US 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). CSREES 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 Pig Species Subcommittee.

Facilities and personnel: Max Rothschild, Department of Animal Science, ISU, serves as Coordinator and was reappointed in 2008. Iowa State University faculty and staff help support the national pig genome coordination effort as part of Iowa State University's contribution.

NRSP8 Objectives: **Objective 1**: Create shared genomic tools and reagents and sequence information to enhance the understanding and discovery of genetic mechanisms affecting traits of interest. **Objective 2**: Facilitate the development and sharing of animal populations and the collection and analysis of new, unique and interesting phenotypes and **Objective 3**: Develop, integrate and implement bioinformatics resources to support the discovery of genetic mechanisms that underlie traits of interest.

Map Development Update: New gene markers were identified with the development of the 60K SNP chip. These new markers are being integrated with the development of Build 9 and the new build 10 as maps now are based on the pig sequencing efforts.

QTL, Candidate Genes and Trait Associations: QTL and trait associations have continued to be reported on all chromosomes for many traits. Candidate gene analyses have proven successful with several gene tests being used in the industry for many traits including, fat, feed intake, growth, meat quality, litter size and coat color. The PigQTLdb (http://www.animalgenome.org/QTLdb/pig.html) is an excellent repository for all of these results.

Sequencing Efforts: The Swine Genome Sequencing Consortium (SGSC) continued its efforts this past year and considerable advances have been made. Build 10 for the Sus scrofa reference genome sequence was released Monday, September 20 thanks to the efforts of many people and great collaboration across the world. The sequence and accompanying information was in a final version and released from TGAC's ftp (FTP site: ftp.tgac.bbsrc.ac.uk; User: pig10; Password: Sscrofa10). This final version was based on the latest freeze of the physical map. The assembly is the result of the integration of all the sequenced clones and contigs produced by SOAPdenovo and Cortex whole genome shotgun (WGS) assemblies. These WGS assemblies were generated using Illumina reads sequenced at BGI and the Sanger Institute (~40X coverage). As part of the release AGP files with information about the source of every contig were provided. The WGS contigs were submitted to EMBL/Genbank, and after that the WGS contigs were to be renamed in the AGP with the corresponding accession numbers. This assembly provides an almost complete coverage of the pig genome. Additional details will be presented as they become available. **The "marker" paper has recently been published** in which the Consortium sets outs its plans for the analysis and publication of a draft pig genome sequence. These plans were presented to participants in the Pig Genome III conference held at the Wellcome Trust Sanger Institute, 2-4 November 2009 when a series of analysis working groups were established. Please see *BMC Genomics* 2010, **11:**438 (http://www.biomedcentral.com/1471-2164/11/438).

Database Activities: While database activities were transferred to the Bioinformatics Coordinator, the Pig Genome Database continues to receive considerable updating. News and updates were set up to report the genome sequencing progress (http://www.animalgenome.org/pigs/genomesequence/) and to link to most updated pig genome information resources. New QTL continue to be curated into the Pig QTL Database. Up to

date there are noe 5,986 QTLs in the database representing 581 pig traits and can be seen at (http://www.animalgenome.org/QTLdb/pig.html). Efforts are being made to update the newest pig genome information in several areas including (1) alignment with pig QTL among other genome features (http://www.animalgenome.org/gbrowse) and (2) blast service to allow the community pig gene analysis and annotation activities. The NAGRP Bioinformatics Team has set up a pig gene Wish List which is seen at (http://www.animalgenome.org/cgi-bin/host/ssc/gene2bacs) which is playing an active role to help the pig genome annotation activities.

Shared Materials: The last of the microsatellite primers and second generation novel 70-mer oligonucleotide microarray have been shared by the coordination program. The other shared materials will be SNP chips. The Pig Genome Coordinator supported community activities to find associations with PRRS and has provided 800 chips for that activity in 2009-2010 and has also supported PCV2 shared activities by providing SNP chips for genoptyping. The coordinator is looking for new projects (meat quality, sow longevity) to help support by providing SNP genotyping.

Porcine SNP chip: Illumina and the International Porcine SNP Chip Consortium developed a porcine 60K+ SNP and have shipped it to many researchers worldwide. Researchers that did not place an order can contact Illumina for further information or questions at http://www.illumina.com/contactMe.ilmn?CS=1. The original publication was Ramos et al. 2009.

International Efforts: Communication with all international groups and individuals is excellent.

Communication: The bimonthly *Pig Genome Update* has now published 100 issues and has been distributed electronically to over 1,800 people worldwide.

Travel and Meeting Support: Some conferences have received support funding from the Coordinator. Travel of some scientists was partially funded to attend important pig gene mapping meetings.

Future Activities: The goals are to help support all of the objectives of this project. Major activities include helping facilitate and sharing use of the 60K SNP chip in 2010. Further development of a shared population is ongoing. New bioinformatic tools will also be developed. Constructive suggestions from researchers to help this coordination and facilitation program grow and succeed are appreciated.