BRIEF SUMMARY OF THE PIG GENOME COORDINATION PROGRAM FOR 2006

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Coordination Structure: Iowa State University faculty and staff help support the national pig genome coordination effort as part of Iowa State University's contribution.

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

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 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. USDA held a competitive grant program for $10 million and the grant was awarded to a team of international team led by the University of Illinois and the Sanger Center, UK and which included the Pig Genome Coordinator. Additional funding from a number of countries has helped to make this a real international effort. My role has been to speak to producer groups which I have done on several occasions.

Database Activities: The Pig Genome Database has received 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, and pig BAC physical maps, new microsatellite markers from Sino-Danish genome project, and pig SNPs from dbSNP, 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. A big thanks goes to Scott Fahrenkrug, Michael Murtaugh and Bhupinder S. Juneja, University of Minnesota, Joan Lunney, USDA ARS Beltsville Agricultural Research Center, Christine Elsik , Michael Dickens and Anand Venkatraman, Texas A&M University, Joe Cassady, North Carolina State University, Cathy Ernst, Michigan State University, Max Rothschild and James Reecy Iowa State University, David Galbrath and Leukena Cheam, University of Arizona. Validation is being made at three university laboratories funded in large part by coordination funds.

Other future activities will include development of a porcine SNP chip.

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

Communication: The bimonthly *Pig Genome Update* has now published 82 issues and has been distributed electronically to 1,385 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: Constructive suggestions from researchers to help this coordination and facilitation program grow and succeed are appreciated.