

Prerequisite Criteria

How is the NRSP consistent with the mission? 8000 character max.

INTRODUCTION

The NRSP-8 National Animal Genome Research Support Program has played a major role in enabling genomic discoveries in livestock animals and aquaculture species. As outlined in the “Blueprint for USDA Efforts in Agricultural Animal Genomics 2008-2017,” infrastructure provides the critical foundation upon which genomics-oriented discovery science can be channeled into substantial advances in agricultural practices. Infrastructure, as defined by the Blueprint, includes genomic tools (e.g., maps, genome assemblies), integrative bioinformatics tools and databases, genetic resource populations, and education and training of students, scientists, and the public. *The mission of NRSP-8 focuses on providing support for these crucial infrastructure components.* Developed infrastructure is, in turn, used to leverage more substantial funding support for livestock genomics research from a variety of public and private sources. As detailed in the “Accomplishments” section, NRSP-8 has been highly successful in the previous period in enabling substantial advances in animal genomics and facilitating a broad array of research activities of importance to its component species groups. This success and the rapid advance of genomic technologies emphasize the need for continued NRSP-8 infrastructure support.

The advent of next-generation sequencing (NGS) technologies, and the associated exponential decreases in sequencing costs and increases in throughput, have produced seismic shifts in approaches towards, and the scope of, animal genomics research. For example, while production of high-quality reference genomes for agricultural animals remains a substantial undertaking, sequencing costs are now outweighed by the infrastructure needed to assemble hundreds of millions of multi-platform reads, annotate genes, genome features, and nucleotide variants, and curate this information in a manner accessible to stakeholders. Additionally, as whole genome sequences become available for most target species, NGS makes broad re-sequencing efforts a viable approach for characterizing variation in breeds and strains and linking this variation to economically-relevant phenotypes. Whereas reference genome assemblies mostly were generated at large sequencing centers, 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 already generating enormous datasets that can quickly overcome the informatics resources of an individual’s lab or even small species groups. These new challenges are reflected in our updated objectives for this renewal, as briefly outlined below and expanded on in the Implementation section.

Our first objective is to 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. 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 annotation.

Our second objective is to develop strategies to identify and exploit genes and allelic variations that contribute to economically relevant phenotypes and traits, in part through improving functional annotation of the genomes of our species. The tremendous power of genome-wide variant analysis is leading to the identification of markers linked to important production traits in agricultural 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 proteomic and metabolomic assays to knock-out/down approaches.

Our third objective is to facilitate analysis, curation, storage, distribution and application of the enormous datasets now being generated by NGS and related technologies with regard to our target species. 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 data/genetic material otherwise sorely lacking across the animal genomics community. The organizational structure of NRSP-8 serves to bring together domestic scientists within a given livestock/aquaculture group, and facilitate rapid transfer of successful approaches to commercial national and international stakeholders.

How does this NRSP pertain as a national issue? 10,000 characters max.

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, spread through and impacting agriculture within every state and region of the U.S. The 2010 document “A Science Roadmap for Food and Agriculture” contains seven grand challenges. While animal genomics research directly or indirectly can be related to each challenge, Grand Challenge 1 - *We must enhance the sustainability, competitiveness, and profitability of U.S. food and agricultural systems* - directly pertains to NRSP-8 infrastructure support functions. Needed approaches to meet Grand Challenge 1 include “Enhance animal productivity by maximizing their genome capacities and developing new animal breeds and stocks....” Animal genomics also has clear national-level roles to play in mitigating climate change impacts (Challenge 2), ensuring a safe, secure, and stable food supply (Challenge 4), and improving human health and nutrition (Challenge 5) through genome-directed selection of breeds and lines that produce food products in a manner meeting national environmental and nutritional needs. 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 NRSP-8-affiliated researchers. 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, a program developed originally

for poultry data analysis in Texas may be readily adapted by researchers working with striped bass in North Carolina.

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 2,242 members around the world. The QTLdb program, developed by the NRSP-8 Bioinformatics Coordination Project team, has been cited in over 150 peer-reviewed publications. Similarly, the PAG conferences are held jointly with the annual NRSP-8 meeting, with 651 animal genome scientists participating in this international meeting in 2012. The chance to compare notes 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 Accomplishments.

B. Continued Need. As detailed above, the NRSP-8 mission is closely aligned with the challenges described in the recent 2010 Science Roadmap. These challenges for food production are long-term in nature and are heightened by rising world 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 wide array of species, the need for national genomics infrastructure support (as provided by NRSP-8) is only expected to increase. Also, while genomics has been applied primarily to breeding and selection, a key deliverable is more biological information on traits.

Whole genome sequences from several species groups were finished and/or refined in the last 5 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 capture and utilization of trait-associated 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 the 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 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 are routinely obtaining whole genome sequences 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 querying vast amounts of re-sequencing data, and development of tools to facilitate annotation and curation of genome assemblies for small research communities (e.g., aquaculture species). 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 challenges.

The structure, past success, and established interpersonal relationships of NRSP-8 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, bioinformatics, epigenetics) allows for rapid dissemination of advances in tools and techniques 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 infrastructure for agricultural animal genomics.

RATIONALE

Priority Established by ESCOP/ESS (8,000 characters max)

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 applied in a number of ways. Below is a brief summary of the relationship of animal genomics research, for which NRSP-8 provides the necessary infrastructure, to the Updated Challenge Areas of the National Association of State University and Land Grant Colleges/Experiment Station Committee on Organizational Policy 2010 update to "A Science Roadmap for Food and Agriculture".

Grand Challenge 1

We must enhance the sustainability, competitiveness, and profitability of U.S. food and agricultural systems.

A key means by which advances in U.S. 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). Selection of superior genotypes across potentially varied production environments is greatly enhanced by integrating genomic data with relevant phenotypes and biological information.

Grand Challenge 2

We must adapt to and mitigate the impacts of climate change on food, feed, fiber, and fuel systems in the United States.

Genome-enabled selection practices are increasingly able to take into account the effect of genotype on the ability of an animal to utilize and assimilate different diets and different downstream impacts on the environment. Cross-disciplinary research in nutrition and genomics promises tailored diets that most effectively utilize genetic growth potential while minimizing environmental impact. Additionally, genomics can enhance selection of animals better adapted for changing climatic conditions.

Grand Challenge 3

We must support energy security and the development of the bioeconomy from renewable natural resources in the United States.

As sustainability and energy costs become increasingly important factors in the success of animal agriculture, incorporating these complex factors into breeding and management strategies will require the power of genomic selection and a much-improved understanding of gene function.

Grand Challenge 4

We must play a global leadership role to ensure a safe, secure, and abundant food supply for the United States and the world.

Genomics can enhance the safety of the food supply through animal identity and traceability systems based on molecular markers. Additionally, genomics allows rapid selection of lines of livestock resistant to infection, increasing animal welfare while optimizing productivity. Animal genomics research can additionally target other production bottlenecks, such as maturation times and fecundity, to enhance productivity and nutritional value.

Grand Challenge 5

We must improve human health, nutrition, and wellness of the U.S. population.

Healthy, low-priced animal protein choices are the result of a vigorous and profitable animal agriculture industry. Genome-based enhancement of the beneficial nutritional profiles of livestock can lead to healthier dietary options and improved human health.

Grand Challenge 6

We must heighten environmental stewardship through the development of sustainable management practices.

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 sustainability in agriculture.

Grand Challenge 7

We must strengthen individual, family, and community development and resilience.

A profitable and growing agricultural sector leads to strong farm families and farm communities. Agricultural animal genomics is focused on enhancing animal improvement programs to lower production costs and increase throughput and yields, thereby increasing profitability. At the same time, these genomic technologies can add aspects of sustainability and biosecurity to production practices, leading to long-term market stability.

RELEVANCE TO STAKEHOLDERS (8,000 characters max)

A. Stakeholders. The membership constitutes the primary group benefiting from activities, although non-members, and in fact, the global scientific community benefit in parallel. Obviously, genotype (the genome) is of critical consideration for many disciplines of animal science (e.g., physiology, behavior, nutrition) whose researchers benefit from NRSP-8 supported resources and knowledge. Members participate in governance, but all interested parties can have input. One mechanism is via the NRSP-8 supported AnGenMap (<http://www.animalgenome.org>), which allows for essentially a daily conversation among its 2200+ members, including many in the stakeholder community. International scientists are another important stakeholder group. Approximately one-third of the 651 PAG animal scientist-attendees and one-third to one-half of AnGenMap members are international. Commercial breeders, producers, and other entities that rely on agricultural animals constitute another critical stakeholder group. Each NRSP-8 species committee incorporates industry representatives that

participate in governance, but many additional industry scientists and leaders attend PAG, utilize AnGenMap, receive newsletters and employ genomic tools/data deriving from NRSP-8-supported infrastructure. The general public constitutes the ultimate stakeholder group for the efforts of NRSP-8. The public pays the bills (via taxes, food costs, etc.) and consume the products of animal agriculture; it is meant to be the beneficiary of genetic improvement in the form of a safe, nutritious, high quality food supply, at reasonable cost and with minimal environmental impact. Further, the public's communication systems (e.g., newspapers, magazines, radio, internet) utilize NRSP-8-generated materials (e.g., websites, newsletters, research articles) as well as the knowledge of species coordinators and member researchers who engage in education/training, interviews, and meetings/workshops to provide objective science-based information in regard to animal genomics and agriculture.

B. Stakeholder Involvement. A few examples of stakeholder synergy in the recent period may help to illustrate the community-building impact of NRSP-8. First, the dairy (Holstein) industry, USDA-ARS, NSRP-8 and other U.S./international scientists formed a highly successful collaboration to utilize the BovineSNP50 genotyping chip for implementation of whole genome selection. Second, the PRRS Host Genetics Consortium brought together swine breeding companies, the National Pork Board, USDA-ARS, NRSP-8 and other U.S. scientists to identify genetic mechanisms controlling host response to PRRS virus infection in nursery pigs. Third, the Equine Genetic Diversity Consortium, consisting of scientists from 25 institutions worldwide, is analyzing a 50K SNP dataset from 36 breeds for signatures of selection, intra- and inter-breed diversity. While these are just a few examples, as noted below (Integration and Documentation section), all the coordinators have engaged in species-specific and, in some cases, cross-species interactions with academic and industry stakeholder groups.

While face-to-face interactions at PAG and other venues remain important, increasingly stakeholder interaction is through Internet resources. This is why the AnGenMap on-line discussion group is so important to NRSP-8 (detailed below in Outreach). Furthermore, each species group has its own species-specific website, with links to maps, databases, newsletters, resources and community links, and all of these are combined at the NRSP-8 Bioinformatics Coordination Site (www.animalgenome.org). Stakeholders increasingly utilize NRSP-8 bioinformatic resources alongside academic researchers, helping to ensure the accuracy of sequence assemblies, the accessibility of newly developed programs, and the real-world relevance of project directions. Communication at the individual, commodity, and national levels greatly facilitates feedback and, as necessary, redirection of resources to support stakeholder needs and ensure quality outputs. NRSP-8 addresses the needs of stakeholders by providing the resources, community, and visibility to allow the leveraging of limited resources in support of the "Blueprint" pillars (Infrastructure, Discovery Science, Science to Practice).

C. Renewal Justification. There is continued need for, and relevance of, NRSP-8 for U.S. scientists and stakeholders who depend on NRSP-8 initiatives and resources. No other public or private program can provide these unique services and infrastructure. As the demand for animals and animal products continues to grow, it is essential that the U.S. have a visible program to maintain its global competitive advantage. 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 to generate practical results of value for animal agriculture and human health. The NRSP-8-derived value of supporting genome research in our designated animal species will undoubtedly continue to have far-reaching impact on scientific endeavors for the betterment of society. Animal genomics faces a challenge today that parallels that faced by medical genetics. It is likely that many young people in the U.S. today will have their own genome sequenced. How can that immense amount of information be stored, analyzed, communicated and interpreted in a way that positively impacts his or her health and lifespan? What collateral information and infrastructure will be needed for these sequences to have real value? Similarly, how will animal producers and scientists (and ultimately society) be able to benefit from genomic advances? These technologies evolve at a remarkable pace, and it is imperative to share genomics tools and reagents, animal populations, and bioinformatics tools, and to pool our scientific expertise. Renewal is further supported by the significant impact that NRSP-8 has had on stakeholders at all levels. The tools, resources, information, and collaborations attributed entirely or in part to NRSP-8 support have led to a number of important advances and discoveries (see the Accomplishments 2008-2012 attachment).

The most obvious and important example of this progress has been obtaining, refining, and using the reference genome sequence assemblies for the majority of our target species. The reference assemblies have enabled other approaches aimed at gaining a full appreciation of animal genetic diversity within many of our species, the use of genomic selection in animal breeding, better implementation of new transcriptomic and proteomic approaches, and a reference to which to turn in the analysis of the phenotypic effects of any gene of interest. Still, many challenges remain. Stakeholders depend on the reference assemblies in the way we previously depended on encyclopedias and dictionaries. At the moment, they frequently find missing and/or incorrectly assembled genes and regulatory elements. The reality is that their best access to the genome may be out-of-date or difficult to interpret. The overarching challenge remains the complexity of genome sequences and data, and the difficulty in connecting those data to the equally complex outcome – the phenotype. It is difficult to envision exactly how we can develop a full appreciation of the functional connections between DNA sequence and, for example, feed conversion efficiency or disease resistance. However, many difficult-to-envision concepts and dreams have been realized by research supported by NRSP-8 in the past, and we can confidently predict that this will continue to occur in its next cycle.

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.

In order to realize the combined agricultural and biomedical potential of livestock, poultry, and aquaculture species, a thorough knowledge of the structure and organization of individual genomes is crucial to sustain and accelerate future genetic improvement. Earlier advances in genome sequencing throughput have enabled the generation of draft reference genome sequences for most, but not all, economically important agricultural animals, as described in the Accomplishments from the current NRSP-8 cycle. However, these draft quality genome sequences still contain numerous gaps and mis-assemblies. In some cases, whole chromosomes

are absent. Accurate and well-annotated reference sequences are essential for most genome-wide analyses, including the dissection of the genetic architecture of complex traits and enhanced breeding using genomic selection strategies. Importantly, these approaches are most beneficial when coordinated synergistically into an integrated discovery program.

The recent advent of next generation sequencing technology has greatly expanded the power of DNA sequencing and, more important, has democratized the process, such that individual breeders and geneticists can cost-effectively “re-sequence” multiple animals within breeds and lines, and unique individuals, analogous to the on-going 1000 Human Genomes project. Coordinated and collective analysis of these sequences will allow for a full understanding and appreciation of the genetic diversity of agricultural animal species and the influences of domestication and subsequent selection. Furthermore, these studies will aid in improving reference genome assemblies, identify new and important new genetic polymorphisms that influence economic traits, and identify selective sweeps that are the fingerprints of the past century of genetic improvement within most breeds of animals.

The specific aims for this objective include:

- i) Initiate acquisition of draft genome assemblies for economically important species for which none are yet available.
- ii) Improve draft genome assemblies to close gaps and improve assembly order.
- iii) Coordinate analysis of re-sequencing data to identify SNPs, CNVs, and insertion-deletions, and better annotate gene models within the reference assemblies.

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.

This objective aims to help the research community enter the post-genome-sequencing era by facilitating translation of genomic findings into genetic improvement of all species. To achieve this goal, strategies and tools are needed to utilize genome-wide sequences and SNP data in genomic selection for improvement of economically important animal traits, as well as determine gene identities and functions. These studies will contribute to development of databases of genes and allelic variation and facilitate conversion of genomic information into applied tools for improved breeding efficiency.

The specific aims for this objective include:

- i) Utilize low, medium, and high-resolution SNP-chips, as well as genome re-sequencing data in genome-wide association studies to identify loci, genes and allelic variants associated with economically important phenotypes.
- ii) Develop strategies, models, algorithms, pipelines and statistical tools to facilitate practical application of genomic selection in livestock, poultry and aquaculture species.
- iii) Apply approaches for functional evaluation of genes or gene products associated with important phenotypes, including transcriptome sequencing, proteomic and metabolomic studies, and knock-out/down analyses.
- iv) Facilitate coordination of available transcriptome and other data resources for improvement of annotation of reference genomes for agricultural animal species.

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.

Advances in genomics, genetics, and their associated technologies allow researchers to rapidly acquire vast amounts of experimental data in all livestock and aquaculture species. To better understand the genetic mechanisms underlying important traits, bioinformatics/computational tools will be necessary to analyze and integrate high throughput data on a grand scale. It is prohibitively costly for each scientist to individually develop these tools and databases to handle this information load; in addition, common file types, protocols and standards will maximize the efficiency of research output and data exchange. Thus, there is a need to support core bioinformatics resources and facilitate access to freely available resources. In short, this objective will provide and integrate the “analytical tools and databases” and “real-time communication” resources needed to enhance the research coordinated in Objectives 1 and 2.

The specific aims for this objective include:

- i) Maintain and expand web-accessible resources that facilitate livestock/aquaculture genomic research and develop/promote data sharing standards and tools necessary to integrate these resources.
- ii) Facilitate livestock and aquaculture data dissemination and communication by providing tools and resources to assist with data access and promote community discussion and awareness of current events, available resources, and other items of interest.
- iii) Develop analytical pipelines and relational databases to help facilitate genome-wide research approaches to understand the genotype-to-phenotype basis of production traits in livestock, poultry and aquaculture.

MANAGEMENT, BUDGET, AND BUSINESS PLAN (16,000 characters max)

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. The 6 species coordinators for aquaculture, cattle, equine, poultry, sheep, and swine are joined by a bioinformatics coordinator. The coordinators facilitate the availability of shared genomic resources (e.g., tools, reagents, 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, working with the members of their respective committees and amongst themselves, also 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 stimulate this communication and provide focal points for input from the committee members and other stakeholders.

The coordinator model has served NRSP-8 well, it is flexible, and the structure allows for continuous refinements. For example, aquaculture, poultry and bioinformatics have shared

responsibility among co-coordinators (poultry: J. Dodgson, H. Cheng; bioinformatics: J. Reecy, S. Lamont, M. Rothschild, C. Tuggle; aquaculture: J. Liu and C. Rexroad III). It is likely that additional co-coordinator groups may be selected, although, for technical reasons, it is expected that financial issues will be handled through only one Experiment Station per coordination group. Co-coordinators bring different perspectives to the job (e.g., different species expertise among the multiple bioinformatics group) and provide more opportunities for member and stakeholder input.

Coordinators will meet with their respective species committee members at least once each year at annual meetings (e.g., 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 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 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 not more than 5 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. Due to growing inputs from companies and other organizations regarding intellectual property, efforts will be made to encourage the 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) \$85,500 in salary costs for the individual that maintains and develops resources at animalgenome.org, (2) \$15,500 to support the PRRS Host Genetics Consortium and BirdBase websites, (3) \$2,000 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 and will not be used to directly fund research programs. Based on prior experience (see appendix titled Coordinators Expenses, which gives a brief summary of the primary tool and resource development expenditures for each coordinator in the last project), these funds likely will support the development and annotation of their respective genomes (e.g., 2009 – turkey genome sequencing by Poultry Coordinator, 2010 – BAC library for oyster by Aquaculture Coordinator) and resources made widely available to NRSP-8 members (e.g., 2011 – Pig 60K SNP chips by Swine Coordinator, 2010- Agilent microarrays by Poultry Coordinator). 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 very substantial minimal 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.

Successful basic and applied agricultural genetics and genomics research is by necessity highly collaborative and multi-disciplinary. Most projects are performed by teams consisting of experts in molecular technologies, data management and statistical analysis of large datasets, specific

phenotyping of large populations, and devising practical downstream applications. External and internal research proposals to private, institutional or federal funding agencies are typically evaluated to some degree on the quality and specific components of the research team. This integrated research team approach will continue for the foreseeable future.

It is a vital mission of this NRSP to provide a framework in which such animal genomics research teams can be established and thrive, and in which both fundamental and applied knowledge can be generated in the most efficient fashion. To accomplish this aim, the results of our original animal genome research are presented at a host of regional, national and international meetings, and published in a wide variety of peer-reviewed, publically-available journals. Furthermore, industry groups, in communication with our applied and extension experts, have and will continue to acquire major results and implications of our research via trade journal articles that are written by journalists familiar with their reader's backgrounds and interests. We predict that the NAGRP bioinformatics website, as well as the individual species websites, will be increasingly utilized by the 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.

Beyond publication and bioinformatics avenues of integration, it is important to note that the vast majority of NRSP-8 members are in academia and engage in teaching and outreach as part of their daily responsibilities. Information and, in some cases, 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 individuals. As noted below, the coordinators actively encourage and financially support attendance of such lab trainees at our annual meetings and other relevant venues.

B. Partnerships and engagement.

The framework and partnerships from the existing NRSP 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 this interaction. Our programs will increasingly begin to evaluate and use other platforms, such as iPlant/iAnimal, 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 will also be open to evaluating new systems for data management and analysis that meet our needs and promote efficient sharing of data and technologies.

The ability of the NRSP-8 program to leverage acquisition of additional animal genomics research funds is supported by data indicating that in FY2011 \$22.4 M in federal, \$6.9 M in other grants or contracts, and \$1.9 M in industry support has been secured, which is up from \$9.0 M federal, \$2.1 M other grants and contracts and \$1.5 M industry funding over FY2010. The

increase in external grants, contracts and industry support is encouraging and likely indicates our success in providing information that industry sees as essential to achieving their goals.

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 in our annual meetings. In the past 5 years, many breeding companies have embraced genomics methods (dense SNP genotyping, genomic selection, etc.). 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 attendance of >3,200, PAG is the largest international scientific conference reporting on non-human genomics research. Over the course of several 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 the newest high throughput sequencing and genotyping technologies and the means of storing, analyzing, and sharing this 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 35% since 2008, and total scientific attendance in 2012 was 2,788, with 1,643 U.S. attendees and 1,145 international attendees. Of those attendees, 651 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 2012 PAG conference included Aquaculture, Buffalo Project, Cat & Dog, Cattle/Sheep, Equine, Poultry, Swine, a combined Cattle/Sheep/Swine workshop, Animal Epigenetics, 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, and Sequencing Complex Genomes. 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. Please see the attached appendix on Coordinator Expenses. 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, hap-map data, microarrays, and now certain essential whole genome and/or RNA sequencing data. We envision that this flexible and diverse use of funds will continue.

Outreach and Communications (20,000 characters max)

A. Plan

i. *Target Audience.* Primary beneficiaries of NRSP-8 will be research scientists that are either engaged directly in animal genome research or utilize genomic data in complementary areas of animal science. Direct beneficiaries also include ever-increasing numbers of commercial animal breeders and producers who apply genomic data and related technologies to enhance aspects of animal health, welfare, productivity, and management, as well as, government agencies and breed organizations utilizing genomic methods for animal identification, disease surveillance, and regulatory monitoring. Taken together, support of research, education, and communication activities in animal genomics 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. NRSP-8 will continue to be visible at national and international scientific meetings and workshops. As stated above, a leading example is the annual International PAG Conference. NRSP-8 is showcased in species-specific and comparative genomics sessions, as well as through committee meetings where scientific presentations and reports are required from 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 international conference. Additionally the Poultry Genome Coordinator and the Swine Genome Coordinator each publish separate newsletters which go well beyond the actual members of NRSP and are circulated to over 2500 people who are scientists, students, and extension workers.

ii. *Engagement of Stakeholders.* The genome committee for each animal species will have one or more representative(s) 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 animal industries and both the committee and the species coordinators. Species coordinators will continue to present and interact at national and regional producer meetings and breed organizations. They will also facilitate communication of research outcomes to the general public. The poultry genome and swine genome newsletters and AnGenMap discussion group will also be used to engage stakeholders worldwide.

iii. *Measurement of Accomplishments and Impacts.* The most important measurements of NRSP-8 impact will be through scientific productivity and milestones. Information on scientific progress will be disseminated in peer-reviewed research articles, books, book chapters, popular press articles, newsletters, and both scientific and industry presentations. Every year, chairs of each species committee will detail the scientific productivity and milestones achieved through an annual report that will include presentations and attendance at both scientific and stakeholder meetings by coordinators and NRSP-8 members. In addition, a generation of new scientists will be trained by NRSP-8 members in animal genomics and bioinformatics, while contributing to NRSP-8 projects. Each of the species coordinators supports a competitive award for graduate

student travel to the annual PAG conference; participation by students at this conference ensures early exposure to animal genomics research and its applications.

iv. 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 such as PAG meeting. Suggestions on when and where to meet will be made by the coordinators and advisers on a year-to-year basis and voted on by the overall technical committee. Major conferences provide enhanced opportunities for information and technology transfer among international scientists and between species groups in all aspects of agricultural genomics encompassing both public and private sectors. Other mechanisms of communication include the swine and poultry genome newsletters (hard copy or electronic) to both scientists and interested non-scientists and species-specific genome home pages on the internet to reach agricultural scientists, industry, consumers, students and others interested in the application of genomics to animal agriculture. Species' genome pages have also been established by NCBI, which include access and direct links to existing genomic databases and related resources. In addition, homepages constructed and maintained by individual animal species coordinators frequently provide additional information and helpful links to genomic resources within the agricultural research community. AnGenMap, an on-line discussion group for the animal genomics community that includes >2,240 members from more than 40 countries/regions, continues to be used for communication between research scientists. Coordinators and other members of NRSP-8 promote advances in genomics for their respective species through invited presentations at scientific conferences and 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 NIH, international consortia, industrial partners, and breed organizations for animal agricultural genomics endeavors.

v. Distribution of Research Results. The primary in-house mechanism for distribution of results and accomplishments will be via annual reports (available on NIMSS). Summary reports are prepared by the technical committee chair, with input from chairs of the species committees 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.

B. Past Successes

NRSP-8 impacts are best measured by the major milestones in animal genomics as listed in the attachment Accomplishments 2008-2012. 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 world-wide. These efforts have achieved the advancement of animal genomics at a pace that has substantially exceeded most predictions.