

PIG TALES

Newsletter of the International Swine Genome Sequencing Consortium (SGSC) Pig Genome Sequence Project

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Significant Progress Reported at SGSC Meeting Hosted by INRA in Toulouse, France



Jane Rogers, WTSI, leads a discussion at the SGSC Meeting in Toulouse on Future planning efforts and funding needs.

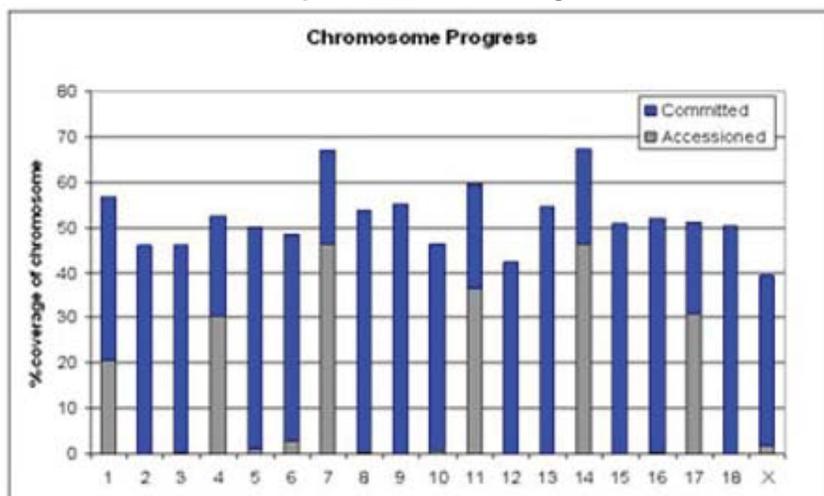
The SGSC was hosted by Denis Milan in Toulouse, France on October 17 and 18. Sean Humphray, The Wellcome Trust Sanger Institute (WTSI), gave a detailed overview of the strategy and progress to date of the pig sequencing project. A clone-by-clone sequencing strategy, based on the minimum tiling path of BAC clones, being employed in the project and the status of accessioned and sequenced regions of pig chromosomes to date was discussed (see Figure below). To date, over 265,000 CHORI BACs have been fingerprinted (16.2 genome complexities) and over 620,000 BES have been deposited for public access. A manuscript has been submitted with respect to completion of the whole genome contig map. The current map has placed 172 contigs with an average length of 15Mb that covers 2.58Gb representing >98% of the pig euchromatin. Sean discussed approaches to building SSCY and SSCX contig maps to support sequencing. Since the CHORI-242 is female, 495 additional BACs from the INRA contig map with at least one BES anchored on X or Y will be selected. These BACs from the INRA male BAC library will be fingerprinted and added to the map. Additional funding will be required to sequence SSCX (deeper coverage than 3X) and a focused project will be necessary for SSCY. Larry Schook, University of Illinois, has established a male Duroc cell line that is being used by the WTS to flow sort chromosomes to make fosmid and plasmid libraries. Sean also provided an update on the fosmid library that has been constructed from DNA used to construct the CHORI-242 BAC library. This fosmid library (WTSI_1005) has 500,000 (7x) clones (1,300 x 384 well plates) and colonies have been picked and replicated into 500 plates. To date, 73,000 fosmid end sequences have been completed and are publicly available.

Craig Beattie, University of Illinois at Chicago, provided an update on additional RH map activity. They have currently assigned ~8,000 markers on the IMNpRH12,000 rad panel. This includes: ~2,097 microsatellites (MSs), 2,140 ESTs, and 1,370 genes (annotated from the human sequence), ~1,900 BESs and 140 SNPs. 90% of the BESs were previously mapped during the construction of BAC fingerprint contigs (FPC) on the IMpRH7,000 rad Panel. Approximately 750 of the MSs and 2,200 of the ESTs/genes are also ordered on the IMpRH7,000 rad panel. Sung-Jong Oh, Korean National Livestock Research Institute, shared their success in whole-genome shotgun sequencing of the Duroc 2-14 shotgun plasmid libraries.

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They have made their third deposit of sequence reads. Their total activity to date is 107,328 reads that represents over 69 Mb. Additionally, by the end of 2006, they expect to finish approximately 100 Mb of sequence. Full-length cDNA development and sequencing being carried out in Japan was reviewed by Hirohide Uenishi. A total of 10,000 full-length cDNAs are being developed from a variety of tissues to contribute to the annotation of the genome.

Sequence Clone Progress



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Clones (7,381) selected and sent for sequencing covering 53% of the map
Total sequence = 309 Mb from 1,746 accessioned clones, 25.8 Mb finished

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Finally, Denis Milan overviewed the SNP discovery effort underway that has been funded by INRA. Seven breeds are included in the project (Large White, Pietran, Landrace, Wild Boar, The National Spanish Iberian breed, Meishan, and the minipig). A total of 1M reads are planned and roughly 500K have been completed to date (200K each on Large White and Landrace and 100K on Meishan). All sequence reads will be released in to the public domain and soon as the quality is verified.

Sequencing Priorities

The strategy for clone selection and sequencing pipeline has been finalized. The planned order of contig selection for sequencing is: (1) SSC7, SSC14 and SSC4 are the highest priority since additional EU funding targeting these chromosomes has been received; (2) SSCX; and (3) SSC 1, SSC11, SSC17, SSC5, SSC6, SSC2, SSC3, SSC8, SSC9, SSC10, SSC12, SSC13, SSC15, SSC16, and SSC18. The first round of clones have been identified and committed for sequencing. Project progress can be monitored at Pre-ensembl (http://pre.ensembl.org/Sus_scrofa/index.html).

Adopt a Gene, BAC or QTL

As illustrated in the headline story, the pig genome project has already selected over 50% of the BAC clones of the minimal tiling path. Shotgun libraries are now being constructed from these BAC clones and being prepared to enter the sequencing pipeline.

Hence we have flexibility in the selection of BACs and the order in which they enter the sequencing pipeline. This affords us an opportunity to target specific genes, chromosomal regions containing putative QTLs or other known candidate genes.

We encourage investigators to forward requests for target genes and chromosomal regions. It is our intent to address ongoing genomic studies by prioritizing the order of BACs being sequenced.

If you wish to submit a request for a specific BAC that contains a specific gene or QTL please visit www.piggenome.org and visit the "Adopt A Gene" page. This will allow you to forward your request for further consideration. The Project Directors will review requests. After consultation with the Technical Support and Steering Committee members a decision will be made with respect to placing the requested BACs into the sequencing pipeline.

SPONSORS

European Union SABRE Funding
Institute for Pig Genetics (TOPIGS), Netherlands
INRA Genoscope
Iowa Pork Producers Association
Iowa State University
Korean National Livestock Research Institute
NAIS, Japan
National Pork Board, U.S.A.
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Sino-Danish Pig Genome Initiative Funded By the Danish Advanced Technology Fund: Joins forces with the International Swine Genome Sequencing Consortium

The Danish Advanced Technology Fund has decided to contribute DKK 24,130,000 (US\$4) to the project "Pigs and Health" with anticipation of additional industry and major contributions from Chinese partners, including the Beijing Genomics Institute. A substantial portion will support de novo sequencing of regions of the pig genome that are considered relevant for pig and/or human health. The effort will be coordinated and integrated into the International Swine Genome Sequencing Consortium project. Selected BAC clones from the physically mapped tiling collection at the Wellcome Trust Sanger Institute will be sequenced by a combination of the "traditional" capillary method and new Solexa and 454 technologies. This sequencing will be performed mainly at the Beijing Genomics Institute with the goal to produce "finished" sequence of as many BAC clones as possible. Funding is also allocated to re-sequencing of especially relevant DNA regions in different pig breeds and reference families. The DNA sequences and their variation will be analyzed by a network of bioinformatics groups in Denmark and China focusing on comparative genomics, evolutionary genetics, integrative biology and association/linkage studies. A major goal of the genetic mapping is to develop genetic tests and genotype assisted breeding to improve the disease resistance of production pigs. Genetically modified pigs will also be produced using Somatic Cell Nuclear Transfer cloning from engineered pig fibroblasts. Such pigs will be used as models for the study of disease processes of medical relevance as well as for the development and testing of new procedures and drugs for disease diagnostics, prevention, and early treatment.

SGSC CALENDAR OF EVENTS

Jan. 13-17, 2007	Plant & Animal Genome XV, San Diego, California joint with NC-1008 and NAGRP Annual Meetings Contact Larry School schook@uiuc.edu
Mar. 14-18, 2007	SGSC, St. Croix, US Virgin Islands Contact Larry School schook@uiuc.edu

SABRE Project

EU Framework 6 Provides €23M to launch a SABRE "Cutting Edge Genomics for Sustainable Animal Breeding"

An innovative four-year, pan-European FP6 Integrated Project is utilizing the latest techniques in animal genomics has been funded by the EU Framework 6. This project will develop economically and environmentally sustainable production systems for cattle, pigs and chickens. The SABRE program was designed to provide a range of new breeding strategies to improve animal health and welfare, reduce chemical and energy inputs, minimize livestock waste and pollution and maximize food safety and quality. Objectives provide (1) fundamental knowledge on the genomics and epigenetics; (2) an understanding of biological systems central to sustainability including; and (3) the identity of genes and markers allowing focused breeding for sustainability goals. Related to the pig genome sequencing effort is support to finish sequencing (6X) coverage and annotation of two pig chromosomes (SSC4 and SSC14) and support the development of SNP panels and linkage disequilibrium maps.