

Projected Outcomes

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.