Pig genome sequence ready for analysis. The Swine Genome Sequencing Consortium (SGSC, http://piggenome.org) is pleased to announce that the sequence data and assembly on which the draft pig genome sequence publications will be based are now available for analysis. This draft pig genome sequence (Sscrofa10.2) has been released by the International Swine Genome Sequencing Consortium under the terms of the Toronto Statement (Nature 2009, 461: 168). Sscrofa10.2 replaces the previous assembly, Sscrofa10, which had assembly errors. The International Swine Genome Sequencing Consortium is coordinating genome-wide analyses, as described in BMC Genomics 2010 11:438. Funders of the pig genome project are acknowledged in this marker paper. The sequence data, from which this assembly was constructed, comprise hierarchical shotgun sequence data providing 4-6x genome coverage from BAC clones representing a minimal tile path across the genome plus >30x genome coverage in whole genome shotgun sequence (WGS) Illumina reads. All the WGS data and most of the BAC data are derived from blood cells of a single Duroc female pig (Duroc 2-14; CHORI-242 BAC library) but also includes some data from other BAC libraries from other breeds.

The Consortium is grateful to Mario Caccamo and his colleagues at The Genome Analysis Centre, Norwich, UK for their work in finalizing the assembly. We are also grateful for the efforts of Martien Groenen and colleagues, Wageningen and Bertrand Servin and colleagues, INRA, Toulouse for their contributions to checking the quality of the multiple iterations of the assembly over the summer. The sequence data and assembly have been posted on the NCBI ftp site at: ftp://ftp.ncbi.nih.gov/genbank/genomes/Eukaryotes/vertebrates_mammals/Sus_scrofa/Sscrofa10.2/ All those who wish to analyze or use the sequence data are strongly encouraged to access the data from this NCBI ftp site in order to ensure that everyone is working with an identical primary dataset. Annotation of this draft pig genome sequence (Sscrofa10.2) has been initiated by the Ensembl team and the genome team at NCBI will also start their annotation effort soon. The annotation currently visible in the Ensembl and NCBI genome browsers should be used with caution – Ensembl is currently displaying the 2009 assembly (Sscrofa9) and the information displayed in the NCBI Map Viewer is based on the flawed assembly 10. The Consortium is holding a series of regular Skype conference calls to discuss and coordinate the analysis and annotation activities and to develop the main and companion papers describing the genome sequence and its use. We are aiming to produce substantive draft manuscripts before the end of the year. If you wish to join these discussions then please contact Larry Schook: schook@illinois.edu or Alan Archibald: alan.archibald@roslin.ed.ac.uk

Congratulations to the Swine Genome Sequencing Consortium. The mid-continent region of the Federal Laboratory Consortium recently present its Excellence in Technology Transfer Award to Swine Genome Sequencing Consortium that developed the Porcine SNP Beadchip, a tool marketed as "a cost-effective and high-quality solution for interrogating genetic variation in multiple porcine breeds." Illumina Inc., headquartered in San Diego, licensed the technology and sells it as part of their genetic analysis kits. Gary Rohrer accepted the award on behalf of the team

PAG 2012 registration is now open. The website has been redesigned and can be found at http://www.intlpag.org/web/ . This year another great meeting is planned. The swine workshop will be Saturday January 14 and chaired by Daniel Ciobanu. Students wishing to apply for travel funding should go to http://www.intlpag.org/web/index.php/attend/travel-grants

Genome Canada grant to study "Maintaining healthy and more profitable pig production." Under a new grant funded by Genome Canada, researchers in Canada, the USA and the UK, led by Graham Plastow, Univ. Alberta, John Harding, Univ. Saskatchewan, and Bob Kemp, PigGen Canada, will apply genomics to help reduce the impact of the two most common diseases in commercial pig production - Porcine Circovirus Associated Disease (PCVAD) and Porcine Respiratory and Reproductive Syndrome (PRRS). Scientists will study mechanisms that make pigs genetically less susceptible to these diseases, identify new diagnostic tools for breeders and expand the understanding of disease control mechanisms. This should lead to new strategies for disease control in addition to new drugs, improved vaccines, and a safer pork product by reducing the use of antibiotics. Researchers will also study public perceptions about the use of genomic technologies to prevent disease in pork production.

What's new on the NAGRP animal genome web site (#3 2011).
1) Announcing Release 15 of the Animal QTLdb with 14,239 total QTL in the database: (Break down: Cattle QTL: 4,802; Chicken QTL: 2,451; Pig QTL: 6,347; Sheep QTL: 639. New QTL added to the database since the Release 14: Cattle: 120; Pig: 3; Sheep: 185.http://www.animalgenome.org/QTLdb/).
2) Another change is that QTL data submission to the Animal QTLdb is now required by several journals prior to the publication of your paper. We encourage you to submit your QTL data directly to the database through the curator web portal (http://www.animalgenome.org/QTLdb/app.html) to speed up the review of your paper.
3) Good news for AnGenMap listserv users - the File Share Platform can now be used as an alternative to share non-plain-text files that are normally not allowed as email attachments on the AnGenMap listserv (e.g. .PDF, .doc, .xls, .ppt, .xlm, etc.) http://www.animalgenome.org/community/angenmap/faq.php#11
4) An experimental pig genome database is under development. A number of new functions and utilities are under development (http://www.animalgenome.org/pig/genome/db/). If you have any new ideas for the pig genome database to better serve your purpose, please feel free to send your suggestions, note "pig genome database" in the "subject:" line, to bioinfo-team@animalgenome.org
5) A local copy of the Biomart has been installed on AnimalGenome.ORG to serve the livestock research community. Currently, queries against the pig, cattle, chicken and horse genomes are supported. More species will be added upon the availability of the data. See: http://www.animalgenome.org:8181/
6) The Blast Extension Analysis Program (BEAP) has been modified to assist users for easier setup. See the updated manual for details. (http://www.animalgenome.org/tools/beap/)
7) The NAGRP data repository has been expanded to host supplementary data for publications. If you are looking for an online host for additional data to your publication, feel free to contact us at bioinfo-team@animalgenome.org (http://www.animalgenome.org/repository/pub/)
8) The new pig genome assembly has been actively improved during the summer. The most recent build 10.2 has been submitted to NCBI and is available for blast analysis on the NAGRP blast server (http://www.animalgenome.org/blast/)

As always, suggestions from the livestock community are always welcome. We are here to serve to community. You can either call Jim Reecy at +1-515-294-9269 or send them a note at bioinfo-team@animalgenome.org.

NIFA is pleased to announce that Dr. Lakshmi Matukumalli has accepted a position of National Program Leader of Animal Breeding, Genetics and Genomics within the Institute of Food Production and Sustainability, Division of Animal Systems. Dr. Matukumalli has held positions at George Mason University and a joint position with USDA/ARS before joining the NIFA family. He was a key member of the bovine genome group at ARS and made significant contributions in analyzing the bovine genome sequence. Dr.Matukumalli can be reached at lmatukumalli@nifa.usda.gov or by phone at 202-401-1766.

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

4th International Symposium on Animal Functional Genomics, October 10-12, 2011. Dublin, Ireland. See http://www.isafg2011.org.

The International Conference on Feed Efficiency in Swine. Hilton Hotel/Qwest Center. Omaha, Neb. November 8-9 Cosponsored by Iowa State University and Kansas State University. See more information, including registration and lodging details on the event website http://www.ans.iastate.edu/ICFES/

National Swine Improvement Federation Annual Meeting, December 1-2, 2011, Lincoln, NE, for information contact Jim Schneider at jim.schneider@ars.usda.gov

Plant & Animal Genome Conference, PAG XX, Jan. 14-18, 2012, Town & Country Hotel, San Diego, CA. Information available at http://www.intl-pag.org/ .

Human Genome Meeting (HGM2012), March 11-14, 2012, Sydney, Australia. See http://www.hgm2012.org

Items for *Pig Genome Update 110* can be sent to me by no later than December 20 please.

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