Pig Genome Update #123

April 1, 2016

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1. Recent meetings summary

a. Gathering On FAANG Workshop (GO-FAANG)

The FAANG (Functional Annotation of ANimal Genomes) Consortium held the GO-FAANG Workshop in Washington, DC on October 7-8, 2015. The Workshop gathered together from around the world a group of 100-plus genome scientists, administrators, representatives of funding agencies and commodity groups to discuss the latest advancements of the Consortium, new perspectives, next steps and implementation plans The Workshop was streamed live and recorded, and all talks, along with speaker slide presentations, are available at www.faang.org.

The GO-FAANG Workshop objectives included establishing priorities for research efforts; planning the management structures required for efficient use and sharing of samples, data and computational tools; and identifying resources needed to accomplish these goals. Three plenary talks and presentations by funding agency representatives set the stage for what is possible in functional annotation of genomes. An emphasis was then placed on small group discussions; these were designed to develop policies and approaches to maximize the success of this crucial next phase in animal genomics. Reference datasets are being established under pilot projects; plans for tissue sets, morphological classification, and methods of sample collection for different tissues were organized; and core assays and data and meta-data analysis standards were established. For more information, please visit the www.faang.org website.

b. Plant and Animal Genome (PAG):

The 2016 NRSP-8 Swine Workshop was held January 9, 2016 in San Diego, CA in conjunction with the Plant and Animal Genome XXIV Conference. A joint session was held with the Cattle, Sheep and Goat Workshop in the morning focused on the theme of Genome Editing. The afternoon Swine Workshop program (see https://pag.confex.com/pag/xxiv/webprogram/Session3175.html) included invited presentations by four young scientists from Konkuk University in South Korea, the University of Barcelona, the Roslin Institute, and the University of Florida, who spoke about their work in emerging areas of pig genomics. The Jorgensen Pig Travel Award winner, Jeremy Howard, from NSCU was introduced and he gave a lightening talk on his area of research. There were also ten presentations from nine different NRSP-8 participating locations. The presentations covered a range of topics from functional genomics to SNP analysis, as well as a broad range of important phenotypes, and sparked discussion among attendees throughout the workshop. Drs. Clutter and Matukumalli gave administrator's reports and Drs. Tuggle and Ernst gave their coordinators' report, as well as conducted a discussion on community needs and resources. At the morning joint session, 176 attendees signed in, including 80 (45%) from 20 different countries outside the US. Attendees from the US represented 21 universities, 14 industry companies and 2 government agencies. In the afternoon, the Swine Workshop had 33 people sign in, although it is estimated that at least 75 were present for the invited talks. Among those signing in, 12 attendees represented 7 countries outside the US, and the 21 US attendees were from 10 universities, 3 industry companies and 2 government agencies. During the business meeting, Dr. Tuggle was elected as the new chair-elect, and Dr. Kiho Lee (Virginia Tech) will chair the 2017 Swine Workshop.

2. Update on new functional genomics project FAANG activities- Special Symposium on FAANG to be held during JAM (Joint Annual Meetings of ASAS, ADSA, CSAS)-ISAG overlap day

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) A meeting report of the GO-FAANG Workshop described above was written by a small group representing the FAANG Subcommittees and attendees. This has been submitted to *Animal Genetics* for publication, pending peer review.

b) A full day **FAANG Symposium** has been organized for July 23, 2016, which can be attended by registrants of either the Joint Annual Meeting of Animal Science Societies (https://asas.org/meetings/jam-2016/home) or the International Society of Animal Genetics (ISAG; https://asas.org/meetings/isag2016/home). Seven world-class speakers will provide 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. This Symposium promises to be excellent, and a very good reason to attend one or both of these great meetings!

c) Two FAANG pilot projects coordinated by Institut National de la Recherche Agronomique (INRA) in France and University of California-Davis (UC Davis) in USA were started in 2015. The Davis project has been supported by NRSP-8 funding from the Swine, Bovine, and Chicken Coordinators, as well as the National Pork Board. These projects aim at identifying regulatory elements within domesticated animal genomes by refined functional annotation of biologically important representative tissues. For both projects, the first phase consisted of sampling of a wide variety of tissues from reference animals in four species: chicken, pig and cattle (both UC Davis and INRA) and goats (INRA only). Different protocols were used to perform multiple assays (histology, chromatin assays, gene expression, DNA conformation and accessibility). Specific representative tissues were selected (cerebellum, cortex, hypothalamus, liver, lung, adipose tissue, muscle and spleen for UC Davis; liver and immune cells (CD4+ and CD8+) for INRA for core molecular assays development and data production (beginning in 2016). In addition to RNA-seq, UC Davis focused on ChIP-seq (histone marks and CTCF) and chromatin accessibility assays (DNase-seq) while INRA focused on small RNA-seq sequencing, chromatin accessibility assays (ATAC-seq), and genome-wide Chromosome Conformation Capture (Hi-C). Preliminary results for ChIP-seq, ATAC-seq and Hi-C assay development were presented at the Plant and Animal Genome XXIV Conference during the FAANG workshop (see http://www.faang.org/bbs?s=PAG2016_workshop..txt).

d) During 2015-2016, new projects joined the FAANG community. Several of these projects aim at identifying the impact of genetic variation on the functional features of the pig and cattle genomes, with the ultimate goal to identify causative variations affecting complex traits. In one, the 'WUR-pigENCODE' project, led by Wageningen University (NL) in collaboration with the University of Illinois (US), is adding new functional annotations to previous methylome studies. In another, a complete range of FAANG annotation is being generated in parallel to eQTL and allele specific expression approaches in dairy cattle. This project is being led by scientists in Australia. Finally, two projects recently funded by the Genome Canada Competition – "Genomics and Feeding the Future" – are linked to FAANG. These projects focus on dairy cattle and feed efficiency and pigs and disease resilience.

e) 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).

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3. Update on USDA-NIFA-AFRI

In case you missed it: A Dear Colleague Letter was emailed to Angenmap from Dr. Matukumalli in March on the following opportunity:

NSF-USDA Joint Funding Opportunity – "Early Concept Grants for Exploratory Research (EAGERs) to Develop and Enable Breakthrough Technologies for Animal and Plant Phenomics and Microbiomes". Up to $300,000 over 2 years can be requested. Interested PIs are required to email a two-page pre-proposal summary to papm@nsf.gov by May 12, 2016, 5:00 PM proposer's local time. More information can be found at the website: http://www.nsf.gov/pubs/2016/nsf16058/nsf16058.jsp, or by contacting Lakshmi Matukumalli,lmatukumalli@nifa.usda.gov or 202-401-1766.

The AFRI request for applications for the yearly genome-oriented opportunities is anticipated to be released approximately early to mid-April, with deadlines approximately 6 weeks later. 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.

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4. Reminder on Joint Annual Meeting (ASAS, ADSA, CSAS) and ISAG registration deadlines.

A reminder that the Joint Annual Meeting of ASAS, ADSA and several other groups is being held July 17 - 23 in Salt Lake City. As well, the International Society of Animal Genetics (ISAG) meeting is being held in the same city, from Jul 23 - 27. As discussed above, there is one day overlapping with the JAM (Joint Annual Meetings of ASAS, ADSA, CSAS) and ISAG meetings, where the FAANG Symposium discussed above will be held.

The next early registration deadline for JAM is June 3, 2016, while the deadline for full registration for the ISAG meeting is prior to the start of the meeting, at which time only the higher on-site registration will be available. Importantly, registration for either meeting allows you to attend the FAANG Symposium on July 23!

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5. Upcoming additional meetings information

Besides the JAM and ISAG 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)

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

Update on PEDV Resistance Genetics project: Dr. F. Bertolini presented a poster on the first results from a collaborative project headed by M. Rothschild et al. See the poster abstract at: https://pag.confex.com/pag/xxiv/webprogram/Paper20373.html. Dr. Bertolini also gave a summary at the Swine Workshop.

Update on FAANG project: Dr. H. Zhou presented a poster summarizing the FAANG project; see the poster abstract at: https://pag.confex.com/pag/xxiv/webprogram/Paper20545.html. There were also several reports given at the FAANG Workshop covering the Davis project that have NRSP-8 support: see https://pag.confex.com/pag/xxiv/webprogram/Session3544.html.

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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