**ANNUAL SUMMARY REPORT**

**PROJECT:** NRSP-8

**PROJECT TITLE:** National Animal Genome Research Project

**PERIOD COVERED:** January 1 to December 31, 2017

**ANNUAL MEETING DATE:** January 13-17, 2018

**Leadership**

Mohamed (Moh) Salem, Chair

Molly McCue, Chair-elect

# Objectives

Objective 1: Advance the status of reference genomes for all species, including basic annotation of worldwide genetic variation, by broad sequencing among different lines and breeds of animals.

Objective 2: Develop strategies to identify and exploit genes and allelic variation that contribute to economically relevant phenotypes and traits, in part through improving functional annotation of the genomes of our species.

Objective 3: Facilitate analysis, curation, storage, distribution and application of the enormous datasets now being generated by next-generation sequencing and related "omics" technologies with regard to animal species of agricultural interest.

# MINUTES OF THE ANNUAL BUSINESS MEETING:

The NRSP-8 business meeting was preceded by two days of species workshops, area subcommittees, and the combined Animal Genome Workshop presented on Sunday afternoon. More than 150 participants from about 20 countries attend the workshop.

The combined workshop included four plenary presentations as follows:

Christopher K. Tuggle, Iowa State University, presented “Towards Understanding the Function of the Porcine Genome”. Dr. David E. MacHugh, University College Dublin presented “Comparative and Integrative Genomics of Bovine and Human Tuberculosis: A One Health Perspective”. Dr. Erez Lieberman Aiden, Baylor College of Medicine, presented “De novo Assembly of Plant and Animal Genomes with Chromosome-Length Scaffolds using Hi-C”. Dr. Jack Dekkers, Iowa State University, presented “Training the Next Generation of Animal Breeders in the Genomics Era”. Mrs. Katherine CH Amrine, Insight Data Science, presented “Emerging Careers in Data Science and Genomics”. Dr. Caird E. Rexroad III, USDA, and Dr. James M. Reecy, Iowa State University, presented “Genome to Phenome: A USDA Blueprint for Animal Production”

The business meeting was called to order by the Chair, Dr. Mohamed Salem (Middle Tennessee State University), and was recorded by the Secretary, Molly McCue (University of Minnesota). Coordinator reports were presented:

* Juan Medrano---Cattle update—updated cattle genome assembly, water buffalo and Brahman draft sequences being built. FAANG in cattle is growing with additional NIFA funding. Green database—repository of phenotypic data from any livestock species. Data, DN, tissue etc. can be stored and will provide continuity into the future. Students and speakers to PAG have been supported by the coordinator funds. Brenda Murdock was the workshop organizer and put together a great program.
* Swine—Chris Tuggle: 68 folks at the workshop. Coordinator funds used for speakers and students. New assembly and annotation of the new assembly. 5 station reports. 3 FAANG projects were funded by NIFA.
* Sheep/Goat----Noelle Cockett and Steven White. Continued to run a join workshop with the cattle group. FAANG sheep happening. Looking at CNVs in both sheep and goat. Working on annotation in the sheep and goat genomes. Great international input for conference calls. Noelle added---hallmarks of the meeting is sharing results about identifying what additional resources are needed. She commented that a single year of FAANG funding would not be enough and that continued funding needs to happen. And she asked that other species should also do the same. She re-iterated that we need to rally our commodity groups and Noelle proposed that we use the letters and videos to carry forward for more support.
* Poultry---Hans Chen poultry workshop coordinators have funded a mini-symposium on gene editing in birds and things look really promising. Gal 6.0 will be out shortly. Being annotated by NCBI.
* Ernie Bailey, Molly McCue and Sam Brooks—Jessica Petersen and Stephen Coleman organized the workshop. 90 attendees on Saturday and 45 on Sunday. 18 station reports. EqCab 3at NCBI and is being annotated should be up in 2 weeks. Funded 20 students to attend the meeting. Annette McCoy is the next co-chair. Havemeyer Foundation meeting in Paloma Italy Sept. 12-15th.
* Jim Reecy---bioinformatics. Thanks to Juliiang Hou for another year of great work at animal genome.org. Dramatic increase in data hosting at animal genome.org, but also encouraging that open science be used since you also get a DOI citation index. Over the next year will be bringing a post-doc on board to help by training on the FAANG data analysis pipelines including hands on and hack-a-thon training. Carl Schmitz asked about fees for open science—Jim reported no fees.
* Steven Roberts---aquaculture John Liu stepped down as a co-coordinator. Eric Patman stepped into that role. Added an industry supported poster session, new Eastern oyster genome. 50x affy SNP in salmon. FAANG for all salmonid genomes. Supported 6 seed projects.

USDA administrative reports:

* Eric Young---lead admin advisor. Updated us on the new project proposal. Peer reviews were very positive and the writing committee is working on revisions from the peer review. Will go to the next stage of review this week. Then goes to the NRSP review committee to look for alignment of the various criteria. Final decision made in September at the national meeting of the Ag Experiment Station directors. After this week there will be a call to fill out appendix E to become an official member of the new project. Everyone has to renew with the new project. In the next couple months, the call for nominations for coordinators and/or co-coordinators. Process will be described in an email form Eric Young.
* Jerry Taylor asked why to coordinator decisions were made by the advisors and there was not a vote. Eric said there has not been reasons to vote in the past, except on rare occasions when the species community has been asked to vote.
* Mark Mirando---Parag was headed to the airport, so Mark is giving the report. AFRI science coordinator and PO for reproduction. He is filling in for Lakshmi. 2017, 2018 and 2019 budgets. May 2016--- 2017 fiscal year budget that started in Oct 2016; 25 million increase. AFRI biggest competitive program. FY18--- NIFA explanatory notes discusses the president’s proposal. NIFA lost only ~6% compared to up to 25% elsewhere. The final is ultimately up to the congress and what they add to the appropriations bill. President has proposed nearly 350 million and house and senate has ~375. FY19 process underway. AFRI RFAs should be out in ~ 2 months. 3 RFAs—foundational, ag system
* Dr. Alison Van Eenennaamu, University of California, Davis, is the chair elect for 2018.
* Moh Salem passed the gavel to Molly McCue as the incoming NRSP-8 chair. Meeting adjourned.

# ACCOMPLISHMENTS AND IMPACTS:

## AQUACULTURE TECHNICAL REPORT

### Leadership

Coordinator: Steven Roberts, Washington State University

Co-coordinator: Eric Patman, Auburn University, Alabama

Species Leaders:

Catfish: Sylvie Quiniou, ARS Stoneville, Mississippi

Oyster: Dina Proestou, ARS University of Rhode Island, Rhode Island

Salmonids: Yniv Palti, ARS Leetown, West Virginia

Striped Bass: Ben Reading, North Carolina State University, North Carolina

### 2018 Aquaculture Workshop Report

Workshop Chair: Geoffrey Waldbieser, USDA ARS

Chair elect: Catherine Purcell

### Theme

Genome Assembly and Application of Genomic Selection in Aquaculture

### Attendees

Number = 50+

Number of institutes: 42

### Invited Presentations (4)

1. **Assembly and Computational Use of Aquatic Genome Models,** Wesley Warren, McDonnell Genome Institute at Washington University, St. Louis,
2. **A Strategy to Assemble High-Quality Reference Genomes for All Vertebrate Orders**, Adam M. Phillippy, National Human Genome Research Institute, National Institutes of Health, Bethesda,
3. **Assembly and Computational Use of Aquatic Genome Models,** Nuala O’Leary, NIH/NCBI, “The National Center for Biotechnology (NCBI)
4. **Applied Genomics for Conservation of Distinct Stocks and Phenotypic Diversity in Chinook Salmon**, Shawn Narum, Columbia River Inter-Tribal Fish Commission,

### Contributed Presentations (15)

### Poster Session Participants (30)

### Business Meeting Minutes

Time: Saturday January 13, 2018, 5:30-6:00 pm

Place: Pacific Salon 3/4, Town and Country Hotel, San Diego, CA

1. Call to order. Dr. Steven Roberts called the business meeting to order at 5:30 pm, following the Aquaculture Workshop.
2. Dr. John Liu has stepped down for his role as chair of the NRSP-8 Aquaculture section; he was thanked for his dedicated service in this role. For now, Dr. Eric Peatman will be stepping into that role in Dr. John Liu’s place.
3. The Species Coordinator reports have been submitted electronically.
4. FAASG (Functional Annotation of All Salmonid Genomes) initiative kicked off with a meeting in Victoria, B.C., Canada and a white paper (Functional Annotation of All Salmonid Genomes (FAASG): an international initiative supporting future salmonid research, conservation and aquaculture; BMC Genomics. 2017 Jun 27;18(1):484. doi: 10.1186/s12864-017-3862-8.). They will be seeing what will happen with the E.U. efforts with annotation, and they are soliciting ideas for funding projects.
5. RFP Announcements: there will be small funding amounts available from NRSP-8 research grants (these would be in the range of ~$10k.
6. PAG Aquaculture Workshop Chairs:
	1. Dr. Geoff Waldbieser was thanked for the wonderful job he did as chair of the 2018 Aquaculture session.
	2. Dr. Catherine Purcell will be chairing next year’s Aquaculture session.
	3. Dr. Tiago Hori (Center for Aquaculture Technologies) and Dr. Louis Plough (University of Maryland – Center for Environmental Science) were nominated to serve as Secretary (Chair-elect) for the 2019 workshop. As both Tiago and Louis were willing to serve in this role, the positions were decided for the following two years, as follows:
	4. Tiago Hori: Secretary (Chair-elect) 2019, Chair of the workshop in 2020
	5. Louis Plough: Secretary (Chair-elect) 2020, Chair of the workshop in 2021
7. Dr. Caird Rexroad III: Gave updates on the report-in-progress, Genomes to Phenomes: USDA Blueprint for Animal Production. He is trying to ensure that aquaculture is well represented in this report; if anyone would like to contribute to the draft, please contact him. In addition, anyone who wishes to be more involved in this report was invited to the writing workshop for this report on Sunday (January 14th) morning.
8. Discussion on funding priorities: there is a need for groups to get together to collaborate and communicate, and start discussions with the NIFA leaders; aquaculture needs to speak up more to get funding and compete for larger funding amounts. Please share any feedback/experiences about what has/has not been successful.
9. The names of the six travel award recipients were announced [*most not present at the meeting*]: André L. S. Garcia, University of Georgia; Erin M. Roberts, University of Rhode Island; Huitong Shi, Auburn University; Melissa K. Holborn – University of Guelph; Rafael M.O. Silva, University of Georgia; Yujia Yang, Auburn University.
10. Meeting was adjourned.

### AQUACULTURE TECHNICAL REPORT ACCOMPLISHMENTS AND IMPACTS:

**Objective 1: Advance the status of reference genomes for all species, including basic annotation of worldwide genetic variation, by broad sequencing among different lines and breeds of animals.**

Sequenced the YY genome of channel catfish using a YY sequencing template that avoid any X chromosome sequences in the assembly. The genome assembly was validated through linkage mapping of more than 250,000 SNP markers.

Eastern oyster (Crassostrea virginica) genome assembly v. 3.0 completed; 99% of sequences are assembled into the known number of chromosomes (10). Gene annotation completed using the automated NCBI pipeline.

The new version of the rainbow trout genome was annotated and released by the NIH-NCBI (GenBank assembly Accession GCA\_002163495). Approximately 88% of the new assembly sequences are aligned within chromosomes to generate contiguous chromosome sequences.

A draft genome for Chinook salmon was assembled and submitted to NCBI which was released publicly on December 11, 2017 (accession #s: project: PRJNA402052; genome assembly: PIPH000000000; transcriptome assembly: GGDU00000000). The assembly was produced from a diploid wild male collected in the interior Columbia River (Johnson Creek). We produced a 2.36 Gb genome assembly with 72.2% (1.70 Gb) of the de novo assembly anchored to 34 chromosomes, with contig N50 of 19.1Kb, scaffold N50 of 153.3Kb (prior to chromosome placement), and anchored chromosome N50 of 45.4Mb.

Efforts are ongoing to complete assembly of the striped bass (Morone saxatilis) and white bass (M. chrysops) genomes using Dovetail Hi-C and Chicago sequencing strategies.

**Objective 2: Develop strategies to identify and exploit genes and allelic variation that contribute to economically relevant phenotypes and traits, in part through improving functional annotation of the genomes of our species.**

Identified a candidate for sex determination gene in catfish through positional and functional evidence. Experimental knockout of the candidate gene converted genetic males (XY) to phenotypic females.

Medium-density Affymetrix SNP array containing ~27K Crassostrea gigas SNPs and ~11K Ostrea edulis SNPs has been developed.

Expressed exome capture sequencing (EecSeq) method developed using the eastern oyster. NCBI Accession # PRJNA423022.

A 50K transcribed gene Affymetrix chip was built. The chip contains ~21K transcribed SNPs with allelic-imbalances associated with important aquaculture production traits including WBW, muscle yield, and resistance/susceptibility to bacterial cold-water disease. The chip identified major QTL explaining genetic variance of body-weight-gain and muscle yield.

Columnaris disease (CD) is distributed around the world, and recently it has been identified as an emerging problem for the U.S. rainbow trout aquaculture industry. As a first step in developing selective breeding strategies for improving the resistance to CD, we scanned the genomes of two important domestic rainbow trout breeding populations for chromosome segments that contain genes that significantly affect resistance to CD. The research is conducted by scientists from USDA-ARS in collaboration with Troutlodge, Inc.

The striped bass genome sequence assembly was used to evaluate epigenetic markers of sperm quality (DNA methylation status) and gene pathways underlying male reproductive dysfunction.

Domestic white bass when crossed with domestic striped bass were shown to produce sunshine hybrid striped bass with 18% better growth to market size than wild-captured white bass from Lake Erie crossed with domestic striped bass in two independent replicate studies through time.

**Objective 3: Facilitate analysis, curation, storage, distribution and application of the enormous datasets now being generated by next-generation sequencing and related "omics" technologies with regard to animal species of agricultural interest.**

Hands-on comparative genomics workshop held at the National Shellfisheries Association annual meeting

NRSP-8 supported and facilitated a workshop of the Functional Annotation of All Salmonid Genomes (FAASG) Consortium: an international initiative supporting future salmonid research, conservation and aquaculture.

A JBrowse integrated web portal of the draft striped bass genome resource is hosted online for use as an unrestricted public resource. Database URL: http://appliedecology.cals.ncsu.edu/striped-bass-genome-project/.

### Communication:

* NRSP-8 Aquaculture leaders participated in establishing the FAASG (Functional Annotation of All Salmonid Genomes) consortium. **Impact(s):** The consortium will allow coordinating data sharing and establish an infrastructure for providing high quality functional annotation of salmonid genomes.

### Research support mini-grants (coordinator grants):

Approximately 6 mini-grants (~$10,000/each) supported projects that fall under all three primary objectives and include a variety of species. Awards listed:

1. Evaluating the genetic potential for environmental adaptation in eastern oysters through resequencing, Marta Gomez-Chiarri et al.
2. Genetic Variation Related to Growth Performance in Domestic and Wild Striped Bass, Benjamin J. Reading et al.
3. Annotating the rainbow trout genome with Iso-seq technology for FAASG, Moh Salem
4. Target capture sequencing to map the genetic basis of salinity tolerance in Crassostrea virginica, Morgan Kelly and Jerome La Peyre
5. Outlining parent-of-origin effects in wild x domestic hybrid striped bass for eQTL potential, Jason Abernathy and Adam Fuller
6. Detection of candidate vAh resistance genes in channel catfish using RNA-seq, Rex Dunham and John Liu

### Travel support and opportunities for trainings:

Travel of 6 students/postdocs was funded to attend the Aquaculture workshop at PAG meetings (2018). The purpose of the travel award program is to help graduate students and postdocs to travel to the annual PAG meeting to present their research.

Awardees:

* 1. André L. S. Garcia, University of Georgia, “Genomic Evaluation for Harvest Weight and Residual Carcass Weight in Channel Catfish Using Single-Step Genomic BLUP”;
	2. MelissaK.Holborn, UniversityofGuelph, “GenomeWideAssociationAnalysis for Resistance to the Causal Agent of Bacterial Kidney Disease in a North American Commercial Atlantic Salmon”;
	3. Erin M. Roberts, University of Rhode Island, “Differential Expression of Apoptosis Pathway Gene Families in Response to Immune Challenge in Crassostrea gigas and Crassostrea virginica”;
	4. Huitong Shi, Auburn University, "Identification of Resistance QTL and Candidate Genes Against Enteric Septicemia of Catfish";
	5. RafaelM.O. Silva, UniversityofGeorgia, “GWASforDetectingQTLAssociated with Columnaris Disease in Two Rainbow Trout Breeding Populations”;
	6. Yujia Yang, Auburn University, “Identification of Sexually Differentially Methylated Regions in Channel Catfish Provides Evidence of Epigenetic Control of Its Sex Determination”.

### Leveraged funds and stakeholders’ use of project outputs

Leveraged funds from diverse projects totaling more than one million dollars from federal sources. Selected grants are highlighted below.

The Genetic Basis of Low Salinity Tolerance in the Eastern Oyster: Baseline Data for Consistent Aquaculture Production in Coastal Areas, Plough, Louis, $148,422.

Sequencing of Y-chromosome and analysis of sex determination in catfish, Liu, John, $500,000.

### Major impact products (could be potential impact):

Draft genomes were assembled for Eastern oyster and Chinook salmon and an improved genome reference was reported for rainbow trout. The new genome references should help in identify genes in control of economically important aquaculture production traits,

### Publications

Jin Y, Zhou T, Li N, Liu S, Xu X, Tan S, Shi H, Yang Y, Yuan Z, Wang W, Pan Y, Gao D, Dunham R, Liu ZJ. 2018. JAK and STAT members in channel catfish: Identification, phylogenetic analysis and expression profiling after bacterial infection. Developmental and Comparative Immunology, in press.

Yuan Z, Huang W, Liu S, Xu P, Dunham R, Liu ZJ. 2018. Historical demography of common carp estimated from individuals collected from various parts of the world using the pairwise sequentially Markovian coalescent approach. Genetica, in press.

Yang Y, Fu Q, Liu Y, Wang X, Dunham R, Liu S, Bao L, Zeng Q, Zhou T, Li N, Qin Z, Jiang C, Gao D, Liu ZJ. 2018. Comparative transcriptome analysis reveals conserved branching morphogenesis related genes involved in chamber formation of catfish swimbladder. Physiological Genomics, in press.

Fu Q, Yang Y, Li C, Zeng Q, Zhou T, Li N, Liu Y, Liu S, Li D, Liu ZJ. 2017. The CC and CXC chemokine receptors in channel catfish (Ictalurus punctatus) and their involvement in disease and hypoxia responses. Developmental and Comparative Immunology 77: 241-251.

Fu Q, Yang Y, Li C, Zeng Q, Zhou T, Li N, Liu Y, Li Y, Wang X, Liu S, Li D, Liu ZJ. 2017. The chemokinome superfamily: II. The 64 CC chemokines in channel catfish and their involvement in disease and hypoxia responses. Developmental and Comparative Immunology 73: 97-108.

Geng X, Liu S, Yuan Z, Jiang Y, Zhi D, and Liu ZJ. 2017. A genome wide association study reveals that genes with functions for bone development are associated with body conformation in catfish. Marine Biotechnology 19: 570-578.

Wang X, Liu S, Dunham R, Liu ZJ. 2017. Effects of strain and body weight on low-oxygen tolerance of channel catfish. Aquaculture International 25: 1645-1652. DOI: 10.1007/s10499-017-0125-2

The Aquaculture Genomics, Genetics and Breeding Workshop, Abdelrahman H, ElHady M, Alcivar-Warren A, Allen S, Al-Tobasei R, Bao L, Beck B, Blackburn H, Bosworth B, Buchanan J, Chappell J, Daniels W, Dong S, Dunham R, Durland E, Elaswad A, Gomez-Chiarri M, Gosh K, Guo X, Hackett P, Hanson T, Hedgecock D, Howard T, Holland L, Jackson M, Jin Y, Kahlil K, Kocher T, Leeds T, Li N, Lindsey L, Liu S, Liu ZJ\*, Martin K, Novriadi R, Odin R, Palti Y, Peatman E, Proestou D, Qin G, Reading B, Rexroad C, Roberts S, Salem M, Severin A, Shi H, Shoemaker C, Stiles S, Tan S, Tang KFJ, Thongda W, Tiersch T, Tomasso J, Tri Prabowo W, Vallejo R, van der Steen H, Vo K, Waldbieser G, Wang H, Wang X, Xiang J, Yang Y, Yant R, Yuan Z, Zeng Q, and Zhou T. 2017. Aquaculture genomics, genetics and breeding in the United States: current status, challenges, and priorities for future research. BMC Genomics 18: 191. DOI 10.1186/s12864-017-3557-1

Wang X, Liu S, Yang Y, Fu Q, Abebe A, Liu ZJ. 2017. Identification of NF-κB related genes in channel catfish and their expression profiles in mucosal tissues after columnaris bacterial infection. Developmental and Comparative Immunology 70: 27-38.

Li N, Zhou T, Geng X, Jin Y, Wang X, Liu S, Xu X, Gao D, Li Q, Liu ZJ. 2017. Identification of novel genes significantly affecting growth in catfish through GWAS analysis. Molecular Genetics and Genomics, in press. doi.org/10.1007/s00438-017-1406-1

Yuan Z, Liu S, Bao L, Zhou T, Liu ZJ. 2017. Comparative genome analysis of 52 fish species suggests differential associations of repetitive elements with their living aquatic environments. BMC Genomics, in press.

Zhong X, Wang X, Zhou T, Jin Y, Tan S, Jiang C, Geng X, Li N, Shi H, Zeng Q, Yang Y, Yuan Z, Bao L, Tian C, Liu S, Li Q, Liu ZJ. 2017. Genome-wide association study reveals multiple novel QTL associated with low-oxygen tolerance in hybrid catfish. Marine Biotechnology 19: 379-390. DOI: 10.1007/s10126-017-9757-5.

Li Y, Geng X, Bao L, Elaswad A, Huggins KW, Dunham R, Liu ZJ. 2017. A deletion in the Hermansky-Pudlak syndrome 4 (Hps4) gene appears to be responsible for albinism in channel catfish. Molecular Genetics and Genomics, in press. DOI 10.1007/s00438-017-1302-8

Nunes, José de Ribamar da Silva, Liu S, Pértille F, Perazza C, Vera Maria Fonseca de Almeida Val, Hilsdorf AWS, Liu ZJ, & Coutinho LL. 2017. Large-scale SNP discovery and construction of a high-density genetic map of tambaqui (Colossoma macropomum) through genotyping-by-sequencing. Scientific Report 7: 46112.

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Gao S, and Liu ZJ. 2017. Taste receptors and gustatory associated G proteins in channel catfish, Ictalurus punctatus. Comparative Biochemistry and Physiology, part D, Genomics and Proteomics 21: 1-9. doi.org/10.1016/j.cbd.2016.10.002.

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Tian C, Tan S, Bao L, Zeng Q, Liu S, Yang Y, Zhong X, Liu ZJ. 2017. DExD/H-box RNA helicase genes are differentially expressed between males and females during the critical period of male sex differentiation in channel catfish. Comparative Biochemistry and Physiology part D 22: 109-119.

Fu Q, Zeng Q, Li Y, Yang Y, Li C, Zhou T, Li N, Liu S, Yao J, Jiang C, Li D, Liu ZJ. 2017. The chemokinome superfamily in channel catfish: I. CXC subfamily and their involvement in disease defense and hypoxia responses. Fish and Shellfish Immunology 60: 380-390.

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## CATTLE TECHNICAL REPORT

### COOPERATING AGENCY AND PRINCIPAL LEADERS:

University of California, Davis: Juan F. Medrano

University of California, Davis: Alison Van Eenennaam, Co-coordinator

University of Missouri-Columbia: Jerry Taylor, Co-coordinator.

**Progress toward Objective 1.** Shared genomic tools and reagents and sequence information.

An important focus of the community has been towards improving the bovine genome assembly.

Development of a new Dominette bovine genome reference assembly

A group of collaborating scientists (Tim Smith, Juan Medrano, Ben Rosen, Sergey Koren, Robert Schnabel, Derek M. Bickhart, Aleksey Zimin, and Chris Elsik) worked toward developing an improved bovine reference genome assembly and its annotation. Multiple data types were generated, such as PacBio long-read sequences, Illumina paired-end sequences. an optical map and improved gene predictions based on RNA-Seq and Iso-Seq data. All of the data were derived from tissue samples from L1 Dominette 01449 (Dominette), the reference animal. The goal of the group was to generate an improved “gold level” cattle reference genome assembly. Approximately 80X PacBio and 80X Illumina paired-end coverage of Dominette were produced. A Falcon *de-novo* assembly was generated followed by scaffolding of contigs using the Dominette Optical Map, Dovetail Genomics Chicago library/HiRise and HiC and a recombination map of 59K autosomal SNPs. In parallel, the Falcon assembly was refined using specialized software, CANU and MaSuRCA, resulting in chromosome length scaffolds. Additionally, full-length transcripts were sequenced using Iso-Seq from 30 tissues from Dominette to support improved annotation. Chris Elsik (University of Missouri, Columbia) has led the annotation effort for the new sequence assembly. A public version of the new ARS-UCD assembly will be submitted to NCBI in January 2018, shortly after the PAG meeting. Funding for this project came from Cattle Genome Coordinator Funds, USDA/MARC, UC Davis, Neogen/Geneseek and Zoetis.

As described by Bob Schnabel et al. (PAG abstract W151) comparing imputation accuracy between markers ordered according to the new ARS-UCD assembly and UMD3.1, approximately 2,000 markers changed positions by greater than 10 Mb or are on different chromosomes in the new assembly. For these markers, average accuracy increased between 1–13%. The overall mean accuracy was increased modestly, but the largest increases in accuracy occurred for low minor allele frequency (<0.03) variants, which has significant implications for imputation to sequence level genotypes.

In addition to the Dominette ARS-UCD reference assembly, 2017 was a productive year to generate new cattle assemblies that will provide useful tools for research and commercial applications:

* Zoetis (G. Rincon, PAG abstract W157) generated a complete high quality *de-novo* Holstein bull annotated reference assembly.
* A collaboration between USMARC, University of Adelaide and NHGRI (A. Rhie PAG abstract W149) reported the development of a unique assembly from an F1 hybrid (Angus x Brahman) and a novel method for resolving completely phased haplotype assemblies from both breeds.
* LIC, New Zealand, Ben Rosen at USDA/Beltsville and others are completing long read *de-novo* assemblies of a Holstein bull and a Jersey bull.
* A draft genome assembly and annotation for river buffalo was published (Giga Sci 6(10), 2017).

Functional Annotation of Animal Genomes (FAANG) initiative

Huaijun Zhou and collaborators at U.C. Davis with the support of both USDA NIFA and NRSP8 Bovine Genome Coordinator funds are following the blueprint of the human and mouse ENCODE projects for identifying the functional roles of regulatory elements in the cattle genome. The goals are to annotate promoter, enhancer, and silencer region specific chromatin marks, and to determine the functional roles of regulatory regions in relevant tissues in each species. Cattle tissues were collected from four (2 males and 2 females) 14 month old Line 1 Hereford animals. The samples from eight tissues (skeletal muscle, liver, adipose, spleen, hypothalamus, brain cortex/whole, cerebellum, and lung) from the animals were processed for RNA-Seq, DNase-Seq, ATAC-Seq, ChIP-Seq, DNA-methylation, Hi-C and other assays. Data are being integrated to functionally annotate regulatory elements within the bovine genome.

We expect that the FAANG cattle initiative will be significantly expanded with added collaborations and assays supported by the recent FAANG Program Area NIFA funding.

**Progress towards Objective 3:** Bioinformatics and database resources

Cattle GRIN Genomics Database

Harvey Blackburn at USDA-ARS National Animal Germplasm Program (NAGP), Colorado State University Experimental Station and EMBRAPA have joined efforts to develop a genomic database that will serve as a repository for DNA data from the large animal genomics projects which have valuable data that need permanent archiving for future research. This effort, coupled with the existing capacities to store phenotypic and production system data in the Animal-GRIN database as well as germplasm/tissue samples, will facilitate the communities’ efforts to maintain genomic data for future use. Efforts have also been ongoing to interface the Animal-GRIN system with the Internet 2 effort, which the USDA ARS, as a whole, has been engaged in developing. The genomics database is ready to accept data. Web-interface on front-ends/back-ends are being built to facilitate user requests.

Database and bioinformatics activities are also coordinated by Jim Reecy (NRSP8 Bioinformatics Coordinator) at the NAGRP site (http://www.genome.iastate.edu/cattle/).

**Meetings**: Coordinator funds supported student travel awards for PAG-XXVI in January 2018 and will do the same for PAG XXVII in January 2019.

**Plans for the future:** Priorities are to support the continued efforts towards the annotation and release of the bovine genome reference assembly and the cattle FAANG initiatives, and data sharing and the creation of sample and data repositories that will benefit other cattle research investigators. We will expand our efforts to include the cattle industry and international collaborators in the application and the utilization of cattle genomic resources. For any informational items that you would like distributed via future newsletters please contact Alison Van Eenennaam (alvaneenennaam@ucdavis.edu) or either of the two other co-coordinators. Constructive suggestions from researchers on areas to support in bovine genomics are also welcomed.

## HORSE TECHNICAL REPORT

### Leadership:

Coordinators:

Ernest Bailey, University of Kentucky

Samantha Brooks, University of Florida

Molly McCue, University of Minnesota

Workshop:

 2018 Chair: Jessica Petersen, University of Nebraska

 2018 Co-chair: Stephen Coleman, Colorado State University

2019 Chair Stephen Coleman, Colorado State University

2019 Co-chair Annette McCoy, University of Illinois

2018 Equine Workshop Report

The workshop met Saturday afternoon (Jan 12) and Sunday morning (Jan 13). The first day was devoted to infrastructural development of the equine genome while the second day was devoted to applications.

### Attendees:

January 12: 90

January 13: 45

### Posters:

35 presented

Station Reports were provided by scientists from 20 laboratories including those at Colorado State University, Cornell University, University of Florida, Mississippi State University, University of Kentucky, University of Louisville, University of Minnesota, Michigan State University, University of Illinois, University of Nebraska, Texas A&M University, University of California-Davis, Argentina, Mongolia, Uppsala Sweden, Italy, Denmark and France.

### Workshop Presentations

On January 12, 12 presentations were made and a coordinated discussion section held. Key presentations were:

1. Invited Speaker: Chongyuan Luo on Epigenomic Diversity in the Mammalian Brian
2. Samantha Brooks: Update on NRSP8 Genome to Phenome Conference
3. Edward Rice: Ecab 3.0
4. Erin Burns: Update on FAANG initiative for horse and other species

On January 13, 6 presentations were given.

Travel support awards were made for 24 Students from the NRSP8 Coordinator Funds. Winner of the Jorgenson Travel award was Moriel Singer-Berk from the University of California-Davis.

### Progress on the Workshop Objectives:

**1: Advance the status of reference genomes for all species, including basic annotation of worldwide genetic variation, by broad sequencing among different lines and breeds of animals.**

The new assembly of the horse genome, Ecab 3.0, was reported to be in process at NCBI and Ensembl. The new assembly is based on the existing Sanger sequence data along with Illumina HiSeq short reads, CHiCago and Hi-C long-insert libraries, Gap-filling with PacBio and a 10x Chromium library to identify and phase variants. The final assembly has 4.5Mb contig N50, 85Mb scaffold N50, and 70Mb more sequence assigned to chromosomes.

A de novo assembly of the equine MHC was produced using the 10x GenomicsTM ChromiumTM linked read gel-bead system. The study produced six long contigs in the MHC region with very few gaps, allowing determination of the correct order of the class I and class II genes on the ELA-A3 haplotype and to obtain high fidelity full length genomic sequences for all of those genes.

To supplement the reference genome derived from a mare, an annotated assembly of the male specific region of the Y chromosome has also been completed and will be released upon acceptance of the descriptive manuscript. This resource will be made available through the NCBI and UCSC genome browsers.

**2: Develop strategies to identify and exploit genes and allelic variation that contribute to economically relevant phenotypes and traits, in part through improving functional annotation of the genomes of our species.**

A biobank of over 80 tissues, 2 cell lines, and 6 fluid types was recently established from two extensively phenotyped healthy adult Thoroughbred mares. RNA-sequencing (both mRNA and smRNA-seq) and ChIP-sequencing for four histone modifiers was initiated across 8 tissues that were prioritized in alignment with the overall across-species FAANG initiative. The biobank has led to a substantial international investment of the equine community, with 24 individuals representing 16 research institutions in 10 countries providing support for transcriptome characterization of tissue relevant to their investigations. As a result, mRNA and smRNA-seq datasets are currently available from 30 tissues to contribute to horse genome annotation. Seven laboratories also volunteered to lead other analyses, including karyotyping, centromere mapping of fibroblast cells, reduced representation bisulfite sequencing of the 8 priority tissues, fibroblast functional assays and further phenotyping through sequencing of microbiome samples. Notably, over $44,000 was contributed by individual members of the research community in addition to the funding provided by Grayson Jockey Club Foundation to support this work. ChIP-seq assays are currently being performed for two tissues and optimized for the other six prioritized, with expected completion in the Spring of 2018.  All of these data are made publically available following FAANG guidelines (8 prioritized tissues immediately available and researcher-funded tissues available after a 6-month embargo period if requested).

**3: Facilitate analysis, curation, storage, distribution and application of the enormous datasets now being generated by next-generation sequencing and related "omics" technologies with regard to animal species of agricultural interest.**

The equine community continues to add information to the [animalgenome.org](http://animalgenome.org/) repository and AnimalQTL db, including new custom tracks in 2017 for CNV and SV. <https://www.animalgenome.org/repository/horse/6_horse-breeds_variants/> <https://www.animalgenome.org/cgi-bin/QTLdb/EC/summary>.

ENA reports release of 932 sequences for EquCab in 2017. <https://www.ebi.ac.uk/ena/data/warehouse/search?query=%22tax_eq(9796)%20AND%20first_public%3E2017-01-01%22&domain=sequence>.

Work continues on developing a large database of genetic variants for the horse based on short-read whole genome sequences. With the release of EquCab 3.0 approximately 700-800 genomes will be re-mapped using a standard state of the art pipeline being developed in conjunction with Interval Bio (www.interval.bio). This database will allow for both open and restricted data sharing by investigators. Working with the University of Minnesota with funding from USDA NIFA Genome tools grants, Interval Bio plans to have the database, GUI, and API available in September 2018.

Several groups are working towards improving the annotation of the new EquCab 3.0 genome release. In addition to use of the RNA- and ChIP-seq data generated as part of the FAANG consortium there are on-going efforts to use RNAseq datasets from large numbers of horses in diverse tissues including using network-based approaches to functionally annotate lncRNA and small RNAs across equine tissues.

Communication:The coordinators maintain an email list and use it to broadcast information for USDA-NRSP8, the USDA, the Havemeyer Foundation and other information relevant to the workshop. In addition to the PAG conference, the Dorothy Russell Havemeyer Foundation International Equine Genome Mapping Workshop a meeting of the International Society for Animal Genetics is held every other year. Many of the NRSP8 members also participant in the biennial Equine Science Society Conferences.

In 2017 the Brooks lab, we continued our online extension short course designed to translate discoveries in equine genetics to application by stakeholders. 37 participants took this course from locations in four countries and included 16 participants utilizing a translation into Brazilian Portuguese provided by Laura Patterson-Rosa. Given the strongly positive evaluations of the course, we are now renovating the material to accommodate a rolling admission system better tailored to the adult professional audience.

### Summary of Funding Reported in support of Equine Genomics

Based on 16 Stations reporting: 6 international and 10 US

|  |  |  |  |
| --- | --- | --- | --- |
| **Institution** | **Internal** | **Industry** | **Federal** |
| US | $505,693  | $918,165  | $1,094,329  |
| International | $674,009  | $243,111  | $1,533,801  |
| Total | $1,179,702  | $1,161,276  | $2,628,130  |

### Specific Industry and Federal Grants Reported

**Finno, University of California – Davis; total for 2017 $585,064**

Center for Equine Health, The effect of alpha-tocopherol supplementation on vitamin E metabolism in healthy horses and horses with neuroaxonal dystrophy $34,244

Center for Equine Health, Validation of putative genetic variants for equine neuroaxonal dystrophy $29,795

Center for Equine Health, Validation of putative genetic variants for juvenile idiopathic epilepsy in Arabian horses, $8,452

Center for Equine Health, Genetic investigation of idiopathic persistent hypocalcemia in the Thoroughbred $12,491

Priority Partnership Collaboration Award Secrets in the bones: how functional genomics will broaden our understanding of catastrophic breakdown in racehorses $30,580

Grayson Jockey Club Foundation, Unraveling complex traits by defining genome function (Part I) $199,177

Arabian Horse Association Genetic Investigation of occipitoatlantoaxial malformation (OAAM) in Arabian Horses $6,294

NIH 1K01OD015134 Molecular pathogenesis of alpha-tocopherol associated neuroaxonal dystrophy in animal models $101,354 direct costs/year

NIH L40 TR001136 Molecular pathogenesis of alpha-tocopherol associated neuroaxonal dystrophy in animal models $70,000 direct costs/year

NIH Office of Dietary Supplements Biomarkers of alpha-tocopherol efficacy in animal models of neurodegeneration $92,677 direct costs/year

**Hill, UC Dublin/Plus Vital; total for 2017 $664, 373**

Enterprise Ireland Innovation Partnership Programme, 2017-19 (IP 2016 0503) Assessment of the Energetic Benefits of Plusvital Supplements/Nutrients on Thoroughbred Horses, €295,286

Enterprise Ireland R&D Fund grant (to Equinome Ltd.), 2015–17 (158281/RR, 158282/RF): A catalogue of genomic variation contributing to racing success in Thoroughbred horses: enabling genomic prediction for commercial genetic testing of elite performance potential. €192,270

Science Foundation Ireland Principal Investigator Career Advancement Programme, 2012-17: Integrated genomics approaches to understanding genetic contributions to system-wide exercise physiology parameters in a large animal model, €1,863,205.

**MacLeod, University of Kentucky; total for 2017 $144,490**

2016-2017.  American College of Veterinary Surgeons. Comparative chondrogenic potential of equine fetal progenitor cells and adult mesenchymal stem cells. Total direct support: $22,943

2016-2019.  Morris Animal Foundation. Developmental Progenitor Cells of Articular Cartilage. Principal Investigator, Total direct support: $121,547.

**McCue and Mickelson, University of Minnesota; total for 2017 $804,890**

Metabolomics in Equine Metabolic Syndrome: Molecular pathophysiology and biomarker discovery, American Quarter Horse Association, ME McCue and JR Mickelson, $77,556 total, 10/2016 – 10/2017. Funds for 2017 = $77,556.

Functional Prioritization of Candidate Genes and Alleles for Equine Metabolic Syndrome, Morris Animal Foundation, ME McCue, $197,000 total, 2017 – 2019. Funds for 2017 = $97,000

Integrated metabolomic and genomic approach to metabolic variation across horse breeds (2016-2018). Morris Animal Foundation Post-Doctoral Fellowship to Felipe Avila, Budget $100,000. Funds for 2017 = $50,000.

Functional Prioritization of Candidate Genes and Alleles for Equine Metabolic Syndrome (2017-2019). Morris Animal Foundation Post-Doctoral Fellowship for Elaine Norton, ME McCue Mentor. Budget for 2017 = $45,000**.**

Tools to Link Phenotype to Genotype in the Horse, USDA/NIFA/AFRI, ME McCue and JR Mickelson; $500,000 total, 2017 – 2020. Funds for 2017 = $166,667

Functional Prioritization of Genes and Alleles for Equine Metabolic Syndrome, USDA/NIFA/AFRI, ME McCue and JR Mickelson $499,000 total, 2017 – 2019. Funds for 2017 = $166,667

Discovering causal variants for complex disease using functional networks in the horse (2015-2017). USDA-NIFA Post-Doctoral Fellowship for Rob Schaefer, ME McCue Mentor, Budget $150,000. Funds for 2017 = $75,000.

Tools for Precision Medicine in the Horse (2016-2018) Minnesota Agricultural Experiment Station, Multistate Competitive Grants Program. ME McCue $68,000, funds for 2017 = $34,000

Genetic variants responsible for health and performance in the Quarter Horse (2017) American Quarter Horse Foundation, ME McCue Budget $67,171, 2017 budget = $33,000

Genetic Basis of Recurrent Exertional Rhabdomyolysis (2017-2021) NIH Office of Research Infrastructure Programs, F30 Dual-Degree Fellowship for Samantha Beeson, ME McCue Mentor, Budget $240,600. Funds for 2017= $60,000

**Bellone, UC Davis total for 2017;** **$46,106**

2016-2018 *Grant awarded from Morris Animal Foundation,*(D16EQ-820)Project Title: “Genetic Investigation of Bilateral Corneal Stromal Loss in Friesian Horses.” Funds for 2017: $10,300

2016-2019 $136,996 *Grant awarded from Morris Animal Foundation,*(D16EQ-028) “Genomic Investigation of Equine Recurrent Uveitis in Appaloosa Horses.”  Funds for 2017: $35,806 *Bellone (PI) McCue and Lassaline (Co-investigators)*

**Mienaltowski, UC Davis; total for 2017 $10,800**

Morris Animal Foundation; Grant Title: “Decoding Equine Tendon Transcriptomes to Understand Tendon Growth, Maturation, and Aging”; $10,800

**Valberg, Michigan State University; total for 2017 $141,816**

2016/2018 Morris Animal Foundation $142,909 Muscle Calcium Regulatory Proteins Unique to Horses: Implications for Exertional Rhabdomyolysis CoPI Valberg SJ coPI Thomas D, ~$47, 637/year

2016/2017 American Quarter Horse Association $19,359 Prevalence of the Mutation for Immune Mediated Myositis in the American Quarter Horse. PI CJ Finno, coPI Valberg SJ.

2017/2018 American College of Veterinary Internal Medicine $51,003 Identifying the genetic basis for a novel exertional myopathy. PI SJ Valberg

**Walner and Brem, University of Vienna; total for 2017 $305,397**

Characterization of stallion lines in Austrian horse breeds with Y-chromosomal markers - Austrian government funded (DANFE 101184/2) Applicant: Wallner B;86.000 €

Y-chromosomale Haplotypen prähistorischer Pferde zur Analyse der Domestikation, früher menschlicher Siedlungsgesellschaften, Migrationsvorgänge und kriegerischer Auseinandersetzungen (Austrian Academy of Sciences, IF\_2015\_17) Applicant: Gottfried Brem 160.000€

**Brooks University of Florida; total for 2017: $325, 591**

6/2017-5/2018 Identification of polymorphisms for the Sunshine coat color dilution. Etalon Inc. Funds for 2017= $1,926

5/2017 Excellence Award for Assistant Professors. UF Provost $5000

11/2016- 4/2018 Transcriptome Analysis of Supporting Limb Laminitis (AWD01050) AAEPF Funds for 2017= $95,526

10/2016 – 9/2017 Genetics of Anhidrosis in the American Quarter Horse (AWD00241) AQHF Funds for 2017= $53,247

11/2013 – 4/2017 Comparative Animal Genomics in Qatar (00092985) QNRF Funds for 2017= $169,892

**Swiderski, Mississippi State University; total for 2017 $206,045**

2015-2018.  USDA/NIFA/AFRI. Protein Networks Mediating Airway Hyper-responsiveness in Horses. Swiderski CE (PD), Bowser JE, Nanduri B, Claude A, Eddy A. Budget: $438,153. Funds for 2017= $194,345

2016-2018.  Morris Animal Foundation. Cryopreserved precision cut lung slices for investigating the regulation of airway contraction in horses. Swiderski CE (PI), Bowser JE, Lopez-Soberal. Budget: $10,800. Funds for 2017=$5,200

2017-2018. Mississippi State University Office of Research. Does Continuous Exposure to Oxygen/Carbon Dioxide Improve Viability of Isolated Bronchial Rings. Swiderski CE, Bowser JE, Dittmar W. Budget: $3,000 Funds for 2017= $ 1,500

2016-2018. College of Veterinary Medicine, Mississippi State University. Determining the Role of a Novel Ion Channel in a Severe, Neutrophilic Asthmatic Phenotype. Swiderski CE (PI), Hunter CL, Nanduri B, McCarthy F, Costa LRR. Budget: $10,000. Funds for 2017=$5,000

**Gabriella Lindgren, SLU; total for 2017 $399,000**

2017-2020. Swedish Research Council (VR), 3.475.000 SEK = 449.000 USD. Tracing the genetic origin of the horse mane: an innovative model to identify genetic factors that regulate hair growth. Main applicant: Gabriella Lindgren, SLU, Uppsala. Co-PI: Juan Negro, Donana Biological Station, Seville. For 2017: 869.000 SEK = 110.000 USD.

2017-2019. Swedish Research Council (FORMAS), 2.996.000 SEK = 379.000 USD. Genomic studies of horses lead the way to unravel genetic regulation of locomotion pattern and performance traits. Main applicant: Gabriella Lindgren, SLU, Uppsala. For 2017: 1.000.000 SEK = 126.000 USD.

2016-2018, Swedish-Norwegian foundation for equine research (Stiftelsen Hästforskning, SHF), 3.861.000 SEK = 488.000 USD. Mapping performance, genetic variation and health in the Coldblooded trotter. Main applicant in Sweden: Gabriella Lindgren, SLU, Uppsala, main applicant in Norway: Eric Strand, NMBU, Oslo. For 2017 1.287.000 SEK = 163.000 USD.

**Monika Bugno-Poniewierska, Tomasz Ząbek, Katarzyna Ropka-Molik, Tomasz Szmatoła, Klaudia Pawlina, Agnieszka Fornal, Magdalena Wojtaszek, Katarzyna Kowalska - National Research Institute of Animal Production and Monika Stefaniuk-Szmukier - Univerity of Agriculture Krakow; total for 2017 $1,980,198**

Name of Grant Agency -National Science Center; "Analysis of changes in transcriptome profile of blood and skeletal muscle in Arabian horses during training regime, using by the method based on Next Generation Sequencing - RNA-seq"; Grant identification number 2014/15/D/NZ9/05256; $206,000

Name of Grant Agency -National Centre for Research and Development; Title of Grant” Directions of use and protection of genetic resources of livestock in conditions of sustainable development"; Grant identification number BIOSTRATEG2/297267/14/NCBR/2016

**Task1 –** $1,209,632: The use of the achievements of molecular genetics in the selection and elimination of animals affected by diseases of genetic origin

**Task 2** - $564,566: Development of new methods of preservation and selection criteria for donors of isolated genetic material for use in programs related to preserving biodiversity of breeds.

**Hamilton, University of Sydney; total for 2017 $166,157**

2017 ~ $USD 107,657 Racing Australia (Industry body) grant "Development of an assay to detect gene doping in Thoroughbred horses"

Dr. Anna Bautina (collaborator) at the National Measurement Institute

2017 $58,500 Racing Australia (Industry body) grant private genotyping consultancy.

### Publications for 2017

Al Abri, M.A., König von Borstel, U., Strecker, V. and Brooks, S.A. (2017) 'Application of Genomic Estimation Methods of Inbreeding and Population Structure in an Arabian Horse Herd', *Journal of Heredity*, 108(4), 361-368, available: http://dx.doi.org/10.1093/jhered/esx025.

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Bauer A, Hiemesch T, Jagannathan V, Neuditschko M, Bachmann I, Rieder S, Mikko S, Penedo MC, Tarasova N, Vitková M, Sirtori N, Roccabianca P, Leeb T, Welle MM. A Nonsense Variant in the ST14 Gene in Akhal-Teke Horses with Naked Foal Syndrome. G3 (Bethesda). 2017 Apr 3;7(4):1315-1321. doi: 10.1534/g3.117.039511.

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## POULTRY TECHNICAL REPORT

### Leadership

Mary Delany, Dept. of Animal Science, UC Davis, served as Coordinator with Hans Cheng, USDA, ARS, ADOL, as Co-Coordinator.

### The NRSP-8 Poultry Workshop

The workshop was held January 14-15, 2017 at the Plant & Animal Genome Conference, San Diego CA, attendance overview:

Attendance during the 1.5-day workshop averaged n=75 with peak attendance in excess of 120.

Representatives of 16 agricultural experiment stations attended from across the US including the membership of NRSP-8 Poultry group: Iowa State, Michigan State, University of Arizona, Univ of Delaware, Univ of Georgia, University of California Davis, University of Minnesota, Beckman Research Institute, USDA-ARS.

Attendees also included members of the poultry layer and broiler breeding companies, U.S. government officials, and scientists from the United Kingdom, Germany, Canada, Sweden, Netherlands, Thailand, and China

### Grants

* Kent Reed, Univ of Minnesota:

Effect of AFB1 on immune tissues of turkeys from diverse genetic backgrounds. USDA-UMN Multi-State Project, 2016-2018, $94,221;

USDA National needs fellowship for enhancing animal production: Addressing national need in poultry production. USDA-NIFA-NNF. 2016-2021, $241,000;

Antibiotic-free alternatives to improve health and performance in commercial turkeys. USDA-NIFA-AFRI. 2016-2018, $464,000;

Influence of thermal challenge on turkey muscle development and meat quality. USDA-NIFA-AFRI. 2014-2018, $975,000.

* Marcia Miller: Beckman Research Institute, City of Hope Medical Center, CA:

USDA NIFA Foundational Program *Understanding Antimicrobial Resistance*.  Award: $387,518.00.  Period of Performance:  06/01/2017-05/31/2020.  MHC-Y-Directed Immune Responses during Colonization of Chickens by *Campylobacter.*

* Doug Rhoads, Univ Arkansas:

Marker Assisted Selection for Ascites Resistance in Broilers.  NIFA-AFRI; 11/2014-10/2017; $467,000; PI: Rhoads

* H. Zhou, UC Davis:

$9,212,800 from USAID, USDA, Egg Industry Center, France-Berkeley Fund including newly funded $737,800 during that period.

### Impacts

Our members are highly focused on fundamental, translational and applied research to benefit U.S. Agriculture and through genomics improve poultry health and contribute to the productivity of the relevant industries. Below are listed some of the highlights from 2016-17 research. Many of the efforts are focused on projects that directly impact poultry health and production.

**Extreme temperature variations** threaten the quality of poultry muscle as a healthy, high quality food product. Identification of molecular mechanisms associated with altered muscle development will result in development of mitigation strategies based on improved genetic selection, nutritional intervention, and other strategies to improve poultry muscle food quality and quantity. **Likewise, exposure to aflatoxin (AFB1)** causes annual industry losses estimated in excess of $500 M. Increasing innate resistance to AFB1 could result in numerous health benefits. Transformational improvements in AFB1 resistance require a multidisciplinary approach to identify protective alleles with potential to reduce disease. Genetic markers to improve AFB1-resistance have a potentially high commercial value and positive economic impact to industry, owing to improvements in health and well-being, productivity, and a safer product for consumers. **The gastrointestinal health of an animal is key to its successful growth and development.** Elimination of subtherapeutic antibiotics for growth promotion and health in poultry will leave a critical void. This project will improve our mechanistic understanding of host-microbiome interactions in the avian host and identify feasible approaches towards modulating the turkey intestinal microbiome resulting in enhanced health and performance.

**Whole** **genome resequencing was utilized to identify and fine map 31 potential QTLs for ascites** which would be a major breakthrough in methods to map complex traits in domestic animals.  We have been examining the basis for resistance and susceptibility to bacterial diseases in bacterial chondronecrosis with osteomyelitis in broilers.

**Provision of unique poultry genetic materials** (chicks, fertile eggs, DNA) to group members enabled multi-state collaborative research on topics including genetics of resistance to heat and pathogens, and allele-specific expression.

**BRI SMRT was utilized to sequence BAC clones corresponding to the MHC-*Y* region in the red jungle fowl (RJF) reference genome**.  The MHC-*Y* genomic sequence revealed the presence of 91 genes within 649 kbp contained within four contigs.  The 91 genes are located within dense arrays of repetitive sequences. This represents most but perhaps not all the RJF MHC-*Y* haplotype. The MHC-Y region is likely segmented and subject to variation among haplotypes in gene copy number.  In addition, we sequenced 137 kbp of the closely adjacent ribosomal RNA region.  Within this sequence are four ribosomal RNA units along with intervening sequence.  These data (soon to be published) add substantially to the genome assembly for chicken chromosome 16

**ChIP-seq and ATAC-seq assays developed and other -omic data generated for regulatory elements annotation will be important for not only poultry but the entire animal genome community.**  Identification of genes that are associated with resistance to heat stress and Newcastle disease virus can be used to genetic enhancement of disease resistance of chicken in adaption to hot climate. Knowledge of genes associated with enhanced immune response may inform further information on vaccine efficacy in poultry production. Understanding the impact of gut associated pathogen on microbiota composition at different development stages will provide great insights in improve gut health and subsequently increase production efficiency and animal well-being.

**Understanding of the driver mutations for Marek’s is a key gap in our knowledge of genomic-based causation contributions by the host.** Ikaros is the first discovered Marek’s disease driver gene.  Based on human and mouse studies, somatic mutations in the Zn-finger binding domains will lead to uncontrolled proliferation of T cells.  Marek’s disease virus Meq is likely to prevent apoptosis of these rapidly growing cells by inhibiting bcl-xL.

**Bioinformatics and annotation projects provide poultry researchers with the ability to effectively translate genomics data into knowledge** that can be applied to agricultural systems. A search of the CRIS database identifies almost 260 actively funded genomics projects; this represents millions of dollars of investment in animal production. The direct **economic impact** of our research is to enable this investment to be more readily applied to production systems. In addition to the economic impact, strategies to reduce or eliminate the severity animal disease also broadly impact society.

## SHEEP AND GOATS TECHNICAL REPORT

### Leadership

Coordinator: Noelle Cockett

Co-coordinator: Stephen White

**PARTICIPANTS:**

 Cornell University: Heather Huson\*

Louisiana State University: James E. Miller\*1

North Carolina A & T: Mulumebet (Meli) Worku\*1

Oklahoma State University: Udaya DeSilva\*

Pennsylvania State University: Wansheng Liu\*1

Texas A&M University: Clare Gill\*1, Penny Riggs\*

University of Florida: Raluca Mateescu\*

University of Idaho: Brenda Murdoch\*1

University of Massachusetts-Amherst: Janice Telfer\*1, Cynthia Baldwin\*

University of Vermont: Stephanie McKay\*1

USDA/ARS: Michelle R. Mousel\*1, Stephen N. White\*1

USDA ARS: Jennifer Woodward-Greene

Utah State University: Noelle E. Cockett\*

Virginia State University: Brian Sayre\*, Glenn Harris\*

Virginia Tech: Rebecca Cockrum\*1

\*Voting member.

1In attendance at the 2018 NRSP-8 meeting.

### BRIEF SUMMARY OF MINUTES OF ANNUAL MEETING:

The 2018 annual meeting of the NRSP-8 Cattle, Sheep, and Goat committee was held on Jan 13-14 in conjunction with the Plant and Animal Genome XXVI meeting. The morning session of the scientific meeting on Jan 13th was held as a joint session in with the Swine Committee with a total of 6 presentations. Theses presentations included an over view of the genomic tools and improvements, genomic resources, manual annotation, the identification of regulatory region, disease challenge models and complex trait, and implications for genomic prediction from sequence data. The Saturday afternoon and Sunday morning sessions of the combined Cattle/Sheep/Goat workshops included 17 presentations covering a wide variety of topics, from the numerous different cattle genome assemblies, imputation, copy number variation, annotation of immune gene clusters, analyses of the microbiome, methylation, feed efficiency, genetic signatures, and high-resolution atlas of gene expression in sheep. Attendance at the sessions was good with more than 220 people attending the Cattle/ Swine scientific session, including delegates from Academia, Industry and Governments and at least 24 countries. Attendance at the Cattle/Sheep/Goat 1 workshop included 100 people from 16 countries, and in attendance at the Cattle/Sheep/Goat 2 workshop there were 128 people from 22 different countries. Additionally, there were 42 cattle and 25 sheep and goat posters presented. Brenda Murdoch was thanked for serving as President of the NRSP-8 Cattle, Sheep and Goat Committee in 2017-18. Rebecca Cockrum will serve as President in 2018-19. Ben Rosen was elected as the 2018-2019 Secretary, and he will serve as President in 2019-2020.

### ACCOMPLISHMENTS AND IMPACTS:

***Objective 1:* Advance the status of reference genomes for all species, including basic annotation of worldwide genetic variation, by broad sequencing among different lines and breeds of animals.**

The NRSP-8 sheep co-coordinators are participants in the International Sheep Genome Consortium (ISGC) (<http://www.sheephapmap.org/>). This multi-institutional organization has assumed a key role in the coordination and prioritization of ovine genomic resources. An ongoing project of the ISGC is development of a whole genome reference assembly. In 2010, sequence data were generated at two sequencing facilities (Beijing Genomics Institute and the Roslin Institute) from DNA of a Texel ewe and a Texel ram, respectively. The ovine whole genome assembly built on these two sequences was released in October, 2012 as Oar v3.1 through NCBI. Kim Worley (BCM-HGSC) has used PacBio sequence data with PBJelly to fill in gaps and improve the male Texel sheep assembly. The assembly is more contiguous, with the contig N50 increasing from 41.7 kb to 165.2 kb. Also, almost 25% of the contigs are larger than 100kb (8,527; increased from 2,355). This version of the ovine genome reference sequence (Oar v4.0) was released in August, 2015 through NCBI. Using funds from a 2013 NIFA/AFRI grant (K. Worley, PD), a very high quality “de novo” whole genome sequence has been constructed using genomic DNA from a Rambouillet ewe (Benz 2616) and 66-fold PacBio long-read sequence data with Hi-C proximity ligation sequence data for scaffolding. This version (Oar­\_rambouillet\_v1.0), which has a total sequence length of 2.87 Gbp, a contig N50 of 2.5Mb and 0 gaps between scaffolds, has been released in GenBank (<https://www.ncbi.nlm.nih.gov/assembly/GCA_002742125.1>).

The Ovine FAANG Project, which has been awarded a 2016 NIFA/AFRIgrant (B. Murdoch PD), includes investigators from several US institutions (USDA/ARS MARC, Washington State University, Utah State University, University of Idaho, BCM-HGSC and Virginia Tech), CSIRO (Australia), Roslin Institute (UK) and AgResearch (New Zealand). This project will contribute to the core activities of FAANG by providing transcriptome data and detailed annotation of genes and regulatory features in the sheep. All transcriptome and regulatory data generated in the Ovine FAANG Project will directly connect to the *de novo* reference genome sequence generated from Benz 2616. Over 100 tissues were collected from Benz 2616 in April 2016; these tissues are archived in EMBL-EBI BioSamples under identifier GSB-7268 and sample accession number SAMEA104495037. The protocols used in collection can be found on the FAANG ftp site:

ftp://ftp.faang.ebi.ac.uk/ftp/protocols/samples/USU\_SOP\_Ovine\_Benz2616\_Cell\_Isolation\_20160426.pdf

ftp://ftp.faang.ebi.ac.uk/ftp/protocols/samples/USU\_SOP\_Ovine\_Benz2616\_Tissue\_Collection\_20160426.pdf

Ovine FAANG sequence was generated by K. Worley (BCM-HGSC) during the first half of 2017 from 20 samples for miRNA sequence, 9 samples for mRNA sequence and 5 samples for long-read mRNA sequence. Ongoing efforts by BCM-HGSC will phase the genome and incorporate the long-read transcript data into the annotations of the Oar­\_rambouillet\_v1.0 assembly. B. Murdoch (U. of Idaho) is using cap analysis of gene expression (CAGE) to identify active promoters and confirm transcription start sites, and ATAC-seq will be used by S. White and M. Mousel (USDA-ARS/Washington State U.) to assess chromatin accessibility.

WC1 co-receptors belong to the scavenger receptor cysteine-rich (SRCR) superfamily and are encoded by a multi-gene family. Each type I transmembrane bovine WC1 protein contains an extracellular SRCR domain arrangement that can be characterized as [a1-(b2-c3-d4-e5-d6) -(b7-c8-d9-e10-d’11)] or [a1-(b2-c3-d4-e5-d’11). The repetitive nature of the exon duplication and gene duplication makes annotation of the WC1 locus challenging; thus, techniques worked out in this project will have an impact on annotation of other gene and exon duplicated loci.

Expression of particular WC1 genes defines functional subpopulations of lymphocytes known as WC1 gamma delta T cells. WC1 genes can be grouped as WC1.1-type or WC1.2-type based on the sequence of their N-terminal a1 SRCR domain, which is 4 amino acids longer for WC1.2 type a1 SRCR domains. Reciprocal expression of either WC1.1-type or WC1.2-type proteins is correlated with gamma delta T cell responsiveness to pathogens, which explains how so many large homologous open reading frames have been maintained for millions of years. We have previously identified complete genomic sequences for 13 different bovine WC1 genes through annotation of the bovine genome Btau\_3.1 build. In 2017, we made significant progress in verifying caprine gene models obtained through annotation of the PacBio sequenced San Clemente goat genome, by comparison to the Yunan goat genome and cloning of corresponding full-length WC1 cDNA from the UMass Boer goat herd. We also cloned homologous WC1 cDNA from the UMass Dorset sheep flock. Because each goat breed contains non-overlapping WC1 genes or cDNA, we estimate that there are 28 caprine and ovine WC1 genes, some of which may be pseudogenes or encode soluble SRCR domains instead of a transmembrane receptor. In order to resolve this question, we are pursuing a next generation sequencing overview of WC1 gene transcripts. We have almost completed the cloning and sequencing of 7 porcine WC1 cDNA from Yorkshire x Duroc cross piglets from a local farm, with sequence from the 5’ UTR to the 3’ UTR. Only 2 of the 7 are currently annotated in the swine genome; thus, we plan to complete swine WC1 gene annotation and database deposition in 2018.

***Objective 2:* Develop strategies to identify and exploit genes and allelic variation that contribute to economically relevant phenotypes and traits, in part through improving functional annotation of the genomes of our species.**

While sheep scrapie has well-defined genetic resistance, the genetics of goat scrapie have not been as well understood. There are multiple amino acid substitutions in the PRNP gene which are known to be underrepresented in scrapie positive goats, but for which the incubation times from inoculation to development of disease have not been characterized. An oral challenge experiment has demonstrated highly significant extended scrapie incubation in animals singly heterozygous for either PRNP S146 or K222 that now extend beyond an average age of 6 years, which is also longer than the commercial lifetimes of many goats.

Entropion is thought to be a recessive genetic disorder and is defined as a laxity of the horizontal lid margin allowing inversion of the eyelid causing lashes or external hairs to rub against the ocular surface. A GWAS was conducted with the severity of entropion categorized as 0, 1, or 2 eyes afflicted in 513 white-faced sheep. Six genomic regions were significantly associated severity of entropion. Further evaluation of these data is ongoing to narrow the region which contains the underlying causal mutation(s). Once the causal mutation(s) are identified producers could use marker assisted selection to more quickly progress to an entropion free flock.

*Coxiella burnetii* is a zoonotic gram-negative organism broadly endemic in most of the world, and domestic ruminants (especially small ruminants) are blamed for disease outbreaks in human populations. We are generating phenotypic data in small ruminants to enable additional research on *C. burnetii* related traits.

An association of sheep KCC3b with blood sodium concentration suggested a role for the R31I variant in dimer function. To our knowledge, this is the first report of any KCC3 genotype association with sodium phenotypes in any mammal. KCC3 is an important hypertension gene with known roles in potassium transport, but the mechanism underlying this association with blood sodium is not well understood at present.

Understanding parasite resistance in sheep. This project was funded in the beginning of 2016 with the aim understanding parasite resistance and resilience and generating estimated breeding value regarding this trait for the industry. To date this project has collected fecal samples, performed FEC and collected blood samples for year one animal and is now entering year two of collections.

Meiotic recombination is an essential process in gametogenesis that ensures proper chromosome segregation and contributes to genetic variation. Interestingly, genetic recombination can differ in different breeds of sheep (Suffolk exhibit 61, Icelandic 64 and Targhee 66 meiotic recombination event per spermatocyte) and is approximately 20% higher than what has been observed in cattle breeds. The characterization and quantification of meiotic recombination should provide valuable information towards improved reproduction and genetic predictions in sheep.

To encourage and enable increased phenotypic collection of carcass trait in sheep data the University of Idaho and WSU were awarded funds to host a carcass scanning school. This school is intended to train personnel in the collection of accurate carcass data.

Estimation of the effective population size in sheep based on recombination rate by the LD method**.** Effective population size (Ne) is a key parameter in population genetics and is widely applied in determining the rate of genetic drift and loss of genetic variability. It is crucial to consider in animal breeding, selection and conservation. The linkage disequilibrium (LD) method performs better in the Ne estimation when genome-wide SNPs applied. Genome-wide SNP data of three commercial sheep breeds, including Texel, Merino and Suffolk, were downloaded from the ISGC database. Chromosome-specific recombination rates were estimated for all autosomes from estimated LD between SNP pairs and the known map length of chromosome. We found that the decay in LD over distance between SNPs within sheep populations is consistent with the recent population decrease. However, our estimated Ne for these sheep populations were about 40% higher than the previously report, possibly because we used the estimated recombination rate, not the theoretical value of 1 Mb = 1 centi-Morgan.

Identifying genetic variants responsible for photosensitivity and hyperbilirubinemia in Southdown sheep: A **p**hotosensitivity and hyperbilirubinemia disease was first described in New Zealand Southdown sheep in 1942. It was determined to be a sub-lethal recessively inherited trait. It was subsequently seen in California in the 1960s. In collaboration with Drs. Bud Tennant (deceased) and Nate Sutter, whole genome sequencing was performed on a known heterozygote individual. Sequencing identified a deleterious mutation within *Slco1b3*, a gene expressed in the liver known to be involved in bilirubin uptake. This manuscript has been accepted and is in press in *American Journal of Veterinary Research.*

Increasing Annual Lamb Productivity through the Identification of Genes and Diagnostic for Selection of Out of Season Breeding: Several approaches were taken to identify regions of the genome contributing to out of season breeding. GWAS was performed using HD SNP chip data on 257 ewes of various breeds. Analysis across breed and within the Dorset and Polypay breeds identified several QTLs that are biologically plausible in genetic control of out of season lambing. In particular, identified pathways involved eye development and known hormones involved in reproductive capability. This manuscript will be submitted to *BMC Genomics* this month.

Identification of genes associated with mature body size and growth:615 ewes, across 22 breed, were characterized for mature body size using 28 measures of various body parts to get an accurate representation of skeletal size. Principal component analysis was performed on the measurements to represent overall body size (PC1) and body thickness (PC2). 184 of these ewes are genotyped on the HD SNP chip. We plan to perform GWAS for mature body size and body thickness both across and within breed. We have birth weight and weaning weight data on 104 individuals we plan to analyze for growth trait associations along with mature body size. Analysis is ongoing.

Characterizing genetic variants responsible for coat color changes in United States sheep breeds: The genetic basis for brown coat color has been identified in several US sheep breeds. Experiment.com/moorit-sheep was used to raise funds to perform Sanger sequencing of *TYRP1* in several U.S. sheep breeds known to have color variation. Two mutations were associated with brown versus black. This project will be presented at the 11th World Congress on Genetics Applied to Livestock Production.

Genome-wide association studies identify candidate genes for coat color and mohair traits in the Iranian Markhoz goat:The Iranian Markhoz goat is an Angora type goat that was investigated for genetic variants related to coat color and fleece traits. Significant associations to coat color were found within or near the *ASIP,* *ITCH*, *AHCY*, and *RALY* genes on chromosome 13 for black and brown coat color and the *KIT* gene on chromosome 6 for white coat color. Individual mohair traits were analyzed for genetic association along with principal components that allowed for a broader perspective of combined traits reflecting overall mohair quality and volume. A multitude of markers demonstrated significant association to mohair traits highlighting potential candidate genes of *POU1F1* on chromosome 1 for mohair quality, *MREG* on chromosome 2 for mohair volume, *DUOX1* on chromosome 10 for yearling fleece weight, and *ADGRV1* on chromosome 7 for grease percentage. Variation in allele frequencies and haplotypes were identified for coat color and differentiated common markers associated with both brown and black coat color. This manuscript is under revision in *Frontiers in Genetics.*

***Objective 3:* Facilitate analysis, curation, storage, distribution and application of the enormous datasets now being generated by next-generation sequencing and related "omics" technologies with regard to animal species of agricultural interest.**

A sheep genomes database, created by the ISGC using funds from a second 2013 NIFA/AFRI grant (N. Cockett, PD), currently contains whole genome sequences from 935 sheep from 21 countries and 69 breeds. H. Daetwyler (La Trobe University, Australia) presented the analyses of these sequences (Run 2) and alignment to Oar v3.1 during the January, 2018 ISGC meeting. Over 50 million SNPs and indels were identified with high confidence using two variant-calling platforms. Data in the database is publicly available (<http://www.ebi.ac.uk/eva/?eva-study=PRJEB14685>) via European Variation Archive (EVA), which provides public access of genome information, data storage and variant accessioning. Variants are available as raw (unfiltered) or filtered data following application of a comprehensive QC protocol and information about the variants can be found through dbSNP. Run 3 will align all Run2 sequences and any new sheep genomes to the Oar­\_rambouillet\_v1.0 assembly and will be available at the end of 2018 to coincide with annotation of the assembly.

The whole genome sequence for the photosensitivity and hyperbilirubinemia heterozygote was submitted to NCBI’s SRA (SRR5749462).

### IMPACT / USEFULNESS OF FINDINGS:

### USEFULNESS OF FINDINGS:

The Ovine FAANG project will provide the enhanced functional annotation of the ovine genome in order to enable research in this sheep. Furthermore, this project will facilitate the understanding of gene regulation in sheep and other livestock species by generating and distributing curated transcriptome data.

The European Food Safety Authority (EFSA) convened a large expert panel that recognized the goat *PRNP* S146 and K222 alleles as scrapie resistance alleles in the latter half of 2017 (Ricci et al 2017), based in part on NRSP8 member data. They concluded that the evidence for scrapie resistance from both the S146 and K222 alleles is stronger today than the public evidence was in 2001 at the time of an important decision recommending use of scrapie resistant sheep bearing R171 (ARR haplotype). They also recommended European member states adopt genetic selection for these alleles as part of scrapie eradication efforts. While no implementation rules have been issued at present, the EFSA decision confirms the strength of the scientific evidence and sets the stage for formal adoption in government-run scrapie eradication efforts.

The KCC3b R31I substitution data open new avenues of research into the relationship of a known potassium transporter with sodium handling in mammals. Furthermore, they suggest sheep as a biomedical model for studying function in the hypertension gene KCC3.

The characterization of WC1 genes in ruminants and swine has utility in several areas: improved vaccine design against multiple important pathogens targeted to recruit gamma delta T cells, potential selective breeding based on SNPs in WC1 genes linked to resistance to pathogens, and the possible involvement of WC1 as a receptor in PRRSV infection of swine. Because WC1 genes are present in most mammalian and avian species, elucidation of WC1 genes in agriculturally important ruminants and swine has global application potential in improving food security and in containing zoonotic diseases in non-human animal reservoirs. This project also helps support undergraduate and graduate agricultural research training.

### Total Leveraged Funding Summary for 2015-2017

Federal Funding:                    $  3,138,500

State/Local/Institutional:        $  360,500

Industry:                                  $       46,200

**Total                                      $ 3,545,200**

### PUBLICATIONS:

**Refereed manuscripts and book chapters: 19**

Baldwin, C.L et. al. (11 authors on committee) National Academies of Sciences, Engineering, and Medicine. 2017. Revisiting Brucellosis in the Greater Yellowstone Area. The National Academies Press: Washington, DC. 209 pgs; ISBN 978-0-309-45831-3 | DOI 10.17226/24750 [<https://www.nap.edu/download/24750>]

Cinar, M.U., Schneider, D.A., Waldron, D.F., O’Rourke, K.I., White, S.N. Goats singly heterozygous for PRNP S146 or K222 orally inoculated with classical scrapie at birth show no disease at ages well beyond six years. The Veterinary Journal. (in press)

Dechow, C.D., Liu, W.-S. (2017) Genome-wide DNA methylation patterns and differential methylation in leukocytes from Holstein cattle with variable milk yield. BMC Genomics (manuscript under revision).

Dechow, C., Liu, W.-S., Idun, J., Maness, W. (2017) Two dominant paternal lineages for North American Jersey artificial insemination sires. J. Dairy Sci. (In Press). Ghadikolaei, A.N., Yeganeh, H.M., Miarei-Aashtiani, S.R., Staiger, E.A., Huson, H.J., Genome-wide association studies identify candidate genes for coat color and mohair traits in the Iranian Markhoz goat, *Frontiers in Genetics* (under revision Jan 2018)

Kiser, J.N., Neupane, M., White, S.N., Neibergs, H.L. Identification of genes associated with susceptibility to *Mycobacterium avium* ssp. *paratuberculosis* (Map) tissue infection in Holstein cattle using gene set enrichment analysis-SNP. Mammalian Genome. (in press)

Kiser, J.N., White, S.N., Johnson, K.A., Hoff, J., Taylor, J.F., Neibergs, H.L. Identification of loci associated with susceptibility to *Mycobacterium avium* subspecies *paratuberculosis* (Map) tissue infection in cattle. Journal of Animal Science. 95(3):1080-1091. 2017.

Liu, W.-S., Zhao, Y.Q., Lu, C., Ning, G., Ma, Y., Diaz, F., O'Connor, M. (2017) A novel testis-specific protein, PRAMEY, is involved in spermatogenesis in cattle. Reproduction 153, 847–863.

Mason, K.L., Gonzalez, M.V., Chung, C., Mousel, M.R., White, S.N., Taylor, J.B., Scoles, G.A. Detection of *Anaplasma ovis* and validation of improved A. marginale cELISA kit for diagnostic use in domestic sheep. Journal of Veterinary Diagnostic Investigation. 29(5):763-766. 2017.

Noelle E. Cockett, Brian Dalrymple, James Kijas, Brenda Murdoch, Kim C. Worley. Mapping the sheep genome, Chapter 5, *Achieving sustainable production of sheep* Burleigh Dodds Series in Agricultural Science (Book 22), Edited by Prof J.P.C. Greyling, Burleigh Dodds Science Publishing September 15, 2017

Notter, D. R., Mousel, M. R., Lewis, G. S., Leymaster, K. A., and Taylor, J. B. Evaluation of Rambouillet, Polypay, and Romanove-White Dorper x Rambouillet ewes mated to terminal sires in an extensive rangeland production system: lamb production. J. Anim. Sci. 95:3851-3862. 2017.

Oliveira, R.D., Mousel, M.R., Pabilonia, K.L., Highland, M.A., Taylor, J.B., Knowles, D.P., White, S.N. Domestic sheep show average *Coxiella burnetii* seropositivity generations after a sheep-associated human Q fever outbreak but lack detectable shedding by placental, vaginal, and fecal routes. PLoS One 12(11): e0188054. 2017.

Posbergh, C.J. & Huson, H.J., (2018) Making Moorit: Mutations in TYRP1 are responsible for brown coat color in different United States sheep breeds, *Proceedings 11th World Congress of Genetics Applied to Livestock Production*, (accepted, under revision Nov 2017).

Posbergh, C.J., Kalla, S.E., Sutter, N.B., Tennant, B.C., Huson, H.J., A mutation responsible for hyperbilirubinemia and photosensitivity in Southdown sheep similar to Rotor Syndrome *American Journal of Veterinary Research* (accepted July 2017, In Press

Posbergh, C.J., Thonney M.L., Huson H.J., The eyes have it: genomic approaches identify novel gene associations with aseasonality in sheep, *BMC Genomics* (submitted Jan 2018)

PrabhuDas M, Baldwin CL, Bollyky PL, Bowdish DME, Drickamer K, Febbraio M, Herz J, Kobzik L, Krieger M, Loike J, McVicker B, Means TK, Moestrup S, Post SR, Tatsuya Sawamura T, Silverstein S, Speth RC, Telfer JC, Thiele GM, Wang X-Y, Wright SD, El Khoury J. A Consensus Definitive Classification of Scavenger receptors. *Journal of Immunology* 2017; 198(10):3775-3789. doi: 10.4049/jimmunol.1700373. PMID: 28483986

Tezgel AÖ, Jacobs PT\*, Backlund CM, Telfer JC, Tew GN Synthetic Protein Mimics for Functional Protein Delivery. *Biomacromolecules* 2017; 18(3):819-825. doi: 10.1021/acs.biomac.6b01685. Epub 2017 Feb 27. PMID: 28165726.

White, S.N., Oliveira, R.D., Mousel, M.R., Gonzalez, M.V., Highland, M.A., Herndon, M.K., Taylor, J.B., Knowles, D.P. Underdominant KCC3b R31I association with blood sodium concentration in domestic sheep suggests role in oligomer function. Animal Genetics 48(5):626-627. 2017.

Zhang, Y.Y., Deng, X.G., Liu, W.-S., Deng, X.M. (2017) Estimation of recombination rate and effective population size with ovine genome-wide SNP-chip. Sciencepaper Online 201704-232

**Ph.D. thesis:**

Payal Damani Yokota “Regulation of expression of the gamma delta T cell co-receptor and pattern recognition receptor multi-gene family WC1.” 2017.

Kimberly Davenport “Understanding the ramification of meiotic recombination variation in male sheep” 2017.

**Published abstracts and proceedings: 25**

Cinar, M.U., Mousel, M.R., Herndon, M.K., Taylor, J.B., White, S.N. Tenascin-XB (TNXB) amino acid substitution E2004G is associated with mature weight and milk score in American Rambouillet, Targhee, Polypay, and Suffolk sheep. 2018. Plant & Animal Genomes XXVI, San Diego, CA, USA. Plant & Animal Genomes XXVI, San Diego, CA, USA.

Cinar, M.U., Schneider, D.A., Waldron, D.F., O’Rourke, K.I., White, S.N. Genetics of Goat Scrapie Resistance. 2017. American Goat Federation, Denver, CO, USA.

Cinar, M.U., Schneider, D.A., Waldron, D.F., O’Rourke, K.I., White, S.N. Goat PRNP alleles S146 and K222 result in long disease-free periods following scrapie inoculation. 2017. U.S. Animal Health Association, San Diego, CA, USA.

Cinar, M.U., Schneider, D.A., Madsen-Bouterse, S.A., Dassanayake, R.P., Waldron, D.F., O’Rourke, K.I., White, S.N. ADRU Scrapie Research Update, including Genetics of Goat Scrapie Resistance. 2017. USDA Animal Plant Inspection Service (APHIS), USA.

Damani-Yokota, P., Telfer, J.C., and Baldwin, C.L. Variegated gene expression and Sox13-mediated regulation of WC1 molecules, hybrid PRR/Co-receptor exclusive to γδ T cells. 2017 (talk and poster. American Association of Immunologists (AAI) meeting. Washington, D.C., USA. May 12-16.

Davenport K.M., Kalbfleisch T.S., McKay S., Heaton M.P, Murdoch B.M. Characterizing allelic variation in the recombination hotspot mediator gene PRDM9 in U.S. sheep. 2018. International Plant & Animal Genomes XXVI Conference, San Diego, CA. USA.

Davenport K.M., Rodriguez A.M., Sawyer R.J., Badigian T.M., Jaeger H.K., Follett M.A., Murdoch B.M. Investigating genetic associations with meiotic recombination in rams. 2017. 36th International Society of Animal Genetic Conference, Dublin, Ireland.

Dechow, C.D., Liu, W.-S. Genome-wide DNA methylation patterns and differential methylation in leukocytes from Holstein cattle. 2017 Conference Abstract, ADSA Annual Meeting, June 25-28, Pittsburg, PA. P380

Gillespie A., Connelley T., Telfer J.C., Baldwin C.L. Interaction of γδ TCR with the WC1 hybrid coreceptor/pathogen recognition receptor in cattle. 2017. American Association of Immunologists (AAI) meeting. (poster) Washington, D.C., USA. May 12-16.

LePage, L., Hsu, H., Nandi, D., Buck, J., Boisvert, N., Damani-Yokota, P., Yirsaw, A., Gillespie, A., Hudgeons, E., Amir, M., Park, H., Baldwin, C.L. and Telfer, J.C. WC1 is a hybrid co-receptor and a pathogen-associated molecular pattern receptor and co-receptor for the gamma delta TCR. 2017. (talk and poster) American Association of Immunologists (AAI) meeting. Washington, D.C., USA. May 12-16.

LePage, L., Hsu, H., Nandi, D., Buck, J., Boisvert, N., Damani-Yokota, P., Yirsaw, A., Gillespie, A., Hudgeons, E., Amir, M., Park, H., Baldwin, C.L. and Telfer, J.C. Molecular and functional variation of the γδ T cell pattern recognition receptor/co-receptor WC1 gene family among livestock. 2017 (poster and talk) NIFA-USDA Program Director meeting and CRWAD meeting, Chicago, IL, USA. December.

Liu Y, Harris R.A., Qin X., Richards S., Rogers J., Han Y., Meng Q., Smith T.P., Dalrymple B.P., White S.N., Murdoch B.M., Kijas J.W., Cockett N., Muzny D.M., Worley K.C. 36th Rambouillet Sheep Genome and FAANG RNA Resources. 2017. International Society of Animal Genetic Conference, Dublin, Ireland.

Liu, W.-S., Zhang, YY., Wang, A.H. Sex chromosome-linked cancer/testis antigens (CTAs) and male fertility in cattle. 2017. Conference Abstract, the 36th International Society for Animal Genetics Conference (ISAG), July 16-21, Dublin, Ireland. MT342.

Lu, C., Wu, W.W., Zhang, J.B., Zhao, Y.Q., Ocon-Grove, O.M., Diaz, F., Liu, W.-S. Blockage of the bovine PRAMEY protein with an anti-PRAMEY antibody leads to an increased rate of polyspermy in in vitro fertilization (IVF). 2017 Conference Abstract, the 50th Annual Meeting of the Society for the Study of Reproduction (SSR2017), July 1316, Washington, D.C. P284.

Massa, A.T., Mousel, M.R., Murdoch, B., White, S.N. ChIP-seq genome-wide identification of regulatory elements in sheep alveolar macrophages. 2018. Plant & Animal Genomes XXVI, San Diego, CA, USA.

Massa, A.T., Mousel, M.R., Murdoch, B., White, S.N. Gene regulation in sheep alveolar macrophages: Genome-wide identification of active enhnacers. 2017. International Society for Animal Genetics, Dublin, Ireland.

Mousel, M.R., White, S.N. Genomic regions associated with entropion in Columbia, Polypay, and Rambouillet breeds of sheep. 2017. International Society for Animal Genetics, Dublin, Ireland.

Mousel, M.R., White, S.N., Herndon, M.K. Genomic regions associated with entropion affecting one or both eyes of domestic sheep. 2018. Plant & Animal Genomes XXVI, San Diego, CA, USA.

Murdoch, B., White, S.N., Mousel, M.R., Massa, A.T., Worley, K., Archibald, A., Clark, E., Dalrymple, B., Kijas, J., Clarke, S., Brauning, R., Smith, T.P.L., Hadfield, T., Cockett, N. The Ovine Functional Annotation Project. 2017. International Society for Animal Genetics, Dublin, Ireland.

Murdoch, B., White, S.N., Mousel, M.R., Massa, A.T., Worley, K., Archibald, A., Clark, E., Dalrymple, B., Kijas, J., Clarke, S., Brauning, R., Smith, T.P.L., Hadfield, T., Cockett, N. The design of the functional annotation of the sheep genome project. 2018. Plant & Animal Genomes XXVI, San Diego, CA, USA.

Oliveira, R.D., Mousel, M.R., Gonzalez, M.V., Taylor, J.B., Knowles, D.P., White, S.N. Genome-wide association with monocyte count in domestic sheep. 2018. Plant & Animal Genomes XXVI, San Diego, CA, USA.

Stewart, W.C., Murphy, T.W., Notter, D.R., Mousel, M.R., Lewis, G.S., Leymaster, K.A., Taylor, J.B. Wool characteristics of Rambouillet, Polypay and Romanov-White Dorper x Rambouillet ewes in an extensive rangeland production system. 2017. American Society of Animal Science, Western Section Meeting. Fargo, ND, USA.

Telfer, J.C. and Baldwin, C.L. (invited talk) “WC1 hybrid pathogen recognition receptors and signaling co-receptors direct immune responses by bovine γδ T cells to pathogens” CRWAD meeting, December 2017.

White, S.N., Oliveira, R.D., Mousel, M.R., Gonzelz, M.V., Highland, M.A., Taylor, J.B., Knowles, D.P. Underdominant KCC3b R31I association with blood sodium concentration in domestic sheep suggests role in dimerization. 2017. International Society for Animal Genetics, Dublin, Ireland.

Zhang, Y.Y., Liu, W.-S., Deng, X.M. (2017) Estimation of the effective population size in sheep based on recombination rate by the LD method. Conference Abstract, International Plant and Animal Genome Research (PAG) XXVI, January 13-18, 2017. San Diego, CA. P1148.

**Invited Seminars:**

1. Developing the functional annotation of the sheep genome. Murdoch BM, White SN, Mousel MR, Massa AT, Worley KC, Archibald AL, Clark EL, Dalrymple B, Kijas J, Clarke S, Brauning R, Smith TPL, Hadfield T, Cockett N. International Sheep Genomics Consortium. Jan 15, 2018.
2. The Ovine FAANG Project. Murdoch BM, White SN, Mousel MR, Massa AT, Worley KC, Archibald AL, Clark EL, Dalrymple B, Kijas J, Clarke S, Brauning R, Smith TPL, Hadfield T, Cockett N. International Sheep Genomics Consortium. Jan 15, 2018.
3. Rambouillet Sheep Genomic Resources. Liu Y, Harris RA., Qin X, Richards S, Rogers J, Han Y, Vee V, Wang M, Meng Q, Heaton MP, Smith T.P.L., Dalrymple B, White SN, Murdoch BM, Kijas JW, Cockett N, Muzny DM, Gibbs R, Worley K. Plant & Animal Genomes XXV Conference, January 14, 2017.
4. Update on the Rambouillet Assembly, the 5.0 Reference, and plans for FAANG RNA Sequencing. Liu Y, Harris RA, Qin X, Richards S, Rogers J, Han Y, Vee V, Wang M, Meng Q, Heaton MP, Smith TPL, Dalrymple B, White SN, Murdoch BM, Kijas JW, Cockett N, Muzny DM, Gibbs R, Worley K. Plant & Animal Genomes XXV Conference, January 16, 2017.
5. Genome-Wide Landscape of Active Enhancers in Sheep Alveolar Macrophages. Massa A, Mousel M, Murdoch BM, White S. Plant & Animal Genomes XXV Conference, January 16, 2017.
6. Understanding the Ramification of Recombination Variation in Sheep. Davenport K and Murdoch BM. Plant & Animal Genomes XXV Conference, January 16, 2017.
7. Gene regulation in Sheep Alveolar Macrophages: Genome-Wide Identification of Active Enhancers. Massa A, Mousel M, Murdoch BM, White S. 36th International Society of Animal Genetic Conference, Dublin July 20, 2017.
8. Investigating Genetic Associations with Meiotic Recombination in Rams. Davenport K, Rodriguez AM, Sawyer RJ, Badigian TM, Jaeger H, Follet MA, Murdoch BM. 36th International Society of Animal Genetic Conference, Dublin July 20, 2017.
9. Strategies to employ molecular markers towards improved prediction of carcass quality. Murdoch B. Increased Efficiency of Sheep Production NCERA214 Lansing, Michigan June 11-14, 2017.
10. The Future of Sheep Production: Capturing Genetic Variation. Cockett N and Murdoch B. American Sheep Industry. Superior Farms board meeting. Denver, CO January 25-28, 2017.
11. Idaho cow-calf herds; a genetic resource for understanding and improving cow reproduction and calf growth efficiency. Murdoch B. NRSP8 Hatch report. San Diego Jan 14, 2017.
12. Ovine FAANG Project. Murdoch B. International Sheep Genome Consortium. San Diego Jan 16, 2017.
13. Ovine FAANG progress Murdoch B. FAANG consortium meeting International Plant and Animal Genome San Diego Jan 17, 2017.

### WORK PLANNED FOR NEXT YEAR:

1. Generation of Ovine FAANG Project data.
2. Annotation of sheep macrophage regulatory sites.
3. Development of *Coxiella burnetii* phenotypes.
4. Evaluation of genomic regions identified in GWAS of entropion.
5. Continued characterization of meiotic recombination differences.
6. Annotation of swine WC1 genes based on sequencing of full-length cDNA clones
7. Continued characterization of ovine and caprine WC1 genes and cDNA discovered via next generation sequencing overview
8. Completion of annotation of new Pac-Bio sequenced genomes and deposition of sequence into GenBank database
9. We will continue to work on the transcriptome of the bovine and ovine Y chromosome
10. WC1-pathogen binding studies

## SWINE TECHNICAL REPORT

### Leadership

Coordinator: Chris Tuggle

Co-coordinator: Cathy Ernst

2017 Chair (for 2018 Workshop): Christopher Tuggle (Iowa State University) cktuggle@iastate.edu

2017 Chair-elect: Christian Maltecca (North Carolina State University) christan.maltecca@ncsu.edu

The 2018 NRSP-8 Swine Workshop was held January 13, 2018 in San Diego, CA in conjunction with the Plant and Animal Genome XXV1 Conference. A joint session was held with the Cattle, Sheep and Goat Workshop in the morning, and two talks on porcine genomics were provided by Pablo Ross, University of California, Davis and Graham Plastow, University of Alberta, Canada. Dr. Ross described the UC-Davis’s efforts to annotate the porcine genome with RNAseq, histone Chipseq and ATAC-seq methods. Dr. Plastow described a natural challenge model for pig disease resilience that has been funded by Genome Alberta and Genome Canada. A companion project to the Canadian effort was recently funded by USDA-NIFA; this project is headed by Jack Dekkers (Iowa State University).

In the afternoon, the Swine Workshop had 68 persons attending, and the following institutions were represented in the US (Iowa State University, Michigan State University, University of Nebraska-Lincoln, University of Missouri, USDA-ARS-BARC, USDA-ARS-MARC, USDA-ARS-NADC), and outside the US (University of Alberta (Canada), European Bioinformatics Institute (UK), Roslin Institute (UK), Huazhong Ag. University(China)). The afternoon program included two invited presentations by two young scientists Thibaud Hourlier (EBI) and Hamid Beiki (Iowa State), who spoke about their work to annotate the new swine genome assembly. Following these two talks, the group heard from 4 scientists who have short summaries of their posters; these speakers were chosen by the Swine Subcommittee for their interesting poster abstracts. The 2017 Jorgensen Pig Travel Award winners Kaitlyn R. Daza (MSU) and Hiruni Wijesena, (UNL) were then introduced and each gave a lightening talk on their area of research. After the break, Drs. Archie Clutter and Parag Chitnis gave administrator’s reports and Drs. Jim Reecy and Chris Tuggle gave short coordinators’ reports (Bioinformatics and Swine, respectively), as well as conducted a discussion on community needs and resources. Four Swine Subcommittee Station representatives then provided Station reports. The presentations covered a range of topics from functional genomics to gene expression during disease challenge to evaluation of new SNP chips, and sparked discussion among attendees. At the end of the presentations, the group held a roundtable to discuss joint projects that could qualify for funding by the NRSP-8 Swine Coordination funds. Three possible projects were discussed and will be followed up.

During the business meeting, Dr. Dan Ciobanu from University of Nebraska was elected as the new chair-elect, and Christian Maltecca from North Carolina State University will chair the 2019 Swine Workshop covering October 1, 2017-September 30, 2018.

### Partial summary of funding awarded to Swine committee scientists (2017 only)

|  |  |
| --- | --- |
| Federal | $1,959,966 |
| Industry | $ 113,905 |
| Internal/Institutional | $ 174,401 |
| Total | $2,248,272 |

### Impacts 2017

1. NRSP8-supported research has improved the functional annotation of the porcine genome.
2. Application of new long-read technology (PacBio Iso-seq) has increased the depth and breadth of annotation of the new Sscrofa 11.1 assembly.
3. Newly validated genotyping tools will increase the depth of knowledge regarding genetic variation in industry populations.

### 2016-7 Swine Genome Committee Publications (refereed journal articles)

Bertolini F., J.C.S. Harding, B. Mote, A. Ladinig, G.S. Plastow and M.F. Rothschild. 2017. Genomic investigation of piglet resilience following porcine epidemic diarrhea outbreaks. Animal Genetics. 48(2):228-232. doi: 10.1111/age.12522.

Casiró S, D. Velez-Irizarry, C.W. Ernst, N.E. Raney, R.O. Bates, M.G. Charles and J.P. Steibel. 2017. Genome-wide association study in an F2 Duroc x Pietrain resource population for economically important meat quality and carcass traits. J. Anim. Sci. 95:545-558.

Choi, I., R.O. Bates, N.E. Raney and C.W. Ernst. 2017. Association of a corticotropin-releasing hormone receptor 2 (CRHR2) polymorphism with carcass merit, meat quality and stress response traits in pigs. Canadian J. Anim. Sci. 97:536-540.

Cole JB, Bormann JM, Gill CA, Khatib H, Koltes JE, Maltecca C, Miglior F. 2017. BREEDING AND GENETICS SYMPOSIUM: Resilience of livestock to changing environments. J Anim Sci. 95(4):1777-1779.

Daza, K.R., J.P. Steibel, D. Velez-Irizarry, N.E. Raney, R.O. Bates and C.W. Ernst. 2017. Profiling and characterization of a longissimus dorsi muscle microRNA dataset from an F2 Duroc x Pietrain pig resource population. Genom. Data. 13:50-53.

Funkhouser, S.A., R.O. Bates, C.W. Ernst, D. Newcom and J.P. Steibel. 2017. Estimation of genome-wide and locus-specific breed composition in pigs. Translational Anim. Sci. 1:36-44.

Funkhouser, S.A., J.P. Steibel, R.O. Bates, N.E. Raney and C.W. Ernst. 2017. Evidence for transcriptome-wide RNA editing among Sus scrofa PRE-1 SINE elements. BMC Genomics.18:360.

Garcia-Baccino, C.A., S. Munilla, A. Legarra, Z.G. Vitezica, N.S. Forneris, R.O. Bates, C.W. Ernst, N.E. Raney, J.P. Steibel and R.J. Cantet. 2017. Estimates of the actual relationship between half-sibs in a pig population. J. Anim. Breed. Genet. 134:109- 118.

Howard JT, Pryce JE, Baes C, Maltecca C. Invited review: Inbreeding in the genomics era: Inbreeding, inbreeding depression, and management of genomic variability. J Dairy Sci. 2017;100(8):6009-6024

Howard JT, Tiezzi F, Huang Y, Gray KA, Maltecca C. 2016. Characterization and management of long runs of homozygosity in parental nucleus lines and their associated crossbred progeny. Genet Sel Evol. 24;48(1):91.

Kommadath, A., H. Bao, I. Choi, J.M. Reecy, J.E. Koltes, E. Fritz-Waters, C. J. Eisley, J. R. Grant, R.R.R. Rowland, C. K. Tuggle, J.C.M. Dekkers, J.K. Lunney, L.L. Guan, P. Stothard, and G.S. Plastow. 2017. Genetic architecture of gene expression underlying variation in host response to porcine reproductive and respiratory syndrome virus infection. Scientific Reports 7:46203. doi: 10.1038/srep46203.

Liu, H., T.P.L. Smith, D.J. Nonneman, J.C.M. Dekkers, C.K. Tuggle 2017. A high-quality annotated transcriptome of swine peripheral blood. BMC Genomics 18:479. doi: 10.1186/s12864-017-3863-7.

Tiezzi F, de Los Campos G, Parker Gaddis KL, Maltecca C. 2017. Genotype by environment (climate) interaction improves genomic prediction for production traits in US Holstein cattle. J Dairy Sci. 100(3):2042-2056

Waide, E., C.K. Tuggle, N.V.L. Serão, M. Schroyen, A. Hess, R.R.R. Rowland, J.K. Lunney, G. Plastow, and J.C.M. Dekkers. 2017. Genome-wide Association of Piglet Responses to one of two Porcine Reproductive and Respiratory Syndrome Virus isolates. J. Animal Science. 95:16-38.

Wijesena HR, CA Lents, J-J. Riethoven, MD Trenhaile-Grannemann, JF Thorson, BN Keel, PS Miller, ML Spangler, SD Kachman, DC Ciobanu, 2017. Integration of Genomic Approaches to Uncover Sources of Variation in Age at Puberty and Reproductive Longevity in Sows, J Anim Sci. 95(9):4196-4205. doi: 10.2527/jas2016.1334.

Wurtz K.E., J.M. Siegford, R.O. Bates, C.W. Ernst and J.P. Steibel. 2017. Estimation of genetic parameters for lesion scores and growth traits in group-housed pigs. J Anim Sci. 95:4310-4317.

2016-7 Swine Genome Committee Publications (other publications)

Beiki, H. M. Schroyen, A. Rakhshandeh, N. Gabler, J. Dekkers, and C. Tuggle. 2017. Rewiring of porcine mRNA and miRNA networks in response to selection for residual feed intake. Proceedings of International Society of Animal Science meeting, Dublin, Ireland, #MT275, p.65

Bertolini, F., T. Yang, Y. Huang, J. Harding, M.F. Rothschild, G.S. Plastow. 2017. A Genomic Investigation of Porcine Periweaning Failure to Thrive Syndrome (PFTS). Plant & Animal Genome XX, San Diego, California. Abstract #W915

Bertolini, F., K. Zurbrigg, T. van Dreumel, T. O’Sullivan, M.F. Rothschild. 2017. Investigating the genomic basis of pigs that have died in transit. 36th International Society for Animal Genetics Conference, Dublin, Ireland. Abstract #MT246

Bertolini F., T. Yang, Y. Huang, J.C.S. Harding, M.F. Rothschild and Plastow G.S. 2017. Failure to Thrive Syndrome (PFTS): is there a genetic component? PAG, 25h Plant and Animal Genomics Conference, 14-18 January, San Diego, CA, US.

Funkhouser, S.A., J.P. Steibel, D. Newcom and C.W. Ernst. 2017. Evaluation of four US pig breeds using the Affymetrix Axiom Pig HD Array. Plant and Animal Genome XXV Conference. San Diego, CA. https://pag.confex.com/pag/xxv/meetingapp.cgi/Paper/25073.

Huang, J., M. Schroyen, Y.Nguyen, N. Gabler, D. Nettleton, J.C.M. Dekkers, C.K. Tuggle. 2017. Identifying tissue specific gene expression using RNAseq data from multiple porcine tissues. 25h Plant and Animal Genomics Conference, 14-18 January, San Diego, CA, US. Abstract P1163.

Huang, J., M. Schroyen, N. Gabler, J. Dekkers, and C. Tuggle, 2017. Combining transcriptome and epigenetic analysis of H3K36me3 and H3K4me3 marks to explore mechanisms of liver-specific gene expression in pigs. Proceedings of International Society of Animal Science meeting, Dublin, Ireland, #WT70 p.79.

Jacobi, SK., L Xi, C Maltecca, L Borst, A Smith, J Odle. 2017. Dietary Prebiotics and Arachidonic Acid (ARA) Modulate Intestinal Injury and Microbial Taxa Following Acute Dextran Sodium Sulfate Induced Colitis. The FASEB Journal 31 (1 Supplement), lb324-lb324.

Kern C., Y. Wang, P. Saelao, K. Chanthavixay, I. Korf, C. K. Tuggle, C. Ernst, P. Ross, and H. Zhou.  2017. Genome-wide analysis of H3K4me3 and H3K27me3 in three tissues in pigs.  Proceedings of International Society of Animal Science meeting, Dublin, Ireland, #MT10, p.41

Lee K, Ryu J, Uh K, Ray C. 2017. Use of CRISPR/Cas9 to induce targeted mutagenesis during porcine embryogenesis. Plant and Animal Genome Conference, San Diego, CA. January 14-18, 2017.

Liu, H., N. Manchanda 1, D. Nonneman, T.P.L. Smith, C.K. Tuggle. 2017. Cataloguing multi-tissue transcriptomes by PacBio IsoSeq and Illumina RNA-seq, and its application in annotating new-generation swine reference genome assemblies: Lessons learned from and recommendations given. 25h Plant and Animal Genomics Conference, 14-18 January, San Diego, CA, US. Abstract #P1162.

Thorpe, MK., L Xi, C Maltecca, KR Walters, A Smith, J Odle, SK Jacobi 2017. Dietary Prebiotics and Arachidonic Acid Alter Intestinal Phospholipid Composition and Time-Dependently Change Fecal Microbiome in Formula-Fed Piglets The FASEB Journal 31 (1 Supplement), 968.11-968.11.

Trakooljul, N., H. Zhou, P. Ross., I. Korf, M.E. Delany, H. Cheng, C.K. Tuggle, C.Ernst, S. Ponsuksili, K. Wimmers. 2017. Comparative DNA Methylome of the Chicken and Pig: An Evolutionary Bridge Between Avian and Mammalian 25h Plant and Animal Genomics Conference, 14-18 January, San Diego, CA, US. Abstract P0274.

Uh K, Ryu J, Errington J, Ray C, Lee K. 2017. Parthenogenetic activation of porcine oocytes using Zn2+ chelators. International Conference on Pig Reproduction.

Vella, G., M. Schroyen, H. Beiki, C. L. Loving, and C. K. Tuggle. 2017. Porcine bloodomics: Identification of porcine neutrophil-specific genes through gene expression correlations to neutrophil abundance and comparative expression data.  Proceedings of International Society of Animal Science meeting, Dublin, Ireland, #MT164, p.55.

Velez-Irizarry, D., S. Casiro, Y.L. Bernal Rubio, R.O. Bates, N.E. Raney, J.P. Steibel and C.W. Ernst. 2017. Expression QTL for longissimus dorsi muscle gene transcripts co-localized with phenotypic QTL for meat quality traits in an F2 Duroc x Pietrain resource population. Proceedings of the 36th International Society for Animal Genetics Conference, Dublin, Ireland. p. 132. http://www.isag.us/Docs/Proceedings/ISAG2017\_Proceedings.pdf?v3.

Wijesena, H. R., Lents, C. A., Keel, B. N., Thorson, J. F., Sullivan, G., Kachman, S., Ciobanu, D. Variation in Gene Expression In The Hypothalamic Arcuate Nucleus of Gilts With Differences in Pubertal Status and Subjected To Dietary Energy Restriction. Plant and Animal Genome Conference, San Diego, January 14-18, 2017

Ciobanu, D., Wijesena, H. R., Lents, C. A., Trenhaile-Grannemann, M. D., Riethoven, J.-J., Thorson, J. F., Keel, B. N., Miller, P., Spangler, M., Kachman, S. Integration of genomic resources to uncover pleiotropic regions associated with age at puberty and reproductive longevity in sows. Plant and Animal Genome Conference, San Diego, January 14-18, 2017.

Wijesena H.R., C.A. Lents, M.D. Trenhaile - Grannemann, J.J Riethoven, B.N. Keel, J.F. Thorson, P.S. Miller, R.K. Johnson, M.L. Spangler, S.D. Kachman, D.C. Ciobanu, 2017, The roles of age at puberty and energy restriction in sow reproductive longevity: a genomic perspective, Midwest ASAS Annual Meeting, March 13-15, 2017.

Wurtz, K.E., J.P. Steibel, R.O. Bates, C.W. Ernst, N.E. Raney and J.M. Siegford. 2017. Genome-wide association analyses of skin lesions and their genetic correlations with production traits in group-housed swine. National Pork Board Pig Welfare Symposium.

Wurtz, K.E., J.M. Siegford, R.O. Bates, C.W. Ernst and J.P. Steibel. 2017. Genetic correlations between skin lesions and growth traits in group housed pigs. Proceedings of the 7th International Conference on the Assessment of Animal Welfare at Farm and Group Level, 7, 217.

Wurtz, K.E., J.P. Steibel, R.O. Bates, C.W. Ernst, N.E. Raney and J.M. Siegford. 2017. Genome wide association analyses of lesion scores in group-housed swine. Proceedings of the 13th North American Regional Meeting of the International Society for Applied Ethology, 13, 32.

Zhou, H., P. Ross, C. Kern, P. Saelao, Y. Wang, M. Halstead, K. Chanthavixay, I. Korf, M. Delany, H. Cheng, J. Medrano, A. Van Eenennaam, C. Tuggle, and C. Ernst.   2017. Identification of regulatory elements in livestock species.  Proceedings of International Society of Animal Science meeting, Dublin, Ireland, #WT58 p.78.

## BIOINFORMATICS REPORT

OVERVIEW: Coordination of the NIFA National Animal Genome Research Program's (NAGRP) Bioinformatics is primarily based at, and led from, Iowa State University (ISU), with additional activities at the University of Arizona (UA), and is supported by NRSP-8. The NAGRP is made up of the membership of the Animal Genome Technical Committee, including the Bioinformatic Subcommittee.

FACILITIES AND PERSONNEL: James Reecy, Department of Animal Science, ISU, serves as Coordinator with Susan J. Lamont (ISU), Max Rothschild (ISU), Chris Tuggle (ISU), and Fiona McCarthy (UA) as Co-Coordinators. Iowa State University and University of Arizona provide facilities and support.

OBJECTIVES: The NRSP-8 project was renewed as of 10/01/13, with the following objectives: 1. Create shared genomic tools and reagents and sequence information to enhance the understanding and discovery of genetic mechanisms affecting traits of interest; 2. Facilitate the development and sharing of animal populations and the collection and analysis of new, unique, and interesting phenotypes; and 3. Develop, integrate, and implement bioinformatic resources to support the discovery of genetic mechanisms that underlie traits of interest.

PROGRESS TOWARD OBJECTIVE 1: Create shared genomic tools and reagents and sequence information to enhance the understanding and discovery of genetic mechanisms affecting traits of interest. (See activities listed below.)

PROGRESS TOWARD OBJECTIVE 2: Facilitate the development and sharing of animal populations and the collection and analysis of new, unique, and interesting phenotypes.

The partnership with researchers at Kansas State University, Michigan State University, Iowa State University, and the U.S. Department of Agriculture continues as the database and website interface developed for this collaboration (https://www.animalgenome.org/lunney) have continually been improved and updated with newly generated data. This resource continues to help the consortium by offering a localized source of information and continued facilitation of data analysis.

PROGRESS TOWARD OBJECTIVE 3: Develop, integrate, and implement bioinformatic resources to support the discovery of genetic mechanisms that underlie traits of interest.

### The following describes the project's activities over this past year.

### Multi-species support

The Animal QTLdb and the NAGRP data repository have been actively supporting the research activities for multiple species. The QTLdb has been accommodating active curation of QTL/association data for seven species (cattle, catfish, chicken, horse, pig, rainbow trout, and sheep). The collaborative site at iPlant continues to play an integral role in sharing the web traffic load by hosting JBrowse for interactive QTL/association data map alignment with annotated genes and other genome features (http://i.animalgenome.org/jbrowse). The advantage of JBrowse is that it easily allows user quantitative data — XYPlot/Density, in BAM or VCF format — to be loaded directly to a user’s browser for comparisons in the user’s local environment. New data sources and species continue to be updated. The virtual machine site to host the Online Mendelian Inheritance in Animals (OMIA) database (Dr. Frank Nicholas at the University of Sydney; http://omia.animalgenome.org/) and the Hybrid Striped Bass website (Benjamin Reading of North Carolina State University; http://stripedbass.animalgenome.org/annotator/index) continues to provide collaborative researchers convenient tools to create, maintain, and manage their sites with complete control.

### Ontology development

This past year we continued to focus on the integration of the Animal Trait Ontology into the Vertebrate Trait Ontology (http://bioportal.bioontology.org/ontologies/VT). We have continued working with the Rat Genome Database to integrate ATO terms that are not applicable to the Vertebrate Trait Ontology into the Clinical Measurement Ontology (http://bioportal.bioontology.org/ontologies/CMO). Traits specific to livestock products continue to be incorporated into a Livestock Product Trait Ontology (LPT), which is available on NCBO’s BioPortal (http://bioportal.bioontology.org/ontologies/LPT). We have also continued mapping the cattle, pig, chicken, sheep, and horse QTL traits to the Vertebrate Trait Ontology (VT), LPT, and Clinical Measurement Ontology (CMO) to help standardize the trait nomenclature used in the QTLdb. At the request of community members, at least 24 new terms were added to the VT in 2017. Now the VT data download has been made possible through the Github portal (https://github.com/AnimalGenome/vertebrate-trait-ontology) where users can automate their data updates. Anyone interested in helping to improve the ATO/VT is encouraged to contact James Reecy (jreecy@iastate.edu), Cari Park (caripark@iastate.edu), or Zhiliang Hu (zhu@iastate.edu). The VT/LPT/CMO cross-mapping has been well employed by the Animal QTLdb, CorrDB, and VCMap tools. Annotation to the VT is also available for rat QTL data in the Rat Genome Database and for mouse strain measurements in the Mouse Phenome Database. We have also been integrating information from multiple resources, e.g. FAO - International Domestic Livestock Resources Information, Oklahoma State University - Breeds of Livestock web site, and Wikipedia, as well as requests from community members, to continue development of a Livestock Breed Ontology (LBO; https://www.animalgenome.org/bioinfo/projects/lbo/) with an AmiGO display of the hierarchy. The LBO data is also available on BioPortal (<http://bioportal.bioontology.org/ontologies/LBO>).

### Software development

The NRSP-8 Bioinformatics Online Tool Box has been actively maintained for use by the community (https://www.animalgenome.org/bioinfo/tools/). Software upgrades and bug fixes were continually made. The CateGOrizer, Expeditor, VCmap, and other tools are continually used by community members.

AgBase and the AnimalGenome.org websites provide multiple reciprocal reference links to facilitate resource sharing.

### Minimal standards development

The Animal QTLdb and CorrDB have been continually developed to use MIQAS for data curation and data integration (https://www.animalgenome.org/QTLdb/doc/minfo/). We have continued to work on refining MIQAS to help define minimal standards for publication of QTL and gene association data (<http://miqas.sourceforge.net/>).

### Expanded Animal QTLdb functionality

In 2017, a total of 41,093 new QTL/association data were curated into the database, bringing the total number of data to 145,842 QTL/associations. Currently, there are 26,076 curated porcine QTL, 108,040 curated bovine QTL, 8,363 curated chicken QTL, 1,304 curated horse QTL, 1,932 curated sheep QTL, and 127 curated rainbow trout QTL in the database (https://www.animalgenome.org/QTLdb/). All data have been ported to NCBI, Ensembl, UCSC genome browser, and Reuters Data Citation Index in a timely fashion. Users can fully utilize the browser and data mining tools at NCBI, Ensembl, and UCSC to explore animal QTL/association data. In addition, we have continued to improve existing and add new QTLdb curation tools and user portal tools. The new improvements include accommodation of multiple genomes for QTL/association mapping; providing a "permanent record locator" for reviewers and authors to locate QTL/association data; and allowing mapping of trait data across the QTLdb and CorrDB databases using VT, LPT, and CMO ontology terms. In addition, trait-centric views and gene-centric views of QTL/association data have been developed to facilitate user analysis of data in terms of interrogating and displaying genotype-to-phenotype information in a synopsis. We have also enabled a function to allow web users to identify traits with both QTL/association data and genetic/phenotypic/environmental correlation data, and to traverse between the QTLdb and CorrDB for information.

### Further development of Animal Trait Correlation Database (CorrDB)

Our development of the CorrDB focused on co-development of curator tools and curation environments with that of the QTLdb. This helped with resources and tool sharing on trait ontology development and management, literature management, breed ontology management, and bug reporting tools for data quality control. The newly developed CorrDB curator tools are available to the public for any user to register for an account to curate correlation data.

### Facilitating research

The Data Repository for the aquaculture, cattle, chicken, horse, pig, and sheep communities to share their genome analysis data has proven to be very useful and has been actively used (https://www.animalgenome.org/repository). New data is continually being added. A total of 345 new data files on different animal genomes and supplementary data files to publications have been added to the repository over the last reporting period, representing a 33% data increase. Nearly 50 researchers and/or labs used the NAGRP data share platform to transfer or share their data files. This was double the number in the previous year. Over 20 groups chose to use our Supplementary Data platform to host files for their new publications, which was a 3-fold increase from the previous year.

The data downloads from the repository generated over 12TB of data traffic in 2017. Throughout 2017, our helpdesk at AnimalGenome.ORG handled over 90 inquiries/requests for services affecting community research projects. Our involvement ranged from data transfer and hosting, data deposition, web presentation, and data analysis, to software applications, code development, etc.

### Community support and user services at AnimalGenome.ORG

We have been maintaining and actively updating the NRSP-8 species web pages for each of the six species. We have been hosting a couple dozen mailing lists/websites for various research groups in the NAGRP community (https://www.animalgenome.org/community/). This includes groups like AnGenMap, FAANG international consortium, CRI-MAP users, and recent meetings like “Livestock High-Throughput Phenotyping and Big Data,” “Genome to Phenome: A USDA Blueprint for Improving Animal Production,” etc. A web service to facilitate gathering of signatures Calling for Restoration of NIFA/AFRI Foundational Program to Support the Animal Breeding, Genetics and Genomics Research played a positive role for the efforts.

The Functional Annotation of ANimal Genomes (FAANG) website (https://www.faang.org/) is hosted by AnimalGenome.ORG. The website has been developed and maintained to serve not only as a FAANG-related information hub, but also as a platform for this international consortium’s communication, collaboration, organization, and interaction. It serves over 467 members and 11 working committees and sub-committees, with 14 listserv mailing lists, a bulletin board, and a database for membership and working group management. The actively hosted materials include meeting minutes, presentation slides, and video records of scientific meetings and related events, all interactively available to members through the web portal. The “Funding Opportunities” information service has been improved to accommodate varying situations and to allow scientists to engage in open or private discussions to facilitate collaborations. Increases in the number of web hits and data downloads continued in 2017. AnimalGenome.org received over 8.6 million web hits from 625,282 individual sites (visitors), resulting in about 1 million data downloads that generated over 1 TB of internet traffic.

### Site maintenance

Along with newly acquired computer servers, the NAGRP program has also retained and made good use of old hardware to form an internal networked development environment, where loads for data backup, virtual machine management, customer portal hosting, databases, and web services can be well distributed.

### Reaching out

We have been sending periodic updates to about 3,000 users worldwide to inform them of the news and updates regarding AnimalGenome.org. “What’s New on AnimalGenome.ORG web site” emails were sent out 3 times in 2017.

### PLANS FOR THE FUTURE

OBJECTIVE 2. Facilitate the development and sharing of animal populations and the collection and analysis of new, unique, and interesting phenotypes. We will seek to partner with any NRSP-8 members wishing to warehouse phenotypic and genotypic data in customized relational databases. This will help consortia/researchers whose individual research labs lack expertise with relational databases to warehouse and share information.

OBJECTIVE 3. Develop, integrate, and implement bioinformatic resources to support the discovery of genetic mechanisms that underlie traits of interest.

We will continue to work with bovine, mouse, rat, and human QTL database curators to develop minimal information for publication standards. We will also work with these same database groups to improve phenotype and measurement ontologies, which will facilitate transfer of QTL information across species. We will continue working with U.S. and European colleagues to develop a Bioinformatics Blueprint, similar to the Animal Genomics Blueprint recently published by USDA-NIFA, to help direct future livestock-oriented bioinformatic/database efforts.