



Pig Genome Update

No. 113 October 1, 2012

Funds available for genome community. Funds are available from now until August 1, 2013 for shared genotyping and phenotyping activities in the pig community. The best types of projects are those who have not received funds in the past and who are between two or more stations for genotyping with the SNP chips (60K or new 10K) or for collection of specialized phenotypes. Please contact the Swine Genome Coordinator to discuss your requests.

The Animal QTLdb included 633 new pig QTL in its recent #18 release, making the total number of pig QTL in the database 7,451. With this release, the NAGRP bioinformatics team has done a number of improvements to the Animal QTLdb, which includes a procedure to withdraw obsolete QTL data from NCBI, a new experimental search function for animal breeds associated with QTLs, a new trait hierarchy navigator, and improved QTLdb curator/editor tools. Users are encouraged to register an account to enter new QTL data. Find out more from <http://www.animalgenome.org/QTLdb>. In addition, the pig genome build 10.2 annotations are ported to the BioMart (<http://www.animalgenome.org:8181/>) for customized downloads; and pig oligoArray elements are BLAST mapped to pig genome build 10.2, available for download from http://www.animalgenome.org/repository/pig/Genome_build_10.2_mappings (kindly provided by Zhiliang Hu, NAGRP bioinformatics team).

A new custom low density chip is now available for imputation work. GeneSeek, a supplier of genotyping services has announced the GeneSeek **Genomic Profiler for Porcine LD** (GGP-Porcine). This custom low density BeadChip utilizes Illumina Infinium chemistry and features approximately 8,500 SNPs for high density chip imputation. The GGP – Porcine BeadChip also includes gene markers from several well-known reproduction, growth, feed efficiency, and meat quality traits at no added expense. These include the following markers: EPOR, MC4R, HMGA, CCKAR, PRKAG, and CAST. Details on these markers will be available from GeneSeek. In addition, researchers can request additional markers including the HAL, Rendement Napole (RN), Resistance marker to *E.coli* (F4 ab/ac), a SNP parentage panel, and the Estrogen Receptor (ESR) which impacts litter size in Large White or Yorkshire by paying additional royalty fees for these optional licensed tests. The chip was developed as a result of a collaborative effort involving leading academic, USDA, and GeneSeek researchers. The price (per sample) will be \$39 per sample for a DNA or \$42 for tissue submission.

The PAG XXI and NRSP8 Swine Genome meetings are around the corner. Online registration is now open for PAG-XXI/NRSP8 at <http://www.intlpag.org>. The meeting will be January 12-16, 2013, in San Diego. Speakers include Eric Perakslis (US FDA), Michael Eisen (UC Berkeley), Daniel Chourrout (Sars Centre, Norway), Greger Larson (Durham U.), Steve Jacobsen (UCLA), Gonçalo Abecasis (U. of Michigan), Michele Morgante (U. of Udine, Italy) and Gary Muehlbauer (U. of Minnesota), see the program at <http://www.intlpag.org>. Students can apply for the Jorgensen Travel Award (\$1000) at <http://www.intlpag.org/2013/index.php/travelhotel/travel-grants>. The poster abstract deadline and the deadline for reduced registration fees is Nov. 1, 2012.

USDA National Institute of Food and Agriculture (NIFA) has delayed the estimated release date for the RFAs for the 2013 AFRI Foundational Grants, Fellowship Grants and most challenge area grants (including Food Security) to approximately October 1, 2012. Go to <http://www.nifa.usda.gov/funding/rfas/afri.html> to get updated information.

The Federal government will likely operate on a Continuing Resolution that will hold FY 2013 funding close to that for FY 2012 until at least next year when a new Congress takes office. The effects on USDA, NIFA and AFRI aren't yet clear. It's also unclear if and when Congress will pass the Agriculture Reform, Food, and Jobs Act (2012 Farm Bill) which would reauthorize NIFA and AFRI through 2017 (at about current funding levels). The Senate Committee version also includes a provision to establish a non-profit, non-governmental Foundation for Food and Agriculture Research (FFAR) and provides FFAR with \$100M in funding that must be matched equally with non-Federal funds. The Farm Bill is currently stuck in the House. Finally, OMB recently released its Sequestration Report that estimates additional 8.2% cuts to USDA NIFA and ARS research activities if budget sequestration were to occur according to last year's budget agreement. (Kindly provided by Jerry Dodgson).

A big thanks and best wishes go out to Dr. Muquarrab Qureshi on his promotion to the position of Assistant Director, Institute of Youth, Family, and Community in the National Institute of Food and Agriculture (NIFA) as of June 3. Muquarrab previously served as Director of the Division of Animal Systems and the National Animal Genome Research Program (NAGRP). He's provided excellent leadership to the NAGRP as Director and has been a good friend to all of animal genomics. We wish him the best of luck as he takes on this challenging new position. Leadership of NAGRP has transferred to Dr. Lakshmi Matukumalli who was appointed as National Program Leader of Animal Breeding, Genetics and Genomics in NIFA last year.

The swine genome coordinator is always glad to hear from NRSP-8 members and other readers about ways that the coordination effort can be improved or provide resources that are needed. Also, if you have items of general interest to the swine genetics and genomics communities that can be include in this newsletter please share.

The sequencing and assemblies of genomes are often international collaborative efforts that conclude upon publication of a reference sequence. In order to ensure the continued utility of these assemblies, however, it is crucial that such projects plan for a means to update reference genomes with new data as it becomes available. As an assembly matures, this will likely require focused curatorial efforts rather than whole genome reassembly. The Genome Reference Consortium (GRC) was organized at the completion of the human genome sequencing project to perform this curation and oversee future updates to the reference assembly. GRC experimental work is performed at the Genome Institute at Washington University, St. Louis (TGI) and The Wellcome Trust Sanger Institute (WTSI). The National Center for Biotechnology Information (NCBI), the WTSI and the European Bioinformatics Institute (EBI) provide the database support and software tools to support this effort. Funding for the GRC comes from the operating budgets of its members. Since its inception, the GRC has expanded its role to address the maintenance and modernization of the mouse and zebrafish reference assemblies. In addition to publicly released updates to both the human and mouse reference genomes, the GRC has also developed and published a new assembly model that better allows for the representation of genome variation and the timely release of inter-build sequence updates in the form of assembly patches (PLOS Biol. 2011 Jul;9(7):e1001091).

Several of the GRC's curatorial software tools and database support may be extensible to other groups working to update assemblies. While the human, mouse and zebrafish reference genomes are all clone-based assemblies, these tools can be adapted to any assembly for which there are tiling path and AGP files. The GRC uses a customizable commercial software package to manage curation of discreet genome regions, while GRC-developed software is used to manage tiling path updates, produce and store alignments between assembly components, provide quality assessments and generate AGP files for loading of an assembly to NCBI's Assembly database. GRC quality assessments include file validation, component alignment statistics, contig building reports and monitoring of the effects of assembly updates on annotation. In addition, GRC software and tools can be used to provide external evidence in support of component alignments, to evaluate proposed assembly changes prior to database updates and to produce test assemblies in advance of public releases. Groups interested in learning more about GRC tools and their applicability to other assemblies are encouraged to contact the GRC via the "Contact Us" link on their website: <http://www.genomereference.org>. (kindly provided by Valerie Schneider NCBI).

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

Innovate 2012: Funding Livestock Research and Outreach in the Future. Oct. 3 to 5, 2012 Shell Beach, CA. For information: <http://asas.org/meetings/innovate-2012>

International PRRS Symposium, held in conjunction with the National Swine Improvement Federation Annual Meeting, Nov. 29-30, 2012, Marriott Hotel Kansas City Downtown, Kansas City, MO; contact: <http://www.prrssymposium.org>

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

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 17-19, 2013. For details see <http://intlpagasia.org/>

Human Genome Meeting/International Congress of Genetics: Genetics and Genomics of Global Health and Sustainability, April 13-18, 2013, Suntec, Singapore. Details at <http://www.hgm2013-icg.org/>

Items for *Pig Genome Update 114* can be sent to me by no later than December 15 please.

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