

# Pig Genome Update # 121

February 15, 2015

## List of Contents

1. PAG wrap-up including announcement of new FAANG Initiative.
2. New high density SNP-Chip available!
3. New RFAs for USDA-NIFA grants.
4. Porcine Translational Research Database has recently been updated.
5. Upcoming meetings- highlighting meetings with close deadlines.
6. We want to hear from you!

### **1. Summary of Plant and Animal Genome 2015 January 10-14, 2015, San Diego**

The 2015 Swine NRSP-8 Workshop was held January 10, 2015 in San Diego, CA in conjunction with the 2015 Plant and Animal Genome Conference. The titles and abstracts of all Lectures, Posters, and Workshop talks can be found at: <https://pag.confex.com/pag/xxiii/webprogram/>. In addition, the winner of the Neil A. Jorgenson Travel Award for Swine, Melanie Trenhaile, has provided a brief summary of selected Swine-related posters. These summaries are found here: <http://www.animalgenome.org/pig/community/columns/20150125>. Melanie is a MS student of Daniel Ciobano of UN-Lincoln. Thanks for your hard work on this, Melanie!

A joint session was held with the Cattle, Sheep and Goat groups in the morning and then each sub-committee had separate afternoon sessions. The Swine program had five invited international speakers representing four different European countries. In addition, there were ten presentations from nine different NRSP-8 participating locations. The presentations were very interesting and initiated considerable discussion among the attendees. Dr. Clutter gave an administrator's report and Drs. Ernst and Tuggle gave their coordinators' report as well as conducted a discussion on the use of coordinator's funds to support collaborative research. At the morning joint session, 177 attendees signed in representing 100 different locations. Sixty-six of these attendees were from 19 different countries. In the afternoon, the workshop had 60 people sign in representing 35 different locations. Thirty-four of the attendees represented 19 different countries. During the business meeting, Dr. Kiho Lee from Virginia Tech University was elected as the new secretary and Dr. Cathy Ernst of Michigan State University was elected to chair the 2016 Swine Workshop. (majority of this information was kindly provided by Gary Rohrer).

One discussion that was a bit different from previous years was a mid-afternoon discussion on ideas for using the NRSP-8 Coordinator funds, and the development of policies requiring matching funds to access NRSP-8 funding. One major topic of discussion was a new high density SNP chip, and a number of Stations were interested in this. Please see item #2 for more details.

A major event at PAG was the announcement and further organization of the Functional Annotation of Animal Genomes (FAANG) Consortium. The following text is a summary of the purposes of FAANG; for further information please see the FAANG website ([www.faang.org](http://www.faang.org)). At the NRSP-8 Workshop on Sunday, there was an introductory talk by Dr. Elisabetta Giuffra (INRA) and a standing-room only crowd then participated in a roundtable discussion on implementing FAANG. A further meeting on Monday afternoon attracted 62 persons, where a Steering Committee was set up and discussions of a Fall meeting in Washington, DC was started. More details as they become available.

The most significant challenge in the post-genomic era is connecting genotype to quantitative phenotype

in basic and applied biology - the genome to phenome challenge. Significant progress has been made in associating sequence variation with quantitative phenotypes motivated by the importance of animals as food sources, models for human health, and key ecological actors. In domesticated animals, the wealth of phenotypic diversity of different breeds and populations and decades of research have been key to such progress, and coupled with advances in sequencing the genomes of these species provides unique opportunities to study genome-phenome relationships.

FAANG has been created as we all recognize the importance of coordinating this effort to maximize efficiency and data quality as demonstrated by the ENCODE project. The major goal of FAANG is to identify all functional elements in animal genomes.

FAANG aims to deliver standardized datasets from a limited set of individuals representing species that have reference quality draft genome assemblies and substantial publicly available phenotypic datasets.

The FAANG project will establish an infrastructure capable of efficiently analyzing genome-wide functional data for animal species. Such large-scale analyses will contribute to our understanding of how variation in gene sequences and functional components determine phenotypic diversity. This understanding will inform the development and exploitation of improved models for predicting complex phenotypes from sequence information.

Please join our initiative by signing up at the website!

## **2. New 650K SNP Chip -- Available soon!**

A high-density pig SNP array has been developed by Affymetrix with over 650,000 SNP selected by Martien Groenen and tested by Alan Archibald in collaboration with Affymetrix. The SNP on the array are equally spaced along pig chromosomes, and also include unassigned contigs from build 10.2. The array includes 56K confirmed SNPs from the Illumina SNP60 chip, thus it should be possible to input data for populations already typed using the SNP60 chip. These SNP have high MAF, and represent a variety of European and Asian breeds. Genotyping of a limited number of samples for US laboratories will be supported by the NRSP8 Swine Genome Coordination Program. For more information or to participate with samples, please contact Cathy Ernst (ernstc@msu.edu).

## **3. New RFAs released on USDA funding opportunities**

### ***A. Agriculture and Food Research Initiative: Food Security Challenge Area Grants***

<http://www.grants.gov/web/grants/view-opportunity.html?oppId=272432>

Note: letters of Intent are no longer required for this opportunity.  
Applications due June 4, 2015

All three different areas are relevant to animal geneticists:

1. Agricultural Production Systems
2. Breeding and Genomics of Crops and Livestock
3. National Strategy for Sustainable Crop and Livestock Production in the United States

### ***B. USDA Higher Education Challenge (HEC) Grants Program***

<http://www.nifa.usda.gov/fo/educationchallengehigheredhep.cfm>

Applications are due March 19, 2015

## **4. Porcine Translational Research Database has recently been updated**

This database currently has 7,538 gene entries including 4,813 sequences with full 5' and 3' representation (an estimated 22.4% of the genome). These sequences include the vast majority of genes that are commonly studied in rodents, pigs or humans. The database also includes extensive error annotations (2,949 gene entries) for the current NCBI and Ensembl (build 10.2) versions of the genome including; 742 genes that have been sequenced more than once, 904 genes that are missing from the genome and 1,046 loci that contain a partial open reading frame. The database also contains extensive information on reagent availability for the pig including 2,227 real-time PCR assays and 602 antibodies. The database can be accessed at <http://www.ars.usda.gov/services/docs.htm?docid=6065>. (kindly provided by Harry Dawson).

## **5. Upcoming meetings- highlighting meetings with close deadlines**

(for meetings of relevance to the genomics community over the next 6-12 months, see: <http://www.animalgenome.org/pig/community/meetings.html>)

### **A. Midwest ASAS/ADSA Meeting March 15-18, 2015, Des Moines, IA**

The 2015 Joint ADSA-ASAS Midwest Section meeting is scheduled for March 15-18 in Des Moines, IA. See <https://www.asas.org/membership-services/asas-sections/midwest-section/meetings> for details. In addition to the regular breeding and genetics sessions, a Functional Genomics symposium has been organized by the Breeding and Genetics program committee. Dr. Huaijun Zhou (UC-Davis) will present a talk in this symposium on his newly NIFA-funded project to identify functional components of the pig, chicken and cattle genomes. This project is also being supported by the Swine, Poultry, and Cattle Genome Coordinators and the National Pork Board.

**B. The 6<sup>th</sup> International Symposium on Animal Functional Genomics (ISAFG 2015)** will be held in Piacenza, Italy from the 27<sup>th</sup> to the 29<sup>th</sup> of July, 2015.

The purpose of ISAFG 2015 is to bring together academic researchers, industry representatives and policy makers to exchange knowledge on the leading-edge developments in functional genomics and its applications in the livestock sector. The symposium themes include important topics, ranging from structural and comparative genomics to systems biology.

### **Conference Themes**

- Comparative genomics
- Epigenetics
- Transcriptomics
- Proteomics
- Microbiome
- Systems Biology

### **Important Dates**

- March 31<sup>st</sup> 2015: deadline for early bird registration
- June 15<sup>th</sup> 2015: deadline for abstract submission
- July 10<sup>th</sup> 2015: deadline for regular registration

(Information taken from ISAFG website; see <http://www.isafg2015.it/>)

## **6. We want to hear from you!**

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 planned for Feb 15, June 15 and October 15 each year. Any contribution should be sent to the Coordinators one week prior to these dates.



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