

Pig Genome Update No. 105 November 1, 2010

New White Paper on swine genome progress and future directions was recently prepared in response to a request by the USDA and other agencies to benchmark progress in livestock genomes. The white paper received inputs from swine genome researchers around the globe including researchers from the International Swine Genome Sequencing Consortium (SGSC). The white paper can be seen at <u>http://www.animalgenome.org/pigs/community/WhitePaper/</u>. Your thoughts are appreciated.

A data repository was set up by the NRSP-8 Bioinformatics Team for the pig genome research community to share data. It can be seen at (<u>http://www.animalgenome.org/repository/pig/</u>). Currently available data sets are the Illumina 60K SNP locations for build 10 contributed by Martien Groenen. Those who wish to share data, please contact the Swine Genome Coordinators Max Rothschild (<u>mfrothsc@iastate.edu</u>), or Bioinformatics Coordinator Jim Reecy (<u>jreecy@iastate.edu</u>), or send an email directly to the NAGRP Bioinformatics Team (<u>bioinfo-team@animalgenome.org</u>).

Build 10 for the Sus scrofa reference genome sequence was recently released 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 TGAC's ftp (FTP site: ftp.tgac.bbsrc.ac.uk ; User: pig10 ; Password: Sscrofa10). This final version was 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 were 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 future. (kindly provided by Mario Caccamo (TGAC) and the International Swine Genome Sequencing Committee).

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] or Alan Archibald [alan.archibald@roslin.ed.ac.uk]).

New publishing format for *Pig Genome Update* **coming soon.** Starting January 1, 2011 the *Pig Genome Update* will be published 4 times a year. Your input and ideas are always welcome. Please contribute.

PAG 2011 Swine Workshop and other PAG happenings. This year at the NRSP-8 Swine Sub-Committee Workshop on January 15, 2011, we will celebrate the "end of the beginning"- the completion of the draft pig genome sequence. We have a great joint session planned with the Cattle/Sheep group in the morning, as this was very successful last year. At this joint session, we will hear from both academia and the industry regarding the nature of the genome (A. Archibald) and the use of it to understand traits of interest (B. Harzilius). In the afternoon, we will have several talks on annotating (J. Loveland) and analyzing the genome (M. Groenen, H.-J. Megens, O. Madsen). We will finish with a talk on GWAS in reproduction and disease (D. Ciobanu). Hope to see you all there! (kindly submitted by Chris Tuggle).

The Sunday the NRSP8 workshop will feature Professor Morris Soller giving the NRSP8 Distinguished Lecture. The PAG plenary talks and other activities at PAG XIX promise to deliver a quality meeting. Now is the time to register. Please note: NRSP-8 coordination funding will be available to partially support travel or registration for committee members or members of their labs. If interested, please contact <u>memfrothsc@iastate.edu</u> prior to December 1.

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

National Swine Improvement Federation Annual Meeting and Genetic Symposium, Kansas City, Missouri, December 2 -3, 2010, for details please email stalder@iastate.edu.

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

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

Swine in Biomedical Research, July 17-19, 2011, Chicago IL, for details contact Larry Schook at schook@uiuc.edu

Items for *Pig Genome Update 106* can be sent to me by no later than December 15 please.

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