

# NRSP 8, National Animal Genome Research Program

**Duration:** 10/01/18 – 9/30/23

## Prerequisite Criteria

*How is the NRSP consistent with the mission?*

## INTRODUCTION

Livestock and poultry are top US agricultural commodities accounting for more than half of the agricultural cash receipts, at least \$100 billion each year. On the other hand, the US imports ~90% of its seafood, at a deficit of more than \$14 billion per year. Therefore, advances in livestock, poultry and aquaculture production capacity and efficiency are essential to advance national and global food security, especially with increasing consumer demand for animal welfare, growing restrictions on antibiotic use, and changing environments. To enable agri-animal industries to increase production and meet this growing demand, we need robust animals with superior health and production traits. A major requirement for increasing production efficiency is genetically improved strains of animals with sufficient genetic diversity to allow continued improvements in traits including yield, disease and pest resistance, efficient reproduction, and stress tolerance, while assuring nutritional quality and animal welfare. The continued development of tools that enable genomic selection for production, disease resistance and genetic diversity will greatly benefit these agri-animal industries.

Infrastructure, including genomic tools (e.g., maps, annotated reference genome assemblies, genotyping platforms), integrative bioinformatics tools, databases and genetic resource populations play a critical role in enabling genomic discoveries in livestock, poultry and aquaculture species. Since 2003, NRSP-8 National Animal Genome Research Program (NAGRP) has played a major role in enabling genomic discoveries in livestock, poultry and aquaculture species. As outlined in the “2014 USDA Research, Education, and Economics Action Plan,” ([https://www.ree.usda.gov/ree/news/USDA\\_REE\\_Action\\_Plan\\_03-2014.pdf](https://www.ree.usda.gov/ree/news/USDA_REE_Action_Plan_03-2014.pdf)) infrastructure is the critical foundation upon which genomics-oriented discovery science is built; and these tools, coupled with the education and training of students, scientists, and the public, are critical to translating genomic discoveries into substantial advances in agricultural practices. *The mission of NRSP-8 is to develop and sustain these crucial infrastructure components.* This infrastructure is, in turn, used to leverage additional funding for agri-animal genomics research from both public and private sources. As detailed in the **Past Successes** section and the **Accomplishments Report**, NRSP-8 has been highly successful in the previous period in substantially advancing animal genomic infrastructure, catalyzing a broad array of research activities resulting in **> \$94 million dollars in leveraged funds**, and facilitating communication across all agri-animal species groups. Prior success and the rapidly evolving and complex genomic technologies and landscape underscore the need for continuation of NRSP-8 and its mission of supporting the agri-animal genomics research community and industry partners.

The constant advancement of next-generation sequencing (NGS) technologies and assay applications and the exponential decreases in sequencing costs and increases in throughput, have produced seismic shifts in research approaches and have substantially broadened the scope of animal genomics. For example, while production of high-quality annotated reference genomes for agricultural animals remains a considerable undertaking—the infrastructure needed to assemble billions of multi-platform reads, annotate genes, genome features, and nucleotide variants, and curate this information in a manner accessible to

stakeholders—outcomes far outweigh the sequencing costs. As whole genome sequences become available for most target species, broad NGS re-sequencing efforts and high-throughput genotyping arrays (‘chips’) have become valuable approaches for characterizing variation in breeds and strains, and for linking this variation to economically relevant phenotypes. In the past, reference genome assemblies were mostly generated at large sequencing centers, today NGS has “democratized” sequencing such that most universities and many companies can now use it to study their own populations of interest. These changing strategies are rapidly generating enormous datasets that have quickly overcome the informatics resources within individual labs and small species groups. These new “big data” challenges are reflected in our updated objectives for this renewal, as briefly outlined below and expanded on in the **Objectives section**. Harnessing the power of big data in agri-animal genomics research is only possible through coordinated teamwork efforts such as those successfully exhibited by the NRSP-8 species consortia.

NRSP-8 is an umbrella organization to promote the needs of the animal genomics community. With limited funds available to species coordinators, NRSP-8 helps to provide critical infrastructure for agri-animal genomic discoveries including genomics and bioinformatics tools and databases, genetic resource populations with economically-important phenotypes, and education and training of students, scientists, and the public.

Our first objective is to advance the quality of reference genomes for all agri-animal species through providing high contiguity assemblies, deep functional annotations of these assemblies, and comparison across species to understand structure and function of animal genomes. The NRSP-8 community, organized around species groups, the AnGenMap list-server, and NRSP-8 meetings in conjunction with the annual Plant and Animal Genome Conference (PAG), provides the core infrastructure and leadership necessary for organizing these efforts, including sharing of DNA resources, collaborative use of computational power, and community-based genome annotation.

Our second objective is to advance genome-to-phenome prediction by implementing strategies to identify and validate genes and allelic variants predictive of biologically and economically important phenotypes and traits. The tremendous power of genome-wide variant analysis is leading to the identification of markers linked to important production traits in agri-animal species. These analyses also suggest the involvement of candidate genes, whose functions are often unknown in the studied species. NRSP-8 support is critical to developing powerful functional “-omic” strategies, from improved annotation to proteomics, metabolomics, metagenomics, and metatranscriptomics to knock-out/down and genome-editing approaches.

Our third objective is to advance analysis, curation, storage, application, and reuse of heterogeneous big data to facilitate genome-to-phenome research in agricultural animal species of agricultural interest. This bioinformatic capacity is a critical component of infrastructure support enabled by NRSP-8. NRSP-8-supported approaches in this area include continued expansion of the tools and capabilities of the bioinformatics coordination program (<http://www.animalgenome.org/>), development of community-wide pipelines and portals for variant analysis and curation, training of students, scientists, and stakeholders in high-throughput data analysis, and development of collaborative platforms that facilitate species-group level access to timely genomic data.

Across all objectives of this renewal, the NRSP-8 proposes to continue providing enabling technologies and support activities, and to disseminate new data/genetic material across the animal research community. The organizational structure of NRSP-8 serves to bring together domestic scientists within a given livestock/poultry/aquaculture group, and facilitate rapid transfer of successful approaches to commercial

national and international stakeholders.

“Blueprint for USDA Efforts in Agricultural Animal Genomics 2008-2017,” was used as a guide in formulating the objectives for the previous NRSP-8 objectives. While this proposal was due for submission, a new Blueprint document “Genome to Phenome: An USDA Blueprint for Animal Production” was being prepared. The updated blueprint, when available will be used as a guide to adjust the objectives of this proposal.

*How does this NRSP pertain as a national issue?*

#### **A. National Scope**

The membership of the NRSP-8 encompasses scientists from the dairy and beef cattle, poultry, equine, sheep, goat, swine, and aquaculture sectors, and is impacting agriculture in every state and region of the U.S. The use of genomics to improve the genetics of US animal-based commodities has been adopted by nearly all the food and fiber animal-breeding industries for which genomic tools have been developed. NRSP-8 scientists across the country were instrumental in creating many of these genomic tools, showing the broad scope and applicability of the NRSP-8 project.

Another indication of the broad scope of NRSP-8 can be seen in the participation in and utilization of NRSP-supported forums, tools, and conferences. The AnGenMap discussion server has about 4,000 members across the nation and around the world, of them about 3,000 are on AnGenMap mailing list. The QTLdb program, developed by the NRSP-8 Bioinformatics Coordination Project team, is used by hundreds of scientists globally- for example, QTLdb for cattle has been cited in over 770 peer-reviewed publications. Similarly, the Plant and Animal Genome (PAG) conferences are held jointly with the annual NRSP-8 meeting, with 776 animal genome scientists participating in this international meeting in 2017; cumulatively over 9,200 animal genome scientists have attended PAG from 1999 to 2017. The chance to communicate with colleagues throughout the genomics community and to access the most recent developments from genomics industry representatives has been critical for much of the past progress outlined under the Past Successes section and the Accomplishments report.

In addition to these broad indications of the importance, impact and national scope of NRSP-8 activities, animal genomics research can be directly related to goals and challenges put forth in two recent national policy documents on agricultural research, education and engagement:

1. Animal genomics is directly relevant to two Strategic Goals (SG) in the document “2014 USDA Research, Education, and Economics Action Plan” introduced above—SG#3 “Help America promote agricultural production and biotechnology exports as America works to increase food security” and SG#4 “Ensure That All of America’s Children Have Access to Safe, Nutritious, and Balanced Meals.” In SG#3, animal genomics has a national role in Strategy #2 – “USDA will generate fundamental knowledge through research in genomic sciences and biotechnology to enhance agricultural sustainability and productivity.” Genomics is accelerating the genetic improvement in sustainable production through increasing feed efficiency in cattle, pigs and poultry as well as other major commodities. In addition, animal genomics has a clear role to play in improving resilience of animals to infectious disease, and thus addresses ‘sustainability and productivity’ as well as the safety of animal food products (SG#4). Public health is also impacted as many animal pathogens also infect people.

2. In the just-published document “The Challenge of Change” (<http://www.aplu.org/projects-and-initiatives/international-programs/challenge-of-change/index.html>), the overarching Grand Challenge is described as “Sustainably feed an expanding population and improve prospects for food and nutrition security for all.” The specific Grand Challenges in this document are described in detail in the Rationale section. Here, we highlight that animal genomics is directly addressing several of the listed challenges, including those related to *Food Availability* through genetic improvement. These include Challenge 1 “Increase yields, profitability, and environmental sustainability simultaneously,” and Challenge 2 “Develop the varieties and breeds needed for sustainable food systems.” NRSP-8 scientists are also addressing Challenges related to *Food Access* including “Create and share resources that serve all populations,” as many of the efforts in NRSP-8 focus on creation of genetic/genomic information resources that anyone nationally or globally can use for genetic research and improved food access. Finally, as discussed above, animal genomics research is directly addressing the *Food Utilization* Challenge 7 “Ensure a safe and secure food supply that protects and improves public health” through research on identifying the genetic architecture of animal resilience to pathogens that can cause human disease, and creating tools to improve such resilience.

The applicability of animal genomic research (and its support via NRSP-8) to a wide array of national issues and animal production needs is reflected both in recent USDA-NIFA proposal requests, which often incorporate a genomics component, and in the diverse applications of the genomic techniques employed by USDA-affiliated researchers. Many modern biological questions, especially those related to practical questions related to food and agricultural research, now use genome-wide tools for screening, detection, and analysis of genes, RNAs and proteins. These projects range from nutritional genomics to comparative immunology to marker-assisted breeding, but often share the same core genomic technologies and needs for bioinformatics support. For example, an algorithm developed originally for swine genome variant analysis in North Carolina may be readily adapted by researchers working with similar data in chicken populations in Arkansas.

## **B. Continued National Need for Genomic Tools and Resources**

As detailed above, the NRSP-8 mission closely aligns with the challenges described in “2014 USDA Research, Education, and Economics Action Plan” and “The Challenge of Change.” These challenges for food production are long-term in nature and are heightened by rising world human populations and environmental obstacles such as climate change. As animal genomic tools and technologies are increasingly integrated into the breeding and production practices of a broad range of species, the need for national genomics infrastructure support (as provided by NRSP-8) is only expected to increase. While genomics has been applied primarily to breeding and selection, a key deliverable is enhanced biological information on traits of interest. Such information can be applied in other research areas important for animal science, including nutrition, reproduction, meat science, welfare, and disease resistance.

Whole genome reference sequences for several species groups were delivered and/or refined in the last five years, while sequencing was initiated and nears completion in several others. **The focus of the proposed renewal turns, therefore, from the structural assembly of primary “reference” sequences to the further refinement of these resources and the capture and utilization of trait-affecting genome variation through a variety of approaches.** These new approaches are based on having the reference assembly in hand and therefore depend on the quality of this initial reference sequence. It is difficult to overstate the magnitude of this change, which can be compared to parallel developments in computing and digital communications. When NRSP-8 began in the 1990s, few among us expected that we would see

complete genome sequences available for our species, and many of our stakeholders found minimal relevance of genomics to their work. *Today, many, if not most, breeding companies across the nation and the world are routinely obtaining whole genome sequences for representative individuals from production lines* and can do so in a matter of weeks or days! This progression marks an exciting era for animal genomics, as diverse phenotypes are connected to genotypes and science translates to practice. However, this transition is also marked by significant new challenges. These include, among others, development of databases suitable for holding and examining, and querying vast amounts of re-sequence data, and development of data and tools to facilitate multilevel functional annotation and curation of genome assemblies to maximize the value of genome-wide association studies (GWAS). While many GWAS studies identify single nucleotide polymorphisms (SNPs) associated with phenotypes in animal populations, such SNPs commonly occur outside of the coding portions of genes. These regions may regulate the expression of genes and are often in more highly variable regions of the genome; thus, these results may not be transferable to another population within the same species or even to crossbred animals including the breed for which the GWAS was performed. One way to increase the value of GWAS results is to identify those variants that impart functional changes. Such variants, if present in other populations, are much more likely to also control phenotypic variation in these other populations. Identifying functional variants/SNPs is one of the objectives of the newly organized Functional Annotation of Animal Genomes (FAANG) consortium, and for which NRSP-8 researchers are integral members. As commercial stakeholders/collaborators increasingly implement genome-enabled animal selection programs, portals for data access and entry of phenotypic information will need to become more sophisticated, and yet more user-friendly. NRSP-8 funding will continue to be needed to address these diverse and evolving national challenges.

The structure, past success, and established interpersonal relationships of NRSP-8 and its members are tremendous assets in facing the new realities of animal genome sciences. Additionally, the broad participation of members with expertise across species and sub-disciplines (e.g., transcriptomics, SNP mapping, functional genomics databases, and bioinformatic tools) allows for rapid dissemination of genome advances and provides a larger combined base of expertise available to the animal genomics stakeholder community. These aspects of NRSP-8 strongly position it for continued success in its mission to enhance the global infrastructure for agricultural animal genomics.

## **RATIONALE**

### *Priority Established by ESCOP/ESS*

NRSP-8 leverages funding to enhance the sharing of genomic resources: tools, reagents, data, animal populations, and bioinformatics. The resulting products support the research community, commodity groups, industry and government regulatory agencies by providing efficient and accurate tools and information on genome sequences, genetic variation, and the relationship of genotype to phenotype that can be broadly applied in many ways. Below is a summary of the relationship of animal genomics research, for which NRSP-8 provides the necessary infrastructure, to help combating the seven food security challenge areas determined by the “Challenge of Change commission.” APLU (Association of Public and Land-grant Universities) established this commission to identify food security challenges and make recommendations on the actions needed to meet global food demands by 2050.

**Grand Challenge 1:** *We must enhance the yields, profitability and environmental sustainability of food and agricultural systems.*

Improvement of feed conversion ratios via genetic selection decreases impact of livestock production upon environment. A key means by which advances in agricultural production can be made is through selection of animals with superior trait performance (e.g., carcass yield, disease resistance, feed-conversion ratio, robustness, athleticism). While applying genetic tools to improve production and resilience of animals, we must account for animal health and welfare, as well as social, cultural, and ethical considerations. Genetic methods of improvement must become more efficient while minimizing environmental impacts. Genomics selection of superior genotypes will help addressing this challenge i.e. enhancing the animal production yields and profitability while reducing the adverse environmental impacts.

**Grand Challenge 2:** *We must develop the breeds needed for sustainable food systems to adapt to rapidly growing human population, along with climate change and weather variability.*

Genome-enabled selection practices need to increasingly account for the effects of genotype on the utilization and assimilation of different animal diets and the potential downstream environmental impacts. Cross-disciplinary research in nutrition and genomics promises tailored diets to maximize genetic growth potential while minimizing environmental impact. Additionally, genomics can enhance selection of animals better adapted for changing climatic conditions. Sustainable management includes efficient livestock utilization of nutrients, water, and space with high survival and minimal environmental impact. Selection of animals best suited for production in a given environment via genomic technologies (precision management systems) optimizes agricultural sustainability.

**Grand Challenge 3:** *We must take measures to decrease food loss and waste through more efficient distribution systems.*

Pre- and post- harvesting environments affect shelf-life, nutritional content and quality of food-animal products. Various genomics approaches allow understanding the biochemical processes through which the animal interacts with the environment pre-, post- and during the harvesting process. Genomics research on local breeds and species will allow us to optimize regionally available food systems. Selection of animals best suited for production in a given environment via genomic technologies (precision management systems) can reduce food loss and waste by creating efficient local distribution systems and by selection for animals that produce products with improved shelf-life and quality.

Also, we must expand genetics/genomics education so that specialists in small urban communities are trained to develop opportunities for urban agriculture to increase availability of nutritious food options in urban environments.

**Grand Challenge 4:** *We must create and share resources that serve all populations.*

We must provide genomics-based advice and education domestically and globally to increase access to the best and regionally most suitable animal management and breeding practices. Animal genomics research must contribute to ‘big data’ for the assessment of needs based on geocoded information on nutritional outcomes and food distribution.

**Grand Challenge 5:** *Ensure inclusive and equitable food systems.*

Healthy, reasonably-priced animal protein choices are the result of vigorous and profitable animal agriculture industries. A profitable and growing agricultural sector leads to strong farm families and farm

communities. Agri-animal genomics is focused on enhancing animal improvement programs to lower production costs, increase throughput and yields and decrease animal disease, thereby increasing profitability. Concurrently, these genomic technologies can add aspects of sustainability and biosecurity to production practices, leading to long-term market stability.

**Grand Challenge 6:** *We must address the dual burdens of undernutrition and obesity to ensure full human potential.*

Animal products are excellent source of proteins, fats, vitamins and minerals. Animal proteins contain all the essential amino acids needed for healthy growth especially in children. Genome-based enhancement of beneficial nutritional profiles of livestock can lead to healthier dietary options and improved human health affected by both undernutrition and overnutrition. In addition, models of overnutrition and obesity in livestock species (e.g. swine, equine) provide a unique opportunity to study the molecular pathophysiology of these diseases and underlying genetic susceptibilities.

**Grand Challenge 7:** *Ensure a safe and secure food supply that protects and improves public health.*

Genomics can enhance the safety of the food supply through animal identity and traceability systems based on molecular markers. Genomics allows rapid selection of lines of livestock resistant to infection, increasing animal welfare while optimizing productivity. Animal genomics research must collaborate with veterinary and human medicine to improve our understanding of the animal-human-environmental health continuum through the ONE Health initiative. Genomics-based selection must gradually reduce and find alternatives for the use of antibiotics in animal production. This is an important measure of treating antibiotic resistance in consumers of animal products.

## **RELEVANCE TO STAKEHOLDERS**

### **A. Stakeholders**

The membership of NRSP-8 includes researchers with an interest in animal genomes, and as such, they constitute the primary group benefiting directly from its activities. However, the beneficiaries are much broader than the participants. Obviously, genotype (the genome) and its relationship to biological function (the phenome) is of critical consideration for many disciplines of animal science whose researchers benefit from NRSP-8 supported resources and knowledge. International scientists are another important stakeholder group (**Figure 1**). The global animal research community, draws on the resources developed by NRSP-8, and the beneficiaries are the global agri-animal industries including commercial breeders, producers, and other entities that rely on agricultural animals. Ultimately, the general public constitutes the ultimate stakeholder group for the efforts of NRSP-8. Thus, it is hard to overstate the impact that accelerated genetic improvement enabled by genomic information has had on decreasing the global environmental footprint of animal protein production.

**Figure 1.** Worldwide distribution of ~3,000 members on AnGenMap server and/or mail list.



## B. Stakeholder Involvement

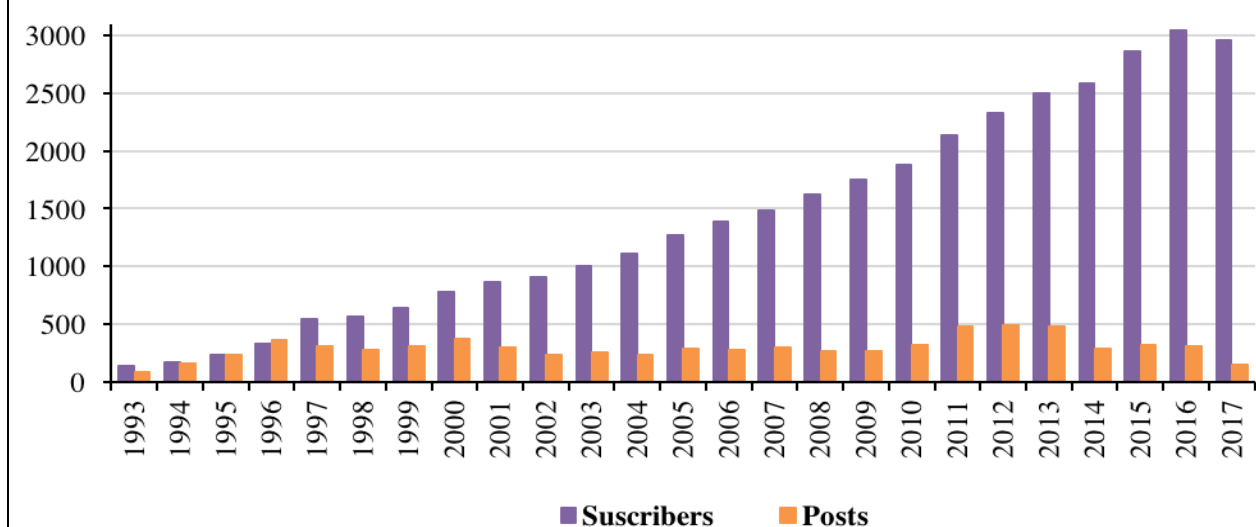
Members participate in governance and all interested parties can have input. One mechanism is via the NRSP-8 supported AnGenMap (<https://www.animalgenome.org/community/angenmap/>), which allows for daily conversation among the ~ 3,000 members, which has grown considerably over time (**Figure 2**). AnGenMap provides each species group with its own website, with links to maps, databases, newsletters, resources and community links, and these are combined at the Bioinformatics Coordination Site ([www.animalgenome.org](http://www.animalgenome.org)). NRSP-8- materials that provide objective science-based information in regard to animal genomics and agriculture are generated by species coordinators and member researchers who engage in education/training, interviews, and meetings/workshops. Each NRSP-8 species committee incorporates industry representatives that participate in governance, and many additional industry scientists and leaders attend PAG, utilize AnGenMap, receive newsletters and employ genomic tools/data deriving from NRSP-8-supported infrastructure.

The annual PAG meeting in San Diego is the largest agri-genomics meeting in the world, and hence, provides a unique opportunity for researchers from around the globe to come together and share research findings, discuss problems and plan for the future. Approximately one-third of the PAG animal scientist-attendees and one-third to one-half of AnGenMap members are international. Out of such discussions have come bold initiatives such as the 1000 Bull Genomes Project and Genomes and Functional Annotation of Animal Genomes (FAANG) Project. Additionally, this meeting attracts industry stakeholders who are keen to understand how genomic developments might be integrated into their genetic improvement programs.



Industries are beneficiaries of the genomic advancements, and a number are now using genomic information to accelerate the rate of genetic improvement. Companies are directly contributing funds, in kind support and genetic resources to help advance genomic understanding. For example, the University of Missouri, in collaboration with GeneSeek, developed an Illumina SNP-chip for genotyping 250,000 locations in the beef cattle genome (GGP F250). The assay was designed using sequence data from the 1000 Bull Genomes Project and over 400 individuals sequenced from multiple taurine breeds, for which some of the sequencing was supported by breed associations who will ultimately benefit from the research. Similarly, companies from other animal industries have been active collaborators and often co-funders of re-sequencing, GWAS, and applied genomic selection experiments of relevance to their industry.

**Figure 2.** Number of subscribers and post per year on the AnGenMap list serve. All data is cumulative per year except for 2017, which is cumulative through August 1, 2017.



### C. Renewal Justification.

As can be seen from the **2013-2017 Accomplishment Report**, previous NRSP-8 funding assisted in genome reference assemblies and improvements for multiple species, with these improved assemblies eliminating most of the regions with ambiguous sequences and in some cases provided sequence for previously unsequenced autosomes (**2013-2017 objective 1**). During this time, one or more SNP genotyping arrays were created for all the major livestock, poultry and aquaculture species and alleles contributing to major economic traits were identified in all species (**2013-2017 objective 2**). In addition, bioinformatics platforms to facilitate collaborative research were developed including a collaborative VCF information-mining platform (**2013-2017 objective 3**). From 2013-2017, NRSP-8 participants leveraged the NRSP-8 investments in tools and infrastructure with more than \$94.5 million dollars of research funding towards investigating fundamental mechanisms of genome biology and physiology and pathophysiology affecting production efficiency, product quality, animal health, disease resistance and food safety.

This renewal seeks to advance the progress enabled by the initial sequencing efforts. It is hard to imagine that just 10 years ago, there were no high-density SNP chips being used in animal breeding programs. The

implementation of genomic selection is now routine in many industries, and over a million US dairy cows have been genotyped. Despite these successes, there are still vexing problems that remain in translating genomic data into useful information. Although many species now have reference genome assemblies, there remain significant gaps and mis-assemblies that complicate analysis and the discovery of genome to phenome relationships. Additionally, the importance of regulatory elements and noncoding regions of the genome on quantitative traits is becoming increasingly evident. Data from the human research community suggest that more than 80% of the SNPs associated with disease traits are in regulatory elements and non-coding regions. The ultimate goal of NRSP-8 is to understand genomic variation and translate that basic mechanistic research into application. Ideally the three objectives outlined in this renewal will result in new knowledge that will improve the utility and predictive ability of genomic information. As detailed below, research described under Objective 1 will be a particularly important contribution to the goals of the FAANG consortium by better identifying and annotating the functional elements that are important in regulating gene expression and ultimately phenotype. Objective 2 outlines specific aims that will be important in understanding trait variation and its genetic causes, and simultaneously developing agricultural animals as biological model systems while maximizing the economic gains from genetic and genomic selection. The advent of genome editing tools opens up an exciting opportunity to precisely investigate and dissect the genetic variation associated with quantitative trait variation. It is clear that the connection between the genome and phenotype is complex. Consequently, a wide group of scientists with diverse skills and expertise with access to high-throughput genomic tools and bioinformatics must work together to achieve an understanding of this connection in order to generate practical results of value for animal agriculture and human health. Objective 3, the analysis, curation, storage, application, and reuse of heterogeneous big data to facilitate genome-to-phenome research, is perhaps the most challenging. How will the tremendous amount of sequence data that is being generated, be curated and harvested into useful information? As commercial stakeholders/collaborators increasingly implement genome-enabled animal selection programs, data access and entry of phenotypic information will need to become more plug and play. This challenge of taking big genomic data and basic science and producing actionable, predictive information is perhaps the grand challenge of our time. While previous iterations of NRSP-8 were essential to produce the genomic information now available, these next five years will be the real challenge – and that is how to integrate data and systems thinking to produce knowledge that can be translated into the desired outcomes.

## OBJECTIVES

**Objective 1:** Advance the quality of reference genomes for all agri-animal species by providing high contiguity assemblies, deep functional annotations of these assemblies, and comparison across species to understand structure and function of animal genomes.

Recent advances in second and third generation sequencing technologies have enabled the generation of draft reference genome sequence assemblies for almost all economically important agricultural animals, as described in the Accomplishments Report from the current NRSP-8 cycle. However, these genome assemblies still contain numerous gaps and local mis-assemblies, especially for highly repetitive sequence regions, such as those found in centromeres. In some cases, whole chromosomes are absent/unassigned, such as the Y chromosome in some mammals and several micro-chromosomes for all the sequenced birds. Functional annotation, at the transcriptomic, proteomic and epigenetic levels, of accurate reference assemblies are essential for most genome-wide analyses, including the dissection of the genetic architecture of complex traits and enhanced breeding using genomic selection strategies. Furthermore, identifying conserved genomic elements across animal species will provide insights into gene function and underlying regulatory mechanisms. This objective advances the quality of reference genomes for all agri-animal species

through providing deeply annotated, high contiguity assemblies, obtained through comprehensive and integrated analyses of transcriptomic data with chromatin architecture and modification data across a wide range of tissues/cells and biological states. This Objective will provide a resource to enhance the research specifics in Objectives 2 and 3.

The specific aims for this objective include:

1. Initiate creation of draft genome assemblies for economically important species and breeds for which assemblies are not yet available.
2. Improve existing genome assemblies to close gaps and improve assembly order, especially for highly repetitive sequence regions, such as those in centromeres and on the sex chromosomes.
3. Coordinate analysis of re-sequencing data to identify SNPs, CNVs, and InDels, and better annotate gene models within the reference assemblies.
4. Develop and apply approaches for identifying and functionally annotating regulatory elements through comprehensive and integrated analyses of transcriptomic data with chromatin architecture and histone modification data across a wide range of tissues and cells at different biological states.
5. Associating functional information (e.g., tissue expression, physiological processes and interaction information) with regulatory and expression elements in the genomes.
6. Compare structural and functional components of genomes across animal species to understand biological function through identifying conserved genomic elements.
7. Expand the training of students and postdocs in application of next-generation technologies to structural and functional animal genomics.

**Objective 2:** Advance genome-to-phenome prediction by implementing strategies and tools to identify and validate genes and allelic variants predictive of biologically and economically important phenotypes and traits.

The goals of this Objective are to advance genome-to-phenome prediction by facilitating translation of genomic findings into biologically relevant information for genetic improvement of all species. To achieve this goal, genome-phenome association studies, functional validation methods, deep phenotype collection, comparative genomics, metagenomics and phenomics are important approaches that will produce valuable insights. In addition, analytic tool development to effectively leverage all information as well as implementation will be critical for agri-animal research communities to realize the potential of these findings to simultaneously develop agri-animals as biological model systems while maximizing the economic gains from genetic and genomic selection.

The specific aims for this objective include:

1. Exploit the power of high-resolution SNP-chips, genome re-sequencing, and genotyping-by-sequencing in genome-phenome association studies for detection and validation of genomic variants that are predictive of economically important phenotypes.
2. Advance strategies, models, algorithms, pipelines and analytic tools to facilitate the identification, validation and incorporation of novel genetic elements and causal and/or highly predictive variants to allow the most accurate prediction of phenotypic performance based on genotypes. Newly identified variants will be used in Objective 1 to further annotate genomes.
3. Develop and adopt various approaches, including (e.g., CRISPR/Cas9 genome editing) for functional analysis, and evaluation and verification of functional allelic variants of causal genes important for production traits.
4. Support deep phenotyping of important traits at the molecular, cellular, tissue and organismal levels, including the use of high-throughput technologies such as transcriptome sequencing, proteomics and

metabolomics studies, whole-animal parameter monitoring, and in vitro gene mutagenesis screening analyses and other tools to support precision monitoring.

5. Use comparative approaches to identify genetic variation within and across species that is associated with phenotypic variation that results from common treatments or environments, or between natural and domesticated populations.
6. Support comparative phenomics, with an emphasis on the use of farm-animal models that mimic human processes to benefit human health.
7. Develop well-characterized animal populations/genetic lines/models that allow for study of biology of various economically important phenotypes and traits.
8. Advance metagenomic studies to help in discovery of novel pathogens, understanding host-pathogen interaction and determining the role of microbiota in agri-animal nutrition, health and reproductive performance.
9. Train the next generation of animal breeders in applying and developing new methods based on high-throughput genomic data to make genetic progress.

**Objective 3:** Advance analysis, curation, storage, application, and reuse of heterogeneous big data to facilitate genome-to-phenome research in animal species of agricultural interest.

The genomic “Big Data” era is here. In the last five years, advances in next-generation DNA sequencing technologies have allowed to produce enormous amounts of data in all livestock, poultry and aquaculture species. To better understand the genetic mechanisms that underlie important traits, in the next five years agri-animal scientists will direct tremendous attention to data refining in addition to data collection. To achieve this goal, bioinformatics/computational tools, resources and expertise will be necessary on an unprecedented scale. The bioinformatics team of the NRSP-8 project will provide in-house bioinformatics tools, databases and resources in addition to assisting researchers to utilize other open-source tools and resources housed elsewhere. The team will provide resources for “real-time communication” to facilitate research coordination needed for Objectives 1 and 2. Furthermore, Objective 3 will address the need to train students/postdocs to be future leaders in agriculture-oriented computational science.

The specific aims for this objective include:

1. Facilitate livestock/poultry/aquaculture genomic research by development/promotion of data sharing standards, workflows and tools necessary to integrate these resources.
2. Facilitate communication and training within the livestock, poultry and aquaculture groups to promote community discussion and awareness of community needs, current events, available resources, and other items of interest.
3. Facilitate genome-wide research approaches to understand the genotype-to-phenotype basis of important traits in livestock, poultry and aquaculture through providing opportunities to curate and reuse data created by the community.
4. Help in training students/postdocs to be future leaders in agriculture-oriented computational science.

## **MANAGEMENT, BUDGET, AND BUSINESS PLAN**

### **A. Management and Activities Plan**

The purpose of NRSP-8 is to provide and/or enhance infrastructure for the animal genome community as a whole. NRSP-8 accomplishes its mission by working with a structure that is organized by animal species and managed by species-specific coordinators and co-coordinators. In addition, due to the need to address

the critical and rapidly growing need for data management and analysis, the infrastructure includes a bioinformatics coordinator and co-coordinators. These individuals facilitate the availability of shared genomic resources (e.g., tools, reagents, protocols, samples, and data) to the members of each species committee, often by leveraging the limited resources of the coordinator with those available from federal (e.g., NIH, USDA AFRI), international, industry, and state sources. The coordinators and co-coordinators, working with the members of their respective committees and amongst themselves, help to develop, stimulate and coordinate new initiatives by providing leadership that is recognized nationally and internationally. Finally, NRSP-8 fosters communication among its members and stakeholders through, among other things, e-mail newsletters and participation in meetings and conferences. Species coordinators and co-coordinators stimulate this communication and provide focal points for input from the committee members and other stakeholders.

The coordinator and co-coordinator model has served NRSP-8 well; it is flexible, and the structure allows for continuous refinements and shared responsibility. Coordinators and co-coordinator will meet with their respective species committee members at least once each year at annual meetings (e.g., typically the species workshop at PAG) and solicit ideas and plans for project development and resources to share. Coordinators will communicate by e-mail, newsletters, and other means to make resources known to community members and solicit input throughout the year. Coordinators and co-coordinators will meet with the NAGRP Director and Administrative Advisors at least once each year and as needed through conference calls and e-mail communications. Coordinators may employ subcommittees within each of the species committees to take on special tasks or to provide recommendations to the coordinator. The frequency of communication within and across each species group affords many opportunities for periodic review of the current management plan and potential revisions. This latter point is critical given how quickly the field of genomics advances and how new technologies can alter plans and objectives.

Application for species coordinators and co-coordinators will take place prior to funding, or when needed during the funded period. Either individual coordinators or co-coordinator groups may apply. When coordinators change, the out-going coordinator will work with the new coordinator to achieve a smooth transition, or in the case of group efforts, some co-coordinators may stay on while others change. In addition, each species committee has rotating chairs that interact with coordinators and may be suitable replacements or may assist during transitions. Applications will be solicited by the NIFA administrator 60 days in advance of the start date for an approved renewal proposal and be widely publicized. Applications shall include a 2-page letter of application and intent, complete *curriculum vitae*, and up to five letters of recommendation. The NIFA Administrator and the Regional Administrative Advisers shall review applications and select the coordinators based on merit, experience, and involvement within the species community.

As a federally-funded organization, we strive to make all reagents and information available to the entire public as soon as possible. Of particular note is the Bioinformatics Coordination webpage at [www.animalgenome.org](http://www.animalgenome.org). Due to growing inputs from companies and other organizations regarding intellectual property, efforts will be made to encourage sharing of information while still protecting their proprietary information, when needed.

## **B. Budget**

We request support of \$500,000 per year. Funds for the Bioinformatics Coordinator (\$110,000 per year) will be used for: (1) \$80,000 in salary costs for the individual that maintains and develops resources at [www.animalgenome.org](http://www.animalgenome.org), (2) \$20,000 in salary cost for a part-time post-doctoral fellow to support

bioinformatics analysis of FAANG related data, (3) \$3,000 to support host servers, and (4) \$7,000 to support Coordinator and PAG student travel. For details, see appendix titled Budget.

Each of the six Species Coordinators will receive \$65,000 per year. The requested funding will be used by the coordinators to provide for communication and sharing of resources to enhance the progress of the membership of the overall Technical Committee. Funds will not be used to directly fund their personal research programs. Based on past history, these funds likely will support the development and annotation of their respective genomes, subsidizing the generation of shared reagents (e.g., SNP chips), support to produce preliminary data for grant submissions, travel to PAG or other relevant meetings (**see Accomplishments Report**). These resources and services are essential for genomics-driven research, help form cohesion within each species group, and often provide preliminary data for larger efforts in the future. As noted in the Integration and Documentation section, the coordination funds are heavily leveraged, in the sense that they assist or provide seed resources that eventually generate Federal grant and/or industry funding to members. While many genomics tools have become more efficient in terms of cost-per-data unit, they still require a substantial expense to initiate and, thus, require coordination within each species community, as each has different needs. It is also important to note that, as a federally-funded organization, we strive to make all information generated available to the entire public as soon as possible.

### **C. Business Plan**

Species and bioinformatics coordinators work with the NIFA Director of the NAGRP each year to justify current and past expenditures and plan for future budget periods. Although the requested budget outlines the proposed distribution, this can be altered through discussions between the NAGRP Director and the coordinators, if special needs arise. The NAGRP Director in consultation with the Administrative Advisers makes the final decision annually as to the distribution of funds among the coordinators. As noted above, each coordination group will receive funding through a single Experiment Station budget affiliated with the coordinator or one of the co-coordinators. In addition to flexibility in annual budgets among NRSP-8 coordinators, we request that all coordinators (or coordinator groups), with permission of the relevant Experiment Station Director, be afforded the option of carrying funds over from one fiscal year to a subsequent fiscal year within the proposed 5-year project term. Opportunities to provide genomic resources change from year to year, and coordinators cannot predict what tool or resource will be most effective and useful to the genome community 3-5 years from now. Not only do the tools and resources change as new technology advances, but frequently a critical opportunity will require more support than is feasible within a single FY budget to a single coordinator. A carryover option would allow for more responsible allocation of resources within the overall 5-year plan.

## **INTEGRATION AND DOCUMENTATION OF RESEARCH SUPPORT**

### **A. Integration with extension or academic programs and use by other potential stakeholders**

Modern agriculture will require revolutionary steps to meet projected demands in the 21<sup>st</sup> century. Contemporary high-scale basic and applied agricultural genetics and genomics research necessitate high-level multidisciplinary collaboration between academic, government, private industry and international partners. Most projects are performed by multidisciplinary and collaborative teams consisting of experts in molecular and advanced genomic technologies, data management and statistical analysis of large “omic” datasets, specific phenotyping of large populations, and devising feasible downstream applications. External and internal research proposals to private, institutional, or federal funding agencies are typically evaluated to some degree on the quality, integration and specific components of the research team. Federal

funding opportunities sometimes require involvement of multi-disciplinary research teams. In addition, involvement of stakeholder, especially industrial, perspectives is very important. This integrated research team approach greatly strengthens the scientific discovery process and will continue for the foreseeable future of agriculture research.

The main mission of the NRSP-8 is to provide a structure in which collaborative animal genomics research teams can be established and succeed, and in which both fundamental and applied knowledge can be generated in the most efficient fashion. To accomplish this aim, six main research consortia for aquaculture, cattle, equine, poultry, sheep, and swine, joined by a bioinformatics team, meet regularly and continuously to share data, generate knowledge and provide expertise. Results of this animal genome research are presented at multiple regional, national, and international meetings, and published in a wide variety of peer-reviewed, publically -available journals. Furthermore, industry groups, in communication with applied and extension experts, will continue to be informed, acquiring major results and the translational implications of our research via trade journal articles written by scientists familiar with their reader's backgrounds and interests. We predict that the NAGRP bioinformatics website, individual species' websites, and genomics-related websites such as FAANG ([www.faaang.org](http://www.faaang.org)), will be increasingly utilized by research teams to communicate results to the public and, on a case by case basis, provide education materials to stakeholders. This means of communication will be actively encouraged by the species coordinators.

The NRSP-8 members serve the USDA educational mission. It is important to note that the vast majority of NRSP-8 members are in academicians and engage in teaching, extension services, and outreach as part of their daily responsibilities. Information and, in some cases, the support that these members receive from NRSP-8 assist them in these activities. Most NRSP-8 research is accomplished through the efforts of undergraduate and graduate students, as well as postdoctoral trainees. Thus, the collaborations generated by NRSP-8 directly influence the training and careers of these junior scientists who clearly represent our future scientific leaders. As noted below, the coordinators actively encourage and financially support the specific attendance of such lab trainees at our annual meetings and other relevant venues, thus providing opportunities for training the next generation animal breeders.

## **B. Partnerships and engagement**

The framework and partnerships generated in the existing NRSP-8 project will continue to be utilized and in many cases enhanced. Species-specific collaborations, websites, and databases, particularly within the NAGRP bioinformatics program, will be maintained. The NRSP-8 bioinformatics team has been receptive to users' suggestions and needs, and the current portfolio of sites, programs, and databases is a direct result of these interactions. Our programs will increasingly evaluate and use other platforms, such as CyVerse, to assist with the complex and computationally intensive tasks using supercomputing cyber-infrastructure. This program takes advantage of the more universal aspects of high-throughput sequence and genotype analysis to provide a common means to perform our work and enable data sharing. This area is rapidly changing, and we are open to evaluating new systems for data management and analysis that meet our needs and promote efficient sharing of data and technologies. This is especially true for the International FAANG Consortium. It is expected that significant amount of epigenomic data will be generated and shared with the animal genome community nationally and internationally.

The ability of the NRSP-8 program to leverage acquisition of additional animal genomics research funds is supported by data indicating that between 2013 and 2017 NRSP-8 members leveraged funds to acquire an additional **\$84,292,482** in federal, **\$5,753,434** in industry and **\$4,440,844** in internal funding to support

animal genomics research. These successes are encouraging and likely indicate our success in providing information that industry sees the generated information as being essential to achieving their goals. Further, NRSP-8 researchers were instrumental in additional new funding being directed to animal genomics research through the USDA NIFA AFRI program; in 2018, it is expected that \$5 million will be provided for development of resources for agri-animal functional genomics research associated with the FAANG consortium.

Species coordinators and, indeed, many NRSP-8 members have close relationships with relevant animal agriculture industries and engage in joint projects with, or receive financial support from these companies. As noted below, industry is well represented and actively participates in our annual meetings. In the past five years, many breeding companies have embraced genomics methods (dense SNP genotyping, genomic selection, etc.) and have directly contributed to NRSP-8 efforts. As a result, NRSP-8-industry cooperation has grown in parallel, and we anticipate that this trend will continue.

### **C. Support of research activities nationwide**

We will continue to utilize annual species group meetings, currently associated with the annual PAG conference. With a total annual attendance of ~3,400, PAG is the largest international scientific conference reporting on non-human genomics research. Over the course of five days, numerous opportunities are available for presenting and discussing current and future research and promoting essential interactions within and across species groups. This has often been the means by which multi-disciplinary research teams are brought together and the momentum of established teams is maintained. The NRSP-8 and PAG meeting has also been a major opportunity for the animal genomics community to acquire knowledge on advances and the newest product offerings from the private sector, including the latest high throughput sequencing and genotyping technologies and the means of storing, analyzing, and sharing data. The PAG meeting is also an efficient mechanism by which the needs of the research communities and the stakeholders can be brought to the attention of the species coordinators for group discussion and potential support from their coordinator funds.

The PAG meeting attendance has increased by 30% since 2010, and total scientific attendance in 2017 was 3,399, with 57% U.S. attendees and 43% international attendees. Of those attendees, 776 indicated an affiliation with the animal genome programs. Overall, >1,700 scientific abstracts were submitted, and 121 scientific and 27 industry workshops were organized. Animal-related workshops at the 2017 PAG conference included Aquaculture, Buffalo Project, Cat & Dog, Cattle/Sheep/Goat, Camelids, Equine, Poultry, Cattle/Swine workshop, Animal Epigenetics, Animal Genomics and Adaptation to Climate Change, Avian Genomics-Going Wild, Domestication Genomics, and the multi-species NRSP-8 Animal Genome workshop. General workshops of interest to animal genome researchers included, but were not limited to, Functional Genomics, Gene Expression Analysis, Gene Introgression, Host-Microbe Interactions, NCBI, Sequencing Complex Genomes, and FAANG. In addition to NRSP-8 lab scientists, the various relevant commodity groups and Federal agencies are well represented at the PAG meeting and are encouraged to participate in our meetings. Representatives of national media are also in attendance.

The species coordinators have traditionally invested their funds in the promotion of communication and efforts that enhance the entire group's effort (see Accomplishments report). Examples include partial PAG meeting travel support for graduate and postdoctoral students, support of the AnGenMap forum, support of scientific meetings of a more specific nature that occur outside of the main NRSP-8 venue at PAG, and specific activities that generate essential group tools and resources, such as SNP panels and arrays, HapMap data, microarrays, and now certain essential whole genome and/or RNA sequencing, and



epigenomic data. We envision that this flexible and diverse use of funds will continue.

## **Outreach and Communications Plan**

**Target Audience.** The primary beneficiaries of NRSP-8 include:

1. Research scientists directly engaged in animal genome research.;
2. Scientists utilizing genomic data in complementary areas of animal science and veterinary medicine.;
3. Graduate and postdoctoral students who benefit from training opportunities in animal genomics.;
4. Commercial animal breeders and producers who apply genomic data and related technologies to enhance animal health, welfare, productivity, and management.: and
5. Government agencies and breed organizations utilizing genomic methods for animal identification, disease surveillance, and regulatory monitoring.

Support of research, education, and communication activities in animal genomics also benefits all consumers of animal agriculture through resulting improvements in the quality, safety, wholesomeness, economic efficiencies, and environmental soundness of animal products and production systems.

**Engagement of Target Audiences.** Research scientists will continue to be engaged through NRSP-8 visibility at national and international scientific meetings/workshops. The leading example of this engagement is the annual International Plant and Animal Genome (PAG) Conference. NRSP-8 is showcased in species-specific and comparative genomics sessions. In each species-specific workshop, station reports are required from scientists at participating Experiment Stations. NRSP-8 has held its annual meeting jointly with PAG for 16 years and NRSP-8 representatives play a major role in the organization and programming for this high-profile conference. PAG is also a primary avenue for engagement of the next generation of animal genomic researchers. Each species supports a competitive award for graduate student travel to the annual PAG conference; and most species coordinators also provide additional travel support for graduate students and postdoctoral fellows presenting their work. Participation by students at this conference ensures early exposure to animal genomics research and its applications. Additionally, the Poultry Genome Coordinator, Swine Genome Coordinator, and Aquaculture Genome Coordinator each publish separate newsletters that go well beyond the actual members of NRSP-8 and are circulated via the AnGenMap listserv to about 3,000 scientists, students, and extension specialists.

**Engagement of Stakeholders.** The genome committee for each animal species will have one or more representatives from an industry group or other appropriate stakeholder selected in consultation with national industry organizations. Industry participants will be invited to attend all technical committee meetings and serve as liaisons between industry and the committee and the species coordinators. Species coordinators will continue to present and interact at national and regional producer meetings, breed organizations and other appropriate venues. Coordinators will also facilitate communication of research outcomes to the general public. Currently the poultry, swine and aquaculture coordinators circulate quarterly genome newsletters. Moving forward all species coordinators will provide quarterly newsletters applicable to target audiences and stakeholders. The AnGenMap discussion group will also be used to engage stakeholders worldwide.

**Measurement of Accomplishments and Impacts.** Scientific productivity is the most important measurements of NRSP-8 impact. The species committees in conjunction with the species coordinators will document scientific productivity in an annual progress report. These reports will detail the scientific accomplishments including:

1. Published peer-reviewed scientific papers;
2. Presentations at scientific meetings by coordinators and NRSP-8 members;
3. Scientists trained in animal genomics and bioinformatics by NRSP-8 members while contributing NRSP-8 projects;
4. Attendance at the PAG species workshops, the PAG NRSP-8 workshop and the technical committee meeting; and
5. Additional funding obtained by NRSP-8 members from leveraging NRSP-8 investments in animal genomics.

**Communication of Activities, Accomplishments, and Impact.** Annual technical committee meetings facilitate interactions between scientists working with different animal species. NRSP-8 will continue to coordinate its meetings with other multi-state technical committees and with scientific conferences and workshops including the PAG meeting. NRSP-8 members communicate advances in genomics through invited presentations at scientific conferences, offering information and technology transfer among international scientists across species groups and with researchers in public and private sectors. AnGenMap, an online discussion group for the animal genomics community, includes about 3,000 members from more than 50 countries/regions, continues to be used for communication among scientists (**Figures 1 and 2**). Each species has a genome page established by NCBI that includes access and direct links to existing genomic databases and related resources.

Other mechanisms of communication include the species-specific quarterly genome newsletters that communicate scientific advances to both scientists and interested non-scientists. Scientific advances are disseminated to the public through popular press articles, webinars and industry presentations. Species-specific genome webpages reach agricultural scientists, industry members, consumers, students and others interested in the application of genomics to animal agriculture. These homepages, constructed and maintained by individual animal species coordinators, frequently provide additional information and helpful links to genomic resources within the agricultural research community. Coordinators and other members of NRSP-8 promote advances in genomics for their respective species through the development and promotion of meetings involving stakeholder groups. NRSP-8 leaders will continue to participate in the writing of white papers and other activities to advance animal genome research. Such activities have proven critical in attracting the cooperation of the NSF, NIH, international consortia, industrial partners, and breed organizations for animal agricultural genomics endeavors.

**Distribution of Research Results.** The primary in-house mechanism for distribution of results and accomplishments will be via annual reports (available on NIMSS). The technical committee chair prepares summary reports with input from the species chairs and species coordinators. In addition to reporting results and accomplishments, annual reports outline future work plans for each species. Other reporting mechanisms include peer-reviewed research publications and reviews, as well as conference presentations. A majority of the requested funding is for species coordinators to distribute among community driven projects. To better promote and share these project results, they will be featured on the [www.animalgenome.org](http://www.animalgenome.org) site with direct links to any genomic data that is generated from these projects. This will extend the impact of these projects and promote interaction among species groups.

### **Past Successes**

NRSP-8 impacts are best measured by the major milestones in animal genomics as listed in the attached Accomplishments Report. Most targeted species have advanced past the whole genome sequencing phase

with the position of genes determined to a large extent, allowing dissection of the functional polymorphisms responsible for the variation of economically important traits. This reflects extensive coordination of effort among scientists, facilitated in no small part by effective outreach and communication strategies of NRSP-8. The project has made good use of its annual technical committee meetings, species and comparative workshops, newsletters, and internet home pages to foster effective communication between member scientists and other stakeholders worldwide. These efforts have achieved the advancement of animal genomics at a pace that has substantially exceeded most predictions.

**TABLE 1. NRSP-8 BUDGET REQUEST FEDERAL FISCAL YEAR (FFY) 2019-2023**

<b>Coordination group</b>	<b>FFY 2019</b>	<b>FFY 2020</b>	<b>FFY 2021</b>	<b>FFY 2022</b>	<b>FFY 2023</b>
Aquaculture	\$65,000.00	\$65,000.00	\$65,000.00	\$65,000.00	\$65,000.00
Cattle	\$65,000.00	\$65,000.00	\$65,000.00	\$65,000.00	\$65,000.00
Horse	\$65,000.00	\$65,000.00	\$65,000.00	\$65,000.00	\$65,000.00
Poultry	\$65,000.00	\$65,000.00	\$65,000.00	\$65,000.00	\$65,000.00
Sheep/goat	\$65,000.00	\$65,000.00	\$65,000.00	\$65,000.00	\$65,000.00
Swine	\$65,000.00	\$65,000.00	\$65,000.00	\$65,000.00	\$65,000.00
Bioinformatics	\$110,000.00	\$110,000.00	\$110,000.00	\$110,000.00	\$110,000.00
<b>Total</b>	<b>\$500,000.00</b>	<b>\$500,000.00</b>	<b>\$500,000.00</b>	<b>\$500,000.00</b>	<b>\$500,000.00</b>

## EXAMPLES OF PAST COORDINATOR EXPENSES

Year	2013	2014	2015	2016
<b>Aquaculture</b>	Improving the Rainbow Trout Genome Assembly using Molecuro Technology	Resource coordination workshops focused on oysters and other shellfish	Speaker Travel Awards (4 Students to PAG)	Functional Annotation of All Salmonid Genomes (FAASG) Workshop
<b>Cattle</b>	Support in the development of the cattle (Dominette) Optical Map; Dominette Illumina sequencing; PAG Awards and travel	Development of the new cattle (Dominette) reference assembly: PacBio genomic sequencing; PAG Awards and travel.	Development of the new cattle (Dominette) reference assembly: PacBio genomic and IsoSeq sequencing, Bioinformatics analysis, Dovetail Chicago Library; FAANG cattle purchase support; PAG Awards and travel.	Development of the new cattle (Dominette) reference assembly: PacBio IsoSeq sequencing, Illumina sequencing, Dovetail HiC library; PAG Awards and travel.
<b>Horse</b>	Student travel to PAG; Website development; SNP Chip development	Student travel to PAG; matching funds for SNP chip development	Student travel to PAG; Matching funds for FAANG-related activities	Student travel to PAG; Matching funds for reference genome work
<b>Poultry</b>	Student travel to PAG; infrastructure/staff support of genetic lines and well-characterized phenotypes & physiological studies	Student travel to PAG; infrastructure/staff support of genetic lines and well-characterized phenotypes & physiological studies	Support to Warren/Cheng/Brown leveraging USDA & stakeholder funding to improve the chicken genome assembly (SNP genotyping)	Improving the chicken genome draft sequence by PacBio sequencing (Washington Univ, Warren)
<b>Sheep/goat</b>	Contribution to the sheep reference genome assembly, Support NRSP8 member and student travel to NRSP8, ISGC, IGGC meetings	Purchase HD genotyping chips for sheep projects, Contribution to improved sheep reference genome, Support NRSP8 member and student travel to NRSP8, ISGC, IGGC meetings	Purchase HD genotyping chips for sheep projects, Contribution to improved sheep, Support NRSP8 member and student travel to NRSP8, ISGC, IGGC meetings reference genome	Purchase of reagents and supplies for sample collection to enable FAANG sheep genome annotation, Support NRSP8 member and student travel to NRSP8, ISGC, IGGC meetings
<b>Swine</b>	Travel: Jorgenson Travel Award winner, Workshop speakers, new Subcommittee members. Support for PEDV genotyping project and FAANG pilot project	Travel: Workshop speakers. Validation of Affymetrix 650K Genotyping chip	Support for Multi-station research project on Iso-seq analysis.	Support for Multi-station FAANG research, and bioinformatics support staff
<b>Bioinformatics</b>	PRRS Host Genome Consortium (PHGC) Database <a href="https://www.animalgenome.org/lunney/">https://www.animalgenome.org/lunney/</a>	Bioinformatics support for Epigenetics Group (multiple species)	Striped Bass Genome Database ( <a href="https://www.animalgenome.org/bioinfo/services/">https://www.animalgenome.org/bioinfo/services/</a> )	Support for Functional Annotation of Animal Genomes <a href="https://www.faang.org/">https://www.faang.org/</a>

## SUMMARY OF NRSP-8 ACCOMPLISHMENTS (2013-2017)

### **Overview of accomplishments for all NRSP-8 technical committees**

The most important accomplishment of the NRSP-8 has been the formation of a large community of scientists working worldwide to advance animal genomics through the sharing of resources, development of open-access multi-species bioinformatic tools, sequencing and assembly of genomes, organization of workshops and conferences, communication of results, support for travel for students and invited speakers, preparation of multi-institutional grant proposals, and formation of large collaborative research groups. The communication and sharing of information among the different species technical committees fostered by NRSP-8 has led to significant achievements under each of the three objectives outlined for 2013-2017. Across committees, the experience of one group has often informed and influenced the directions and approaches taken by other groups and this shared knowledge has accelerated tool development and discovery for all supported species. A summary of the important accomplishments and impacts for each of the technical committees (aquaculture, cattle, horse, poultry, sheep/goat, swine and bioinformatics) are included below. Here we highlight a few of the accomplishments shared across multiple species for each of the three objectives.

**Objective 1: Advance the status of reference genomes for all species, including basic annotation of worldwide genetic variation, by broad sequencing among different lines and breeds of animals.** Between 2013 and 2017, reference genomes were assembled for the pig, turkey, sheep, goat, catfish pacific oyster, rainbow trout and striped bass. In addition, genome reference assemblies were improved for the chicken, cow, horse, pig and rainbow trout with researchers capitalizing on short-read sequencing technologies, optical mapping, Pacific Biosciences sequencing and other technologies. Across all species, these improved assemblies reached high-quality chromosome levels, eliminated most of the regions with ambiguous sequences, and in some cases provided sequence for previously unsequenced autosomes. Genome annotation and gene predictions were enhanced in several species using a variety of methods including RNA sequencing (RNA-Seq) of protein coding RNA, micro RNA (miRNA), and long non-coding RNA (lncRNA), full-length transcript sequencing using Iso-seq, and coordinated efforts to manually annotate genes.

Efforts were initiated in the cow, pig, chicken, horse, sheep, rainbow trout and pacific oyster to annotate additional functional elements of the genome as part of a new initiative, the Functional Annotation of ANimal Genomes (FAANG) consortium. The FAANG consortium was formed in 2014 with the goal of accelerating genome-to-phenome discovery in NRSP-8 species. In the first phases of this effort, a number of investigations have been proposed or initiated across 80-105 tissues, depending on the species. These include whole genome sequencing; whole genome bisulfite sequencing; RNA sequencing (mRNA, miRNA, ncRNA) and transcriptome assembly; ATAC-seq; ChIP-seq with DNase I, histone modification marks, insulator-binding protein CCCTC-binding factor, and important transcription factors; and the study of the genome-wide chromatin interactome using Hi-C. Is it worth noting that this is the first time some of these technologies have been applied to some of these species. Work is ongoing among members of the FAANG project to standardize collection techniques, experimental protocols, and data analysis pipelines to maximize the utility of the data produced by this effort.

**Objective 2: Develop strategies to identify and exploit genes and allelic variation that contribute to economically relevant phenotypes and traits, in part through improving functional annotation of the genomes of our species.** From 2013 to 2017, single nucleotide polymorphism (SNP) high-throughput genotyping arrays were developed for several species including Equine (54K, 65K, 670K and 2M arrays), chicken (670K), cattle (250K functional allele array), sheep (600K), goat (52K), swine (670K) and rainbow trout (57K, 50K functional allele arrays). For all species, the impacts of these SNP genotyping arrays include: permitting genome-wide analyses such as genome-wide association studies (GWAS) and genomic signatures of selection for identification of genomic regions harboring alleles for traits of interest; allowing for, and improving the accuracy of predicted breeding values; enabling genomic selection; and permitting estimation of genetic diversity in breeds and populations of interest. Across species tools developed under this objective have allowed for identification of alleles responsible for important economic and disease traits, including alleles important in infectious diseases such as GBP5 associated with resistance/susceptibility to primary PRRS virus infection in pigs. In addition, the dairy industry has used SNP-chips to genotype nearly over one million dairy cattle allowing application of genomic selection which has reduced

animal selection generation interval (from 5 years to less than one year) and has increased genetic merit prediction accuracy by more than 30 percent with an estimated annual benefits of \$100 million per year.

**Objective 3: Facilitate analysis, curation, storage, distribution and application of the enormous datasets now being generated by next-generation sequencing and related "omics" technologies with regard to animal species of agricultural interest.** Successful efforts have been made to develop platforms to facilitate collaborative research for collection and analysis of new, unique, and interesting phenotypes, and to develop, integrate, and implement bioinformatic resources to support the discovery of genetic mechanisms underlying agriculturally important traits. For example, the Animal Quantitative Trait Loci database (Animal QTLdb) was updated with 104,272 new quantitative trait loci (QTL). To date, the database contains 95,332 cattle, 6,633 chicken, 1,245 horse, 16,516 pig, 1,412 sheep and 127 rainbow trout loci that have been associated with many traits of interest. Further, the data repository for the aquaculture, cattle, chicken, horse, pig, and sheep communities to share their genome analysis data has proven to be very useful for the community with 1,140 data files, totaling 140 GBGb, shared through this platform. Finally, a collaborative VCF information-mining platform was developed to allow for sharing discovered genetic variants between researchers.

In addition to direct contributions to each of the three objectives, NRSP-8 participants have leveraged the NRSP-8 investment in tools and infrastructure into at least \$94.5 million dollars in funding to study diverse animal models to investigate fundamental mechanisms of genome biology and physiology and pathophysiology affecting production efficiency, product quality, animal health, disease resistance and food safety and to develop additional bioinformatics resources (see **Table 1**). Finally, the annual NRSP-8 workshops have become an essential component for the development of collaborations, training and dissemination of new information to government, academic, and industry stakeholders in animal agriculture. NRSP-8 species coordinators' funds have been used to support travel for 146 postdoctoral and graduate students to the NRSP-8 meetings that are held in conjunction with the annual Plant and Animal Genome (PAG) meeting.

	<b>Federal</b>	<b>Private/Industry</b>	<b>Intramural</b>	<b>Total</b>
<b>Horse</b>	\$14,605,017	\$4,799,843	\$3,440,344	<b>\$22,845,204</b>
<b>Poultry</b>	\$18,675,963	\$150,000		<b>\$18,825,963</b>
<b>Cattle</b>	\$27,831,461	\$73,000		<b>\$27,904,461</b>
<b>Swine</b>	\$8,229,905	\$621,591	\$533,500	<b>\$9,384,996</b>
<b>Aquaculture</b>	\$5,553,103			<b>\$5,553,103</b>
<b>Sheep/goat</b>	\$3,644,000	\$109,000	\$467,000	<b>\$4,220,000</b>
<b>Bioinformatics /multispecies</b>	\$5,753,033			<b>\$5,753,033</b>
<b>Total</b>	<b>\$84,292,482</b>	<b>\$5,753,434</b>	<b>\$4,440,844</b>	<b>\$94,486,760</b>

## AQUACULTURE

<http://www.animalgenome.org/aquaculture/>

### Direct contributions to Objective 1:

- Reference genome for catfish (2016). **Impact(s):** The genome reference will allow understanding the genes controlling performance traits. Technologies can be developed based on this information allowing superior catfish breeds that will help farmers increase profits.
- Rainbow trout high-density 57K SNP chip was developed and characterized (2013). Approximately 50K of the SNPs were validated in a panel of 18 rainbow trout populations at the standard 97% call rate of the Affymetrix SNP polisher software. **Impact(s):** The SNP chip allowed improved accuracy of predicting breeding values for bacterial cold water disease resistance compared to a traditional pedigree-based model in rainbow trout aquaculture.
- Reference genome for the Pacific oyster (2012). **Impact(s):** This genome provides a basis for numerous phenotype studies and provides insight into performance under changing environmental conditions.
- Striped Bass Genetic Map (2012). The first genetic map of the genome of the striped bass was developed and published. **Impact(s):** This medium-density linkage map was based on 298 microsatellite markers and is enabling detection of QTL affecting production traits.
- Rainbow Trout Reference Genome sequence (2012): A pooling and tagging scheme was used for sequencing of ~15,000 clones from the BAC fingerprinted physical map minimal tiling path (MTP). **Impact(s):** The map helped in assembling the trout genome.
- Improved Rainbow Trout Reference Genome sequence (2017): The longest available read length of the Illumina technology was used to improve the genome sequence producing longer and better anchored scaffolds to chromosomes. **Impact(s):** The genome assembly led to SNP genotyping tools that are being used to accelerate genetic improvement.
- Striped bass genome sequence assembly containing ~35 K scaffolds was produced (2015). **Impact(s):** The assembly should accelerate analysis of the striped bass genome, to identify and characterize genes affecting important production traits.

### Direct contributions to Objective 2:

- A 675K SNPs array was developed for catfish (2017). **Impact(s):** This array allowed for genetic mapping and validation of the reference genome sequence assembly as well as for identification of a genetic markers associated with aquaculture production traits in catfish.
- A 57K SNPs array was developed for rainbow trout (2014). **Impact(s):** This array allowed for genetic mapping and improving assembly of the reference genome and evaluation genomic selection in rainbow trout.
- A 50K cSNPs array was developed for rainbow trout (2016). **Impact(s):** This array allowed for allelic-imbalance analysis of genes that are associated with muscle yield and fillet quality traits and also with bacterial cold-water disease survivability.
- Bulk segregant RNA-seq (BSR-Seq) was used to analyze differentially expressed genes and associated SNPs with disease resistance against enteric septicemia of catfish (ESC) (2013). A total of 1,255 differentially expressed genes were found between resistant and susceptible fish. **Impact(s):** These genes are candidates for further functional genomics work to validate their role in providing catfish with susceptibility to ESC.
- QTL mapping families for stress response and bacterial cold-water resistance (BCWD) in rainbow trout (2013). **Impact(s):** The families are being used to study genes responsible for stress response and BCWD.



- Illumina GoldenGate genotyping arrays were designed for *Crassostrea gigas* and *Ostrea edulis* (2014). **Impact(s):** These assays were used to genotype 1,000 individuals from wild and selected populations as well as families bred for commercially important traits.
- Large intergenic noncoding RNAs (lncRNAs) were identified by RNA-Seq analysis of rainbow trout transcriptome (2016). **Impact(s):** Many of the lncRNAs are tissue-specific and functionally associated with important biological processes including resistance to the rainbow trout BCWD and muscle growth.
- RNA-Seq analysis of miRNAs associated with different production quality traits in trout (2015 and 2017). **Impact(s):** Several miRNAs with epigenetic role associated with egg quality and muscle quality traits were identified.

### **Direct contributions to Objective 3:**

- Rainbow trout QTL database (2012) available through the Animal Genome website of the NRSP-8 bioinformatics group (<http://www.animalgenome.org/cgi-bin/QTLdb/index>) and is being continually updated. **Impact(s):** QTLs are available for industry to improve aquaculture production traits in rainbow trout.
- Bioinformatics pipeline was developed for genotyping SNPs from raw sequence data for the GT-seq method (2014). **Impact(s):** The pipeline provides significant cost reduction for genotyping.
- *C. gigas* transcriptome information derived from 2.2 billion sequences from 114 RNA-seq datasets has been organized and deposited into a publicly available database: GigaTON (2015). **Impact(s):** The user interface provides powerful and user-friendly tools to search and retrieve annotation, expression, and polymorphism information of important genes related to aquaculture traits.

### **Communication:**

- A strategic planning workshop for aquaculture genomics, genetics and breeding was held at Auburn University (2016). **Impact(s):** The workshop led to a white paper published in BMC Genomics that placed goals and priorities for future research in the aquaculture genomics, genetics and breeding in the US.
- NRSP-8 Aquaculture leaders participated in establishing the FAASG (Functional Annotation of All Salmonid Genomes) consortium. **Impact(s):** The consortium will allow coordinating data sharing and establish an infrastructure for providing high quality functional annotation of salmonid genomes.

### **Research support mini-grants (coordinator grants):**

- Approximately 25 mini-grants (~\$10,000/each) supported projects that fall under all three primary objectives and include a variety of species.

### **Travel support and opportunities for trainings:**

- Travel of 25 students/postdocs was funded to attend the Aquaculture workshop at PAG meetings (2012-2016). The purpose of the travel award program is to help graduate students and postdocs to travel to the annual PAG meeting to present their research.

### **Leveraged funds and stakeholders' use of project outputs**

Leveraged funds from diverse projects totaling more than \$5,553,103 from federal sources. Selected grants are highlighted below.

- Whole genome mapping of disease resistance/susceptibility-associated SNPs in catfish. USDA National Institute of Food and Agriculture Competitive Grant no. 2015-67015-22975. **\$500,000**. John Liu (PD).

This project is designed to address the following two objectives: 1). Genome wide scan of QTLs conferring resistance to ESC and columnaris using F2 and F4 fish using the 250K catfish SNP array; and 2). Fine QTL analysis by genotyping a large number of F2 and F4 individuals using evenly-spaced markers from mapped QTL regions. **Impact(s):** The impact of this grant will be to determine genes that will be used to select for fish resistant catfish

- Closing the tilapia genome assembly. USDA National Institute of Food and Agriculture Competitive Grant no. 67015-23088. **\$270,000**. Tom Kocher (PD).  
This project aims to improve the platform for genetic improvement of tilapia by developing a definitive sequence of the tilapia genome. **Impact(s):** The ultimate goal of the project is to improve the health and production of tilapia and related aquaculture species.
- Sequencing the Genome of the Eastern Oyster. USDA National Institute of Food and Agriculture Competitive Grant no. 2015-67016-22942. **\$242,051** Marta Gonez-Chiarri (PD).  
This project propose to develop these key resources and tools by performing the sequencing, assembly, and annotation of a reference genome and transcriptome for the Eastern oyster *C. virginica*. Genome researchers and bioinformatics experts, in collaboration with the Eastern Oyster Genome Consortium, will use state-of-the-art sequencing and assembly strategies to achieve these aims. **Impact(s):** The reference genome and transcriptomes for the Eastern oysters will aid the research community in the discovery of candidate genes and markers associated with traits of commercial, biological, and ecological importance in oysters.
- Development of 675K SNP arrays for whole genome mapping and genetic studies in catfish. USDA National Institute of Food and Agriculture Competitive Grant no. 2015-67015-22907. **\$485,000** John Liu (PD).  
This project addresses major limitations to adopting genome technologies in aquaculture that currently are the lack of a high- throughput technology for the analysis of genomic variations in relation to phenotypic variations. We need a high-density SNP array technology that allows high- efficiency, cost-effective, whole-genome coverage, analysis of genetics of important performance traits such as disease resistance. This project is poised to resolve these challenges, with three specific objectives: 1) Developing the catfish 675K SNP arrays; 2). Genetic mapping of whole genomic sequence scaffolds; 3). Enhancing and validating the catfish whole genome assembly. **Impact(s):** This project will address the most significant problem currently existing in catfish genomics. This project will develop a technology for the most efficient analysis of performance traits, and will literally transform the isolated whole genome sequence tags into a well-assembled reference genome assembly, thereby enabling its application in breeding and selection programs.
- Homozygous clonal rainbow trout lines as genomic resources. USDA National Institute of Food and Agriculture Competitive Grant no. 2016-67015-24472. **\$485,000**. Gary Thorgaard (PD).  
Doubled haploid lines have unique value as genomic tools because they have minimal heterozygosity and allow full chromosomal haplotypes to be identified. These lines have been used for the rainbow trout genome sequencing project and for QTL studies. The experimental objectives will include: (1) Establish at least 12 lines within the USDA. (2) Transfer cryopreserved semen from each line as an ongoing repository. (3) Generate a repository of frozen tissues and genomic DNA. (4) Conduct baseline karyotype analysis and SNP typing by re-sequencing of two of the lines. (5) Attempt to induce sex reversal to females in the YY lines and test their fertility. **Impact(s):** The project will assure continued availability of the lines to the trout research community, develop sperm, tissue and DNA repositories and improve propagation methods.
- SNP markers for muscle, growth and fillet quality traits in rainbow trout. USDA National Institute of Food and Agriculture Competitive Grant no. 2014-67015-21602. **\$500,000**. Mohamed Salem (PD).  
The project aims to find genes and to develop genetic markers that would be used in USDA marker-assisted selection programs to develop food fish strains with superior muscle growth and fillet quality in rainbow trout. This project is expected to produce a large number of true genetic markers that provide a valuable resource for determination of genetic merit of growth and carcass traits in rainbow trout. Project outcomes including, knowledge, expertise, methods, tools, and technologies, will be disseminated to the US aquaculture industry/stakeholders including the US largest producers of rainbow trout food fish and eggs. **Impact(s):** These

genetic markers may be quickly adapted to other species and give the US aquaculture industry a competitive advantage.

**Major impact products (could be potential impact):**

Recently, the first genome-wide SNP arrays have been developed and applications of the SNP-chip technology in genomic selection have just begun to be adapted by commercial breeders of some aquaculture species including catfish (600K), salmon (286K), rainbow trout (57K) and oyster (190K).

## CATTLE

<http://www.animalgenome.org/cattle/>

### Direct contributions to Objective 1:

- An improved bovine genome reference sequence assembly of Dominette (the reference animal) based on multiple data types developed by the bovine community (optical map, Illumina paired-end, PacBio sequence, and improved gene predictions based on RNA-Seq and Iso-Seq data) will be released in Fall of 2017. **Impact(s):** This improved assembly will help with the identification of genetic markers associated with economically important traits in cattle.

### Direct contributions to Objective 2:

- A 250K functional variant assay was made available to cattle researchers. The assay was designed using various sources of sequence data derived from AFRI-funding and is focused on the detection of genic variants likely to be functional in taurine cattle. **Impact(s):** This tool will assist researchers to identify genetic identifying causative SNPs that are associated with economically important traits and which are likely to be useful in marker-assisted selection across multiple breeds.

### Direct contributions to Objective 3:

- A database (Animal-GRIN) has been developed to serve as a permanent archive for DNA data, germplasm/tissue samples, and phenotypic and production system data from large animal genomics projects. **Impact(s):** This database will allow for future data mining and value capture from the data and samples collected by publicly funded research.

### Communication:

- A bovine genome newsletter was prepared by the bovine coordinators and distributed to the AnGenMap listserv. **Impact(s):** This helped inform the bovine research community of ongoing developments with the bovine genome.
- Two industry conferences were held, the “2015 Applied Reproductive Strategies in Beef Cattle (ARSBC) Conference Grant”, and “New Approaches to Bovine Respiratory Disease Prevention, Management, and Diagnosis” with support from USDA, National Institute of Food and Agriculture Conference Grants (2014-67015-21562; 2015-67015-23693). Proceedings were produced from both conferences, and the latter was published in Animal Health Reviews.

### Research support mini-grants (coordinator grants):

- Livestock FAANG project (lead by H. Zhou, P. Ross and I Korf) Coordinator funds (\$30,000). [The project allowed for sample collection from 4 individuals (2 males and 2 females). These funds were used as leverage that resulted in ~\$500,000 grant from the USDA NIFA and another ~\$100,000 from National Pork Board, Aviagen etc. for FAANG data collection on these samples.

### Leveraged funds and stakeholders’ use of project outputs:

From 2013-2017, the investigators and stakeholders leveraged the tools and resources generated through NRSP-8 to obtain at least \$27,904,461 additional funding from federal sources, in funding from private foundations and industry sources. Selected grants are highlighted below.

- Integrated program for reducing bovine respiratory disease complex in beef and dairy cattle. USDA National Institute of Food and Agriculture Competitive Grant no. 2011-68004-30367. **\$9,750,000**. Jim Womack (PD). The objective of this Coordinated Agricultural Project was to use genomic tools to identify genetic markers associated decreased susceptibility to bovine respiratory disease. This is the most important disease in both the beef and dairy cattle industry with estimated losses of more than one billion dollars annually. This project used genome sequences to fine map genetic variants associated with respiratory disease, with the aim of delivering a tool that the industry can use to select for cattle that are less susceptible to respiratory disease. **Impact(s):** The impact of this grant will be decreased morbidity and antibiotic use in cattle production, and improved animal health and welfare.
- 2015-2017: USDA NIFA 2015-67015-23183. “Application of a functional variant assay and sequence imputation to identify large-effect QTL underlying feed efficiency and component traits in beef cattle.” Taylor JF, RD Schnabel, JE Decker, CS Seabury and HL Neibergs. 4/1/15-03/31/17. **\$500,000**. This grant supported the development of the GGP-F250 functional assay. The accomplishment is that we successfully designed an assay for which 173,609 variants can be assayed with a marker call rate of at least 90%. These variants are highly enriched for rare functional variation within the bovine genome and include 82,979 variants that alter amino acids within gene products, 665 Indels that either alter frame or add/delete amino acids, 2017 splice site variants and 44,358 variants within untranslated regions. The assay is currently publicly available through GeneSeek. **Impact(s):** Impacts of this grant include 23,541 variants within QTL regions detected in the BRD and Feed Efficiency grant that were identified and included on the assay and 1978 BRD case-control and 4609 Feed Efficiency project animals have been genotyped with the assay to fine-map QTL. The assay also contains 2,224 variants for which no homozygotes were detected. These are currently being mapped to genes known to be essential for life to identify candidates for lethal alleles segregating in cattle. Finally, the assay is expected to aid in the process of imputing genotypes to whole genome sequence, because, contrary to the currently used assays which are strongly enriched for common variants, the GGP-F250 is enriched for rare variants and the linkage disequilibrium that exists among rare variants will aid in the imputation of genotypes for this class of variant.
- 2013-2017: USDA-NIFA-AFRI. 2013-68004-20364. “Identification and management of alleles impairing heifer fertility while optimizing genetic gain in Angus cattle.” Patterson DJ, JF Taylor, A Van Eenennaam, S Brown and M Smith. **\$2,997,040**. This grant supported the whole genome sequencing of the 100 registered Angus bulls that have had the greatest impact on the breed as determined by the number of registered descendants. These animals, along with sequences obtained on 162 additional animals from 12 other taurine breeds, were used to identify variants genome wide. With support from the three other USDA grants (Bovine Respiratory Disease, Feed Efficiency and Functional Variant), we designed the GGP-F250 assay for which 173,609 variants can be assayed with a marker call rate of at least 90%. These variants are highly enriched for rare functional variation within the bovine genome and include 82,979 variants that alter amino acids within gene products, 665 Indels that either alter frame or add/delete amino acids, 2017 splice site variants and 44,358 variants within untranslated regions. **Impact(s):** The assay is currently publicly available through GeneSeek allowing genetic gain assessment for important production phenotypes in Angus cattle.
- 2016-2019: NIH 1R01HD084353. “Linking Fertility-Associated Gene Polymorphisms to Aberrant Sperm Phenotypes.” Sutovsky P, RD Schnabel, JF Taylor. 7/1/2016-6/30/21. **\$2,149,000**. This grant has just started but plans to sequence 100 bulls with either sperm abnormalities or with extreme differences for conception rate to identify mutations in genes known to be expressed in sperm that are responsible for the defects and variants that are candidates for genetic variation in male fertility. We have begun the collection of sperm samples from US and Canadian AI companies. **Impact(s):** The project is expected to identify and validate sperm phenotype biomarkers encoded by fertility associated polymorphic genes, and to improve sire management by genetic selection and automated semen evaluation. This project will also yield new methods and potentially new treatments for human male and idiopathic infertility.
- Gene Seek and Zoetis provided industry funds and support to leverage the cost of developing the new bovine genome assembly, **\$73,000**.

### **Travel support and opportunities for trainings:**

- Funding was used to bring students to the annual PAG meeting based on a competitive travel award. Coordinator funds were also used on several occasions to help support the NRSP8 speaker at PAG.

### **Major impact products (could be potential impact):**

- Genomic selection has dramatically improved the rate of genetic progress within the US dairy industry. The dairy industry has used SNP-chips to genotype over 1 million dairy cattle. Application of GS reduced animal selection generation interval (from 5 years to less than one year) and has increased prediction accuracy by more than 30 percent for an estimated annual benefits of \$100 million per year.
- Genomic selection is starting to be implemented in the US beef industry.
- Development of a 173,609 SNP functional variant assay containing variants highly enriched for rare functional variation within the bovine genome and including 82,979 variants that alter amino acids within gene products, 665 Indels that either alter frame or add/delete amino acids, and 2017 splice site variants. The assay is currently publicly available through GeneSeek.

## **HORSE**

<http://www.uky.edu/Ag/Horsemap/>

### **Direct contributions to Objective 1:**

- A new reference genome build (EqCab 3.0) was created for the horse and shared among workshop participants. Public release and publication is expected in late 2017. Morris Animal Foundation, NRSP-8 coordinator and other federal funds supported this work. **Impact(s):** The new assembly improved gene annotation, increased contig N50 from 112 Kb to 1.4 Mb, and eliminated most of the regions with ambiguous sequence (“Ns”). The improved reference will increase the power and efficacy of genomics research to discover the genes and alleles underlying disease and economically important performance traits in the horse.
- The annotation of the horse genome was improved through investigations of gene expression and splice variation that occurs among diverse tissues. Data supporting wide- scale annotations of the horse genome were published in several reports (2013-2016). **Impact(s):** Improved annotation provides context for the discoveries by making it possible to identify the functional aspects of genetic variation.
- SNP and insertion-deletion polymorphism discovery was performed using whole genome sequence from 153 horses as part of an effort to design 2M and 670K SNP Affymetrix SNP arrays. **Impact(s):** This work documents the extent of variation that exists among 24 horse breeds and made genotypes from 485 horses across 2M SNPs publically available providing raw material for use in developing research tools. (Schaefer RJ, *et al.* Developing a 670k genotyping array to tag~ 2M SNPs across 24 horse breeds. *BMC Genomics* 18.1 (2017): 565).

### **Direct contributions to Objective 2:**

- An assay tool to assay ~65K SNPs (SNP70) was developed to replace the ~54K SNP (SNP50) tool in 2013. The development of this tool was a collaborative activity of the NRSP-8 community and made publicly available. An imputation pipeline between these two moderate-density arrays was developed. (McCoy AM, McCue ME. Validation of imputation between equine genotyping arrays. *Animal Genetics* 45:153, 2014.

PMCID: PMC4000747.) **Impact(s):** Developing this tool and imputation pipeline made it possible to continue to perform genome-wide analyses that impact the health and welfare of horses.

- SNP discovery based on whole genome sequence from 153 horses was used to construct the next generation 2M and 670K SNP Affymetrix SNP arrays for equine whole genome analyses. The 670K array is designed for imputation and enables data from prior lower density SNP arrays to be imputed up to ~1.8M SNPs. The equine 670K SNP chip was made available in 2015. (Schaefer RJ, *et al.* Developing a 670K genotyping array to tag~2M SNPs across 24 horse breeds. *BMC Genomics* 18.1 (2017): 565.). **Impact(s):** This 670K array and imputation resource improves genome coverage more than 30-fold over the medium density (54K and 65K) SNP arrays. More than 20,000 670K genotyping arrays have been used to date. This increase in SNP density will allow for GWAS in genetic diverse breeds of economic importance such as the American Quarter Horse (~4 million registered individuals).
- Because of the closing of the commercial operation of the BAC library, the primary CHORI 241 BAC library was moved from the Children's Hospital of Oakland to the laboratory of Samantha Brooks (co-coordinator) at the University of Florida. **Impact(s):** This will ensure continued access to the library for equine researchers. This resource is key for investigating the broader aspects of structure and organization of the horse genome.

### **Direct contributions to Objective 3:**

- Horse technical committee members joined the FAANG initiative to generate gene expression data for 38 of tissues from two horses. In connection, competitive, extramural industry funding was obtained to further develop this dataset. **Impact(s):** This resource will empower research in the area of functional genomics.
- The horse genomics community actively utilized the collaborative resources provided in the AnimalGenome.org Data Repository. The site hosts large shared files, prepublication works and polymorphism data.
- Horse specific transcriptome assemblies not yet curated by NCBI were made available at AnimalGenome.org and through GitHub ([https://github.com/drtamermansour/horse\\_trans](https://github.com/drtamermansour/horse_trans)). **Impact(s):** This resource increases the publically availability of equine transcriptional data and will improve genome annotation.
- With the assistance of horse genome researchers, the AnimalQTL database added horse to the species list. **Impact(s):** This resource provides rapid access to 1,245 equine QTL and associated metadata.
- Horse genome workshop members deposited 1,524 genomic SRA archives for the horse. These accessions contain many fully re-sequenced genomes, as well as targeted datasets generated by diverse NGS platforms. **Impact(s):** This resource increases the publically availability of equine whole genome sequence and transcriptomic data.

### **Communication:**

- Additional workshops were conducted for NRSP-8 participants in connection with the International Society of Animal Genetics ([ISAG] 2016 [Salt Lake City], ISAG 2014 [Xian, China], ISAG 2012 [Cairns, Australia], and ISAG 2017 [Dublin, Ireland]). **Impact(s):** These meetings facilitated communication and collaborations among international scientists working on all species and extended discussions conducted at the annual NRSP-8 workshops.
- Additional workshops were conducted with support of the Dorothy Russell Havemeyer Foundation that focused on issues related to horse genomics (2013 [Azores, Portugal], 2015 [Hannover, Germany], 2018 [planned, Pavia, Italy]). **Impact(s):** These workshops include the entire international horse genomics research community and facilitate exchange of information and collaboration between scientists.
- Following the identification of critical needs in coordinating collaborations across institutions for new and evolving projects, an initiative to provide a database of ongoing work is now hosted through collaboration

with the Interbull.org service. **Impact(s):** This database currently provides a listing of projects recruiting samples, but may eventually expand to include file sharing for exchange of SNP and NGS datasets.

#### **Research support mini-grants (coordinator grants):**

- Matching funds provided to support development of the SNP70 SNP genotyping array (~65K SNPs) for discovery research on the genomics of horses.
- Matching Funds provided to support development of the 670K SNP genotyping array. Primary funding from USDA-NIFA (Dr. Molly McCue PI) along with coordinator funds were used to develop a 2M test array. 670K SNPs were selected to tag ~1.8M SNPs across 24 horse breeds.
- Matching funds provided for EqCab 3.0. Primary funding from the Morris Animal Foundation. Improved predictions from assembly.
- Matching funds provided to develop FAANG resources for horse; primary funding came from Grayson-Jockey Club Research foundation project Developing resource for functional genomics research.

#### **Leveraged funds and stakeholders' use of project outputs:**

From 2012-2017, the equine investigators leveraged the tools and resources generated through NRSP-8 to obtain **\$22,845,204** in additional funding. This included **\$14,605,017** in funding from federal sources, **\$4,799,843** in funding from private foundations and industry sources and **\$3,440,344** in intramural funding. Selected grants are highlighted below.

- **“Genetic diversity and selection in the domestic horse.”** Dr. Molly McCue PI, Dr. James Mickelson Co-I, and others **\$499,481** USDA-AFRI. **Impact(s):** This proposal quantified genetic diversity and to identify functional alleles that cause variation in size, locomotion and athletic phenotypes among 36 domestic horse breeds.
- **“Tools to Link Genotype to Phenotype in the Horse.”** Dr. Molly McCue PI, Dr. James Mickelson Co-I, and others. **\$499,727** USDA-NIFA. In this proposal builds upon the recent development of high-density SNP arrays to develop tools that further facilitate GWAS in the horse by: **1)** enabling complementary GWAS approaches including gene, haplotype, and pathway-based analyses through SNP-to-gene mapping and the construction of a haplotype map; **2)** increasing marker density by developing an imputation resource; and **3)** constructing context-specific co-expression networks for integrated network-based association analysis. Prioritization of candidate genes is assisted by: **4)** refining the physical annotation of mRNAs, lncRNAs, and miRNAs; and **5)** improving functional annotation of these loci through tissue-specific gene expression and gene co-expression networks. Finally, the identification of functional alleles will be accelerated by **6)** developing a comprehensive catalog of genetic variants from WGS of >450 horses.
- **“Functional Prioritization of Candidate Genes and Alleles for Equine Metabolic Syndrome.”** Dr. Molly McCue PI, Dr. James Mickelson Co-I. **\$499,815** USDA-NIFA. Genome wide association in Welsh Ponies (WP) and Morgan horses has identified >180 chromosomal regions of interest (ROI) harboring >3,000 positional candidate genes associated with Equine Metabolic Syndrome (EMS) phenotypes. The objectives of this proposal are to **1)** prioritize candidate genes using skeletal muscle and/or adipose tissue gene expression or alterations in serum metabolite abundance to support their role in EMS pathophysiology; and **2)** identify the functional alleles underlying EMS phenotypes.
- **“Discovering Causal Variants for Complex Disease Using Functional Networks in the Horse.”** Dr. Rob Schaefer PI, Dr. Molly McCue mentor. **\$150,000** USDA-NIFA. The goals of this grant are to develop software tools to integrate available sources of genomic data and functional data (WGS, SNP, RNA-sequencing, proteomics and metabolomics) in agricultural species to better understand complex phenotypic traits using metabolic syndrome in the domestic horse as a test case.



- “**Protein Networks Mediating Airway Hyper-Responsiveness In Equine Airways.**” Dr. Chipper Swiderski **\$438,153** USDA-AFRI. This grant seeks to better understand the etiopathogenesis of Recurrent Airway Obstruction in the horse through proteomic studies and improved annotation of genes expressed during disease exacerbation.
- “**Comparative Genomics in Qatar.**” Dr. Doug Antczak and Dr. Samantha Brooks, **\$1,030,000** Qatar National Research Foundation- National Priorities Research Program. This project will document variation and signatures of selection in desert breeds of horse, as part of a larger effort to improve genomic resources in desert adapted hoof stock.
- “**Identification of Genetic Factors Responsible for Establishment of Equine Arteritis Virus Carrier State in Stallions.**” Dr. Uri Balasuriya PI, Dr. Ernie Bailey Co-PI and others. **\$2,930,000** USDA-AFRI.

#### **Travel support and opportunities for training:**

- Travel of 64 students/postdocs was funded to attend the Equine workshop at PAG meetings (2012-2016). The purpose of the travel award program is to help graduate students and postdocs to travel to the meeting to present their research.
- Support for five NRSP-8 members to attend GO-FAANG workshop in Washington DC to provide leadership horse group in connection with this initiative.
- Member sent to participate in Hack-a-thon in Europe 2016 in support of FAANG activities. Integration with international efforts to develop functional genomics databases for animal genomics.

#### **Major impact products (could be potential impact):**

- Development of 4 SNP genotyping arrays (54K, 65K, 670K and 2M). **Impact(s):** These arrays allow for efficient and economic performance of dozens of genome-wide analyses in the horse.
- Genomic diagnostics in the horse have now expanded to include commercially available tests over 100 markers contributing to more than 40 diverse traits. **Impact(s):** Costs per test are falling, and as adoption of genomic selection and mandatory genetic testing increases across the industry, translating in to reduced economic losses due to genetic disease.
- Diagnostic tests created for markers related to performance, disease and color, including *DMRT3* and gait, *TBX3* and dun color, *SHOX* and dwarfism, *BAGALT7* and dwarfism, *ACAN* and dwarfism, *RFWD3* and Appaloosa color pattern, *SERPINB11* and hoof quality, *KIT* and spotting in donkeys, *HOXD3* and occipitoalantoaxial malformation, *CXCL16* and susceptibility to equine arteritis virus.
- Additional targets for investigation were identified through genome-wide analyses including signatures of selection in 38 horse breeds, genomic loci contributing to osteochondrosis, recurrent laryngeal neuropathy and others.
- Molecular tests to identify chromosome abnormalities were reported and additional test are being developed. **Impact(s):** Chromosome abnormalities are the most common genetic cause of infertility and disease amongst horses and molecular tests are much less expensive than conventional karyotyping.
- The major histocompatibility complex plays a major role in the occurrence and consequences of allergic and infectious diseases. Determinants playing a role in specific diseases were identified and methods were developed to improve our ability to identify yet other MHC determinants. **Impact(s):** MHC is a genetically complex region but plays a major role in immune responses. Knowledge of the MHC remains incomplete for all species and but research is turning up applications, especially with respect to vaccine design and immune therapy.

## POULTRY

<https://www.animalgenome.org/poultry/>

### Direct contributions to Objective 1:

- The chicken genome build (Gallus\_gallus-5.0) was released to the public in 2015. **Impact(s):** This improved build, which was aided by long single molecular sequencing and finished BACs, yielded a gain of 180 Mb in assembled bases and provided coverage to 3 previously missing autosomes. As the reference genome, this invaluable resource greatly enhances the ability to identify genes and genetic variations associated with traits of agronomic interest.
- A turkey draft genome was generated from next generation sequencing and a turkey BAC contig (physical) map.
- Guidelines for standardized gene nomenclature for chicken genes were developed to assign nomenclature to (1) MHC genes; (2) genes highly expressed in egg white, yolk and eggshell; (3) histone; and (4) myosin genes. **Impact(s):** This nomenclature was shared with NCBI and Ensembl.

### Direct contributions to Objective 2:

- Very high-density SNP mapping (ca. 600K SNP) panels have been developed and along with 60K SNP chips. **Impact(s):** These genotyping arrays are being employed in genome-wide association studies (GWAS) and genomic selection (GS).
- Efforts have been initiated to annotate the chicken genome, especially with respect to regulatory elements. In brief, datasets for transcripts, histone marks, methylation and more have been integrated to identify promoters, enhancers, and silencers. **Impact(s):** This information is vital to help connect genotypic variation to phenotypic variation.
- Transcript and comparative genome hybridization arrays were developed and distributed.

### Direct contributions to Objective 3:

- Over 40 unique chicken research lines and their derived materials have been shared with amongst investigators to expand studies on the chicken genome.
- DNA from the East Lansing international reference mapping population has been sent to many laboratories throughout the world. Similarly, DNA from the junglefowl used to generate the reference sequence assembly has been widely distributed.

### Communication:

- Provided support for members to attend GO-FAANG meeting and/or other multi-state research project meetings to enhance communications of activities, communicate about resources.

### Research support mini-grants (coordinator grants):

- Provided \$30,000 in funds towards the USDA AFRI Animal ENCODE proposal; Huaijun Zhou, UC Davis – PI.
- Financial support provided to W. Warren, Washington U., St Louis, for sequencing of microchromosomes, which has aided to fill in gaps in the genome assembly.
- Financial support provided to M. Delany, UC Davis, to create a capture arrays and sequence the wg-2 mutation in the Wingless-2.331 congenic inbred line.

- Financial support provided to H. Zhou, UC Davis, for challenge experiments involving highly pathogenic Newcastle Disease Virus (NDV) and the Fayoumi and Leghorn strains in order to characterize genetic resistance.
- Financial support provided to B. Muir, Purdue U. to create a synthetic resource population using 8 diverse genetic lines to fine map genetic resistance to Marek's disease.
- Financial support provided to M. Miller, City of Hope, for further sequencing of microchromosome 16 BAC clones to improve understanding of the MHC/Rfp-Y complex.

### **Leveraged funds and stakeholders' use of project outputs:**

From 2013-2017, the investigators and stakeholders leveraged the tools and resources generated through NRSP-8 to obtain at least \$18,675,963 additional funding from federal sources and \$150,000 in funding from industry sources (Cobb Vantress supported efforts towards the improvement of the chicken genome assembly). Selected grants are highlighted below:

- 2013-2017: USDA NIFA 2013-67015-21357. "Improving the chicken genome assembly and annotation." Warren W, CT Brown, H Cheng H, and J Dodgson. **\$485,690**. This grant supported the improvement of the chicken genome assembly and annotation by filling in known gaps within and between existing scaffolds, and refining microchromosome linkage maps for localization of unplaced sequences. **Impact(s):** With the biology becoming reliant on a genome assembly, the higher quality chicken assembly aided all efforts especially with respect to identifying genes and pathways of agronomic importance. Furthermore, other avian genomes were improved as they also rely on the chicken genome assembly as their reference as well.
- 2012-2017. USDA NIFA 2012-67015-19419. "Enhancing genetic resistance to Marek's disease in chicken via allele-specific expression screens and genome-wide selection." This grant supported the identification of genes and genetic markers associated with resistance to Marek's disease (MD), a herpesvirus-induced lymphoma of chickens. Hypothesizing that differences in gene expression (when, where, and how much) are the major contributors of phenotypic variation for complex traits such as disease resistance, SNPs that exhibit allele-specific expression (ASE) in response to Marek's disease virus infection were identified. These ASE SNPs were found to account for over 83% of the genetic variance and were 125% more accurate in genomic selection compared to pedigree evaluation (i.e., BLUP). **Impact(s):** These results support the hypothesis that phenotypic variation in traits is primarily due to changes in regulation of gene expression rather than other sources such as differences in protein composition. Furthermore, we have identified most of the genes that confer MD genetic resistance, which should help reduce the ~\$1-2 billion in annual losses associated with MD.
- 2013-2018. USAID AID-OAA-A-13-00080 "Improving food security in Africa by enhancing resistance to disease and heat in chickens; Feed the future innovation lab for genomics to improve poultry" Zhou H. Bunn D, Gallardo G, Lamont S, Dekkers J. et al. **\$6,000,000**. This grant uses contemporary high-throughput genetic technologies of SNP chips and functional genomics, along with targeted genome resequencing and extensive statistical and bioinformatic analyses to dissect and identify the genetic factors of the chicken that enhance its resistance against NDV and heat stress by assessing diverse populations of chickens, including well- characterized research lines and highly relevant local African ecotypes. **Impact:** The project has significantly improved institute capacity (infrastructure has developed in Africa) and human capacity building, including by training of students and scientists both on-site in Africa and in the US in essential skills that enable the African partners to sustain and disseminate the results of this project. Project outcomes are expected to reduce poverty, hunger, and malnutrition, and empower women through increased agricultural productivity achieved by decreasing the major losses that currently occur as a result of Newcastle disease and heat stress in African chickens.
- 2015-2017. USDA NIFA 2015-67015-22940 "Genome wide identification and annotation of functional regulatory regions in livestock species" H. Zhou, P. Ross, I. Korf. **\$500,000**. This grant supported research

effort in functionally annotating regulatory elements in the three major farm animal species by integrative bioinformatic analysis of RNA-seq, DNase-seq and ChIP-seq data from the eight most important tissues. **Impact:** This will generate first line of re-annotation of gene structure and landscape of functional regulatory elements in chicken, bovine, and swine genomes, and will develop a framework to continue a more in-depth functional annotation of these genomes and other agricultural animals.

- 2011-2016. USDA NIFA “System Biology Analysis & Modeling Of Complex “Omic” Data: A Service Center Approach”. Zhou H. Drake K. **\$750,000**. This grant has supported an effort in collaboration with Seralogix, to provide sophisticated systems biology and modeling analysis with visualization for a total of 12 projects generating more than 100 data analysis module reports. These projects include microarray and RNA-seq data from cattle, sheep, chicken and mice in the areas of nutrition, reproduction, growth and disease. **Impacts:** Results have contributed greatly to our understanding and formulation of new hypotheses that are advancing the fields of animal infection, nutrition, reproduction, and physiology.
- 2015-2018. USDA NIFA 2015-67015-23093 and BBSRC BB/M028208/1. “US-UK Collaborative Research: Host Resistance to Avian Pathogenic E. coli” Lamont, S.J. (PD), Wolc, A; Kaiser, P. (dec.), Stevens, M., Vervelde, L. **\$499,999** (USDA). This grant supported the genomic, molecular and cellular characterization of the host-pathogen interactions between chickens and avian pathogenic E. coli (APEC), through the use of unique inbred chicken lines in both countries that differ in resistance to avian pathogenic E. coli (APEC), analysis of transgenic chickens in which all cells of the myeloid lineage express a fluorescent protein to aid the phenotyping of APEC-infected cells, definition of the transcriptome of infected cells, association of resistance with bird genetic variation (in structure and expression) through GWAS and RNA-seq analysis, and validation of selected research findings for translation into industry application. **Impact(s):** The impacts of this grant will be a reduction of the negative impact of respiratory APEC on the poultry industry, improved poultry health and vaccine strategies, and decreased use of antibiotics in food animals.

#### **Travel support and opportunities for trainings:**

- Provided financial support for over 40 students, postdocs, members, and speakers to attend the PAG Poultry Workshop (2013-2017).

#### **Major impact products (could be potential impact):**

- Genomic selection is now routinely implemented in both the meat (broiler) and egg (layer) breeding companies. This has greatly accelerated the genetic progress required by the industry to meet the growing consumer demand. Furthermore, poultry health and welfare have been enhanced.
- The chicken genome assembly reached the stage that scientists can confidently identify genes and genetic variations associated with biological traits, many of which are highly relevant to the poultry industry.
- The draft assembly of the turkey genome has been released, which affords the opportunity for efforts similar to those in the poultry industry, e.g., biological characterization, genomic selection.

## SHEEP/GOAT

<http://www.animalgenome.org/sheep/>

### Direct contributions to Objective 1:

- Reference genomes were published for goat in Nature Biotechnology in 2013 and for sheep in Science in 2014. An improved reference genome for the goat was published in Nature Genetics in 2017 that leveraged single molecule sequencing plus chromatin conformation capture to create a genome assembly with chromosome length scaffolds. **Impact(s):** The reference genomes advanced the status of mammal genome assembly and annotation technology at the time of publication. They also enabled comparative genomic insight into rumen biology, and expanded understanding of genes underlying numerous economically important traits. The improved goat genome reference elevated the standard for quality of mammal reference genome assemblies. Together, these results will underpin all future efforts to improve genetics of productive efficiency in sheep and goats.

### Direct contributions to Objective 2:

- A sheep 600K SNP chip and a goat 52K SNP chip were both released for research in 2014. **Impact(s):** This dramatic increase in SNP density for sheep and the first genome-wide medium density panel for goat have enabled powerful new tools including genome-wide association and genomic selection to dissect and improve numerous traits in sheep and goats.

### Direct contributions to Objective 3:

- A sheep genomes database has been assembled to provide a public, large-scale warehouse for global sheep genetic diversity. The database now includes re-sequencing data from almost 1,000 sheep genomes with an overall total of nearly 100 million identified sequence variants. **Impact(s):** This resource will accelerate the identification of causal variants for numerous traits and enable previously inconceivable analyses.

### Communication:

- Strategic planning conference calls with international attendance were held in 2015 and 2016, in addition to annual meetings at PAG and biennial meetings at International Society for Animal Genetics (ISAG). **Impact(s):** These contributed to the development and implementation of the Ovine FAANG Project tissue collection in the U.S. and recent successful leveraged grant funding.

### Research support mini-grants (coordinator grants):

- Ovine FAANG (Functional Annotation of ANimal Genomes) Project tissue collection (\$15,000 Coordinator funds). Sample collection of 100 tissues from a new reference genome sheep was conducted in 2016. **Impact(s):** Use of the reference genome animal to generate functional annotation data will enable state-of-the-art annotation, and this was recognized by a \$500,000 grant from USDA-NIFA (led by Brenda Murdoch and Noelle Cockett) to generate annotation data for FAANG using these samples.

### Leveraged funds and stakeholders' use of project outputs:

From 2013-2017, the investigators and stakeholders utilized the tools and resources generated through NRSP-8 to acquire leveraged funds from diverse projects totaling **\$4,220,000**. The overall total leveraged funds include **\$3,644,000** from combined federal sources, **\$467,000** in local/institutional funds, and **\$109,000** from industry. **Impact(s):** Diverse leveraged funds supported projects to improve the functional genome annotation, provided

large-scale genetic variant datasets and analyses, and informed causal variant searches for numerous important traits. Selected grants are highlighted below.

- **Ovine FAANG Project.** USDA National Institute of Food and Agriculture Competitive Grant 2017-67016-26301. **\$500,000.00.** Brenda Murdoch (PD). The majority of a mammalian genome does not consist of coding genes but rather copious portions that influence the timing, tissue, and spatial regulation of the expression of genes. This project will generate data from numerous tissues of the reference genome sheep to elucidate transcription details at unprecedented resolution, identify numerous regulatory elements including promoters, enhancers, silencers and insulators, and perform numerous other assays including measures of DNA methylation and open chromatin. **Impact(s):** The outcomes of this project will provide the sheep research community with cutting edge functional genome annotation resources and enable comparison of genome regulation across animal species by the global FAANG (Functional Annotation of ANimal Genomes) consortium.
- **Genome-Wide Association Analysis for the Identification of Alpine Goats With High Milk Production.** USDA National Institute of Food and Agriculture Competitive Grant 2015-67031-23776. **\$100,000.00.** Yonathan Tilahun (PD). This project used genome-wide association analysis to identify genomic regions and genes associated with dairy production in Alpine goats. **Impact(s):** These results provide a foundation for improved understanding of lactation, and they enable enhanced selective breeding in the economically important Alpine goat breed.
- **Genomics of Resilience in Sheep to Climatic Stressors.** USDA National Institute of Food and Agriculture Capacity Building Competitive Grant 2013-38821-21389. **\$600,000.00.** Arthur Goetsch (PD). Environmental extremes are a key constraint on agricultural production, and sheep have genetic diversity relating to many traits. This project will identify genetic variation important for resilience to stressors present in extreme environments by surveying sheep from divergent breeds and geographic locations. **Impact(s):** This project has defined useful phenotypic measures for assessing resilience to conditions including heat load as well as feed and water availability. Assessment of genomic bases for these traits is progressing. This will enable selective breeding to improve sheep resilience to environmental extremes.
- **Building the Sheep Genomes Database.** USDA National Institute of Food and Agriculture Competitive Grant 2013-67015-21372. **\$500,000.00.** Noelle Cockett (PD). This project addresses the need for generation and collection of sheep sequences including genetic and genomic variants to benefit the whole research community. Objectives include sequence data generation on a genetically diverse set of sheep, identification of genetic variants, and public accessibility of these data plus sequence data from outside sources. **Impact(s):** Sequence data from nearly 1000 animals including over 80 million genetic variants have been made public. This resource has identified many genetic variants and provided valuable assessments of their frequency and geographic distribution among global domestic sheep.

#### **Travel support and opportunities for trainings:**

- Travel of 12 students was funded to attend the Sheep and Goat workshop at Plant & Animal Genome (PAG) meetings (2012-2017). **Impact(s):** The purpose of the travel award program is to help graduate students to travel to the annual PAG meeting to present their research.

#### **Major impact products (could be potential impact):**

- Development of 45 genetic locus tests, overarching genomic selection, and potential for gene editing systems. Genetic locus tests for 43 economically important traits plus 2 biomedical model mutations have been developed since 2014, including tests for loci with large influence effects on reproductive prolificacy, growth/milk production, muscular development, and pathogen susceptibility. In addition, the first genomic selection results for each species hold promise for incorporating unprecedented numbers of genes and traits into

genomics-enabled breeding gains moving forward. Finally, reference genome sequences underpin the broad utility of new knockout and gene editing systems now available for both sheep and goats.

## SWINE

<http://www.animalgenome.org/pigs/>

### Direct contributions to Objective 1:

- A global group with significant contributions by several NRSP-8 scientists created the first draft assembly of the swine genome (2012). **Impact(s):** The genome assembly led to SNP genotyping tools that have been used by the swine genetics industry to accelerate genetic improvement. The assembly has accelerated the analysis of the swine genome, to understand and manipulate genes of major importance (such as a CD163 KO pig that is resistant to porcine reproductive and respiratory syndrome virus (PRRSV) infection).
- A global group led by NRSP-8 scientists formed the Immune Response Annotation Group (IRAG) and worked closely with the Wellcome Trust Sanger Institute on the community annotation of immunity associated genes in the pig genome (2012), resulting in the detailed manual annotation of over 1,400 genes in the first draft assembly of the swine genome. **Impact(s):** This annotation work expanded swine bioinformatic capabilities for immune response associated genes, as well as identifying hundreds of missing genes in the assembly. These data are of high importance as geneticists use the genome assembly for genetic improvement of pigs.
- A dramatically improved swine genome assembly (2016) was created by researchers in the UK with contributions to gene annotation by NRSP-8 scientists. **Impact(s):** The one hundred-fold increase in quality of the sequence data and gene annotations will dramatically improve the use of the porcine genome, through increasing the accuracy of SNP analysis, gene mapping of traits and regulatory network analysis.

### Direct contributions to Objective 2:

- A public-private collaboration, supported with NRSP-8 Swine Coordination funds, assessed the recently released GeneSeek Genomic Profiler for Porcine LD (GPP-LD) SNP chip list for accuracy of imputing genotypes for the Illumina Porcine SNP60. **Impact(s):** This project demonstrated the accuracy and cost-efficient use of the GPP-LD for implementation of genotype imputation for genomic selection in pigs. Data and tools are publicly available at [https://www.msu.edu/~steibelj/JP\\_files/imputation.html](https://www.msu.edu/~steibelj/JP_files/imputation.html).
- Methods were published for conducting meta-analyses to combine genome-wide association (GWAS) studies, and these methods were used to combine SNP and phenotypic data for a meta-analysis of meat quality data for three populations from MSU and US-MARC (collaboration funded by the National Pork Board). SNP marker data for National Swine Registry (NSR) populations has been used to establish baselines for breed identification. **Impact(s):** A strategy has been proposed for implementing use of SNP markers for breed composition estimation in the Yorkshire breed. (Funded by NSR). This project provided improved methods for genomic selection, GWAS and eQTL analyses in pigs.
- A candidate genetic marker (GBP5) associated with resistance/susceptibility to primary PRRSV infection has been identified based on transcriptomic data performed with PRRS Host Genetics Consortium (PHGC) trial samples. **Impact(s):** These results provide a promising candidate gene for further functional work to validate its role in the host response to PRRSV infection. This genetic variant (now included on the GPP-LD SNP chip) will help breeders select for pigs, regardless of breed, with the favorable genotype for PRRS resistance
- Important progress was made in the dissection of the QTL associated with PCV2 viremia located at the proximal end of SSC12. Potential genes and functional polymorphisms were evaluated using long-reads genomic sequences, gene annotation and RNA-seq. **Impact(s):** Initial results indicate novel genes and mechanisms potentially involved in PCV2 innate immune response. Marker-assisted selection for the favorable allele will decrease susceptibility to PCVAD and will provide a complementary solution to vaccination.
- Identified SNP markers and combinations of markers associated with age at puberty (AP), in particular early onset puberty, and sow reproductive longevity by conducting a genome-wide characterization of the cross between commercial Landrace and Nebraska Index Line (NIL), which has been subjected to long-term selection



for litter size. **Impact(s):** Candidate genes and SNPs located in the QTL region for litter size traits identified by GWAS, genome and RNA sequencing could explain some of the observed phenotypic variation. Following validation, some of these polymorphisms could be used in selection to improve sow fertility.

- Genomic and phenotypic predictors of PRRS resistance in pregnant gilts and their fetuses have been identified in collaboration between NRSP-8 and Canadian researchers. Gene expression data suggested that the immune response to PRRSV infection is faster in resistant versus susceptible fetuses, thus possibly contributing to different levels of fetal pathology. **Impact(s):** Overall, the findings provide insight into anti-viral immune responses that may help researchers to determine new ways to reduce the impact of PRRS in pregnant gilts and to select for genetically resistant breeders.

### **Direct contributions to Objective 3:**

- The PRRS Host Genomic Consortium (PHGC) Database <http://www.animalgenome.org/lunney/index.php> was developed by scientists at Iowa State, Kansas State and BARC to house the large amounts of phenotypic and genotypic data that are collected across several research labs in the PRRS research community. The database has been expanded to include SNP genotype data and tissue gene expression data from arrays, next generation sequencing, RNA-seq and NanoString codeset data. **Impact(s):** The PHGC database is continuing to be used to identify genes and pathways linked to phenotypes recorded in the database. The website has been used by many researchers interested in the genetic control of the phenotypic response to PRRSV infection and vaccination. It has enabled real-time data sharing among users from geographically disparate locations; the website has had up to 93,000 visitors in the last few years, from >1,000 unique Internet IP addresses.
- A public website providing information on genomic data for the USDA-NIFA funded project 2011-68004-30336 was created to increase stakeholder awareness of genome-based analyses in swine phenotypic traits of economic importance ([www.Swinefeedefficiency.com](http://www.Swinefeedefficiency.com)). **Impact(s):** The website is used by visitors from over 1,000 unique IP addresses each month.

### **Communication:**

- NRSP-8 members and others wrote and published a refereed journal article describing the goals of the Functional Annotation of Animal Genomes (FAANG) consortium in 2015. **Impact(s):** Cited 27 times by PubMed articles through February 2017, this paper greatly increased the visibility of this new project, as well as established the standards and methods required to participate, a critical organizational step for the FAANG consortium.
- The Swine and Bioinformatics Coordination Program develop and continues to host an open website ([www.faang.org](http://www.faang.org)) which provides information and coordination of the community developing this effort. **Impact(s):** The website is a clearinghouse for information on FAANG for contributors as well as the general public. The site has been visited over 65,000 times by unique IP addresses since 2015.
- The Swine and Bioinformatics Coordinators and others wrote and published a refereed journal article describing a public Workshop on FAANG “Gathering On-FAANG” ([GO-FAANG], October 7-8, 2015) in Washington DC. **Impact(s):** Increased visibility of the FAANG project to non-attendees through this publication will advance both the understanding of FAANG goals and opportunities for funding of animal genomics research worldwide.

### **Research support mini-grants (coordinator grants):**

- A public-private collaboration between 2 NRSP-8 supported Experiment Stations (MI, IA) and Affymetrix, Inc. successfully tested a high-density 670K (HD) SNP genotyping platform for swine. **Impact(s):** Science-based evaluation of the HD chip across US swine breeds will expand proven genetic tools available for researchers and industry for genetic improvement.

- A second public-private collaboration featured NRSP-8 organization of support from the National Pork Board (\$30,000) as well as coordinator support to leverage Federal research dollars. With this support, a USDA-NIFA funded project was funded, to functionally annotate the genome of swine and other species (2015-67015-22940 “Genome wide identification and annotation of Functional Regulatory regions in Livestock Species” Zhou, H., Korf, I., Ross, PA. **\$499,842**. The overall goal of this project is to generate a comprehensive resource of functional regulatory elements for the chicken, cattle, and pig genomes. All work relies on the genomic and bioinformatics tools developed by NRSP-8 researchers and researchers across the globe. **Impact(s):** This pilot project will lay the foundation for improved use of the swine genome for genetic improvement by industry. Financial support by a major commodity group also demonstrated the clear support of industry for this pre-competitive research.
- Contributions from Bioinformatics, Poultry, Sheep and Swine Genome Coordination Programs (\$10,000) were leveraged to successfully obtain conference funding (~\$30,000) from Government (USDA-NIFA, NSF) and industry (Illumina, Inc.) to hold a Workshop on the new Functional Genomics of Animal Genomes (FAANG) in Washington DC, attended by six participating funding agencies across three countries, as well as private companies. **Impact(s):** The livestock genetics and federal agencies communities became familiar with the importance of data that identifies the functional components of the genome for any species. Through in-depth discussions in two small groups, the FAANG community created excellent working relationships and developed a plan for sharing of resources and information.

#### **Leveraged funds and stakeholders’ use of project outputs:**

Leveraged funds from diverse projects totaling \$9,384,996. The overall total leveraged funds include \$8,229,905 from combined federal sources, \$533,500 in local/institutional funds, and \$621,591 from industry. Selected grants are highlighted below.

- 2013-2017: USDA-NIFA-AFRI. 2013-68004-20362. “Genetically Improving Resistance of Pigs to PRRS Virus infection.” Dekkers, J. C.; Tuggle, C. K.; Stalder, K.; Reecy, J., **\$2,998,931**. The long-term objective is to enhance the ability of pigs to resist and minimize the impact of the most costly infectious disease in the US pork industry: Porcine Reproductive and Respiratory Syndrome (PRRS). The project is building on prior genetic analyses as well as novel such analyses, both made possible by genomic tools derived from the work of NRSP-8 members. **Impact(s):** To date, this group has validated the effect of a genetic marker previously identified to be associated with improved host response to PRRS virus infection under experimental PRRS-only challenge, under conditions that are closer to conditions that pigs experience in the field. They also demonstrated that genetic selection for improved host response of pigs to PRRS infection is possible. The identified genetic marker is available to the industry, which will help to address the enormous economic and animal welfare impacts of PRRS in the US and global industry.
- 2013-2017: USDA-NIFA-AFRI “Translational Genomics For Improving Sow Reproductive Longevity” Ciobanu, D. C.; Kachman, S. D.; Lents, C. A.; Safranski, T. J. **\$1,166,650**. The long-term goal of this project is to develop a panel of genetic markers that will predict at weaning, gilts with superior propensity for reproductive longevity, which in turn will reduce culling rates and the cost associated with developing replacement sows. This project is capitalizing on prior genetic results using SNP panels created using NRSP-8-supported genomic and bioinformatics resources. **Impact(s):** The integration of RNA and genome sequence data and evaluation of a novel approach for genome-wide associations has the potential to lead to the discovery of functional mutations that could reduce age at puberty, improve fertility and reproductive longevity, leading to an increase in sow net values in the commercial herds.
- 2015-2017 USDA-NIFA-AFRI “The TET Family regulates embryogenesis by controlling both DNA and histone methylation.” Lee, K. **\$334,263** This project is studying the action of TET family genes, which are epigenetic regulators in various cell types, during early porcine embryogenesis to expand our knowledge of how epigenetic marks are regulated during embryogenesis. The researchers are testing the specific involvement of TET family genes on epigenetic modifications, occurring after fertilization, through recent molecular analysis technologies. These studies are using the genome assembly to design tools for mutating

specific TET genes, as well as use the annotation of the porcine genome assembly to perform the epigenetic analyses. **Impact(s):** Understanding the action of key epigenetic regulators, such as TET family, during embryogenesis will allow improvements in availability of in vitro-derived embryos and increase embryo viability in domestic species.

- 2014-2017 USDA-NIFA-AFRI “Reducing production losses using behavioral and genomic tools to identify pigs suited for group living.” Siegford, J.M. **\$749,059**. In pigs, social behaviors can affect performance of all pigs in a group or result in injury or lameness. This overall goal of this project is to ensure global food security by improving use of behavior in breeding programs to reduce loss from non-infectious diseases in group-housed pigs. The scientists will use genotyping tools and resources supported by NRSP-8 project outputs to estimate genetic parameters and perform genome-wide prediction and association of social behavioral traits expressed by group-housed pigs to determine underlying genomic control of these traits. **Impact(s):** By examining social behaviors of group-housed pigs and understanding genetic control of these traits, we will develop tools allowing producers to better select and manage group-housed pigs, including gestating swine. Importantly, such information will reduce animal losses occurring from non-infectious diseases such as injury and lameness.

#### **Travel support and opportunities for trainings:**

- NRSP-8 Swine Coordination program provided competitively award funds for five graduate students to travel and present their genomics research at the Plant and Animal Genome meetings from 2013 to 2017. **Impact(s):** Increased visibility of young scientists and additional experience in presenting their research work will improve the education and professional development of these promising animal genome scientists.

#### **Major impact products (could be potential impact):**

- Porcine reproductive and respiratory syndrome (PRRS) is the most economically important disease of pigs worldwide and isolates vary greatly. The PRRS Host Genetics Consortium (PHGC) researchers compared host responses to genetically different PRRS virus isolates. NRSP-8 researchers statistically evaluated and affirmed that the resistance associated swine chromosome 4 (SSC4) allele had an effect on viremia with faster virus clearance and positive effects on weight gain. Estimates of heritability of genetic resistance to PRRSV infection were moderate for different PRRSV isolates. **Impact(s):** Genetic selection in the swine industry for increased resistance to genetically distinct PRRSV isolates is now possible.

## **BIOINFORMATICS**

<http://www.animalgenome.org/bioinfo/>

### **Direct contributions to Objective 3:**

- **Continued curation and development of the Animal Quantitative Trait Loci database (QTLdb).**
  - Horse and catfish were added to the Animal QTLdb.
  - Animal QTLdb database (regularly updated), a total of 104,272 new QTL/association data has been curated into the Animal QTLdb. The database contains Cattle: 95,332; Chicken: 6,633; Horse: 1,245; Pig: 16,516; Sheep: 1,412; Rainbow trout: 127 QTL reports. **Impact(s):** The database provides a set of useful molecular breeding tools allowing selection for improved production traits in various species.
  - Development of curation tools for Animal QTLdb—allow batch entry of pre-tabulated data. **Impact(s):** This has greatly accelerated the speed of data entry for large volumes of data using a semi-automated method.
  - Additional support tools for Animal QTLdb have been released—enabled multiple genomes for cattle, chicken, and sheep. **Impact(s):** Allows QTL/association data alignment to each respective genome.
  - New data alliances with UCSC Genome Browser and the Monarch Initiative have been established. **Impact(s):** This allows users to obtain Animal QTLdb data via more avenues.
  - Integration of the Animal Trait Ontology into the Vertebrate Trait Ontology (<http://bioportal.bioontology.org/ontologies/VT>). We have continued working with the Rat Genome Database to integrate ATO terms that are not applicable to the Vertebrate Trait Ontology into the Clinical Measurement Ontology (<http://bioportal.bioontology.org/ontologies/CMO>). Traits specific to livestock products continue to be incorporated into a Livestock Product Trait Ontology (LPT), which is available on NCBO's BioPortal (<http://bioportal.bioontology.org/ontologies/LPT>). We have also continued mapping the cattle, pig, chicken, sheep, and horse QTL traits to the Vertebrate Trait Ontology (VT), LPT, and Clinical Measurement Ontology (CMO) to help standardize the trait nomenclature used in the QTLdb. Now VT data download has also been made possible through the Github portal. **Impact(s):** Allows users to query Animal QTLdb data more effectively.
  - The VT/LPT/CMO cross mapping has been employed by the Animal QTLdb and VCMMap tools. Annotation to the VT is also available for rat QTL data in the Rat Genome Database and for mouse strain measurements in the Mouse Phenome Database. We have also been integrating information from multiple resources, e.g. FAO - International Domestic Livestock Resources Information, Oklahoma State University - Breeds of Livestock web site, and Wikipedia, as well as requests from community members, to continue development of a Livestock Breed Ontology (LBO; <http://www.animalgenome.org/bioinfo/projects/lbo/>).
  - The Animal QTLdb has undergone continued upgrades to use MIQAS for data curation and data integration (<http://www.animalgenome.org/QTLdb/doc/minfo/>). Minimal standards for curation into the Animal QTLdb have been established (<http://www.animalgenome.org/QTLdb/doc/minfo/>). **Impact(s):** This will increase the quality of the data present in Animal QTLdb.
  - Expansion of the Data Repository for the aquaculture, cattle, chicken, horse, pig, and sheep communities to share their genome analysis data. **Impact(s):** This resource has proven useful for the community (<http://www.animalgenome.org/repository>). To date there are 1,140 data files, totaling 140 Gb, shared through this platform. This includes supplementary data files to publications deposited by the authors.
- **Development of a Collaborative VCF Info Mining Platform.** A recent effort was to establish a partner relationship with the European Variation Archive (EVA) in order to make shared VCF files more accessible and adherent to a better file format standard. **Impact(s):** This platform is continually used by the community and allows for more efficient on-line file sharing.
- **Collaboration with and support of community research groups.**

- PRRS project database and web site: Partnered with researchers at Kansas State University, Michigan State University, Iowa State University, and U.S. Department of Agriculture, to further developed and improve the web-interfaced relational databases to store and disseminate phenotypic and genotypic information from large genomic studies in farm animals and better serve the needs of researchers. New animal genotype and phenotype data were added. The database/web site operations have been smooth with little or no down-time (<http://www.animalgenome.org/lunney>).
- Set up a virtual machine site to host the Online Mendelian Inheritance in Animals (OMIA) database created and maintained by Dr. Frank Nicholas at the University of Sydney (<http://omia.animalgenome.org/>).
- Provided a dedicated virtual machine platform to a USDA-funded project to develop cyber resources for the Striped Bass Genome Database activities, led by Benjamin Reading and Charles Opperman at North Carolina State University (<http://stripedbass.animalgenome.org/>). The database and web site have been maintained for the past 3 years.
- Developed and maintained the web site and tools for the Functional Annotation of ANimal Genomes (FAANG) consortium. The efforts included setting mailing lists for each committee and subcommittee, a user forum, interactive meeting sites, platform for collaborative funding applications, tools for the coordination of sample collections, and online publishing capabilities, etc., to support this large international collaboration (<http://www.faang.org/>). We also helped to support the GO-FAANG meeting in Washington DC on October 7-8, 2015.
- A collaborative site at iPlant has been set up to share some of the web service loads, including the JBrowse server to serve the cattle, chicken, pig, sheep, and horse communities for QTL/association data alignment with annotated genes and other genome features (<http://i.animalgenome.org/jbrowse>).
- **NAGRP Tool Box has been actively maintained for online use by the community** (<http://www.animalgenome.org/bioinfo/tools/>).
- **Overall impact(s):** The Bioinformatics helpdesk annually helps more than 60 research groups. Involvement has ranged from data transfer, data assembly, and data analysis, to software applications, code development, information resources, etc.

**National Animal Genome Research Program (NSRP-8)  
2018 Project proposal renewal request**

**Reviewer Comments and Response to Reviewers (in blue)**

**Reviewer number 1**

It is very encouraging to perceive the progress of the NRSP-8 program during the last couple of years. As reported in the progress report NRSP-8 seems to have made substantial progress in addressing the stated objectives and goals. NRSP-8 as an umbrella organization appears to have greatly supported the needs of the animal genomics community. The program has made significant improvements in terms of resource scaling, added functionality and engaging researchers from diverse animal genomics communities. Significant developments include efforts in fostering the large community of scientists, development of critical infrastructure to conduct genome-level studies, advance an open-access multi-species bioinformatics tool set, support for sequencing and assembly of genomes, organization of workshops and conferences for effective communication between groups to share results and forge future collaborations, support travel for students and invited speakers, preparation of multi-institutional grant proposals through leveraging NRSP-8 resources to procure additional funding , and formation of large collaborative research groups.

The NRSP-8 has made great strides in adapting new technologies for genome analysis – for example the focus on reference genome sequencing and follow-up population-level genomic studies based on high throughput resequencing technologies; application of the SNP-chip technologies for genomic selection, application of RNA-Seq methods for improved annotations of reference genomes, gene expression studies, development of software tools to integrate available sources of genome and functional data (WGS, SNP, RNA-sequencing, proteomics and metabolomics) in agricultural species to better understand complex phenotypic traits using metabolic syndrome in domesticated animals are a few notable achievements.

The development of the informatics portal (<https://www.animalgenome.org/bioinfo/tools/>) to search, visualize, and share agricultural genomics data is particularly important as it provides a valuable data resource to the community. This site hosts a comprehensive list of all bioinformatics tools and databases developed under the NRSP-8 program and proves to be an extremely useful resource to connect geographically distributed animal genomics communities.

Particularly the initiation of the FAANG consortium in 2014 appears to have accelerated collaborative activities between various animal genomics groups.

The NRSP-8 workshops are an important activity for dissemination of information to stakeholders from the academic, government and industry groups, provides a forum for scientists, students and post docs to share their research and foster future collaborations. The NRSP-8 has effectively used their funding to promote travel for students and post docs to PAG meetings annually. Overall, the reported activities point to promising achievements in the field and fully justify the investments to this program.

## **Reviewer number 2**

### **Overall:**

This proposal is well thought out and on target. While relatively little detail is provided on how many objectives will be achieved, this reviewer finds that level of detail acceptable. I recognize that this document is as much a vision as a recipe for success. Given the success and impact of this group in the past – I am comfortable with most of the details. That being said, there are a few points that could use some more specifics. One concern that I have long held, is that identifying a causative variant is *really* tough... With SNP chips we can identify genomic regions quite readily, but it takes a lot of meiosis to get recombinations within a small region that provide insights that allow one to tease apart the causality of adjacent variants that are in high linkage disequilibrium. There may be new ways to consider this problem using gene editing, for example. This technology is both expensive and unproven in high volume.

Regarding Obj.2.2, we agree with the reviewer. Developing models, algorithms, pipelines to facilitate the identification of causal variants may be hard due to the need for so many meiosis events. However, there is still a need to find more highly predictive variants and/or causal variants when possible. Therefore, the word “causal” was replaced with “causal and/or highly predictive”.

Regarding Obj.2.3, we still think that applying various approaches like CRISPR is needed to characterize the genetic variations previously identified through GWAS as putatively associated with traits. While we acknowledge that these technologies are currently expensive and unproven, there are likely to become more affordable and to be supported by more robust evidence over time.

Some details on how the money from the last proposal was spent would be helpful. There are examples of past coordinator expenses – but these do not provide amounts spent on these items. Similarly, “Research support mini-grants” are listed with few items identifying funding levels.

Examples of past coordinator expenses were provided with the budget request. In addition, the Rewriting Committee invested ample efforts on preparing an accomplishment report that reflects the ROI rather on collecting detailed data on how the money was spent. According to Dr. Eric Yong, the NRSP-8 Accomplishment report was well perceived by the NIFA communications office and by kglobal (ESCAP's communications firm). We will be glad to collect more data on how money was spent, however, given that the budget of each species is handled by a separate experimental station, this will require extra time beyond the current deadline, January 15, 2018.

Addressing the outputs of the two meetings recently held in Beltsville on “Livestock High-Throughput Phenotyping and Big Data Analytics” and “Genome to Phenome: A USDA Blueprint for Animal Production” as they might impact NRSP-8 objectives. Most of the attendees of those meetings were NRSP-8 members.

As the reviewer mentioned below, it is tough to tie this to the G2P workshop in Beltsville before the report is finalized. Therefore, we added a statement that the updated blueprint will be used as a guide.

*“Blueprint for USDA Efforts in Agricultural Animal Genomics 2008-2017,” was used as a guide in formulating the objectives for the previous NRSP-8 objectives. While this proposal was due for submission, a new Blueprint document “Genome to Phenome: An USDA Blueprint for Animal Production” was being prepared. The updated blueprint, when available will be used as a guide to adjust the objectives of this proposal”.*

### **Rationale – Grand Challenges:**

GC1: How will this challenge be accomplished through funding NRSP-8 differently?

*We added this statement “Genomics selection of superior genotypes will help addressing this challenge i.e. enhancing the animal production yields and profitability while reducing the adverse environmental impacts.”*

GC2: I challenge the assertion that “Genome-enabled selection practices increasingly account for the effects of genotype on the utilization and assimilation of different animal diets and the potential downstream environmental impacts.” It may be a reasonable goal, but I don’t think we are using genome enabled selection accounting for effects on genotype except for a few large QTL/QTN. I think we are even further away from predicting impacts on downstream impacts. Again, I don’t take issue with this statement as a goal, but I think the statement needs to be adjusted. The GC2 statement calls for development of breeds – I think that could be a laudable objective, particularly in pulling together experiment station resources from multiple states... like was done with NC-1, NC-2, etc.

*We changed the statement to “Genome-enabled selection practices **need to increasingly...**”*

GC3: This seems to be a bit of a reach - I really don’t see where genomics can influence these post-harvest challenges.

*To further explain this point we added this statement “Pre- and post- harvesting environments affect shelf-life and quality of the food-animal products. Various genomics approaches allow understanding the biochemical processes through which the animal interacts with the environment pre-, post- and during the harvesting process. In addition, genomics can be used to select for animals that yield products of improved shelf-life and quality and reduced food waste”.*

GC5: I am not sure that low-priced is a goal, but rather fair or reasonable priced products. The producer needs to maintain profitability for the enterprise to be sustainable. Certainly, improving efficiencies will help in that effort.

*Whanged “low-priced” to “reasonably-priced”.*

GC6: A statement about the benefits of animal protein in the diets of people in moderation – especially young children.



We added this statement *“Animal products are excellent source of proteins, fats, vitamins and minerals. Animal proteins contain all the essential amino acids needed for healthy growth especially in children”*.

### **Objectives:**

The sequencing and assembly parts of the objective as written should be accomplished in a year or two – then what? There are several breeds that could use breed specific assemblies (Holstein, Angus, Jersey, Nelore, etc.). It would be interesting to phase the chromosomes of a few important animals from these same breeds. How will the functional annotation be done to accurately ascribe function?

The first specific objective 1.1 was changed to *“Initiate creation of draft genome assemblies for economically important species and breeds for which assemblies are not yet available”*.

Objective 1.2 already mentioned phasing out chromosomes *“Improve existing genome assemblies to close gaps and improve assembly order, especially for highly repetitive sequence regions, such as those in centromeres and on the sex chromosomes”*.

This statement was added to Obj. 1.4 *“The aim is to deliver well-standardized and documented datasets from a set of individuals representing species with reference quality genome assemblies and substantial publicly available phenotypic datasets”*.

It would be nice to tie this to the G2P workshop in Beltsville - I concede that this is tough before the report is finalized... maybe just add a statement that the updated blueprint will be used as a guide.

As in objective 2 -it would make sense to add a statement about using the report from the high-throughput-phenotyping workshop as a guide for prioritizing goals. I think it would make sense for NRSP-8 to provide leadership in warehousing, sharing, and coordinated development of software, scripts, and other software tools.

As mentioned above, page 3 at the end of the introduction to the objectives, this statement was added:

*“Blueprint for USDA Efforts in Agricultural Animal Genomics 2008-2017,” was used as a guide in formulating the objectives for the previous NRSP-8 objectives. While this proposal was due for submission, a new Blueprint document “Genome to Phenome: An USDA Blueprint for Animal Production” was being prepared. The updated blueprint, when available will be used as a guide to adjust the objectives of this proposal”*.

### **Reviewer number 3**

The NRSP-8 project renewal request demonstrates, in clear and persuasive language, the critical need for support of infrastructure for animal genomics research. The accomplishments for the 2013-2017 period are significant for all species.

As outlined in a recent report sponsored by the National Academy of Sciences<sup>1</sup>, among the highest priorities for animal agriculture research investment are optimizing livestock sustainability and productivity. Genomics research is critical for advancing sustainability of animal production. Another application of genomics research not mentioned is the enhancement of nutritional quality and healthfulness of meat products (Strategic Goal 4 of the 2014 USDA Research, Education and Economics Action Plan). It might be worth considering the potential to improve human nutritional outcomes, especially with the public interest in health outcomes linked to meat consumption. For example, genomics has the potential to increase omega-3 levels and other important nutrients, and increase lean meat content, in animal food products.

The is addresses under the contribution of animal genomics to **Grand Challenge 3** from the APLU document:

*“Pre- and post- harvesting environments affect shelf-life, nutritional content and quality of food-animal products. Various genomics approaches allow understanding the biochemical processes through which the animal interacts with the environment pre-, post- and during the harvesting process. Genomics research on local breeds and species will allow us to optimize regionally available food systems. Selection of animals best suited for production in a given environment via genomic technologies (precision management systems) can reduce food loss and waste by creating efficient local distribution systems and by selection for animals that produce products with improved shelf-life and quality.”*

Under the rationale section, the proposal refers to the “Challenge of Change,<sup>2</sup>” a document from APLU that is aimed primarily at global food security, which is an interesting choice of reference for the rationale. While much U.S. genomics research is relevant to Challenge of Change, such as understanding climate resilience / tropical adaptation in livestock, disease resistance and potential for zoonotic transmission, one tends to think of U.S. genomics selection as having focused primarily on improved performance of domestic breeds up to now. The question that arises is whether U.S. animal genomics research will shift towards global issues, or continue to focus primarily on U.S. food systems. I respectively suggest the writers consider instead using the One Health concept in the rationale, as this provides a global context for discussing the impact of genomics on food security, antimicrobial resistance, environmental sustainability, animal welfare and human health.

The reviewer is correct that throughout the rationale as presented under the grand challenges and in other places in the document that the concepts of one health are mentioned including food security, environmental impacts, animal health and welfare and impacts on human health. It is unclear how reorganizing these arguments under the umbrella of “one health” will change the outcomes and emphasis

of the NRSP-8. In fact, much of the “one health” community is currently focused on supporting efforts that span two or more components of the animals, humans and the environment triad. Reframing NRSP-8 under the “one health” concept, may unfairly give the impression that the downstream work that NRSP-8 supports is focused across the one health space, whereas NRSP-8 is mainly focused on tools that support research in the “animal” component of the “one health” triad.

Involvement of an industry liaison is a good way to bridge between academia and industry. However, the impact on the animal agriculture industry is not well measured in the accomplishments and impacts section. Is it possible to encourage industry partnership and measure or give examples of the impact on industry? Also, stronger partnerships with NIH and NSF would be highly beneficial to this program.

The committee wonders if the reviewer had a chance to look at the Accomplishment Report that was provided as a separate document in addition to the Accomplishment section in the main document. As example *across species tools developed under objective 2 have allowed the dairy industry used SNP-chips to genotype nearly half a million dairy cattle allowing application of genomic selection which reduced animal selection time (from 5 years to 1 week) and increased genetic merit prediction accuracy by more than 30 percent with an estimated annual benefits of \$100 million per year.*

Several themes consistently emerge in regard to animal genetics and biotechnology research: (1) Social license, (2) Animal welfare, (3) Precision agriculture and (4) Capacity-building.

1. I highly encourage the NSRP-8 coordinators to consider how the program might support outreach and education efforts that would improve the public understanding and perception of animal biotechnologies. Public engagement is critical to preserving the availability of technologies such as gene-editing, and even genomic selection, for future use. As we have seen with GMOs, vaccines and other technologies, lack of transparency and erosion of public trust can have dire consequences for science.

While increasing outreach is a laudable goal, the scope of the NRSP-8 is limited by the budget. Active engagement by industry is sought in this proposal by including industry representatives as part of the technical communities and through species-specific websites and the inclusion of newsletters to update industry as well as other stakeholders for each species and through the bioinformatics coordinator. Without increasing the total budget allotment for NRSP-8 it was unclear to the writing committee how we could dramatically increase the amount of resources invested in outreach that would address the broad goals encompassed by NRSP-8.

2. Genetic selection has resulted in dramatic improvements in livestock performance in the last 50-100 years. For some species, these gains are still needed, yet for others it is time to shift to addressing challenges to health and wellbeing, and the environment.

Use of genetic technologies to advance the health and well-being and environmental impacts of animal agriculture is encompassed broadly throughout the document and references to “phenotype and important phenotypes” would include phenotypes that are relevant to health, well-being and the environment. As mentioned in the proposal, “While applying genetic tools to improve production and resilience of animals, we must account for animal health and welfare”

3. A topic of high interest at meetings including the Genome to Phenome 2017 meeting is the development of precision tools including rapid diagnostics, precision monitoring, digital- or cloud-based programs for animal management and others. High-throughput phenotyping tools, to make associations between genotype and phenotype, are needed.

These tools are addressed under Objective 2.4, to clarify we have added the phrases in red: *“Support deep phenotyping of important traits at the molecular, cellular, tissue and organismal levels, including the use of high-throughput technologies such as transcriptome sequencing, proteomics and metabolomics studies, whole-animal parameter monitoring, in vitro gene mutagenesis screening analyses and other tools to support precision monitoring.”*

4. There is a major need for agricultural scientists skilled in bioinformatics, data analytics, computer sciences, etc. I highly encourage the NRSP-8 program to support training opportunities in these fields for their students, in addition to the annual Plant and Animal Genome meeting.

Given the limited funds available for NRSP-8, we recommend using short-term face-to-face courses and online classes. The following objectives were modified to capture reviewer’s recommendation.

Obj. 1.9. Train the next generation of animal breeders in applying and developing new data analytics methods based on high-throughput genomic data to make genetic progress through online and face-to-face short courses.

Obj. 3.4. Help in training students/postdocs to be future leaders in agriculture-oriented bioinformatics, data and computational sciences.

Additional recommendations:

- High-density SNP chips that work across breeds, especially in the beef industry, that would allow selection for traits such as heat tolerance or disease resistance

This is directly supported under objectives 2.1.

- Identification of SNPs/QTLs that facilitate antimicrobial stewardship (e.g. resistance to BRD in cattle or coccidiosis in poultry, which often lead to antibiotic treatment for secondary infections).

This is directly supported under objectives 2.8.

- Better understanding of the role of regulatory elements and non-coding DNA in determining phenotype.

This is supported under objectives 1.4 and 1.5 as well as 2.2 and 2.5

- Infrastructure support for metagenomic/microbiome research to better understand gut health, reference populations linked with animal genome, microbial dynamics and selection pressure, and animal health and welfare under antibiotic-free production practices

This is addressed and directly supported under Objective 2.8: *“Advance metagenomic studies to help in discovery of novel pathogens, understanding host-pathogen interaction and determining the role of microbiota in agri-animal nutrition, health and reproductive performance.”*

#### REFERENCES

<sup>1</sup>Committee on Considerations for the Future of Animal Science Research; Science and Technology for Sustainability Program; Policy and Global Affairs; Board on Agriculture and Natural Resources; Division on Earth and Life Sciences; National Research Council. Critical Role of Animal Science Research in Food Security and Sustainability. Washington (DC): [National Academies Press \(US\)](#); 2015 Mar 31. Summary available from: <https://www.ncbi.nlm.nih.gov/books/NBK285709/>

<sup>2</sup><http://www.aplu.org/projects-and-initiatives/international-programs/challenge-of-change/index.html>

# Mid Term Review(Submitted)

Status: Complete

Project ID/Title: NRSP4: Facilitating Registration of Pest Management Technology for Specialty Crops and Specialty Uses

## Mission and Relevance

### 1. Mission:

The activity of an NRSP focuses on the development of enabling technologies, support activities (such as to collect, assemble, store, and distribute materials, resources and information), or the sharing of facilities needed to accomplish high priority research, but which is not of itself primarily research. Ideally, an NRSP would facilitate a broad array of research activities. The primary purpose of NRSPs shall not be solely to conduct research, as there are other available mechanisms for creating these types of projects including the multistate research projects and the National Research Project (NRP) options. Examples of NRSP activities might include collection of data that are widely used by other research groups and efforts; development of databases; or development of critical technologies."

**Are the activities of this NRSP consistent with the mission of the NRSP program?**

Yes ▼

### 2. (20 points) Relevance to National Issue:

All NRSPs must involve a national issue, relevant to and of use by most, if not all regions. These projects draw on the best minds and resources within and outside the State Agricultural Experiment Station (SAES) system to address the issues.

**Does this NRSP address a national issue?**

Yes ▼

### Comments

NSRP4 serves a vital need for specialty, field and ornamental crop minor use crop protection product registration. Specialty crops are important to every region of the country, and all benefit from work of NRSP-4, which is for practical purposes synonymous with the IR-4 Project. The NRSP-4 project also has specific regional representation in laboratories around the country, a unique feature among NRSP projects.

Application of environmentally-sound crop protection methods for specialty commodities is indeed a national issue. IR-4 directly addresses the need for pesticide use on specialty crops when development of such methods is not economically warranted by registrants. The level of impact varies by region, but all regions are engaged and benefit to some extent. There is special emphasis on biopesticide registration support, international harmonization activities involving MRLs, pollinator protection, public health, and invasive species management products.

It should also be noted that IR-4 brings in most of its funding from industry and other government sources, greatly leveraging the NRSP funding and maintaining a strong partnership between the SAES system and major industry partners.

### Total Points

20 ▼

### 3. (20 points) Relevance to Stakeholders:

**Is there evidence of stakeholder use of project outputs?**

Yes

Are there project outcomes that aide in development of or contribute to the discussion of public policy?

Yes

### If so, please describe

partnerships with stakeholders across the country. The results of the program directly impact stakeholders as new uses are approved and implemented. The recently released economic impact study again documented the impacts of the program.

IR-4 leadership and the CLC engage in a range of activities that touch on public policy as it relates to pesticide regulation and use, but it is an area that could be expanded. The program staff already carry a heavy workload, but it is a topic worthy of discussion by program leadership to build on its previous work on economic impact. This might be an area of interest for public policy experts to delve into using the IR-4 history and connections.

As an example of recent activity, the ornamental and pollinator protection workshops generated important discussion among stakeholders and those involved in public policy. Deliberate stakeholder engagement and participation in IR-4 management meetings and "hill" visits conveys needs, with opportunity to impact public policy. The potential for policy impact and discussion is facilitated through integration of IR-4 information into the "information supply chain".

### Total Points

18

## Implementation of the NRSP

### 1. (15 points) Management and Business Plan:

Each NRSP must have a well-developed business plan that describes how the project will be managed and funded for a five-year period. This plan includes a management structure to adequately integrate the efforts of multiple participants. The plan should include provisions for linking multiple sources of funding and leveraging those sources with the limited off-the-top research funds. The plan should demonstrate that alternative funding sources have been sought. This plan should include efforts to bring in new agencies, organizations, industry, foundations, etc. to help address the issues and provide funding for the project. All project proposals must provide evidence of contributions from experiment stations across the nation beyond what is available through off-the-top funds.

The midterm review must reflect progress toward meeting funding expectations. Failure to meet funding goals may result in alterations to the off the top budget contribution provided by the SAES system.

### Comments

The IR-4 Project currently relies to a relatively small extent on funding from NRSP-4, but NRSP-4 remains an important coordinating vehicle for the project. It is the largest of the NRSP projects from the standpoint of resource leveraging. Major additional funding comes directly from USDA-NIFA and USDA-ARS, and project funding comes from competitive grants and contracts. The project therefore requires a more thoroughly developed business plan than other NRSP projects. The administrative leadership has been examining the business plan on an ongoing basis, but especially now it is important to review and examine the business model with an eye toward maximum flexibility and continued partnership development.

Diminishing resources have led to infrastructure reorganization, and in some cases removal and redistribution of activities across each region. This was done because of careful planning and work by the Path Forward Working Group. We would have liked to see some discussion on this effort and planned activities and prospects of support moving into the next review/renewal period.

While the business plan is reasonable, the program would greatly benefit from an independent audit of both its management and

business practices. There are concerns that in an era of limited funding the resources provided to the program could be managed and used more efficiently, potentially via a new business model. For instance, concerns regarding the level of staffing and its efficient use have been raised in recent years. Such an audit could address management issues and enhance the level of confidence in the program. In an era of limited funding, availing itself of the use of electronic systems to enhance communications and reduce travel costs is one area the program could improve upon. Future administration by land-grant institutions is another area for concern, and one that has not yet been adequately addressed. Facilities and administration (F&A) costs will continue to increase, while AES resources will continue to decline. Thus, it is imperative that the program address the need to offset its F&A costs or it will be asked to relocate, as recently occurred at Cornell University.

#### Total Points

10

### 2. (15 points) Progress Toward Objectives and Projected Outcomes:

a. Objectives, milestones and deliverables should be described in sufficient detail such that progress can be measured.

b. The midterm review of the project must demonstrate productivity, progress toward original objectives and the relationship between projected goals, actual accomplishments and any impacts to date. As appropriate, this assessment must include an evaluation of stakeholders' use of project outputs to date.

#### Comments

This is the traditional strength of the program. The system is well established and the projects move efficiently through the system. There are occasional bumps, but leadership has been willing to critically self-evaluate and address problems as they arise. Objective description is clear and progress toward those objectives is documented in the IR-4 midterm summary. Stakeholders' use of results is well documented.

#### Total Points

14

### 3. (15 points) Integration:

a. Project proposals should indicate how efforts are integrated with extension or academic programs and how results might be of use by other potential stakeholders.

b. In the midterm review, the project must address actual collaborations and any new partnerships built during the project period. The report should address the degree to which the full team is engaged in project planning and implementation. Discuss plans to correct any weaknesses that may have been identified

#### Comments

The report indicates the expansion of international partnerships that facilitate data sharing and knowledge, and international trade. NRSP-4 is generally well integrated with extension, and many individual projects supported through IR-4 are with extension agents and specialists. By nature of its mission, IR-4 is less well integrated into academic programs. Partnerships within several USDA agencies and EPA are reported. This is an important aspect of IR-4 that should continue.

At the local level, the IR-4 program at UCD has been integrated with extension programs over the years but generally not academic programs. It has been hosted by the Department of Environmental Toxicology for space and administrative purposes and while generally not contributing to the department's academic mission (research and teaching), it has been a significant contributor to its outreach mission.



At MSU the program is well-connected with the faculty and other professionals involved in the fundamental mission of the program. These relationships help maintain strong connections to key stakeholder/industry groups. The vitality of the program is maintained through these individual relationships. However, the relationship with field-based Extension is not particularly strong. As key faculty retire we need to look at strengthening the ties with Extension for program execution and delivery.

#### Total Points

12

#### 4. (15 points) Outreach, Communications and Assessment:

All project proposals must have a sound outreach, communications and an assessment plan that seek to communicate the program's goals, accomplishments and outcomes/impacts. The communication plan must detail how results will be transferred to researchers and other end users and contain the following elements:

a. Clear identification of the intended audience(s) of the NRSP. Since this is a Research Support Project, in most instances the primary beneficiary of the results will be other scientists. However, careful consideration should be given to other possible users of the information (such as consumers, producers, governmental agencies (local, state and federal), general public, etc.)

Yes

b. Clear description of the engagement of stakeholders in the definition and/or conduct of the research support project.

Yes

c. Thorough description of the methodology to measure the accomplishments and impacts of the National Research Support Project and effectiveness of the communication plan. Methods such as surveys, town meetings, conferences, analyses of reference data (e.g. citation index, etc.), and use of professional evaluators should be considered.

Yes

d. Specific description for development of communication pieces describing the activities, accomplishments, and impacts of the NRSP. The communication pieces will be used with SAES/ARD directors, stakeholders and their organizations, funding sources and agencies, and congressional delegations.

Yes

e. Suggested mechanisms for distribution of the results of the research support project. Examples include sharing the results at annual meetings of stakeholders, providing material to the Budget and Advocacy Committee of the APLU Board on Agriculture Assembly and other appropriate committees within the SAES/ARD organization, and assisting NIFA in preparation of appropriate documents highlighting the impacts of the project.

The midterm review must demonstrate the extent to which the NRSP is working to effectively communicate project results to those who need them and their use by target audiences

Yes

#### Comments

The IR-4 Project has a well-developed communications arm through its website and other vehicles including technical reports, newsletters, and social media. They engage with scientists at state experiment stations and elsewhere, and with stakeholders at all levels, including USDA partners, industry, and legislators. There is always room for improvement in areas of communication; it is especially difficult for a project such as this one to gain public recognition.

The communications operations have been strong, but are probably ready for an update. As we face the challenges of the coming decades we need to look at modernizing communication methods and exploring the uses of social and other new media. Communications materials sufficiently convey important content and activities, but care should be taken not to over saturate stakeholders and policy makers, so communications must be measured, focused and deliberate. The national IR-4 website link referred to in the report appears to be broken. Are there opportunities to link the IR-4 website to major partners?

**Total Points**

13

# Mid Term Review(Submitted)

Status: Complete

**Project ID/Title:** NRSP6: The US Potato Genebank: Acquisition, Classification, Preservation, Evaluation and Distribution of Potato (Solanum) Germplasm

## Mission and Relevance

### 1. Mission:

The activity of an NRSP focuses on the development of enabling technologies, support activities (such as to collect, assemble, store, and distribute materials, resources and information), or the sharing of facilities needed to accomplish high priority research, but which is not of itself primarily research. Ideally, an NRSP would facilitate a broad array of research activities. The primary purpose of NRSPs shall not be solely to conduct research, as there are other available mechanisms for creating these types of projects including the multistate research projects and the National Research Project (NRP) options. Examples of NRSP activities might include collection of data that are widely used by other research groups and efforts; development of databases; or development of critical technologies."

**Are the activities of this NRSP consistent with the mission of the NRSP program?**

Yes ▼

### 2. (20 points) Relevance to National Issue:

All NRSPs must involve a national issue, relevant to and of use by most, if not all regions. These projects draw on the best minds and resources within and outside the State Agricultural Experiment Station (SAES) system to address the issues.

**Does this NRSP address a national issue?**

Yes ▼

## Comments

Potato, the top vegetable crop in the USA and world, produces more food per acre than any other major crop, which, along with its unmatched palatability makes it our most valuable resource for feeding an increasing global population. The National Potato Council statistical yearbook for 2016 lists 25 states with over \$1M in crop production for a national total of ~\$4B farmgate. Of course, with 60% of the potato crop eaten as processed foods, the value of NRSP6 germplasm magnifies and extends to all states' food economies as value-added potato products. This prominence also makes potato germplasm an important factor in issues of major social concern, like nutrition, health, and healthcare costs, pesticide impact on people and environment, and climate change. Germplasm of potato is of particular value, since potato has more useful related exotic species and allele diversity than any other major crop. The job of mining the benefits of potato germplasm is certainly not winding down. On the contrary, new challenges to the crop continue to arise, and form the basis of vital and vigorous research efforts by SAES, USDA/ARS, and industry research and breeding. Additionally, new techniques for trait evaluation, and especially germplasm selection and enhancement through DNA technology greatly increase our power to deploy germplasm. A need exists for new techniques for germplasm uses, for example to improve seed germination, long-term storage, and interspecific crossability—the kind of things genebank staff are particularly well-suited to advance. This situation has resulted in many professional researchers and breeders who require access to potato germplasm resulting in demand for NRSP6 germplasm to be increased over 25% from the previous 5-year project term. Since potato is "prohibited" for import except with special quarantine permit, scientists depend on the NRSP6 germplasm already in the USA.

NRSP6 provides critical support to the USDA Potato Genebank, enabling it to provide high-impact enabling technologies, germplasm and associated information readily available to researchers and breeders to facilitate genetic improvement and research. The Genebank accomplishes this by acquiring new useful germplasm, classifying it, multiplying it in vigorous, disease-free form, evaluating it for useful traits, and distributing it free to researchers across the USA and abroad. The genebank collection contains over 5,000 seed populations of about 100 species, and 1,500 clonal varieties and genetic stocks. Demand for these materials continues to steadily increase to over 10,000 units (seed or tuber samples) per year. These stocks, many collected from

now inaccessible wild lands in Latin America over the past 75 years, thus represent an irreplaceable and well-curated genetic resource. Scientists cannot access them from any other source in the US, and importation from other genebanks or re-collecting is impractical or impossible. These living collections require constant curation and will be lost forever without reliable long-term, continual, and persistent funding for their maintenance. The Genebank makes full and effective use of technology to enhance access to the germplasm and associated documentation. All available information on the materials—origin, taxonomy, useful traits, how to order-- is maintained fully on-line. The Potato Genebank maintains a complete website with contact information, new germplasm offerings, germplasm news, technical tips, and administrative reports. All of these efforts promote the use of the germplasm resource to improve the potato crop in ways that directly benefit the nation's farmers and consumers.

#### Total Points

### 3. (20 points) Relevance to Stakeholders:

**Is there evidence of stakeholder use of project outputs?**

**Are there project outcomes that aide in development of or contribute to the discussion of public policy?**

#### If so, please describe

In the past couple of years, breeders achieved a revolutionary remaking of potato as a diploid inbred crop using haploidizing technology and selfing mutants discovered in NRSP6 germplasm-- by NRSP6 staff. NRSP6 further supported the effort in the current project term by importing valuable new stocks and testing techniques. The ploidy manipulation technique that resulted in Yukon Gold was also developed with NRSP stocks--by NRSP6 staff. Wisconsin collaborators isolated and incorporated the gene providing durable resistance to late blight from a wild species collected in Mexico, preserved and studied in the genebank long before its potential was recognized. Washington state collaborators incorporated potent nematode resistance. In 2017, Idaho collaborators reported incorporation of resistance to greening (responsible for 10-15% waste) -- discovered by NRSP6 staff. Collaborators used NRSP6 stocks to develop breeding stocks resistant to verticillium and scab, and donated those back to the genebank. NRSP6 staff helped Oregon State researchers identify germplasm with high folate and resistance to nematodes. NRSP6 staff produced custom hybrids and propagules to help industry partners breed lines with much greater levels of an anti-appetite compound aimed at reducing obesity. At least 70% of named US cultivars contain exotic germplasm from the genebank in their pedigrees. For example, in Wisconsin, of the past 8 cultivar releases from the breeding program, 6 have wild species germplasm as parents obtained directly from NRSP6. NRSP6 staff bred cold tolerant families from which two new cultivars were selected for release in 2018 in Peru. Sequencing the potato genome depended on the use of genetic stocks from NRSP6 developed by collaborators at Virginia Tech. The revolutionary intragenic innate potato lines from Simplot in Idaho were developed through the use of exotic germplasm from NRSP6. Two new potato pests—Zebra chip and Dickeya-- have become very serious in recent years. In the current NRSP6 project, we are cooperating with state and federal scientists in Colorado, Texas, New York, and Washington, screening for and finding potent resistance in exotic germplasm from NRSP6. All these advances would not have been possible using germplasm in the common breeding pool. They needed to be accessed from exotic germplasm. And that exotic germplasm is only available in the USA from NRSP6. The use of NRSP6 germplasm by stakeholders has been very robust in the past, increasing knowledge and breeding products that have had a great positive impact on the crop-- and this process is increasing in the current project term.

Yes, ready access to this large genetic resource primarily contributes to basic knowledge and provides resilience to potato as a food source. Improved varieties result in better nutrition, thereby improving quality of life and lowering healthcare costs. Increased potato productivity lowers costs, resulting in more disposable income and a raised standard of living. Natural genetic resistances to crop pests and diseases reduces the need for pesticides, thus lower impact on farm workers, consumers, and the environment. Improved efficiency of water and fertilizer use further reduces environmental impact. A potato crop more tolerant to environmental stresses is able to better adapt to climate change. In addition to these scientific advances, genebank staff contribute to discussion of public policy by hosting tours of students and faculty and via invited lectures in the US and abroad during which national policy issues related to conserving germplasm are discussed.

#### Total Points

# Implementation of the NRSP

## 1. (15 points) Management and Business Plan:

Each NRSP must have a well-developed business plan that describes how the project will be managed and funded for a five-year period. This plan includes a management structure to adequately integrate the efforts of multiple participants. The plan should include provisions for linking multiple sources of funding and leveraging those sources with the limited off-the-top research funds. The plan should demonstrate that alternative funding sources have been sought. This plan should include efforts to bring in new agencies, organizations, industry, foundations, etc. to help address the issues and provide funding for the project. All project proposals must provide evidence of contributions from experiment stations across the nation beyond what is available through off-the-top funds.

The midterm review must reflect progress toward meeting funding expectations. Failure to meet funding goals may result in alterations to the off the top budget contribution provided by the SAES system.

## Comments

Management, Budget and Business Plan – NRSP6 -- \$150K/yr.

Midterm assessment comments follow the approved FY16-20 project outline's Management and Business Plan narrative.

“Genetic diversity management. DNA-marker-based studies will show us where genetic diversity is concentrated and vulnerable to loss, so we can prioritize stocks for preservation and optimize techniques as needed. [We will continue to test methods of selecting core collections for more efficient germplasm sampling. We will continue DNA-marker-based studies aimed at understanding relative genetic heterogeneity of germplasm subgroups and how this impacts sampling when collecting, preserving and evaluating the germplasm. We will continue studies on efficiency of rapid visual categorization (cogs) for partitioning diversity within taxa.] “

“Technical research. Studies will be done to improve the efficiency of growing, mating, and storing the stocks, providing results that help the genebank and our clients. [We will investigate more porous potting medium for over-watering protection, techniques for promoting flowering, systems for training plant canopy for better growth, fine tune fertilization and germination methods. We will test fertilization effect on long-term germination. We will use our tissue culture facilities and expertise to start working on use of microbes for bioassays and as selection agents. We will systematically test bridge-crossing techniques to bring *S. jamesii* and similar primitive diploids into the breeding pool. We will continue breeding toward an ideal universal diploid cultivated tuberosum parent for introgressing diploid exotic wild germplasm.] “

Comments:

Staff met the first goal through accelerated work during the first two years of the FY16-20 project. In the past two years, US Potato Genebank staff:

- performed systematic tests to optimize media and watering.
- made a good start in converting a specialty potato to an inbred diploid.
- created and tested the fourth backcross generation of an optimized bridge species line to make exotic species with high insect and disease resistance accessible to cultivar breeding.
- obtained a UV scope and mainstreamed microscopic verification of pollen quality.
- made a breakthrough in seed germination technology, finding that some seedlots germinate much better in alternating temperature.

“Records. Maintain local data records and those on-line in GRIN and Intergenebank databases [We will transition to the new GRIN. We will make photographs and tissue samples of the field tubers of the cultivar collection and post them online. We will digitize PTIS herbarium records and link them to GRIN provenance records. We will keep the PCGC Vulnerability Statement document updated and revise the NRSP6 Procedures Manual.]“

These yearly goals were accomplished, except that the PTIS herbarium was moved to UW-Madison in summer 2017. In the first two years of the current project, Potato Genebank staff also created high quality scans of representative plants, flowers and tubers from each accession in the species *boliviense* (223) and *microdontum* (114). These will be attached to the on-line accession record in GRIN. Staff will continue scanning all accessions.

“Human resources. Project direction will be accomplished through a Technical Advisory Committee and USDA/ARS National Plant Germplasm System leadership. Local administration is by the ARS Project Leader, ARS and UW staff and associated ARS scientists and administration at Madison. We will: Manage staff time and budget to maximize efficiency and flexibility. Strive to make prudent decisions on what we should do in-house and what should be contracted or purchased. Direct experienced base staff to tasks requiring technical expertise and reserve routine work for part-time staff. Hold regular group meetings to make sure the team is working together cooperatively and safely. Conduct annual self-review of overall project progress each year with local staff, and individual staff performance evaluations. Hold TAC meeting on-site every other year to report, tour facilities, provide “face time” with

all local staff, and solicit management input from national experts. Each year prepare the Annual Report, UW Department of Horticulture Professional Activity Report, and ARS Performance Plan Appraisal, as ways to invite feedback on methods, focus and management. “

Two primary formal evaluations provide a summary assessment of the project's general accomplishments: USDA/ARS annual performance rating for the Project Leader, and the review of the past and future project plan for the corresponding 5-year USDA/ARS federal genebank CRIS. The Project Leader's annual progress report got a rating of “Superior” and for FY16, and “Outstanding” (the highest possible) for FY17. Review of the past performance and plan for new federal genebank 5-year CRIS project starting in FY18 recently received a perfect score (24 of 24 possible points) by outside peer reviewers.

“ARS contributions. Associated base research budgets from ARS scientists and various sources of outside grant funds also support technical research, labor, supplies and equipment that directly enhance NRSP6 service. See Appendix E and F for details of structure and contributions. ARS administration costs at the Midwest Area and National Levels are also significant. USDA/ARS and USDA/APHIS also provide data management services through GRIN, and for quarantine, respectively.”

The NRSP investment in NRSP6 leverages significant additional federal resources, as USDA/ARS provides \$665K support for the federal genebank CRIS.

“University of Wisconsin contributions. The University of Wisconsin Department of Horticulture (HORT) will provide lab and office space for on-campus R&D that supports the NRSP6 service, with administrative and secretarial support for Madison personnel provided jointly by ARS and HORT. The University of Wisconsin Peninsula Agricultural Research Station at Sturgeon Bay (PARS) will continue to be the headquarters of NRSP6. PARS will contribute much of the needed facilities and associated resources: 10 greenhouses, 5 large screen houses, office and storage buildings, two labs, field plots, travel and farm vehicles, security and maintenance, utilities (including the major input of heat and light for greenhouses), plus some secretarial service. We will also use greenhouse and field resources at remote locations with cooperators at the UW-Hancock field station. HORT also provides administration of personnel for local state employees and graduate students associated with the genebank. UW provides accounting services for the NRSP6 budget.”

The UW-Madison CALS continued these home-state contributions. In response to significant reductions in state support for the UW-Madison, USDA agreed to contribute \$35K/y beginning in FY17 at the PARS. This represents a reallocation of current funding, rather than new monies. New charges of \$900/acre for plot land began in FY15, and totaled \$1200 and \$1395 for 2016 and 2017, respectively.

“Grants and Collaborators. ARS scientists will continue to seek grants and engage numerous state, federal, international, and industry collaborators who contribute expertise, facilities, equipment and funds to joint projects of mutual interest. Project Leader will continue as chairman of the Crop Germplasm Committee, which provides ~\$10K in germplasm evaluation funds each year, expressly intended for evaluation of NRSP6 genebank stocks.”

US Potato Genebank staff solicited and received a \$13K CGC grant for potato in 2016, and one for \$20K in 2017. The work for the 2017 grant attracted matching contributions from industry, and more than matching contributions in kind from other SAES scientists who also wanted to screen the tubers prepared by NRSP6 staff.

“No fees for service. Charging fees for services has been suggested several times in the past, but always determined to be impractical and counterproductive because implementation would be costly and complicated, it would depress germplasm distribution and use, and, it would contradict USDA policy of free exchange and perhaps inhibit donations of germplasm to NRSP6. “ Staff continue to oppose implementing a charge system for genebank accessions, but this idea should be carefully evaluated. No USDA policy proscribes the practice, and reasonable cost recovery fees for users would bring additional resources to the project. “MRF contributions. NRSP6 is the NPGS working genebank for the top vegetable, so is perpetual in nature and national in scope. Over 25% of germplasm distributions go to ESCOP scientists. For over 65 years, the important elements of funding and administration for NRSP6 have developed as a partnership of SAES, USDA/ARS, and UW. Continued significant funding and technical/administrative inputs on a multistate basis are seen as necessary to keep this partnership healthy and maintain this project's impact and efficiency.”

Two University of Wisconsin professional staff with over 25 years in highly-experienced linchpin positions currently provide staff support in tissue culture to the NRSP6 program. It is critical that NRSP6 continue to provide support for these employees, so they can keep working and serving the germplasm needs of SAES potato researchers.

As detailed in the section “Relevance to Stakeholders”, potato is a major crop with many researchers and breeders who spend several millions of dollars each year doing germplasm research and are wholly dependent on availability of the stocks provided by NRSP6.

“Industry contributions: Gifts from private companies prove the practical value of NRSP6, and keep us tuned to the needs of the industry. Such gifts totaled over \$45K in each of the past two years. Robust support of this kind will continue to be sought.” NRSP6 garnered over \$45K from industry in both FY16 and FY17. We hope to expand this private sector support. However, national germplasm leaders caution that expecting industry to assume major support for basic public genebank services is problematic for these reasons: Private companies can drop projects and come back to them later, but germplasm needs unbroken commitment or will be lost forever. Potato germplasm is almost exclusively sourced from Latin America, where germplasm ownership issues have blocked sharing. Any stocks imported must go through years of US quarantine testing. So NRSP6 collection built up over the past 65 years represents the only practical source of exotic potato germplasm for US scientists. Industry focuses on the most profitable products and projects in the short-term, while germplasm seeks diversity with a view to long-range benefits. Industry restricts access to germplasm and information, and directs research (that they are paying for) toward their own narrower interests, while national genebanks aim to maximize germplasm study and use by free and broad access.

“NRSP Review Committee approved recommendation to approve NRSP6 proposal and budget with the requirement that the committee look at alternative funding models (e.g., increase ARS budget; look for support from key institutions) and report back to the NRSP RC at the mid-term review on progress toward the goal of eliminating or significantly reducing NRSP funding at the end of this cycle.”

Each year since 2010, NRSP6 staff successfully attracted private sector financial support from both major commercial potato breeders in the amount of \$45-50K/yr. Cutbacks in Wisconsin state support for their Agricultural Research Station system, borne in

part by the Peninsular Agricultural Research Station, eroded the value of these private sector investments, however. Little activity has occurred to expand the support network to other industrial sectors, grower groups, or foundations. This situation, exacerbated by a change in Lead AA at the University of Wisconsin, is currently being addressed. A group of NCRA and other allied parties are currently formulating a plan with options to seek support from users and beneficiaries of the potato scientific research and commercial ecosystem. Irrespective of the success of enhanced efforts to build support, we recommend continuation of the current NRSP6 budget. The above midterm assessment shows the essential and successful program enjoying strong and increasing need for germplasm services. Increasing opportunities to leverage the \$150K outlay with USDA/ARS, SAES, and industry investment exist and have not been adequately explored. Current efforts to reevaluate current practices and engage stakeholders will yield a stronger and more effective foundational resource for potato science and its associated industries.

#### Total Points

5

### 2. (15 points) Progress Toward Objectives and Projected Outcomes:

a. Objectives, milestones and deliverables should be described in sufficient detail such that progress can be measured.

b. The midterm review of the project must demonstrate productivity, progress toward original objectives and the relationship between projected goals, actual accomplishments and any impacts to date. As appropriate, this assessment must include an evaluation of stakeholders' use of project outputs to date.

#### Comments

The latest distribution statistics (for FY 2017) demonstrate strong and increasing productivity and demand for NRSP6 services with 12,101 units of germplasm in 246 orders sent to 35 states and 9 foreign countries. NRSP6 staff added valuable new cultivars and breeding and genetic stocks. Staff continued annual collecting expeditions to the southwestern USA to study and collect the two wild potato species native to the United States. Maintenance of germplasm continued with botanical seed increase of about 200 families. This involves hand pollinating 20 parent plants of each family in the greenhouse, harvesting fruit; extracting, processing and storing seeds. Maintenance of clonal stocks required about 3,150 tissue culture transfers. Normal greenhouse tuber increase of about 100 cultivars were made available to requesters. Almost two acres of small field plots were planted for numerous studies related to germplasm use and evaluation. All these efforts require monitoring of disease free status and viability of the germplasm, so over 800 virus assays were done as well as 1,600 duplicate germination tests. As detailed elsewhere, NRSP6 continued a very active program in basic research and evaluation, both in-house and with specialist collaborators in numerous states.

The section on relevance of the project noted several current examples of direct use of NRSP6 resource by multiple state and federal users to breed advanced lines and cultivars. A recent example demonstrates the coordinating and promotion function of the genebank: The Potato Crop Germplasm committee was invited to recommend a grant project for evaluation. NRSP6 staff solicited candidate grants, organized voting to prioritize them, and managed the paperwork to administer the funding. The selected grant to screen for a serious new tuber rot disease was awarded to a state researcher in Colorado. NRSP6 staff also engaged a second expert pathologist at Cornell to conduct advanced screening on remnant tubers of a spectrum of species available at Sturgeon Bay. Thus, some species with promising resistance were identified in advance of the actual award of the grant. A consortium was organized to multiply the useful information this study would yield. NRSP6 staff negotiated the agreement of an industry partner to GBS genotype 50 populations of the promising species. They also obtained an additional \$20K in outside support from industry to grow replicated tuber samples of these populations in two greenhouse locations, in specialized commercial tuberizing growth chambers, and in the controlled environment Biotron facility at UW Madison. In the end, NRSP6 staff coordinated state and industry scientists at CO, NY, and WI to screen the germplasm for the most potent sources of tuber rot resistance, assessed the interaction and variability of growing environment, assessed the interaction with supplemental applied calcium fertilizer, and provided precise genetic characterization. In addition, NRSP6 staff already made successful crosses between the resistant wild species and commercial cultivars.

#### Total Points

15

### 3. (15 points) Integration:

a. Project proposals should indicate how efforts are integrated with extension or academic

programs and how results might be of use by other potential stakeholders.

b. In the midterm review, the project must address actual collaborations and any new partnerships built during the project period. The report should address the degree to which the full team is engaged in project planning and implementation. Discuss plans to correct any weaknesses that may have been identified

### Comments

The UW-Madison CALS fields a strong interdisciplinary team of potato scientists in the Departments of Entomology, Horticulture, and Plant Pathology, with related research across four agricultural research stations. The project leader, an ARS employee, holds a zero-dollar faculty appointment in the UW-Madison Department of Horticulture, participates in graduate training, and is well integrated into the local potato research milieu. Summer interns undertake short term research projects, often resulting in peer reviewed journal publications. NRSP6 staff attend and participate in professional meetings, and provide service leadership (for example, the project leader is the chairman of the Potato Crop Germplasm Committee). The project leader is the Editor and Chief of the American Journal of Potato Research, thus keeping NRSP6 aware of the topics and people doing the latest potato research. The project leader personally reviews every germplasm order, often contacting the requester to make sure the most appropriate materials will be delivered. This often leads to cooperation in which NRSP6 synthesizes custom propagules and hybrids.

In addition to the already-mentioned longstanding relationships with many research collaborators around the country and abroad, USDA/ARS provides a supporting team of federal scientists at UW Madison. Thus, NRSP6 leverages input from a taxonomist, a germplasm pre-breeder, a pathologist, and a physiologist who advise and assist with the NRSP6 germplasm mission.

### Total Points

15

#### 4. (15 points) Outreach, Communications and Assessment:

All project proposals must have a sound outreach, communications and an assessment plan that seek to communicate the program's goals, accomplishments and outcomes/impacts. The communication plan must detail how results will be transferred to researchers and other end users and contain the following elements:

a. Clear identification of the intended audience(s) of the NRSP. Since this is a Research Support Project, in most instances the primary beneficiary of the results will be other scientists. However, careful consideration should be given to other possible users of the information (such as consumers, producers, governmental agencies (local, state and federal), general public, etc.)

Yes

b. Clear description of the engagement of stakeholders in the definition and/or conduct of the research support project.

Yes

c. Thorough description of the methodology to measure the accomplishments and impacts of the National Research Support Project and effectiveness of the communication plan. Methods such as surveys, town meetings, conferences, analyses of reference data (e.g. citation index, etc.), and use of professional evaluators should be considered.

Yes

d. Specific description for development of communication pieces describing the activities, accomplishments, and impacts of the NRSP. The communication pieces will be used with SAES/ARD directors, stakeholders and their organizations, funding sources and agencies, and congressional delegations.

Yes



e. Suggested mechanisms for distribution of the results of the research support project. Examples include sharing the results at annual meetings of stakeholders, providing material to the Budget and Advocacy Committee of the APLU Board on Agriculture Assembly and other appropriate committees within the SAES/ARD organization, and assisting NIFA in preparation of appropriate documents highlighting the impacts of the project.

The midterm review must demonstrate the extent to which the NRSP is working to effectively communicate project results to those who need them and their use by target audiences

### Comments

NRSP6 staff have well-established relationships with national breeders and researchers as long-term colleagues and actively participate in potato research meetings. For example, Project leader Bamberg has attended and presented research at each of the 35 past annual meetings of the Potato Association of America since 1983, and 33 of the annual meetings of the North Central Regional Potato Genetics Technical meeting. Staff member del Rio was invited to be on the organizing committee at the joint meeting of professional potato research and industry groups in Cusco, Peru in 2018. Project Leader Bamberg serves as the Editor in Chief of the world's premier research journal, American Journal of Potato Research and chairman of the federal Crop Germplasm Committee, and genebank staff member Jansky is the current President of the nation's professional potato research society, The Potato Association of America. In the past two years, the staff (not counting the associated germplasm programs at Madison) published 9 peer reviewed papers, one book chapter, and 2 invited reviews.

NRSP6 makes effective use of technology, maintaining a website (<https://www.ars-grin.gov/nr6/>) with a page "In the News" that documents all its media exposure. For example, see [https://www.ars-grin.gov/nr6/press2/1708\\_interview.pdf](https://www.ars-grin.gov/nr6/press2/1708_interview.pdf) It also provides a portal to GRIN, USDA's Germplasm Resources Information Network, providing a customer on-line access to all germplasm data, and a platform for ordering stocks. NRSP6 announces new materials three times per year to an email list of over 300 customers. NRSP6 established close communication and cooperative projects with the private sector -- SeedSavers potato collection in Kenosha, WI, and industry—Kemin, Simplot, Pepsico-FritoLay, CETS. The NRSP6 Technical Advisory Committee, consisting of the nation's top experts in potato germplasm technology, breeding, and administration meets annually to advise genebank staff. Staff fully mesh their germplasm activities with the federal national programs for germplasm acquisition (PEO), quarantine (APHIS), germplasm databasing (GRIN), and long-term germplasm backup in Ft. Collins, CO. NRSP6 staff meet annually with all other national curators and USDA/ARS genebank administrators as the Plant Germplasm Operations Committee.

Assessment takes several forms. Formal staff reviews are conducted each year by UW and USDA. The corresponding USDA/ARS genebank CRIS also goes through peer review every five years as does NRSP6. Prior to the annual NRSP6 technical committee meeting, a list of germplasm orders from each region is provided to the corresponding technical rep, who solicits remarks about the quality of service from the recipients.

### Total Points

# Mid Term Review(Submitted)

Status: Complete

Project ID/Title: NRSP9: National Animal Nutrition Program

## Mission and Relevance

### 1. Mission:

The activity of an NRSP focuses on the development of enabling technologies, support activities (such as to collect, assemble, store, and distribute materials, resources and information), or the sharing of facilities needed to accomplish high priority research, but which is not of itself primarily research. Ideally, an NRSP would facilitate a broad array of research activities. The primary purpose of NRSPs shall not be solely to conduct research, as there are other available mechanisms for creating these types of projects including the multistate research projects and the National Research Project (NRP) options. Examples of NRSP activities might include collection of data that are widely used by other research groups and efforts; development of databases; or development of critical technologies."

**Are the activities of this NRSP consistent with the mission of the NRSP program?**

Yes ▼

### 2. (20 points) Relevance to National Issue:

All NRSPs must involve a national issue, relevant to and of use by most, if not all regions. These projects draw on the best minds and resources within and outside the State Agricultural Experiment Station (SAES) system to address the issues.

**Does this NRSP address a national issue?**

Yes ▼

### Comments

NRSP 9 focuses on the collection, cataloging, synthesis and dissemination of animal nutrition data that serve animal research and education. The NRSP committee accomplishes these goals through three committees: coordinating activities, feed composition and modeling. These groups meet regularly and hold weekly conference calls for committee members and administrative advisors.

The committee develops and promotes science based animal nutrition requirements for most all species of agricultural animals and aquaculture. The committee is rather diverse representing select nutritionist and modelers from several land grant universities and this group is very dedicated to this national issues of animal nutrition. With the five year renewal, the committee made significant efforts to invite new members to join the committee and expand expertise to other animal species.

Points: 19/20; 18/20; 18/20; 19/20 rating per four reviewers

### Total Points

19 ▼

### 3. (20 points) Relevance to Stakeholders:

**Is there evidence of stakeholder use of project outputs?**

Yes ▼

Are there project outcomes that aide in development of or contribute to the discussion of public policy?

Yes

If so, please describe

Overall, all reviewers agree that the efforts of NRSP 9 have been instrumental in updating animal nutritional requirements for agricultural animals, including a feed composition database. The NRSP 9 efforts are the first in several years to evaluate and update nutritional recommendations for beef, dairy, swine and poultry diets and to formulate new models, physiological and performance data and new feed components. The committee is working closely with the National Academies of Science and databases created by NANP were instrumental in the release of the National Academies Beef and Dairy reports. The committee continues collaboration with the National Academies continues with the update of nutrient requirements for other species.

Points: 20/20; 10/20; 19/20; 15/20

Total Points

16

## Implementation of the NRSP

### 1. (15 points) Management and Business Plan:

Each NRSP must have a well-developed business plan that describes how the project will be managed and funded for a five-year period. This plan includes a management structure to adequately integrate the efforts of multiple participants. The plan should include provisions for linking multiple sources of funding and leveraging those sources with the limited off-the-top research funds. The plan should demonstrate that alternative funding sources have been sought. This plan should include efforts to bring in new agencies, organizations, industry, foundations, etc. to help address the issues and provide funding for the project. All project proposals must provide evidence of contributions from experiment stations across the nation beyond what is available through off-the-top funds.

The midterm review must reflect progress toward meeting funding expectations. Failure to meet funding goals may result in alterations to the off the top budget contribution provided by the SAES system.

### Comments

The project is well managed by a coordinator that sets up weekly meetings with the committee and these meetings are well attended. The three committees – coordinating, modeling and feed composition work well together. Post-doctoral scholars are used by the committee on several short-term projects and as the primary dedicated NANP staff. Group may want to rethink this strategy as post-doctoral research associates move on to other positions quickly, leaving the project without a dedicated staff.

The committee reports that MRF funding constitutes less than 10% of the total project funding. Other resources leveraged by the group are investments of the participants' time through funds from experiment stations, universities, government agencies and private companies. Companies have contributed feed ingredients data worth millions of dollars. Some concern on how the value of in-kind contributions are calculated. Overall, seems to be on target to meet funding expectations.

Points: 15/15; 13/15; 12/15; 12/15

Total Points

13

**2. (15 points) Progress Toward Objectives and Projected Outcomes:**

a. Objectives, milestones and deliverables should be described in sufficient detail such that progress can be measured.

b. The midterm review of the project must demonstrate productivity, progress toward original objectives and the relationship between projected goals, actual accomplishments and any impacts to date. As appropriate, this assessment must include an evaluation of stakeholders' use of project outputs to date.

**Comments**

All reviewers agree that the project is making sufficient progress towards the stated objectives in the proposal. One reviewer indicated that the committee is on track with milestones and deliverables towards 8/10 objectives. Another reviewer agrees that progress is being made but ask that the NRSP team develop a better strategy to clearly list the outputs resulting from the research.

Points: 15/15; 15/15; 10/15; 14/15

**Total Points**

14

**3. (15 points) Integration:**

a. Project proposals should indicate how efforts are integrated with extension or academic programs and how results might be of use by other potential stakeholders.

b. In the midterm review, the project must address actual collaborations and any new partnerships built during the project period. The report should address the degree to which the full team is engaged in project planning and implementation. Discuss plans to correct any weaknesses that may have been identified

**Comments**

All reviewers agree that the NRSP team has done a good job of integrating with extension and academic programs. The project has provided training resources for students and the project plans to develop additional materials for curriculum, extension and industry use. Participants regularly present data and have held symposia at the Federation for Animal Science Societies.

The weekly meetings have most if not all the team members engaged in discussions, project planning and implementation. One reviewer commented this committee is a model for integration activities.

Points: 15/15; 13/15; 12/15; 13/15

**Total Points**

13

**4. (15 points) Outreach, Communications and Assessment:**

All project proposals must have a sound outreach, communications and an assessment plan that seek to communicate the program's goals, accomplishments and outcomes/impacts. The communication plan must detail how results will be transferred to researchers and other end users and contain the following elements:

a. Clear identification of the intended audience(s) of the NRSP. Since this is a Research Support Project, in most instances the primary beneficiary of the results will be other scientists. However, careful consideration should be given to other possible users of the information (such as consumers, producers, governmental agencies (local, state and federal), general public, etc.)

Yes

b. Clear description of the engagement of stakeholders in the definition and/or conduct of the research support project.

Yes

c. Thorough description of the methodology to measure the accomplishments and impacts of the National Research Support Project and effectiveness of the communication plan. Methods such as surveys, town meetings, conferences, analyses of reference data (e.g. citation index, etc.), and use of professional evaluators should be considered.

N/A

d. Specific description for development of communication pieces describing the activities, accomplishments, and impacts of the NRSP. The communication pieces will be used with SAES/ARD directors, stakeholders and their organizations, funding sources and agencies, and congressional delegations.

Yes

e. Suggested mechanisms for distribution of the results of the research support project. Examples include sharing the results at annual meetings of stakeholders, providing material to the Budget and Advocacy Committee of the APLU Board on Agriculture Assembly and other appropriate committees within the SAES/ARD organization, and assisting NIFA in preparation of appropriate documents highlighting the impacts of the project.

The midterm review must demonstrate the extent to which the NRSP is working to effectively communicate project results to those who need them and their use by target audiences

Yes

## Comments

Item c.) was listed as N/A as it received two "Yes" and two "No" responses.

There are several examples related to outreach, communications and assessments that have been championed by the NRSP team:

- Dissemination of the results of the NRSP 9 project are the focus of the coordinating committee. This committee keeps project focused.
- The NRSP 9 team is in the process of reviewing and implementing an improved communication plan.
- The NRSP 9 team has released their results through presentations at national meetings, National Academies reports, information on website (although this needs improvement), weekly conference calls with participants and administrative advisors and workshops.
- NIFA National Program Leader is very engaged in the project and provides excellent guidance and leadership for the NRSP 9 committee.
- Group has worked with SAES to develop impact statements related to the initial 5 years of the project and used the SAES directors' network to publicize a previous national forum.
- At the advice of NRSP-RC, this committee has initiated a study on the global impact of the project.
- Members of the committee also share data with colleagues in other multistate groups that are focused on animal nutrition, physiology or performance. NC 2040 and NC 2042, dairy cattle focused committees are examples where this information is shared.
- Committee has updated animal nutritional databases, improved the formulation of animal diets and developed improved standards

for nutritional requirements.

- Overall, this committee is using various forms of communication to disseminate results to stakeholders.
- Committee has engaged an external evaluator to assess the impact of NRSP 9 on the animal industry.

Points: 15/15; 13/15; 10/15; 12/15

**Total Points**

13