PIG TALES

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

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Patrick Chardon, INRA and Co-Chair of the Swine Genome Sequencing Consortium Retires

The SGSC will miss the great leadership of Patrick. He has announced his retirement from INRA. His seminal contributions to understanding the porcine major histocompatibility complex are broadly recognized. His laboratory's creation of genomic platforms provided the foundation for the pig genome sequencing project. Patrick's great smile and team work will be greatly missed.

Mike Stratton, Deputy Director of Wellcome Trust Sanger Institute, Elected to the Royal Society

Professor Mike Stratton, Deputy Director and Joint Head of the Cancer Genome Project at the Wellcome Trust Sanger Institute, has been elected to the Fellowship of the Royal Society. Professor Stratton is one of the leading cancer researchers in the world. Mike also serves as the Co-Principal Investigator for the USDA sponsored pig genome sequencing project. The SGSC is extremely proud of Mike's achievements in cancer biology and his tremendous support and leadership in the pig genome sequencing project. Congratulations!





The Sanger Center Pig Genome Sequencing Team

The progress and quality of the pig genome sequencing effort is the result of the treemendous team. Pictured left is the current team being led by Carol Churcher and Richard Clark. We are very grateful for their dedication and the high quality outcomes they have provided the SGSC.

Front row L to R: Clare Murnane, Anthea Cassidy, Deborah Atkin

Pig Annotation Workshop 16-18 July 2008 Wellcome Trust Sanger Institute Kudos to Mario Caccamo, European Bioinformatics Institute and Alan Archibald, Roslin for organizing the Pig Annotation Workshop that will be held at the Wellcome Trust Sanger Institute from July 16 to 18. Registration closed on June 6 but to receive additional information please contact Mario (marioc@ebi.ac.uk) or Alan (alan.archibald@roslin.ed.ac.uk).

Back row L to R: Darren Ware, Glen Threadgold, Ryan Beveridge, Richard Clark, Claire McKeeve, Sylvia Keigwin. Mid row L to R: Kate Fraser, Paul Hunt, Carol Churcher, Xiaonan Wang, Lucy Matthews

Sequencing Progress: The March Continues with Pace and Quality

Tremendous progress is continuing to be made and the target date of June, 2009 for completion is still in sight. Specific information regarding the overall project and specific BAC clones can be viewed at http://www.sanger.ac.uk/Projects/S_scrofa/. Specifically, sequencing of chromosomes 7 and 14 are going well. Chromosome 17 has sequence coverage of about 90%. A total of ~14,000 BAC clones have been selected for sequencing and sent to the pipeline. These BAC clones cover about 86.1% of the physical map. To date over 1,600 Mb of total sequence (61.2 Mb of finished quality) from 9,797 clones has been completed. About 5,000 clones have been sequenced to the "improved/finished" stage. We estimate that about 60.5% of the genome had been sequenced.



Pig X/Y BBSRC grant

The Wellcome Trust Sanger Institute (WTSI) and Department of Pathology, University of Cambridge have been awarded funding from BBSRC to determine the sequence of the sex chromosomes in pig to a high standard. From high quality analyzed sequence it is planned:

- 1) To determine the gene content and genomic organization of the sex chromosomes
- 2) To identify transcribed sequences mapping to pig sex chromosomes involved in spermatogenesis
- 3) To use historical breeding records and archive DNA to identify Y chromosome variants potentially associated with fertility traits
- 4) To provide a sequence resource that can be used to identify candidate genes for X-linked QTL

Extensive human and mouse sequencing has provided evidence that certain X and Y genes appear to be shared between most mammals whilst also defining lineage specific sex chromosome genes. There is limited information on primates and other mammals so it is important to utilize and extend the available sequence for the pig sex chromosomes to encompass another mammal. Encompassing all branches of mammalian evolution will allow a better study of the X and Y chromosomes.

At WTSI work will carry on with the X chromosome sequencing (funded by the USDA project) with BBSRC funding providing the resources to finish BAC and fosmid clones to a comparable level of human and mouse. Further refinement of the physical map is required using BACs from the CHORI 242 library and a new (produced at WTSI) chromosome X fosmid library. A fosmid library of the Y chromosome is to be produced at WTSI which will be fingerprinted and mapped. To aid map assembly of the highly repetitive Y chromosome other information will be utilised such as:

- 1) The existing small BAC contigs assembled round the Y and X-Y homologous genes included in the first generation gene map of the Y chromosome
- 2) Probes developed from other Y chromosome genes and cDNA clones
- 3) Sequence from putative assembled round the Y and X-Y homologous genes included in the first generation gene map of the Y chromosome
- 4) Probes developed from other Y chromosome genes and cDNA clones
- 5) Sequence from putative chromosome BACs deposited in Genbank

From the Y map fosmid clones will be selected for shotgun sequencing, improvement and finishing followed by analysis and manual annotation (for X and Y). Sequence data will be made publicly available as per WTSI guidelines. [contributed by Carol Churcher, WTSI]

SPONSORS

Agricultural Research Service, USDA European Union SABRE Funding Institute for Pig Genetics (TOPIGS), Netherlands INRA Genescope Iowa Pork Producers Association Iowa State University Korean National Livestock Research Institute National Institute of Agrobiological Sciences, Japan National Pork Board, U.S.A. North Carolina Pork Board, U.S.A. North Carolina Agricultural Research Service North Carolina State University University of Illinois Wellcome Trust Sanger Institute BBSRC, UK



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SNP Chip Development is Underway

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 (~60K) SNP chip for pigs. The consortium is aiming to develop this research tool by late 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. A SNP discovery program funded through the CSREES National Research Initiative is supporting efforts at the University of Illinois, University of Missouri, ARS-MARC and Wageningen University. 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. Illumina will be providing the technology platform. Interested parties should contact Marylinn Munson (mmunson@illumina.com) to inquire about pricing and placing orders.

SGSC CALENDAR OF EVENTS

July 16-18, 2008	Annotation and Assembly Workshop
	Hinxton, UK
July 23, 2008	Domestic Animal Sequencing Workshop
	ISAG, Amsterdam
August 22	Orders for Illumina Pig Chip due