



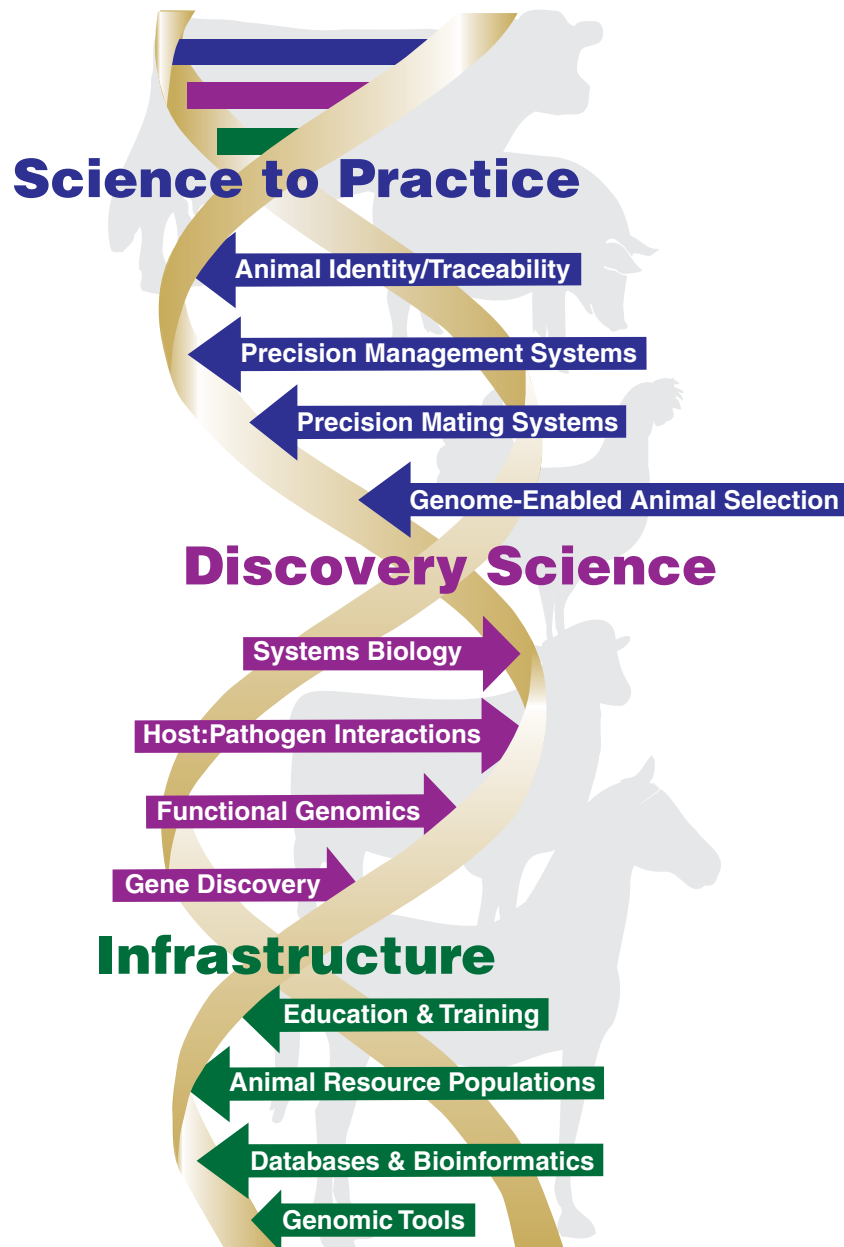
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September 2007

Blueprint for USDA Efforts in Agricultural Animal Genomics 2008–2017



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USDA Animal Genomics Strategic Planning
Task Force

Abstract

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Following the recommendation of the National Science and Technology Council's Interagency Working Group on Animal Genomics, a task force was established in January 2006 to develop a blueprint for USDA efforts in agricultural animal genomics. This task force of Agricultural Research Service (ARS), Cooperative State Research, Education, and Extension Service (CSREES), and university scientists and administrators developed a "Blueprint" for future research, education, and extension efforts in agricultural animal genomics, based on a vast array of stakeholder input. The Blueprint is designed as a pyramid, with "Science to Practice" at the top, supported by fundamental and mission-oriented research in "Discovery Science," and is based on a solid foundation of "Infrastructure." The Blueprint will guide activities in this critical area of science over the coming decade.

Keywords: animal genomics, animal genomes, food animal, animal production, animal selection, genome mapping, bioinformatics, comparative genomics, functional genomics, genetic selection, systems biology.

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EXECUTIVE SUMMARY

Animal improvement programs have greatly increased the ability of animal agriculture to provide high quality, low cost and safe animal products to the American consumer. A large part of this change is a result of investments made by USDA in quantitative animal genetics and animal molecular biology research as well as the ability of private industry to rapidly adopt these new technologies. Investments in genomic technology, from gene discovery to sequenced genomes, and state-of-the-art technology developed by the biomedical research community, have animal agriculture poised at the threshold of the genomic revolution. Although quantitative geneticists have made tremendous progress in improving the efficiency of meat, milk, and egg production, there is still a significant need for increased production efficiency. For example, if Americans are to fully meet the *2005 Dietary Guidelines for Americans*, U.S. dairy producers will need to increase annual production of milk and milk products (especially fat-free or low-fat dairy products) by an estimated 65% (Buzby et. al., 2006). In addition, by 2020-2030 world demand for meat and dairy products is expected to increase 40-50% (Rosegrant et. al., 2001; FAO, 2002), which will stimulate the competitiveness of American food animal products. Genome-enabled technologies will also lead to improvements in product quality, including nutrient-fortified lean meat, milk, and eggs to satisfy increasing demand for healthier food from aging or obese consumers. Animal genomics will

also provide the ability to understand and improve genetic traits that were difficult to measure with quantitative genetics approaches (e.g., disease resistance, animal well-being, feed efficiency, and product quality) and will lead to enhanced functionality and well-being of animals in environmentally neutral production systems. In the near future, genome-enabled technologies will be used to trace animals and animal products throughout the food production chain resulting in enhanced biosecurity as well as increased food safety and consumer confidence. Thus, with additional USDA-supported efforts, new genomic technologies will be available to livestock, poultry, and aquaculture producers to improve the efficiency, sustainability, biosecurity, and social acceptance of agricultural animal production.

To meet these national needs, a blueprint for future research, education, and extension efforts in agricultural animal genomics has been developed by a task force of ARS, CSREES, and university scientists and administrators. The *Blueprint* is built on a vast array of stakeholder input and is designed as a pyramid, with *Science to Practice* at the top supported by fundamental and mission oriented research in *Discovery Science*, and is based on a solid foundation of *Infrastructure*.

The goals and recommendations of the *Blueprint* are consistent with the President's American Competitiveness Initiative (2006) which stresses the importance of targeting “..investments



toward the development of deeper understanding of complex biological systems..". The *Blueprint* is consistent with the 2005-2010 USDA Strategic Plan, including its **Goal 1** (Enhance International Competitiveness of American Agriculture), **Goal 2** (Enhance the Competitiveness and Sustainability of Rural and Farm Economies), **Goal 4** (Enhance Protection and Safety of the Nation's Agriculture and Food Supply), and **Goal 5** (Improve the Nation's Nutrition and Health). Appendix I provides additional information regarding how the *Blueprint* aligns with these USDA Goals.

Science to Practice Priorities:

Quantitative genetics has been used for many years in selecting animals for improved production (e.g., growth, yield, efficiency) and has achieved remarkable results. The addition of animal genomic technology to quantitative genetics programs has the potential to lead to more accurate and rapid animal improvement, especially for phenotypic traits that are difficult to measure (e.g. disease resistance, animal well-being, feed efficiency, product quality). Genomic technologies also offer new opportunities to develop precision management systems to optimize the production environment based on an animal's genotype. In the short-term, research, education, and extension efforts in animal genomics are expected to deliver the following genome-based technologies to animal producers:

- 1) Whole-genome-enabled animal selection.

- 2) Prediction of genetic merit of individual animals from genome-based data combined with phenotypes.
- 3) Integration of genomic data into large scale genetic evaluation programs and the use of genomic information to design precision mating systems.
- 4) Precision management systems to optimize animal production, health, and well-being.
- 5) Genomic capabilities that enable parentage and identity verification (traceability).

Discovery Science: Critical gaps in our understanding of gene structure and function in animals must be filled before animal genomics technologies can be successfully applied to animal industries. Agricultural animals form a unique resource to study the fundamental underlying biological mechanisms of gene structure and function, regulation of gene expression, and the genetic contribution to phenotypic variation because, unlike humans, animals have been artificially selected to express or repress specific traits. Advances in discovery science will require interdisciplinary teams of scientists that address complex agricultural issues with state-of-the-art equipment and approaches that include systems biology and comparative genomics. The following are priorities in discovery science for animal genomics:

- 1) Identify genes and gene products that regulate important traits in agricultural animals such as disease resistance, animal well-being, feed efficiency, and product quality.

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- 2) Understand mechanisms that regulate agriculturally relevant genes in a systems biology framework.
- 3) Define the mechanisms through which specific genes and genetic variation influence phenotypes and phenotypic variation.
- 4) Understand the roles and interactions of host animal and microbial genomes and environmental influences (e.g., animal feed, vaccines) for improving animal health, well-being, and production efficiency.

Infrastructure: A solid infrastructure is needed to support advances in discovery science. The priorities for a solid infrastructure are:

- 1) Genomic tools to connect genotype to phenotype and elucidate pathways of complex traits for all agricultural animal species. These genomic tools include comprehensive, high resolution genome maps and assembled and annotated genomic sequences.
- 2) National, comprehensive databases and the statistical and bioinformatics tools that integrate genomic, phenotypic, and experimental information for each species.
- 3) Genetic resources such as centralized animal populations that are deeply phenotyped as well as repositories for cell lines, DNA and RNA collections, and gene expression resources for all species. The mission of the National Animal Germplasm Program should be broadened to become a coordinated national repository for genomic

- 4) Education and training of students, scientists, and the public on genome-enabled animal sciences and opportunities that help prepare the next generation of scientists. Particular emphasis should be placed on integrating quantitative genetics, genomics, immunology, nutrition, physiology, biochemistry, cell biology, developmental biology, ecology, engineering, physics, mathematics, and computer science with development of scientists who have a keen appreciation for, and knowledge of, animal production systems. Additional emphasis on extension and outreach will enable and facilitate effective translation of genomics research and resulting technologies to the agricultural animal production sector and the public.



INTRODUCTION

Agricultural animal research has been successful in developing technology and methodologies that have enhanced production efficiency of the beef, dairy, swine, poultry, sheep, and aquaculture industries. Excellent examples of the changes that have taken place over the last ~50 years are: 1) The dairy industry's coupling of genetic selection and efficacious use of artificial insemination has more than doubled the annual milk yield per cow while reducing the size of the national dairy herd by about 50%; 2) Genetics, nutrition and other management changes resulted in a "modern day" broiler that requires approximately one-third the time and over a threefold decrease in the amount of feed consumed to produce a market-age broiler; and 3) The pounds of feed needed to produce a pound of pork is estimated to have been halved. While quantitative geneticists have been successful in improving production traits, genomic technology has potential to lead to more accurate and rapid animal improvement, especially for phenotypic traits that are difficult to measure (such as disease resistance, animal well-being, feed efficiency, and product quality). The potential for future improvements in animal production efficiency, quality of animal products, animal health and animal well-being lies in the elucidation and understanding of interactions of the various components of animal biology in concert with all of the parameters of the production environment. To begin to fully understand these interactions, a redirection of the traditional "reductionist

science" approach to a "systems biology" approach is required. It is also clear that publicly supported agricultural research must be focused on enhancing the nutrient composition of meat, milk, and eggs and enhancing the functionality and well-being of animals in environmentally neutral production systems.

In the past two decades, molecular biology has changed the face of agricultural animal research, primarily in the arena of genomics and the relatively new offshoot areas of **functional genomics, proteomics, transcriptomics, metabolomics and metagenomics**. Recently, the agricultural research community has been able to capitalize on the infrastructure built by the human genome project (Collins et al., 2003; International HapMap Consortium, 2005) by sequencing two of the major agricultural animal genomes, *Gallus domesticus* (International Chicken Genome Consortium, 2004; Wong et al., 2004) and *Bos taurus* (Gibbs et al., 2002). The 2006 calendar year marked a major milestone in the history of agricultural animal research since annotated draft genome sequences were completed for chickens and cattle and sequencing was initiated for the porcine and equine genomes. We now have in place a powerful toolbox for understanding the genetic variation underlying economically important and complex phenotypes of agricultural animals.



STAKEHOLDER INPUT

The priorities and recommendations contained in this *Blueprint* are based on a substantial amount of stakeholder input that was provided to USDA National Program Staff by scientists, producers, animal industry and commodity groups, other federal research agencies, and the general public.

In 1990, an Allerton Conference entitled “*Mapping Domestic Animal Genomes: Needs and Opportunities*” was hosted by the University of Illinois while a Banbury Conference was held at Cold Spring Harbor on “*Mapping Genomes of Agriculturally Important Animals*”. Participants at these workshops recommended to USDA that genetic maps be developed for each of the agriculturally important species (cattle, swine, poultry, sheep, and fish).

A second Allerton Conference entitled “*Genetic Analysis of Economically Important Traits in Livestock*” was convened in 1996. The primary recommendation of the workshop was a call for building the research infrastructure necessary to enable researchers to identify important genes that control economically important traits and, eventually, gain an understanding of the function of individual genes and their interactions across the genome (Schook, 1997).

In 2002, the National Academy of Sciences hosted a public workshop entitled “*Exploring Horizons for Domestic Animal Genomics*” (National Academies

Press, 2002). The workshop participants identified the need to produce high-coverage, draft genome sequences of some domestic animal species (cattle, chicken, swine, dog, and cat) for deposit into the public domain databases. Furthermore, it was recognized that there would be a need to scale up bioinformatics resources to make effective use of the information that would result from the genome sequencing projects. Based upon the experiences of the National Plant Genome Initiative, it was also discussed that funding for such large-scale projects would likely need to come from a variety of sources, including the U.S. Federal government, private industry, and international partners.

In 2002, a third Allerton Conference entitled “*Beyond Livestock Genomics*” was conducted to develop an initial plan for the full utilization of genomic information to promote animal health and productivity. The overarching recommendation from this workshop was that additional basic research was needed to identify genomic mechanisms and novel genes/proteins in a variety of tissues under a variety of environmental conditions (Hamernik et al., 2003). Functional genomics was recognized as the vehicle for capitalizing on the investment of obtaining whole genome sequence information. The need to increase bioinformatics infrastructure, teaching, and outreach efforts in animal genomics was recognized also. To further define priorities for animal bioinformatics, an electronic workshop was conducted in 2002. Priorities for animal genome database development included: 1) data repository, 2) tools for genome analysis,



3) annotation, 4) practical application of genomic data, and 5) a biological framework for DNA sequence (Hamernik and Adelson, 2003).

An Interagency Working Group (IWG) on Domestic Animal Genomics was chartered in September of 2002 by the U.S. National Science and Technology Council. The membership of the IWG included representatives from the Department of Agriculture (USDA), Department of Energy (DOE), Food and Drug Administration (FDA), National Institutes of Health (NIH), National Science Foundation (NSF), Office of Science and Technology Policy (OSTP), Office of Management and Budget (OMB), Department of Homeland Security (DHS) and the U.S. Agency for International Development (USAID). The IWG identified the following broad strategic goals: 1) Bring into place the programmatic elements needed to advance the study and understanding of domestic animal genomes, including large-scale DNA sequencing; functional characterization of expressed genes (functional genomics); tools for data storage, analysis and visualization (bioinformatics); and study of similarities among genomes of different species (comparative genomics); 2) Leverage the national infrastructure for large-scale DNA sequencing that has been established for the Human Genome Project and other vertebrate and model organism genomes; 3) Advance and utilize the enabling tools and infrastructure of functional genomics and bioinformatics to enhance the understanding not only of basic science and disease mechanisms,

but also to address critical agricultural missions, including animal health and well-being, food safety, and human nutrition; 4) Ensure that genomics data are freely available in the public domain and genomics reagents and resources are available to the public; 5) Increase the training opportunities for genomics and bioinformatics at all levels of education; and 6) Coordinate and encourage international cooperation to achieve these goals.

In early 2004, as the sequencing goals of the IWG appeared to be within reach, the IWG charged the USDA with evaluating how bioinformatics and functional genomics programs should be developed further to allow full utilization of annotated genome sequences and associated tools. An Animal Genomics Workshop was convened by USDA administrators in ARS and CSREES in 2004. The workshop resulted in a list of priorities in each of these areas for the “post-sequencing era” for agricultural animal genomics (Green et al., 2007). A primary recommendation resulting from this workshop was that “USDA should expeditiously develop a coordinated long-term strategic plan for efforts in agricultural animal genomics”. Thus, in January 2006 the USDA Undersecretary for Research, Education, and Economics appointed an Animal Genomics Strategic Planning Task Force to develop a *Blueprint* intended to guide future decision making and priority setting by the Department and its relevant agencies.



In 2006, the ARS and CSREES conducted a joint stakeholder workshop in the area of animal production and well-being where previous input was further validated by scientists, producers, and representatives of animal commodity groups and animal industries. A summary of the ARS and CSREES stakeholder workshop is available at: (http://www.ars.usda.gov/research/programs/programs.htm?np_code=101&docid=13166). Additionally, in July 2006, a US-EC Livestock Genomics Symposium was held under the auspices of the US-EC Joint Task Force on Biotechnology. The priorities identified in this session allowed USDA to assure that efforts between the European Commission and U.S. research programs were complementary in achieving impacts in agricultural animal genomics and also identified areas for transatlantic collaboration (Burfening et. al., 2006). Input from both of these events was used in the formulation of the USDA *Blueprint*.

SCIENCE TO PRACTICE

Application of basic science to improve animal production practices is the goal of animal genomics research. In the short-term, the combined use of genomic information with existing animal breeding and animal management programs will provide immediate impacts, such as more accurate and accelerated rates of genetic improvement of breeding stock (especially for traits that have been traditionally difficult to measure), animals that are more adaptable and better suited to various production environments, and

new genome-based technologies to enable parentage and identity verification (i.e., traceability). Delivery and adoption of new genome-based technologies will require integrated activities involving basic scientists, educators (classroom and extension specialists), animal breeding and artificial insemination organizations, and producers working together to utilize these technologies. In the long-term, animal genomics efforts will lead to efficient and economical production of human pharmaceutical proteins in animals, new technologies for manipulation of gene expression in animals (i.e., RNA interference, transgenesis, etc.), and improved methods for conserving biodiversity and unique animal germplasm. Because of the existing widespread use of quantitative genetics in animal breeding programs in the U.S. and the rapid rate at which genomic information is being discovered, the initial applications of genomics efforts will be the combined use of genomic data with quantitative genetics for animal improvement, management, and biosecurity. Thus, USDA-supported research, education, and extension efforts in animal genomics are expected to deliver the following genome-based technologies to livestock producers in the short term:

- 1) **Whole genome enabled animal selection resulting in a significant reduction in selection cost and generation interval.** One of the first and most exciting avenues to explore is the possibility of using dense single nucleotide polymorphism (SNP) maps coupled with haplotype information



within species to enable “whole-genome selection” for traits important in the overall breeding objective. Such approaches should accelerate the rate of genetic improvement, while simultaneously reducing progeny testing costs to the animal industries. In addition, precise genetic improvement will be obtained because SNP markers can be used to monitor selection for more than one trait throughout the entire genome.

- 2) Prediction of genetic merit from genome-based data combined with phenotypes.** In order to fully harness the power of genomic information for genetic improvement, a meshing together of quantitative genetics theory and platforms with genomic data will be required. Additionally, significant research and software development is required to integrate all forms of genomic information, following validation, into large-scale genetic evaluation systems. A critical step in the process of moving to genome-enabled animal improvement is the development of standardized systems for recording performance phenotypes for complex and difficult to measure traits. This is particularly true for traits that capture the genetic variation of animals for adaptation to their production environments (stress resistance, behavior, innate resistance to disease) and for measures of efficiency of nutrient utilization (e.g. feed efficiency), amongst others. A major effort will be required for these traits to be defined and

parameterized, followed by evaluation in genetic resource populations to identify genomic control mechanisms underpinning observed variation.

- 3) Integration of genomic data into large scale genetic evaluation programs and the use of genomic information to design precision mating systems.** Not only will genomic information be of use in prediction of genetic values for complex traits, the resulting tools from such approaches will also allow design of precision mating systems. More precise information at the genomic level can be incorporated into mating system design to minimize the cumulative effects of inbreeding from selection and predict matings that will optimize the use of non-additive genetic variation for traits where hybrid vigor is of importance. Knowledge of epigenetic effects will also be required to fully capture the value of this use of genomic data.
- 4) Precision management systems to optimize animal production.** Genomic information will also provide the basis for development of precision management systems. Knowledge of an animal’s genotype will allow precise sorting of animals into the optimal production environment, resulting in enhanced animal well-being. For example, the genotype of some beef and dairy cattle may be more suited to pasture-based production systems rather than confinement systems. Feeding regimens and preventative health care programs can also be



designed to match an animal's genotype and lead to increased production efficiency, targeted market endpoints, and new opportunities for niche markets. The expected amount of genomic information will require development of decision support systems for use in the industries to implement and manage such genome-enabled precision management systems. The ability to precisely control expression of selected genes (such as inactivation of the myostatin gene to increase lean muscle mass) may also lead to increased production efficiency, more consistent meat quality, and healthier animals.

- 5) **Genomic capabilities that enable parentage and identity verification (traceability).** Development of high-throughput genotyping systems that allow for individual animal identification and parentage identification will likely have an immediate impact on all animal industries. High-throughput SNP genotyping systems are affordable and will likely be commercially available for most agricultural animal species in the near future. In today's world, biosecurity is a major issue due to the concentration of animal populations and widespread movement of animals. Genomic techniques and technology should be harnessed to provide a quick, affordable, and foolproof means of animal identification for traceability resulting in increased food safety and consumer confidence in the food supply.

DISCOVERY SCIENCE

Critical gaps in our understanding of gene structure and function in animals must be filled before genome-enabled technologies can be successfully applied to animal improvement, management, and biosecurity programs. Rapid progress in discovering new knowledge related to animal gene structure and function will require interdisciplinary teams of scientists, access to state-of-the-art equipment, technology, and approaches that include systems biology and comparative genomics.

Instead of analyzing individual components or aspects of the organism, systems biology incorporates all biological components and their interactions. Systems biology will promote identification and determination of the function(s) of a complete set of genes and regulatory elements and will integrate analysis of DNA sequences, transcriptional regulation, proteomics, and metabolic networks and pathways. The ultimate goal is to understand how genotype contributes to phenotype and phenotypic variation. Animal populations that have been selected for specific phenotypes and that have been well-characterized at the molecular and whole animal levels provide a valuable resource for discovery research in this area.

Comparative genomics will be an essential tool to take advantage of knowledge obtained from species with finished genome sequences (i.e., human, mouse, rat) to advance the knowledge of genomes



from agricultural animals. DNA sequences that have been highly conserved across species are likely to have functional significance, either as genes or as regulatory elements. Agricultural animals will play a significant role in revealing the basic biology of how chromosomes evolved and how functional elements within a genome are organized to produce different phenotypes. Comparative genomics will also point to specific targets for understanding and potentially modulating gene expression. Since it is not likely that the genomes from all animals of agricultural importance will be sequenced in the near future, comparative genomics will provide an important tool for extrapolating genetic information between closely related species (such as chickens and turkeys or cattle and sheep).

The priorities for advancing discovery science in the short-term are:

- 1) Identify genes and gene products that regulate important traits in agricultural animals.** Previous research in agricultural animal genomics has identified a substantial number of genomic regions harboring Quantitative Trait Loci (QTL) for a variety of economically important traits. Fine-mapping of these QTL and identification of many more gene and genic interaction effects for a wide array of traits of economic and societal importance are expected in the near future. Comparative genomics will be an important tool to discover genes that are common
- 2) Understand mechanisms that regulate agriculturally relevant genes in a systems biology framework.** Although progress has been made in understanding the mechanisms that regulate individual genes in isolated systems (i.e., in isolated cell cultures), many of the basic mechanisms that regulate gene expression in the context of the whole animal still need to be determined. Expression profiling of large numbers of genes across diverse tissues, animal populations, and environmental conditions using DNA chips, microarrays, or next-generation sequencing will identify novel genes and characterize spatial and temporal expression of these genes. Additional technologies to knock out (such as RNA-interference; RNAi) or knock-in (i.e., transgenesis with opportunities for spatial and temporal control of the transgene) gene expression will need to be optimized for more efficient use in animals.



3) **Define the mechanisms through which specific genes and genetic variation influence phenotypes and phenotypic variation.** Discovery science is also needed to unravel the complexities of epistasis and the interactions of genotype by environment and how they affect phenotype. Development of clear and standardized descriptions or ontologies for defining phenotypes (especially for phenotypes that are difficult to measure) for animals are needed. Efficient, systematic, and comprehensive phenotypic screening procedures and tools that will permit comparison among laboratories are also needed. The identification of haplotypes within and between breeds of animals will enhance the mapping of traits and the ultimate identification of mutations underlying those traits that may give rise to phenotypic variation.

4) **Understand the role of host genomes and microbial genomes to improve animal health and well-being.** Despite efforts to control the production environment (e.g. housing systems, feeding systems, thermal environment), animals are not born and raised in isolation. The interaction of host, beneficial and pathogenic microbes, and environment ultimately determines whether an animal remains healthy or is challenged by disease. Consequently, understanding the variation in how an animal responds to various microbes and environments can have profound influences on the outcome of the interactions. Current efforts of most scientists are directed

toward understanding the genetics or physiology of the host, finding pathogenicity genes in viruses or other pathogens, and examining how animal feeds and environmental parameters influence the composition of the microbial community in the digestive tract. While these approaches have been successful, further advances in animal health and well-being will require a systems biology approach by interdisciplinary teams of scientists. State-of-the-art metagenomics technologies can be used to understand the genetic composition of poorly characterized microbial communities in the rumen and gastrointestinal tract of animals. Functional genomics efforts will define the microbial response in the rumen or gastrointestinal tract to different hosts or changes in environmental conditions such as nutrition, management, or therapeutics. Future genomics efforts will allow selection of animals for superior disease resistance, vaccine response, or adaptability to various production environments. In addition, improved vaccines, diagnostics and therapeutics can be developed; producers can devise better precision feeding systems to improve efficiency of nutrient utilization and enhance animal well-being; and use of antimicrobials and pesticides can be reduced in agricultural animal production.



INFRASTRUCTURE

A solid infrastructure is needed to facilitate advances in discovery science in animal genomics in a time and cost-effective manner. Infrastructure refers to state-of-the-art genomic tools and resources that are available to the scientific community as well as a highly trained and skilled workforce. The infrastructure needed to advance animal genomics efforts does not require additional bricks and mortar. The priorities for a solid infrastructure in animal genomics are:

- 1) Genomic tools to connect genotype to phenotype and elucidate pathways of complex traits for all animal species important to agriculture.** These genomic tools include: comprehensive, high resolution genome maps and assembled and annotated genomic sequences.

Genome Maps: Genetic maps are the basis for identifying genome regions that affect genes of economic importance in agricultural animals. Genetic linkage maps are needed for all agricultural animal species so that each species can utilize the most current selection practices. Linkage maps for all species must be of sufficient density so that genomes can be scanned effectively and efficiently for economically important loci. Physical maps are needed so that researchers can characterize specific regions of the genome. Maps based on segregation of markers in irradiated hybrid cell lines provide the resolution needed to order

markers and genes in very narrow regions of the genome (less than 100,000 bases apart) and are excellent resources for developing comparative maps between species. Whole genome physical maps are composed of ordered BAC clones, which contain large segments of cloned DNA (100,000-200,000 bases) necessary to develop markers for use in commercial animal populations.

Assembled and Annotated Genomic Sequences:

An assembled genome sequence is a compilation of all of the available DNA sequence into long contiguous (contigs) stretches of DNA and assignment of DNA contigs to specific chromosomes. Assembled genome sequences provide insight into the evolutionary processes that occurred during development of a species; allow basic studies on the architecture of a genome; allow characterization of genetic variation that underlies traits; and provide information regarding organization of genes and their impact on expression of genes in different tissues. An annotated genome sequence contains information regarding the gene name, gene structure, function of the gene product, cellular location of the gene product, as well as how this knowledge was determined (i.e., literature citation). A finished, annotated genome sequence should be available for the most economically important species (currently these species include: cattle, chicken, and swine). The target for these species should be a 10-fold or greater coverage of the genome. The next tier of economic importance (for example: catfish, equine (currently at 6.8X), salmon,



sheep, tilapia and turkey) should have a high quality draft genome sequence (approximately 6X). This level of genome sequence quality is necessary for accurate functional genomic studies as well as comparative analyses. Additional species (for example: goat, oyster, shrimp, and trout) should have a low quality draft genome sequence (approximately 2X). This level of coverage, coupled with genetic and physical maps, would advance the basic biology of these species as well as allow for limited comparative analyses.

2) National, comprehensive databases and the statistical and bioinformatics tools that integrate genomic, phenotypic, and experimental information for each species. To effectively use the resources being generated from efforts in animal genomics, there is a need to design, construct and maintain large comprehensive databases and the statistical and bioinformatic tools that integrate information from these databases for a variety of applications. As annotated sequence data, haplotype maps, SNP maps, expression profiling data, and other genomic data become available, these data will need to be integrated with phenotypic, pedigree, and experimental data into a common, national database. These databases will require a standardized ontology of genotypes and phenotypes and mechanisms to encourage centralization of producer-generated phenotypic data. The National Center for Biotechnology Information (NCBI) at the NIH is

currently the warehouse for genome sequence information. However, NCBI does not have adequate resources to continue to maintain and curate all genome sequence databases. In addition, agricultural animal species have unique population characteristics (such as inbreeding or crossbreeding that are not present in other species) and require unique statistical tools for appropriate analyses.

3) Centralized animal genetic resource populations that are deeply phenotyped and available to the research community. A centralized facility with sufficient technical expertise to preserve unique experimental animal populations, collect genotypic and phenotypic information on these animals, and make the populations available to the agricultural and biomedical research communities (i.e., the Jackson labs model) is needed. The emphasis in these animal populations should be on the development of rich phenotypic measures for common traits of interest as well as complex and difficult to measure traits such as feed efficiency, disease resistance, animal well-being, product quality, and environmental adaptability. Resource populations of animals with divergent responses to microbes, vaccines and therapeutics are also needed. Repositories for cell lines, DNA and RNA collections, and gene expression resources for all species should also be developed, maintained and made readily accessible to the scientific community.



The mission of the National Animal Germplasm Program should be broadened to become a coordinated national repository for genomic DNA, appropriate DNA libraries, tissues and specialized cell lines for access by publicly-funded, U.S. scientists.

- 4) **Education and training of students, scientists, and the public on genome-enabled animal science and opportunities that help prepare the next generation of researchers to work in interdisciplinary teams.** Particular emphasis should be placed on integrating quantitative genetics, genomics, immunology, nutrition, physiology, biochemistry, cell biology, developmental biology, ecology, engineering, physics, mathematics, and computer science with development of scientists who have a keen appreciation for and knowledge of animal production. There is a dearth of qualified candidates for scientific and technical support positions in the animal industry. The critical mass of expertise in animal genomics at colleges and universities across the globe that train these scientists is diminishing at a rapid pace. The U.S. faces the very real possibility of losing our ability to train new scientists in the integrated fields of quantitative genetics, statistics, and computational biology for animals unless this trend is reversed. Undergraduate animal sciences and related curricula should contain sufficient exposure to “omics” concepts and technologies, as well as the social science aspects of

consumer acceptance of the application of genome-enabled technologies to animal production systems. In addition, faculty development, student recruitment and services, curriculum development, instructional materials, and innovative teaching methodologies in agricultural animal genomics are needed. A national animal genomics commodity-specific model for extension and outreach (based on “regional” extension specialists) will enable and facilitate effective translation of genomics research and resulting technologies to the animal production sector and the public.

CONCLUSION

Quantitative animal genetics and animal improvement programs have led to tremendous improvements in the efficiency of agricultural animal production during the last 50 years. Investments in genomic technology from gene discovery to sequenced genomes, as well as state-of-the-art technology developed by the biomedical research community, have animal agriculture poised at the threshold of the genomic revolution. Application of new genomic technologies to animal producers will improve the efficiency, sustainability, biosecurity, and social acceptance of animal production. This *Blueprint* describes future research, education, and extension efforts needed to develop and deliver animal genome-enabled technologies to the animal industry. The *Blueprint* contains specific

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Discovery Science

Infrastructure



recommendations for Infrastructure, Discovery Science, and Science to Practice. A summary of these recommendations is provided in Appendix II.



A word about the USDA Animal Genomics Strategic Planning Task Force:

*Following the recommendation of the Interagency Working Group on Animal Genomics, a task force was established in January 2006 by USDA's Under Secretary for Research, Education and Economics, Joseph Jen. This task force was charged with developing a **Blueprint** for USDA efforts in agricultural animal genomics. Members include:*

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Appendix I
Alignment of Blueprint Priorities With National Issues and USDA Strategic Goals

	Competitiveness of American products*	Production Efficiency**	Animal Health & Well-Being***	Biosecurity***	Product Quality****	Food Safety***	Traceability****	Sustainability**
Science to Practice								
Whole Genome Selection	X	X	X	X	X			X
Prediction of Genetic Merit	X	X	X		X			X
Precision Mating	X	X	X		X	X		X
Precision Management	X	X	X		X			X
Genome-Based Traceability	X			X	X	X	X	X
Discovery Science								
Gene Discovery	X	X	X	X	X	X	X	X
Systems Biology & Gene Mechanisms	X	X	X	X	X	X		X
Genetic Basis of Phenotypic Variation	X	X	X	X	X	X		X
Animal Health & Well-Being	X	X	X	X	X	X		X
Infrastructure								
Genomic Tools	X	X	X	X	X	X	X	X
Databases	X	X	X	X	X	X	X	X
Genetic Resources	X	X	X	X	X	X	X	X
Education and Outreach	X	X	X	X	X	X	X	X

* Relates to USDA Goal 1 (Enhance International Competitiveness of American Agriculture)

** Relates to USDA Goal 2 (Enhance the Competitiveness and Sustainability of Rural and Farm Economies)

*** Relates to USDA Goal 4 (Enhance Protection and Safety of the Nation's Agriculture and Food Supply)

**** Relates to USDA Goal 2 (Enhance the Competitiveness and Sustainability of Rural and Farm Economies) and Goal 5 (Improve the Nation's Nutrition and Health)

Appendix II

Summary of the Animal Genomics Blueprint Priorities

Science to Practice:

1. Whole genome enabled animal selection.
2. Prediction of genetic merit of individual animals from genome-based data combined with phenotypes.
3. Integration of genomic data into large scale genetic evaluation programs and the use of genomic information to design precision mating systems.
4. Precision management systems to optimize animal production, health, and well-being.
5. Genomic capabilities that enable parentage and identity verification (traceability).

Discovery Science:

1. Identify genes and gene products that regulate important traits in agricultural animals such as disease resistance, animal well-being, feed efficiency, and product quality.
2. Understand mechanisms that regulate agriculturally relevant genes in a systems biology framework.
3. Define the mechanisms through which specific genes and genetic variation influence phenotypes and phenotypic variation.
4. Understand the roles and interactions of host animal and microbial genomes and environmental influences (e.g., animal feed, vaccines) for improving animal health, well-being, and production efficiency.

Infrastructure:

1. Genomic tools to connect genotype to phenotype and elucidate pathways of complex traits for all agricultural animal species. These genomic tools include comprehensive, high resolution genome maps and assembled and annotated genomic sequences.
2. National, comprehensive databases and the statistical and bioinformatics tools that integrate genomic, phenotypic, and experimental information for each species.
3. Genetic resources such as centralized animal populations that are deeply phenotyped as well as repositories for cell lines, DNA and RNA collections, and gene expression resources for all species. The mission of the National Animal Germplasm Program should be broadened to become a coordinated national repository for genomic DNA, appropriate DNA libraries, and specialized cell lines.
4. Education and training of students, scientists, and the public on genome-enabled animal sciences and opportunities that help prepare the next generation of scientists. Particular emphasis should be placed on integrating quantitative genetics, genomics, immunology, nutrition, physiology, biochemistry, cell biology, developmental biology, ecology, engineering, physics, mathematics, and computer science with development of scientists who have a keen appreciation for and knowledge of animal production systems. Additional emphasis on extension and outreach will enable and facilitate effective translation of genomics research and resulting technologies to the agricultural animal production sector and the public.

