US PIG GENOME COORDINATION PROGRAM ACTIVITIES

Supported by Regional Research Funds, Hatch Act for the Period 1/1/07-12/31/07

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Presented January 12, 2008

Overview: Coordination of Pig Genome Coordination Program is under the National Animal Genome Research Program (NAGRP) and is the effort of 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 the project is underway.

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

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. This year new physical maps continue to progress. For one measure of the map's progress please see the recently published paper (http://genomebiology.com/2007/8/7/R139).

QTLs 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 proved 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. New funding continues to be secured. The Coordinator has attended the SGSC meetings, lobbied for funding and sp to producer groups. A recent publish paper which describes some of the sequencing progress to date can be seen at (http://genomebiology.com/2007/8/8/R168) . This year considerable progress has been made on the sequencing and 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 1,675 QTLs in the database representing 246 pig traits. In addition, 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. It can be seen 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 we have developed a second generation novel 70-mer oligonucleotide microarray for profiling expression of the pig (Sus scrofa) genome. The Swine Protein-Annotated Oligonucleotide Microarray has been developed as an OPEN SOURCE collaboration between investigators and institutions with an interest in pig physiology. 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 spotted with already synthesized oligonucleotides 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 has included the labs of Scott Fahrenkrug, University of Minnesota, Joan Lunney, USDA ARS Beltsville Agricultural Research Center, Christine Elsik , Georgetown University, Cathy Ernst, Michigan State University, and Max Rothschild, Iowa State University.

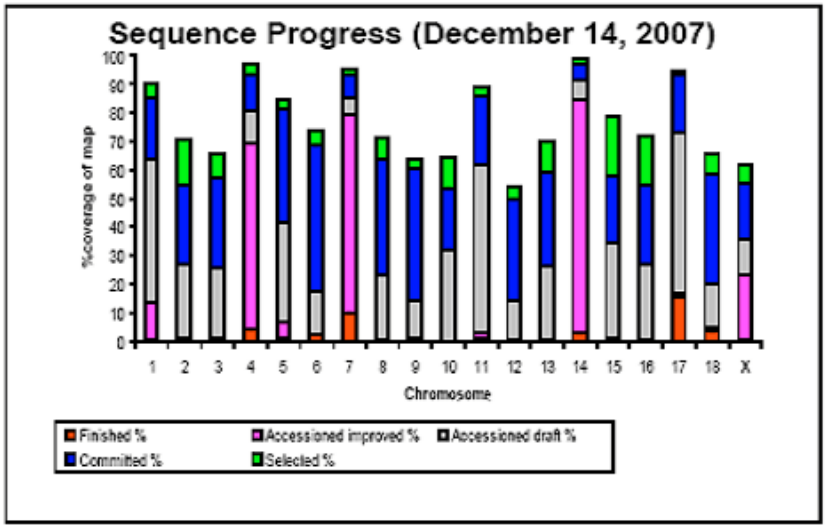
Porcine SNP chip: A consortium from the USDA (ARS, CSREES), University of Illinois, Iowa State University and the National Pork Board is currently undertaking a concerted effort to develop a high density (~50K) SNP chip for pigs. The consortium is aiming to develop this research tool by mid 2008. It is envisioned that this chip will be employed widely by the porcine research community to drive gene discovery and association analyses and eventually whole genome selection. The SNPs included for this project will be selected from those in public databases on February 1, 2008. The consortium would like to invite researchers interested in access to this technology to join their group. In addition, investigators possessing SNP information that has not been placed in public databases are encouraged to submit their information as soon as possible so that the most useful set of SNPs can be included in the final product. At present, neither the cost per chip nor the commercial provider of the technology has been finalized. To help define both of these, the consortium is now seeking to quantify the likely demand for the finished chip. Please contact either: Mohammad Koohmaraie (Mohammad.Koohmaraie@ARS.USDA.GOV), Max Rothschild (mfrothsc@iastate.edu) or Larry Schook (schook@uiuc.edu) if your research program/institution would consider purchasing and employing the 50K pig SNP chip. Also, please indicate the approximate number of chips required initially and per year so that we can include you in the mailing list concerning chip production and supply. Our aim is to achieve the maximum economy of scale across the pig genomic community and in turn achieve the lowest unit cost per chip.

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

Communication: The bimonthly *Pig Genome Update* has now published 88 issues and has been distributed electronically to 1,484 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: Major activities include the rewriting of the NRSP8 project and the development of a SNP chip in 2008. Constructive suggestions from researchers to help this coordination and facilitation program grow and succeed are appreciated.



12,328 clones has been selected and sent for sequencing that provide 76.8% coverage of the map. The total sequence is 1,115 Mb from 6,902 sequenced clones and 2,902 have improved/finished, thus 49.7 Mb is finished.

(Reprinted from Swine Sequencing newsletter)