



# Pig Genome Update

## No. 103 July 1, 2010

**Information on the next sequencing efforts are expected shortly.** Please stay tuned for an announcement in the near future.

**Sequencing pig genome assembly** and the publications that are likely to result will continue to be of primary importance. Pig Genome Update 101 (March 1) and Pig Genome Update 102 (May 1) were devoted to primarily explaining the process and much of the opportunities. Please see:

<http://www.animalgenome.org/pigs/newsletter/No.101.html> and  
<http://www.animalgenome.org/pigs/newsletter/No.102.html>.

**The SGSC has submitted a “marker” paper for publication** in which the Consortium sets out its plans for the analysis and publication of a draft pig genome sequence. These plans were presented to participants in the Pig Genome III conference held at the Wellcome Trust Sanger Institute, 2-4 November 2009 when a series of analysis working groups were established.

**The SGSC would welcome the input of members of the community** in the analysis and annotation of the draft sequence. **“Annotation”** comprises manual correction and improvement of the gene models for individual genes on a gene-by-gene basis. We are using the Wellcome Trust Sanger Institute’s Otterlace tools for these manual annotation tasks – training can be provided as necessary. Individuals who make significant contributions to the manual annotation effort will be recognized through authorships of the relevant paper(s). **“Analysis”** comprises global analyses of particular aspects of genomic structure (e.g. repetitive sequences, segmental duplications,..) or of gene families (e.g. the immunoglobulin superfamily) or of genes with effects on specific traits (e.g. immunity, reproduction, olfaction). The outputs from “analysis” groups will be a few sentences or paragraphs in the main sequence paper plus possibly a companion paper that describes and discusses the specific analyses in greater detail. Authorship would be recognized in accordance with scientific convention. The paper describing the draft cattle genome sequence (Science 324, 522) provides an indication of “analysis” groupings – the text of the paper illustrates the outputs from such analyses. Members of the community who wish to contribute to the analysis and annotation of the draft pig genome sequence should contact the relevant analysis group leader or the coordinators, for example, if they wish to establish additional analysis groupings (Larry Schook [[schook@illinois.edu](mailto:schook@illinois.edu)] or Alan Archibald [[alan.archibald@roslin.ed.ac.uk](mailto:alan.archibald@roslin.ed.ac.uk)]).

**The International Symposium on Animal Genomics for Animal Health (AGAH) was held in Paris, France, May 31 - June 2, 2010.** The goal of the AGAH was to identify critical needs and opportunities to advance the use of animal genomics to solve problems in animal health. The symposium included major talks by leaders in the field addressing both host and microbial genomics, functional responses of hosts to infections and nutritional and immune interventions, and host and pathogen genetic controls of those responses. It is clear that genomic developments, such as SNP chips, nextgen sequencing, etc., have changed the way genomics of animal health studies can proceed. Yet there is still a need for improved datasets with deeper phenotypes for the most important animal diseases, both for production agriculture and developing economies. The AGAH attracted 170 attendees from 30 countries who attended and presented 39 oral and 70 poster presentations. It provided an excellent opportunity to discuss current and future research with leaders in the fields of animal and microbial genomics and animal health. The full program is available at <https://colloque.inra.fr/agah2010>. The meeting ended with a Roundtable discussion on "What are the critical needs/future applications in animal health: input of research and links with industry." The summary of these discussions, as well as numerous papers from the AGAH, will be published in BMC proceedings. (Kindly submitted by Joan Lunney).

**What's new on NAGRP animal genome web site.** (1) Release 11 of the Animal QTLdb is complete. As of April 23, 2010, a total of 1643 new QTL have been added to the Animal QTLdb since last release before the New Year. The new data included 1532 cattle QTL and 111 pig QTL. We encourage all users to add your own new QTL data through the Curator web form: found at the URL: <http://www.animalgenome.org/QTLdb/app.html>. (2) A major improvement to the CateGORizer online tool is made to improve its performance. The improvement included faster algorithms and more efficient ways to handle large data sets and can be seen at URL: <http://www.animalgenome.org/bioinfo/tools/catego/>. (3) Animal QTLdb frequently asked questions has been updated with new items. The most recent additions are to address possible confusions that some downloaded QTL data may "appear" like "duplicates". The FAQ explained why and provided hints as how to correctly examine the downloaded data. (4) A generic online tool has been in development (<http://www.animalgenome.org/cgi-bin/util/2gff>) to help users to convert their mapping data file into GFF3 format, which is useful to upload to GBrowse for map alignments of the genome features. In addition, the same data is also available in SAM data format <http://www.animalgenome.org/cgi-bin/QTLdb/SS/index>. The SAM data format is to assist users using SAM Tools. For details using SAM tools, see: <http://samtools.sourceforge.net/>. Please let us know if you have data that are not on our input file format list. Check out the "what's new" page (<http://www.animalgenome.org/news/whatsnew.html>) for more up-to-date information (kindly provided by the NAGRP Bioinfo Team who may be contacted at [bioinfo-team@animalgenome.org](mailto:bioinfo-team@animalgenome.org)).

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

International Society of Animal Genetics conference will take place in Edinburgh (UK), July 26-30, 2010. For details see <http://www.isag.org.uk/society/conferences.asp>

The 9th World Congress on Genetics Applied to Livestock Production (WCGALP), Aug. 1-6, 2010, Leipzig, Germany. For more details visit <http://www.wcgalp2010.org/>.

The 9th International Veterinary Immunology Symposium, August 16-20, 2010, Tokyo, Japan For more details visit <http://9th-ivis.jtbcom.co.jp>.

Plant and Animal Genome XIX Conference, *January 15-19, 2011, San Diego CA. For details see <http://www.intl-pag.org/>*

Swine in Biomedical Research, July 17-19, 20011, Chicago IL, for details contact larry Schook at [schook@uiuc.edu](mailto:schook@uiuc.edu)

**Items for *Pig Genome Update 104*** can be sent to me by no later than August 15 please.

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