

Pig Genome Update #124

Oct 1, 2016

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1. Recent meetings summary

a. JAM 2016

The Joint Annual Meeting of the American Society of Animal Science, American Dairy Science Association and Canadian Society of Animal Science was held July 19-23, 2016 in Salt Lake City, UT (<https://asas.org/meetings/jam-2016/home>). Breeding and Genetics sessions were coordinated by topic facilitating interaction among scientists working with different species. Session topics included Genomic Evaluation – Methods, Genomic Evaluation – Applications, Selection for Improved Efficiency, Selection for Health and Fertility, and Novel Traits and Selection Objectives, all of which included presentations by pig geneticists. A highlight of the Breeding and Genetics program was presentations on genetics of heat stress in pigs, which were presented in the novel traits session and also in the Breeding and Genetics Symposium – Resilience of Livestock to Changing Environments.

b. Functional Annotation of Animal Genomes Symposium 2016

The FAANG Symposium was held on the day overlapping the two JAM and ISAG meetings, July 23, 2016. Approximately 450 scientists from both the JAM and ISAG communities attended this full-day Symposium. Seven world-class speakers provided up-to-the-date information on the use of functional annotation to explore human and model species genomes, early results on the use of such data for understanding results from Genome-wide Association studies, as well as new methods to assemble animal genomes. A description of funded FAANG-associated projects was provided, as well as a summary of progress made by the FAANG subcommittees. For example, the Animals, Samples, and Assays committee has finalized protocols for sample collection as well as several of the core assays. In addition, pipelines for data analysis have been proposed by the Bioinformatics and Data Analysis committee. Finally,

the group discussed plans for the PAG 2017 and ISAG 2017 meetings. For the latter, the group agreed to suggest to ISAG that FAANG speakers be incorporated into three Workshops, Comparative and Functional Genomics, Epigenetics, and especially into a renamed Genome Sequencing and Annotation Workshop).

c. ISAG 2016

The International Society of Animal Genomics meeting was held in Salt Lake City, UT July 23-27, 2016. The local organizing committee, chaired by Clare Gill of Texas A&M, did a great job and the venue and entertainment was terrific. Four plenary sessions and many workshops were held. Workshops of relevance to swine genomics included: Genetically Engineered Livestock; Genetics of Immune Response and Disease Resistance; Comparative and Functional Genomics; Domestic Animal Epigenetics; and the Pig Genetics and Genomics Workshop. The latter included 9 talks covering genotype-phenotype association, the porcine gut microbiome, the pig metabolome, regulatory pathway analyses, as well as genome editing to create porcine models of disease relevant to biomedicine.

The next meeting of ISAG will be in Dublin 16-21 July 2017. At the ISAG business meeting, presentations for several possible 2019 locations were also made, including: Toronto, Canada; Llieda Spain; and Piacenza, Italy.

d. Livestock Genomics

This meeting is held every two years in Cambridge, UK, organized by the European Molecular Biology Laboratory-European Bioinformatics Institute. The meeting attracts European leaders in livestock genomics as well as some 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. Thirty-five talks were presented at the meeting from 14-16 September 2016. Several species-agnostic bioinformatic tool presentations, and two roundtable discussions on data genotype to phenotype and handling multiple genome assemblies were also held.

Seven talks and several posters reported pig genome data. Chris Tuggle presented a talk on the porcine blood transcriptome, including the use of PacBio data from other tissues to validate these transcript assemblies, which was supported by NRSP-8 (see below). Other swine-related talks included a presentation by Elisabetta Giuffra on the FAANG projects in the pig and other species, and Amanda Warr on the current status of the new PacBio-based Genome Assembly of TJ Tabasco, which was the pig whose genome sequence was reported in 2012. Importantly, there was a call for anyone to submit data that could be of use in annotation of this new genome assembly (such as RNAseq data) to submit as soon as possible to NCBI or ENA. The intent is to maximize such information for the genome assembly annotation, which will be done by Ensembl over several months; this will start soon. Several talks on linking porcine genotypes to phenotypes were also presented by scientists from U. Llieda and U. Bologna. The pdf of the meeting program, which includes the Abstracts of speakers and posters, is available here: <http://www.ebi.ac.uk/~streeter/livestock-2016/meeting-booklet.pdf>. Slides of talks should be available soon. Contact Ian Streeter (streeter@ebi.ac.uk) for more information.

e. Large Animal Genetic Engineering 2016

This new meeting was held in Bethesda, MD September 18-20, 2016, and was organized by Utah State. Many very interesting projects on the use of pigs as biomedical models were presented, including many individual gene knockouts but also transgene insertions including some projects with up to 6 transgenes at one time for xenotransplantation. Controversy over the timelines and throughput of FDA approvals of genetically modified/genome-edited organisms for food consumption were a major topic, which many felt was an impediment to using this promising new technology in agricultural production. However, there was a clearly high level of enthusiasm for CRISPR approaches to make dramatically rapid advances to understand porcine physiological mechanisms. Plans were discussed to have a repeat meeting in September of 2018 in Park City, Utah.

2. Update on new functional genomics project FAANG activities (beyond the Special Symposium on FAANG held during JAM-ISAG).

As described in prior PG Updates, the FAANG Consortium has been organized and held meetings. The following text is a summary of the activities of FAANG since the last PG Update; for further information please see the FAANG website (www.faang.org).

a) **The meeting report of the GO-FAANG Workshop held in October 2015 was accepted for publication.** An e-copy of this paper by Tuggle et al. is available at: <http://www.ncbi.nlm.nih.gov/pubmed/27453069>.

b) Responding to FAANG member requests, a new webpage has been developed to provide information on new funding opportunities for FAANG related proposals (available on FAANG website, member's area page).

3. Update on USDA-NIFA-AFRI

In July 2016, Dr. Lakshmi Matukumalli provided guidance to several members of the genome community on the following. He indicated that AFRI Animal Genome:Tools and Resources panel would like to see 4-6 proposals per species submitted for FAANG-related projects, which would be scientifically independent but would be complementary to each other and linked to the overall goals of FAANG. The genome Coordinators were notified of this suggestion and each group is handling any group discussion or coordination. Chris Tuggle sent out a note to all members of the Swine Sub-committee and a conference call is being scheduled with those interested. This will be an important topic for the Subcommittee to discuss at the PAG 2017 meeting.

Dr. Matukumalli further indicated that the AFRI request for applications for the yearly genome-oriented opportunities (Tools and Resources) is anticipated to be released approximately early February, which is earlier than last year. However, the intent by AFRI is to provide about 3 months between the RFA release and the deadlines. Be sure to read and consider applying for these opportunities! If a letter of support, including matching funds from NRSP-8, would be useful, please let the Co-coordinators know early in the process.

4. Reminder on PAG 2017, Midwest ASAS-ADSA 2017, ASAS-CSAS 2017, ADSA 2017 meeting registration deadlines.

A reminder that the 25th Plant and Animal Genome Meeting (<http://www.intlpag.org/>), will be held January 14-18, 2017 in San Diego CA (as usual, location is the Town and Country Hotel). This meeting will include the Swine Genome Subcommittee Workshop on January 14. The PAG25 early registration deadline is October 31, 2016 (see: <http://www.intlpag.org/2017/attend/registration-and-fees>), and the abstract submission deadline is October 28, 2016 (see: <http://www.intlpag.org/2017/abstracts/poster-submission>).

The Midwest Section meeting of the ASAS and ADSA will be held March 13-15, 2017 in Omaha, NE. Registration for the Midwest ASAS-ADSA meeting will open October 2016; (watch here for further details:

<https://www.asas.org/membership-services/asas-sections/midwest-section/meetings>.) Midwest ASAS-ADSA 2017 abstracts are due by October 26, 2016. See <https://asas.confex.com/asas/mw17/cfp.cgi> for more details.

Information on ASAS-CSAS 2017, to be held July 8-12, 2017 in Baltimore, MD is available here: <https://asas.org/meetings/annual-2017/home> Lowest cost registration deadline is February 9, 2017.

Information on ADSA 2017, to be held July 25-28 in Pittsburgh, PA is available here: <http://www.adsa.org/2017/>

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 2017, not in 2018, to avoid the World Congress to be held in 2018. ISAG will then go back to biannual year meetings in the future; continuing in 2019. The location for the 2019 meeting is being discussed.

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

Update on FAANG project: Dr. H. Zhou presented a poster summarizing the FAANG project at the ISAG meeting. Please email Dr. Zhou at hzhou@ucdavis.edu with any questions.

Update on High Density Genotyping: Two 96 sample assays have been processed on the Affymetrix Axiom™ PigHD_V1 Array including samples representative of the Yorkshire, Duroc, Landrace and Hampshire breeds in the US, and the genotype data is currently being evaluated. Please contact Cathy Ernst (ernstc@msu.edu) or Jack Dekkers (jdekkers@iastate.edu) with any questions.

Update on PacBio Iseq Data analysis: Illumina and PacBio Iseq data has been received from Dr. Tim Smith for eight tissues. Error correction of the latter has been completed for 4 tissues using the Illumina data. Additional tissues and cell samples to be analyzed in the same way are

being planned. Please email Dr. Chris Tuggle (cktuggle@iastate.edu) or Dr. Tim Smith (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 1 and October 1 each year. Any contribution should be sent to the Coordinators one week prior to these dates.

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