

US PIG GENOME COORDINATION PROGRAM ACTIVITIES

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

Max F. Rothschild, US Pig Genome Coordinator

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). 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, has served as Coordinator since 1993 and was last 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.

NRSP-8 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. The 60KSNP chip information can now be integrated with the development of Build 10.2 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. Several new genome wide association studies (GWAS) are being published in the pigs.

 **Sequencing Efforts:** The Swine Genome Sequencing Consortium (SGSC) was pleased to announce the publication of a high quality draft genome sequence for the pig (*Sus scrofa*). The paper entitled "*Analyses of pig genomes provide insight into porcine demography and evolution*" describing the sequencing, analysis and annotation of this draft genome sequence was published in *Nature* in the November 15 issue. In parallel a series of companion papers has been published in BMC journals. In addition, this annotation can be visualized in Gbrowse against version 10.2 of the swine genome at <http://www.animalgenome.org/cgi-bin/gbrowse/pig>.

Database Activities: The Pig Genome Database continues to receive considerable updating. The Animal QTLdb included 633 new pig QTL in its recent #18 release, making the total number of pig QTL in the database 7,451. With this release, the NAGRP bioinformatics team has done a number of improvements to the Animal QTLdb, which includes a procedure to withdraw obsolete QTL data from NCBI, a new experimental search function for animal breeds associated with QTLs, a new trait hierarchy navigator, and improved QTLdb curator/editor 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 ported to the BioMart <http://www.animalgenome.org:8181/> for customized downloads; and pig oligoArray elements are BLAST mapped to pig genome build 10.2, available for download from http://www.animalgenome.org/repository/pig/Genome_build_10.2_mappings.

Shared Materials and Funding: The Pig Genome Coordinator has recently supported community activities to find associations with many different traits and has provided nearly 2,000 chips/genotyping for those several projects from 2009-2012. The coordinator is looking for new projects to support by providing SNP genotyping.

Porcine SNP chip update: Illumina and the International Porcine SNP Chip Consortium developed a porcine 60K+ SNP and has shipped it to many researchers worldwide. The original publication was Ramos et al. 2009. Prices for the chip have been dropping and are reasonable. **A new custom low density chip** is now available for imputation work. GeneSeek, a supplier of genotyping services has announced the GeneSeek Genomic Profiler for Porcine LD (GGP-Porcine). This custom low density BeadChip utilizes Illumina Infinium chemistry and features approximately 8,500 SNPs for high density chip imputation. The GGP - Porcine BeadChip also includes gene markers from several well-known reproduction, growth, feed efficiency, and meat quality traits at no added expense. These include the following markers: EPOR, MC4R, HMGA, CCKAR, PRKAG, and CAST. Details on these markers will be available from GeneSeek. In addition, researchers can request additional markers including the HAL, Rendement Napole (RN), Resistance marker to E.coli (F4 ab/ac), a SNP parentage panel, and the Estrogen Receptor (ESR) which impacts litter size in Large White or Yorkshire by paying additional royalty fees for these optional licensed tests. The chip was developed as a result of a collaborative effort involving leading academic, USDA, and GeneSeek researchers. The price (per sample) is about 40% of the cost of the 60K chip.

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

Communication: The periodic *Pig Genome Update* has now published 115 issues and has been distributed electronically to over 2000 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.

2013 Activities: The goals are to help support all of the objectives of this project. Major activities include helping facilitate collection of phenotypes and sharing use of the 60K and 8 K SNP chips in the future. Further development of shared populations is ongoing. New bioinformatic tools 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. NRSP-8 is being revised and contributions from members of the pig genome community are appreciated.

Final considerations: This coordinator's report marks the last planned yearly report that will be issued by myself. After 20 years it is time for a change of leadership in the Swine Genome Coordination program and I will be stepping down September 30, 2013 if a replacement can be chosen. We as a community should be quite proud of all we have accomplished. This work has gone from discovering microsatellite markers, genes and initial QTL to having a pig genome sequence, gene markers used in industry and a much better understanding of the genetic control of the traits of interest in the pig. As Coordinator I have tried to help facilitate these activities and thanks to many, many colleagues around the US and the world we have been successful. I thank each of you for your help and support and for your friendship in these matters. I pledge to help the next Coordinator continue to work with our community and I wish whoever is chosen great success.