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. A rewrite of NRSP8 was completed in 2008. New objectives are listed at the end of this report.

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.

Old Objectives: 1. Develop high resolution comparative genome maps aligned across species that link agricultural animal maps to those of the human and mouse genomes; 2. Increase the marker density of existing linkage maps used in QTL mapping and integrate them with physical maps of animal chromosomes, and 3. Expand and enhance internationally shared species genome databases and provide other common resources that facilitate genome mapping.

Map Development Update: New gene markers continue to be identified and mapped and integration of the maps continues to have taken place as QTL maps are expanded.

QTL and Candidate Genes: QTL have continued to be reported on all chromosomes for many traits. QTL studies continue to find imprinted QTL. Candidate gene analyses have proven successful with several gene tests being recently released and 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. A total of 95% of the physical map has been selected in 15,882 BAC clones for sequencing. A total 14,233 of these clones have sequence available, contributing 2,438Mb, which is approximately 85% of the map. The plan is to select a further 1,100 clones over the next 4-5 months, which will bring the total number of clones for the project to 17,000. In addition, efforts will also be made to close the remaining map gaps, in which the entire genome is currently in 166 map contigs. Some bioinformatics efforts will be made to discover where remaining gaps can be closed, both by the addition of new clones into the map and by the manual manipulation of existing clone sequence. For further details, please go to www.sanger.ac.uk/Projects/S_scrofa/ or mail pig-help@sanger.ac.uk. This progress is seen at the end of this report.

Database Activities: 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/). New QTL continue to be curated into the Pig QTL Database. Up to date there are 11,831 QTLs in the database representing 246 pig traits. Another 200 more QTL have been recently curated and are going through a quality control process before their release in the near future. New functions have been added to the PigQTLdb tools to align pig RH map-human comparative maps, pig BAC physical maps, new microsatellite markers from Sino-Danish genome project, pig SNPs from dbSNP, Affy and Oligo microarray elements against pig QTL. Most recently, a new function has been added to allow users to download all curated QTL data when they browse the QTL chromosome map views. The database is available at http://www.animalgenome.org/QTLdb/pig.html. Database activities were transferred to the Bioinformatics Coordinator.

Shared Materials: The last of the microsatellite primers have now been distributed and no new production is planned. Thanks to efforts of a number of groups and individuals a second generation novel 70-mer oligonucleotide microarray,. the Swine Protein-Annotated Oligonucleotide Microarray, has been developed as an OPEN SOURCE collaboration between investigators and institutions. The sequences of the oligonucleotides, the consensus sequences they represent, and the annotation of the consensus sequences are provided at no cost to the entire research community. Microarrays can be purchased by going to: http://www.pigoligoarray.org/ or to http://www.animalgenome.org/pigs/resources/array_request.html to order them. This year validation of the arrays has been taking place and has been sponsored in part by the pig genome coordination program. This validation will be reported soon in upcoming publications. The other shared materials will be SNP chips. The Pig Genome Coordinator will support community activities to find associations with PRRS and will be providing 800 chips for that activity in 2009.

Porcine SNP chip: Illumina and the International Porcine SNP Chip Consortium recently announced that the porcine 50K+ SNP panel is available and being shipped. researchers that did not place an order can contact Illumina for further information or questions at http://www.illumina.com/contactMe.ilmn?CS=1. Inoitial publications involving the development of the chip and its initial use will be available in 2009.

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

Communication: The bimonthly *Pig Genome Update* has now published 94 issues and has been distributed electronically to 1,625 people worldwide.

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

Future Activities: Objectives from the recently renewed NRSP-8 term (10/01/08-09/30/13) are 1) Create shared genomic tools and reagents and sequence information to enhance the understanding and discovery of genetic mechanisms affecting traits of interest; 2) Facilitate the development and sharing of animal populations and the collection and analysis of new, unique and interesting phenotypes and 3) Develop, integrate and implement bioinformatics resources to support the discovery of genetic mechanisms that underlie traits of interest. To meet these new goals major activities include helping facilitate and sharing use of the 60K SNP chip in 2009. Further development of a shared PRRS 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.

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