



Pig Genome Update

No. 95 March 1, 2009

Sequencing Project Progress is on target to complete in 2009 but needs your inputs. The Pig X chromosome sequencing project is making excellent progress through the sequencing pipeline at the Sanger Institute, with unfinished sequence data now available for over 750 clones. As the large genome finishing teams begin work to ensure the finished sequence meets our usual high standard of accuracy, discussions are underway within the Finishing Department to set finishing guidelines for these clones. In order to increase the efficiency of the finishing process we are considering whether to continue tagging regions where the data are derived only from a single sub-clone. Currently, these tags appear as miscellaneous feature tags in the EMBL headers, to indicate to researchers that the region tagged does not conform to the usual standard as described in the header. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality ≥ 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one sub-clone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC. If we no longer asked finishers to scrutinize and tag these regions we would speed up the finishing process. We don't believe that this would introduce inaccuracies in the finished sequence, but are currently carrying out checks to ensure this is the case. We would also appreciate hearing from anyone who uses the finished sequence to let us know whether you're aware of any inaccuracies in the sequence of single sub-clone regions. We are also interested in feedback from you to let us know where you access our finished data. Do you look in EMBL at individual finished clones, and therefore see the miscellaneous feature tags in the EMBL header? Or do you wait until the sequence has been annotated and access this from Vega? If you could let us know that would give us an idea of how useful our miscellaneous feature tags are to you. Please send your emails to pig-help@sanger.ac.uk by 20 March 2009. We look forward to hearing your opinions to help us generate finished data as efficiently as possible while still providing as much information as you need (kindly provided by Carol Churcher and colleagues).

With the renewal of a new NRSP-8 project, members are encouraged to provide input to the NRSP-8 Bioinformatics coordination team to help identify the highest priority needs of the animal genome research community. For those members that did not previously get a chance to fill out a survey form at the Plant and Animal Genome meeting, the bioinformatics team has placed the same survey on-line. <http://www.animalgenome.org/bioinfo/survey3.php>. Please provide your input by Monday March 3th. The Bioinformatics Team tries to provide at no cost to the users tools/databases/computational resources that meet their needs. To address the needs, that either go beyond the resources provided to the Bioinformatics Team or are specific to a very small group of users, some survey questions address the willingness to share the expenses for the development or provision of such resources. Thank you to all NRSP-8 members that have filled out the survey. Your input is greatly appreciated. This information will help the coordination team set priorities for the future of the project. We want to work toward meeting the needs of the NRSP-8 member (kindly provided by Zhi-Liang Hu and James Reecy).

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>.

A Banff Swine Genomics Workshop was held to further engage Canadian scientists and industry personnel in collaborative projects and grant development. A first draft discussion paper was prepared by Graham Plastow as background from the meeting. Copies can be obtained from Graham Plastow and any comments and suggestions would be appreciated. Please feel free to provide comments directly to Graham as well. His email address is Graham.Plastow@ales.ualberta.ca and phone number is (780) 492-1496.

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.

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).

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>)

Midwest ASAS, ADSA regional meetings. March 16-19 in Des Moines IA. Details at <http://adsa.asas.org/midwest/2009/>

British Pig Breeders Roundtable in 2009 – April 27th– 29th, Kent, UK for information please contact marie-anne.robertson@genesis-faraday.org

"Enabling protein value chains" – University of Alberta livestock genomics conference, Edmonton, Alberta, 28th-30th April 2009, contact Graham Plastow at Plastow@ualberta.ca.

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 96* can be sent to me by no later than April 15 please.

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