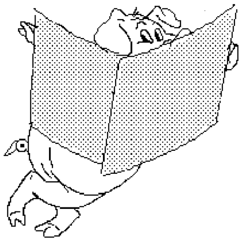

Pig Genome Update

No. 111 April 1, 2012

The Swine Genome Sequencing Consortium continues to make good progress towards the goal of publishing a good quality annotated reference genome sequence for the pig. The genome assembly (Sscrofa10.2) which is the template for the Consortium's analysis and annotation efforts and the basis for the pig genome sequence paper was deposited at NCBI in late August 2011 (ftp://ftp.ncbi.nih.gov/genbank/genomes/Eukaryotes/vertebrates_mammals/Sus_scrofa/Sscrofa10.2/). This is the definitive source for the analyses. The NCBI genome team have released an annotated copy of this draft genome sequence (see ftp://ftp.ncbi.nlm.nih.gov/genomes/Sus_scrofa/GFF/). This annotated pig genome sequence is available in the NCBI Genome Browser. Members of the Consortium have also been working with the Ensembl team. The Ensembl team recently completed their Gene Build for Sscrofa10.2. The Ensembl gene models are based on sequence evidence including alignments with expressed sequences comprising not only cDNA and EST information in the public databases but also more than 250 Gigabases of RNA-seq data generated by members of the Consortium. The preliminary Ensembl analysis is available on the Pre-Ensembl site (http://pre.ensembl.org/Sus_scrofa/Info/Index) and the full annotated genome will be available in the Ensembl genome browser in Ensembl release 67 in a few weeks time (the version currently visible in the Ensembl genome browser is an older assembly – Sscrofa9).

The Swine Genome Sequencing Consortium has released the pig genome sequence data in a timely manner as the project has progressed in accordance with the principles of the Toronto Statement on Pre-publication data sharing (see: Toronto International Data Release Workshop Authors: Prepublication data sharing. Nature 2009, 461:168-70.). Briefly, The Toronto Statement places obligations on the producers of such data sets, including genome sequence data, in respect of prepublication release of the data and confirms the principle that allows the data producers (i.e. the Consortium) to publish the first global analyses of the data set. In 2010 the Consortium published its plans for its first global analyses of the genome sequence and for publication (see: Archibald et al 2010 BMC Genomics 11: 438 http://www.biomedcentral.com/1471-2164/11/438).

The pig genome sequence paper is in draft and a wide range of companion papers are currently also in draft, under review or in press. It is envisaged that the main paper will not only describe the main and pig-specific features of the draft genome sequence and its utility in agricultural and biomedical uses of pigs but also explore how the sequence together with sequences of Wild Boar and other Suids generated by Martien Groenen and colleagues informs our understanding of speciation and domestication.

The Consortium remains open to new groups joining the efforts to characterise and publish the pig genome. Interested scientists / groups should contact either Larry Schook (schook@uillinois.edu) or Alan Archibald (alan.archibald@roslin.ed.ac.uk). (kindly provided by Alan Archibald on behalf of the Swine Genome Sequencing Consortium)

Sunny San Diego and PAG-XX drew a new record crowd of over 2800 attendees. An excellent swine workshop followed by a PRRS meeting made for a great start. There were some super plenary talks presented by Lee Hood, Stephen Quake, Carlos Bustamante and Robert Williams, among others. Next year's PAG-XXI/NRSP-8 will be January 12-16, 2013, once again in San Diego. Note that in March, 2013 there will also be a new 2.5 day conference, PAG-ASIA, in Singapore (see www.intl-pag.org).

NRSP-8 rewrite is beginning soon. The NRSP-8 is scheduled to end in September of 2013, so if it is to continue, it must be revised and resubmitted for review by NIFA and the Experiment Stations again this year. The approximate deadline is this September for submitting the revised project. New draft objectives for NRSP-8 will be circulated shortly. All members of NRSP-8 may receive requests to contribute to assembling past accomplishments and publications and for input into the new proposals. Please respond promptly, as we're on a tight deadline and this will be a huge help to the writing teams. (kindly provided by J. Dodgson)

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

33rd International Society for Animal Genetics Conference in Cairns, Australia on July.15-20, 2012. For details see http://www.isag.us/2012/

International Conference of Quantitative Genetics in Edinburgh, Scotland on June 17-22, 2012. For details please see http://www.icqg2012.org.uk/

American Society of Animal Science (ASAS), Dairy Science (ADSA), and Canadian Society of Animal Science (CSA) Joint Annual Meeting in Phoenix, AZ on July 15 – 19, 2012. For details see http://www.jtmtg.org/2012/

PAG-XXI/NRSP-8 will be January 12-16, 2013, for details see http://www.intlpag.org/web/

Gordon Research Conferences: Quantitative Genetics & Genomics, Genetics of Complex Disease, February 17-22, 2013, Galveston, TX for details see http://www.grc.org/programs.aspx?year=2013&program=quantgen

PAG Asia to be held in Singapore, March 2013. For details see http://www.intlpag.org/web

Items for *Pig Genome Update 112* can be sent to me by no later than June 15 please.

Max F. Rothschild
U.S. Pig Genome Coordinator
2255 Kildee Hall
Department of Animal Science
Iowa State University
Ames, Iowa 50011
Phone: 515-294-6202
Fax: 515-294-2401
mfrothsc@iastate.edu

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