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 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 **14,479** pig QTLs from **507** publications curated into the database, a 4 % increase over the end of 2014. Those QTLs represent **592** different traits. Throughout 2015, the NAGRP bioinformatics team has continued their efforts to make improvements to the Animal QTLdb, which includes a new mirror site in China, facilitate the addition of gene network analysis data, improved search tools and data analysis tools. 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.

International Efforts: Communication with all international groups and individuals is excellent. Two international meetings were organized and/or held in 2015 that have a significant international component.
1. The Swine Genome coordinators have been working with a large number of individuals in many countries to develop a new initiative, called Functional Annotation of ANimal Genomes (FAANG). This group proposes a project to identify all functional elements in animal genomes, and has presented their plans on a website organized by the Swine Coordination effort (see www.faang.org). A first international Workshop (GO-FAANG), chaired by Chris Tuggle and held in Washington DC. Approximately 100 attendees were from 24 US states and 13 non-US countries; many additional scientists attended via the web. An important component of this Workshop was the participation of 6 funding agencies from US, Canada, and Europe, who were very supportive of the goals of FAANG and provided guidance on obtaining funding for FAANG-related research. Talk videos are available: http://www.animalgenome.org/community/FAANG/bbs?s=go-faang..txt.
2. A unique opportunity to advance discussions on genomics presented itself when the organizers of the 2016 Joint Annual Meeting (JAM) of the ASAS, ADSA, CSAS and other organizations scheduled a day of programmatic overlap with the 2016 International Society of Animal Genetics (ISAG) meeting. Both groups meet on July 23, 2016 in Salt Lake City, Utah, and several FAANG members including Chris Tuggle and Stephen White (NRSP-8 Sheep Coordinator) proposed that this day be devoted to a Symposium on FAANG. The proposal was approved and this Symposium is being planned. See https://www.asas.org/meetings/isag2016/program for current details.

Communication: The *Pig Genome Update* has now published 122 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:
Melanie Trenhaile, University of Nebraska-Lincoln, 2015 Neal Jorgenson Travel Award winner
Elisabetta Giuffra, INRA, 2015 NRSP-8 special speaker on FAANG
Huaijun Zhou, University of California-Davis, Midwest ASAS Functional Genomics Workshop

<u>2016 commitments:</u>
Jeremy Howard, North Carolina State University, 2016 Neal Jorgenson Travel Award winner
We are also partially supporting the travel of speakers to the Cattle/Swine joint and Swine Workshops:
Randy Prather, University of Missouri, and Bruce Whitelaw, Roslin Institute, Cattle/Swine Workshop
Min-Kyeung Choi, Konkuk University, and Francisco Peñagaricano, University of Florida, Swine Workshop

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!

<u>Prior approved Projects:</u>
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.

Newly approved projects during reporting period:

1. 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.
2. 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 both of these projects, the Swine Genome Coordinators had a co-PI role, so the proposals were vetted through the Advisory Committee for approval.