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.

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 continue to be identified and mapped and integration of the maps continues to have taken place as QTL maps are expanded. Maps now based on the pig sequencing efforts and the 60K SNP chip are being developed.

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 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 160 attendees came to this historic meeting where speakers presented updates on several subjects related to the sequencing effort and plans for the future. The deadline has passed for new clones to enter the sequencing pipeline. However, some new clones are being identified as a possible resource for future sequence gap closure. These identified BACs currently stand at ~150 and have been identified using physical map and sequence information. All chromosomes are over 90% sequenced taking the genome to 95.72% from 16,974 sequenced clones. About 94% of the genome is at the "Improved" status (15720 clones). There is 123Mb of finished quality data within the 2.994Gb currently available. Sanger will continue with chromosome X/Y sequencing – chromosome X clones sequenced in the genome project will be finished and the map will continue to be refined using a fosmid library too. Sanger has produced a chromosome Y fosmid library which is currently being fingerprinted. This will be used to select up to 1100 fosmid clones for sequencing and finishing. This work is funded by BBSRC. In collaboration with TGAC (Norwich, UK) the remaining BAC clones which have been selected from the fingerprint map will be pooled and sequenced on the Illumina platform. A further 10X coverage of Duroc sow DNA will be produced on the Illumina platform to be combined with the BGI data and assembled (also in collaboration with TGAC). Automatic annotation will continue to be provided by Ensembl. Another annotation jamboree is to be organized in 2010

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 4,928 QTLs in the database representing 499 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. Efforts are being made to align the current genome assembly against pig

QTL among other genome features (http://www.animalgenome.org/gbrowse/). 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 and 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 was published. 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. The coordinator is looking for new projects (meat quality, PCV2) to help support by providing SNP genotyping.

Porcine SNP chip: Illumina and the International Porcine SNP Chip Consortium developed a porcine 60K+ SNP and has 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. An initial publication involving the development of the chip and its initial use has been published and additional publications will be available in 2010.

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 1,700 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: To meet the new objectives major activities include helping facilitate and sharing use of the 60K SNP chip in 2010. Further development of a shared PRRS population is ongoing and other shared populations are likely in 2010. 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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