

PIG TALES

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

Project Directors

Jane Rogers

Wellcome Trust Sanger Institute

Larry Schook

University of Illinois-Urbana

Technical (*) and
Steering Committee(#)

A. Archibald*#

Roslin Institute

C. Beattie*

University of Illinois-Urbana

J. Beaver*#

University of Illinois-Urbana

M. Boggess#

National Pork Board

J. Cassady#

North Carolina State University

P. Chardon*#

INRA-Jouy-en-Joysas

K. Eversole#

Alliance for Animal Genome
Research

M. Fredholm*

Danish Ag and Vet

R. Green#

USDA/ARS

D. Hamernik#

USDA/CSREES

S. Humphray*#

Wellcome Trust Sanger Institute

B. Liu*

Beijing Genome Center

D. Milan*#

INRA-Toulouse

S-J Oh*

National Livestock Research
Institute

F.A. Ponce de Leon*

University of Minnesota

G. Rohrer*

USDA/ARS

M. Rothschild*#

Iowa State University

H. Uenishi*

National Institute of Agrobiological
Sciences

M-C Wu*

Taiwan Livestock Research Institute

Countdown Towards the Year of the Pig Begins!

Welcome to the inaugural issue of *Pig Tales*, the Official Newsletter of the Pig Genome Sequencing Project! This quarterly newsletter has been developed by the International Swine Genome Sequencing Consortium to permit the broadest distribution of information on the pig genome project. It is our hope that through this newsletter and its related website (www.piggenome.org) the fullest utility of the sequence information can be achieved. Also, this pig genome sequencing project represents an integrated international effort and it is our hope to further stimulate interactions and discussions. We recognize that obtaining the pig genome sequence is only the beginning of our journey and that it is essential that we develop a strong communication vehicle.

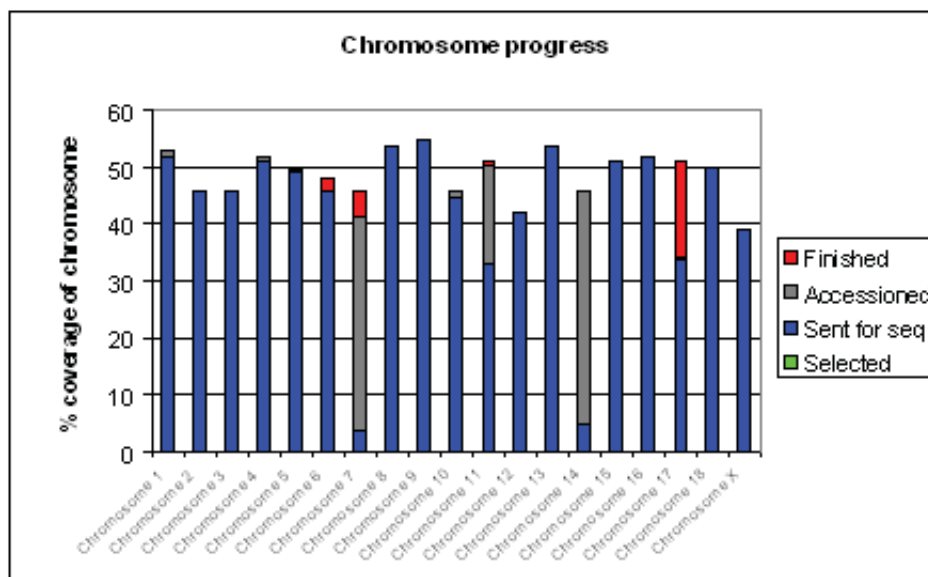
The newsletter will provide updates on the selection of regions for sequencing as well as progress in filing the sequencing pipeline. Below is a diagram developed by Sean Humphray to permit all of us to visualize which areas are being sequenced, submission of sequence reads (accessions), and assembled regions (4X coverage). Please visit the website (www.piggenome.org) for further information on these updated graphics. Suggestions to the format are welcome and can be submitted using the website. We are encouraging users to share their applications of the sequence information to the SGSC membership. Towards that end, we have a section on *First Fruits* to highlight the utilization of the sequence during this period of the project. Please forward your successes so we can share with the community.

The newsletter is also designed to provide updates on *Related Activities* and to share the successful application of the sequence information. Again, this newsletter is for the community so please forward your ideas and detailed successes for broad distribution.

Pig Tales will be distributed quarterly and provide a *Calendar of Events*. Please forward any events you wish to have shared. Finally, we wish to recognize our *Sponsors*. Obviously this is a significant project and their support is an essential component to our overall success. It is also essential that we continue to identify potential sponsors to ensure our goal of a 6X coverage of the genome. Recruiting new members and sponsors is an active process and a responsibility of all members of the SGSC.

Our next meeting is scheduled for the International Society for Animal Genetics meeting in Porto Seguro, Brazil. We hope you can attend!

Jane Rogers, The Wellcome Trust Sanger Institute
Larry Schook, University of Illinois at Urbana-Champaign



"FIRST FRUITS"

Congratulations to our colleagues at the Korean National Livestock Research Institute! The Korean NLRI was not only the first SGSC member to pledge sponsorship but also the first to begin depositing their whole genome shotgun reads in the Ensembl/NCBI trace repository. Their running total is now over 320,000 reads!

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 addressing 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.



Introducing T.J. Tabasco: DNA, Libraries, and Cell Lines

The sequencing template for the pig genome project was provided by T. J. Tabasco. She was a Duroc gilt (University of Illinois Farm pig 2-14) and was used as a source of DNA for the construction of the porcine BAC CHORI-242 library (<http://bacpac.chori.org/>) by Pieter De Jong.

Cell lines derived from ear notch fibroblasts were provided to construct various whole genome plasmid and fosmid libraries. Specifics on the libraries, their designations and how to receive them can be obtained from Sean Humphray, The Wellcome Trust Sanger Institute (sjh@sanger.ac.uk). Adult and fetal fibroblasts were also derived from Duroc 2-14. These lines have been shown in two independent studies to be clonable. RNA from various tissues during developmental stages is also available. To obtain the cells lines or receive more information on the lines or RNA please contact Larry Schook, University of Illinois at Urbana-Champaign (schook@uiuc.edu or www.swinegenomics.com).

SPONSORS



Special Tribute to Dr. Joseph Jen

The Swine Genome Sequencing Consortium wishes to express a special acknowledgement to Dr. Joseph Jen, former USDA Undersecretary for Research, Education and Economics. Through his effective leadership as Chair of the US Office of Science and Technology's

Interagency Working Group on Domestic Animal Genomics, he provided the vision and initial resources for sequencing the pig genome. His efforts led to securing industry support and international resources to achieve this milestone. All of us are indebted to his efforts on our behalf. Dr. Jen retired from USDA in April of this year after five years of dedicated service. We wish him the very best in his retirement. We are also indebted to the following Sponsors who have already made commitments to the pig genome project.

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



The 3X BAC skim of the porcine genome is supported by the National Research Initiative of the USDA Cooperative State Research, Education and Extension Service, grant number #2006-35216-16668.

SGSC CALENDAR OF EVENTS

- Aug. 20-25 ISAG 2006, Porto Seguro, Brazil 30th International Conference on Animal Genetics
Contact Larry Schook schook@uiuc.edu
- Oct. 16-17 INRA, Toulouse, France
Contact Denis Milan milan@toulouse.inra.fr
- Jan. 13-17 Plant & Animal Genome XV, San Diego, California joint with NC-1008 and NAGRP Annual Meetings
Contact Larry Schook schook@uiuc.edu

USDA-CSREES National Research Initiative Funded BAC-Skim Sequencing Project

The long-term goal of the USDA-CSREES funded project is to provide the foundations for completing a 6-7X draft sequence of the pig, as well as to support targeted high resolution analysis of QTL containing regions for identifying genes involved in growth, disease resistance, reproduction and muscle development in the pig. Thus, using funding provided by the USDA-CSREES NRI we are completing a 3X clone-by-clone genome sequence draft using a minimal tiling path BAC contig of CHORI-242. This clone-by-clone genome sequence will be then supplemented with 3X whole-genome shotgun sequencing (funding provided by other sponsors). The USDA-CSREES project aims are: (1) Complete contig and map construction; (2) Construction of BAC clone libraries, sequencing, assembly and annotation; and (3) Develop a communication plan, train potential users, release of sequence information and publish a draft assembly. The project period began in April, 2006 and will be completed by April, 2008.