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From Animal Genomes to Phenomes: What's Next for Genomics

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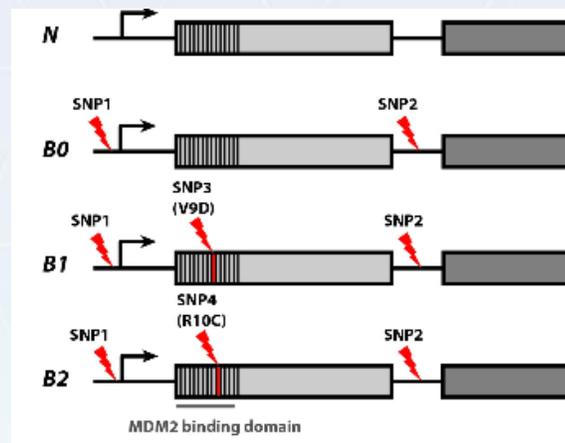


Image from: Schwochow et al., 2017, PLoS One



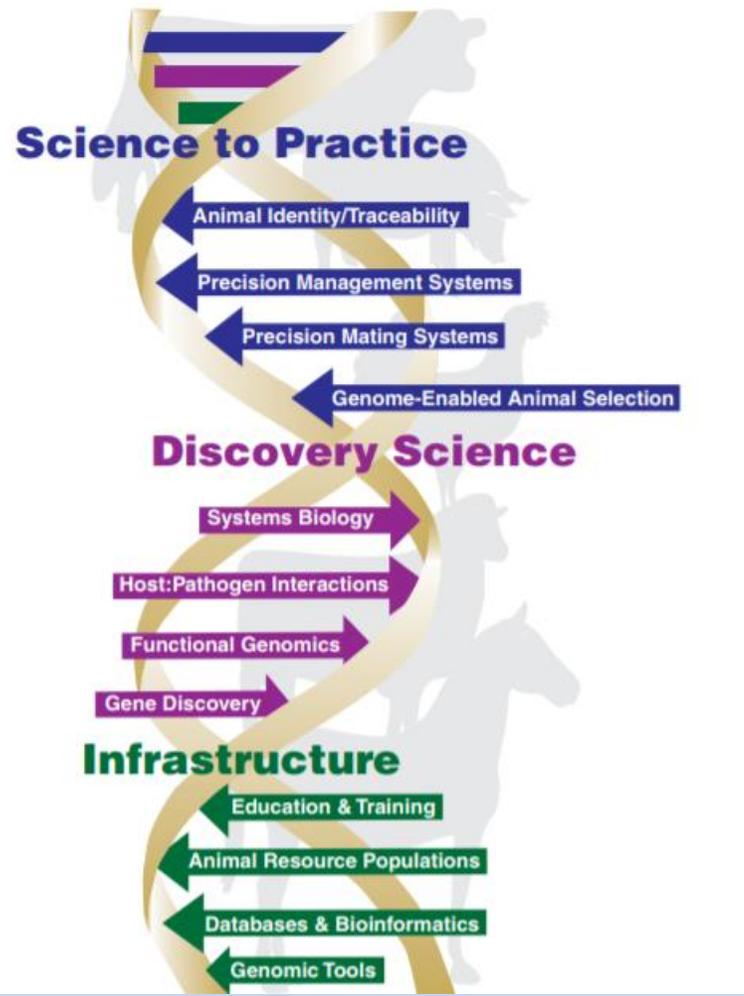
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September 2007

Blueprint for USDA Efforts in Agricultural Animal Genomics 2008–2017



In the decade that followed, many of the goals set forth in the blueprint were accomplished.

Genomes have been assembled and annotated for major agricultural species, including:

Chicken – 2004, 10X coverage

Cattle – 2009, 10X coverage

Turkey – 2010, 6X coverage

Swine – 2012, 10X coverage

Sheep – 2014, 6X coverage

Catfish – 2016, 6X coverage

Goat – 2017, 2X coverage

Genome Data Viewer

Meleagris gallopavo: Turkey_5.1 (GCF_000146605.3) Chr 5 (NC_015015.2): 1 - 59,006,440

Reset All Share this page FAQ Help Browser Agreement Version 4.8.3

Ideogram View

Unplaced/unlocalized scaffolds: 185,142

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15

16 17 18 19 20 21 22 23 24 25 26 27 28 29 30

Z W MT

Search

Location, gene or phenotype

Enter a location, gene name or phenotype

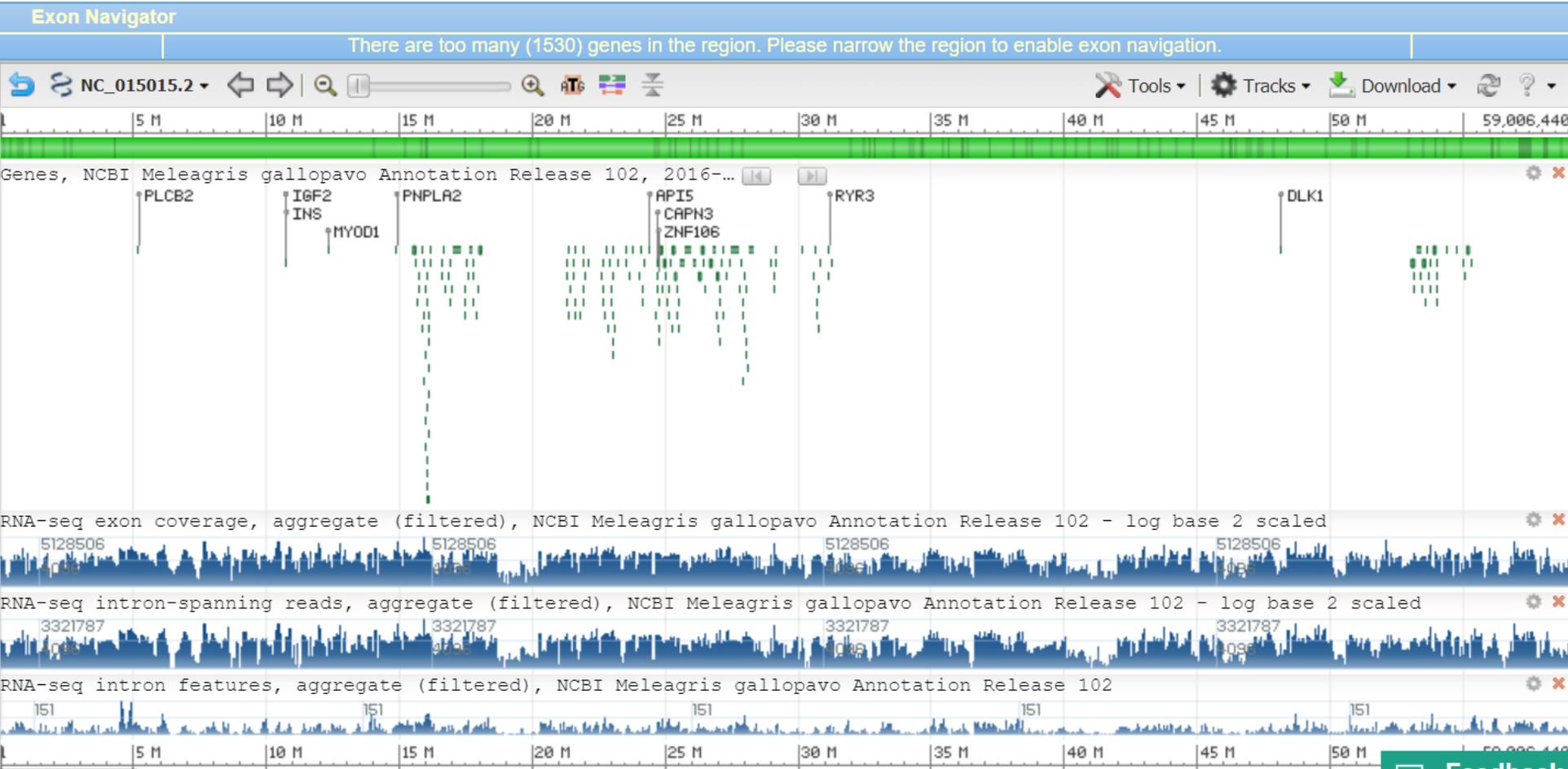
Search examples:

User Data and Track Hubs

BLAST

Add Tracks

History



Affymetrix Introduces Axiom® Turkey Genotyping Array

PRODUCT NEWS 📅 Nov 21, 2015

“Affymetrix, Inc. has introduced Axiom® Turkey Genotyping Array, developed in collaboration with the USDA’s Agricultural Research Service, Aviagen and Hendrix Genetics.”

- Includes 643,845 SNPs
- Enables turkey breeders to screen birds for economically important traits
- Markers associated with meat characteristics, health outcomes, and fertility

Over the past 10 years, genome-enabled technologies have become integral components of commercial animal breeding for many species as advances in DNA sequencing and genotyping dramatically increased the ability to obtain genome information.

International research consortia are using genomics to identify:

- **biomarkers for incidence of myopathies in live birds**
Occurrence of muscle myopathy is closely associated with up-regulation of protein metabolism and increased translation of proteins (Kuttappan et al., 2017).

Poultry breeding companies are using genome information to accelerate genetic improvement, although details of this are confidential.

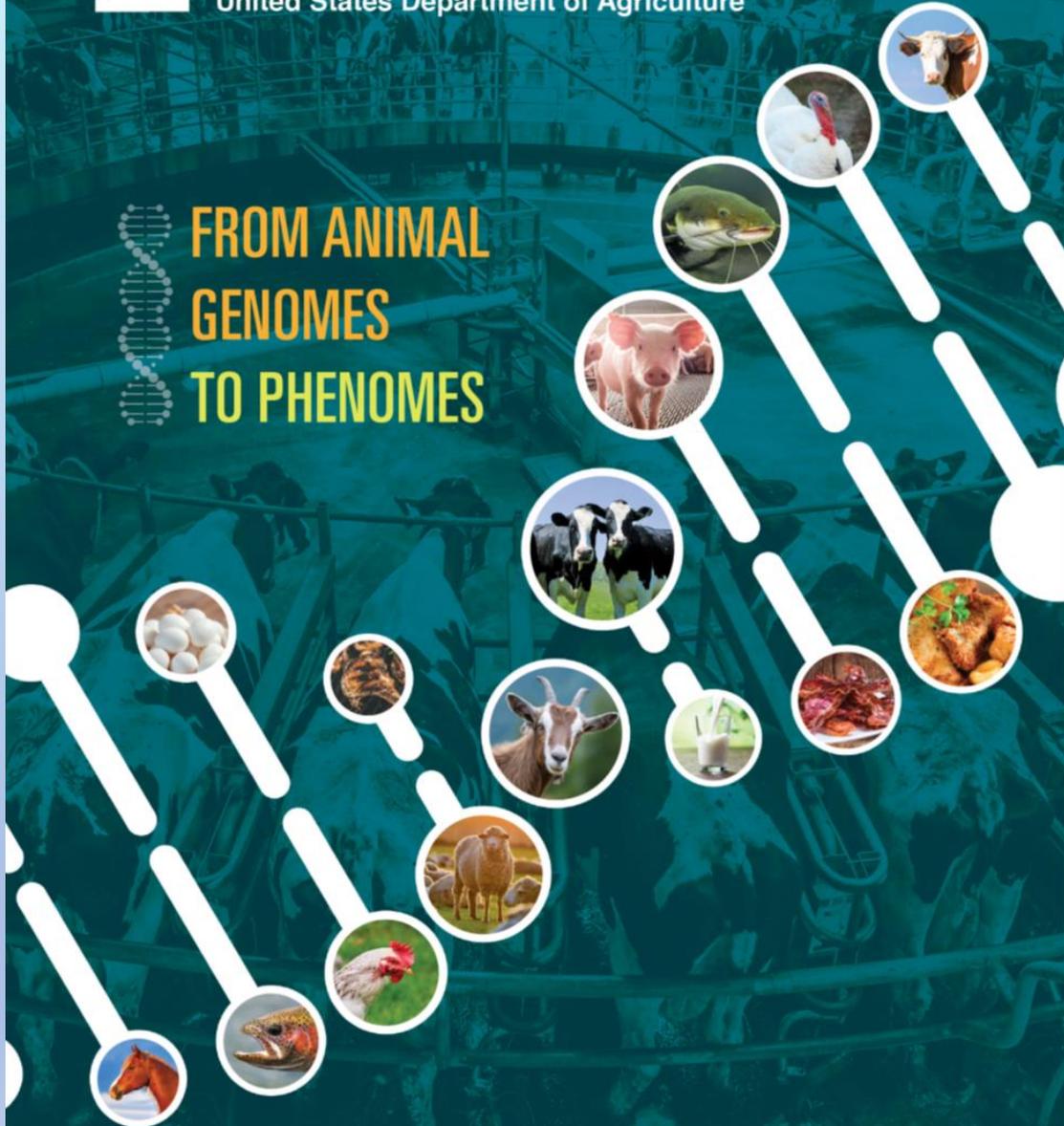
- **chickens that are more resilient to the negative effects of heat stress**
Genes associated with cell movement and immune signaling could be promising candidates for selection to improve humoral-mediated immune responses in heat-stressed poultry (Monson et al., 2018).

- **genetic differences of laying hens producing either a high or low breaking strength egg shell**
Osteopontin, which inhibits the growth of calcite crystals, had higher gene expression in hens with low shell strength (Zhang et al., 2019).



United States Department of Agriculture

FROM ANIMAL
GENOMES
TO PHENOMES



1. Science to Practice

a. Precision Selection and Management

2. Discovery Science

a. Genome and Functional Biology

The term “genome to phenome” describes the connection and causation between the **genetic makeup** of an animal (**genome**) and the totality of all phenotypes, or the **observable physical or physiological traits** or characteristics (**phenome**).

b. Bioinformatic and Computational Biology

d. Biotechnology

e. Animal Populations and Germplasm Preservation

Science to Practice: Precision Selection and Management

Attending to the State of the Art

- Primary use is to help identify specific genes or **SNP markers** that represent genetic diversity or the cost-effective level that are associated with **economically important traits**.
- High-throughput platforms for genotyping large numbers of these markers in a **single assay**
- Based on the individual's phenotype that seeks to determine the genetic basis of traits and **improve predictions of performance in offspring**

phenotypic, environmental, and genomic information. Comprehensive phenotypes should

Identify genes in a wide range of age with high reproductive, fitness, metabolic, welfare, disease susceptibility and disease resistance traits.

- Identify causal alleles

Poultry *identifying and characterizing the alleles that directly affect the biochemical mechanisms that underlie differences in phenotypes (and therefore economically important traits) will significantly expressed efforts to optimize breeding strategies.*

measured only in older females (egg production over extended periods).



Discovery Science: Genome and Functional Biology

Advancing the State of the Art

- Catalog gene expression

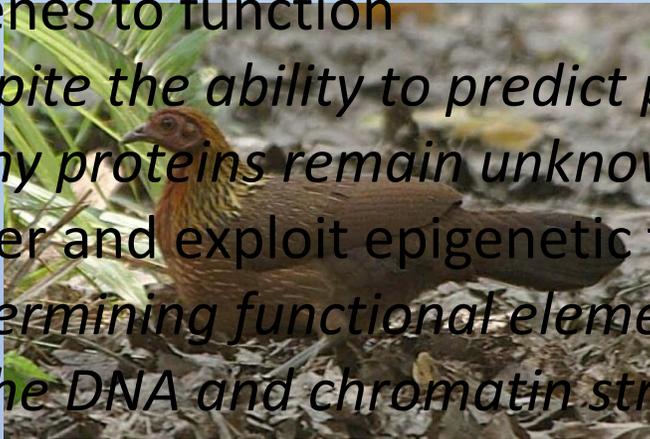
Determining mechanisms that underlie phenotypic variation and regulation of gene expression across tissues and biological states is essential for incorporating molecular phenotypes into genetic improvement programs, especially between commercial animals and their unselected ancestors.

- Link genes to function

Despite the ability to predict protein sequences from DNA sequences, the functions of many proteins remain unknown.

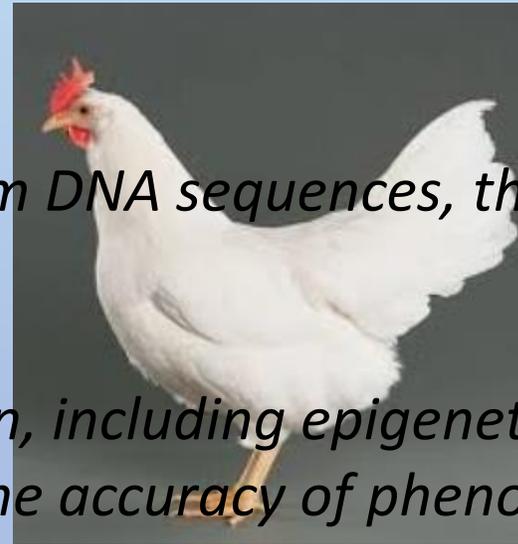
- Discover and exploit epigenetic factors

Determining functional elements of gene expression, including epigenetic modifications of the DNA and chromatin structure, will improve the accuracy of phenotype prediction.



6–12 eggs within the first year of life

Photo credit: Peter Price, orientalbirdimages.org



200 eggs within the first year of life

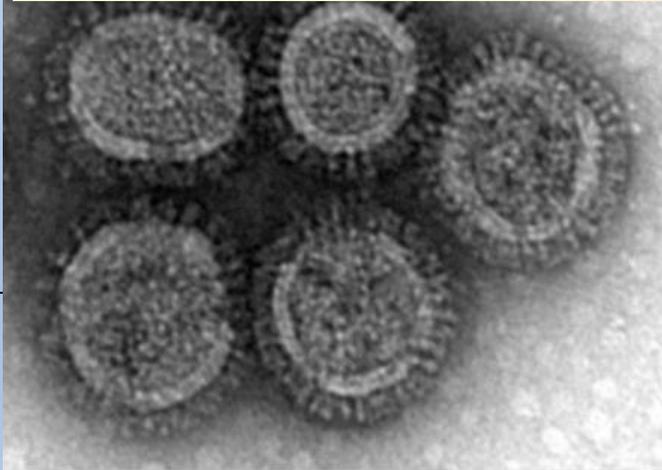
Discovery Science: Host-Pathogen Interactions

Advancing the State of the Art

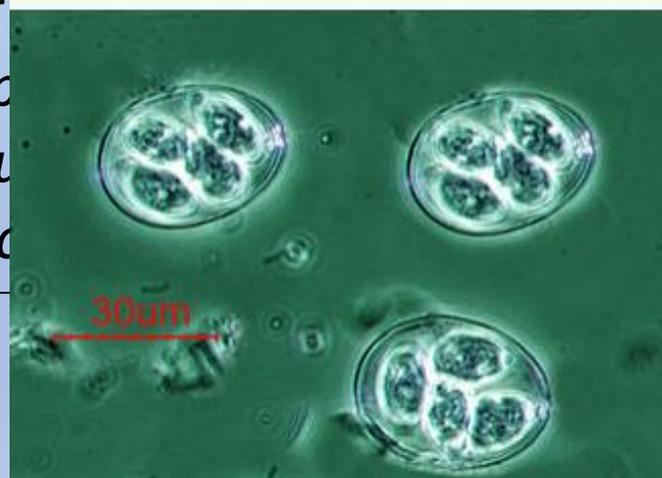
- Identify pathogens and diagnose diseases

Reemerging/new diseases need to be addressed due to changes in management, climate and other abiotic factors. Host genomic and immunological knowledge will need to be integrated with outbreak tracking tools and complete annotated genomes and pathogen variance characterization to provide information associated with disease phenotypes.

Avian H5N1 virus



Eimeria maxima



Mycoplasma gallisepticum

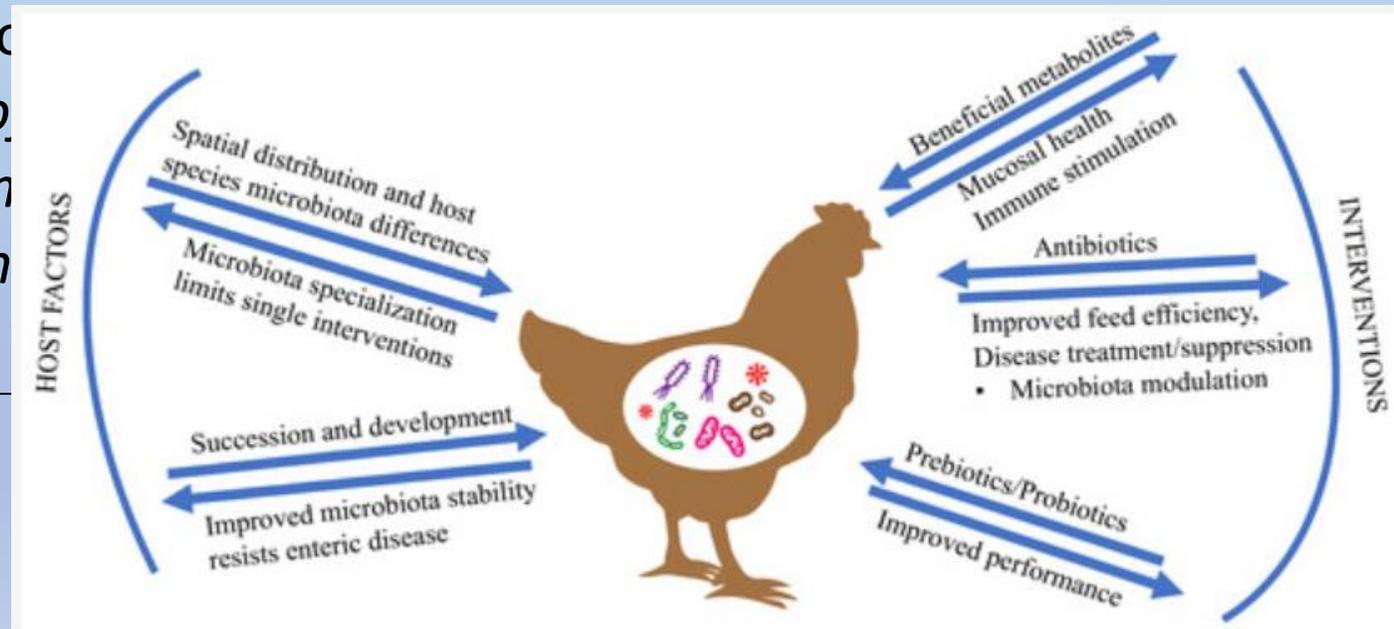


Photo: Dr. Takeshi Noda, University of Tokyo

Discovery Science: Microbiome and Metagenomics

Advancing the State of the Art

- Microbial genomes, transcriptomes, and metabolomes
The role of microbial populations (including bacteria, viruses, archaea, protists, and fungi) in animal health, production efficiency, and food safety has been confirmed in some cases. A proportion of observed phenotypic variation in animals may be due to differences in microbial populations.
- Building the micro...
The inclusion of... of prediction in... characterize th... populations.



...prove the accuracy...nsive methods to...analysis of entire

Figure from Maki et al., 2019, *Microorganisms*

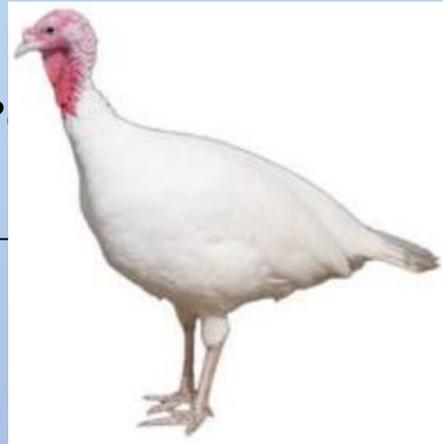
Infrastructure: Genome Tools and Resources

Advancing the State of the Art

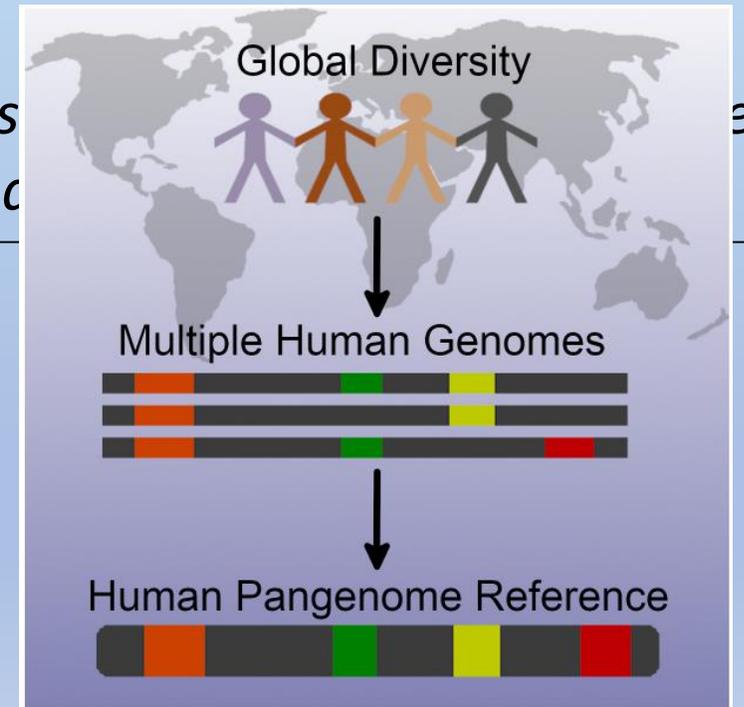
- Develop pan-genomes for agricultural animals

Existing reference genomes often represent a single, inbred individual. All animal species of agricultural importance should be characterized by pan-genome assemblies that, as with the human genome, provide full annotations of genomic features.

- Call for multiple annotated reference variants



encompass
gained and



Graphic by Peter Audano

Infrastructure: Animal Populations and Germplasm Preservation



Sue Lamont with an inbred chicken from a line used for disease resistance/tolerance studies at Iowa State University.

Advancing the State of the Art

- Improve cryopreservation protocols

Species-specific protocols must be developed to the degree they can be routinely used to preserve sufficient germplasm for all agriculturally important animals.

Chicken line	Week	Number					Percent		
		Eggs Set	Unfertile	Early Dead	Viable	Hatch	Total Fertility	Viable Embryos	Hatched
ADOL	1	94	91	0	3	3	3.2	3.2	100
Line 0	2	83	84	0	0	n/a	0	0	n/a
	3	96	82	0	0	n/a	0	0	n/a
VA Tech	1	89	86	0	3	3	3.4	3.4	100
Hi BW	2	93	89	0	4	3	4.3	4.3	75
	3	93	93	0	0	n/a	0	0	n/a
AR	1	89	49	4	36	36	44.9	40.4	100
Regressor	2	88	66	0	22	22	25	25	100
	3	93	88	0	5	4	5.4	5.4	80

Protecting Food Animal Gene Pools for Future Generations

*A paper in the series on
The Need for Agricultural Innovation to
Sustainably Feed the World by 2050*



Using different preservation techniques, breeds such as the Mulefoot hog, Buckeye chicken, San Clementine goat, Gulf Coast sheep, and Narragansett turkey can be preserved to ensure genetic diversity in livestock and poultry around the world. (Photo collage by Megan Wickham. Photos courtesy of the USDA, Wikimedia Commons, and Curtis Youngs.)

ABSTRACT

The world's population is expected to reach more than 9 billion by 2050, creating a grand societal challenge: ramping up agricultural productivity to feed the globe. Livestock and poultry products are keys to the world supply of protein, but genetic diversity of livestock is fading.

The number of breeds has declined as farming practices have focused on a small number of high-producing breeds to meet low-cost market demands. In fact, up to 25% of global livestock breeds are either at risk of being lost, or have already been lost. In the face of the mounting depletion in genetic diversity among livestock species, there is an

urgent need to develop and maintain an intensive program of sampling and evaluation of the existing gene pools. Genetic diversity can be preserved through living populations or cryopreserved for future use. Living populations can adapt to changes in the natural or production environment, provide value in research, and contribute to specialty

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The world's population is expected to reach more than 9 billion by 2050.

Livestock and poultry products from **7 domesticated species** are key components of the world's supply of dietary protein.

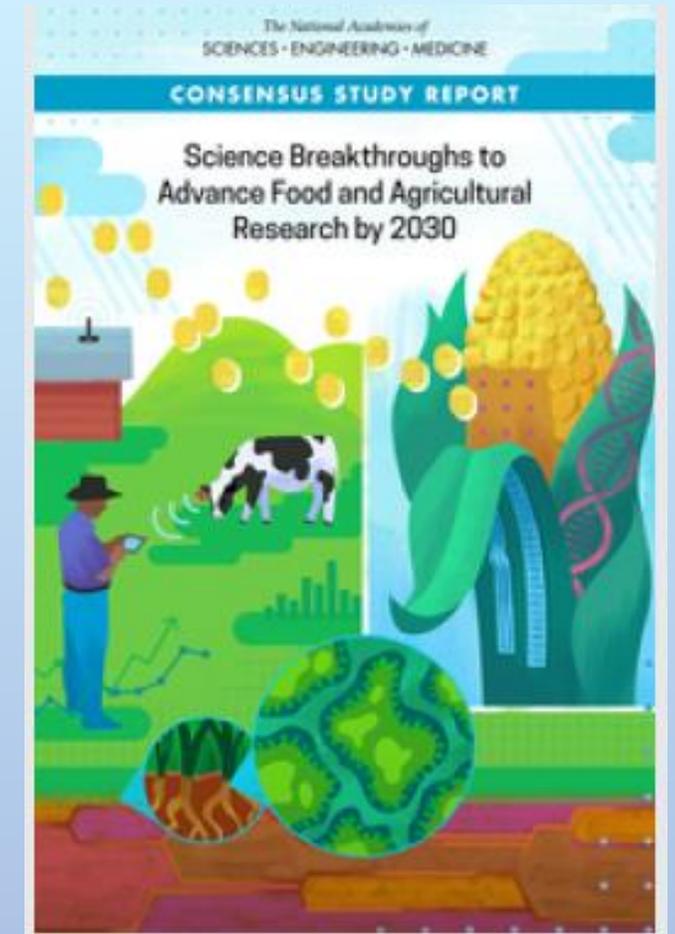
There are 7,745 agricultural breeds left in the world (FAO 2019). *The urgent process needed today to address the most challenging problems requires leveraging capabilities across the scientific and technological enterprise in a convergent research approach.*

Will need a two-fold increase in animal protein through:

- 1) 10-fold increase in the rate of genetic improvement;
- 2) development of precision livestock production systems.

Breeds not at risk = 7%

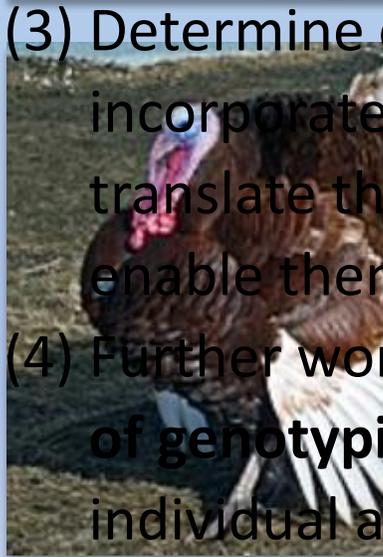
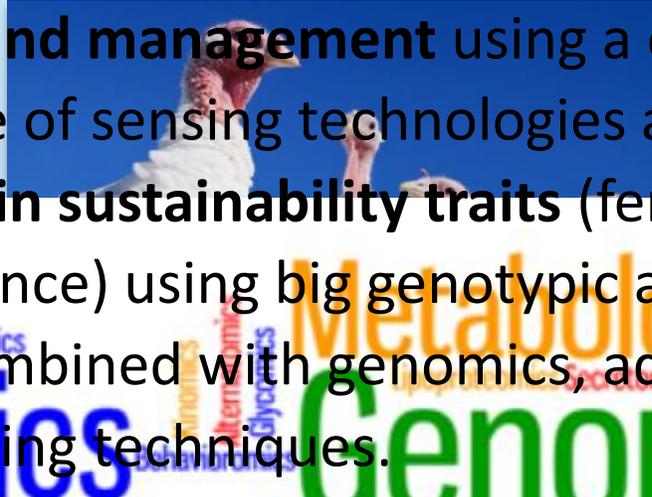
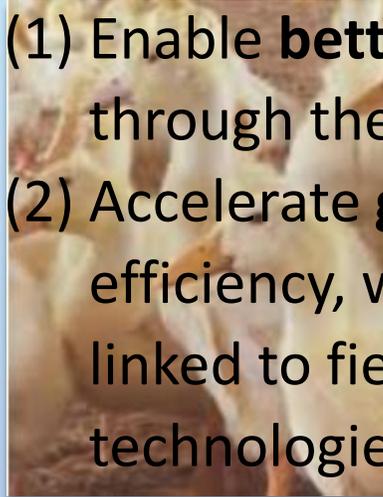
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Impacts of the Genome to Phenome Blueprint for the Poultry Industry: the “Omics” Revolution

- (1) Enable **better disease detection and management** using a data-driven approach through the development and use of sensing technologies and predictive algorithms
- (2) Accelerate **genetic improvement in sustainability traits** (fertility, improved feed efficiency, welfare, disease resistance) using big genotypic and sequence data sets linked to field phenotypes and combined with genomics, advanced reproductive technologies, and precision breeding techniques.
- (3) Determine **objective measures of sustainability and animal welfare**, how those can be incorporated into precision systems, and how the social sciences can inform and translate these scientific findings to promote consumer understanding of trade-offs and enable them to make informed purchasing decisions.
- (4) Further work will be needed to **continue to reduce the costs and increase performance of genotyping platforms**, particularly for industries in which the economic value of an individual animal is low relative to genotyping costs.

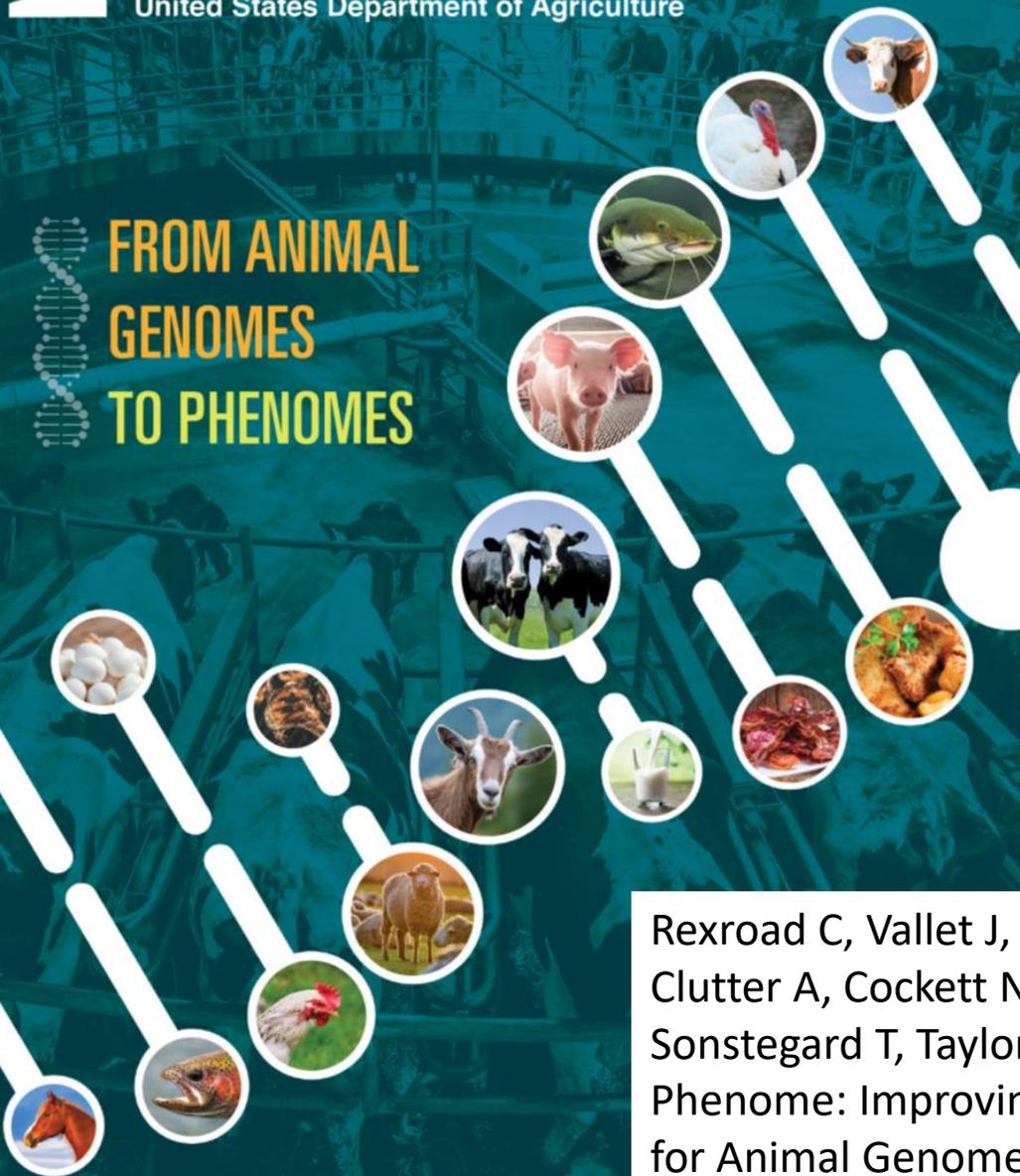


Proteomics
Genomics
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Metabolomics
Epigenomics
Morphomics
Regulomics
Fluxomics
Intercomics
Glycomics
Lipidomics
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Phenomics
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Immunomics
Reproductiveomics
Developmentalomics
Environmentalomics
Nutritionalomics
Behavioralomics
Socialomics



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 FROM ANIMAL
GENOMES
TO PHENOMES



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