Swine Genome Mapping Consortium Workshop

January 15, 2006, San Diego, CA

A workshop about the consortium was held in San Diego on January 15, 2006 in conjunction with the Plant and Animal Genome XIV meeting, January 14 - 18, 2006. The program for the workshop is available at : http://www.intl-pag.org/14/14-swine-seq.html.

The workshop was attended by a large group of participants. An overview of the consortium and its achievements in 2005 was given by Larry Shook of University of Illinois at Urbana-Champaign. The Consortium was founded on September 23, 2003 in France. Three phases have been completed in time. The swine genome is approximately 2.7 GB with 18 autosomes and, X and Y chromosome. The human genome is approximately 2.9 GB. The resources used are. 1. genetic linkage map with over 2000 mapped markers. 2. Radiation Hybrid (RH) map with over 7000 markers 3. Four BAC libraries: RP-44, Roslin, INRA and CHORI-242; and 4. Physical map. The DNA from a single Duroc sow that was used to produce the CHORI-242 BAC library will be sequenced to generate the reference genome.

The results of the comparative map and full-Length cDNA sequencing were also presented. The comparative map has coverage of 90.3% based on a conservative estimation. The map provides scaffolds for BAC physical map assembly and is also integrated with linkage map via micro-satellites. The tissue is harvested for RNA from adult female day 55 cloned piglets. More clones are on the way. This has provided abundant EST sequence data. The potential deficiencies are that rare transcripts remain poorly characterized and resources for functional analysis are poorly organized.

The steps for a high resolution porcine RH map for sequence assembly were described by Craig Beattie of University of Nevada-Reno. The RH map assists in the comparative mapping. Mapping of about 6900 markers will be completed by the end of June, 2006. Description of the porcine genome physical mapping project at the institute for the domestic pig (*Sus scrofa)* is available at: http://www.sanger.ac.uk/Projects/S_scrofa/.

Currently seven breeds and one animal per breed has been used in the SNP discovery. The list of breeds included Large White, Landrace, Pietrain, Maishan, Iberian, North European wild boar and minipig from Goettingen, Germany. The list presented however did not include Durocs. A SNP discovery software "TIGR-contig" has been developed in collaboration with MARC. Currently 6426 SNPs in the gene back are from MARC.

The SNP genotyping is also done at the Beijing Genomic institute in China. A number of breeds were used in genotyping including Durocs. Genotyping has been done for about 3000 SNPs.

The industry and translational activities of the Consortium were described by Max Rothschild of Iowa State University. He described the plans for development and distribution of information to the consumers, the circulation of information through news letters like the ANGENMAP discussion group and creation of web pages that will be

updated routinely. The web sites include: www.sanger.ac.uk, www.swinegenomics.com and www.genome.iastate.edu.

Kellye Eversole, from the Eversole foundation and the Alliance for Animal Genome Research discussed the post-Sequencing Activities. These activities included SNP discovery.

The institutions participating in the consortium are: University of Illinois, the Sanger Institute, the Roslin Institute in Edinburgh, Scotland; the University of Nevada, Reno; INRA Cellular Genetics Laboratory, Toulouse, France; USDA Agricultural Research Service Meat Animal Research Center, Clay Center, Nebraska, and Iowa State University.

The financial contributors to the project are from UK, France, South Korea, Holland, US. In the US, the contribution is provided by USDA, the National Pork Board, Iowa Pork Board, Iowa State University, North Carolina Pork Council and North Carolina State University.

A $10 million grant to the consortium from United States Department of Agriculture was announced by Agriculture Secretary Mike Johanns at the end of the workshop. However, there is still need for more funds for sequencing and SNP discovery. Support from Canada was also requested.