

## **NRSP-8 Swine Genome Committee Report Covering October 1, 2016 – September 30, 2017**

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 lightning 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, Koltjes 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. Easley, 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, 25<sup>h</sup> 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. 25<sup>h</sup> 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. 25<sup>h</sup> 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 25<sup>h</sup> 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 Zn<sup>2+</sup> 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](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.