





Building the Tools to Solve the Genome to Phenome Puzzle in Agriculture

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AG2PI is funded by USDA-NIFA awards 2020-70412-32615 2021-70412-35233 2022-70412-38454



USDA-NIFA Agricultural Genome to Phenome Initiative

- 2018 Farm Bill directed NIFA to establish a new competitive grant program to support research concerning genomes and phenomes of crops and animals of importance to US agriculture, authorizing up to \$40,000,000 annually 2019 2023.
 - https://nifa.usda.gov/program/genome-phenome-initiative
- U.S. Congress appropriated only \$1M in fiscal year 2020
 \$1M in fiscal year 2021
 \$2M in fiscal year 2022

Creating a Shared Vision Across Crop & Livestock Communities



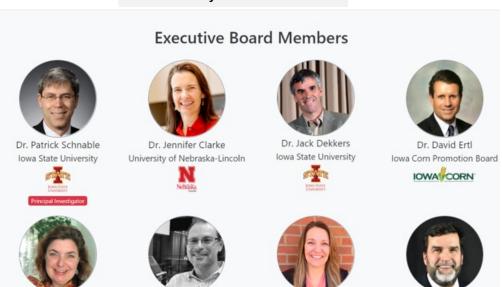
Overall objective:

Assemble a transdisciplinary community prepare it for an anticipated large-scale R&D effort in AG2P

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Project Team



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AG2PI aims to connect crop and livestock scientists to each other and to scientists working in data sciences, statistics, engineering and social sciences to identify shared problems and collaborate on solutions in agricultural genome to phenome

science



What's Required to Realize this Vision?

- A **community** of interactive biologists (crop + livestock), engineers, data scientists and members of the greater community
- More data (phenotypes, genotypes and environment/management practices) ideally from coordinated, multi-disciplinary, multi-location, multi-year projects

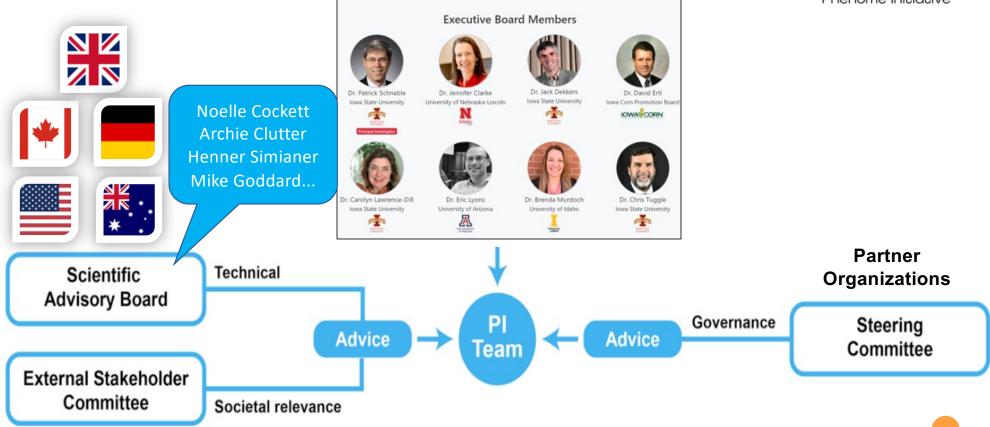
Genotype (G) + Environment (E) + G \times E = Phenotype (P)

- New technologies and analysis methods
- Substantial new R&D investments



Organizational Structure 2020-2023







External Stakeholder Member Organizations







NSIF





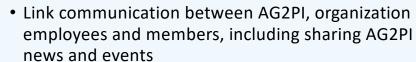




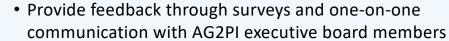


























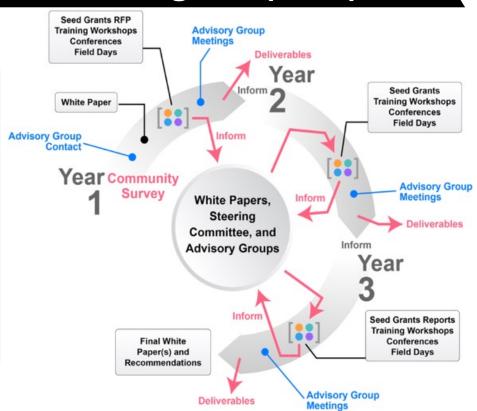


Poultry Breeders of America

Activities & Deliverables 2020 grant (\$1M)













Summary























Community **Events**





Goals

- Expose Ag G2P community to research activities and resources across crops and livestock
- Share research methods, approaches, capacities
- Identify research and capacity gaps and challenges for AG2P research
- Provide a platform for introducing teams that can develop joint solutions

Selection of Past Field Day Topics:

- Automating Phenotyping
- Genomic Selection and Phenotyping in Dairy Cattle
- U.S. Aquaculture
- Precision Livestock Management
- Breeding Challenges in Fruit Trees
- AI and Agriculture
- IP in Livestock and Crop Breeding and Genetics
- Quantitative Multi-omics to Unravel G2P in Crops and Livestock
- International Centers & Partnerships: Genetic Improvement Resources and Opportunities
- Incorporating Domain Knowledge in Genetic/Genomic Prediction & Analysis Models
- Leveraging Microbiomes in Agriculture



Goals

- Build technical strengths and future collaborative AG2P communities
- Offer a suite of workshops to enable researchers from all backgrounds and computational skill levels to develop best practices, common vocabularies, and technical expertise around genomic and phenomic cyberinfrastructure, data tools and pipelines, statistics, and experimental techniques

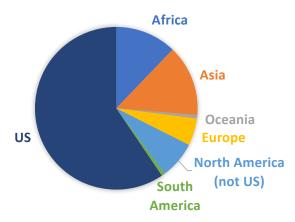
Selection of Past Workshop Topics:

- Foundations of Computation: Introduction for Biologists
- Introduction to Scientific Computing
- Unix and Git Skills
- Genotype to Phenotype for Non-Biologists
- Introduction to SNP Data Analysis
- A Guide to GWAS
- Hands-On Machine Learning with Agricultural Applications
- Structural Variant Detection in Animal Populations
- Developing Mobile Computer Vision Applications for Improved Recognition of Livestock
- The APSIM Software Platform to Predict and Explain Genotype x Management x Environment Interactions
- Intermediate Omics Data-Enabled Genomic Prediction and Mediation Analysis

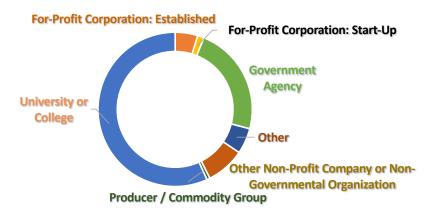




2022 AG2PI SURVEY RESPONDENTS, BY LOCATION



2022 AG2PI SURVEY RESPONDENTS, BY EMPLOYER TYPE



15-question survey

* These topics came from AG2PI Scientific Advisory Board and Steering Committee

Deployed in June of 2022

Purpose: to narrow the scope of future funding to areas that are **most critical** to advancing G2P research as well as those that are **easiest to achieve**

Participants at a September 2022 workshop were asked to rank the same topics and compile survey results



White paper draft based on Sept 2022 Workshop sent to NIFA: "Current Challenges and the Future of Agricultural Genomes to Phenomes in the U.S."

We recommend that AG2PI funding be used to address the following critical milestones:

- 1. Provide resources to evaluate and **improve Ag G2P predictive tools**, including generation of *benchmark testing datasets*.
- 2. **Remove current public-private barriers** for collaborating with commercial entities that maintain *large phenotypic datasets*.
- 3. Establish a single comprehensive public genome/phenome knowledge base that enables FAIR data sharing as a foundation for building on Federal investments in agricultural genomes.
- 4. Accelerate the **training of scientists required for agricultural G2P research,** including toward developing and evaluating data analytics training programs.
- 5. Expand the diversity of people engaged in agricultural G2P activities, including researchers, students and producers.
- 6. **Identify additional gaps** in knowledge, multidisciplinary team development, education/training, and analytical or quantitative methods relevant to agricultural G2P and *initiate actions to fill those gaps*.

Send your thoughts and suggestions to AG2PI!







Goals

- Bring people together to develop a vision for the future of Ag G2P and build community
- Identify opportunities and resources within the crop and livestock communities
- Support discussions across research and stakeholder communities
- Communicate and disseminate findings
- Develop white papers to inform USDA NIFA towards future AG2P research and development

Past Conferences:

- Seed Grant mini-conferences
- Listening Sessions at national meetings
- Sept. 22 Conference/Workshop:
- "Thinking Big: Visualizing the Future of AG2PI"



White Paper

Future Conference:

- 2023: June 15-16, Kansas City MO
- Mark your calendars and register!





Summary





















Contact Us

Events

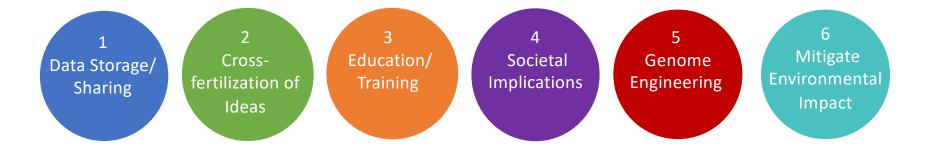




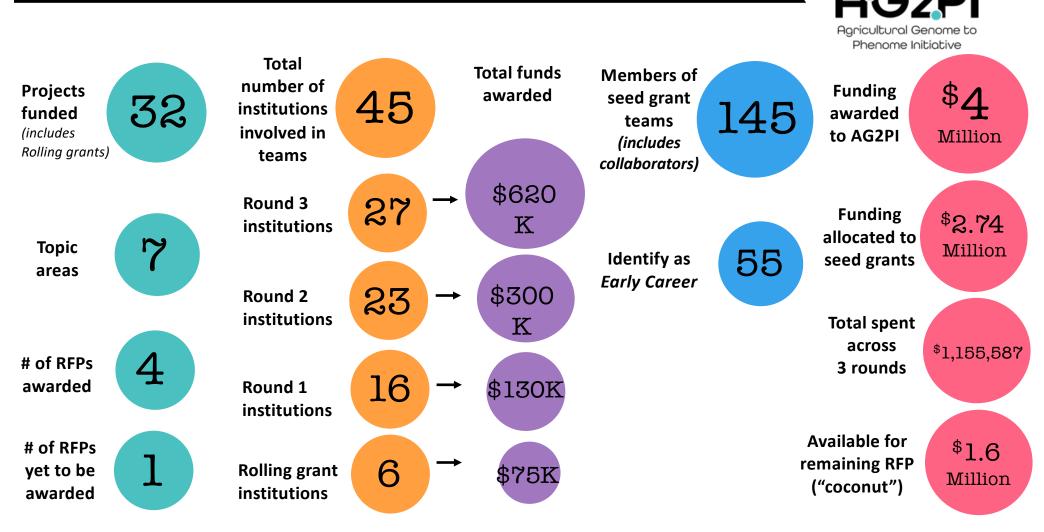
Goals

- Promote collaboration and support the development and cross-pollination of tools, data, and ideas to enable and facilitate future AG2P research
- Foster first steps towards the development of community solutions
 - Research needs and opportunities, physical infrastructure needs, promote capabilities in data processing, analysis and management

Focus areas funded



Seed Grants Overview – By the Numbers





How Can ASAS members participate in AG2P? \$2.5 Million will be in new RFA...

Develop a Vision → Congress wants this from the community (us)

Identify the research and/ or physical infrastructure needs and opportunities

Develop Community Solutions → **Congress wants this too!**

- Identify the key components (tools, people, sensors, etc.) necessary for success
- Identify a list of priorities and potential path(s) forward

Working Groups

Consider working with others to form or participate in a working group





Further ideas on ASAS Participation in AG2PI

- What is important to animal agriculture G2P research?
- What do our respective stakeholders need to make genetic progress in a changing environment?
- How can we work with others to expand what we can deliver?
- How can we help inform NIFA as they establish a new competitive grant program to support research the area of AG2P importance to US agriculture?
- U.S. Congress appropriated **\$2,500,000** in fiscal year 2023 for AG2PI, RFA to be released soon.

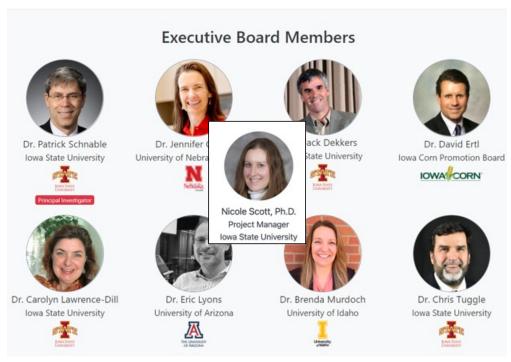






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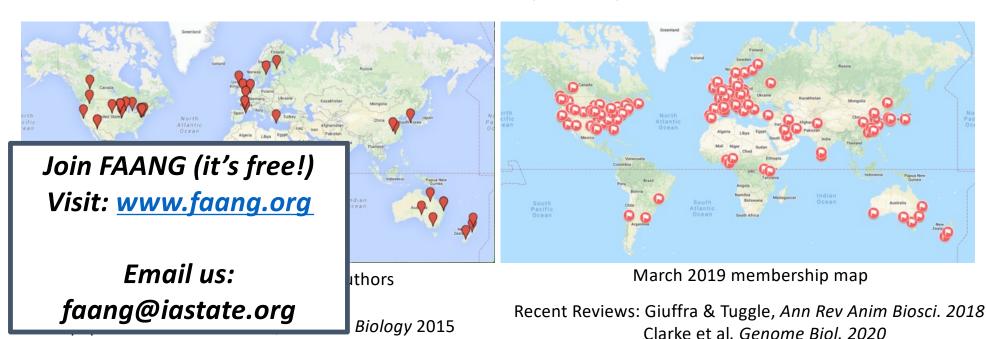




Introduction to **F**unctional **A**nnotation of **AN**imal **G**enomes (FAANG)--Goals and Opportunities

Organic growth of FAANG during 2014-2022 Current FAANG

contributors = 571 (Feb 2023)



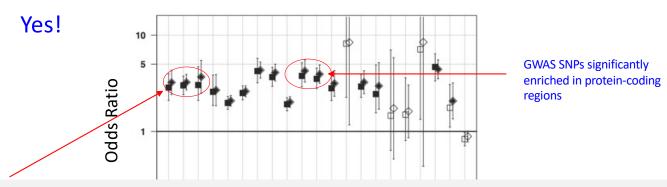
Why is FAANG important?

- Understanding the genotype to phenotype link:
 - Improving fundamental understanding of biology
 - Providing information to accelerate genetic improvement- linking trait-associated SNP with function at that SNP location > most important SNP to select for (against)?

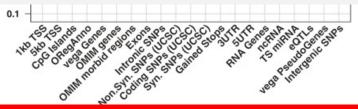


Beyond protein-coding part of genome

Is trait-associated genetic variation located (enriched) in genes?



But also enriched in regions flanking/outside known coding regions!



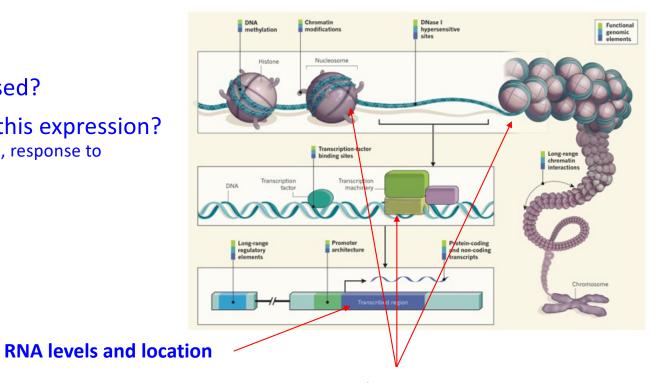
Thus we need to *annotate the function* of the ENTIRE genome of our animals

ated variants

Large-scale genome functional annotation: described by ENCODE

To understand function:

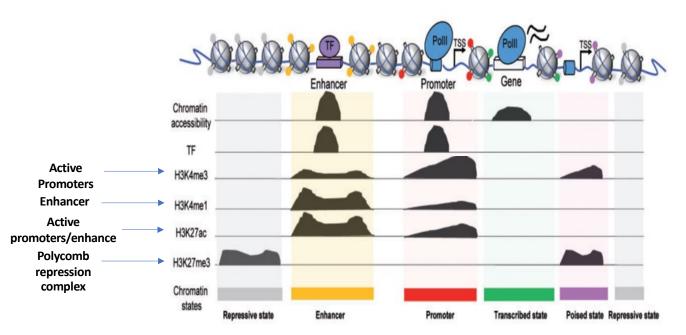
- a) what part is expressed?
- b) what part controls this expression? (specific tissue or cell type, response to infection, etc):



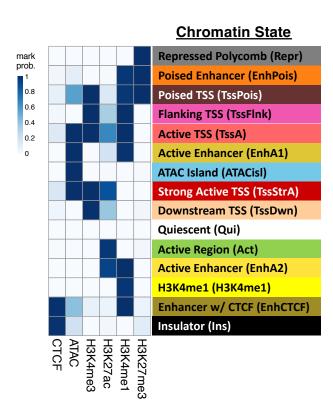


Biochemical assays of Chromatin structure

Combinations of signals from different chromatin modifications predict genome function



Jiang, S and Mortazavi, A. 2015. Briefings in Functional Genomics, 17(2), 2018, 104-115



Research on Livestock functional genomics

- National Porcine FAANG project funded by NIFA-AFRI
 - USDA Center of Excellence- headquartered at ISU
- One of three funded by USDA (also bovine, chicken) in 2018
- Sheep, horse, aquaculture also funded in recent years
- Large EU projects funded in 2019
 - Monogastrics (Swine+chicken)
 - Bovine
 - Aquaculture
- More than \$40 Million awarded world-wide for FAANG research



Functional Annotation of the Porcine Genome

• **Overall goal:** catalog functional elements in the porcine genome for >40 biological states, create Chromatin state map

Aim 1 Adult tissues

extend FAANG pilot of 8 -> 25 tissues

Aim 2 Fetal tissues

- Identify and correlate allele-specific expression and AS chromatin modification
- Parent-of-origin effects (reciprocal crosses Meishan x WhiteCross)

Aim 3 Immune System

- Stimulated macrophages and PBMC
- Single cell analysis of blood PMBC and immune tissues
- Circulating Blood Cells- flow-sorted into functional types

Aim 4 Data Integration

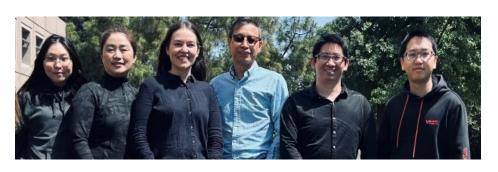
• Integrate all public and project data to develop a higher-order regulatory understanding of the porcine genome, including a predicted chromatin state map.



<u>Aim 1: Adult tissues</u> (UC-Davis)

extend FAANG pilot of 8 -> 26 tissues

Liqi An, Ying WANG, Claire PROWSE-WILKINS, Huaijun ZHOU, Zhangyuan PAN, Dailu GUAN



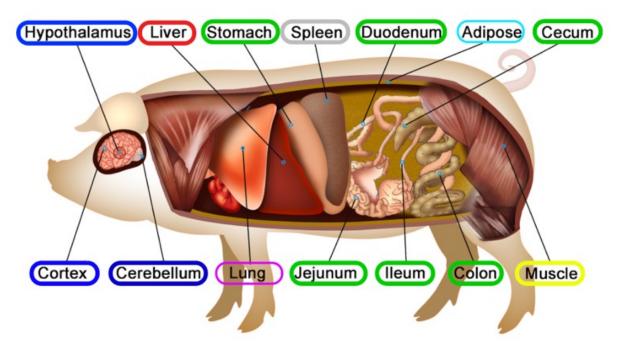
Finished

Core tissues (8): cortex, cerebellum, hypothalamus, liver, lung, spleen, and adipose muscle (Kern, et. al., Nat Commun 2021).

Gut-associated tissues (6): stomach, duodenum, jejunum, ileum, cecum, colon (Pan Z. et al. Nat Commun 2021).

Ongoing:

Remaining adult tissues (12)

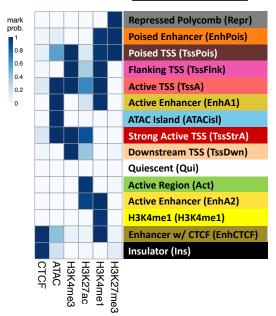


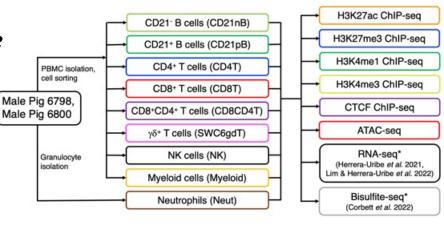
Aim 3: Functional Annotation of Circulating Porcine Immune **Cell Populations**

Published:

Herrera-Uribe et al. 2020 Herrera-Uribe & Wiarda 2021 Corbett et al. 2022

Chromatin State







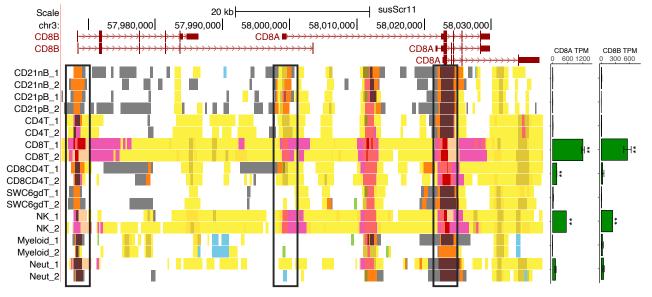


Corbett

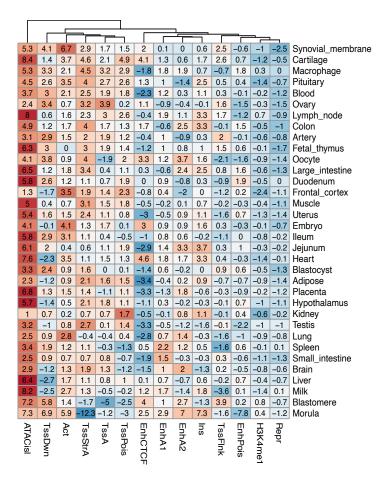
Ryan Juber Herrera Uribe

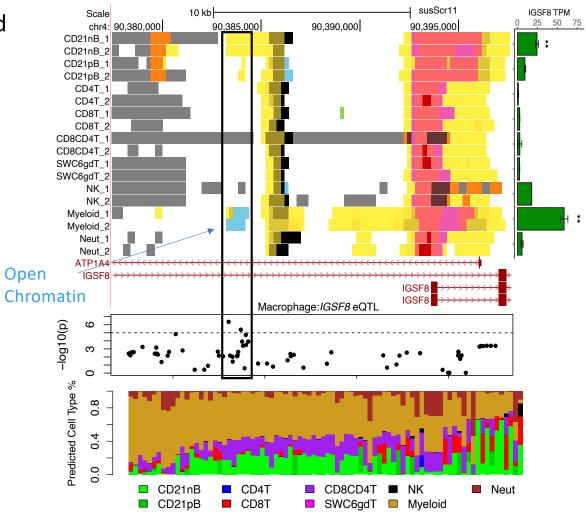
Collaboration:

Lingzhao Fang, et al. Aarhus U **Crystal Loving, USDA-NADC Cathy Ernst, Michigan State**



Active chromatin states are enriched for Pig GTEx eQTL in many tissues





Acknowledgments- FAANG and PIGGI@iastate.edu group (that's Pig ImmunoGenomics and Genetics in Iowa!)



Tuggle







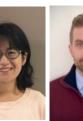
Uribe



Haibo Liu



Lance Daharsh



Pengxin Yang



Ryan Corbett



Crystal Loving



Jayne Wiarda



Kristen **Bvrne**



Sathesh Sivasankaran

Agricultural Research



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IOWA STATE UNIVERSITY

We thank all pig **FAANG** members and collaborators!



Huaijun Zhou, et al.



Cathy Ernst, et al.



Tim Smith, Dan Nonneman **MARC**



Joan Lunney **BARC**



United States Department of Agriculture

National Institute of Food and Agriculture

NIFA Project 2018-67015-2701

