# USDA PIG GENOME COORDINATION PROGRAM ACTIVITIES

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**Overview:** Coordination of Pig Genome Coordination Program is under the National Animal Genome Research Program (NAGRP) and is the effort of personnel at Iowa State University (ISU) and Michigan State University (MSU). Support is allocated from NRSP-8 and provided to the Agriculture Experiment Stations by off the top funding. The NAGRP is made up of the membership of the Animal Genome Technical Committee, including the Swine Species Subcommittee.

**Facilities and personnel:** Chris Tuggle, Department of Animal Science, ISU, and Cathy Ernst, Department of Animal Science, MSU, have served as Joint Coordinators since 2013 and have a renewed five-year appointment that will end in 2023. Iowa State University staff help support the national pig genome coordination effort as part of Iowa State University's contribution.

**NRSP8 Objectives (2018-2023): Objective 1:** Advance the quality of reference genomes for all agri-animal species by providing high contiguity assemblies, deep functional annotations of these assemblies, and comparison across species to understand structure and function of animal genomes.
**Objective 2:** Advance genome-to-phenome prediction by implementing strategies and tools to identify and validate genes and allelic variants predictive of biologically and economically important phenotypes and traits.
**Objective 3:** Advance analysis, curation, storage, application, and reuse of heterogeneous big data to facilitate genome-to-phenome research in animal species of agricultural interest.

**Policy Updates:** We developed an Advisory Committee, who will provide guidance on policy as well as help evaluate requests for funding. The members of this Advisory Committee represent the swine industry, swine genomics and biotechnology researchers, NRSP-8 Stations and participating USDA labs. The members are: Jack Dekkers (ISU), Chris Hostetler (National Pork Board), Joan Lunney (USDA-BARC), Randy Prather (U. Missouri), and Juan P. Steibel (MSU). Thanks to this group for volunteering for this important role!

**Database Activities:** The Pig Genome Database continues to receive considerable updating through the work of the Bioinformatics team. The PigQTLdb (http://www.animalgenome.org/QTLdb/pig) is an excellent repository for QTL and candidate gene association results. As of December 2019, in the Animal QTLdb there are **30,170** pig QTLs from **687** publications curated into the database. Those QTLs represent **688** different traits. Throughout 2019, the NAGRP bioinformatics team has continued their efforts to make improvements to the Animal QTLdb. Users are encouraged to register an account to enter new QTL data. Find out more from http://www.animalgenome.org/QTLdb. In addition, the pig genome build 11.1 annotations are continuing to be updated in the BioMart (http://www.animalgenome.org:8181) and for the Animal QTLdb.

**Shared Materials and Funding:** NRSP8 funds are available to support community activities to find associations with many different traits. In 2014, a policy was developed and approved by the Advisory Committee that for swine genomics projects to be eligible for NRSP8 Coordination support, the project must materially involve two or more NRSP8 member groups (university or ARS research locations) and that substantial funding will only be provided for projects that have matching funding from another agency. Any questions on this policy, please contact the Coordinators.

**Porcine SNP chips update:** In addition to the 60K Illumina and the GeneSeek GGP-Porcine LD and HD chips, a new high density SNP chip is being developed by Affymetrix. An NRSP-8 supported project provided validation of this chip for integration with 60K and GeneSeek chip data; see summary of this at the 2017 PAG meeting SNP chip presentation.

**National and International Efforts:** Communication with several national and international groups and individuals is excellent. Several international meetings were organized and/or held in 2019 that had a national or international component.

1. At the 37th biennial International Society of Animal Genetics (ISAG) conference in Llieda, Spain from July 8 to 13, 2019, several talks related to pig genomics, including one provided by Claire Rogel-Gaillard on the current understanding of the microbiome's role in pigs, indicating that substantial heritability of the components of the microbiome have been documented. She further discussed large-scale experiments that show so-called "enterotypes" (similar microbiota populations) can be recognized and that one enterotype rich in the *Prevotella* spp. is associated with increased weight gain and better vaccination responses in young pigs. Several informative Workshops with significant numbers of talks on porcine research included Pig Genetics and Genomics, Epigenetics, Genetics of Immune Response and Disease Resistance, and Comparative and Functional Genomics. At the Pig Workshop, topics included genome assemblies of new Suina species (A. Archibald), finding deleterious mutations using large-scale genotyping of industrial populations (M. Groenen), the role of circular RNAs in biology (A. Robic), the use of genome editing to create a proof-of-concept model for removing boar-taint (S. Kurtz), the integrative analysis of blood and fecal microbiota parameters between breeds (M. Moroldo), the analysis of gene expression in semen microbiota (A. Clopp), comparison of gene editing and traditional breeding for the swine industry (E. Jonas), and the use of genome-wide CRISPR libraries in screens for genes required for Japanese Encephalitis virus (S. Xie). Pig-centric talks in other workshops included those on new tools for epigenetics analysis (GRID-seq, J. Li), the multi-omic analysis of functional DNA elements in commercial and Chinese breeds (S. Zhao), and pipelines to discover novel miRNAs in pig tissues (E. Murwol-Sanchez). Finally, there were several comparative genomic talks that included pig, including one on chromatic accessibility measures across pig, goat, chicken , and cattle (S. Djebali), and a search for enhancer-gene pairs in pig, chicken, sheep and cattle (M. Halstead). The entire Program, including all abstracts and speaker titles, is available here.

2. The WWW.FAANG.ORG website, hosted by www.animalgenome.org through the NRSP-8 Bioinformatics Coordination team, has continued to be developed. A new webpage has been developed to provide information on new funding opportunities for FAANG related proposals (see also below; available on FAANG website, member's area page).

**Communication:** The *Pig Genome Update* has now published 127 issues and has been distributed electronically to over 3,100 people worldwide. PGU will be electronically published two times a year, and in addition to general updates, the issues will be published to coincide with major events of interest to the genome community:

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| Feb/March | (a wrap-up report of the PAG meetings); |
| September/October | (summer meetings report, PAG abstract submission deadlines, preparations). |

**Travel and Meeting Support:** Travel of several scientists was partially funded to attend important pig genomics meetings in the reporting period. These included:
Ryan Corbett, Michigan State University 2019 Neal Jorgenson Travel Award winner
Lianna Walker, University of Nebraska-Lincoln 2019 Neal Jorgenson Travel Award winner
We also partially supported the travel of speakers to the 2019 Cattle/Swine joint and Swine Workshops:
Jack Dekkers,_Iowa State University

2020 commitments:

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| Hiruni Wijesena, University of Nebraska-Lincoln | 2020 Neal Jorgenson Travel Award winner 1 |
| Kaitlyn R. Daza, Michigan State University | 2020 Neal Jorgenson Travel Award winner 2 |
| Martien Groenen, Wageningen University | |
| Brittany Keel, USDA-ARS-Meat Animal Research Center | |

**Research Support Activities:** The goals are to help support all of the objectives of this project. Major activities included helping facilitate collection of phenotypes and sharing use of SNP chips in the future. New bioinformatic tools relevant to the swine genomics community will also be developed with help of the bioinformatics team. Constructive suggestions from researchers to help this coordination and facilitation program grow and succeed are appreciated. ***Reminder***: funding is available for new projects- preliminary ideas can be a starting point and are welcome- please contact the Coordinators!

**Prior approved Projects:**

1. FAANG project led by Huaijun Zhou, University of California-Davis. This project also had funding promised by the NRSP8 Bovine and Poultry Coordinators, as well as funding by the National Pork Board. This project revived funding in the amount of $500,000 from USDA-NIFA-AFRI.
2. PEDV genetics resistance project led by Max Rothschild with collaborators Daniel Ciobanu and Canadian swine genetics companies.
3. A proposal submitted by Jack Dekkers along with Cathy Ernst and Juan P. Steibel (MSU) to validate the new Affymetrix 650K chip and provide initial data on integration with 60K genotype data.
4. A proposal by Tim Smith and Dan Nonneman of USDA-MARC along with Chris Tuggle to add additional tissues to a PacBio IsoSeq project for functional annotation of the genome of the animal whose genome is being sequenced at MARC. It is important to note that for projects #3 and #4, the Swine Genome Coordinators had a co-PI role, so the proposals were vetted through the Advisory Committee for approval.
5. To best make use of available NRSP-8 funding in 2016-2017, a part-time postdoctoral position was proposed to be supported, to be housed at Iowa State University. This postdoc will be tasked with bioinformatic analysis of the PacBio Isoseq/Illumina RNAseq data being created and analyzed in the Smith/Nonneman/Tuggle project above, to maximize the use of these data across nine tissues to annotate the new TJ Tabasco assembly. Dr. Hamid Beiki was hired in December 2016, and is working to further improve the porcine 11.1 annotation.
6. Functional Annotation of Skeletal Muscle Transcripts in Developing Pig Fetuses
7. Annotation of Gilt Transcript Diversity in Social, Sexual and Feeding Behavior Centers
8. Annotation of the Immunome: Transcriptomes of the major blood cell types in the pig

**Newly approved projects during reporting period:**

9. Dr. Haibo Liu was hired and partially supported by NRSP8 funding with the task to provide a Bioinformatics Workshop at PAG 2020.
10. Developing tools to Determine Transcriptional Regulatory Networks in Porcine Tissues and Cells.
11. Assessing boar dominance in pooled semen to allow for selection in progeny generated from pooled semen
12. New pig FAANG tissues for Whole Genome Bisulfite sequencing.

The record of these mini-grants in generating new funds is quite good: a total of over $3.0 million has been awarded to projects with <$150,000 (in total) NRSP-8 funding over the past five years. We anticipate that collaborative projects such as those listed above will continue through maintaining communication with current members of the Swine Sub-committee, and that a substantial portion of the budget will be provided to researchers for this opportunity.