

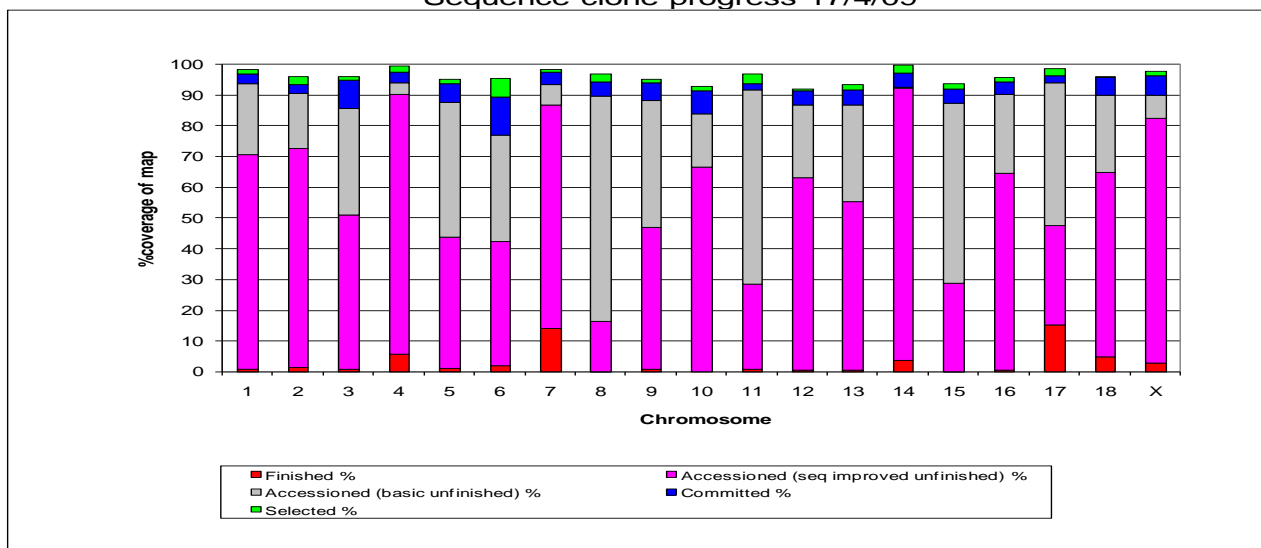
Pig Genome Update

No. 96 May 1, 2009

The Swine Genome Sequencing Project is entering the final stages of clone selection. Every effort is being made to identify clones that will contribute new sequence data. Radiation hybridizations are planned to identify new extending clones from each map contig. So far, clones selected and sent for sequencing cover 96.26% of the physical map and clones sequenced cover 89.18%. Currently, 16,707 clones are in the sequencing pipeline. Of these, 15,485 have sequence (4x) with 10,381 having been improved (>6x). Sequence data have reached a total of 2,635Mb with 72.39Mb at finished quality. The completion date is December 31, 2009. We are on track to have achieved >98% sequence coverage at ~6X coverage.

Community feedback is needed: 1) The Ensembl team has taken the Pig assembly and plans to run the automated Genebuild. The timeframe is expected to be 5 months as it is not an easy process. This will add Pig to the list of species found on the Ensembl website. The best QC for the analysis will be feedback from the community and we would like lots of it! Guidance to problematic areas means they can then be corrected in time for a second Genebuild upon completion of the project; 2) Manual annotation for some clones is a possibility, but resources are limited. Therefore, it would be hugely beneficial for the community to identify any sequenced clone that would benefit from increased annotation provided by manual intervention and 3) One advantage of opting for the BAC by BAC sequencing approach was to allow targeted sequencing of important regions first. These regions identified by the swine community are sequenced as "Top Priorities" and allow rapid sequence feedback to the community long before completion of the project. So far, 28 regions of interest have been prioritized spanning 518 clones or ~3% of the genome. If you know of a region that would benefit from prioritized sequencing, please email pig-help@sanger.ac.uk. The deadline is 31st June to send a request carol@sanger.ac.uk (kindly provided by Richard Clark and Carol Churcher).

Sequence clone progress 17/4/09



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Clones sequenced cover 89.18% of the physical map.

Pig Breeders Roundtable was held in Canterbury, UK. Over 50 researchers and industry personnel discussed advances in swine breeding and the role genomics has played in those advances. Advice and input from the community was also sought to help with the final stages of the sequencing effort. Early results from multiple SNP experiments on boar taint, genetic abnormalities and other traits were presented.

The Swine Genome Sequencing Consortium (SGSC) will co-host with The Wellcome Trust Sanger Institute a workshop from November 2 to 3, 2009 in Hinxton, UK. In anticipation of the completion of the pig genome sequencing project, this workshop will focus on “Pig Genome Assembly and Annotation”. The SGSC workshop will be held in conjunction with the EU PigNet Genome Meeting that will be held at the same location from November 3 to 4 and will focus on strategies for full utilization of the pig genome sequence information. All investigators are encouraged to attend and fully participate in these two workshops. Registration and Program details will be released soon. Interested parties should contact either Larry Schook (schook@illinois.edu), Alan Archibald (alan.archibald@roslin.ed.ac.uk), or Martien Groenen (Martien.Groenen@wur.nl).

The NRSP-8 Bioinformatics Coordination team has released an update for Pig QTLdb, which includes a number of new improvements. Within this update, there are 569 newly curated QTL and data download functions that allow users to download pig QTL data by either their linkage location ("cM") or genome location ("bp", for chromosomes that have preliminary genome assemblies are available). The QTL genome location data are available in GFF format so that users can directly import it for analyses in external programs such UCSC for genome feature alignments. Please see <http://www.animalgenome.org/QTLdb/pig.html> for details. Data can be downloaded for the entire Pig genome, for specific chromosomes, or for a refined chromosomal view. In addition, GBrowse has been installed so that pig QTL can be visualized in combination with pig transcripts, mRNA, annotated genes, etc. Currently, this option is only available for pig chromosomes 1, 4, 5, 7, 11, 13, 14, 15, 17, and X. As the pig genome assembly is updated, the GBrowse display will be updated as well. Users can find links to GBrowse either at the Pig QTLdb web site, or use this link <http://www.animalgenome.org/cgi-bin/gbrowse/pig/> (kindly provided by Zhi-Liang Hu).

USDA Grant update. The 2008 Farm Bill authorized the creation of the Agriculture and Food Research Initiative (AFRI), which replaces the National Research Initiative (NRI). AFRI offers research, education, extension project opportunities that focus on six key areas of importance to agriculture, nutrition, food safety, environment, and rural communities. CSREES released the AFRI program announcement on the agency's Web site http://www.csrees.usda.gov/funding/afri/pdfs/program_announcement.pdf and on <http://grants.gov/>. The program announcement provides an overview of the legislation that created the AFRI program and describes programs being offered in Fiscal Year 2009. The program descriptions contain the program priorities, deadline dates, budget limitations, and contact information. The program announcement does not contain all information needed to submit an application. That information will be contained in the AFRI Request for Applications (RFA). The AFRI RFA is anticipated in January 2009. Important information regarding the **Animal Genome, Genetics, and Breeding Program:** The program name for the Animal Genome program has been changed to “**Animal Genome, Genetics, and Breeding**” Letters of Intent are required for research priorities 1 through 4 and the letter of intent deadline is **March 5, 2009**. The proposal deadline for research priorities 1 through 4 is **May 14, 2009** (kindly provided by D. Hamernik and P. Burfening).

Illumina and the International Porcine SNP Chip Consortium are pleased to announce that the porcine 50K+ SNP panel is available and being shipped. If you did not place an order please do not hesitate to contact Illumina for further information or questions at <http://www.illumina.com/contactMe.ilmn?CS=1>.

PAG XVII, January 10-14, 2009 was a great success. The swine workshop and the swine sequencing workshop both had excellent presentations including one on the usefulness of the new 60K SNP chip. The abstracts are now posted on the web. See <http://www.intl-pag.org/> for more information. Planning is well underway for next year and your involvement is encouraged.

Please provide your input The Pig Genome Coordinator is always glad to hear from NRSP-8 members and other readers about ways to improve the coordination effort or provide resources that are needed and with which the coordination program can help

Upcoming meetings (see: <http://www.animalgenome.org/pigs/community/meetings.html>)

Statistical Genetics of Livestock for the Post-Genomic Era, May 4-6, 2009. University of Wisconsin, Madison, WI. Additional information can be found by contacting grosa@wisc.edu.

Systems Biology: Integrative, Comparative, and Multi-Scale Modeling: The 18th Annual Growth Factor and Signal Transduction Conference, June 11-14, 2009, Iowa State U., Ames, Iowa. See <http://www.bb.iastate.edu/~gfst/phomepg.html>

7th U.C. Davis Transgenic Animal Research Conf., Aug. 17-22, 2009, Granlibakken Resort and Conference Center, Tahoe City, CA. See <http://conferences.ucdavis.edu/transgenic>

Next generation sequencing: challenges and opportunities. October 1-3, 2009, Casa Convalescencia, Barcelona, Spain <http://ngs2009.uab.es>

Plant & Animal Genome Conference, PAG XVIII, Jan. 9-13, 2010, Town & Country Hotel, San Diego, CA. Information available at <http://www.intl-pag.org/>.

Items for *Pig Genome Update 97* can be sent to me by no later than June 15 please.

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