

# Pig Genome Update #126

Oct 11, 2018

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## 1. Recent meetings summary

### a. Biology of Genomes 2018 (Cold Spring Harbor Laboratory)

The use of CRISPR technology to edit genomes was widespread across many talks at this meeting. Jef Boeke (NY Genome Center) discussed his interesting work modifying large chunks of the yeast genome in synthetic biology approaches, even to the point of creating whole “neochromosomes”. Molly Gasperini (U. Washington) discussed high multiplexing of guide RNAs to modify more than 1,000 sites in the human genome to test function of predicted enhancers. High-dimensional, CRISPR-based genome editing evaluation of 16,000+ SNPs in yeast was discussed by Eilon Sharon (Stanford U.). Such techniques, impressive in their scope, may be of interest in livestock functional genomics to test SNPs associated with traits, especially those that can be scored in vitro.

Elaine Ostrander (NHGRI) discussed a strategic planning process for NHGRI called Genomics 2020 (<https://www.genome.gov/10001307/longrange-planning/>). She asked for suggestions on how to structure their NIH grant processes in the future. As the USDA is now working closely with NIH (i.e., on a Comparative Genomics joint call, see below #3): it could be useful for our community to engage with this discussion. Email this group at [genomics2020@mail.nih.gov](mailto:genomics2020@mail.nih.gov) with your suggestions!

Arang Rhie described the Vertebrate Genomes Project (<https://vertebrategenomesproject.org/>), which had a full day Workshop at PAG 2018. The VGP intends to exploit new technologies to assemble the genome sequence of 10,000 or more vertebrate species (see more in the report on Livestock Genomics meeting below). Rhie discussed a project using a “trio-binning” approach with parental short-reads and offspring long-reads to assemble parental haplotypes using data from a Brahman cross with Angus (<https://www.biorxiv.org/content/early/2018/02/26/271486>). This approach could be useful in pigs as well, potentially to establish and use breed haplotypes.

## **b. Genome Writer's Guild meeting 2018**

This interesting small meeting focused on all aspects of genome editing (GE), technologies, uses and outcomes in agricultural (including pigs and cattle) and biomedicine, and the societal implications of GE. Several talks focused on engaging the public, to explain and discuss the science and implications of GE, including presentations by Johnny Kung (Harvard Medical School) and Charlie Arnot (Center for Food Integrity). Tammy Lee (Recombinetics) described the process ahead for gaining approval for GE pigs, including “castration-free” swine. Jeff Essner (Iowa State U.) told the audience of new GE strategies to modify pig fibroblasts more efficiently, in collaboration with Recombinetics.

## **c. Livestock Genomics 2018**

This meeting is held every two years in the UK, organized by the European Molecular Biology Laboratory-European Bioinformatics Institute (EMBL-EBI). The meeting attracts European leaders in livestock genomics as well as many speakers from around the globe. It is a smaller meeting with most attendees providing a talk and/or a poster, thus providing excellent opportunities to gain knowledge in livestock genomics thought leaders. Twenty-two talks were presented at the meeting from 20-21 September 2018. Six speakers and several poster presenters reported pig genome data, and seven additional speakers covered results broader in scope but of relevance to pig genomics.

Two speakers discussed phylogeny of species in the suid ancestry (whole genome sequence of pygmy hog, Langqing Li (Wageningen U.); and African genome assemblies, (Lel Eory, Roslin I.)). Transcriptome-level analyses was reported by the other four speakers. Chris Tuggle (Iowa State U.) described the use of PacBio Isoseq data from nine tissues to improve the annotation of the pig genome. Stefan Seeman (U. Copenhagen) described a comparative study of X chromosome lncRNA between pig, human, and mouse. Jun-mo Kim (Chung-Ang U.) used network analysis to elucidate the gene expression changes during the estrous cycle in reproductive tissues, and Martina Zappaterra (U. of Bologna) looked at differential expression in muscles from pigs differing in intracellular fat content.

There were also talks on Ensembl tools relevant to livestock by EMBL-EBI staff; including tools for analyzing GWAS associated variants (Daniel Zerbino) and livestock species annotation (Kostas Billis), and an update on the Data Coordinating Centre and FAANG metadata standards (Peter Harrison). Paul Flicek (EMBL-EBI) concluded the meeting with an interesting look on the status and aspirations of the Vertebrate Genome Project. He introduced the metric of x.y.z score for each assembly, and described the current stage of testing technologies to get to the goal of a \$10,000 assembly per species. 260 different species 50 million years apart in evolution have been selected to represent vertebrates at the ordinal level; 15 VGP genomes have been released thus far. Flicek described the enormous efforts in coordination of data, metadata quality control and annotation this inspiring project will demand, simply to make the data useful and accessible.

## **2. Update on USDA-NIFA-AFRI and new functional genomics project FAANG activities**

As described in prior PG Updates, the FAANG Consortium has been organized and held meetings and conference calls regularly. Some developments are described below; for further

information please see the FAANG website ([www.faang.org](http://www.faang.org)), which is hosted by [www.animalgenome.org](http://www.animalgenome.org) through the NRSP-8 Bioinformatics Coordination team. A new webpage has been developed to provide information on new funding opportunities for FAANG related proposals (see also below; available on FAANG website, member's area page).

a) Three groups have been awarded substantial funding (totaling \$6M) from the USDA-NIFA-AFRI to create resources for functional analysis of animal genomes (see: <https://www.news.iastate.edu/news/2018/06/13/swinegenomicscoe>). These include a group headed by Pablo Ross (UC-Davis) focused on cattle, and a group headed by Yvonne Dreschler (Western University of Health Sciences) focused on chicken. The third group is headed by Chris Tuggle, with a focus on pigs, and includes ISU collaborators James Reecy and James Koltes, as well as USDA-ARS-MARC (Dan Nonneman, Tim Smith), Michigan State U (Cathy Ernst), UC-Davis (Huaijun Zhou, Pablo Ross), and USDA-ARS-NADC (Crystal Loving). This group was awarded \$2.5 M over 4 years to develop data on the functional components of the pig genome in adult, fetal and immune cells and tissues relevant to economically important traits. A number of techniques will be used to generate RNA expression and epigenetics data, and all data will be deposited in public databases as soon as it is quality-controlled (prior to publication). The project earned the distinction of being named a USDA "Center of Excellence" for pig genomics, as well.

b) Lakshmi Matukumalli announced earlier this year that NIFA is partnering with NIH to request proposals to work on comparative genomics. See <https://nifa.usda.gov/funding-opportunity/comparative-genomics-research-program> for details; there are several opportunities for funding in the next year; however, the funding available may be fully committed before all application deadlines are reached. Questions can be directed to the contacts on the webpage.

### **3. Reminder on ISAFG 2018, PAG 2019 *\*\*Short deadline\*\**, Midwest ASAS-ADSA 2019, ASAS 2019 meeting registration deadlines.**

The 7<sup>th</sup> International Symposium on Animal Functional Genomics is being held next month in Adelaide, Australia, 12-15 November 2018. The program is now available at <http://www.isafg2018.com/program.html>, and looks to be a great meeting on the functions of genomes for a number of animal species. On-line registration is still available until the end of October 2018.

A reminder that the 27th Plant and Animal Genome Meeting (<http://www.intlpag.org/>), will be held January 11-16, 2019 in San Diego CA (as usual, location is the Town and Country Hotel). This meeting will include the Swine Genome Subcommittee Workshop on January 12, being organized this year by the 2019 Chair, Christian Maltecca (North Carolina). There will also be a FAANG Workshop held on January 11, 1-6 PM). The PAG27 early registration deadline is November 2, 2018 (<http://www.intlpag.org/2019/attend/registration-and-fees>), and the poster/abstract submission deadline is October 26, 2018 (see: <http://www.intlpag.org/2019/abstracts/poster-submission>). *However, stay tuned to an expected announcement in mid-late October for an extension of the Abstract deadline.*

The Midwest Section meeting of the ASAS and ADSA will be held March 11-13, 2019 in Omaha, NE. Registration for the Midwest ASAS-ADSA meeting will open October 2018 (<https://netforum.avectra.com/eweb/shopping/shopping.aspx?logoff=yes&site=asas&cart=0&sho>

[psearch=%25midwest&shopsearchCat=Event](#)). Midwest ASAS-ADSA 2019 abstracts are due by 3:00 pm on November 8, 2018 (<https://www.asas.org/taking-stock/blog-post/taking-stock/2018/09/16/2019-midwestern-section-call-for-abstracts-and-early-registration> ).

Check out: <https://www.animalgenome.org/pig/community/meetings> for meeting information updates.

#### **4. Neil A. Jorgenson Travel Award Opportunity **\*\*Short deadline\*\*****

A reminder that the NRSP-8 Swine Genome Coordinator can fund travel to the PAG meeting for a student who presents their swine-genome related research work there. **If you or your graduate student is interested in applying for the Neil Jorgensen Travel award, please send Chris Tuggle and Cathy Ernst your application as soon as possible** (see: <http://www.intlpag.org/2019/attend/travel-grants> , scroll down to Jorgenson Awards). **Applications will be accepted until October 25, 2018, not October 12 as stated on the PAG 27 website.**

#### **5. Upcoming additional meetings information**

Besides the meetings discussed above, there are many other meetings of relevance to the genomics community over the next 6-12 months, see: <http://www.animalgenome.org/pig/community/meetings>). As mentioned above, a reminder that the ISAG community will hold their next meeting in July 2019 at the University of Lleida in Spain. See <https://www.isag.us/2019/> for details. At time of writing, registration and abstract submission details were not yet available.

#### **6. Update on projects supported by NRSP-8 funds - We want to hear from you!**

Update on PacBio Iseq Data analysis: As described above, Chris Tuggle presented the analysis of nine tissues of Iso-seq data at the Livestock Genome meeting. There are plans to present updated results at the ISAFG meeting in November 2019. Please email Chris Tuggle ([cktuggle@iastate.edu](mailto:cktuggle@iastate.edu)), Dan Nonneman ([Dan.Nonneman@ARS.USDA.GOV](mailto:Dan.Nonneman@ARS.USDA.GOV)), or Tim Smith ([Tim.Smith@ARS.USDA.GOV](mailto:Tim.Smith@ARS.USDA.GOV)) with any questions.

The swine genome coordinators are 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. If you have items of general interest to the swine genetics and genomics communities that can be included in this newsletter please share. Our issues are now planned for February and October each year. Any contribution should be sent to the Coordinators one week prior to these dates.

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#### *Joint Coordinators:*

Christopher Tuggle  
2255 Kildee Hall  
Department of Animal Science  
Iowa State University  
Ames, IA 50011

Catherine Ernst  
Anthony Hall, 474 S. Shaw Lane, Room 1205  
Department of Animal Science  
Michigan State University  
East Lansing, MI 48824

Phone: 515-294-4252  
Fax: 515-294-2401

Phone: 517-432-1941  
Fax: 517-353-1699

<http://www.animalgenome.org/pig/>