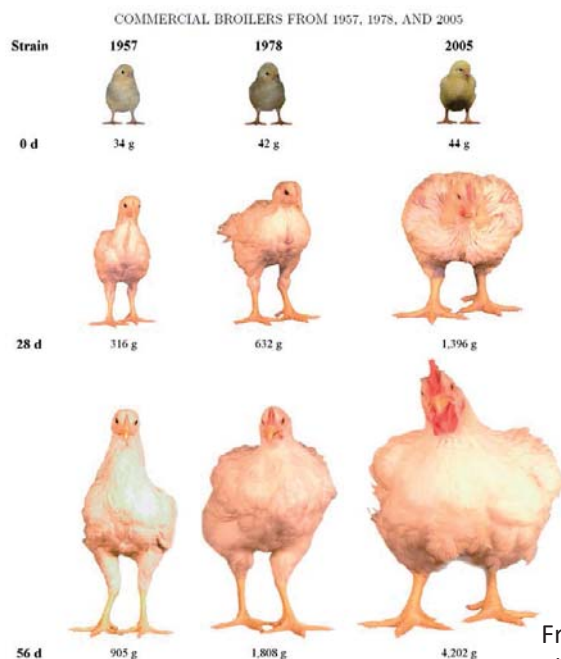# How Genomic Research Will Affect Future Livestock Production
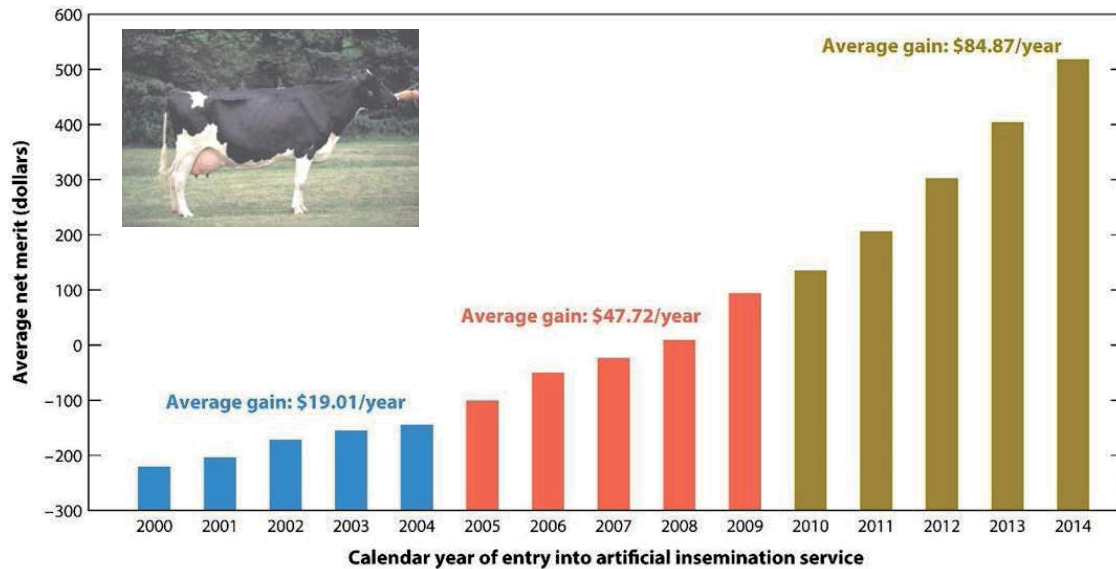
Dr. Steven Kappes

Associate Administrator, USDA, ARS, Office of National Programs

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Genetic selection has been amazingly successful, but genomic technologies promise even greater benefits

From Zuidhof et al., 2014

More importantly, genomics enabled genetic selection in dairy cattle effectively doubled genetic progress

Wiggans GR, et al. 2017.
Annu. Rev. Anim. Biosci. 5:309–27

In 2007, National Program Leaders from USDA developed a blueprint for animal genomics for the decade to follow.

It was broken into three sections, Science to Practice, Discovery Science and Infrastructure. It set goals for animal genomics research, and many have been realized.
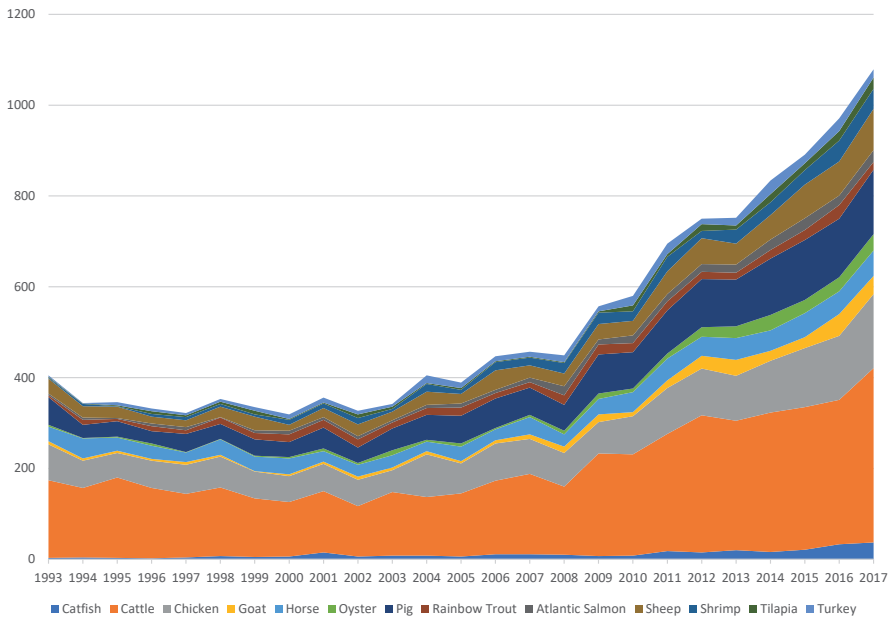
In the decade that followed, research goals of the blueprint were often exceeded

Animal Genome Publications by Year

- 13 species included in 2008 Blueprint
- Journals indexed in Pubmed

Timeframe	# Pubs
2008-2017	7558
1998-2007	3730
Total since 1993	13037
Total since 1949	17203

Legend: Catfish, Cattle, Chicken, Goat, Horse, Oyster, Pig, Rainbow Trout, Atlantic Salmon, Sheep, Shrimp, Tilapia, Turkey
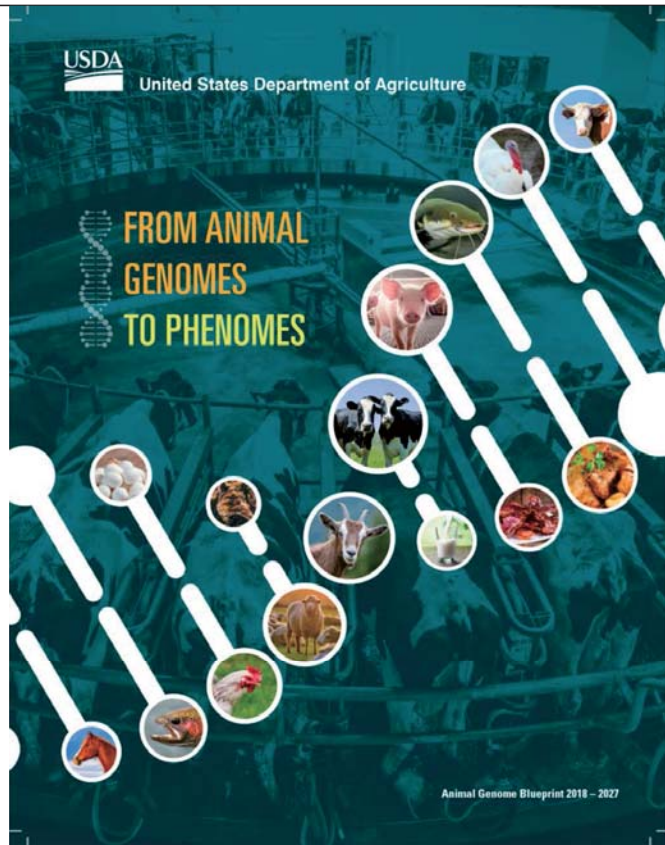
(*genom* OR sequenc* OR GWAS OR SNP OR polymorphi* OR transcript* OR *DNA* OR *RNA*) AND (species OR common name)

Since the original blueprint, new technologies expand the possibilities

- Make targeted changes to the genome
- Understand underlying biology
  - Match genetics to environment
  - Enhance production further by fully implementing genomic selection in all livestock
  - Improve animal health and welfare
  - Increase sustainability
  - Reduce environmental impact
  - Understand the microbiome and its interactions with the host

Led by USDA National Program Leaders, and in collaboration with the livestock genomics community, an updated blueprint for the next decade was developed.

USDA United States Department of Agriculture

FROM ANIMAL GENOMES TO PHENOMES

Animal Genome Blueprint 2018 – 2027

The new blueprint maintained the three sections from the previous blueprint, and adjusted or added new focus areas consistent with new needs and technologies

1. **Science to Practice**
   a. *Precision Selection and Management*

2. **Discovery Science**
   a. *Genome and Functional Biology*
   b. *Host-Pathogen Interactions*
   c. *Phenotyping*
   d. *Microbiome and Metagenomics*

3. **Infrastructure**
   a. *Genome Tools and Resources*
   b. *Education and Training*
   c. *Bioinformatic and Computational Biology*
   d. *Biotechnology*
   e. *Animal Populations and Germplasm Preservation*

- ➢ **Goal 1: Providing Nutritious Food to a Growing Human Population**

- ➢ **Goal 2: Increasing Animal Fitness and Improving Animal Welfare**

- ➢ **Goal 3: Improving Sustainability of Animal Agriculture**

- ➢ **Goal 4: Meeting Consumer Needs and Choices**

Slide presented at NRSP8 meeting at PAG 2018, Rexroad et al.

Science to Practice goals

Expand genomic breeding to more species and production systems
Additional species, products (e.g. aquaculture, sheep)

Broaden focus beyond additive effects
Especially heterosis, epigenetics, epistatic interactions

Collect new and more extensive phenotypes
New technologies, non-traditional phenotypes

Identify causal alleles (QTN)
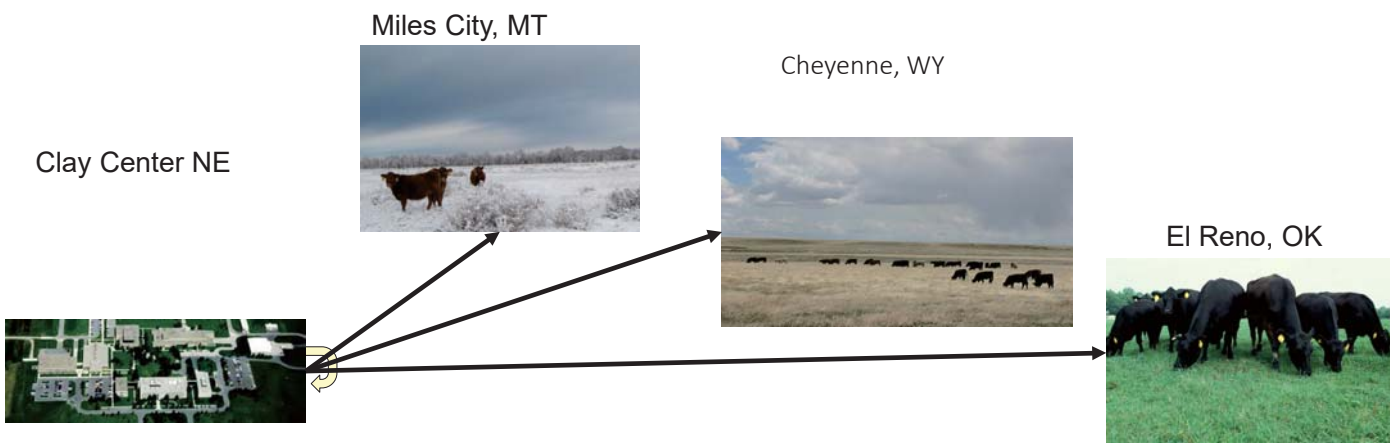Supports precision breeding / management

Integrate GES and biotechnology
Gene editing for efficient transfer of causal alleles

Beef Grand Challenge- Understanding the genotype by environment interaction

600 BEEF CALVES 5 GENOTYPES WEANING TO PLATE

Miles City, MT

Cheyenne, WY

Clay Center NE

El Reno, OK

Production
- Growth
- Ruminal Microbiome
- Genomic analyses
- GxExM

Ecology
- Nutrient cycling (C, N, P)
- Water use
- Methane production
- Resource use/production

Nutrition and Food Safety
- Fatty acid genetics and environmental influence
- Pathogens and AMR
- GxExMxP

Heat stress effects on genomic ranking of milk traits- protein breeding values

APPLICATION / FUTURE WORK

Application: Possible alternate rankings of bulls depending on location of use:

Ranking of US prefix bulls born ≥2004 with ≥ 50 daughters for EBV protein: original and after applying heat stress factor for different climates

Bull name	Original EBV protein rank	EBV protein rank[1] in warm climate	EBV protein rank[2] in cold climate
Coyne	1	2	1
Nobleland	2	1	4
Listen	3	7	2
Tyron	4	4	6
Altagreatest	5	3	7
Ruble	6	12	3
Altastone	7	6	15
Lonzo	8	11	33
Syrup	9	20	11
Picardus	10	95	8
Mercedes	11	55	9
Fathom	12	344	5
Dahlia	13	34	17
Altafairway	14	115	12
Altasuperjet	15	120	10
Robust	27	8	49
Eureka	66	15	126

[1] Defined as: EBV + HS factor * Mean annual Florida THI
[2] Defined as: EBV + HS factor * Mean annual Wisconsin THI

➢ Correlation between alternative rankings of bulls based on heat stress solutions:

0.912 between original model and warm climate (FL)
0.986 between original model and cool climate (WI)

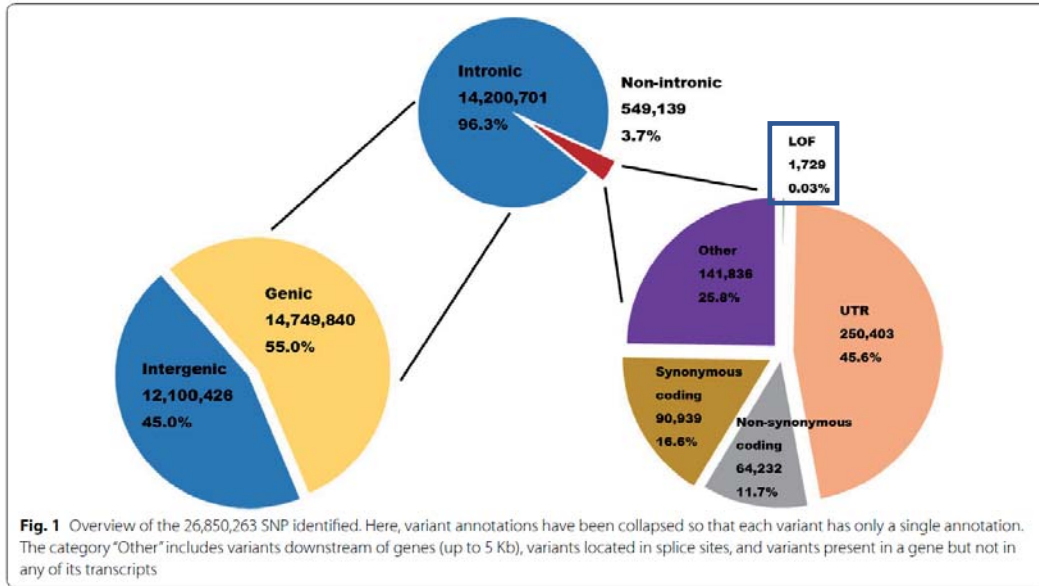Correlations say that heat stress has minor effects on reranking

CONCLUSIONS

▶ Addition of heat stress interaction term to the model improved predictions by a small amount (R^2 difference < 0.0003)

▶ Most warmer, southern hemisphere countries (ARG, URY) had positive heat stress coefficients while cooler, more northern countries were negative

▶ Addition of herd yield level interaction term improved prediction very little (R^2 difference < 0.0002)

▶ Overall, as evidenced by the small correlation gains when adding HS and HL interactions, the current models predict well in a variety of environments

▶ Individual bull differences resulting from addition of interaction term could enhance bull selection when planned usage is solely in one environment

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Epigenetics and causal alleles

Define tissue-specific genes and transcripts
Identify all genome segments expressed in RNA
        (e.g. lncRNA, cRNA, miRNA)
Characterize genome elements contributing to gene expression/pattern of gene expression
   (e.g. promoters, enhancers, imprinted genes)

Using genome sequences, we can get polymorphisms that are predicted to alter protein function, including loss of function (LOF). Protein function changes are immediate candidates for functional DNA variation.

Fig. 1 Overview of the 26,850,263 SNP identified. Here, variant annotations have been collapsed so that each variant has only a single annotation. The category "Other" includes variants downstream of genes (up to 5 Kb), variants located in splice sites, and variants present in a gene but not in any of its transcripts

Impact of Butyrate on rumen epithelial cells   From Keel et al., 2018

Current gene editing work:

Engineering flu resistant pigs
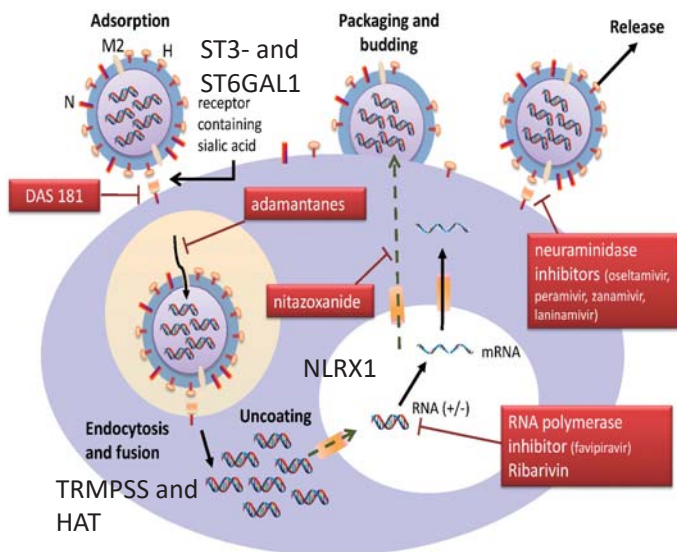
ST3- and ST6GAL1- sialylation of membrane proteins
TRMPSS and HAT- fusion and unpackaging of virus
NLRX1- control of antiviral response

Creating universal transplant recipients for high genetic potential boars

Normal boar   NANOS2 knockout
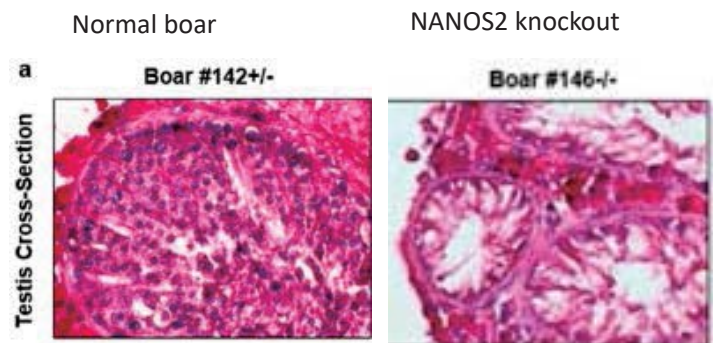
Knockout of sperm production by disabling NANOS2 allows for transplantation of germ cells from high genetic value boars.

Discovery Science

Understanding genome biology
establish high quality annotated reference genomes
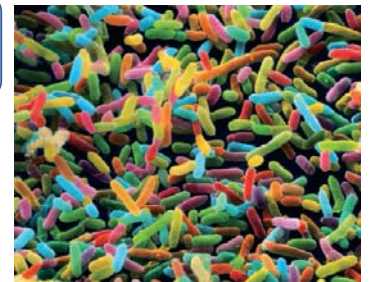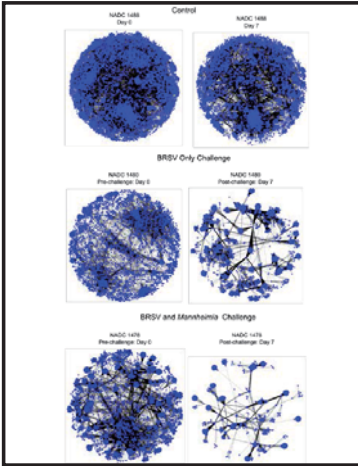
Apply precision Ag technologies
sensors, other tech to automate phenotype collection

Develop tools to reduce animal disease
phenotyping tools, host-pathogen interactions, diagnostics

Microbiome and Metagenomics
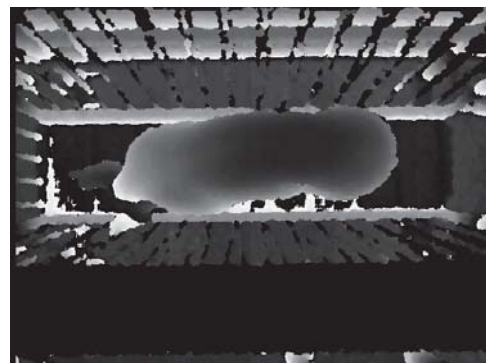Defining the microbiome and characterizing changes

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Precision livestock management technologies will provide us automated phenotyping

Animal weights from 3D imaging

Calculating Pig Volume

- Results showed that the mass can be predicted with an average error of 4.6%, or 2.2 kg.
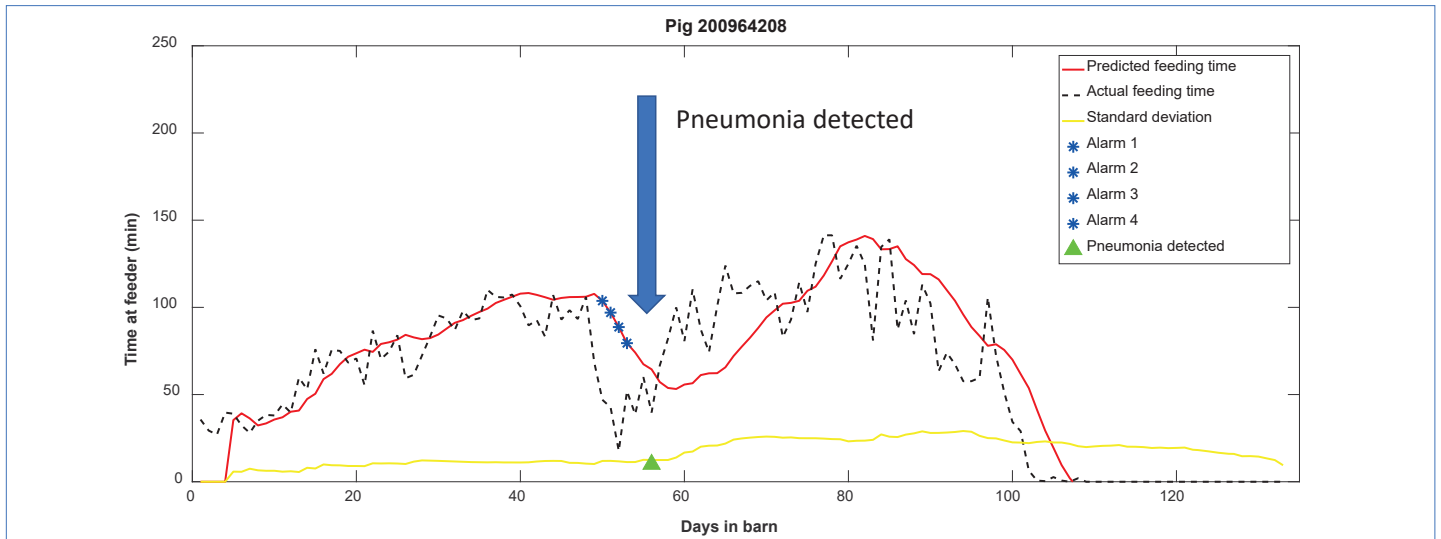- No effects of sire-line or sex
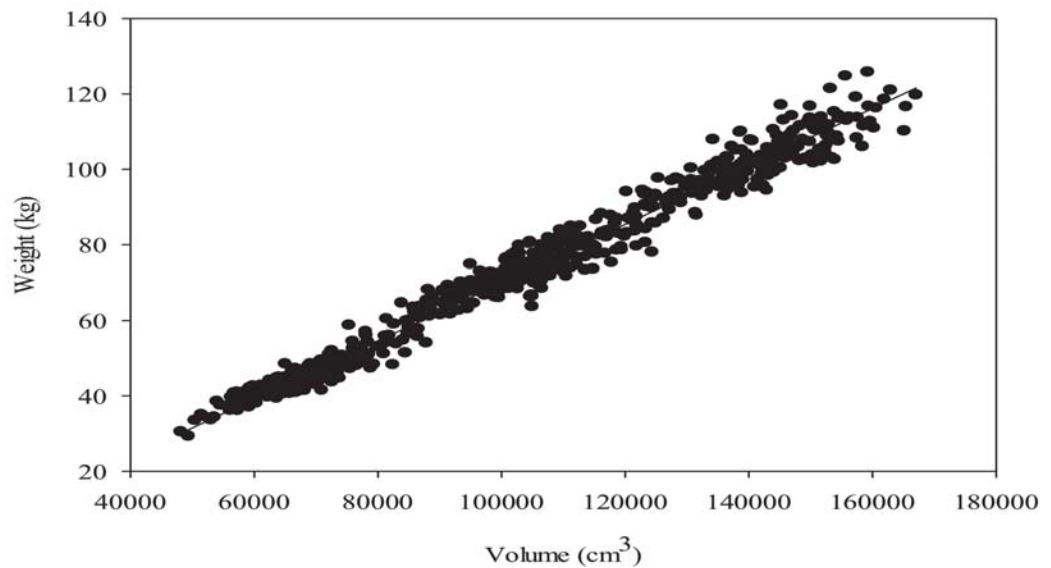
Automated health phenotyping- eating behavior



Antenna array in swine feeding troughs

Reductions in daily feeding behavior signal pneumonia onset

Pig 200964208

Pneumonia detected

Legend:
- Predicted feeding time
- Actual feeding time
- Standard deviation
- Alarm 1
- Alarm 2
- Alarm 3
- Alarm 4
- Pneumonia detected

Y-axis: Time at feeder (min)
X-axis: Days in barn

New capabilities in sequencing will deliver better Microbiome and Metagenomics information

Effort to fully sequence and assemble the ruminal microbiome from cattle using long and short sequence read technologies.

-Complete genome information provides better identification of new species within the rumen.
-Many new bacterial viruses and their hosts were identified, opening a new research area for microbiome modification
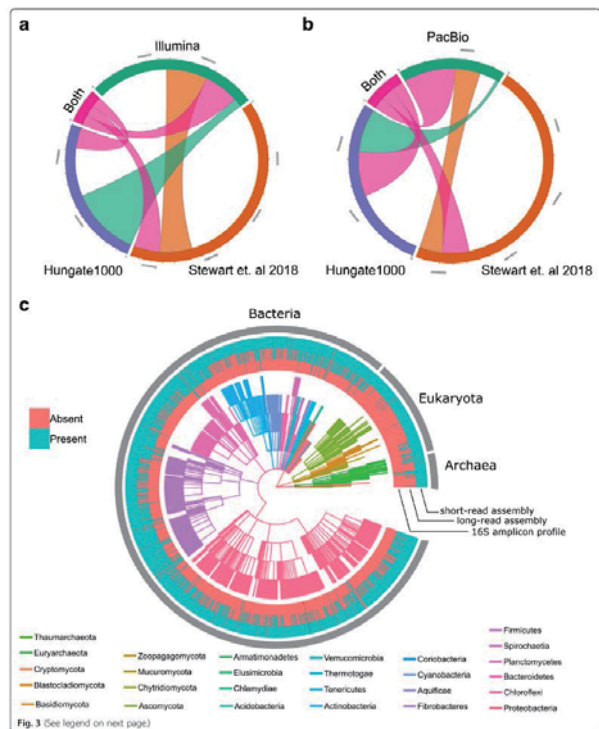

Bickhart et al., 2019

Infrastructure

Training the next generation of animal scientists
develop integrated curriculum, hands on training, active recruitment

Develop advanced genomic tools and resources
pan-genomes, catalog variation, examine diversity in domesticated populations

Big Data
computational capacity, bioinformatics solutions, metadata standards

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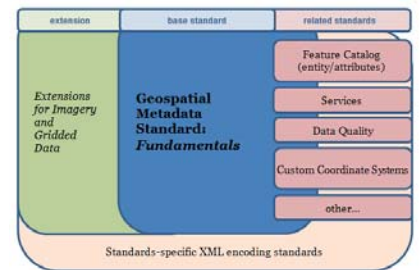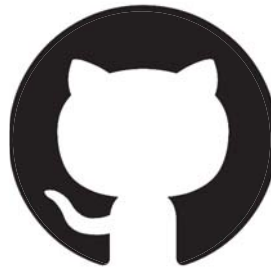
National Agricultural Library is developing a repository for agricultural data to allow full reuse of agricultural data- Ag Data Commons

Future of livestock genomics

- Genome analysis for every livestock and aquaculture species
- Technologies to optimize heterosis in livestock
- Management based on the genome, genome based on the environment
- Optimized microbiome to maximize animal production and reduce environmental effects (i.e., methane)
- Livestock resistant to diseases, reducing the need for antibiotics in livestock
- Automated measures to help in genomic selection and other management decisions
- Data infrastructure making all of this seamless