

USDA PIG GENOME COORDINATION PROGRAM ACTIVITIES

Supported by Regional Research Funds, Hatch Act for the Period 10/1/15-9/30/16

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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 five-year appointment. Iowa State University staff help support the national pig genome coordination effort as part of Iowa State University's contribution.

NRSP8 Objectives (2013-2018): 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. **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. **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.

Policy Updates: We have 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 January 4, 2016, in the Animal QTLdb there are **16,516** pig QTLs from **566** publications curated into the database, a **14 %** increase over the end of 2014. Those QTLs represent **626** different traits. Throughout 2016, 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 10.2 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, and was announced in 2015. As described above, an NRSP-8 supported project will provide validation of this chip for integration with 60K and GeneSeek chip data.

National and International Efforts: Communication with several national and international groups and individuals is excellent. Several international meetings were organized and/or held in 2016 that had a national or international component.

1. At the 2016 Joint Annual Meeting (JAM) of the ASAS, ADSA, CSAS and other organizations a day of programmatic overlap with the 2016 International Society of Animal Genetics (ISAG) meeting was scheduled for July 23, 2016 in Salt Lake City, Utah. Several FAANG members including Chris Tuggle and Stephen White (NRSP-8 Sheep Coordinator) helped develop a Symposium on FAANG for this day.

Talks were presented by speakers who are experienced leaders and scientists in the ENCODE project as well as newly emerging researchers in systems biology/functional genomics in livestock species. 450-500 persons attended, and the program is provided at the ISAG website (direct link: <http://www.isag.us/Docs/DomAnimSequencing2016.pdf>).

2. The ASAS meeting was attended by Dr. Ernst and both she and Dr. Tuggle attended the following ISAG meeting. Short meeting reports were provided in the October 2016 Pig Genome Update.

Communication: The *Pig Genome Update* has now published 124 issues and has been distributed electronically to over 2,800 people worldwide. PGU will be electronically published three 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:

Feb (a wrap-up report of the PAG meetings);

June (summer meetings reminders); and

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:

Jeremy Howard, North Carolina State University, 2016 Neal Jorgenson Travel Award winner

We also partially supported the travel of speakers to the 2016 Cattle/Swine joint and Swine Workshops:

Randy Prather, University of Missouri, and Bruce Whitelaw, Roslin Institute, Cattle/Swine Workshop

Min-Kyeong Choi, Konkuk University, and Francisco Peñagaricano, University of Florida, Swine Workshop.

2017 commitments:

Haibo Liu, Iowa State University, 2017 Neal Jorgenson Travel Award winner

Vanmathy Kasimanickam, Washington State University, Pullman, WA

Alan Archibald, Roslin Institute, Edinburgh, UK

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.

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.

Newly approved projects during reporting period:

1. 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 imminent new TJ Tabasco assembly. Additional projects on analysis of data from multi-station projects is projected. The Advisory Committee approved this use of funds, and a search for a qualified person to fill this position is being made.