



# Pig Genome Update

## No. 104 September 1, 2010

**Editors note:** My apologies for the late newsletter but we held the presses for the important news below!!

**Build 10 for the *Sus scrofa* reference genome sequence will be released Monday, September 20.** Thanks to the efforts of many people and great collaboration across the world, the sequence and accompanying information will be in a final version and released from The Genome Analysis Centre (TGAC)'s FTP site (<ftp.tgac.bbsrc.ac.uk> ; User: pig10 ; Password: Sscrofa10). This final version will be based on the latest freeze of the physical map. The assembly is the result of the integration of all the sequenced clones and contigs produced by SOAPdenovo and Cortex whole genome shotgun (WGS) assemblies. These WGS assemblies were generated using Illumina reads sequenced at BGI and the Sanger Institute (~40X coverage). As part of the release AGP files with information about the source of every contig will be provided. The WGS contigs will be submitted to EMBL/Genbank, and after that the WGS contigs will be renamed in the AGP with the corresponding accession numbers. This assembly provides an almost complete coverage of the pig genome. Additional details will be presented in the coming weeks. (Kindly provided by Mario Caccamo (TGAC) and the International Swine Genome Sequencing Committee)

**The “marker” paper has recently been published** 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. Please see *BMC Genomics* 2010, **11**:438 (<http://www.biomedcentral.com/1471-2164/11/438>).

**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)]).

**What a summer!! Are you jet lagged and meeting blurry??** Several meetings were held this summer but the big two meetings ISAG and WCGALP came back to back and focused on genomics and included a great deal on the pig. Both were outstanding venues with kind hosts and great programs. Over 630 people attended ISAG where talks focused on everything related to genomics and genetics of your favorite species including the pig. The WCGALP in Leipzig was also a great event with nearly 1,400 people and far ranging talking including bioinformatics, quantitative genetics and genomics and what is next on the horizon. For those that like to plan ahead ISAG has chosen Australia for its meeting 2 years from now and China 4 years from now. WCGALP has chosen Vancouver, BC for its next venue 4 years from now.

**Another big meeting was the EEAP meeting in Crete.** For those that missed out the complete "Book of Abstracts" of the Annual Meeting held in Heraklion, Crete (Greece), is available as PDF file on the EAAP website at: [http://www.eaap.org/Crete/Heraklion\\_2010\\_Abstracts.pdf](http://www.eaap.org/Crete/Heraklion_2010_Abstracts.pdf)

**PAG 2011 Swine Workshop.** The current Chair of the Swine Subcommittee, Chris Tuggle, along with Cathy Ernst and Larry Schook, are planning the 2011 Swine Workshop for the PAG meetings which are held every year in January in San Diego. In 2011, the Swine Workshop will be on January 15. The information for PAG is here: <http://www.intl-pag.org/> and the 2011 Swine workshop is here: <http://www.intl-pag.org/19/19-swine.html>. Their plans are to hold a joint Workshop with the Cattle/Sheep group in the morning and then continue meeting in the afternoon, as a Swine only group, as was done in 2010. This year they will also incorporate the Swine Genome Sequencing Workshop, which will not be meeting separately in 2011 at PAG. To fill this program, they plan to emphasize the exciting developments in the genome sequence and its analysis and annotation. Please contact Chris Tuggle ([cktuggle@iastate.edu](mailto:cktuggle@iastate.edu)) if you have suggestions.

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

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

Gordon Research Conference in Quantitative Genetics & Genomics, Feb. 20-25, 2011, Hotel Galvez, Galveston, TX. See <http://www.grc.org/programs.aspx?year=2011&program=quantgen>

Swine in Biomedical Research, July 17-19, 2011, Chicago IL, for details contact Larry Schook at [schook@uiuc.edu](mailto:schook@uiuc.edu)

**Items for Pig Genome Update 105** can be sent to me by no later than October 15 please.

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Supported by Multi-State Research Funds to the National Research Service Program: NRSP-8. National Animal Genome Research Program, Muquarrab Qureshi, NAGRP Director, NIFA