heritability estimated with daughter-parent regression for yield and somatic cell score. Journal of Dairy Science. 90(1):482-492.

Dematawewa, C., Pearson, R.E., Van Raden, P.M. 2007. Modeling Extended Lactations of Holsteins. Journal of Dairy Science. 90(8):3924-3936.

Fetrow, J., Nordlund, K.V., Norman, H.D. 2006. Invited review: Culling: nomenclature, definitions, and recommendations. Journal of Dairy Science. 89(6):1896-1905.

Gengler, N., Wiggans, G.R., Gillon, A. 2005. Adjustment for heterogeneous covariance due to herd milk yield by transformation of test-day random regressions. Journal of Dairy Science. 88(8):2981-2990.

Gengler, N., Wiggans, G.R., Thornton, L.L., Wright, J.R., Druet, T. 2006. Accounting for heterogeneous variances in multi-trait evaluation of Jersey type traits. Journal of Dairy Science. 89(8):3143-3151.

Hayes, B.J., Bowman, A.J., Chamberlain, A.J., Savin, K., Van Tassell, C.P., Sonstegard, T.S., Goddard, M.E. 2009. A validated genome wide association study to breed cattle adapted to an environment altered by climate change. PLoS One. Aug 18:4(8)e:6676.

Jann, O.C., Aerts, J., Jones, M., Hastings, N., Law, A., Mckay, S., Marques, E., Prasad, A., Yu, J., Moore, S.S., Florita, S., Mahe, M., Eggen, A., Silveri, L., Negrini, R., Milanesi, E., Ajmone-Marsan, P., Vakebtubu, A., Marchitelli, C., Janitz, M., Herwig, R., Hennig, S., Savarese, M., Gorni, C., Connor,

E.E., Sonstegard, T.S., Smith, T.P., Drogemuller, C., Williams, J. 2006. A second generation radiation hybrid map to aid the assembly of the bovine genome sequence. BMC Genomics. 7:283-298.

Kachman, S.D., Van Vleck, L.D. 2007. Technical Note: Calculation of standard errors of estimates of genetic parameters with the multiple-trait derivative-free restricted maximal likelihood programs. Journal of Animal Science. 85:2375-2381.

Kuhn, M.T., Hutchison, J.L., Norman, H.D. 2008. Modeling Nuisance Variables for Prediction of Service Sire Fertility. Journal of Dairy Science. 91(7):2823-2835.

Liu, G., Hou, Y., Zhu, B., Cardone, M.F., Jiang, L., Cellamare, A., Mitra, A., Alexander, L.J., Coutinho, L.L., Gasbarre, L.C., Heaton, M.P., Li, R.W., Matukumalli, L.K., Nonneman, D.J., De A Regitano, L.C., Smith, T.P., Song, J., Sonstegard, T.S., Van Tassell, C.P., Eichler, E.E., Mcdaneld, T.G., Keele, J.W. 2010. Analysis of copy number variations among cattle breeds. Genome Research. 20:693-703.

Liu, G. 2009. Applications and Case Studies of the Next-Generation Sequencing Technologies in Food, Nutrition and Agriculture. Recent Patents on Food, Nutrition & Agriculture. 1(1):75-79.

Liu, G., Ventura, M., Cellamare, A., Chen, L., Cheng, Z., Zhu, B., Song, J., Eichler, E.E. 2009. Analysis of recent segmental duplications in the bovine genome. BMC Genomics. 10:571.

Miller, R.H., Norman, H.D., Kuhn, M.T., Clay, J.S., Hutchison, J.L. 2007. Voluntary waiting period and adoption of synchronized breeding in Dairy Herd Improvement herds. Journal of Dairy Science. 90(3):1594-1606.

Mitra, A., Liu, G., Song, J. A genome-wide analysis of array-based comparative genomic hybridization (CGH)data to detect intra-species variations and evolutionary relationships. PLoS One. Nov. 24; 4(11):e7978.

Norman, H.D., Wright, J.R., Kuhn, M.T., Hubbard, S.M., Cole, J.B., Van Raden, P.M. 2009. Genetic and Environmental Factors That Impact Gestation Length in Dairy Cattle. Journal of Dairy Science. 92(5):2259-2269.

Norman, H.D., Wright, J.R., Weigel, K.A. 2009. Alternatives for Examining Daughter Performance of Progeny-Test Bulls between Official Evaluations. Journal of Dairy Science. 92(5):2348-2355.

Paape, M.J., Wiggans, G.R., Bannerman, D.D., Thomas, D.L., Sanders, A.H., Contreras, A., Moroni, P., Miller, R.H. 2007. Monitoring goat and sheep milk somatic cell counts. Small Ruminant Research. 68(1-2):114-125.

Powell, R.L., Norman, H.D. 2006. Major advances in genetic evaluation techniques. Journal of Dairy Science. 89(4):1337-1348.

Ratnakumar, A., Barris, W., McWilliam, S., Brauning, R., McEwan, J.C., Snelling, W.M., Dalrymple, B.P. 2009. A Multiway Analysis for Identifying High Integrity Bovine BACs. Biomed Central (BMC) Genomics. 10:46 (13 pp).

Snelling, W.M., Chiu, R., Schein, J.E., Hobbs, M., Abbey, C.A., Adelson, D.L., Aerts, J., Bennett, G.L., Bosdet, I.E., Boussaha, M., Brauning, R., Caetano, A.R., Costa, M.M., Crawford, A.M., Dalrymple, B.P., Eggen, A., Everts-Van Der Wind, A., Floriot, S., Gautier, M., Gill, C.A., Green, R.D., Holt, R., Jann, O., Jones, S.J., Kappes, S.M., Keele, J.W., De Jong, P.J., Larkin, D.M., Lewin, H.A., Mcewan, J.C., Mckay, S., Marra, M.A., Mathewson, C.A., Matukumalli, L.K., Moore, S.S., Murdoch, B., Nicholas, F.W., Osoegawa, K., Roy, A., Salih, H., Schibler, L., Schnabel, R.D., Silveri, L., Skow, L.C., Smith, T.P., Sonstegard, T.S., Taylor, J.F., Tellam, R., Van Tassell, C.P., Williams, J.L., Womack, J.E., Wye, N.H., Yang, G., Zhao, S. 2007. A physical map of the bovine genome. Genome Biology. 8:R165 (17 pp).

Thallman, R.M., Kuehn, L.A., Allan, M.F., Bennett, G.L., Koohmaraie, M. 2008. Opportunities for collaborative phenotyping for disease resistance traits in a large beef cattle resource population. Developments in Biologicals. 132:327-330.

Tsai, S., Cassady, J.P., Freking, B.A., Nonneman, D.J., Rohrer, G.A., Piedrahita, J.A. 2006. Annotation of the affymetrix porcine genome microarray. Animal Genetics. 37:423-424.

Tshipuliso, N.O., Alexander, L.J., Kotze, A., Ehlers, K., Leesburg, V.L., Macneil, M.D. 2008. Structural assessment of backcrossing using microsatellite markers. South African Journal of Science 38(4):290-292.

Van Raden, P.M., Sullivan, P. 2010. International genomic evaluation methods for dairy cattle. Genetics Selection Evolution. 42:7.

Van Raden, P.M. 2008. Efficient Methods to Compute Genomic Predictions. Journal of Dairy Science. 91(11):4414-4423.

Van Raden, P.M., Dematawewa, C., Pearson, R.E., Tooker, M.E. 2006. Productive life including all lactations and longer lactations with diminishing credits. Journal of Dairy Science. 89(8):3213-3220.

Van Raden, P.M. 2005. Inbreeding adjustments and effect on genetic trend estimates. International Bull Evaluation Service Bulletin 33:81-84.

Van Tassell, C.P., Smith, T.P., Matukumalli, L.K., Taylor, J.F., Schnabel, R.D., Lawley, C.T., Haudenschild, C., Moore, S.S., Warren, W.C., Sonstegard, T.S. 2008. SNP discovery and allele frequency estimation by deep sequencing of reduced representation libraries. Nature Methods. 5:247-252.

Weigel, K.A., Van Tassell, C.P., O'Connell, J.R., Van Raden, P.M., Wiggans, G.R. 2010. Prediction of unobserved single nucleotide polymorphism genotypes of Jersey cattle using reference panels and population-based imputation algorithms. Journal of Dairy Science. 93(5):2229-2238.

Wiedmann, R.T., Smith, T.P., Nonneman, D.J. 2008. SNP discovery in swine by reduced representation and high throughput pyrosequencing. BioMed Central (BMC) Genetics. 9:81.

Wiggans, G.R., Van Raden, P.M., Bacheller, L.R., Tooker, M.E., Hutchison, J.L., Cooper, T.A., Sonstegard, T.S. 2010. Selection and management of DNA markers for use in genomic evaluation. Journal of Dairy Science. 93(5):2287-2292.

Wiggans, G.R., Sonstegard, T.S., Van Raden, P.M., Matukumalli, L.K., Schnabel, R.D., Taylor, J.F., Schenkel, F.S., Van Tassell, C.P. 2009. Selection of single-nucleotide polymorphisms and quality of genotypes used in genomic evaluation of dairy cattle in the United States and Canada. Journal of Dairy Science. 92(7):3431-3436.

Wiggans, G.R., Tsuruta, S., Misztal, I. 2008. Technical Note: Adaptation of an Animal-Model Method for Approximation of Reliabilities to a Sire-Maternal Grandsire Model. Journal of Dairy Science. 91(10):4058-4061.

Williams, C.B., Bennett, G.L., Jenkins, T.G., Cundiff, L.V., Ferrell, C.L. 2006. Using simulation models to predict feed intake: phenotypic and genetic relationships between observed and predicted values in cattle. Journal of Animal Science. 84(6):1310-1316.

Zhang, Z., Todhunter, R.J., Buckler Iv, E.S., Van Vleck, L.D. 2007. Technical note: Use of marker-based relationships with multiple-trait derivative-free restricted maximal likelihood. Journal of Animal Science. 85:881-885.

Zhu, B., Jiang, L., Liu, G. 2010. A dynamic neighboring extension search algorithm for genome coordinate conversion in the presence of short sequence duplications. Gene Expression to Genetical Genomics. 2:29-36.

Research Component 2: Enhancing Animal Adaptation, Well-Being and Efficiency in Diverse Production Systems

1. Basic endocrinology in ruminants.

Amaral, B.C., Connor, E.E., Tao, S., Hayen, J., Bubolz, J., Dahl, G.E. 2010. Heat stress abatement during the dry period influences prolactin signaling in lymphocytes. Domestic Animal Endocrinology. 38(1):38-45.

Baldwin, R.L., Baumann, R.G., Mcleod, K.R. 2007. Influence of abomasal carbohyrdates on subcutaneous, omental, and mesenteric adipose lipogenic and lypolytic rates in growing beef steers. Journal of Animal Science. 85:2271-2282.

Blum, J.W., Elsasser, T.H., Greger, D.L., Wittenberg, S., de Vries, F., Distl, O. 2006. Insulin-like growth factor type-1 receptor down-regulation associated with dwarfism in Holstein calves. Domestic Animal Endocrinology.

Cooper, B., Neelan, A., Campbell, K., Lee, J., Liu, G., Garrett, W.M., Scheffler, B.E., Tucker, M.L. 2007. Protein Accumulation Changes Associated with Germination of the Uromyces appendiculatus Uredospore. Molecular Plant-Microbe Interactions. 20(7):857-866.

Elsasser, T.H., Kahl, S., Li, C., Sartin, J.L., Garrett, W.M., Rodrigo, J. 2007. Caveolae-based nitration at the jak-2 kinase 1007 y-1008-y phosphorylation site; a novel regulatory input to signal transduction processing. Endocrinology 148:3803-3813.

Elsasser, T.H., Li, C., Caperna, T.J., Kahl, S., Schmidt, W.F. 2007. GH-associated nitration of JAK2 at the 1007Y-1008Y epitope impedes phosphorylation at this site: Mechanism for and impact of a GH, AKT and nitric oxide synthase (NOS) axis on GH signal transduction. Endocrinology. 148:3792-3802.

Kahl, S., Elsasser, T.H. 2005. Exogenous testosterone modulates tumor necrosis factor-A and acute phase proteins responses to repeated endotoxin challenge in steers. Domestic Animal Endocrinology. Available:http://dx.doi.org/doi:10.1016/j.domaniend.2005.11.005.

Li, C., Li, R.W., Elsasser, T.H., Kahl, S. 2009. Lipopolysaccharide-induced early response genes in bovine peripheral blood mononuclear cells implicate GLG1/E-selectin as a key ligand–receptor interaction. Functional and Integrative Genomics. 9(3):335-349.

Li, C., Elsasser, T.H., Kahl, S. 2009. AKT/eNOS Signaling Module Functions as a potential feedback loop in the growth hormone signaling pathway. Journal of Molecular Signaling. 4:1.

Li, C., Elsasser, T.H. 2006. Specific cell cycle synchronization with butyrate and cell cycle analysis by flow cytometry for Madin Darby Bovine Kidney (MDBK) cell line. Journal of Animal and Veterinary Advances. 5(11):916-923.

Li, C.J., Kahl, S., Carbaugh, D., Elsasser, T.H. 2006. Temporal response of signal transduction elements during endotoxin challenge in cattle liver cells: Effects of growth hormone treatment. Domestic Animal Endocrinology 32(2):79-92.

Li, C.J., Li, R.W., Wang, Y.H. Elsasser, T.H. 2007. Pathway analysis identifies perturbation of genetic networks induced by butyrate in a bovine kidney epithelial cell line. Functional and Integrative Genomics. 7:193-205.

Looper, M.L., Flores, R., Rorie, R.W., Hallford, D.M., Rosenkrans, C.F. 2008. Endocrine and follicular dynamics are influenced by body condition and somatotropin in post-partum beef cows. Journal of Animal Science. 86:1335-1344.

Michael, D.D., Alvarez, I.M., Ocon, O.M., Powell, A.M., Talbot, N.C., Johnson, S.E., Ealy, A.D. 2006. Fibroblast growth factor-2 is expressed by the bovine uterus and stimulates interferon-tau production in bovine trophectoderm. Endocrinology. 147:3571-3579.

Michael, D.D., Ocon, O.M., Talbot, N.C., Rooke, J.A., Ealy, A.D. 2006. Granulocyte-macrophage colony-stimulating factor increases interferon-tau protein secretion without influencing the rate of interferon-tau gene expression in bovine trophectoderm. Domestic Animal Endocrinology. 56:63-67.

Mccleod, K.E., Baldwin, R.L., Solomon, M.B., Baumann, R.G. 2007. Influence of ruminal and postruminal carbohydrate infusion on visceral organ mass and adipose tissue accretion in growing beef steers. Journal of Animal Science. 85:2256-2270.

Sunny, N.E., Owens, S.L., Baldwin, R.L., El-Kadi, S.W., Kohn, R.A., Bequette, B.J. 2007. Salvage of blood urea nitrogen in sheep is highly dependent on plasma urea concentration and the efficiency of capture within the diegestive tract. Journal of Animal Science. 85(4):1006-1013.

2. Basic endocrinology in swine and poultry.

Adcock, R.J., Kattesh, H.G., Roberts, M.P., Saxton, A.M., Carroll, J.A. 2006. Relationships between plasma cortisol, corticosteroid-binding globulin (CBG) and the free cortisol index (FCI) in pigs over a 24 h period. Journal of Animal and Veterinary Advances. 5(1):85-91.

Barb, C.R., Barrett, J.B. 2005. Neuropeptide Y modulates growth hormone secretion but not luteinizing hormone secretion from prepuberal gilt anterior pituitary cells in culture. Domestic Animal Endocrinology. 29:548-555.

Barb, C.R., Hausman, G.J., Ramsay, T.G. 2006. Leptin in farm animals. In: Castracane, D.V., Henson, M.C., editors. Endocrine Update. New York, NY: Springer. p.263-308.

Caperna, T.J., Shannon, A.E., Poch, S.M., Garrett, W.M., Richards, M.P. 2005. Hormonal regulation of leptin receptor expression in primary cultures of porcine hepatocytes. Domestic Animal Endocrinology. 29:582-592.

Caperna, T.J., Shannon, A.E., Richards, M.P., Garrett, W.M., Talbot, N.C. 2006. Identification and characterization of aquaporin-9 (aqp9) in porcine hepatic tissue and hepatocytes in monolayer culture. Domestic Animal Endocrinology. 32:273-286.

Chen, S.E., McMurtry, J.P., Walzem, R.L. 2006. Overfeeding-induced ovarian dysfunction in broiler breeder hens is associated with lipotoxicity. Poultry Science. 85.70-81.

Daniel, J., Carroll, J.A., Keisler, D., Kojima, C. 2008. Evaluation of immune system function in neonatal pigs born vaginally or by Cesarean section. Domestic Animal Endocrinology. 35(1):81-87.

Dodson, M.V., Fernyhough, M.E., Vierck, J.L., Hausman, G.J. 2006. Adipocytes may not be a terminally differentiated cell type: implications for animal production. Animal Science. 80(3):239-240.

Elsasser, T.H., Li, C., Caperna, T.J., Kahl, S., Schmidt, W.F. 2007. GH-associated nitration of JAK2 at the 1007Y-1008Y epitope impedes phosphorylation at this site: Mechanism for and impact of a GH, AKT and nitric oxide synthase (NOS) axis on GH signal transduction. Endocrinology. 148:3792-3802.

Fernyhough, M.E., Vierck, J.L., Hausman, G.J., Mir, P.S., Okine, E.K., Dodson, M.V. 2005. Primary adipocyte culture: adipocyte purification methods may lead to a new understanding of adipose tissue growth and development. Cytotechnology. 46(2-3):163-172.

Hausman, G.J., Hausman, D.B. 2006. Search for the preadipocyte progenitor proceeds to a new dimension. Journal of Clinical Investigation. 116(12):3103-3106.

Hausman, G.J., Poulos, S.P., Richardson, R.L., Barb, C.R., Andacht, T., Mynatt, R., Kirk, H., Crandall, D., Hreha, A. 2006. Secreted proteins and genes in fetal and neonatal pig adipose tissue and stromal-vascular cells. Journal of Animal Science. 84(7):1666-1681.

Leach, R.M.,Jr., Richards, M.P., Praul, B.C., Ford, B.C., McMurtry, J.P. 2007. Investigation of the insulin-like growth factor system in the avian epiphyseal growth plate. Domestic Animal Endocrinology. 33:143-153.

McMurtry, J.P. 2008. Regulation and Role of Leptin: Poultry. Encyclopedia of Animal Science. Pond, W. Bell, A., Eds.; Taylor & Francis Group: New York, 2008.

Poulos, S.P., Hausman, D.B., Hausman, G.J. 2009. The development and endocrine functions of adipose tissue. Molecular and Cellular Endocrinology.

Poulos, S.P., Hausman, G.J. 2006. Adipogenesis in stromal-vascular cell cultures derived from fetal semitendinosus muscle and subcutaneous adipose tissue. Adipocytes. 2:29-36.

Poulos, S.P., Hausman, G.J. 2006. A comparison of thiazolidinedione-induced adipogenesis and myogenesis in stromal-vascular cells from subcutaneous adipose tissue or semitendinosus muscle from postnatal pigs. Journal of Animal Science. 84(5):1076-1082.

Proszkowiec-Weglarz, M., Richards, M.P. 2007. 5'-AMP-activated protein kinase in avian biology. Avian and Poultry Biology Reviews. 18(4):123-145.

Proszkowiec-Weglarz, M., Richards, M.P., Ramachandran, R., McMurtry, J.P. 2006. Characterization of the AMP-activated protein kinase pathway in chickens. Comparative Biochemistry and Physiology Part B. 143:92-106.

Ramsay, T.G., Richards, M.P. 2007. Beta-adrenergic regulation of uncoupling protein expression in swine. Comparative Physiology and Biochemistry A. 147(2):395-403.

Rhoads, R., Fernyhough, M.E., Liu, X., Mcfarland, D., Velleman, S., Hausman, G.J., Dodson, M.V. 2009. Invited Review: Extrinsic regulation of domestic animal-derived myogenic satellite cells II. Domestic Animal Endocrinology. v:36, issue 3, p. 111-126.

Richards, M.P., Mcmurtry, J.P. 2010. The avian proghrelin system. International Journal of Peptides. Volume 2010, Article ID 749401, 14 pages.

Richards, M.P., Poch, S.M., McMurtry, J.P. 2006. Characterization of turkey and chicken ghrelin genes, and regulation of ghrelin and ghrelin receptor mRNA levels in broiler chickens. General and Comparative Endocrinology. 145(3):298-310.

Rosebrough, R.W., Richards, M.P., Mcmurtry, J.P., 2010. Rapid dietary protein changes and relationships among enzyme activities, their RNA's and plasma hormone levels in the broiler chicken. Avian Biology Research. 3(1):7-16.

Sweazea, K.L., McMurtry, J.P., Braun, E.J. 2006. Inhibition of fatty acid lipolysis does not affect insulin sensitivity to glucose uptake in the mourning dove. Comparative Biochemistry and Physiology, Part B. 144:387-394.

Williams, P., Carroll, J.A., Welsh Jr, T., Collier, C., Laurenz, J. 2009. Temporal pattern and effect of sex on lipopolysaccharide-induced stress hormone and cytokine response in pigs. Domestic Animal Endocrinology. 37:139-147.

3. Reproductive physiology – sperm physiology, semen quality, cryopreservation.

Bakst, M.R., Akuffo, V. 2007. Alkaline phosphatase reactivity in the vagina and uterovaginal junction sperm-storage tubules of turkeys in egg production: implications for sperm storage. British Poultry Science. 48:515-8.

Bakst, M.R., Akuffo, V. 2008. Turkey sperm reside in the tubular glands in the urodeum following artificial insemination. Poultry Science. 87(4):790-2.

Bakst, M.R., Akuffo, V. 2008. Serotonin localization in the turkey vaginal but not sperm storage tubule epithelia. Poultry Science. 87(2):356-61.

Bakst, M.R., Akuffo, V.G., Trefil, P., Brillard, J.P. 2007. Morphological and histochemical characterization of the seminiferous epithelial and leydig cells of the turkey. Animal Reproduction Sciences. 97:303-313.

Bakst, M.R., Long, J.A., Kramer, M.H. 2006. Impact of fenbendazole on turkey semen quality. Journal of Applied Poultry Research. 15:307-311.

Blanco, J.M., Long, J.A., Gee, G., Donoghue, A.M., Wildt, D.E. 2008. Osmotic tolerance of avian spermatozoa: influence of time, temperature, cryoprotectant and membrane ion pump function on sperm viability. Cryobiology. 56:8-14.

Corbin, C.J., Berger, T., Ford, J.J., Roselli, C.E., Sienkiewicz, W., Trainor, B.C., Roser, J.F., Vidal, J.D., Harada, N., Conley, A.J. 2009. Porcine Hypothalamic Aromatase Cytochrome P450: Isoform Characterization, Sex-Dependent Activity, Regional Expression, and Regulation by Enzyme Inhibition in Neonatal Boars. Biology of Reproduction. 81(2):388-395.

Dupuy, V., Sellier, N., Brillard, J., Bakst, M.R. 2006. Comparative staging of embryo development in chicken, turkey, duck, goose, guinea fowl, and quail assessed from 5 hours after fertilization to 72 hours of incubation. Journal of Applied Poultry Research. 15:219-228.

Ellis, R.W., Rupp, G.P., Chenoweth, P.J., Cundiff, L.V., Lunstra, D.D. 2005. Fertility of yearling beef bulls during mating. Theriogenology. 64(3):657-678.

Ford, J.J., Rohrer, G.A., Nonneman, D.J., Lunstra, D.D., Wise, T.H. 2010. Association of Allelic Variants of Thyroid-Binding Globulin With Puberty in Boars and Responses to Hemicastration. Animal Reproduction Science. 119(3-4):228-234.

Ford, J.J., Wise, T.H. 2009. Sertoli Cell Differentiation in Pubertal Boars. Journal of Animal Science. 87(8):2536-2543.

Guthrie, H.D., Welch, G.R. 2010. Using fluorescence-activated flow cytometry to determine reactive oxygen species formation and membrane lipid peroxidation in viable boar spermatozoa. Methods in Molecular Biology (Advanced Protocols in Oxidative Stress II). 594:163-171.

Guthrie, H.D., Welch, G., Long, J.A. 2008. Mitochondrial function and reactive oxygen species action in relation to boar motility. Theriogenology. 70:1209-1215.

Guthrie, H.D., Woods, L.C., III, Long, J.A., Welch, G.R. 2008. Effects of osmolality on inner mitochondrial transmembrane potential and ATP content in spermatozoa recovered from the testes of striped bass (Morone saxatilis). Theriogenology. 69:1007-12.

Guthrie, H.D., Welch, G.R. 2006. Determination of intracellular reactive oxygen species and high mitochrondrial membrane potential in viable boar sperm using fluorescence activated flow cytometry. Journal of Animal Science. 84:2089-2100.

Jimenez-Severiano, H., D'Occhio, M.J., Lunstra, D.D., Mussard, M.L., Davis, T.L., Enright, W.J., Kinder, J.E. 2007. Comparative response of rams and bulls to long-term treatment with gonadotropin-releasing hormone analogs. Animal Reproduction Science. 98(3-4):204-224.

Kealey, C.G., Macneil, M.D., Tess, M.W., Geary, T.W., Bellows, R.A. 2006. Genetic parameter estimates for scrotal circumference and semen characteristics of yearling line 1 Hereford bulls. Journal of Animal Science 84:283-290.

Long, J.A. 2010. Chapter II. Determination of sperm concentration. Section 3. Photometer procedure. In: Bakst, M.R., Long, J.A., editors. Techniques for Semen Evaluation, Semen Storage, and Fertility Determination. 2nd edition. St. Paul, MN: The Midwest Poultry Federation. p. 23-25.

Long, J.A. 2010. Chapter VI. Semen cryopreservation. Section 1. Cryopreservation of poultry sperm using glycerol. In: Bakst, M.R., Long, J.A., editors. Techniques for Semen Evaluation, Semen Storage, and Fertility Determination. 2nd edition. St. Paul, MN: The Midwest Poultry Federation. p. 62-64.

Long, J.A. 2010. Chapter VI. Semen cryopreservation. Section 2. Cryopreservation of rooster sperm using DMA. In: Bakst, M.R., Long, J.A., editors. Techniques for Semen Evaluation, Semen Storage, and Fertility Determination. 2nd edition. St. Paul, MN: The Midwest Poultry Federation. p. 65-67.

Long, J.A. 2010. Chapter VI. Semen cryopreservation. Section 3. Glycerol removal from thawed semen. In: Bakst, M.R., Long, J.A., editors. Techniques for Semen Evaluation, Semen Storage, and Fertility Determination. 2nd edition. St. Paul, MN: The Midwest Poultry Federation. p. 68-71.

Long, J.A. 2010. Chapter VIII. Sperm function assessment. Section 2. ATP assay. In: Bakst, M.R., Long, J.A., editors. Techniques for Semen Evaluation, Semen Storage, and Fertility Determination. 2nd edition. St. Paul, MN: The Midwest Poultry Federation. p. 99-102.

Long, J.A., Bongalhardo, D.C., Pelaéz, J., Saxena, S., Settar, P., O'Sullivan, N.P., Fulton, J.E. 2010. Rooster semen cryopreservation: Effect of pedigree line and male age on postthaw sperm function. Poultry Science. 89(5):966-973.

Long, J.A. 2006. Avian semen cryopreservation: what are the biological challenges? Poultry Science. 85:232-236.

Long, J.A., Guthrie, H.D. 2006. Validation of a rapid, large-scale assay to quantify atp levels in spermatozoa. Theriogenology. 65:1620-1630.

Noirault, J., Brillard, J.P., Bakst, M.R. 2005. Spermatogenesis in the turkey (meleagris gallopavo): quantitative approach in immature and adult males subjected to various photoperiods. Theriogenology. 65:845-859.

Norman, H.D., Hutchison, J.L., Miller, R.H. 2010. Use of sexed semen and its effect on conception rate, calf sex, dystocia, and stillbirth of Holsteins in the United States. Journal of Dairy Science. 93(8):3880-3890.

Pelaez, J. Long, J.A. 2008. Characterizing the glycocalyx of poultry spermatozoa: II. In vitro storage of Turkey semen and mobility phenotype affects the carbohydrate component of sperm membrane glycoconjugates. Journal of Andrology. 29:431-9.

Pelaez, J., Long, J.A. 2007. Characterizing the glycocalyx of poultry spermatozoa: i. identification and distribution of carbohydrate residues using flow cytometry and epifluorescence microscopy. Journal of Andrology. 28(2):342-352.

Purdy, P.H. 2008. Ubiquitination and its influence in boar sperm physiology and cryopreservation. Theriogenology 70:818-826.

Rowe, M., Bakst, M.R., and Pruett-Jones, S. 2008. Good vibrations? Structure and function of the cloacal tip of male Australian Maluridae. Journal of Avian Biology. 39(3):348-354.

Stellflug, J.N., Lewis, G.S., Moffet, C.A., Leeds, T.D. 2008. Evaluation of three-ram cohort serving capacity tests as a substitute for individual serving capacity tests. Journal of Animal Science. 86:2024-2031.

Stellflug, J.N. 2006. Comparison of cortisol, luteinizing hormone, and testosterone responses to a defined stressor in sexually inactive rams and sexually active female-oriented and male-oriented rams. Journal of Animal Science. 84:1520-1525.

Stellflug, J.N., Cockett, N.E., Lewis, G.S. 2006. The relationship between sexual behavior classifications of rams and lambs sired in a competitive breeding environment. Journal of Animal Science. 84:463-468.

Stellflug, J.N., Cockett, N.E., Lewis, G.S. 2007.The influence of breeding intensity on above- and below-average sexual performance rams in single- and multiple-sire breeding environments. Animal Reproduction Sciences. doi:10.1016/j.anireprosci.2007.02.017.

Stellflug, J.N., Lewis, G.S. 2007. Effect of early and late exposure to estrual ewes on ram sexual performance classifications. Animal Reproduction Sciences. 97:295-302.

Trefil, P., Micakova, A., Mucksova, J., Hejnar, J., Brillard, J.P., Bakst, M.R., Kalina, J., Poplstein, M. 2006. Restoration of spermatogenesis and male fertility by transplantation of dispersed testicular cells in the chicken. Biology of Reproduction. 75:575-581.

Vizcarra, J.A., Ford, J.J. 2006. Validation of the sperm mobility assay in boars and stallions. Theriogenology. 66(5):1091-1097.

4. Reproductive physiology – embryonic development and physiology.

Blomberg, L., Schreier, L.L., Guthrie, H.D., Caperna, T.J., Ramsay, T.G., Sample, G.L., Vallet, J. 2010. The effect of intrauterine growth retardation on the expression of developmental factors in porcine placenta subsequent to placentation. Placenta. 31(6):549-52.

Blomberg, L., Hashizume, K., Viebahn, C. 2008. Blastocyst elongation, trophoblastic differentiation, and embryonic pattern formation. 2008. Reproduction. 135:181-95.

Blomberg, L., Schreier, L.L., Talbot, N.C. 2008. Expression Analysis of Pluripotency Factors in the Undifferentiated Porcine Inner Cell Mass and Epiblast During In Vitro Culture. Molecular Reproduction and Development. 75(3):450-63.

Blomberg, L., Miles, J.R., Talbot, N.C., Garrett, W.M., Zuelke, K.A. 2006. Unique expression patterns of differentiation, growth and cell structure factors in the elongating porcine conceptus. Reproduction, Fertility and Development. 18:170.

Blomberg, L., Zuelke, K.A. 2005. Expression analysis of the steroidogenic acute regulatory protein (STAR) gene in developing porcine conceptuses. Journal of Molecular Reproduction and Development. 72:419-429.

Caperna, T.J., Shannon, A.E., Blomberg, L., Garrett, W.M., Ramsay, T.G. 2010. Identification of protein carbonyls in serum of the fetal and neonatal pig. Comparative Biochemistry and Physiology. 156(3):189-196.

Christensen, V.L., Havenstein, G.B., Ort, D.T., McMurtry, J.P., Nestor, K.E. 2007. Dam line and sire line effects on turkey embryo survival and thyroid hormone concentrations at the plateau stage in oxygen consumption. Poultry Science. 86:1861-1872.

Degrelle, S.A., Blomberg, L., Garrett, W.M., Li, R.W., Talbot, N.C. 2009. Comparative Proteomic and Regulatory Network Analyses of the Elongating Pig Conceptus. Proteomics. 9(10):2678-94.

Echternkamp, S.E., Vonnahme, K.A., Green, J.A., Ford, S.P. 2006. Increased vascular endothelial growth factor and pregnancy-associated glycoproteins, but not insulin-like growth factor-I, in maternal blood of cows gestating twin fetuses. Journal of Animal Science. 84(8):2057-2064.

Imakawa, K., Imai, M., Sakai, A., Suzuki, M., Nagaoka, K., Sakai, S., Lee, S.-R., Chang, K.-T., Echternkamp, S.E., Christenson, R.K. 2006. Regulation of conceptus adhesion by endometrial CXC chemokines during the implantation period in sheep. Molecular Reproduction and Development. 73(7):850-858.

Kim, J.G., Nonneman, D.J., Vallet, J.L., Wise, T.H., Rohrer, G.A. Sequence variation and evaluation of inhibin alpha-subunit and steroidogenic acute regulatory protein for reproductive traits in swine. Animal Genetics. 37:424-425. 2006.

Klemcke, H.G., Vallet, J.L., Christenson, R.K. 2006. Lack of effect of metyrapone and exogenous cortisol on early porcine conceptus development. Experimental Physiology. 91(3):521-530.

Miles, J.R., Freking, B.A., Blomberg, L., Vallet, J.L., Zuelke, K.A. 2008. Conceptus development during blastocyst elongation in lines of pigs selected for increased uterine capacity or ovulation rate. Journal of Animal Science. 86(9):2126-2134.

Stepinska, U., Bakst, M.R. 2007. Fertilization. In:Jamieson, B.G.M.,editor. Reproductive Biology and Phylogeny of Aves (Birds). Volume A. Enfield, NH: Science Publishers. p. 149-179.

Vallet, J.L., Miles, J.R., Brown Brandl, T.M., Nienaber, J.A. 2010. Proportion of the Litter Farrowed, Litter Size, and Progesterone and Estradiol Effects on Piglet Birth Intervals and Stillbirths. Animal Reproduction Science. 119(1-2):68-75.

Vallet, J.L., Miles, J.R., Freking, B.A. 2010. Effect of Fetal Size on Fetal Placental Hyaluronan and Hyaluronoglucosaminidases Throughout Gestation in the Pig. Animal Reproduction Science. 118(2-4):297-309.

5. Reproductive physiology – pregnancy maintenance, and uterine and ovarian function.

Allan, M.F., Kuehn, L.A., Cushman, R.A., Snelling, W.M., Echternkamp, S.E., Thallman, R.M. 2009. Confirmation of quantitative trait loci using a low-density single nucleotide polymorphism map for twinning and ovulation rate on bovine chromosome 5. Journal of Animal Science. 87(1):46-56.

Atkins, J.A., Smith, M.F., Wells, K.J., Geary, T.W. 2010. Factors affecting pre-ovulatory follicle diameter and ovulation rate to GnRH in postpartum beef cows. Part I: Cycling cows. Journal of Animal Science 88:2300-2310.

Atkins, J.A., Smith, M.F., Wells, K.J., Geary, T.W. 2010. Factors affecting pre-ovulatory follicle diameter and ovulation rate following GnRH in postpartum beef cows. Part II: Anestrous cows. Journal of Animal Science 88:2311-2320.

Bakst, M.R., Donoghue, A.M., Yoho, D.E., Moyle, J.R., Whipple, S.M., Camp, M.J., Liu, G.Q., Bramwell, R.K. 2010. Comparisons of sperm storage tubule distribution and number in four strains of mature broiler breeders and in turkey hens before and after the onset of photostimulation. Poultry Science. 89:986-992.

Bakst, M.R. 2010. Chapter II. Determination of sperm concentration. Section 1. Hemocytometer procedure. In: Bakst, M.R., Long, J.A., editors. Techniques for Semen Evaluation, Semen Storage, and Fertility Determination. 2nd edition. St. Paul, MN: The Midwest Poultry Federation. p. 11-15.

Bakst, M.R. 2010. Chapter III. Sperm Viability. Section 1. Nigrosin eosin stain for determining live dead and abnormal sperm counts. In: Bakst, M.R., Long, J.A., editors. Techniques for Semen Evaluation, Semen Storage, and Fertility Determination. 2nd edition. St Paul, MN: The Midwest Poultry Federation. p. 28-44.

Bakst, M.R. 2010. Chapter IV. Sperm motility and metabolism. Section 1. Visual scoring of motility using the hanging drip method. In: Bakst, M.R., Long, J.A., editors. Techniques for Semen Evaluation, Semen Storage, and Fertility Determination. 2nd edition. St. Paul, MN: The Midwest Poultry Federation. p. 45-46.

Bakst, M.R., Akuffo, V.G. 2009. Morphology of the Turkey Vagina and Uterus With and Without an Egg Mass. Poultry Science. 88:631-635.

Bischoff, S.R., Tsai, S., Hardison, N., Motsinger-Reif, A.A., Freking, B.A., Piedrahita, J.A. 2009. Functional Genomic Approaches for the Study of Fetal/Placental Development in Swine with Special Emphasis on Imprinted Genes. In: Control of Pig Reproduction VIII (H. Rodriguez-Martinez, J.L. Vallet and A.J. Ziecik, eds.) Journal of Reproduction and Fertility Supplement. 66:245-264.

Blomberg, L., Schreier, L.L., Guthrie, H.D., Caperna, T.J., Ramsay, T.G., Sample, G.L., Vallet, J. 2010. The effect of intrauterine growth retardation on the expression of developmental factors in porcine placenta subsequent to placentation. Placenta. 31(6):549-52.

Busch, D.C., Atkins, J.A., Bader, J.F., Shafer, D.J., Patterson, D.J., Geary, T.W., Smith, M.F. 2008. Effect of Ovulatory Folicle Size and Expression of Estrus on Progesterone Secretion in Beef Cows. Journal of Animal Science 86(3):553-563.

Christensen, V.L., Bagley L., Long, J.A. 2010. Chapter I. Semen collection and dilution. In: Bakst, M.R., Long, J.A., editors. Techniques for Semen Evaluation, Semen Storage, and Fertility Determination. 2nd edition. St. Paul, MN: The Midwest Poultry Federation. p. 7-10.

Cushman, R.A., Allan, M.F., Kuehn, L.A., Snelling, W.M., Cupp, A.S., Freetly, H.C. 2009. Evaluation of Antral Follicle Count and Ovarian Morphology in Crossbred Beef Cows: Investigation of Influence of Stage of the Estrous Cycle, Age, and Birth Weight. Journal of Animal Science. 87(6):1971-1980.

Cushman, R.A., Allan, M.F., Jones, S.A., Rupp, G.P., Echternkamp, S.E. 2007. Localization of Period 1 mRNA in the ruminant oocyte and investigations of its role in ovarian function. Animal Reproduction Science. 99(1-2):93-105.

Echternkamp, S.E., Cushman, R.A., Allan, M.F. 2009. Size of Ovulatory Follicles in Cattle Expressing Multiple Ovulations Naturally and Its Influence on Corpus Luteum Development and Fertility. Journal of Animal Science. 87(11):3556-3568.

Echternkamp, S.E., Cushman, R.A., Allan, M.F., Thallman, R.M., Gregory, K.E. 2007. Effects of ovulation rate and fetal number on fertility in twin-producing cattle. Journal of Animal Science. 85(12):3228-3238.

Echternkamp, S.E., Thallman, R.M., Cushman, R.A., Allan, M.F., Gregory, K.E. 2007. Increased calf production in cattle selected for twin ovulations. Journal of Animal Science. 85(12):3239-3248.

Echternkamp, S.E., Thallman, R.M., Cushman, R.A., Allan, M.F., Gregory, K.E. 2007. Increased calf production in cattle selected for twin ovulations. Journal of Animal Science. 85(12):3239-3248.

Echternkamp, S.E., Cushman, R.A., Allan, M.F., Thallman, R.M., Gregory, K.E. 2007. Effects of ovulation rate and fetal number on fertility in twin-producing cattle. Journal of Animal Science. 85(12):3228-3238.

Freking, B.A., Leymaster, K.A., Vallet, J.L., Christenson, R. 2007. Number of fetuses and conceptus growth throughout gestation in lines of pigs selected for either ovulation rate or uterine capacity. Journal of Animal Science. 85(9):2093-2103.

Freking, B.A., Leymaster, K.A., Vallet, J.L., Christenson, R. 2007. Number of fetuses and conceptus growth throughout gestation in lines of pigs selected for either ovulation rate or uterine capacity. Journal of Animal Science. 85(9):2093-2103.

Geary, T.W., Ansotegui, R.P., MacNeil, M.D., Roberts, A.J., Waterman, R.C. 2010. Effects of flunixin meglumine on pregnancy establishment in beef cattle. Journal of Animal Science 88:943-949.

Geary, T.W., Grings, E.E., Macneil, M.D., De Avila, D.M., Reeves, J.J. 2006. Use of recombinant gonadotropin releasing hormone antigens for immunosterilization of beef heifers. Journal of Animal Science 84:343-350.

Harris, D.L., Huderson, A.C., Niaz, M.S., Ford, J.J., Archibong, A.E., Ramesh, A. 2009. Comparative Metabolism of Benzo(a)pyrene by Ovarian Microsomes of Various Species. Environmental Toxicology. 24(6):603-609.

Hart, H.A., Azain, M.J., Hausman, G.J., Reeves, D.E., Barb, C.R. 2007. Failure of short term feed restriction to effect luteinizing hormone or leptin secretion and subcutaneous adipose tissue expression of leptin or leptin receptor in the prepuberal gilt. Canadian Journal of Animal Science. 87:191-197.

Kayser, J-P.R., Kim, J.G., Cerny, R.L., Vallet, J.L. 2006. Global characterization of porcine intrauterine proteins during early pregnancy. Reproduction. 132(2):379-388.

Kim, J.G., Vallet, J.L. 2007. Placental expression of the membrane form of folate binding protein during pregnancy in swine. Theriogenology. 67(7):1279-1284.

Koch, J.M., Mortiz, J.S., Smith, D.L., Lay, Jr., D.C., Wilson, M.E. 2005. Melengestrol acetate as an effective alternative to induce a decline in egg production and reversible regression of the reproductive tract in laying hens II. Effects on post molt egg quality. Poultry Science. 84:1757-1762

Koch, J.M., Moritz, J.S., Lay, Jr., D.C., Wilson, M.E. 2005. Melengestrol acetate in experimental diets as an effective alternative to induce a decline in egg production and reversible regression of the reproductive tract in laying hens I. Determining an effective concentration of MGA. Poultry Science. 84:1750-1756.

Kuhn, M.T., Hutchison, J.L., Wiggans, G.R. 2006. Characterization of Holstein heifer fertility in the United States. Journal of Dairy Science. 89(12):4907-4920.

Kuehn, L.A., Nonneman, D.J., Klindt, J.M., Wise, T.H. 2009. Genetic relationships of body composition, serum leptin, and age at puberty in gilts. Journal of Animal Science. 87(2):477-483.

Lamb, G.C., Larson, J.E., Geary, T.W., Stevenson, J.S., Johnson, S.K., Day, M.L., Kesler, D.J., Dejarnette, J.M., Landblom, D.G., Ansotegui, R.P. 2006. Synchronization of estrus and artificial insemination in replacement beef heifers using gonadotropin-releasing hormone, prostaglandin F2, and progesterone. Journal of Animal Science 84(11):3000-3009.

Larson, J.E., Lamb, G.C., Stevenson, J.S., Johnson, S.K., Day, M.L., Geary, T.W., Kesler, D.J., Dejarnette, J.M., Schrick, F.N., Arseneau, J.D. 2006. Synchronization of estrus in suckled beef cows before detected estrus and (or) timed artificial insemination using gonadotropin-releasing hormone (gnrh), prostaglandin f2a (pg), and progesterone (cidr). Journal of Animal Science 84:332-342.

Lents, C.A., Heidorn, N.L., Barb, C.R., Ford, J.J. 2008. Central and peripheral administration of kisspeptin activates gonadotropin but not somatotropin secretion in prepubertal gilts. Reproduction. 135:879-887.

Lewis, G.S., Wulster-Radcliffe, M.C. 2006. Prostaglandin F2ALPHA up regulates uterine immune defenses in the presence of the immunosuppressive steriod progesterone. American Journal of Reproductive Immunology. 56:102-111.

Macdonald, G.J., Wise, T.H., Sluss, P.M., Ford, J.J. 2007. Breed differences in clearance of porcine FSH in hypophysectomized rats. Animal Reproduction Science. 102(3-4):328-334.

Macneil, M.D., Geary, T.W., Perry, G.W., Roberts, A.J., Alexander, L.J. 2006. Genetic partitioning of variation in ovulatory follicle size and probability of pregnancy. Journal of Animal Science 84:1646-1650.

Merrill, M.L., Ansotegui, R.P., Burns, P.D., MacNeil, M.D., Geary, T.W. 2007. Effects of flunixin meglumine and transportation on pregnancy in beef cows. Journal of Animal Science 85:1547-1554.

Norman, H.D., Wright, J.R., Hubbard, S.M., Miller, R.H., Hutchison, J.L. 2009. Reproductive status of Holstein and Jersey cows in the United States. Journal of Dairy Science. 92(7):3517-3528.

Ocon, O.M., Maddineni, S., Hendricks, G.L., Elkin, R.G., Proudman, J.A., Ramachandran, R. 2006. Pituitary progesterone receptor expression and plasma gonadotrophin concentrations in the reproductively dysfunctional mutant restricted ovulator chicken. Domestic Animal Endocrinology. 32:201-215.

Ottinger, M., Mobarak, M., Abdelnabi, M., Roth, G., Proudman, J.A., Ingram, D. 2005. Calorie restriction in young and adult japanese quail: effects on the reproductive axis and adrenal systems: relevance to mammals. Experimental Gerontology. 126:967-975.

Paczoska-Eliasiewicz, H.E., Proszkowiec-Weglarz, M., Proudman, J.A., Jacek, T., Mika, M., Sechman, A., Rzasa, J., Gertler, A. 2006. Exogenous leptin advances puberty in domestic hen. Domestic Animal Endocrinology. 31(3):211-226.

Perry, G.A., Smith, M.F., Roberts, A.J., MacNeil, M.D., Geary, T.W. 2007. Relationship between size of ovulatory follicle and pregnancy success in beef heifers. Journal of Animal Science 85:684-689.

Proudman, J.A., Siopes, T.D. 2006. Further studies of the potential role of thyroid hormones and prolactin in the programming of photorefractoriness in turkey hens. Poultry Science. 85:1457-1461.

Roberts, A.J., Al-Hassan, M.J., Fricke, P.M., Echternkamp, S.E. 2006. Large variation in steroid concentrations and insulin-like growth factor binding proteins exists among individual small antral follicles collected from within cows at various stages of estrous cycle. Journal of Animal Science 84:2714-2724.

Roberts, A.J., Klindt, J.M., Jenkins, T.G. 2005. Effects of varying energy intake and sire breed on duration of postpartum anestrus, insulin like growth factor-1, and growth hormone in mature crossbred cows. Journal of Animal Science 83(7):1705-1714.

Sa Filho, O.G., Vilela, E.R., Geary, T.W., Vasconcelos, J. 2009. Strategies to improve fertility in post partum Bos indicus cows submitted to a fixed-time insemination protocol with GnRH and PGF2a. Journal of Animal Science jas.2009-1926v1-20091926.

Tauck, S.A., Berardinelli, J.G., Geary, T.W., Johnson, N.J. 2006. Resumption of postpartum luteal function of primiparous, suckled beef cows exposed continuously to bull urine. Journal of Animal Science 84:2708–2713.

Trott, J.F., Horigan, K.C., Gloviczki, J.M., Costa, K.M., Freking, B.A., Farmer, C., Hayashi, K., Spencer, T., Morabito, J.E., Hovey, R.C. 2009. Tissue-specific Regulation of Porcine Prolactin Receptor Expression by Estrogen, Progesterone and Prolactin. Journal of Endocrinology. 202:153-166.

Vallet, J.L., Miles, J.R., Freking, B.A. 2009. Development of the Pig Placenta. IN: Control of Pig Reproduction VIII (Rodriguez-Martinez, H., Vallet, J.L., Ziecik, A.J., eds.), Nottingham University Press. Proceedings of the Eighth International Conference on Pig Reproduction, May 31-June 4, 2009, The Banff Centre, Banff, Alberta, Canada. Society of Reproduction and Fertility Supplement. 66:265-279.

Vallet, J.L., Freking, B.A. 2007. Differences in placental structure during gestation associated with large and small pig fetuses. Journal of Animal Science. 85(12):3267-3275.

Vallet, J.L., Freking, B.A. 2006. Changes in fetal organ weights during gestation after selection for ovulation rate and uterine capacity in swine. Journal of Animal Science. 84(9):2338-2345.

Vallet, J.L., Freking, B.A. 2005. Effect of selection for ovulation rate and uterine capacity on fetal brain, heart, liver and spleen weights throughout gestation [abstract]. Seventh International Conference on Pig Reproduction (June 12-15, 2005; Congress Center 'Rolduc', Kerkrade, The Netherlands). p. 108.

Vonnahme, K.A., Zhu, M.J., Borowicz, P.B., Geary, T.W., Hess, B.W., Reynolds, L.P., Caton, J.S., Means, W.J., Ford, S.P. 2007. Effect of early gestational undernutrition on angiogenic factor expression and vascularity in the bovine placentome. Journal of Animal Science doi 10:2527/jas.2006-805.

Walker, R.S., Enns, R.M., Geary, T.W., Wamsley, N.W., Mortimer, R.G., Lashell, B.A., Zalesky, D.D. 2005. Evaluation gonadotropin-releasing hormone at fixed-time ai in beef heifers synchronized using a modified co-synch plus cidr protocol. Professional Animal Scientist 21:449-454.

Ward, M.A., Neville, T.L., Reed, J.J., Taylor, J.B., Hallford, D.M., Soto-Navarro, S.A., Vonnahme, K.A., Redmer, D.S., Reynolds, L.P., Caton, J.S. 2008. Effects of selenium supply and dietary restriction on maternal and fetal metabolic hormones in pregnant ewe lambs. Journal of Animal Science. 86:1254-1262.

Wilhelms, K.W., Cutler, S.A., Proudman, J.A., Carsia, R.V., Anderson, L.L., Scanes, C.G. 2006. Effects of atrazine on estrogen-responsive organs and circulating hormone concentrations in sexually immature female Japanese quail (coturnix coturnix japonica). Chemosphere. 65:674-681.

Wilhelms, K.W., Cutler, S.A., Proudman, J.A., Anderson, L.L., Scanes, C.G. 2006. Effects of atrazine on sexual maturation in female japanese quail induced by photostimulation or exogenous gonadotropin. Environmental Toxicology and Chemistry. 25(1):233-240.

Wulster-Radcliffe, M.C., Seals, R.C., Lewis, G.S. 2005. Uterine Response to Multiple Inoculations with Arcanobacterium pyogenes and Escherichia coli in Nulliparous Ewes. American Journal of Reproductive Immunology. 54:249-261.

6. Nutrition, growth biology and physiology in ruminants.

Archibeque, S.L., Freetly, H.C., Ferrell, C.L. 2008. Feeding distillers grains supplements to improve amino acid nutriture of lambs consuming moderate-quality forages. Journal of Animal Science. 86(3):691-701.

Bell, A.W., Ferrell, C.L., Freetly, H.C. 2005. Pregnancy and fetal metabolism. In: Dijkstra, J., Forbes, J. M.,France, J., editors. Quantitative Aspects of Ruminant Digestion and Metabolism. 2nd edition. Wallingford: CABI Publishing. p. 523-550.

Bewley, J.M., Boehlje, M.D., Gray, A.W., Hogeveen, H., Kenyon, S.J., Eicher, S.D., Schutz, M.M. 2010. Assessing the Potential Value for an Automated Body Condition Scoring System through Stochastic Simulation. Agricultural Finance Review. 70(1):126-150.

Brito, A.F., Broderick, G.A. 2007. Effects of different protein supplements on milk production and nutrient utilization in lactating dairy cows. Journal of Dairy Science. 90:1816-1827.

Brito, A.F., Broderick, G.A., Reynal, S.M. 2007. Effects of different protein supplements on omasal nutrient flow and microbial protein synthesis in lactating dairy cows. Journal of Dairy Science. 90:1828-1841.

Brito, A.F., Broderick, G.A. 2006. Effect of varying dietary ratios of alfalfa silage to corn silage on production and nitrogen utilization in lactating dairy cows. Journal of Dairy Science. 89:3924-3938.

Brito, A.F., Broderick, G.A., Reynal, S.M. 2006. Effect of varying dietary ratios of alfalfa silage to corn silage on omasal flow and microbial protein synthesis in dairy cows. Journal of Dairy Science. 89:3939-3953.

Broderick, G.A., Huhtanen, P., Ahvenjarvi, S., Reynal, S.M., Shingfield, K.J. 2010. Quantifying Ruminal Nitrogen Metabolism Using the Omasal Sampling Technique in Cattle--A Meta-Analysis. Journal of Dairy Science. 93:3216-3230.

Broderick, G.A., Stevenson, M.J., Patton, R.A. 2009. Effect of Dietary Protein Concentration and Degradability in Response to Rumen-Protected Methionine in Lactating Dairy Cows. Journal of Dairy Science. 92:2719-2728.

Broderick, G.A., Muck, R.E. 2009. Effect of Alfalfa Silage Storage Structure and Rumen-Protected Methionine on Production in Lactating Dairy Cows. Journal of Dairy Science. 92:1281-1289.

Broderick, G.A., Reynal, S.M. 2009. Effect of Source of Rumen-Degraded Protein on Production and Ruminal Metabolism in Lactating Dairy Cows. Journal of Dairy Science. 92:2822-2834.

Broderick, G.A., Luchini, N.D., Reynal, S.M., Varga, G.A., Ishler, V.A. 2008. Effect on Production of Replacing Dietary Starch with Sucrose in Lactating Dairy Cows. Journal of Dairy Science. 91(12):4801-4810.

Broderick, G.A., Brito, A.F., Olmos Colmenero, J.J. 2007. Effects of feeding formate-treated alfalfa silage or red clover silage on the production of lactating dairy cows. Journal of Dairy Science. 90:1378-1391.

Broderick, G.A. 2006. Improving nitrogen utilization in the rumen of the lactating dairy cow. In: Proceedings of the 17th Florida Ruminant Nutrition Symposium, January, 2006, Gainesville, Florida. p. 11-24.

Broderick, G.A. 2006. Nutritional strategies to reduce crude protein in dairy diets. In: Proceedings of the 21st Annual Southwest Nutrition and Management Conference, February, 2006, Tempe, Arizona. p. 1-14.

Brown, M.A., Lalman, D.L. 2008. Preweaning performance of calves from Bonsmara, Brangus, Charolais, Gelbvieh, Hereford, and Romosinuano sires bred to Brangus cows managed on native rangeland or improved forages. Professional Animal Scientist. 24:67-75.

Brown, M.A., Wang, X., Gao, F., Wu, J., Lalman, D.L. 2008. Postweaning gains in calves sired by six sire breeds evaluated on two preweaning forages and two postweaning management systems. Professional Animal Scientist. 24:224-231.

Calegare, L., Alencar, M.M., Packer, I.U., Ferrell, C.L., Lanna, D.P. 2009. Cow/calf preweaning efficiency of Nellore and Bos taurus x Bos indicus crosses. Journal of Animal Science. 87(2):740-747.

Calegare, L., Alencar, M.M., Packer, I.U., Leme, P.R., Ferrell, C.L., Lanna, D.P. 2009. Preweaning Performance and Body Composition of Calves from Straightbred Nellore and Bos taurus x Nellore Crosses. Journal of Animal Science. 87(5):1814-1820.

Carlson, D.B., Reed, J.J., Borowicz, P.P., Taylor, J.B., Reynolds, L.P., Redmer, D.A., Vonnahme, K.A., Caton, J.S. 2009. Effects of selenium supply and timing of nutrient restriction during gestation on maternal growth and body composition of pregnant adolescent ewes. Journal of Animal Science. 87:669-680.

Casas, E., Lunstra, D.D., Cundiff, L.V., Ford, J.J. 2007. Growth and pubertal development of F1 bulls from Hereford, Angus, Norwegian Red, Swedish Red and White, Friesian, and Wagyu sires. Journal of Animal Science. 85:2904-2909.

Contreras-Govea, F.E., Muck, R.E., Armstrong, K.L., Albrecht, K.A. 2009. Fermentability of Corn-Bean Mixtures from Different Planting Densities. Animal Feed Science And Technology. 149(3-4):298-306.

Contreras-Govea, F.E., Muck, R.E., Armstrong, K.L., Albrecht, K.A. 2009. Nutritive Value of Corn Silage in Mixture with Climbing Beans. Animal Feed Science And Technology. 150(1/2):1-8.

Cooper, A.J., Ferrell, C.L., Cundiff, L.V., Van Vleck, L.D. 2010. Prediction of Genetic Values for Feed Intake from Individual Body Weight Gain and Total Feed Intake of the Pen. Journal of Animal Science. 88(6):1967-1972.

Covey, T., Elam, N., Carroll, J.A., Wester, D., Ballou, M., Hallford, D., Galyean, M. 2010. Supplemental selenium source in Holstein steers challenged with intranasal bovine infectious rhinotracheitis virus: Blood metabolites, hormones, and cytokines. The Professional Animal Scientist. 26:93-102.

Covey, T., Elam, N., Carroll, J.A., Wester, D., Galyean, M. 2010. Supplemental selenium source in Holstein steers challenged with intranasal bovine infectious rhinotracheitis virus and in newly received beef heifers: Performance, morbidity, antibody titers, and blood cell counts. The Professional Animal Scientist. 26:82-92.

El-Dadi, S.W., Baldwin, R.L., Mcleod, K.R., Sunny, N.E., Bequette, B.J. 2009. Glutamate is the major anaplerotic substrate in the tricarboxylic acid cycle of isolated rumen epithelial and duodenal mucosal cells from beef cattle. Journal of Nutrition. 139(5):869-875.

El-Kadi, S.W., Baldwin, R.L., Sunny, N.E., Owens, S.L., Bequette, B.J. 2006. Metabolism of amino acids and glucose by the sheep gatrointestinal tract in response to post-ruminal protein supplies. Journal of Nutrition. 136(5):1261-1269.

Elsasser, T.H., Ingvartsen, K.L., Kahl, S., Capuco, A.V. 2006. In: Ruminant Physiology, Sejrsen, K., Hvelplund, T. Neilsen, M.O., eds. Wagemingem Academic Publishers, Netherlands. pp. 415-447.

Freetly, H.C., Ferrell, C.L., Archibeque, S.L. 2010. Net Flux of Amino Acids Across the Portal-drained Viscera and Liver of the Ewe During Abomasal Infusion of Protein and Glucose. Journal of Animal Science. 88(3):1093-1107.

Freetly, H.C., Nienaber, J.A., Brown Brandl, T.M. 2008. Partitioning of energy in pregnant beef cows during nutritionally induced weight fluctuation. Journal of Animal Science. 86(2):370-377.

Freetly, H.C., Nienaber, J.A., Brown-Brandl, T.M. 2006. Partitioning of energy during lactation of primiparous beef cows. Journal of Animal Science. 84:2157-2162.

Hall, M., Larson, C.C., Wilcox, C.J. 2010. Carbohydrate Source and Protein Degradability Alter Lactation, Ruminal, and Blood Measures. Journal of Dairy Science. 93(1):311-322.

Hall, M.B., Keuler, N.S. 2009. Factors Affecting Accuracy and Time Requirements of a Glucose Oxidase-Peroxidase Assay for Determination of Glucose. Journal of Association of Official Analytical Chemists International. 92:50-60.

Harris, H.L., Cupp, A.S., Roberts, A.J., Funston, R.N. 2008. Heifers fed soybeans or milling by-products utilization of soybeans or corn milling by-products in beef heifer development diets. Journal of Animal Science 86:476-482.

Horn, M.J., Van Emon, M.L., Gunn, P.J., Eicher, S.D., Lemenager, R.P., Pyatt, N., Lake, S.L. 2010. The Effects of Maternal Natural (RRR Alpha-Tocopherol Acetate) or Synthetic (All-Rac Alpha-

Tocopherol Acetate) Vitamin E Supplementation on Suckling Calf Performance, Colostrum IgG, and Immune Function. Journal of Animal Science. 88:3128-3135.

Houlihan, A.J., Russell, J.B. 2006. Factors affecting the activity of bovicin hc5, a bacteriocin from streptococcus bovis hc5: release, stability and binding to target bacteria. Journal of Applied Microbiology. 100:168-174.

Huhtanen, P., Ahvenjarvi, S., Broderick, G.A., Reynal, S.M., Shingfield, K.J. 2010. Quantifying Ruminal Digestion of Organic Matter and Neutral Detergent Fiber Using Omasal Sampling in Cattle--A Meta-Analysis. Journal of Dairy Science. 93:3203-3215.

Ipharraguerre, I.R., Reynal, S.M., Lineiro, M., Broderick, G.A., Clark, J.H. 2007. A comparison of sampling sites, digesta and microbial markers, and microbial references for assessing post-ruminal supply of nutrients in dairy cows. Journal of Dairy Science. 90:1904-1919.

Jenkins, T.G., Ferrell, C.L. 2007. Daily dry matter intake to sustain body weight of mature, nonlactating, nonpregnant cows. Journal of Animal Science. 85(7):1787-1792.

Kalscheur, K.F., Baldwin, R.L., Glenn, B.P., Kohn, R.A. 2006. Milk Producton of Dairy Cows Fed Differing cConcentrations of Rumen Degraded Protein. Journal of Dairy Sci. 89:249-259.

Lanzas, C., Broderick, G.A., Fox, D.G. 2008. Improved Feed Protein Fractional Schemes for Formulating Rations With the Cornell Net Carbohydrate and Protein System. Journal of Dairy Science. 91:4881-4891.

Lekatz, L.A., Caton, J.S., Taylor, J.B., Reynolds, L.P., Redmer, D.A., Vonnahme, K.A. 2010. Maternal selenium supplementation and timing of nutrient restriction in pregnant sheep: Effects on maternal endocrine status and placental characteristics. Journal of Animal Science. 88:955-971.

Lekatz, L.A., Ward, M.A., Borowicz, P.P., Taylor, J.B., Redmer, D.A., Grazul-Bilska, A.T., Reynolds, L.P., Caton, J.S., Vonnahme, K.A. 2009. Cotyledonary responses to maternal selenium and dietary restriction may influence alteration in fetal weight and fetal liver glycogen sheep. Animal Reproduction Sciences. doi:10.1016/j.anireprosci.2009.05.009.

Leytem, A.B., Taylor, J.B., Raboy, V., Plumstead, P.W. 2007. Dietary low-phytate mutant-M 955 barley grain alters phytate degradation and mineral digestion in sheep fed high-grain diets. Animal Feed Science and Technology. 138:13-28.

Lewis, G.S., Wulster-Radcliffe, M.C., Herbein, J.H. 2008. Fatty acid profiles, growth, and immune responses of neonatal lambs fed milk replacer and supplemented with fish oil or safflower oil. Small Ruminant Research. 79:167-173.

Li, R.W., Li, C. 2008. Effects of butyrate on the expression of insulin-like growth factor binding proteins in bovine kidney epithelial cells. The Open Veterinary Science Journal. 2:1-6.

Liao, S.F., Harmon, D.L., Vanzant, K.R., Mcleod, K.R., Boling, J.A., Matthews, J.C. 2010. The Small Intestinal Epithelia of Beef Steers Differentially Express Sugar Transporter Messenger Ribonucleic Acid in Response to Abomasal Versus Ruminal Infusion of Starch Hydrolysate. Journal of Animal Science. 88:306-314. DOI.10.2527jas.2009-1992.

Liao, S.F., Vanzant, E.S., Harmon, D.L., Mcleod, K.R., Boling, J.A., Matthews, J.C. 2009. Ruminal and Abomasal Starch Hydrolysate Infusions Selectively Decrease the Expression of Cationic Amino Acid Transporter mRNA by Small Intestinal Epithelia of Forage-fed Beef Steers. Journal of Dairy Science. 92:1124-1135. DOI:10.3168/jds.2008-1521.

Mertens, D.R. 2005. Rate and extent of digestion. In: Dijkstra, J., Forbes, J.M., France, J., eds. Quantitative Aspects of Ruminant Digestion and Metabolism. 2nd Edition. Cambridge, MA: CABI Publishing. p. 13-47.

Meyer, A.M., Reed, J.J., Neville, T.L., Taylor, J.B., Hammer, C.J., Reynolds, L.P., Redmer, D.A., Vonnahme, K.A., Caton, J.S. 2010. Effects of nutritional plane and selenium supply during gestation on ewe and neonatal offspring performance, body composition, and serum selenium.. Journal of Animal Science. 88:1786-1800.

Neville, T.L., Ward, M.A., Reed, J.J., Soto-Navarro, S.A., Julius, S.L., Borowics, P.P., Taylor, J.B., Redmer, D.A., Reynolds, L.P., Caton, J.S. 2008. Effects of level and source of dietary selenium on maternal and fetal body weight, visceral organ mass, cellularity estimates, and jejunal vascularity in pregnant ewe lambs. Journal of Animal Science. 86:890-901.

Ngwa, A.T., Dawson, L.J., Puchala, R., Detweiler, G., Merkel, R.C., Wang, Z., Tesfai, K., Sahlu, T., Ferrell, C.L., Goetsch, A.L. 2009. Effects of Stage of Lactation and Dietary Forage Level on Body Composition of Alpine Dairy Goats. Journal of Dairy Science. 92(7):3374-3385.

Peng, Y., Brown, M.A., Wu, J., Liu, Z. 2010. Different oilseed supplements alter fatty acid composition of different adipose tissues of adult ewes. Meat Science. 85(3):542-549.

Phillips, W.A., Horn, G.W. 2008. Intake and digestion of wheat forage by stocker calves and lambs. Journal of Animal Science. 86(9):2424-2429.

Phillips, W.A., Grings, E.E., Short, R.E., Heitschmidt, R.K., Mayeux Jr, H.S. 2006. Impact of calving season on stocker and feedlot performance. Professional Animal Scientist. 22:392-400.

Puchala, R., Tovar-Luna, I., Sahlu, T., Freetly, H.C., Goetsch, A. 2009. Technical Note: The Relationship between Heart Rate and Energy Expenditure in Growing Crossbred Boer and Spanish Wethers. Journal of Animal Science. 87(5):1714-1721.

Quigley, J.D., Wolfe, T.A., Elsasser, T.H. 2006. Effects of additional milk replacer feeding on calf health, growth and selected blood metabolites in calves. Journal of Dairy Science. 89:207-216.

Reed, J.J., Ward, M.A., Vonnahme, K.A., Neville, T.L., Julius, S.L., Borowicz, P.P., Taylor, J.B., Redmer, D.A., Reynold, L.P., Caton, J.S. 2007. Effects of selenium supply and dietary restriction on maternal and fetal body weight, visceral organ mass, cellularity estimates, and jejeunal vascularity in pregnant ewe lambs.. Journal of Animal Science. doi:10.2527/jas.2006-785.

Reynal, S.M., Ipharraguerre, I.R., Lineiro, M., Brito, A.F., Broderick, G.A., Clark, J.H. 2007. Omasal flow of soluble proteins, peptides, and free amino acids in dairy cows fed diets supplemented with proteins of varying ruminal degradabilities. Journal of Dairy Science. 90:1887-1903.

Rius, A.G., Connor, E.E., Capuco, A.V., Kendall, P.E., Auchtung, T.L., Dahl, G.E. 2005. Long day photoperiod that enhances puberty does not limit body growth in Holstein heifers. Journal of Dairy Science. 88:4356-4365.

Roberts, A.J., Geary, T.W., Grings, E.E., Waterman, R.C., MacNeil, M.D. 2009. Reproductive performance of heifers offered ad libitum or restricted access to feed for a 140-d period after weaning. Journal of Animal Science 87:3043-3052.

Roberts, A.J., Paisley, S.I., Geary, T.W., Grings, E.E., Waterman, R.C., MacNeil, M.D. 2007. Effects of restricted feeding of beef heifers during the postweaning period on growth, efficiency and ultrasound carcass characteristics. Journal of Animal Science 85:2740-2745.

Russell, J.B., Muck, R.E., Weimer, P.J. 2009. Quantitative analysis of cellulose degradation and growth of cellulolytic bacteria in the rumen. FEMS Microbiology Ecology. 67(2):183-197.

Russell, J.B. 2006. Factors affecting lysine degradation by ruminal fusobacteria. Federation of European Microbiological Societies Microbiology Ecology. 56:18-24.

Russell, J.B., Houlihan, A.J., Rose, J.E., Angert, E.R. 2005. Bacteriocins of gram-positive bacteria and their application in biotechnology. In: Pandalai, S.G., editor. Recent Research Developments in Applied Biotechnology. Kerala, India. Research Signpost. 2:87-101.

Russell, J.B., Strobel, H.J. 2005. Microbial energetics. In: Dikstra, J., Forbes, J. M., France, J., Editors. Quantitative Aspects of Ruminant Digestion and Metabolism. Wallingford, United Kingdom:CABI Publishing. p. 229-262.

Strickland, J.R., Custis, M., Ashley, A.K., Smith, L.L., Klotz, J.L., Krehbiel, C. 2005. Clearance of Para-Aminohippuric Acid in Wethers Consuming Locoweed. New Zealand Veterinary Journal. 53(5):288-292.

Taylor, J.B., Moffet, C.A., Leeds, T.D. 2009. Body weight changes and subsequent lambing rates of western whiteface ewes grazing winter range. Livestock Science. 121:339-342.

Taylor, J.B., Reynolds, L.P., Redmer, D.A., Caton, J.S. 2009. Maternal and fetal tissue selenium loads in nulliparous ewes fed supranutritional and excessive selenium during mid to late pregnancy.. Journal of Animal Science. 87:1828-1834.

Waterman, R.C., Grings, E.E., Geary, T.W., Roberts, A.J., Alexander, L.J., MacNeil, M.D. 2007. Influence of seasonal forage quality on glucose kinetics of young beef cows. Journal of Animal Science 85:2582-2595. doi 10:2527/jas.2007-0023.

Waterman, R.C., Loest, C.A., Bryant, W.D., Petersen, M.K. 2007. Supplemental methionine and urea for gestating beef cows consuming low quality forage diets. Journal of Animal Science online doi:10.2527/jas.2006-425. J. Anim Sci. 85:731-736.

Williams, C.B. 2010. Application of Biological Simulation Models in Estimating Feed Efficiency of Finishing Steers. Journal of Animal Science. 88(7):2523-2529.

Williams, C.B., Bennett, G.L., Jenkins, T.G., Cundiff, L.V., Ferrell, C.L. 2006. Using simulation models to predict feed intake: phenotypic and genetic relationships between observed and predicted values in cattle. Journal of Animal Science. 84(6):1310-1316.

7. Nutrition, growth biology and physiology in poultry.

Angel, R., Saylor, W.W., Mitchell, A., Powers, W., Applegate, T.J., Dhandu, A.S. 2006. Effect of dietary phosphorus concentration, and inclusion of phytase and 25-hydroxycholecalciferol on broiler chicken bone mineralization, litter total and water soluble phosphorus and processing yields and losses. Journal of Poultry Science. 85(7):1200-1211.

Bee, G., Pursel, V.G., Mitchell, A.D., Maruyama, K., Wells, K.D., Solomon, M.B., Wall, R.J., Coleman, M.E., Schwartz, R.J. 2007. Carcass composition and skeletal muscle morphology of swine expressing an insulin-like growth factor-I transgene. Archives of Animal Breeding. 50(5):501-519.

Dozier III, W.A., Corzo, A., Kidd, M.T., Schilling, M.W. 2008. Dietary Digestible Lysine Requirements of Male and Female Broilers From Forty-Nine to Sixty-Three Days of Age. Poultry Science 87:1385-1391.

Corzo, A., Dozier III, W.A., Kidd, M.T. 2008. Valine Nutrient Recommendations for Ross × Ross 308 Broilers. Poultry Science 87:335-338.

Corzo, A., Dozier III, W.A., Kidd, M.T. 2005. Dietary lysine needs of late-developing broilers. Poultry Science. 85:457-461.

Corzo, A., Dozier III, W.A., Kidd, M.T., Hoehler, D. 2008. Impact of dietary isoleucine status on heavy-broiler production. International Journal of Poultry Science 7(6):526-529.

Corzo, A., Kidd, M., Dozier III, W.A., Pharr, T., Koutsos, E. 2007. Dietary threonine needs for growth and immunity of broilers raised in different litter conditions. Journal of Applied Poultry Research. 16:574-582.

Corzo, A., Kidd, M., Dozier III, W.A., Vieira, S. 2007. Marginality and needs of dietary valine for broilers fed certain all-vegetable diets. Journal of Applied Poultry Research. 16:546-554.

Corzo, A., Kidd, M.T., Dozier III, W.A., Walsh, T.J., Peak, S.D. 2005. Impact of dietary amino acid density on broilers grown for the small bird market. Japan Poultry Science. 42:329-336.

deBeer, M., McMurtry, J.P., Brocht D.M., Coon, C.N., 2008. An examination of the role of feeding regimens in regulating metabolism during the broiler breeder grower period 2. Plasma hormones and metabolites. Poultry Science. 87(2):264-275.

de Beer, M., Rosebrough, R.W., Russell, B.A., Poch, S.M., Richards, M.P., Coon, C.N. 2007. An examination of the role of feeding regimen in regulating metabolism during the broiler breeder grower period. 1. Hepatic lipid metabolism. Poultry Science. 86:1726-38.

Dozier, W.A., Behnke, K., Twining, P., Branton, S.L. 2009. Effects of the addition of roller mill ground corn to pelletted feed during a 56 day production period on growth performance and processing yields of broiler chicks. Journal of Applied Poultry Research 18(2):310-317.

Dozier, W.A., Corzo, A., Kidd, M.T., Tillman, P.B., Purswell, J.L., Kerr, B.J. 2009. Digestible Lysine Requirements of Male Broilers From 14 to 28 Days of Age Subjected to Different Environmental Conditions. Journal of Applied Poultry Research. 18:690-698.

Dozier III, W.A., Corzo, A., Kidd, M. 2008. Apparent Metabolizable Energy Needs of Broiler Chicks Subjected to Diverse Ambient Temperature Regimens. Journal of Applied Poultry Research 17:134-140.

Dozier III, W.A., Kidd, M.T., Corzo, A. 2008. Dietary amino acid responses of broiler chickens: A Review. Journal of Applied Poultry Research. 17:157-167.

Dozier III, W.A., Kerr, B.J., Corzo, A., Kidd, M.T., Weber, T.E., Bregendal, K. 2008. Apparent Metabolizable Energy of Glycerin for Broiler Chickens. Poultry Science. 87:317-322.

Dozier III, W.A., Kidd, M.T., Corzo, A., Owens, P.R., Branton, S.L. 2008. Live performance and environmental impact of broilers fed diets varying in amino acids and phytase. Animal Feed Science And Technology. 141:92-103.

Dozier III, W.A., Corzo, A., Kidd, M.T., Branton, S.L. 2007. Dietary apparent metabolizable energy and amino acid density effects on growth and carcass traits of heavy broilers. Journal of Applied Poultry Research. 16:192-205.

Dozier III, W.A., Price, C.J., Kidd, M.T., Corzo, A., Anderson, J., Branton, S.L. 2007. Growth performance, meat yield, and economic responses of ross x ross 308 broilers provided diets varying in metabolizable energy from 3o to 59 days of age during low and moderate temperatures. Journal of Applied Poultry Research. 15:383-393.

Dozier III, W.A., Behnke, K., Kidd, M.T., and Branton, S.L. 2006. Effects of the addition of roller mill ground corn to pelleted feed on pelleting parameters, broiler performance, and intestinal strength. Journal of Applied Poultry Science. 15(2):236-244.

Dozier III, W.A., Gordon, R.W., Anderson, J., Kidd, M.T., Corzo, A., Branton, S.L. 2006. Growth, meat yield, and economic responses of broilers provided three-and four-phase regimens formulated to moderate and high nutrient density during a 56 day production period. Journal of Applied Poultry Research. 15:312-325

Dozier III, W.A., Kidd, W.A., Corzo, A., Anderson, J., Branton, S.L. 2006. Growth performance, meat yield, and economic responses of broilers provided diets varying in amino acid density from thirty-six to fifty-nine days of age. Journal of Applied Poultry Research. 15:383-393.

Dozier III, W.A. 2005. Growth and meat yield responses of male broilers provided feeds subjected to post-grinding during a 41 day production period. Journal of Applied Poultry Research. 14:476-482.

Ekmay, R.D., Coon, C.N., De Beer, M., Rosebrough, R.W., Richards, M.P., Mcmurtry, J.P. 2010. The role of feeding regimens in regulating metabolism of sexually mature broiler breeders. Poultry Science. 89(6):1171-1181.

Foye, O.T., Uni, Z., McMurtry, J.P., Ferket, P.R. 2006 The effects of amnionic nutrient administration, in ovo feeding of arginine and/or beta-hyroxy-beta-methybutyrate (HMB) on insulin-like growth factors, energy metabolism and growth in turkey poults. International Journal of Poultry Science. 5(4):309-317.

Karcher, D.M., McMurtry, J.P., Applegate, T.J. 2005. Developmental changes in amniotic and allantoic fluid insulin-like growth factor (IGF) - I and -II concentrations of avian embryos. Comparative Biochemistry and Physiology Part A. 142:404-409.

Kidd, M.T., Corzo, A., Hill, S.M., Zumwalt, C.D., Robinson, E.H., Dozier III, W.A. 2005. Growth and meat yield responses of broilers provided feed subjected to extrusion cooking. Journal of Applied Poultry Research. 14:536-541.

Kidd, M.T., Corzo, A., Hoehler, D., Miller, E.R., Dozier III, W.A. 2005. Broiler responsiveness (ross x 708) to diets varying in amino acid density. Poultry Science. 84:1389-1396.

Kim, W.K., Donalson, L.M., Mitchell, A.D., Kubena, L.F., Nisbet, D.J. Ricke, S.C. 2006. Effects of alfalfa and fructooligosaccharide on molting parameters and bone qualities using dual energy x-ray absorptiometry and conventional bone assays. Journal of Poultry Science. 85:15-20.

Lammers, P.J., Kerr, B.J., Honeyman, M.S., Stalder, K., Dozier III, W.A., Weber, T.E., Kidd, M.T., Bregendahl, K. 2008. Nitrogen-Corrected Apparent Metabolizable Energy Value of Crude Glycerol for Laying Hens. Poultry Science. 87:104-107.

Lu, J.W., McMurtry, J.P., Coon, C.N. 2007. Developmental changes of plasma insulin, glucagon, insulin-like growth factors, thyroid hormones, and glucose concentrations in chick embryos and hatched chicks. Poultry Science. 86:673-683.

Mazzuco, H., McMurtry, J.P., Kuo, A.Y., Hester, P.Y. 2005 The effect of pre- and postmolt diets high in n-3 fatty acids and molt programs on skeletal integrity and insulin-like growth factor-I of white leghorns. Poultry Science. 84:1735-1749.

Mitchell, A.D., Scholz, A.M. 2008. Efficiency of energy and protein deposition in swine measured by dual energy X-ray absorptiometry (DXA). Archives of Animal Breeding. 51:159-171.

Mitchell, A.D., Pursel, V.G., Elsasser, T.H., McMurtry, J.P., Bee, G. 2005. Effects of dietary conjugated linoleic acid on growth and body composition of control and IGF-I. Animal Research. 54:5.

Proszkowiec Weglarz, M., Richards, M.P. 2009. Expression and activity of the 5'-adenosine monophosphate-activated protein kinase pathway in selected tissues during chicken embryonic development. Poultry Science. 88(1):159-178.

Proszkowiec-Weglarz, M., Richards, M.P., Humphrey, B., Rosebrough, R.W., McMurtry, J.P. 2009. AMP-activated protein kinase and carbohydrate response element binding protein: A study of two potential regulatory factors in the hepatic lipogenic program of broiler chickens. Journal of Comparative Biochemistry and Physiology. 154(1):68-79.

Richards, M.P., Rosebrough, R.W., Coon, C.N., Mcmurtry, J.P. 2010. Feed intake regulation for the female broiler breeder: In theory and in practice. Journal of Applied Poultry Research. 19(2):182-193.

Richards, M.P., McMurtry, J.P. 2009. The avian proglucagon system. General and Comparative Endocrinology. 163(1/2):39-46.

Richards, M.P., Proszkowiec-Weglarz, M. 2007. Mechanisms regulating feed intake, energy expenditure, and body weight in poultry. Poultry Science. 86(7):1478-1490.

Rosebrough, R.W., Russell, B.A., Richards, M.P. 2009. Effects of Short Term Triiodothyronine administration to broiler chickens fed methimazole. Comparative Biochemistry and Physiology. 150:72-78.

Rosebrough, R., Russell, B.A., McMurtry, J.P. 2006. Studies on doses of methimazole (MMI) and its administration regimen on broiler metabolism. Comparative Biochemistry and Physiology. 143:35-41.

Rosebrough, R.W., Russell, B.A., Richards, M.P. 2007. Responses of chickens subjected to thyroid hormone depletion-repletion. Comparative Biochemistry and Physiology. Part A. 147:543-549.

Roush, W.B., Purswell, J.L., Branton, S.L. 2007. An adjustable nutrient margin of safety comparison using linear and stochastic programming in an excel spreadsheet. Journal of Applied Poultry Research. 16:514-520.

Sethi, P.K., McMurtry, J.P., Pesti, G.M., Aggrey, S.E. 2008. Physiological responses to divergent selection for phytate phosphorus bioavailability in a randombred chicken population. Poultry Science. 87:2512-2516.

Shahnazari, M., Lang, D.H., Fosmire, G.J., Sharkey, N.A., Mitchell, A.D., Leach, R.M. 2006. Strontium administration in young chickens improves bone volume and architecture but does not enhance bone structural and material strength. Calcified Tissue International. 80(3):160-166.

Shiraishi, J., Yanagita, K., Nishikawa, F., Tahara, Y., Fujita, M., McMurtry, J.P., Bungo, T. A . 2009. Comparison of the Anorexic Effects of Chicken, Porcine, Human and Bovine Insulin on the Central Nervous System of Chicks. Journal of Poultry Science. 46:144-148.

Sun, J.M., Richards, M.P., Rosebrough, R.W., Ashwell, C.M., McMurtry, J.P., Coon, C.N. 2006. The relationship of body composition, feed intake and metabolic hormones for broiler breeder females. Poultry Science. 85:1173-1184.

Thornton, S.A., Corzo, A., Pharr, G.T., Dozier III, W.A., Miles, D.M., Kidd, M.T. 2006. Valine needs for immune and growth responses in broilers from 3 to 6 weeks of age. British Poultry Science. 47:190-199.

West, M.L., Corzo, A., Dozier III, W.A., Blair, M.E., Kidd, M.T. 2007. Assessment of dietary rivabio excel in practical u.s. broiler diets. Journal of Applied Poultry Research. 16:313-321.

Yan, F., Angel, R., Ashwell, C., Mitchell, A., Christman, M. 2005. Evaluation of the broiler's ability to adapt to an early moderate deficiency of phosphorus and calcium. Journal of Poultry Science. 84:1232-1241.

8. Nutrition, growth biology and physiology in swine.

Barb, C.R., Hausman, G.J. 2009. Insulin-like growth factor-I feedback regulation of growth hormone and luteinizing hormone secretion in the pig: Evidence for a pituitary site of action. Animal. v.3(6) p. 844-849.

Barb, C.R., Kraeling, R.R., Rampacek, G.B., Hausman, G.J. 2006. The role of neuropeptide y and interaction with leptin in regulating feed intake and luteinizing hormone and growth hormone secretion in the pig. Reproduction. 131:1127-1135.

Farmer, H., Petit, H.V., Weiler, H., Capuco, A.V. 2007. Effects of dietary supplementation with flax during prepuberty on fatty acid profile, mammogenesis and bone metabolism in gilts. Journal of Animal Science. 85(7):1675-1686.

Hsu, W.L., Johnson, R.K., Van Vleck, L.D. 2010. Effect of Pen Mates on Growth, Backfat Depth, and Longissimus Muscle Area of Swine. Journal of Animal Science. 88(3):895-902.

Klindt, J.M., Thallman, R.M., Wise, T.H. 2006. Effects of sire line, sire, and sex on plasma urea nitrogen, body weight, and backfat thickness in offspring of duroc and landrace boars. Journal of Animal Science. 84(6):1323-1330.

Kojima, C.J., Jenkins, S.J., Cooper, T.A., Roberts, M.P., Carroll, J.A., Kattesh, H.G. 2009. Effects of syndyphalin-33 on feed intake and circulating measures of growth hormone, cortisol, and immune cell populations in the recently weaned pig. Journal of Animal Science. 87:3218-3225.

Lammers, P.J., Kerr, B.J., Weber, T.E., Bregendahl, K., Lonergan, S.M., Prusa, K.J., Ahn, D.U., Stoffregen, W.C., Dozier III, W.A., Honeyman, M. 2008. Growth performance, carcass characteristics, meat quality, and tissue histology of growing pigs fed crude glycerin-supplemented diets. Journal of Animal Science. 86(11):2962-2970.

Lammers, P.J., Kerr, B.J., Weber, T.E., Dozier III, W.A., Kidd, M.T., Bregendahl, K., Honeyman, M.S. 2008. Digestable and metabolizable energy of crude glycerol in growing pigs. Journal of Animal Science. 86:602-608.

Mateo, R., Carroll, J.A., Hyun, Y., Smith, S., Kim, S. 2009. Effect of dietary supplementation of omega-3 fatty acids and high levels of dietary protein on performance of sows. Journal of Animal Science. 87:948-959.

Mateo, R., Wu, G., Moon, H.K., Carroll, J.A., Kim, S. 2008. Effects of dietary arginine supplementation on the performance of lactating primiparous sows and nursing piglets. Journal of Animal Science. 86(4):827-835.

Mckee, C.A., Eicher, S.D., Carroll, J.A. 2006. Supplemental vitamin C and yeast cell-wall beta-glucan as growth enhancers in newborn pigs and as immunomodulators after an endotoxin challenge after weaning. Journal of Animal Science. 84:2352-2360.

Mitchell, A. 2009. Effect of ractopamine on growth and body composition of pigs during compensatory growth. Animal. 3(1):173-180.

Mitchell, A.D., Scholz, A.M. 2009. Relationships among dual-energy X-ray absorptiometry (DXA), bioelectrical impedance (BIA), and ultrasound measurements of body composition of swine. Archives of Animal Breeding. 52(1):28-39.

Mitchell, A.D., Conway, J.M. 2005. Changes in body composition of pigs fed high or low protein diets during a period of compensatory growth between 60 and 100 kg body weight. International Journal of Body Composition Research. 3(3):117.

Mitchell, A.D., Scholz, A.M., Solomon, M.B. 2005. Estimation of body composition of pigs by a near-infrared interactance probe technique. Archive of Animal Breeding. 49(1):580-591.

Oliver, W.T., Miles, J.R. 2010. A Low-fat Liquid Diet Increases Protein Accretion and Alters Cellular Signaling for Protein Synthesis in 10-day-old Pigs. Journal of Animal Science. 88(8):2576-2584.

Ramsay, T.G., Richards, M.P., Li, C.J., Caperna, T.J. 2010. IGF-I mediated inhibition of leptin receptor expression in porcine hepatocytes. Comparative Biochemsitry and Physiology. 155(1):43-48.

Ramsay, T.G., Stoll, M.J., Caperna, T.J. 2010. Adipokine gene transcription level in adipose tissue of runt piglets. Comparative Biochemistry and Physiology. 155(2):97-105.

Ramsay, T.G., Caperna, T.J. 2009. Ontogeny of adipokine expression in neonatal pig adipose tissue. Comparative Biochemistry and Physiology. 152:72-78.

Ramsay, T.G., Mitchell, A.D 2008. Impact of dietary protein content on uncoupling protein mRNA abundance in swine. Comparative Biochemistry and Physiology. 149:562-571.

Ramsay, T.G., Mitchell, A.D., Richards, M.P. 2008. Uncoupling protein expression in skeletal muscle and adipose tissue in response to in vivo porcine somatotropin treatment. Domestic Animal Endorcinology. 35(2): 130-141.

Yen, J., Klindt, J.M., Kerr, B.J., Buonomo, F.C. 2005. Lysine requirement of finishing pigs administered porcine somatotropin by sustained-release implant. Journal of Animal Science. 83:2789-2797.

9. Lactation physiology, evaluation and regulation.

Akers, R.M., Capuco, A.V., Keys, J.E. 2006. Cellular differentiation in mammary tissue of beef and dairy heifers. Livestock Science. 105:44-49.

Annen, E.L., Fitzgerald, A.C., Gentry, P.C., Mcguire, M.A., Capuco, A.V., Baumgard, L.H., Collier, R.J. 2007. Effect of continuous milking and bST supplementation on mammary epithelial cell turnover. Journal of Dairy Science. 90:165-183.

Capuco, A.V., Annen, E., Fitzgerald, A.C., Ellis, S.E., Collier, R.J. 2006. Mammary cell turnover: relevance to lactation persistency and dry period management. IN:Ruminant Physiology:Digestion, metabolism and impact of nutrition on gene expression, immunology and stress. K. Sejrsen, T. Hvelplund, M.O. Nielsen (eds), Wageningen Academic Publishers, Wageningen, The Netherlands. pp. 363-388.

Elsasser, T.H., Capuco, A.V., Caperna, T.J., Martinez, A., Cuttitta, F., Kahl, S. 2006. Adrenomedullin (AM) and adrenomedullin binding protein (AM-BP) in the bovine mammary gland and milk: Effects of stage of lactation and experimental intramammary E. coli infection. Domestic Animal Endocrinology. Available:http://dx.doi.org/doi:10.1016/j.domaniend. 32:138-154.

Freetly, H.C., Nienaber, J.A., Brown-Brandl, T.M. 2006. Partitioning of energy during lactation of primiparous beef cows. Journal of Animal Science. 84:2157-2162.

Grings, E.E., Roberts, A.J., Geary, T.W., Macneil, M.D. 2008. Milk Yield of Primiparous Beef Cows From Three Calving Systems and Varied Weaning Ages. Journal of Animal Science 86:768-779.

Hadsell, D.L., Torres, D., George, J., Capuco, A.V., Ellis, S.E., Fiorotto, M.L. 2006. Changes in secretory cell turnover, and mitochondrial oxidative damage in the mouse mammary gland during a single prolonged lactation cycle suggest the possibility of accelerated cellular aging. Experimental Gerontology. 41(3):271-281.

Liu, W., Capuco, A.V., Romagnolo, D. 2006. Regulation of expression of cytosolic NADP+-dependent isocitrate dehydrogenase in bovine mammary epithelium. Experimental Biology and Medicine. 231(5):599-610.

Meyer, M.J., Capuco, A.V., Boisclair, Y.R., Van Amburgh, M.E. 2006. Estrogen-dependent responses to the mammary fat pad in prepubertal dairy heifers. J. Endocrinol. 190(3):819-827.

Meyer, M.J., Capuco, A.V., Ross, D.A., Lintault, L.M., Van Amburgh, M.E. 2006. Developmental and nutritional regulation of the prepubertal heifer mammary gland:i. parenchyma and fat pad mass and composition. Journal of Dairy Science. 89:4289-4297.

Meyer, M.J., Capuco, A.V., Ross, D.A., Lintualt, L.M., Van Amburgh, M.E. 2006. Developmental and nutritional regulation of the prepubertal bovine mammary gland: ii. allometric growth, epithelial cell proliferation, and the influence of age at slaughter on parenchyma development. Journal of Dairy Science. 89:4298-4304.

Wang, X.Z., Brown, M.A., Gao, F.Q., Wu, J.P., Lalman, D.L., Liu, W.J. 2009. Relationships of milk production of beef cows to postweaning gain of their calves. Professional Animal Scientist. 25:266-272.

Whitley, N.C., O'Brien, D.J., Quinn, R.W., Keisler, D.H., Walker, E.L., Brown, M.A. 2009. Milk leptin in sows and blood leptin and growth of their offspring. Journal of Animal Science. 87:1659-1663.

10. Evaluating and improving forage quality and digestibility.

Brito, A.F., Broderick, G.A. 2007. Effects of different protein supplements on milk production and nutrient utilization in lactating dairy cows. Journal of Dairy Science. 90:1816-1827.

Brito, A.F., Broderick, G.A., Olmos Colmenero, J.J., Reynal, S.M. 2007. Effects of feeding formate-treated alfalfa silage or red clover silage on omasal flow of nutrients and microbial protein synthesis in lactating dairy cows. Journal of Dairy Science. 90:1392-1404.

Brito, A.F., Broderick, G.A., Reynal, S.M. 2007. Effects of different protein supplements on omasal nutrient flow and microbial protein synthesis in lactating dairy cows. Journal of Dairy Science. 90:1828-1841.

Brito, A.F., Broderick, G.A. 2006. Effect of varying dietary ratios of alfalfa silage to corn silage on production and nitrogen utilization in lactating dairy cows. Journal of Dairy Science. 89:3924-3938.

Brito, A.F., Broderick, G.A., Reynal, S.M. 2006. Effect of varying dietary ratios of alfalfa silage to corn silage on omasal flow and microbial protein synthesis in dairy cows. Journal of Dairy Science. 89:3939-3953.

Broderick, G.A., Stevenson, M.J., Patton, R.A., Lobos, N.E., Olmos Colmenero, J.J. 2008. Effect of supplementing rumen-protected methionine on production and nitrogen excretion in lactating dairy cows. Journal of Dairy Science. 91:1092-1102.

Broderick, G.A., Brito, A.F., Olmos Colmenero, J.J. 2007. Effects of feeding formate-treated alfalfa silage or red clover silage on the production of lactating dairy cows. Journal of Dairy Science. 90:1378-1391.

Bunzel, M., Allerdings, E., Ralph, J., Steinhart, H. 2008. Cross-linking of arabinoxylans via 8-8-coupled diferulates as demonstrated by isolation and identification of diarabinosyl 8-8(cyclic)-dehydrodiferulate from maize bran. Journal of Cereal Science. 47(1):29-40.

Bunzel, M., Funk, C., Ralph, J., Steinhart, H. 2006. Ferulate trimers and tetramers isolated from insoluble maize bran fibre. In: Proceedings of the Dietary Fibre 2006 - Multifunctional Complex of Components, June 12-14, 2006, Helsinki, Finland. p. 103-104.

Bunzel, M., Ralph, J. 2006. NMR characterization of lignins isolated from fruit and vegetable insoluble dietary fiber. Journal of Agricultural and Food Chemistry. 54(21):8352-8361.

Bunzel, M., Ralph, J., Bruning, P., Steinhart, H. 2006. Structural identification of dehydrotriferulic and dehydrotetraferulic acids isolated from insoluble maize fiber. Journal of Agricultural and Food Chemistry. 54(17):6409-6418.

Bush, L.P., Roberts, C., and Schultz, C. 2007. Plant Chemistry and Antiquality Components in Forages. In Collins, Barnes and Nelson (ed). Forages: The Science of Grassland Agriculture 6th Edition. Ch 33. pp 509-528. ISBN: 9780813802329.

Casler, M.D., Jung, H.G. 2006. Relationships of fibre, lignin, and phenolics to in vitro fibre digestibility in three perennial grasses. Animal Feed Science And Technology. 125:151-161.

Dauwe, R., Morreel, K., Goeminne, G., Gielen, B., Rohde, A., Van Beeumen, J., Ralph, J., Boudet, A., Rochange, S., Kopka, J., Halpin, C., Messens, E., Boerjan, W. 2007. Molecular phenotyping of lignin-modified tobacco reveals associated changes in cell wall metabolism, primary metabolism, stress metabolism and photorespiration. Plant Journal. 52:263-285.

Funk, C., Braune, A., Grabber, J.H., Steinhart, H., Bunzel, M. 2007. Moderate Ferulate and Diferulate Levels Do Not Impede Maize Cell Wall Degradation by Human Intestinal Microbiota. Journal of Agriculture and Food Chemistry. 55:2418-2423.

Funk, C., Grabber, J.H., Weber, P., Thilker, J., Steinhart, H., Bunzell, M. 2006. Influence of lignin on the adsorption of hetero-cyclic aromatic amines by insoluble fiber. Dietary Fibre 2006, Multifunctional complex of Components, June 12-14, 2006, Helsink, Finland. 2006 CDROM.

Funk, C., Weber, P., Thilker, J., Grabber, J.H., Steinhart, H., Bunzel, M. 2006. Influence of lignification and feruloylation of maize cell walls on the adsorption of heterocyclic aromatic amines. Journal of Agricultural and Food Chemistry. 54:1860-1867.

Grabber, J.H., Lu, F. 2007. Formation of syringyl-rich lignins in primary maize walls as influenced by cell wall feruloylation and p-coumaroylated monolignols. Planta. 226:741-751.

Hatfield, R.D., Jung, H.G., Broderick, G.A., Jenkins, T. 2007. Nutritional chemistry of forages. In: Barnes, R.F., Nelson, C.J., Moore, K.J., Collins, M., editors. The Science of Grassland Agriculture. Sixth Edition of Forages, Volume II. Ames, IA:Blackwell Publishing. p. 467-485.

Holmgren, A., Brunow, G., Henriksson, G., Zhang, L., Ralph, J. 2006. Non-enzymatic reduction of quinone methides during oxidative coupling of monolignols: implications for the origin of benzyl structures in lignins. Organic and Biomolecular Chemistry. 4(18):3456-3461.

Hristov, A.N., Mcallister, T.A., Ouellet, D.R., Broderick, G.A. 2005. Comparison of purines and nitrogen-15 as microbial flow markers in beef heifers fed barley- or corn-based diets. Canadian Journal of Animal Science. 85:211-222.

Jung, H.G., Casler, M.D. 2006. Maize stem tissues: impact of development on cell wall degradability. Crop Science. 46:1801-1809.

Kostenbauder, M.J., Coleman, S.W., Chase, C.C., Kunkle, W.E., Hall, M.B., Martin, F.G. 2007. Intake and Digestibility of Bahiagrass Hay Supplemented with Molasses or Molasses-urea with or without Soybean Hulls when Fed to Cattle. Professional Animal Scientist. 23:373-380.

Krizsan, S.J., Broderick, G.A., Muck, R.E., Promkot, C., Colombini, S., Randby, A.T. 2007. Effect of alfalfa silage storage structure and roasting corn on production and ruminal metabolism of lactating dairy cows. Journal of Dairy Science. 90:4793-4804.

Leple, J., Dauwe, R., Morreel, K., Storme, V., Lapierre, C., Pollet, B., Naumann, A., Kang, K., Kim, H., Ruel, K., Lefebvre, A., Josseleau, J., Grima-Pettenati, J., De Rycke, R., Andersson-Gunneras, S., Erban, A., Fehrle, I., Petit-Conil, M., Kopka, J., Polle, A., Messens, E., Sundberg, B., Mansfield, S.D., Ralph, J., Pilate, G., Boerjan, W. 2007. Downregulation of cinnamoyl-coenzyme a reductase in poplar: multiple-level phenotyping reveals effects on cell wall polymer metabolism and structure. The Plant Cell. 19:3669-3691.

Phillips, W.A., Northup, B.K., Venuto, B.C. 2009. Dry matter intake and digestion of perennial and annual cool-season grasses by sheep. Professional Animal Scientist. 25:610-618.

Phillips, W.A., Coleman, S.W., Mayeux, H.S. 2006. Changes in body weight, fill and shrink as a result of grazing winter wheat pasture. Professional Animal Scientist. 22:267-272.

Morreel, K., Goeminne, G., Sterch, L., Ralph, J., Coppieters, W., Storme, V., Breyne, P., Steenackers, M., Messens, E., Boerjan, W. 2006. Genetical metabolomics of flavonoid biosynthesis in populus: a case study. Plant Journal. 47(2):224-237.

Ralph, J., Brunow, G., Boerian, W. 2007. Lignins. In: Rose, F., Osborne, K., editors. Encyclopedia of Life Sciences. Chichester, United Kingdom:John Wiley and Sons, Ltd. p. 1-10.

Ralph, J. 2006. What makes a good monolignol substitute? In: Hayashi, T., editor. The Science and Lore of the Plant Cell Wall Biosynthesis, Structure and Function. Boca Raton, FL: Universal Publishers (BrownWalker Press). p. 285-293.

Ralph, J., Akiyama, T., Kim, H., Lu, F., Schatz, P.F., Marita, J.M., Ralph, S.A., Reddy, M., Chen, F., Dixon, R.A. 2006. Effects of coumarate 3-hydroxylase downregulation on lignin structure. Journal of Biological Chemistry. 281(13):8843-8853.

Ralph, J., Lu, F., Akiyama, T., Kim, H., Marita, J.M., Reddy, M.S., Dixon, R.A. 2005. Tools for lignin structural analysis; applications to C3H-downregulation. In: Proceedings of Biosynthesis of Plant Cell Walls, August 4-7, 2005, Pacific Grove, California. p. 11.

Russell, J.B., Muck, R.E., Weimer, P.J. 2009. Quantitative analysis of cellulose degradation and growth of cellulolytic bacteria in the rumen. FEMS Microbiology Ecology. 67(2):183-197.

Schatz, P.F., Ralph, J., Lu, F., Guzei, I.A., Bunzel, M. 2006. Synthesis and identification of 2,5-bis-(4-hydroxy-3-methoxyphenyl)-tetrahydrofuran-3,4-dicarboxylic acid, an unanticipated ferulate 8-8-coupling product acylating cereal plant cell walls. Organic and Biomolecular Chemistry. 4(14):2801-2806.

Schatz, P.F., Ralph, J., Lu, F., Guzei, I.A., Steinhart, H., Bunzel, M. 2005. Synthesis and identification of an unanticipated ferulate 8-8-coupling product present in cereal dietary fibers. In: Edklund, T., Steinhart, H., Thier, H.-P., Winterhalter, P., editors. European Food Chemistry Conference XIII: Macromolecules and their degradation products in food — Physiological, analytical and technological aspects, September 21-23, 2005, Hamburg, Germany. p. 253-261.

Stevenson, D., Muck, R.E., Shinners, K., Weimer, P.J. 2006. Use of real time polymerase chain reaction to determine population profiles of individual species of lactic acid bacteria in alfalfa silage and stored corn stover. Applied Microbiology and Biotechnology. 71(3):329-338.

Stutte, G.W., Monje, O., Hatfield, R.D., Paul, A.-L., Ferl, R.J., Simone, C.G. 2006. Microgravity effects on leaf morphology, cell structure, carbon metabolism and mRNA expression of dwarf wheat. Planta. 224:1038-1049.

Wagner, A., Ralph, J., Akiyama, T., Flint, H., Phillips, L., Torr, K., Nanayakkara, B., Te Kiri, L. 2007. Modifying lignin in conifers: the role of HCT during tracheary element formation in Pinus radiata. Proceedings of the National Academy of Sciences. 104(28):11856-11861.

Weimer, P.J., Russell, J.B., Muck, R.E. 2009. Lessons From the Cow: What the Ruminant Animal Can Teach Us About Consolidated Bioprocessing of Cellulosic Biomass. Bioresource Technology. 100:5323-5331.

Zhang, X.J., Phillips, W.A., Garbrecht, J.D., Steiner, J.L., Hunt, L.A. 2008. A wheat grazing model for simulating grain and beef production: Part 1 - model development. Agronomy Journal. 100(5):1242-1247.

Zhang, X.J., Hunt, L.A., Phillips, W.A., Horn, G.W., Edwards, J., Zhang, H.L. 2008. A wheat grazing model for simulating grain and beef production: Part II - model validation. Agronomy Journal. 100(5):1248-1258.

Zhang, L., Gellerstedt, G., Ralph, J., Lu, F. 2006. NMR studies on the occurrence of spirodienone structures in lignins. Journal of Wood Chemistry and Technology. 26(1):65-79.

11. Determining forage and feed ingredient quality and nutritional value.

Bossen, D., Mertens, D.R., Weisbierg, M.R. 2010. Influence of Fermentation Methods on NDF Degradation Parameters. Journal of Dairy Science. 91(4):1464-1476.

Contreras-Govea, F.E., Albrecht, K.A., Muck, R.E. 2006. Spring yield and silage characteristics of kura clover, winter wheat, and in mixtures. Agronomy Journal. 98:781-787.

Ferreira, G., Mertens, D.R. 2007. Measuring detergent fibre and insoluble protein in corn silage using crucibles or filter bags. Animal Feed Science And Technology. 133(3-4):335-340.

Ferreira, G., Mertens, D.R. 2005. Chemical and physical characteristics of corn silages and their effects on in vitro. Journal of Dairy Science. 88:4414-4425.

Filya, I., Muck, R.E., Contreras-Govea, F.B. 2007. Inoculant effects on alfalfa silage: fermentation products and nutritive value. Journal of Dairy Science. 90(11):5108-5114.

Hartnell, G.F., Hatfield, R.D., Mertens, D.R., and Martin, N.P. 2005. Potential benefits of plant modification of alfalfa and corn silage to dairy diets. In: Proceedings of the 20th Southwest Nutrition and Management Conference, University of Arizona, Tucson. p. 156-172.

Igathinathane, C., Davis, J.D., Purswell, J.L., Columbus, E.P. 2010. Application of 3D Scanned Imaging Methodology for Volume, Surface Area, and Envelope Density Evaluation of Densified Biomass. Bioresource Technology. 101 pp 4220-4227.

Martin, N.P., Hatfield, R.D., Mertens, D.R. 2005. Reinventing alfalfa for dairy cattle and novel uses. Proceedings of the 35th California Alfalfa & Forage Symposium. p. 299-311.

Muck, R.E., Filya, I., Contreras-Govea, F.B. 2007. Inoculant effects on alfalfa silage: in vitro gas and volatile fatty acid production. Journal of Dairy Science. 90(11):5115-5125.

Phillips, W.A., Starks, P.J., Glasgow, S., Coleman, S.W. 2007. Different methods of estimating crude protein concentration of bermudagrass pastures for stocker calf production. Professional Animal Scientist. 23:696-701.

Shinners, K.J., Mertens, D.R., Harrison, J. 2006. Processing whole-plant corn silage: machine, storage, and animal perspectives. In: Silage for Dairy Farms: Growing, Harvesting, Storing, and Feeding. Ithaca, NY: NRAES Publication 181. p. 140-157.

12. Forage and physiological factors associated with toxic endophytes.

Aiken, G.E., Strickland, J.R., Looper, M.L., Bush, L.P., Schrick, F.N. 2009. Hemodynamics are Altered in the Caudal Artery of Beef Heifers Fed Different Ergot Alkaloid Concentrations. J. Anim Sci..2009; 87: 2142-2150.

Aiken, G.E., Kirch, B.H. 2008. Comparison Between Two Tracing Methods with Ultrasonography to Determine Lumen Area of the Caudal Artery in Beef Cattle. J. of Anim Sci. 2009. 87:371-374.

Aiken, G.E., Mc Clanahan, L.K., Kirch, B.H., Schrick, F.N. 2008. Performance and Physiology of Steers Following Grazing of Toxic Tall Fescue as Influenced by Feeding Soybean Hulls on Pasture and Post-Graze Steroid Implantation. Professional Animal Scientist. 2008. 24:392-398.

Aiken, G.E., Mcclanahan, L., Schrick, F.N. 2008. Steer Response to Feeding Soybean Hulls on Toxic Tall Fescue Pasture. Professional Animal Scientist. 2008. 24:399-403.

Aiken, G.E., Kirch, B.H., Strickland, J.R., Bush, L.P., Looper, M.L., Schrick, N.F. 2007. Hemodynamic Responses of the Caudal Artery to Toxic Tall Fescue in Beef Heifers. Journal of Animal Science. 2007. 85:2337-2345.

Brown, K.R., Anderson, G.A., Son, K., Rentfrow, G., Bush, L.P., Klotz, J.L., Strickland, J.R., Boling, J.A., Matthews, J.C. 2009. Growing Steers Grazing High Versus Low Endophyte (Neotyphodium coenophialum)-Infected Tall Fescue Have Reduced Serum Enzymes, Increased Hepatic Glucogenic Enzymes, and Reduced Liver and Carcass Tissue Mass. J. Anim. Sci. 2009. 87:748-760.

Burke, J.M., Coleman, S.W., Chase, C.C., Riley, D.G., Looper, M.L., Brown, M.A. 2010. Interaction of breed-type and endophyte-infected tall fescue on milk production and quality in beef cattle. Journal of Animal Science. 88:2802-2811.

Caldwell, J.D., Coffey, K.P., Coblentz, W.K., Jennings, J.A., Hubbell III, D.S., Kreider, D.L., Looper, M.L., Rosenkrans Jr, C.F. 2009. Performance by fall-calving cows grazing tall fescue pastures with different proportions stockpiled. Forage and Grazinglands [serial online]. doi:10.1094/FG-2009-0312-01-RS.

Carroll, J.A., Arthington, J.D., Chase Jr., C.C. 2009. Early weaning alters the acute phase response to an endotoxin challenge in beef calves. Journal of Animal Science. 87:4167-4172.

Jones, K.L., Schulze, J.L., Strickland, J.R., Cross, D.L., Burns, P., Gilley, R.M., Bassoo, E., Hart, K.B., Thompson, Jr., D.L., King, S.S. 2008. Evaluation of a Controlled-Release Domperidone Delivery Method for the Treatment of Fescue Toxicosis in Beef Heifers. Prof Anim Sci. 24(4):342-348.

Klotz, J.L., Kirch, B.H., Aiken, G.E., Bush, L.P., Strickland, J.R. 2009. Bioaccumulation of Ergovaline in Bovine Lateral Saphenous Veins in Vitro. J Anim Sci. 2009. 87:2437-2447.

Klotz, J.L., Kirch, B.H., Aiken, G.E., Bush, L.P., Strickland, J.R. 2008. Effects of Selected Combinations of Tall Fescue Alkaloids on the Vasoconstrictive Capacity of Fescue-Naive Bovine Lateral Saphenous Veins. Journal of Animal Science. 2008. 86:1021-1028.

Klotz, J.L., Bush, L.P., Smith, D.L., Schafer, W.D., Smith, L.L., Vevoda, A.O., Craig, A.M., Arrington, B.C., Strickland, J.R. 2006. Assessment of vasoconstrictive potential of d-lysergic acid using an isolated bovine lateral saphenous vein bioassay. Journal of Animal Science. 84:3167-3175.

Krauss, J., Harri, S.A., Bush, L., Husi, R., Bigler, L., Power, S.A., Muller, C.B. 2007. Effects of Fertilizer, Fungal Endophytes and Plant Cultivar on Performance of Insect Herbivores and Their Natural Enemies. Functional Ecology. 21:107-116.

Looper, M.L., Edrington, T.S., Moubarak, A.S., Callaway, T.R., Rosenkrans Jr, C.F. 2008. Effects of the ergot alkaloids dihydroergotamine, ergonovine, and ergotamine on growth of Escherichia coli O157:H7 in vitro. Foodborne Pathogens and Disease. 5(5):25-30.

Lorenz, N., Wilson, C., Machado, C.L., Schardl, C.L., Tudzynski, P. 2007. Comparison of Ergot Alkaloid Biosynthesis Gene Clusters in Claviceps Species Indicates Loss of Late Pathway Steps in Evolution of C. fusiformis. Applied and Environmental Microbiology 73:7185-7191. doi:10.1128/AEM.01040-07.

Mc Clanahan, L.K., Aiken, G.E., Dougherty, C.L. 2008. Case Study: Influence of Rough Hair Coats and Steroid Implants on the Performance and Physiology of Steers Grazing Endophyte-Infexted Tall Fescue in the Summer. Professional Animal Scientist. 24:269-276.

Schardl, C.L., Grossman, R.B., Nagabhyru, J.R., Faulkner, U.P., Mallik, U.P. 2007. Loline Alkaloids: Currencies of Mutualism. Phytochemistry. 68:980-996. doi:10.1016/j.phytochem.2007.01.010.

Schultz, C.L., Lodge-Ivey, S.L., Bush, L.P., Craig, A.M., Strickland, J.R. 2006. Effects of Initial and Extended Exposure to an Endophyte-Infected Tall Fescue Seed Diet on Faecal and Urinary Excertion of Ergovaline and Lysergic Acid in Mature Geldings. New Zealand Veterinary Journal. 54(4):178-184.

Strickland, J.R., Aiken, G.E., Klotz, J.L. 2009. Ergot Alkaloid-Induced Blood Vessel Dysfunction Contributes to Fescue Toxicosis. Forage and Grazinglands. 4Nov09.

Tavva, V.S., Palli, S.R., Dinkins, R.D., Collins, G.B. 2007. Applications of EcR Gene Switches Technology in Functional Genomics. Archives of Insect Biochemistry and Physiology. 65:164-179. DOI: 10.1002/arch.20193.2007.

Wang, H., Looper, M.L., Johnson, Z.B., Rorie, R.W., Rosenkrans, C.F. 2009. Signaling pathways used by ergot alkaloids to inhibit bovine sperm motility. In Vitro Cellular and Developmental Biology - Animals. 45(8):483-489.

Xu, R., Zhao, H., Dinkins, R.D., Cheng, X., Carberrry, G., Li, Q.Q. 2006. The 73 kD Subunit of the Cleavage and Polyadenylation Specificity Factor (CPSF) Complex Affects Reproductive Development in Arabidopsis. Plant Molecular Biology. 61:799-815.

13. Rumen and gut microbiome - classification and biology.

Barker, K.J., Purswell, J.L., Davis, J., Parker, H.M., Kidd, M.T., Mcdaniel, C.D., Kiess, A.S. 2010. Distribution of Bacteria at Different Poultry Litter Depths. International Journal of Poultry Science. 9(1): pp 10-13.

Durso, L.M., Harhay, G.P., Smith, T.P.L., Bono, J.L., Desantis, T.Z., Harhay, D.M., Andersen, G.L., Keen, J.E., Laegreid, W.W., Clawson, M.L. 2010. Animal-to-Animal Variation in Fecal Microbial Diversity among Beef Cattle. Applied and Environmental Microbiology. 76(14):4858-4862.

Flythe, M.D. 2009. The Antimicrobial Effects of Hops (Humulus lupulus L.) on Ruminal Hyper Ammonia-Producing Bacteria. The Society for Applied Microbiology, Letters in Applied Microbiology. 48, 712-717.

Flythe, M.D., Andries, K. 2009. The Effects of Monensin on Amino Acid Catabolizing Bacteria Isolated from the Boer Goat Rumen. Small Ruminant Research. 81. 178-181.

Flythe, M.D., Russell, J.B. 2006. The effect of acidic pH on the ability of Clostridium sporogenes MD1 to take up and retain intracellular potassium. Federation of European Microbiological Societies Microbiology Letters. 12:245-252.

Flythe, M.D., Russell, J.B. 2007. Fermentation acids inhibit amino acid deamination by clostridium sporogenes md1 via a mechanism involving a decline in intracellular glutamate rather than protonmotive force. Microbiology. 152(9):2619-2624.

Hall, M., Weimer, P.J. 2007. Sucrose concentration alters fermentation kinetics, products and carbon fates in in vitro fermentations with mixed ruminal microbes. Journal of Animal Science. 85:1467-1478.

Houlihan, A.J., Russell, J.B. 2006. The effect of calcium and magnesium on the activity of bovicin hc5 and nisin. Current Microbiology. 53:365-369.

Mantovani, H.C., Russell, J.B. 2008. Bovicin HC5, a lantibiotic produced by Streptococcus bovis HC5, catalyzed the efflux of intracellular potassium but not ATP. Antimicrobial Agents and Chemotherapy. 52:2247-2249.

Palmonari, A., Stevenson, D.M., Mertens, D.R., Cruywagen, C.W., Weimer, P.J. 2010. pH Dynamics and Bacterial Community Composition in the Rumen of Lactating Dairy Cows. Journal of Dairy Science. 93:279-287.

Park, J.S., J.B. Russell, and D.B. Wilson. 2007. Characterization of a family 45 glycosyl hydrolase from Fibrobacter succinogenes S85. Anaerobe 13:83-88.

Reynal, S.M., Broderick, G.A. 2009. A New HPLC Purine Assay for Quantifying Microbial Flow. Journal of Dairy Science. 92:1177-1181.

Russell, J.B. 2007. The Energy Spilling Reactions of Bacteria and Other Organisms. Journal of Molecular Microbiology and Biotechnology. 13:1-11.

Stevenson, D.M., Weimer, P.J. 2007. Dominance of Prevotella and low abundance of classical ruminal bacterial species in the bovine rumen revealed by relative quantification real-time PCR. Applied Microbiology and Biotechnology. 75:165-174.

Weimer, P.J., Stevenson, D.M., Mertens, D.R. 2010. Shifts in Bacterial Community Composition in the Rumen of Lactating Dairy Cows Under Conditions of Milk Fat Depression. Journal of Dairy Science. 93:265-278.

Weimer, P.J., Stevenson, D.M., Mertens, D.R., Thomas, E.E. 2008. Effect of monensin feeding and withdrawal on populations of individual bacterial species in the rumen of lactating dairy cows fed high-starch rations. Applied Microbiology and Biotechnology. 80(1):135-145.

Welkie, D.G., Stevenson, D.M., Weimer, P.J. 2010. ARISA Analysis of Ruminal Bacterial Community Dynamics in Lactating Dairy Cows During the Feeding Cycle. Anaerobe. 16:94-100. Available: http://www.sciencedirect.com/science.

Xavier, B.M., Houlihan, A.J., Russell, J.B. 2008. The activity and stability of cell associated activity of bovicin HC5, a bacteriocin from Streptococcus bovis HC5. Federation of European Microbiological Societies. 283:162-166.

Xavier, B.M., Russell, J.B. 2006. Bacterial competition between a bacteriocin producing and a non-producing strain of streptococcus bovis in batch and continuous culture. Federation of European Microbiological Societies Microbiology Ecology. 58:317-322.

14. Animal well-being and stress physiology.

Adcock, R., Kattesh, H., Roberts, M., Carroll, J.A., Saxton, A. 2007. Temporal relationships between plasma cortisol, corticosteriod-binding globulin (CBG), and the free cortisol index (FCI) in pigs in response to adrenal stimulation or suppression. Stress: The International Journal on Biology of Stress. 10(3):305-310.

Bowers, S., Gandy, S., Graves, K., Eicher, S.D., Willard, S. 2006. The effects of prepartum milking on postpartum reproductive and production performance in first-calf dairy heifers. Journal of Dairy Research. 73(3):257-263.

Carroll, J.A., Berg, E.L., Strauch, T.A., Roberts, M.P., Kattesh, H.G. 2006. Hormonal profiles, behavioral responses, and short-term growth performance after castration of pigs at three, six, nine, or twelve days of age. Journal of Animal Science. 84:1271-1278.

Carroll, J.A., Forsberg, N.E. 2007. Influence of stress and nutrition on cattle immunity. In: Olson, K.C., Hollis, L.C., editors. Veterinary Clinics of North America: Food Animal Practice. Amsterdam, The Netherlands: Elsevier Saunders. p. 105-149.

Carroll, J.A., McArthur, N.H., Welsh, Jr., T.H. 2007. In vitro and in vivo temporal aspects of ACTH secretion: Stimulatory actions of corticotropin-releasing hormone and vasopressin in cattle. Journal of Veterinary Medicine. 54:7-14.

Chen, C., Johnson, R.K., Newman, S., Kachman, S.D., Van Vleck, L.D. 2009. Effects of Social Interactions on Empirical Responses to Selection for Average Daily Gain of Boars. Journal of Animal Science. 87(3):844-849.

Dennis, R.L., Muir, W.M., Cheng, H. 2006. Effects of raclopride on aggression and stress in diversely selected chicken lines. Behavioural Brain Research. 175(1):104.
Fahey, A., Cheng, H., Marchant Forde, R. 2005. Effects of chronic stress on response to social isolation in three genetic strains of leghorn hens. International Society of Applied Ethology. p. 70.

Eicher, S.D., Wesley, I.V., Sharma, V.K., Johnson, T.R. 2010. Yeast Cell-Wall Products Containing Beta-Glucan plus Ascorbic Acid affect Neonatal Bos-Taurus Calf Leukocytes and Growth after a Transport Stressor. Journal of Animal Science. 88(3):1195-1203.

Eicher, S.D., Schutz, M.M., Willard, S.T., Bowers, S., Gandy, S., Graves, K. 2007. Pre-partum milking effects on parlor behavior, endocrine and immune responses in Holstein heifers. Journal of Dairy Research. 74(4):431-438.

Farran, T.B., Reinhardt, C.D., Blasi, D.A., Minton, J.E., Elsasser, T.H., Higgins, J.J., Drouillard, J.S. 2008. Source of dietary lipid may modify the immune response in stressed feeder cattle. Journal of Animal Science. 86:1382-1394.

Gebremedhin, K.G., Hillman, P.E., Lee, C.N., Collier, R.J., Willard, S.T., Arthington, J.E., Brown Brandl, T.M. 2008. Sweating rates of dairy cows and beef heifers in hot conditions. Transactions ASABE 51(6):2167-2178.

Koch, J.M., Moritz, J.S., Lay Jr, D.C., Wilson, M.E. 2005. Effect of melengestrol acetate (MGA) as an alternative to induce molting on egg quality. Journal of Animal Science. 83(2):22.

Lay Jr, D.C., Kattesh, H.G., Cunnick, J.E., Daniels, M.J., McMunn, K.A., Toscano, M.J., Roberts, M.P. 2008. Prenatal stress on pig development and response to weaning. Journal of Animal Science. 86:1316-1324.

Olanrewaju, H.A., Purswell, J.L., Collier, S.D., Branton, S.L. 2009. Age-related Effects of Varying Ammonia Concentrations on Hematophysiological Variables in Broiler Chickens. International Journal of Poultry Science 8(2):138-144.

Olanrewaju, H.A., Thaxton, J.P., Dozier III, W.A., Purswell, J.L., Branton, S.L. 2008. Interactive Effects of Ammonia and Light Intensity on Hematochemical Variables in Broiler Chickens. Poultry Science 87:1407-1414.

Olanrewaju, H.A., Thaxton, J.P., Dozier III, W.A., Branton, S.L. 2007. Electrolyte Diets, Stress, and Acid-Base Balance in Broiler Chickens. Poultry Science. 86:1363-1371.

Olanrewaju, H.A., Wongpichet, S., Thaxton, J.P., Dozier III, W.A., and Branton, S.L. 2006 Stress and Acid-Base Balance in Chickens. Poultry Science 85:1266-1274.

Qiu, X., Arthington, J.D., Riley, D.G., Chase, C.C., Phillips, W.A., Coleman, S.W., Olson, T.A. 2007. Genetic effects on acute-phase protein response to the stresses of weaning and transportation in beef calves.. Journal of Animal Science. 85:2367-2374.

Roush, W.B., Dozier III, W.A., Branton, S.L. 2006. Comparison of gompertz and neural network models of broiler chickens. Poultry Science. 85:794-797.

Scharf, B., Carroll, J.A., Riley, D.G., Chase, C.C., Coleman, S.W., Keisler, D.H., Weaber, R.L., Spiers, D.E. 2010. Evaluation of Physiological and blood serum differences in heat tolerant (Romosinuano) and heat susceptible (Angus) Bos taurus cattle for determination of markers of sensitivity. Journal of Animal Science. 88:2321-2336, and doi:10.2527/jas.2009-2551.

Schenck, E.L., Lay Jr, D.C., Kattesh, H.G., Cunnick, J.E., Daniels, M.J., Toscano, M.J., Mcmunn, K.A. 2006. The effects of prenatal stress on the ano-genital distance and growth hormone immuno-positive cells in the pituitary gland of the pig. Journal of Animal Science. 84(1):413.

15. Animal well-being – management, housing and environmental factors.

Arthington, J.D., Qiu, X., Cooke, R.F., Vendramini, J.M., Araujo, D.B., Chase, C.C., Coleman, S.W. 2008. Effects of pre-shipping management on measures of stress and performance of beef steers during a feedlot receiving period. Journal of Animal Science. 86:2016-2023.

Bohmanova, J., Misztal, I., Cole, J.B. 2007. Temperature-humidity indices as indicators of milk production losses due to heat stress. Journal of Dairy Science. 90(4):1947-1956.

Brown Brandl, T.M., Berry, E.D., Wells, J., Arthur, T.M., Nienaber, J.A. 2009. Impacts of Individual Animal Response to Heat and Handling Stresses on Escherichia coli and E. coli O157:H7 Fecal Shedding by Feedlot Cattle. Foodborne Pathogens and Disease. 6(7):855-864.

Brown Brandl, T.M., Jones, D.D., Gaughan, J.B. 2006. Modelling the components of livestock stress for precision animal management. American Society of Agri Engineers Special Meetings and Conferences Papers. Paper No. 064204.

Burdick, N., Carroll, J.A., Hulbert, L.E., Dailey, J.W., Willard, S., Vann, R., Welsh Jr, T., Randel, R. 2010. Relationships between temperament and transportation with rectal temperature and serum concentrations of cortisol and epinephrine in bulls. Livestock Science. 129:166-172.

Cheng, H. 2010. Breeding of Tomorrow's Chickens to Improve Well-Being. Poultry Science. 89(4):805-813.

Davis, J.D., Purswell, J.L., Columbus, E.P., Kiess, A.S. 2010. Evaluation of Chopped Switchgrass as a Litter Material. International Journal of Poultry Science. 9(1): 39-42.

Dozier III, W.A., Purswell, J.L., Kidd, M.T., Corzo, A., Branton, S.L. 2007. Apparent Metabolizable Energy Needs of Broilers from 2.0 to 4.0 kg as Influenced by Ambient Temperature. Journal of Applied Poultry Research. 16:206-218.

Dozier III, W.A., Lott, B.D., Branton, S.L. 2005. Live performance responses of male broilers subjected to constant or variable air velocities at moderate temperatures with a high dew point. Poultry Science. 84:1328-1331.

Dozier III, W.A., Thaxton, J.P., Branton, S.L., Morgan, G.W., Miles, D.M., Roush, W.B., Lott, B.D., Vizzier-Thaxton, Y. 2005. Stocking density on growth performance and processing yields of heavy broilers. Poultry Science. 84:1332-1338.

Dozier III, W.A., Thaxton, J.P., Olanrewaju, H.A., Branton, S.L., Roush, W.B. 2006. Stocking density effects of male broilers destined for fast-food markets. Poultry Science. 85:344-351.

Dozier III, W.A., Purswell, J.L., Branton, S.L. 2007. Growth responses of male broilers subjected to high air velocity at either 12 or 24 hours from 37 to 51 days of age. Journal of Applied Poultry Research.

Dozier III, W.A., Purswell, J.L., Kidd, M., Corzo, A., Branton, S.L. 2007. Apparent metabolizable energy needs of broilers from 2.0 to 4.0 kg as influenced by ambient temperature. Journal of Applied Poultry Research. 16:206-218.

Eicher, S.D., Johnson, T.A., Marchant Forde, J.N. 2006. Age at transport effects on behavioral responses in dairy calves to novel stimuli. Journal of Animal Science. 84(1):305.

Eigenberg, R.A., Brown Brandl, T.M., Nienaber, J.A. 2009. Shade Material Evaluation Using a Cattle Response Model and Meteorological Instrumentation. International Journal of Biometeorology. 53:501-507.

Eigenberg, R.A., Bucklin, R.A., Brown Brandl, T.M. 2009. Chapter 6: Instrumentation for Research and Management in Animal Agriculture. In: DeShazer, J.A., ed. Livestock Energetics and Thermal Environmental Management. St. Joseph, MI:American Society of Agricultural and Biological Engineers. p.131-149.

Eigenberg, R.A., Brown Brandl, T.M., Nienaber, J.A. 2008. Sensors for dynamic physiological measurements. Computers and Electronics in Agriculture. 62:41-47.

Eigenberg, R.A., Brown Brandl, T.M., Nienaber, J.A. 2007. Development of a livestock weather safety monitor for feedlot cattle. Applied Engineering in Agriculture, Sept. 2007, Vol. 23(5): 657-660.

Hahn, G., Gaughan, J.B., Mader, T.L., Eigenberg, R.A. 2009. Chapter 5: Thermal Indices and Their Applications for Livestock Environments. In: DeShazer, J.A., ed. Livestock Energetics and Thermal Environmental Management. St. Joseph, MI:American Society of Agricultural and Biological Engineers. p. 113-130.

Koch, J.M., Lay Jr, D.C., Mcmunn, K.A., Moritz, J.S., Wilson, M.E. Motivation of hens to obtain feed during a molt induced by either feed withdrawal, wheat middlings or melengestrol acetate. Poultry Science. 86:614-620.

Kojima, C., Carroll, J.A., Matteri, R.L., Touchette, K., Allee, G. 2007. Effects of weaning and piglet size on neuroendocrine regulators of feed intake. Journal of Animal Science. 85:2133-2139.

Mader, T.L., Davis, M.S., Brown Brandl, T.M. 2006. Environmental factors influencing heat stress in feedlot cattle. Journal Animal Science. 84:712-719.

Marchant Forde, J.N., Pajor, E.A. 2009. Welfare of Gestating Sows. In: Marchant-Forde, J.N., editor. The Welfare of Pigs. Dordrecht, The Netherlands:Springer Science + Business Media B.V. p. 95-140.

Meiszberg, A.M., Johnson, A.K., Sadler, L.J., Carroll, J.A., Dailey, J.W., Krebs, N. 2009. Drinking behavior in nursery pigs: Determining the accuracy between an automatic water meter versus human observers. Journal of Animal Science. 87:4173-4180.

Nienaber, J.A., Hahn, G.L. 2007. Livestock production system management responses to thermal challenges. International Journal of Biometeorology 52:149-157(2007), doi 10.1007/s00484-007-0103-x.

Olanrewaju, H.A., Purswell, J.L., Collier, S.D., Branton, S.L. 2009. Effects of Broiler Rearing Environment on Transmission of F-Strain Mycoplasma gallisepticum From Commercial Layer Hens to Broiler Chickens: Role of Acid-Base Balance. Avian Diseases 8(2):145-150.

Olanrewaju, H.A., Dozier III, W.A., Purswell, J.L., Branton, S.L., Miles, D.M., Lott, B.D., Pescatore, A.J., Thaxton, J.P. 2008. Growth performance and physiological variables for broiler chickens subjected to short-term elevated carbon dioxide concentrations. International Journal of Poultry Science. 7(8):738-742.

Olanrewaju, H.A., Thaxton, J.P., Dozier III, W.A., Purswell, J.L., Roush, W.B., Branton, S.L. 2006. A review of lighting programs for broiler production. International Journal of Poultry Science. 5(3):301-308, 2006.

Pohle, K., Cheng, H. 2009. Furnished Cage System and Hen Well-Being: Comparative Effects of Furnished and Battery Cages on Egg Production and Physiological Parameters of White Leghorn Hens. Poultry Science. 88(8):1559-1564.

Poletto, R., Meisel, R.L., Richert, B.T., Cheng, H., Marchant Forde, J.N. 2010. Aggression in Replacement Grower and Finisher Gilts Fed a High-Tryptophan Diet and the Effect of Long-Term Human-Animal Interaction. Applied Animal Behaviour Science. 122(24):90-110.

Purswell, J.L., Lott, B.D., Dozier III, W.A., Roush, W.B., Branton, S.L. 2008. Assessing Thermal Comfort of Broiler Chicks During Brooding. International Journal of Poultry Science 7(3):202-206.

Purswell, J.L., Thaxton, J.P., Branton, S.L. 2007. Identifying Process Variables for a Low Atmospheric Pressure Stun/Kill System. Journal of Applied Poultry Research. 16:509-513.

Sorrells, A.D., Eicher, S.D., Scott, K.A., Harris, M.J., Pajor, E.A., Lay Jr, D.C., Richert, B.T. 2006. Post-natal behavioral and physiological responses of piglets from gilts housed individually or in groups during gestation. Journal of Animal Science. 84:757-766.

Thaxton, J.P., Dozier III, W.A., Branton, S.L., Morgan, G.W., Miles, D.M., Roush, W.B., Lott, B.D., Vizzier-Thaxton, Y. 2006. Stocking density and physiological adaptive responses of broilers. Poultry Science. 85:819-824.

Toscano, M.J., Lay Jr, D.C., Craig, B.C., Pajor, E.A. 2007. Assessing the adaptation of swine to 57 hours of feed deprivation in terms of behavioral and physiological responses. Journal of Animal Science. 85:441-451.

Williams, J.L., Minton, J.E., Patterson, J.A., Marchant-Forde, J.N., Eicher, S.D. 2008. Lairage during transport has an impact on the swine innate immunity and commensal bacteria diversity. Journal of Animal Science. 86:1232-1244.

Research Component 3: Measuring and Enhancing Product Quality

1. Genetic characterization of body composition and meat quality characteristics.

Alexander, L.J., Kuehn, L.A., Smith, T.P., Matukumalli, L.K., Mote, B., Koltes, J.E., Reecy, J., Geary, T.W., Rule, D.C., Macneil, M.D. 2009. A Limousin specific myostatin allele affects longissimus muscle area and fatty acid profiles in a Wagyu-Limousin F*2* population. Journal of Animal Science 87:1576-1581.

Alexander, L.J., Macneil, M.D., Geary, T.W., Snelling, W.M., Rule, D.C., Scanga, J.A. 2007. Quantitative trait loci with additive effect on palatability and fatty acid composition of meat in a Wagyu-Limousin F*2 population. Animal Genetics 38:506-513.

Casas, E., White, S.N., Shackelford, S.D., Wheeler, T.L., Koohmaraie, M., Bennett, G.L., Smith, T.P.L. 2007. Assessing the association of single nucleotide polymorphisms at the thyroglobulin gene with carcass traits in beef cattle. Journal of Animal Science. 85:2807-2814.

Casas, E., White, S.N., Wheeler, T.L., Shackelford, S.D., Koohmaraie, M., Riley, D.G., Chase, C.C. Jr., Johnson, D.D., Smith, T.P. 2006. Effects of calpastatin and u-calpain markers in beef cattle on tenderness traits. Journal of Animal Science. 84:520-525.

Cepica, S., Masopust, M., Knoll, A., Bartenschlager, H., Yerle, M., Rohrer, G.A., Gelderman, H. 2006. Linkage and RH mapping of 10 genes to a QTL region for fatness and muscling traits on pig chromosome X. Animal Genetics. 37:603-604.

Frylinck, L., Van Wyk, G.L., Smith, T.P., Strydom, P.E., van Marle-Koster, E., Webb, E.C., Koohmaraie, M., Smith, M.F. 2009. Evaluation of Biochemical Parameters and Genetic Markers for Association with Meat Tenderness in South African Feedlot Cattle. Meat Science. 83:657-665.

Garcia, M.D., Thallman, R.M., Wheeler, T.L., Shackelford, S.D., Casas, E. 2010. Effect of Bovine Respiratory Disease and Overall Pathogenic Disease Incidence on Carcass Traits. Journal of Animal Science. 88(2):491-496.

Geesink, G.H., Kuchay, S., Chishti, A.H., Koohmaraie, M. 2006. μ-calpain is essential for postmortem proteolysis of muscle proteins. Journal of Animal Science 84:2834-2840.

Jiang, Z., Michal, J.J., Tobey, D.J., Daniels, T.F., Rule, D.C., Macneil, M.D. 2008. Significant associations of stearoyl-CoA desaturase (SCD1) gene with fat deposition and composition in skeletal muscle. International Journal of Biological Sciences 4(6):345-351.

King, D.A., Shackelford, S.D., Kuehn, L.A., Kemp, C.M., Rodriguez, A.B., Thallman, R.M., Wheeler, T.L. 2010. Contribution of Genetic Influences to Animal-to-Animal Variation in Myoglobin Content and Beef Lean Color Stability. Journal of Animal Science. 88:1160-1167.

Klindt, J.M., Thallman, R.M., Wise, T.H. 2006. Effects of sire line, sire, and sex on plasma urea nitrogen, body weight, and backfat thickness in offspring of duroc and landrace boars. Journal of Animal Science. 84(6):1323-1330.

Kuehn, L.A., Rohrer, G.A., Nonneman, D.J., Thallman, R.M., Leymaster, K.A. 2007. Detection of single nucleotide polymorphisms associated with ultrasonic backfat depth in a segregating Meishan x White Composite population. Journal of Animal Science. 85:1111-1119.

Lindholm-Perry, A.K., Rohrer, G.A., Holl, J.W., Shackelford, S.D., Wheeler, T.L., Koohmaraie, M., Nonneman, D.J. 2009. Relationships among Calpastatin Single Nucleotide Polymorphisms, Calpastatin Expression and Tenderness in Pork Longissimus. Animal Genetics. 40(5):713-721.

Okumura, F., Shimogiri, T., Shinbo, Y., Yoshizawa, K., Kawabe, K., Mannen, H., Okamoto, S., Cheng, H.H., Maeda, Y. 2005. Linkage mapping of four chicken calpain genes. Animal Science Journal. 76:121-127.

Rios-Utrera, A., Cundiff, L.V., Gregory, K.E., Koch, R.M., Dikeman, M.E., Koohmaraie, M., Van Vleck, L.D. 2006. Effects of age, weight and fat slaughter end points on estimates of breed and retained heterosis effects for carcass traits. Journal of Animal Science 84:63-87.

Rohrer, G.A., Thallman, R.M., Shackelford, S.D., Wheeler, T.L., Koohmaraie, M. 2005. A genome scan for loci affecting pork quality in a Duroc-Landrace F2 population. Animal Genetics. 37:17-27.

Stone, R.T., Casas, E., Smith, T.P.L., Keele, J.W., Harhay, G.P., Bennett, G.L., Koohmaraie, M., Wheeler, T.L., Shackelford, S.D., Snelling, W.M. 2005. Identification of genetic markers for fat deposition and meat tenderness on bovine chromosome 5: Development of a low-density single nucleotide polymorphism map. Journal of Animal Science. 83:2280-2288.

Van Vleck, L.D., Cundiff, L.V., Wheeler, T.L., Shackelford, S.D., Koohmaraie, M. 2007. Across-breed adjustment factors for expected progeny differences for carcass traits. Journal of Animal Science. 85:1369-1376.

Wheeler, T.L., Cundiff, L.V., Shackelford, S.D., Koohmaraie, M. 2005. Characterization of biological types of cattle (Cycle VII): Carcass, yield, and longissimus palatability traits. Journal of Animal Science. 83:196-207.

White, S.N., Casas, E., Wheeler, T.L., Shackelford, S.D., Koohmaraie, M., Riley, D.G., Chase, C.C., Johnson, D.D., Keele, J.W., Smith, T.P. 2005. A new snp in capn1 extends the current tenderness marker test to include cattle of bos indicus, bos taurus, and crossbred descent. Journal of Animal Science. 83:2001-2008.

Zhou, H., Deeb, N., Clover, C.M., Ashwell, C.M., Lamont, S.J. 2006. Genome-wide linkage analysis to identify chromosomal regions affecting phenotypic traits in the chicken. II. Body composition. Poultry Science. 85:1712-1721.

Walker, S.C., Christenson, R.K., Ruiz, R.P., Reeves, D.E., Pratt, S.L., Arenivas, F., Williams, N.E., Bruner, B.L., Polejaeva, I.A. 2007. Comparison of meat composition from offspring of cloned and conventionally produced boars. Theriogenology. 67(1):178-184.

2. Physical comparison, evaluation and improvement of meat products.

Dinh, T., Blanton, Jr., J., Riley, D.G., Chase, C.C., Coleman, S.W., Phillips, W.A., Brooks, J., Miller, M., Thompson, L. 2010. Intramuscular fat and fatty acid composition of longissimus muscle from divergent pure breeds of cattle. American Society of Animal Science. Journal of Animal Science. 88:756-766. doi10.2527/JAS2009-1951.

Dodson, M.V., Jiang, Z., Chen, J., Hausman, G.J., Guan, L.L., Novakofski, J., Thompson, D., Lorenzen, C.L., Fernyhough, M.E., Mir, P., Reecy, J.M. 2009. Allied industry approaches to alter intramuscular fat content and composition in beef animals. Journal of Food Science. v.00, Nr.0. p.1.

Duckett, S.K., Neel, J.P., Fontenot, J.P., Clapham, W.M. 2009. Effects of winter stocker growth rate and finishing system on: III. tissue proximate, fatty acid, vitamin, and cholesterol content. Journal of Animal Science. 87(9):2961-2970.

Duckett, S.K., Neel, J.P., Sonon, Jr., R.N., Fontenot, J.H., Clapham, W.M. 2007. Effects of winter stocker growth rate and finishing system on: II. 9-10-11th rib composition, muscle color, and palatability. Journal of Animal Science. 85:2691-2698.

Duckett, S.K., Sonan, R.N., Pavan, E., Neel, J.P., Fontenot, J.P., Scaglia, G., Clapham, W.M. 2006. Effects of forage species on rib composition, color, and palatability in forage-finished beef. Journal of Animal Science. 84(1):387.

Duckett, S.K., Pavan, E., Sonon, R.N., Neel, J.P., Fontenot, J.P., Clapham, W.M. 2006. Effects of forage species on fatty acid composition of beef longissimus muscle from forage-finished beef. Journal of Animal Science. 84(1):387.

Guay, J.F., Fontenot, J.P., Swecker, Jr., W.S., Herbein, J.H., Neel, J.P., Scaglia, G., Clapham, W.M. 2009. Fatty acid metabolism and deposition in subcutaneous adipose tissue of pasture and feedlot finished cattle. Journal of Animal Science. doi: 0:jas.2008-1277.

Kemp, C.M., King, D.A., Shackelford, S.D., Wheeler, T.L., Koohmaraie, M. 2009. The Caspase Proteolytic System in Callipyge and Normal Lambs in Longissimus, Semimembranosus, and Infraspinatus Muscles During Postmortem Storage. Journal of Animal Science. 87:2943-2951.

King, D.A., Shackelford, S.D., Wheeler, T.L., Pfeiffer, K.D., Mehaffey, J.M., Miller, M.F., Nickelson, R., Koohmaraie, M. 2009. Consumer Acceptance and Steak Cutting Yields of Beef Top Sirloin and Knuckle Subprimals. Meat Science. 83:782-787.

King, D.A., Wheeler, T.L., Shackelford, S.D., Pfeiffer, K.D., Nickelson, R., Koohmaraie, M. 2009. Effect of Blade Tenderization, Aging Time, and Aging Temperature on Tenderness of Beef Longissimus Lumborum and Gluteus Medius. Journal of Animal Science. 87:2952-2960.

King, D.A., Wheeler, T.L., Shackelford, S.D., Koohmaraie, M. 2009. Comparison of palatability characteristics of beef gluteus medius and triceps brachii muscles. Journal of Animal Science. 87:275-284.

King, D.A., Wheeler, T.L., Shackelford, S.D., Koohmaraie, M. 2008. Chapter 3. Fresh Meat Texture and Tenderness. In: Kerry, J.P., Ledward, D., editors. Improving the Sensory and Nutritional Quality of Fresh Meat. Cambridge, England: Woodhead Publishing Limited. p. 61-88.

Leeds, T.D., Mousel, M.R., Notter, D.R., Zerby, H.N., Moffet, C.A., Lewis, G.S. 2008. B-mode, real-time ultrasound for estimating carcass composition in live sheep: Accuracy of ultrasound measures and their relationships with carcass composition. Journal of Animal Science. 86:3203-3214.

Liu, M., Solomon, M.B., Vinyard, B.T., Callahan, J.A., Patel, J.R., West, R., Chase, C.C. 2006. Use of hydrodynamic pressure processing and blade tenderization to tenderize top rounds from brahman cattle. Journal of Muscle Foods. 17:79-91.

Riley, J.M., Schroeder, T.C., Wheeler, T.L., Shackelford, S.D., Koohmaraie, M. 2009. Valuing Fed Cattle Using Objective Tenderness Measures. Journal of Agricultural and Applied Economics. 41(1):163-175.

Schenck, E.L., McMunn, K.A., Nielsen, B.D., Richert, B.T., Marchant Forde, J.N., Lay Jr, D.C. 2008. Exercise in stall-housed gestating gilts: Effects on lameness, the musculo-skeletal system, production and behavior. Journal of Animal Science. 86:3166-3180.

Scholz, A.M., Mitchell, A.D., Forster, M., Pursel, V.G. 2007. Two-site evaluation of the relation between in vivo and carcass dual energy x-ray absorptiometry (DXA) in pigs. Livestock Production Science. 110:1-11.

Taylor, J.B., Marchello, M.J., Finley, J.W., Neville, T.L., Combs, G.F., Caton, J.S. 2008. Nutritive value and display-life attributes of selenium-enriched beef-muscle foods. Journal of Food Composition and Analysis. 21(2):183-186.

Wheeler, T.L., Shackelford, S.D., Koohmaraie, M. 2007. Beef longissimus slice shear force measurement among steak locations and institutions. Journal of Animal Science 85:2283-2289.

Miscellaneous References For NP101

1. Food safety – infectious pathogens of animal products.

Clawson, M.L., Keen, J.E., Smith, T.P., Durso, L.M., Mcdaneld, T.G., Mandrell, R.E., Davis, M.A., Bono, J.L. 2009. Phylogenetic Classification of Escherichia coli O157:H7 Strains of Human and Bovine Origin Using a Novel Set of Nucleotide Polymorphisms. Genome Biology [serial online]. 10:R56. Available: http://genomebiology.com/2009/10/5/R56.

Looper, M.L., Edrington, T.S., Callaway, T.R., Rosenkrans, C.F. 2009. Fate of Escherichia coli O157:H7 and Salmonella from contaminated manure slurry applied to soil surrounding tall fescue. Letters in Applied Microbiology. 48:513-516.

Looper, M.L., Edrington, T.S., Rosenkrans, C.F. 2009. Influence of body condition and forage type on prevalence of Escherichia coli O157:H7 and Salmonella in grazing beef cattle. Letters in Applied Microbiology. 49:361-365.

Riley, D.G., Loneragan, G.H., Phillips, W.A., Gray, J.T., Cray, P.J. 2008. Fecal shedding of foodborne pathogens and other enterobacteriaceae by Florida heifers and steers in US beef production segments. Journal of Food Protection.71:807–810.

Rostagno, M.H., Hurd, S.H., Mckean, J.D. 2009. Split Marketing as a Risk Factor for Salmonella Enterica Infection in Swine. Foodborne Pathogens and Disease. 6(7):865-869.

Rostagno, M.H., Wesley, I.V., Trampel, D.W., Hurd, H.S. 2006. Salmonella prevalence in market-age turkeys on-farm and at slaughter. Poultry Science. 85(10):1838-1842.

Standley, T., Paterson, J., Skinner, K., Rainey, B., Roberts, A.J., Geary, T.W., Smith, G., White, R. 2008. The Use of an Experimental Vaccine in Gestating Beef Cows to Reduce the Shedding of Escherichia coli O157:H7 in the Newborn Calf. Professional Animal Scientist 24:260-263.

Toscano, M.J., Stabel, T.J., Bearson, S.M., Bearson, B.L., Lay Jr, D.C. 2007. Cultivation of Salmonella enterica seovar Typhimurium in a norepinephrine-containing medium alters in vivo tissue prevalence in swine. Journal of Experimental Animal Science. 43(4):329-338.

Wells, J., Oliver, W.T., Yen, J. 2010. The Effects of Dietary Additives on Faecal Levels of Lactobacillus spp., Coliforms, and Escherichia coli, and Faecal Prevalence of Salmonella spp. and Campylobacter spp. in U.S. Production Nursery Swine. Journal of Applied Microbiology. 108:306-314.

Wells, J., Shackelford, S.D., Berry, E.D., Kalchayanand, N., Guerini, M.N., Varel, V.H., Arthur, T.M., Bosilevac, J.M., Freetly, H.C., Wheeler, T.L., Ferrell, C.L., Koohmaraie, M. 2009. Prevalence and Level of Escherichia coli O157:H7 in Feces and on Hides of Feedlot Steers Fed Diets With or Without Wet Distillers Grains with Solubles. Journal of Food Protection. 72(8):1624-1633.

2. Animal health.

Bearson, B.L., Bearson, S.M., Uthe, J., Houghton, J., Dowd, S.E., Lee, I., Toscano, M.J., Lay Jr, D.C. 2008. Iron regulated genes of Salmonella enterica serovar Typhimurium in response to norepinephrine and the requirement of fepCDG for norepinephrine-enhanced growth. Microbes and Infection. 10(7):807-816.

Carroll, J.A., Reuter, R.R., Chase Jr., C.C., Coleman, S.W., Riley, D.G., Spiers, D.E., Arthington, J.D., Galyean, M.L. 2009. Profile of the bovine acute-phase response following an intravenous bolus-dose lipopolysaccharide challenge. Innate Immunity. 15(2):81-89.

Chau, G.P., Collier, C.T., Welsh, T.H., Carroll, J.A., Laurenz, J.C. 2009. Beta-1-3-glucan effect on sow antibody production and passive immunization of progeny. Food and Agricultural Immunology. 20(3):185-193.

Hoesing, L.M., Broughton-Neiswanger, .L., Gouine, K., White, S.N., Mousel, M.R., Lewis, G.S., Marshall, K.L., Knowles Jr, D.P. 2010. Evaluation of a Caprine Arthritis-Encephalitis Virus/Maedi-

Visna Virus Indirect Enzyme-Linked Immunosorbent Assay in the Serological Diagnosis of Ovine Progressive Pneumonia Virus in U.S. Sheep. Clinical and Vaccine Immunology. 17(2):307-310.

Hoesing, L.M., White, S.N., Mousel, M.R., Lewis, G.S., Knowles Jr, D.P. 2008. Ovine progressive pneumonia provirus levels associate with breed and Ovar-DRB1. Immunogenetics. 60(12):749-758.

Hoesing, L.M., White, S.N., Lewis, G.S., Mousel, M.R., Knowles Jr, D.P. 2007. Development and Validation of an Ovine Progressive Pneumonia Virus Quantitative PCR. Clinical and Vaccine Immunology. 14(10):1274-1278.

Jenkins, S.J., Cooper, T.A., Roberts, M.P., Mathew, A.G., Carroll, J.A., Kattesh, H.G., Kojima, C.J. 2009. Effects of Syndyphalin-33 on immune function during a Salmonella challenge in recently weaned pigs. Journal of Animal and Veterinary Advances. 8(12):2562-2567.

Moulton, K., Ryan, P., Lay Jr, D.C., Willard, S. 2009. Postmortem Photonic Imaging of Lux-Modified Salmonella Typhimuium Within the Gastrointestinal Tract of Swine Following Oral Inoculation In Vivo. Journal of Animal Science 87:2239-2244.

Scoles, G.A., Goff, W.L., Lysyk, T.J., Lewis, G.S., Knowles Jr, D.P. 2008. Validation of an Anaplasma marginale cELISA for use in the diagnosis of A. ovis infections in domestic sheep and Anaplasma spp. in wild ungulates. Veterinary Microbiology. 130:184-190.

Taus, N.S., Herndon, D.R., Traul, D., Stewart, J.P., Ackermann, M., Li, H., Knowles Jr, D.P., Lewis, G.S., Brayton, K.A. 2007. Comparison of ovine herpesvirus 2 genomes isolated from domestic sheep (Ovis aries) and a clinically affected cow (Bos bovis). Journal of General Virology. 88(1):40-45.

White, S.N., Orourke, K.I., Gidlewski, T.L., Vercauteren, K.C., Mousel, M.R., Phillips, G.E., Spraker, T.R. 2010. Increased risk of chronic wasting disease in Rocky Mountain elk associated with decreased magnesium and increased manganese in brain tissue. Canadian Journal of Veterinary Research. 74:50-53.

White, S.N., Mousel, M.R., Reynolds, J.O., Lewis, G.S., Hoesing, L.M. 2009. Common promoter deletion is associated with 3.9-fold differential transcription of ovine CCR5 and reduced proviral level of ovine progressive pneumonia virus. Animal Genetics. 40(5):583-589.

3. Animal production and environmental effects.

Archibeque, S.L., Freetly, H.C., Cole, N.A., Ferrell, C.L. 2007. The influence of oscillating dietary protein concentrations on finishing cattle. II. Nutrient retention and ammonia emissions. Journal of Animal Science. 85(6):1496-1503.

Archibeque, S.L., Miller, D.N., Freetly, H.C., Berry, E.D., Ferrell, C.L. 2007. The influence of oscillating dietary protein concentrations on finishing cattle. I. Feedlot performance and odorous compound production. Journal of Animal Science. 85(6):1487-1495.

Berry, E.D., Wells, J.E., Archibeque, S.L., Ferrell, C.L., Freetly, H.C., Miller, D.N. 2006. Influence of genotype and diet on steer performance, manure odor, and carriage of pathogenic and other fecal bacteria. II. Pathogenic and other fecal bacteria. Journal of Animal Science. 84:2523-2532.

Ferrell, C.L., Berry, E.D., Freetly, H.C., Miller, D.N. 2006. Influence of genotype and diet on steer performance, manure odor, and carriage of pathogenic and other fecal bacteria. I. Animal performance. Journal of Animal Science. 84:2515-2522.

Flythe, M.D., Kagan, I. 2010. Antimicrobial Effects of Red Clover (Trifolium pratense) Phenolic Extract on the Ruminal Hyper Ammonia-producing Bacterium, Clostridium sticklandii SR. Curr Microbiol (2010) 61:125-131.

Harper, L.A., Flesch, T.K., Powell, J.M., Coblentz, W.K., Jokela, W.E., Martin, N.P. 2009. Ammonia Emissions from Dairy Production Systems in Wisconsin. Journal of Dairy Science. 92:2326-2337.

Knowlton, K.F., Wilkerson, V.A., Casper, D.P., Mertens, D.R. 2009. Manure Nutrient Excretion by Jersey and Holstein Cows. Journal of Dairy Science. 93(1):407-412.

Mader, T.L., Frank, K.L., Harrington, J.A., Hahn, G.L., Nienaber, J.A. 2009. Potential Climate Change Effects on Warm-Season Livestock Production in the Great Plains. Climatic Change. 97:529-541.

Miller, D.N., Berry, E.D., Wells, J.E., Ferrell, C.L., Archibeque, S.L., Freetly, H.C. 2006. Influence of genotype and diet on steer performance, manure odor, and carriage of pathogenic and other fecal bacteria. III. Odorous compound production. Journal of Animal Science. 84:2533-2545.

Powell, J.M., Broderick, G.A., Grabber, J.H., Hymes Fecht, U.C. 2009. Effects of Forage Protein-Binding Polyphenols on Chemistry of Dairy Excreta. Journal of Dairy Science. 92:1765-1769.

Powell, J.M., Russelle, M.P. 2009. Dairy Cattle Management Impacts Manure N Collection and Cycling Through Crops in Wisconsin, USA. Agriculture, Ecosystems and Environment [electronic journal]. 131(2009):170-177.

4. Management and economics.

Bewley, J.M., Boehlje, M.D., Gray, A.W., Hogeveen, H., Kenyon, S.J., Eicher, S.D., Schutz, M.M. 2010. Stochastic Simulation using @Risk for Dairy Business Investment Decisions. Agricultural Finance Review. 70(1):97-125.

Clapham, W.M., Fedders, J.M., Teutsch, C. 2009. RISK ANALYSIS, ANALYSIS OF VARIANCE: GETTING MORE FROM OUR DATA. Forage and Grazinglands. Available: http://www.plantmanagementnetwork.org/fg/element/sum2.aspx?id=7911.

Kruse, R.E., Tess, M.W., Grings, E.E., Short, R.E., Heitschmidt, R.K., Phillips, W.A., Mayeux, H.S. 2008. Evaluation of Beef Cattle Operations Utilizing Different Seasons of Calving, Weaning Strategies, Post-weaning Management, and Retained Ownership. Professional Animal Scientist 24(4):319-327.

Lewis, G.S., Gavin, W.G., Goetsch, A.L., Taylor, J.B.,and Thonney, M.L. 2010. Chapter 10: Sheep and Goats, in Guide for Care and Use of Agricultural Animals in Research and Teaching. 3rd ed. Federation of Animal Science Society, Savoy, IL. p. 129-142.

Roush, W.B., Purswell, J.L., Branton, S.L. 2009. Micosoft Excel Sensitivity Analysis for Linear and Stochastic Program Feed Formulation. Journal of Applied Poultry Research 13(1):85-89.

Tylutki, T.P., Fox, D.G., Durbal, V.M., Tedeschi, L.O., Russell, J.B., Van Amburgh, M.E., Overton, T.R., Chase, L.E., Pell, A.N. 2008. A decision support system for dairy herd nutrition management. Animal Feed Science And Technology. 143:174-202.

5. Miscellaneous genetic and genomic references.

Decker, J.E., Pires, J.C., Conant, G.C., McKay, S.D., Heaton, M.P., Chen, K., Cooper, A., Vilkki, J., Seabury, C.M., Caetano, A.R., Johnson, G.S., Brenneman, R.A., Hanotte, O., Eggert, L.S., Wiener, P., Kim, J.J., Kim, K.S., Sonstegard, T.S., Van Tassell, C.P., Neibergs, H.L., McEwan, J.C., Brauning, R., Coutinho, L.L., Babar, M.E., Wilson, G.A., McClure, M.C., Rolf, M.M., Kim, J., Schnabel, R.D., Taylor, J.F. 2009. Resolving the Evolution of Extant and Extinct Ruminants With High-Throughput Phylogenomics. Proceedings of the National Academy of Sciences. 106(44):18644-18649.

Jiang, Z., Michal, J.J., Tobey, D., Wang, Z., MacNeil, M.D., Magnuson, N.S. 2008. Comparative understanding of UTS2 and UTS2R genes for their involvement in type 2 diabetes mellitus. International Journal of Biological Sciences 4(2):96-102.

Kordonowy, L.L., Mcmurtry, J.P., Williams, T.D. 2010. Variation in plasma leptin-like immunoreactivity in free-living european starlings (Sturnus vulgaris). General and Comparative Endocrinology. 166(1):47-53.

Liu, G., Alkan, C., Zhao, S., Eichler, E.E. 2009. Comparative Analysis of Alu Repeats in Primate Genomes. Genome Research. 19(5):876-885.

Natarajan, S.S., Xu, C., Cregan, P.B., Caperna, T.J., Garrett, W.M., Luthria, D.L. 2008. Utility of proteomics techniques for assessing protein expression. Journal of Regulatory Toxicology and Pharmacology. 54:S32-S36.

6. Miscellaneous production and other references.

Andres, A., Mitchell, A.D., Badger, T.M. 2010. Validation of a new body composition method for infant and children using piglets. International Journal of Obesity. 34(4):775-780.

Barraza, M.L., Strickland, J.R., Zepada, H., Taylor, J.B., Krehbiel, C.R., Bell, G.S. 2006. Gross and histopathological observations of long term catheterized vessels in experimental sheep. Journal of Veterinary Medicine. 53:230-238 (2006).

Cushman, R.A., Allan, M.F., Kuehn, L.A. 2009. Achievements of Research in Reproduction Sciences. In: Rosati, A., Tewolde, A., Mosconi, C., editors. Animal Production and Animal Science Worldwide - WAAP Book of the Year 2007. The Netherlands: Wageningen Academic Publishers. p. 59-65.

Gressley, T.F., Reynal, S.M., Olmos Colmenero, J.J., Broderick, G.A., Armentano, L.E. 2006. Development of a tool to insert abomasal infusion lines into dairy cows. Journal of Dairy Science. 89:3965-3967.

Kovner, I., Taicher, G., Mitchell, A.D. 2010. Calibration and validation of EchoMRI whole body composition analysis based on chemical analysis of piglets, in comparison with the same for DXA. International Journal of Body Composition Research. 8(1):17-29.

Liang, L., Yan, R., Ma, W., Zhang, H., Wang, S. 2006. Exploring RPE as a source of photoreceptors: differentiation and integration of transdifferentiating cells grafted into embryonic chick eyes. Investigative Ophthalmology and Visual Science. 47(11):5066-5076.

Mitchell, A.D. 2007. Impact of research with cattle, pigs and sheep on nutrition concepts: Body composition and growth. Journal of Nutrition. 137(3):711-714.

Peng, Y.S., Brown, M.A., Wu, J.P., Wei, L.X., Wu, J.L., Sanbei, D.Z. 2008. Fatty acid profile and conjugated linoleic ccid (CLA) in the milk fate from Qingphai yak. Professional Animal Scientist. 24:479-487.

Sprangler, M.L., Robbins, K.R., Bertrand, J.K., MacNeil, M.D., Rekaya, R. 2009. Ant colony optimization as a method for strategic genotype sampling. Animal Genetics 40:308-314.

Wu, J., Ma, B., Ren, H., Zhang, L., Xiang, Y., Brown, M.A. 2007. Characterization of metallothioneins (mt-i and mt-ii) in yak. Journal of Animal Science. 85:1357-1362.

APPENDIX 3. ANNUAL REPORT SUMMARIES FOR 2006-2010 NP101

National Program 101: Food Animal Production
FY 2006 Annual Report

Introduction

The food animal production national program is charged with conducting cutting edge research to contribute to increased efficiency and sustainability of production of beef and dairy cattle, poultry, swine, and sheep. Research efforts in the animal sciences over the past century have had dramatic impacts on animal agriculture both in terms of improved biological and economic efficiency of production and in terms of quantity, quality, and safety of animal products. Many major challenges remain, however, requiring the dedicated focus of long-term research teams, particularly in the areas of reproductive longevity and animal well-being, adaptability to production environments, product quality, reduction of feed and energy inputs, enhancements in nutrient retention, and reduction of negative environmental impacts.

During the past year, the structure of the national program changed as a result of the merger of the former national program 105, Animal Well-Being and Stress Control Systems, in to the Food Animal Production program. This merger added four existing research projects to the portfolio and three new unit locations.

The program had a very good year in 2006. In total, 113 full-time scientists working at 20 locations across the U.S. were actively engaged in 45 research projects in the program. Research projects in this program area were approved through the ARS Office of Scientific Quality Review in 2002, making this the fourth year of implementation of these five-year project efforts.

During fiscal year 2006, program increases were appropriated for forage animal pasture research ($108,000 to Lexington, KY), bovine genetics ($270,000 to Beltsville, MD), dairy forage research ($510,000 to Madison, WI), beef cattle feed efficiency genomics ($315,000 to Clay Center, NE), and beef cattle rumen metagenomics ($135,000 to Miles City, MT) bringing the total appropriations in the national program to over $46.5M. Additionally, funds were appropriated for development of new facilities in the program at Lexington, KY ($4M), Marshfield, WI ($8M), and Bozeman, MT ($4M).

Several new permanent scientists were welcomed to the program including: Wayne Coblentz (Madison, WI); Michael Flythe (Lexington, KY); Larry Keuhn (Clay Center, NE); Jeremy Miles (Clay Center, NE); Corey Moffett (Dubois, ID); and Michelle Mousel (Dubois, ID).

The ARS animal production research community was saddened by the death of Larry Satter (retired) from the U.S. Dairy Forage Research Center.

Ronnie Green served as the national program leader for the program with co-lead responsibilities provided by Lewis Smith. Contributions to the national program were also provided by program team members Evert Byington, Cyril Gay, and Robert Heckert.

Several scientists in the national program were recognized with prominent awards, including:

Rick Barb, Athens, GA – Animal Physiology and Endocrinology Award, American Society of Animal Science

Tony Capuco, Beltsville, MD – WestAgro Award, American Dairy Science Association

Jeff Carroll, Lubbock, TX – National Pork Board Innovation Award, Southern Section, American Society of Animal Science

Bill Dozier, Starkville, MS – HyLine International Research Award, Poultry Science Association

Calvin Ferrell, Clay Center, NE – Animal Growth and Development Award, American Society of Animal Science

Mary Beth Hall, Madison, WI – Foundation Scholar Award in Dairy Production, American Dairy Science Association

Mike Looper, Booneville, AR – Outstanding Young Animal Scientist Education Award, Southern Section, American Society of Animal Science

Mike MacNeil, Miles City, MT – Hall of Merit Inductee, American Hereford Association

John Nienaber, Clay Center, NE – Fellow Award, American Society of Agricultural and Biological Engineers

Rex Powell (retired), Beltsville, MD – Distinguished Service Award, Northeast Section, American Dairy Science Association

Vern Pursel (retired), Beltsville, MD – Hall of Fame Inductee, USDA Agricultural Research Service

Dale Van Vleck, Clay Center, NE – International Gamma Sigma Delta Distinguished Achievement in Agriculture Award

George Wiggans, Beltsville, MD – National DHIA Outstanding Service Award

The high quality and impact of research conducted in the program was further evidenced by the fact that scientists delivered 128 invited presentations at international and national symposia during the past year. During the year, two new CRADAs were established and four new patents were filed by researchers in the program. Additionally, a total of $2.7M in extramural grant award funding was received by scientists in the program, supported in many cases by cooperative research programs with partners at land grant universities.

Administrator’s Postdoctoral Awards were granted to Eduardo Casas (Clay Center, NE), Dan Nonneman (Clay Center, NE), John Ralph (Madison, WI), and David Donovan (Beltsville, MD).

Partnerships with land grant and 1890s universities continued to be very important to the success of the national program in 2006. These partnerships are greatly appreciated and take on a variety of forms including work with those in the states of Arkansas, Colorado, Connecticut, Florida, Georgia, Idaho, Illinois, Indiana, Iowa, Kentucky, Maryland, Michigan, Minnesota, Mississippi, Missouri, Montana, Nebraska, New York, Oklahoma, Oregon, South Carolina, Texas, Virginia, West Virginia, and Wisconsin.

Planning for the next 5-year cycle of the national program was a major focal point during the year. A retrospective assessment panel was appointed and documentation (www.ars.usda.gov/research/programs/programs.htm?np_code=101&docid=14389) was prepared for their review which was completed in February 2006. A Joint ARS-CSREES Food Animal Production Stakeholder Workshop was held April 10-12, 2006 in Kansas City, MO. Input from the 145 participants of this workshop was used to guide the development of the newly published 2007-2012 national program action plan (www.ars.usda.gov/research/programs/programs.htm?np_code=101&docid=13753). Project teams and objectives were developed during the last part of the fiscal year for 31 new projects to address this action plan. These new 5-year project plans will undergo peer review prior to scheduled implementation in August of 2007.

The following sections of the report summarize high impact research results addressing the various components of the current national program action plan…

National Program 101: Food Animal Production
FY 2007 Annual Report

Introduction

The food animal production national program is charged with conducting cutting edge research to contribute to increased efficiency and sustainability of production of beef and dairy cattle, poultry, swine, and sheep. Research efforts in the animal sciences over the past century have had dramatic impacts on animal agriculture both in terms of improved biological and economic efficiency of production and in terms of quantity, quality, and safety of animal products. Many major challenges remain, however, requiring the dedicated focus of long-term research teams, particularly in the areas of reproductive longevity and animal well-being, adaptability to production environments, product quality, reduction of feed and energy inputs, enhancements in nutrient retention, and reduction of negative environmental impacts.

During 2007, 110 full-time scientists working at 20 locations across the U.S. were actively engaged in 45 research projects in the program. Research projects in this program area were approved through the ARS Office of Scientific Quality Review in 2002, making this the final year of implementation of these five-year project efforts.

During fiscal year 2007, USDA-ARS operated under a full year continuing resolution with no program increases from the previous year. However, previously “earmarked” funds were redirected during the year to permanent funding including funding for the national animal germplasm program ($390K), dairy cattle genetic improvement ($930K), bovine cloning ($956K), dairy functional genomics ($956K), rumen metagenomics ($50K), beef and swine genomics ($928K), forage animal production ($1.74M), grass-finished beef production ($1.875M) and poultry production and management ($1.67M) research. Total funding in the program for fiscal year 2007 was approximately $46.5M.

Several new permanent scientists were welcomed to the program including: Justin Holl (Clay Center, NE); David King (Clay Center, NE); Jimmy Kotz (Lexington, KY); Larry Kuehn (Clay Center, NE); Tara McDaneld (Clay Center, NE); and William Oliver (Clay Center, NE).

Retiring from the ranks of scientists in the national program during 2007 were Larry Cundiff, John Klindt, and Dale Van Vleck (all Clay Center, NE). The distinguished record of service of these gentlemen in the areas of animal breeding, genetics, and physiology is recognized world-wide in the beef, swine, and sheep industries and they will be missed.

In January 2007, Lewis Smith retired from USDA-ARS after 45 years of dedicated and excellent service as a scientist working in dairy cattle nutrition, research supervisor and administrator, and national program leader. He had served as national program leader for animal nutrition and in recent years as co-lead of the food animal production national program and lead of the aquaculture and animal well-being and stress control systems national programs. He leaves behind a portfolio of dynamic and significant programs marked by his leadership and direction.

Ronnie Green served as the national program leader for the program with co-lead responsibilities provided by Lewis Smith until his retirement. Jeff Silverstein became a welcome addition to the national program staff in October 2007 assuming the co-lead role. Contributions to the national program were also provided by program team members Evert Byington, and Cyril Gay.

Several scientists in the national program were recognized with prominent awards:

Jeff Carroll, Livestock Issues Research Unit, Lubbock, TX
(National Pork Board Research Innovation Award, ASAS Southern Section)

Erin Connor, Bovine Functional Genomics Lab, Beltsville, MD
(ASAS/ADSA Young Scientist Award, Northeast Section)

Bill Dozier, Poultry Research Unit, Starkville, MS
(USDA-ARS Early Career Scientist Award, Mid-South Area)

Cal Ferrell, U.S. Meat Animal Research Center, Clay Center, NE
(ASAS Fellow Award – Research)

Cal Ferrell, U.S. Meat Animal Research Center, Clay Center, NE
(Oklahoma State University "Graduate of Distinction")

Ronnie Green, National Program Staff, Beltsville, MD
(USDA-CSREES TEAM Award for USDA Animal Genomics Blueprint)

Neal Martin, U.S. Dairy Forage Research Center, Madison, WI
(Honorable Mention Laboratory Director of the Year in Tech Transfer, The Federal Laboratory Consortium)

John Nienaber, U.S. Meat Animal Research Center (Clay Center, NE)
(Outstanding Contribution to Nebraska Agriculture, The Society for Engineering in Agricultural, Food, and Biological Systems, Nebraska Section)

Duane Norman, Animal Improvement Programs Lab, Beltsville, MD
(ADSA Land O' Lakes Award)

John Ralph, U.S. Dairy Forage Research Center, Madison, WI
(Exceptional Citation Count in Agricultural Science, Institute for Scientific Information (ISI)) and (Carbohydrate Research Most Cited Paper: 2004-2007. Awarded to the "top 50 most cited" papers for Carbohydrate Research 339:2009-2017)

Larry Satter (deceased), U.S. Dairy Forage Research Center, Madison, WI
(National Dairy Shrine Posthumous Pioneer Award)

Lewis Smith, National Program Staff, Beltsville, MD
(ASAS/ADSA Distinguished Service Award, Northeast Section)

Research Team, Poultry Research Unit, Starkville, MS
(Honorable Mention for Excellence in Tech Transfer, The Federal Lab Consortium, Southeast Region)

The high quality and impact of research conducted in the program was further evidenced by the fact that scientists published 115 refereed journal publications and three book chapters, and delivered 95 invited presentations at international and national symposia during the past year. During the year, 8 new CRADAs were established and 1 new patent was filed granted to researchers in the program. Additionally, a total of $3.27M in extramural grant award funding was received by scientists in the program, supported in many cases by cooperative research programs with partners at land grant universities.

Administrator's Postdoctoral Awards were granted to Larry Kuehn (Clay Center, NE), Robert Li (Beltsville, MD), and Tad Sonstegard (Beltsville, MD).

Partnerships with land grant and 1890s universities continued to be very important to the success of the national program in 2007. These partnerships are greatly appreciated and take on a variety of forms including work with those in the states of Arkansas, Colorado, Connecticut, Florida, Georgia, Idaho, Illinois, Indiana, Iowa, Kentucky, Maryland, Michigan, Minnesota, Mississippi, Missouri, Montana, Nebraska, New York, Oklahoma, Oregon, South Carolina, Texas, Virginia, West Virginia, and Wisconsin.

Completion of planning and implementation for the next 5-year cycle of the national program was the major focal point during the year. The newly published 2007-2012 national program action plan developed from the Joint USDA-ARS-CSREES Stakeholder Workshop held in April 2006, (www.ars.usda.gov/research/programs/programs.htm?np_code=101&docid=13753) served as the basis for the development of 31 new integrative projects to address this action plan. Included in the development of this project portfolio was a thorough analysis of the national program in relation to related program areas including animal health (NP 103), and rangelands, pastures and forages (NP 205). There was some shifting of projects and scientists between these three national programs for the next cycle to more accurately align resources with programmatic goals. These new 5-year project plans underwent peer review through the ARS Office of Scientific Quality Review in May-June 2007. At the end of the fiscal year, 29 of these projects had completed the review process and were fully implemented with the remaining 2 near completion.

Additionally, several years of planning and effort culminated during the year in the publication and implementation of a "Blueprint for USDA Efforts in Agricultural Animal Genomics: 2008-2017" (http://www.ars.usda.gov/SP2UserFiles/Place/00000000/NPS/APP/USDABlueprintProofs7-27-07.pdf). This blueprint will guide decision-making and resource allocation for the coming decade in livestock and poultry genomics research, education, and outreach. The ARS Food Animal Production National Program is a major contributor to USDA efforts in this area and the new five-year projects are carefully aligned to meet the criteria and goals articulated in the Blueprint.

The following sections of the report summarize high impact research results addressing the various components of the 2002-2007 national program action plan…

National Program 101: Food Animal Production
FY 2008 Annual Report

Introduction

The food animal production national program is charged with conducting cutting edge research to contribute to increased efficiency and sustainability of production of beef and dairy cattle, poultry, swine, and sheep. Research efforts in the animal sciences over the past century have had dramatic impacts on animal agriculture both in terms of improved biological and economic efficiency of production and in terms of quantity, quality, and safety of animal products. Many major challenges remain, however, requiring the dedicated focus of long-term research teams, particularly in the areas of reproductive longevity and animal well-being, adaptability to production environments, product quality, reduction of feed and energy inputs, enhancements in nutrient retention, and reduction of negative environmental impacts.

During 2008, 110 full-time scientists working at 20 locations across the U.S. were actively engaged in 33 research projects in the program. Research projects in this program area were approved through the ARS Office of Scientific Quality Review in 2007, making this the first year of implementation of these five-year project efforts.

Total funding in the program for fiscal year 2008 was approximately $46 M.

Several new permanent scientists were welcomed to the program including:

James Klotz, Research Animal Scientist, Forage-Animal Production Research Unit, Lexington, Kentucky

Lea Rempel, Research Physiologist, Meat and Animal Research Center, Clay Center, Nebraska

Amanda Lindholm-Perry, Research Geneticist, Meat and Animal Research Center, Clay Center, Nebraska

Retiring from the ranks of scientists in the national program during Fiscal Year 2008 was John N. Stellflug, from U.S. Sheep Experiment Station, Dubois, Idaho. William Dozier, III, from the Mid South Area Poultry Research Unit, along with Gary Snowden, Mark Allen, and Justin Holl, from Clay Center, Nebraska, have left to work outside the Agency. The distinguished record of service of these gentlemen in the areas of animal breeding, genetics, and physiology is recognized world-wide in the beef, swine, and sheep industries and they will be missed.

Ronnie Green served as the national program leader for the program until his departure in April 2008. Jeff Silverstein assumed these responsibilities. Contributions to the national program were also provided by program team members Evert Byington and Cyril Gay.

Several scientists in the national program were recognized with prominent awards:

Joe Ford, Clay Center, Nebraska, received American Society for Animal Science Fellow

Tim Smith, Clay Center, Nebraska, received ARS Northern Plains Area Outstanding Scientist Award
John Nienaber, Animal Improvement Research Laboratory, Beltsville, Maryland, for Outstanding Contributions to Nebraska Agriculture, Nebraska Section, American Society of Agricultural and Biological Engineers (ASABE)

William Dozier III, Mid South Area Poultry Research Unit received the SE Federal Laboratory Consortium Technology Award

Robert H. Miller, Animal Improvement Research Laboratory, Beltsville, Maryland, American Registry Of Professional Animal Scientists (ARPAS) Chapter Distinguished Service in the Animal Science Award

The high quality and impact of research conducted in the program was further evidenced by the fact that scientists published over 200 referred journal publications and three book chapters, and delivered 120 invited presentations at international and national symposia during the past year. This activity was accompanied by over 40 articles in trade journals and popular press. During the year, 13 new CRADA and MTAs were established and two new patents were filed to researchers in the program.

Administrator’s Postdoctoral Awards were granted to:

Sherrill Echternkamp at US MARC, Clay Center, Nebraska, for “Establishment of Maternal Versus Embryonic Genomic Regulation of Early Embryonic development in Cattle and Identification of Genetic Markers Linked to Oocyte and Embryo Quality”

Heng Wei Cheng at the Livestock Behavior Research Unit, West Lafayette, Indiana, for “Modification of Serotonergic System for Controlling Feather Pecking and Cannibalism in Chickens”.

Partnerships with land grant and 1890s universities continued to be very important to the success of the national program in 2008. These partnerships are greatly appreciated and take on a variety of forms including work with those in the states of Arkansas, Colorado, Connecticut, Florida, Georgia, Idaho, Illinois, Indiana, Iowa, Kentucky, Maryland, Michigan, Minnesota, Mississippi, Missouri, Montana, Nebraska, New York, Oklahoma, Oregon, South Carolina, Texas, Virginia, West Virginia, and Wisconsin.

The following section of the report summarizes high impact research results addressing the various components of the recently implemented national program action plan FY 2008 to 2012…

National Program 101: Food Animal Production
FY 2009 Annual Report

Introduction

Over the past century ARS has worked in concert with academia and meat animal industries around the world to redefine the science of food animal production. The resulting improvements in animal production, efficiency and quality are unparalleled in history and illustrate the extraordinary impact and value of these efforts. This work continues to create real value for the meat animal production industries and consumers worldwide. Today this work is even more important as the USDA and the US and international livestock industries address diverse global societal challenges such as international food security, obesity, and climate change.

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 demonstrated vividly in 2009. 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 2009, 96 full-time scientists working at 20 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 second year of implementation of these five-year project efforts. The total fiscal year 2009 funding for NP101 was $ 49,400,000.

Personnel in NP 101

The 2009 leader for NP 101 was Jeff Silverstein who also served as the leader for aquaculture, NP 106 in 2009. Mark Boggess assumed the responsibility as program leader in October 2009. Significant contributions to NP 101 were also provided by program team members Evert Byington and Cyril Gay.

New additions to the NP 101 team in 2009 included:

Amanda Lindholm-Perry, Research Geneticist, USMARC Clay Center, NE. Dr. Lindhom-Perry previously worked as a Research Scientist at Transgenomic, Inc., as a Product Manager at Streck, Inc, and most recently completed postdoctoral work at the US Meat Animal Research Center.

James Schneider, Research Geneticist, USMARC, Clay Center, NE. Dr. Schneider was previously Senior Geneticist with Babcock Genetics, Inc., Holmen, WI.

Lea Rempel, Research Physiologist, USMARC, Clay Center, NE. Dr. Rempel completed postdoctoral research at USMARC and worked previously at the University of Kansas Medical Center.2

Mark Petersen, Research Leader, Fort Keough LRRL, Miles City, MT. Dr Petersen most recently held a research and teaching position for 18 years at New Mexico State University. Previously he served 8 years at Montana State University and 3 years at University of Wyoming as a Ruminant Nutrition Extension Specialist.

The following scientists retired from the ranks in NP 101:

Mark Allan, USMARC, Clay Center, NE, left to work outside the Agency.

Calvin Ferrell, USMARC, Clay Center, NE, retired.

Thomas Jenkins, USMARC, Clay Center, NE, retired.

David Riley, STARS, Brooksville, FL, left to work outside the Agency.

William Rousch, MSU-PRU, retired.

The distinguished record of service of these gentlemen is recognized world-wide in the beef, swine, poultry, and sheep industries and they will be missed.

The following scientists in NP 101 received prominent awards in 2009:

Harvey Freetly, Clay Center, Nebraska, received the American Society of Animal Science American Feed Industry Association Ruminant Nutrition Research Award in 2009.

Mike Looper, Booneville, Arkansas, was distinguished as the Southern Plains Area, Early Career Research Scientist of the Year and the USDA-ARS, Herbert L. Rothbart Outstanding Early Career Research Scientist of the Year.

Mike MacNeil, Miles City, Montanal was awarded the Western Section American Society of Animal Science Distinguished Service Award.

Tara McDaneld, Clay Center, Nebraska; Timothy Smith, Clay Center, Nebraska; and Tad Sonstegard, Beltsville, Maryland each received the Red Angus Association Industry Service Award.
Mark Thallman, Clay Center, Nebraska received the Beef Improvement Federation Continuing Service Award.

Andy King, Clay Center, Nebraska; Steven Shackelford, Clay Center, Nebraska; and Tommy Wheeler, Clay Center, Nebraska received the Federal Laboratory Consortium Technology Transfer Award for the Mid-Continent Region.

The quality and impact of NP 101 research was further evidenced in 2009 by following:
- Over 200 refereed journal articles published

- Over 100 invited presentations at national and international symposia
- Application for one new patent
- Thirteen new cooperative research and development agreements with stakeholders
- Over 40 new scientific technologies developed relating to genomics and other research, and
- Administration or development of 4 web sites for stakeholders

NP 101 scientists participated in research collaborations with scientists in: Australia, Brazil, Canada, France, Germany, Grenada, Israel, Italy, Kazakhstan, Kenya, Netherlands, New Zealand, Norway, Pakistan, Russia, Scotland, Spain, Sweden, Switzerland, Tunisia and United Kingdom in FY 2009.

National Program 101: Food Animal Production
FY 2010 Annual Report

Introduction

Over the past century ARS has worked in concert with academia and meat animal industries around the world to redefine the science of food animal production. The resulting improvements in animal production, efficiency and quality are unparalleled in history and illustrate the extraordinary impact and value of these efforts. This work continues to create real value for the meat animal production industries and consumers worldwide. Today this work is even more important as the USDA and the United States and international livestock industries address diverse global societal challenges such as international food security, obesity, and climate change.

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 demonstrated vividly in 2010. 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 United States of America in today's very competitive global agriculture community.

During 2010, 99 full-time scientists working at 18 locations across the United States 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 third year of implementation of these five-year project efforts. The gross fiscal year 2010 funding for NP101 was $ 51,491,000.

Personnel in NP 101
New additions to the NP 101 team in 2010 are:

David Parker, Clay Center, Nebraska, Supervisory Agricultural Engineer in the Environmental Management Research Unit.
Clay Lents, Clay Center, Nebraska, Research Physiologist in the Swine Reproductive Research Unit.

The following scientists retired from the ranks in NP 101:

John Nienaber, Clay Center, Nebraska, retired.

John McMurtry, Beltsville, Maryland, left NP 101 to serve as Director of the USDA-ARS Animal and Natural Resources Institute.

The distinguished record of service of these gentlemen is recognized world-wide and they will be missed.

The following scientists in NP 101 received prominent awards in 2010:

Dale Van Vleck, retired, Clay Center, Nebraska, was inducted into the ARS Hall of Fame in 2010.

Curt Van Tassell, Tad Sonstegard, John Cole, Paul VanRaden, and George Wiggans**,** Beltsville, Maryland, received the 2010 Secretary's Honor Award as members of the Cattle Genomics Consortium for novel discoveries leading to the development of a commercial cattle DNA assay and developing methods for incorporating data into the national dairy cattle genetic evaluation system.

David Parker, Clay Center, Nebraska, received the FLC Mid-Continent Notable Technology Award for work on emissions from feedlots for EPA compliance with Rick Todd and Andy Cole of USDA-ARS, Bushland, Texas.

Tami Brown-Brandl, Clay Center, Nebraska, was awarded Engineer of the Year, by the Nebraska Section of the American Society of Agricultural and Biological Engineers.

George Liu, Beltsville, Maryland, was named the 2010 Beltsville Area Early Career Scientist of the Year.

Sherrill Echternkamp, Clay Center, Nebraska, was named a 2010 American Society of Animal Science Fellow Award.

Duane Norman, Beltsville, Maryland, received the Distinguished Dairy Alumnus Award from the Department of Dairy and Animal Science at Pennsylvania State University for his leadership in genetic evaluation research on traits of economic importance to the dairy industry.

George R. Wiggans, Beltsville, Maryland, received the Gamma Sigma Delta International Distinguished Service Award of Merit for his important contributions to the dairy industry and their international impact.

Jeff Carroll, Lubbock, Texas, received the 2010 National Pork Board Research Innovation Award from the Southern Section of the American Society of Animal Science.

Larry Kuehn, Clay Center, Nebraska, received the 2009-2010 Outstanding Recent Alumnus Award from the Department of Animal and Poultry Sciences in the College of Agriculture and Life Sciences at Virginia Polytechnic Institute and State University, Blacksburg, Virginia.

Michael Looper, Booneville, Arkansas, received a 2010 Presidential Early Career Award for Scientists and Engineers, the highest honor bestowed by the United States government on science and engineering professionals in the early stages of their independent research careers.

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

- Over 160 refereed journal articles published
- Over 100 invited presentations at national and international symposia
- Application for two new patents
- Seven new cooperative research and development agreements with stakeholders
- Over 30 new scientific technologies developed relating to genomics and other research, and
- Administration or development of 6 web sites for stakeholders

In 2010 NP 101 scientists participated in research collaborations with scientists in: Australia, Brazil, Canada, China, Czech Republic, Denmark, France, India, Ireland, Italy, Kazakhstan, Kenya, Mexico, Netherlands, New Zealand, Pakistan, Russia, Scotland, Spain, Sweden, Switzerland, Tunisia and United Kingdom.