

Curriculum Vita
James E. Koltes

PROFESSIONAL EXPERIENCE

- Assistant Professor** Department of Animal Science, Iowa State University (8/17– present)
- Assistant Professor** Department of Animal Science, University of Arkansas (7/15 – 7/17)
- Post-Doctoral Fellow** Department of Animal Science, Iowa State University (7/10 – 6/15)
- Post-Doctoral Fellow** Department of Biochemistry, University of Wisconsin (3/09 – 7/10)
- Fulbright Fellow** Unit of Animal Genomics, University of Liege, Belgium (1/08 – 12/08)

EDUCATION

- PhD program: Iowa State University** (8/02 – 12/07)
Major: Genetics
Minor: Statistics
- Undergraduate: University of Wisconsin-Madison** (9/97 – 12/01)
BS degree in Natural Sciences with honors
Majors: Dairy Science and Genetics

HONORS AND AWARDS

- CyThx Honoree- Teaching recognition from ISU students for ANS434 Fall 2020 01/21
- NSF travel fellowship to the Gathering on Functional Annotation of ANimal Genomes (GO-FAANG) workshop (10/15)
- USDA-NIFA Post-Doctoral Fellow: grant number 2011-67012-30692 (07/11 – 12/13)
- NIH-NLM CIBM Traineeship/ Fellow: grant number T15 LM007359 (07/09-07/10)
- Fulbright Fellowship to Belgium (01/08-12/08)
- Belgian-American Educational Foundation Research Fellowship (01/08-12/08)
- Miller Fellowship (07/03-12/07)
- Iowa State University Sports Club Council Advisor of the year: ISU fishing club (04/07)
- Bioinformatics travel grant to Plant & Animal Genome conference (01/06)
- John Airy Endowed Graduate Scholarship (01/04 & 01/05)
- Wisconsin Agricultural & Life Sciences Alumni Association (WALSAA) Active Aggie Senior Activities Award (1 of 2 in the college) (12/01)
- Wisconsin Alumni Association Outstanding Junior Award (1 of 6 university wide: 04/00)
- Hoards Scholar (07/00)
- Schmidt Academic Merit Scholarship (07/98 & 07/99)

PUBLICATIONS

Refereed papers

Citations = 745 h-index = 16 i-10 index = 26 Date accessed= 2/04/21

Full publication profile available at Google Scholar:

<https://scholar.google.com/citations?user=eZFUr0AAAAAJ&hl=en>

*Indicates co-first author

^Indicates corresponding author

42. Chinchilla-Vargas J, Kramer LM, Tucker JD, Hubbell, DS III, Powell JG, Lester TD, Backes EA, Anschutz K, Decker JE, Stalder KJ, Rothschild MF, and **JE Koltes**. 2020. Genetic basis of blood-based phenotypes and their relationship with performance and environment in beef cattle at weaning. *Frontiers in Genetics*. 11: 717. doi: 10.3389/fgene.2020.00717. eCollection 2020
41. Crook TS, Beck PA, Gadberry MS, Sims MB, Stewart CB, Shelton C, **Koltes J**, Kegley EB, Powell J, McLean DJ, and Chapman JD. 2020. Influence of an immune modulatory feed supplement on performance and immune function of beef cows and calves preweaning. *Journal of Animal Science*. 98_(3):skaa073. doi: 10.1093/jas/skaa073
40. Lima AO, **Koltes JE**, Diniz WJS, de Oliveira PSN, Cesar ASM, Tizioto PC, Afonso J, de Souza MM, Petrini J, Rocha MIP, Cardoso TF, Neto AZ, Coutinho LL, Mourao GB, and LCA Regitano. 2020. Potential biomarkers for feed efficiency-related traits in Nelore cattle identified by co-expression network and integrative genomics analyses. *Frontiers in Genetics* 11:189. doi: 10.3389/fgene.2020.00189. eCollection 2020
39. Andrade BGN, Bressani FA, Cuadrat RC, Tizioto PC, Oliveira PSN, Mourao GB, LL Coutinho, Reecy JM, **Koltes JE**, Walsh P, Berndt A, Palhares JCP, and Regitano LCA. 2020. The Nelore rumen and fecal microbiomes: Structure and inter-dependency of bacterial and archaeal populations. *Journal of Animal Science and Biotechnology*. 11, Article number: 6. <https://link.springer.com/article/10.1186/s40104-019-0422-x>
38. **Koltes JE**, JB Cole, NVL Serão, ME McCue, J Woodward, H Zhang, SD McKay, JK Lunney, LM Kramer, RN Dilger, R Reuter, R Clemmens, BM Murdoch, CE Rexroad III, GJM Rosa, RG Mateescu, SN White, M Worku, and JM Reecy. 2019. A vision for development and utilization of high-throughput phenotyping and big data analytics in livestock. *Frontiers in Genetics*. doi: 10.3389/fgene.2019.01197
<https://www.frontiersin.org/articles/10.3389/fgene.2019.01197/abstract>
37. Ramirez BC[^], Xin H, Beermann DH, Halbur PG, Hansen SL, Peschel JM, Rademacher CJ, Reecy JM, Ross JW, Shepherd TP, and **JE Koltes**[^]. 2019. At the intersection of industry and academia: How do we facilitate productive precision livestock farming in practice? *Animals* 9; 635. DOI: <https://doi.org/10.3390/ani9090635>
36. Oliveira PSN, LL Coutinho, Cesar ASM, Diniz WJD, De Souza MM, Andrade BGN, **Koltes JE**, Mourao GB, Zeriotini-Neto A, Reecy JM, and Regitano LCA. 2019. Co-expression

- networks reveals potential regulatory roles of miRNAs in fatty acids composition of Nelore cattle. *Frontiers in Genetics*. 11. <https://doi.org/10.3389/fgene.2019.00651>
35. **Koltes J.E.**, Arora, I., Gupta R., Nguyen D.C., Schiad M., Kim J., Kimple M.E., and S. Bhatnagar. 2019. A gene expression network analysis of the pancreatic islets from lean and obese mice identifies complement 1q like-3 secreted protein as a regulator of β -cell function. *Scientific Reports*. 9, Article number: 10119.
 34. Goncalves, T.M., LCA Regitano, **J.E. Koltes**, A.S.M. Cesar, S.C.S Andrade, G.B. Mourao, G. Gasparin, GCM Moreira, E Fritz-Waters, JM Reecy and LL Coutinho. 2018. Gene co-expression analysis indicates potential pathways and regulators of beef tenderness in Nelore Cattle. *Frontiers in Genomics*, 05 October 2018. <https://doi.org/10.3389/fgene.2018.00441>
 33. Gupta R., **Koltes J.E.**, Schiad M., Appakalai B., Kim J., Kimple M.E., and S. Bhatnagar. 2018. Complement 1q like-3 protein inhibits insulin secretion from pancreatic β -Cells via the cell adhesion G protein-coupled receptor BAI3. *Journal of Biological Chemistry*. 293:18086-18098. doi: 10.1074/jbc.RA118.005403
 32. Cesar A.S.M., Regitano L.C.A., Reecy J.M., Poleti M.D., Oliveira G.B., Oliveira P.P.N., Oliveira G., Moreira G.C.M., Mudadu M.A., Tizioto P.C., **Koltes J.E.**, Fritz-Waters E., Kramer L., Garrick D., Beiki H., Geistlinger L., Mourão, G.B., Zerlotini-Neto A., and L.L. Coutinho. 2018. Identification of putative regulatory regions and transcription factors associated with intramuscular fat content-traits. *BMC Genomics* 19:499. doi: 10.1186/s12864-018-4871-y.
 31. **Koltes J.E.**, Koltes D.A., Mote B.E., Tucker J., and D.S. Hubbell III. 2018. Automated collection of heat stress data in livestock: new technologies and opportunities. *Translational Animal Science*. 2: 319-323. <https://doi.org/10.1093/tas/txy061>
 30. Oliveira G., LCA Regitano, ASM Cesar, JM Reecy, KY Degaki, MD Poleti, AM Felício, **JE Koltes**, and LL Coutinho. 2018. Integrative analysis of microRNAs and mRNAs revealed regulation of intramuscular fat deposition in Nelore cattle. *BMC Genomics* 19:126. <https://bmcbgenomics.biomedcentral.com/articles/10.1186/s12864-018-4514-3>
 29. Iamartino D, E.L. Nicolazzi, C.P. Van Tassell, J.M. Reecy, E.R. Fritz-Waters, **J.E. Koltes**, S. Biffani, T.S. Sonstegard, S.G. Schroeder, P. Ajmone-Marsan, R. Negrini, R. Pasquariello, P. Ramelli, A. Coletta, J.F. Garcia, A. Ali, L. Ramunno, G. Cosenza, D.A. de Oliveira, M.G. Drummond, E. Bastianetto, A. Davassi, F. Brew, A. Pirani, and J.L. Williams. 2017. Design and validation of a 90k SNP genotyping assay for the Water Buffalo (*Bubalus bubalis*). *PLOS One* 12(10): e0185220 <https://doi.org/10.1371/journal.pone.0185220>.
 28. Yazwinski T.A., Tucker C.A., Powell J., Beck P., Wray E., Jones L., **Koltes J.E.**, and Weingartz C. 2017. A Fecal egg count reduction test with cattle treated 118 days earlier

with saline, albendazole in combination with doramectin or an extended release formulation of eprinomectin. *Bovine Practitioner* 51: 28-33.

27. Bao H., A. Kommadath, I. Choi, J.M. Reecy, **J.E. Koltes**, E. Fritz-Waters, C.J. Easley, 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.
26. J.B. Cole, J.M. Bormann, C.A. Gill, H. Khatib, **J.E. Koltes**, C. Maltecca, and F. Miglior. 2017. Resilience of Livestock to Changing Environments. *Journal of Animal Science*. 95:1777-1779.
25. Jia C., Kong X., **Koltes J.E.**, Gou X., Yang S., Yan D., Lu S., and Z. Wei. 2016. Gene Co-expression network analysis unraveling transcriptional regulation of high-altitude adaptation of Tibetan pig. *PLOS One*. Dec 9;11(12): e0168161. doi: 10.1371/journal.pone.0168161.
24. Cesar ASM, Regitano LCA, Poleti MD, Andrade SCS, Tizioto PC, Oliveira PSN, Felicio AM, Nascimento ML, Chaves AS, Lanna DPD, Tullio RR, Nassu RT, **Koltes JE**, Fritz-Waters E, Mourao GB, Zeriotini-Neto A, Reecy JM, and LL Coutinho. 2016. Differences in the skeletal muscle transcriptome profile associated with extreme values of fatty acids content. 2016. *BMC Genomics*. 17:961.
23. Kramer, L.M., **J.E. Koltes**, E.R. Fritz-Waters, M. Mayes, A. Markey, D.J. Garrick, N.T. Weeks and J.M. Reecy. 2016. Identification of epistatic interactions among fatty acid traits in Angus sired cattle. *BMC Genomics*. 17:891.
22. Fleming, D.S., **J.E. Koltes**, E.R. Fritz-Waters, J.M. Reecy, M.F. Rothschild, C.J. Schmidt, C.M. Ashwell, M.E. Persia and S.J. Lamont. 2016. Single nucleotide variant discovery of highly inbred Leghorn and Fayoumi chicken breeds using pooled whole genome resequencing data reveals insights into phenotypic differences. *BMC Genomics*. 17:812.
21. Buchanan, J.W., J.M. Reecy, D.J. Garrick, **J.E. Koltes**, M. Saatchi, Q. Duan, D.C. Beitz, and R.G. Mateescu. 2016. Deriving gene networks from SNP associated with triacylglycerol and phospholipid fatty acid fractions from ribeyes of Angus cattle. *Frontiers in Genetics*. 7:116. doi: 10.3389/fgene.2016.00116. eCollection 2016.
20. Boddicker, R.L.* , **J.E. Koltes***, E.R. Fritz-Waters, L. Koesterke, T. Yin, V. Mani, J.M. Reecy, D. Nettleton, L.H. Baumgard, N.K. Gabler, and J.W. Ross. 2016. Genome-Wide Methylation Profile Following Prenatal and Postnatal Dietary n-3 Fatty Acid Supplementation in Pigs. *Animal Genetics*. Aug 25. doi: 10.1111/age.12468.
19. Weeks N.T., G.R. Luecke, B.M. Groth, M. Kraeva, L. Ma, L.M. Kramer, **J.E. Koltes** and J.M. Reecy. 2016. High performance epistasis detection in quantitative trait GWAS.

International Journal of High Performance Computing Applications.

doi: 10.1177/1094342016658110

<http://hpc.sagepub.com/content/early/2016/07/12/1094342016658110.abstract>

This paper does not show up on pubmed as it is in a computing journal. It was selected as one of the top papers at the 2016 International Workshop on Parallelism in Bioinformatics (PBio2016) and was selected for publication based on it's merit. In addition, an article was written about this work for the Department of Energy's National Energy Research Scientific Computing Center (NERSC) newsletter. This paper has been cited 15 times (02/27/20).

18. Fleming, D.S., **J.E. Koltes**, A.D. Markey, C.J. Schmidt, C.M. Ashwell, M.F. Rothschild, J.M. Reecy, M.E. Persia and S.J. Lamont. 2016. Genomic analysis of Ugandan and Rwandan chicken Ecotypes Using a 600k genotyping array. *BMC Genomics* 17: 407.
17. Schroyen, M., Eislely C.J., **J.E. Koltes**, E. Fritz-Waters, Choi I., Plastow G.S., Guan L.L., Stothard P., Bao H., Kommadath A., Reecy J.M., Lunney J.K., Rowland R.R.R., Dekkers J.C.M., and Tuggle C.K. 2016. Bioinformatic analyses in early host response to Porcine Reproductive and Respiratory Syndrome virus (PRRS) reveals pathway differences between pigs with alternate genotypes for a major host response QTL. *BMC Genomics* 17: 196. <http://www.biomedcentral.com/1471-2164/17/196>
16. Luecke, G.R., N.T. Weeks, B.M. Groth, M. Kraeva, L. Ma, L.M. Kramer, **J.E. Koltes** and J.M. Reecy. 2015. Fast epistasis detection in large-scale GWAS for Intel Xeon Phi Clusters. *Trustcom/BigDataSE/ISPA IEEE*, 3: 228-235. doi:10.1109/Trustcom.2015.637 This paper does not show up on pubmed as it is in a computing journal. This paper has been cited 2 times (02/27/20).
15. Schroyen, M., J.P. Steibel, **J.E. Koltes**, I. Choi, N.E. Raney, C. Eislely, E. Fritz-Waters, J.M. Reecy, J.C.M. Dekkers, R.R.R. Rowland, J.K. Lunney, C.W. Ernst, and C.K. Tuggle. 2015. Whole blood microarray analysis of pigs showing extreme phenotypes after a porcine reproductive and respiratory syndrome virus infection. *BMC Genomics* 16: 516.
14. Cesar, A.S.M., Regitano L.C.A., **Koltes J.E.**, Fritz-Waters E., Gasparin G., Mourao G.B., Oliveira P.S.N., Reecy J.M., and LL Coutinho. 2015. Putative regulatory factors associated with intramuscular fat content. *PLOS ONE*. 10(6):e0128350. doi: 10.1371/journal.pone.0128350. eCollection 2015.
13. **Koltes J.E.** *, Fritz-Waters E.*, Eislely C.J., Choi I., Bao, H., Kommadath A., Serão N.V.L., Boddicker N., Abrams S.M., Schroyen M., Loyd H., Tuggle C.K., Plastow G.S., Guan L.L., Stothard P., Lunney J.K., Liu P., Carpenter S., Rowland R.R.R., J.C.M. Dekkers, and J.M. Reecy. 2015. Identification of a putative quantitative trait nucleotide in Guanylate Binding Protein 5 for host response to PRRS virus infection. *BMC Genomics*. 16:412.

12. **Koltes, J.E.**, D. Kumar, R.S. Kataria, V.L. Cooper, and J.M. Reecy. Transcriptional profiling of *PRKG2*-null growth plate identifies down-stream targets of *PRKG2*. 2015. *BMC Research Notes*. 8:177.
11. Pilcher, C., Jones C., Schroyen M., Severin A., Tuggle C.K., Patience J.F., and **J.E. Koltes**[^]. 2015. Gene expression profiling of longissimus dorsi and adipose tissue in pigs with differing post-weaning growth rates. *Journal of Animal Science*. 93(5): 2134-43.
10. Yang, X.* , **Koltes, J.E***, Park, C.A., Chen, D., and JM Reecy. Gene co-expression network analysis provides novel insights into important factors involved in myostatin regulation across developmental timepoints in mouse skeletal muscle. 2015. *PLoS One*. Feb 19: 10(2):e0117607. doi: 10.1371/journal.pone.0117607
9. Baes C.F., Dolezal M.A., Bapst B., Fritz-Waters E., **Koltes J.E.**, Jansen S., Flury C., Signer-Hasler H., Stricker C., Fernando R., Fries R., Moll J., Garrick D.J., Reecy J.M., and Gredler B. Evaluation of variant identification methods for whole genome sequencing data in dairy cattle. 2014. *BMC Genomics*. Nov 1; 15:948.
8. Koesterke, L., **J.E. Koltes**, N.T. Weeks, K. Milfeld, M. Vaughn, J.M. Reecy and D. Stanzione. Discovery of biological networks using an optimized PCIT algorithm on Stampede's Intel Xeon and Xeon Phi processors. 2014. *Concurrency and Computation Practice and Experience*. 26: 2178-2190.
<http://onlinelibrary.wiley.com/doi/10.1002/cpe.3252/abstract>
This paper does not show up on pubmed as it is in a computing journal. The paper has been cited 17 times (02/27/20).
7. Koesterke, L., **J.E. Koltes**, N.T. Weeks, K. Milfeld, M. Vaughn, J.M. Reecy and D. Stanzione. Optimizing the PCIT algorithm on Stampede's Xeon and Xeon Phi processors for faster discovery of biological networks. 2013. Proceedings of the XSEDE2013 Conference. ACM. New York, NY, USA. doi>[10.1145/2484762.2484794](https://doi.org/10.1145/2484762.2484794).
This paper does not show up on pubmed as it is in a computing journal. This paper won an award as best lightning talk at the XSEDE 2013 conference, has been downloaded more than 181 times and cited 15 times (02/27/20).
<http://dl.acm.org/citation.cfm?id=2484794>
6. Hu, Z-L* , **Koltes, J.E.*** , Park, C.A., Fritz, E.R., and J.M. Reecy. Invited Review: Bioinformatics approaches to livestock animal genomics research. *CABI Reviews*. 2011, 6: 1-15.
5. Lavine, J.A., Raess, P.W., Stapleton, D.S., Rabaglia, M.E., Suhonen, J.I., Schueler, K.L., **Koltes, J.E.**, Dawson, J.A., Yandell, B.S., Samuelson, L.C., Beinfeld, M.C., Belt Davis, D., Hellerstein, M.K., Keller, M.P. and A.D. Attie. Cholecystokinin is upregulated in obese islets and expands β -cell mass by increasing β -cell survival. *Endocrinology*. 2010. 151(8): 3577-88.

4. **Koltes, J.E.**, B.P. Mishra, D. Kumar, R.S. Kataria, L.R. Totir, R.L. Fernando, R. Cobbold, D. Steffen, W. Coppieters, M. Georges, and J.M. Reecy. A Nonsense mutation in the Kinase domain of cGMP-dependant, type II protein kinase (*PRKG2*) is the causative mutation for Angus dwarfism. *Proceedings of the National Academy of Science*. 2009, 106 (46): 19250-5.
3. **Koltes, J.E.**, Z-L. Hu, E. Fritz, and J.M. Reecy. BEAP: BLAST extension and alignment program- a tool for contig construction and analysis of preliminary genome sequence. *BMC Research Notes*. 2009, 2:11.
2. Alexander, L.J., L.A. Kuehn, T.L.P. Smith, L. Matukumalli, B. Mote, **J.E. Koltes**, J. Reecy, T.W. Geary, and M.D. MacNeil. A Limousin specific myostatin allele affects longissimus muscle area and fatty acid profiles in a Wagyu-Limousin F2 population. *J. Animal Science*. 2009, 87(5):1576-81.
1. Tshipuliso, N.O.M, L.J. Alexander, T.W. Geary, W.M. Snelling, D.C. Rule, **J.E. Koltes**, B.E. Mote, and M.D. MacNeil. Mapping QTL for fatty acid composition that segregate between Japanese Black and Limousin breeds. *South African Journal of Animal Science*. 2008. 38 (2): 126-130.

PEER REVIEWED BOOK CHAPTERS

1. **Koltes JE** and F Peñagaricano. 2019. Linking genotype to phenotype: functional annotation as a tool to advance dairy cattle breeding. In Advances in breeding of dairy cattle (ed. Julius van der Weft and Jennie Pryce). Burleigh Dodds Science Publishing, Cambridge, UK (ISBN: 978 1 78676 296 2). <http://dx.doi.org/10.19103/AS.2019.0058.19>

SUBMITTED PAPERS

Andrade BGN, Afli H, Bressani FA, Cuadrat RRC, de Oliveira PSN, Mourão GB, Coutinho LL, Reecy JM, **Koltes JE**, de Souza MM, Zerlotini Neto A, de Medeiros SR, Berndt A, Palhares JCP, and L Regitano. 2021. Fecal and ruminal microbiome components associated with methane emission in beef cattle. Submitted to *Animal Microbiome*

PEER REVIEWED CONFERENCE PAPERS

7. Khanal, P., Sanglard, L.M.P, Koltes, J.E., Sommer, P., Poole, D.H., and N.V.L. Serão. 2017. Genetics of fescue toxicity in Angus cattle: Identification of differentially expressed genes in tolerant and susceptible Angus cows. The proceedings, 11th World Congress of Genetics Applied to Livestock Production. Auckland, New Zealand
6. Cesar, ASM, LCA Regitano, **JE Koltes**, ER Fritz-Waters, G. Gasparin, GB Mourao, DPD Lanna, JM Reecy and LL Coutinho. 2014. RNA sequencing analysis identifies retinoic acid pathway genes as differentially expressed in animals with extreme intramuscular

fat GEBVs in Nellore steers. The proceedings, 10th World Congress of Genetics Applied to Livestock Production. Vancouver, Canada.

5. J. Reecy, J. Carson, F. McCarthy, **J.E. Koltes**, E. Fritz-Waters, J. Williams, E. Lyons, C.F. Baes, and M. Vaughn. 2014. Cyberinfrastructure for Life Sciences - iAnimal resources for genomics and other data driven biology. The proceedings, 10th World Congress of Genetics Applied to Livestock Production. Vancouver, Canada.
4. Baes, C.F., M.A. Dolezal, E. Fritz-Waters, **J.E. Koltes**, B. Bapst, C. Flury, H. Signer-Hasler, C. Stricker, R. Fernando, F. Schmitz-Hsu, D.J. Garrick, J.M. Reecy, and B. Gredler. 2014. Comparison of variant calling methods for whole genome sequencing data in dairy cattle. The proceedings, 10th World Congress of Genetics Applied to Livestock Production. Vancouver, Canada
3. Fleming, D.S., **J.E. Koltes**, E.R. Fritz-Waters, J.M. Reecy, and S. J Lamont. 2014. A Tale of Two Birds: SNP discovery and genomic architecture of highly inbred Leghorn and Fayoumi chicken breeds using whole genome resequencing. The proceedings, 10th World Congress of Genetics Applied to Livestock Production. Vancouver, Canada
2. L. M. Kramer, **J.E. Koltes**, E.R. Fritz-Waters, M. Mayes, A. Markey, M. Saatchi, N.T. Weeks, and J.M. Reecy. 2014. Identification of Epistatic Interactions Among Fatty Acid Traits, in Angus Sired Beef Cattle. The proceedings, 10th World Congress of Genetics Applied to Livestock Production. Vancouver, Canada
1. F. M. McCarthy, C. Gresham, **J. Koltes**, M.T. Arick, E. Lyons, E.T. Dawson, N. Hopkins, and S.C. Burgess. 2014. From data to knowledge: translating functional genomics data into information for livestock production. The proceedings, 10th World Congress of Genetics Applied to Livestock Production. Vancouver, Canada

FULL PAPERS, NOT PEER REVIEWED

1. Iamartino, D, J.L. Williams, T.S. Sonstegard, J. M. Reecy, C.P. Van Tassell, E.L. Nicolazzi, S. Biffani, F. Biscarini, S. Schroeder, D.A. de Oliveira, A. Coletta, J.F. Garcia, A. Ali, L. Ramunno, G., R. Pasquariello, M.G. Drummond, E. Bastianetto, E. Fritz, **J.E. Koltes**, and The International Buffalo Consortium. 2013. The buffalo genome and the application of genomics in animal management and improvement. Proceedings of the World Buffalo Congress. Phuket, Thailand.

ABSTRACTS

107. C.J. Siberski, M.S. Mayes, P.J. Gorden, A. Copeland, M. Healy, B.M Goetz, H. Beiki, L.M. Kramer, L.H. Baumgard, P. Dixon, and **J.E. Koltes**. Inclusion of automated sensor data

as a predictor of feed intake increases the variance explained by a random forest model. Proc. Of the National ASAS meeting. 2020 Madison, WI, USA.

106. A.E. Jantzi, C.J. Siberski, B.M Goetz, M. Healy, K.P. Hayman, P.J. Gorden, L.H. Baumgard, and **J.E. Koltes**. Milking collar activity data is associated with health events and feed intake in lactating Holstein cattle. 2020 Proc. Of the National ASAS meeting. Madison, WI, USA.
105. C.J. Siberski, M.S. Mayes, P.J. Gorden, A. Copeland, M. Healy, B.M Goetz, H. Beiki, L.M. Kramer, L.H. Baumgard, P. Dixon, and **J.E. Koltes**. Predicting health events and feed intake using sensor data in lactating Holstein cows. 2020. Proc. Of the National ADSA meeting. West Palm Beach, FL, USA.
104. M. J. VandeHaar, R. J. Tempelman, **J.E. Koltes**, H. M. White, K. A. Weigel, E. Connor, P. Van Raden, F. Peñagaricano, J. Santos, K. Parker Gaddis, J. Burchard, and J. Durr. Improving dairy feed efficiency, sustainability, and profitability by impacting farmer's breeding and culling decisions. 2020. ICAR Annual Conference. Leeuwarden, The Netherlands.
103. Chinchilla-Vargas J, L. M. Kramer, J. D. Tucker, D. S. Hubbell III, J. G. Powell, T. D. Lester, E. A. Backes, K. Anschutz, J. E. Decker, K. J. Stalder, M. F. Rothschild, and **J. E. Koltes**. Genetic Basis of blood traits in beef cattle and their relationship with production traits at weaning. 2020 Proc. of Midwest ASAS meeting. Omaha, NE, USA.
102. Beiki, H., **J.E. Koltes**, Z-L. Hu, J. M. Reecy. Analysis of Divergent Transcription Events Across Cattle Tissues. 2020. Proc. of Plant and Animal Genome XXVIII. San Diego, CA, USA.
101. MM de Souza, H Beiki, DA Koltes, JG Powell, JA Atchley, LM Meyer, J Tucker, DS Hubbell, III, and **JE Koltes**. Effect of toxic fescue on whole blood gene expression in beef cattle. 2020. Proc. of Plant and Animal Genome XXVIII. San Diego, CA, USA.
100. Chinchilla-Vargas J, L. M. Kramer, J. D. Tucker, D. S. Hubbell III, J. G. Powell, T. D. Lester, E. A. Backes, K. Anschutz, J. E. Decker, K.J. Stalder, M. F. Rothschild, and **J. E. Koltes**. Blood traits in beef cattle and their relationship with production traits at weaning. 2020. Proc. of Plant and Animal Genome XXVIII. San Diego, CA, USA.
99. Petry, B, Copola, A.G.L, Moreira, G.C.M, Godoy, T.F, Jorge, E.C, Peixoto, J.O, Ledur, M.C, **Koltes, J.E**, Coutinho, L.L Functional analysis indicates *SAP30* as putative causal gene for muscle growth in chicken. 2020. Proc. of Plant and Animal Genome XXVIII. San Diego, CA, USA.
98. Beiki, H., **J. Koltes**, Z. Hu, and J. Reecy. Analysis of Alternative Splicing Events Across Cattle Tissues by Genome-Wide Integration of PacBio Iso-seq and RNA-Seq Data. 2019. Proceedings of the 37th International Society of Animal Genetics. Lleida, Spain.

97. M. de Souza, D. Koltes, H. Beiki, T. Tsai, M. Sales, C. Maxwell, J. Zhao, and **J. Koltes**. miRNA and mRNA differential expression in peripheral blood mononuclear cells of pigs exposed to topsoil in early life. 2019. Proceedings of the 37th International Society of Animal Genetics. Lleida, Spain.
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12. Ganesan, S., Madden, J.A., Bhattacharya, P., **Koltes, J.E.**, Devine, P.J., and A.F. Keating. DNA Repair Gene Expression Up-Regulation in Response to Phosphoramidate Mustard Exposure in Cultured Rat Ovaries. 2011. SSR meetings.
11. Richter, E.L., Drewnoski, M.E., Ziemer, C.J., **Koltes, J.E.**, Fritz, E.R., Kolte, A., Reecy, J.M., and S.L. Hansen. High Dietary Sulphur modifies volatile fatty acid profiles and increases hydrogen sulfide gas production. 2011. Midwest Animal Science Meetings. Des Moines, IA, USA.
10. **Koltes J.E.**, Davis S.G., Hu Z-L., Shimoyama M., Dwinell M., Kwitek A.E., and J.M. Reecy. 2011. VCMaP: A Comparative Genomics Viewer and Database Designed to Facilitate Genomic Discovery. Proc of Plant and Animal Genome XIX. (C899) p 267. San Diego, CA, USA.
9. **Koltes, J.E.**, Bhatnagar, S., Broman, A., Chaibub Neto, E., Keller, M.P., Yandell, B.S., and A.D. Attie. 2009. Development of methods and software to find candidate inter-tissue communication molecules mediating obesity and diabetes phenotypes. CIBM Annual Retreat. Madison, WI, USA
8. **Koltes, J.E.** and J.M. Reecy. 2006. Functional analysis of a *PRKG2* nonsense mutation in American Angus dwarf cattle. Proc. Of 30th International Society of Animal Genetics. (C476) p79. Puerto Seguro, Bahia, Brazil.
7. Grant, M.S., **J.E. Koltes**, and J.M. Reecy. 2006. The Effects of Myostatin on Skeletal Muscle Re-Growth Following Disuse Atrophy in Mice. J. Anim. Sci. 84 (Suppl. 2): p53.
6. **Koltes, J.E.**, L.R. Totir, R.L. Fernando, and J.M. Reecy. 2006. Identification of a putative causal mutation for dwarfism in *PRKG2*. Proc of Plant and Anim. Genome XIV. (P527) p233. San Diego, CA.
5. **Koltes, J.**, R. Totir, R. Fernando, and J. Reecy. 2005. Fine-mapping of a 2.8cM region associated with dwarfism in American Angus cattle. Proc. Of the 3rd symposium of Genet of Anim. Health (P24). Ames, IA.
4. **Koltes, J.**, Z-L Hu, and J. Reecy. 2005. Localized development of a high resolution sequence comparative map of bovine chromosome 6. Proc of Plant and Anim. Genome XIII. (P523) p201. San Diego, CA.
3. Mishra, B., **J. Koltes**, R. Totir, R. Fernando, J. Cavanagh, M. Georges, W. Coppieters, and J. Reecy. 2004. Mapping of the gene causing disproportionate dwarfism in American Angus cattle. Proc. of the International Society of Animal Genetics. W003. Tokyo, Japan

2. Berger, P. J., **J. Koltes**, M. H. Healey, M. S. Ashwell, R. D. Shanks, H. Schlessner, and H. A. Lewin. 2003. Putative quantitative trait loci affecting perinatal survival in eleven Holstein families. *J. Dairy Sci.* 86(Suppl. 1): p161.
1. **Koltes, J.**, P. J. Berger, J. C. M. Dekkers, M. H. Healey, M. S. Ashwell, R. D. Shanks, H. Schlessner, and H. A. Lewin. 2003. Evidence for major quantitative trait loci affecting perinatal survival in two elite Holstein sire families. *Proc. The John M. Airy Beef Cattle Symposium. Visions for genetics and breeding.* p131. Ed. J. M. Reecy. Johnston, IA.

INDUSTRY POPULAR PRESS ARTICLES

1. Christensen A, Cooper D, Fourdraine R, Griffiths B, Mathis C, **Koltes J**, Quick A, and M Utts. Farming out data-driven decisions. *Hoard's Dairyman* March 25, 2020 p. 185. Written as part of the Virtual Dairy Brain Coordinated Innovation Network advisory group for the corresponding USDA NIFA project.

RESEARCH REPORTS

12. Oconitrillo MJ, Wickramasinghe H. K. J. P., Stepanchenko N., Siberski CJ, **Koltes JE**, and J. A. D. R. N. Appuhamy. 2020. The Effects of a Zinc-Methionine Supplementation in High Producing Dairy Cows. Iowa State University Animal Industry Report.
11. **Koltes JE**, Poole DH, Schmitz-Esser S, Zhao J, Chewning S, Hubbell D III. and, Serao NVL. 2018. Development of new measurements and tools to mitigate fescue toxicosis in beef cattle. Iowa State University Animal Industry Report.
10. **Koltes J.E.** 2017. Genomic testing tips for beef cattle. Arkansas Cattleman's Report.
9. Su H., **J.E. Koltes**, and D. Garrick. 2016. Evaluating sequence-based customized SNP in addition to GeneSeek LD chip for predicting birth weight in beef cattle. Iowa State University Animal Industry Report.
8. Flemming, D.S., **J.E. Koltes**, A.D. Markey, C.J. Schmidt, C.M. Ashwell, M.F. Rothschild, M.E. Persia, J.M. Reecy and S.J. Lamont. 2015. Genomes of African chickens show evolutionary response to environmental stress. Iowa State University Animal Industry Report.
7. L. M. Kramer, **J.E. Koltes**, E.R. Fritz-Waters, M. Mayes, A. Markey, M. Saatchi, N.T. Weeks, and J.M. Reecy. 2014. Fatty acid SNP Interaction analysis in Angus Sired Beef Cattle. Iowa State University Animal Industry Report.
6. Schroyen, M., Steibel J.P., I. Choi, **J.E. Koltes**, C. Eisley, E. Fritz-Waters, J.M. Reecy, J.C.M. Dekkers, Rowland R.R.R., Lunney J.K., Ernst C.W., and C.K. Tuggle. 2014. Identifying Molecular Differences in Pigs with Extreme Phenotypes for Weight Gain and Viral Load in Response to PRRS. Iowa State University Animal Industry Report.

5. Flemming, D.S., **J.E. Koltes**, E.R. Fritz-Waters, J.M. Reecy and S.J. Lamont. 2014. SNP discovery and genomic architecture of highly inbred Leghorn and Fayoumi chicken breeds using whole genome sequencing. Iowa State University Animal Industry Report.
4. Su H, **J Koltes**, M Saatchi, J Lee, R Fernando, and D Garrick. 2014. Characterizing Haplotype Diversity in Ten US Beef Cattle Breeds. Iowa State University Animal Industry Report.
3. Easley CJ, E Fritz-Waters, I Choi, **JE Koltes**, N Boddicker, J Reecy, JK Lunney, S Carpenter, CK Tuggle, P Liu, and JCM Dekkers. 2014. Analysis of gene expression in a region associated with host response to porcine reproductive and respiratory syndrome virus challenge. Iowa State University Animal Industry Report.
2. **Koltes, J.E.**, B.P. Mishra, L.R. Totir, R.L. Fernando, W. Coppieters, M. Georges, and J.M. Reecy. 2006. Angus dwarfism: the short story about ISU's discovery of a causal mutation for dwarfism in American Angus. Iowa State University Animal Science leaflet.
1. **Koltes, J.E.** and J.M. Reecy. 2006. NRSP-8 update of Iowa State University's molecular genetic research in beef cattle, highlighting the discovery of a putative causal mutation for Angus dwarfism. USDA NRSP-8 Research report. San Diego, CA.

PATENTS

GENETIC TEST FOR THE IDENTIFICATION OF DWARFISM IN CATTLE – USPTO # 7,700,291

GRADUATE STUDENTS ADVISED

Membership in Interdepartmental Programs

Interdepartmental Genetics and Genomics Graduate faculty (IGG)
Interdepartmental Bioinformatics and Computational Biology (BCB)

Students Advised as Committee Chair

Name	Major	Degree	Degree Start (end)
Cori Siberski	Animal Breeding & Genetics	PhD	January 2020
Kayla Lucas	Animal Breeding & Genetics	MS	August 2019
Abigail Jantzi	Animal Breeding & Genetics	PhD	August 2019

Committee Member Appointments

Name	Major	Degree	Degree Start
Lucas Koester	VMPM	PhD	2018
Josue Chinchilla-Vargas	Animal Science	PhD	2019
Thi-Hong-Ha Vu	Bioinfo. & Comp. Bio (BCB)	PhD	2019
Maria Oconitrillo Hidalgo	Animal Science	MS	2019

Penxing Yang	BBMB	PhD	2019
Handagala Wickramasinghe	Animal Science	PhD	2020
Chiron Anderson	Microbiology	PhD	2020

Adjunct Faculty at University of Guelph, Guelph, Ontario, Canada (Committee member)

Name	Major	Degree	Degree Start
Lucas Lopes	Animal Breeding & Genetics	PhD	2020

COMPLETED GRADUATE PROGRAMS AS COMMITTEE CHAIR

Name	Major	Degree	Degree Start (End)
2. Cori Siberski	Animal Breeding & Genetics	MS	August 2017 – December 2019

Thesis: Investigating automated sensor measures as possible indicator traits of feed intake and health traits in dairy cattle

1. Sarah Chewning (Arkansas)	Animal Science	MS	June 2016 – July 2018
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Thesis: Investigation of Bacterial Taxa as Biomarkers of Fescue Toxicosis and Heat Stress in Grazing Beef Cows

COMPLETED GRADUATE PROGRAMS- As Committee Member

Name	Major	Degree	Degree Completed
Leticia Sanglard (ISU)	Animal Breeding & Genetics	MS	March 2018

Visiting PhD students mentored (as faculty)

Name	Dates at Iowa State Institute
3. Bruna Petry	09/22/19 - 09/21/20 University of São Paulo, Brazil

Fellowship Project Title: Functional Analysis of the SAP30 gene and it's relation to muscle development. **Funding:** FAPESP scholarship

2. Marina Rocha	07/01/18 – 12/31/18 Federal University of São Carlos, Brazil/ EMBRAPA
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Fellowship Project Title: Genome-wide methylation profile and co-methylation analysis applied to feed efficiency in Nelore cattle. **Funding:** FAPESP scholarship

1. Andressa Lima	02/01/18 – 07/30/18 Federal University of São Carlos, Brazil/ EMBRAPA
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Fellowship Project Title: Identification of functional variants in regulatory regions associated with residual feed intake in Nelore cattle. **Funding:** FAPESP scholarship

Visiting Scientists and Students mentored (as a post-doc and student)

Visiting Scientists: Atul Kolte (2011), Chandra Mukhopadhyay & Thilak Pon Jawah Koilpillai (2012), Muhammad Saif Ur Rehman (2012), Amit Kumar Fnu (2013), Sanjeev Singh (2013), Lawrence Leslie Leo Prince Fnu (2013), Mir Asif Iquebal (2013), Sajidkhan Yusufzai (2013), Sarika Jaiswal (2013), Rajendran Ramanujam (2013), Varun Sankhyan (2014). Visiting PhD Students: Tassia Mangetti Goncalves (2014), Priscilla Silva Neubern De Oliveira (2013), Aline

Cesar (2013, 2015), Xuerong Yang (2012). *Veterinarians and Vet students*: Kathy Parton DVM, and Susan Piripi (2004 – 2007).

Post-Doctoral Mentor

Mentee

Marcela Marie de Souza

Dates

November 2018 – December 2020

TEACHING EXPERIENCE

Iowa State University

- **Instructor:** Animal Science 434 Dairy Systems Management (Dairy Capstone). Instructor: 2020, 2019, co-Instructor: Fall 2018, guest lecturer 2017. Responsible for coordinate of lectures across dairy management topic areas, lectures, homework, development of assessments (quizzes and exams) and lab modules. Currently developing hands-on dairy lab experiences. (junior/ senior level, class size = 40-60)
- **Instructor:** Animal Science 351x Introduction to Domestic Animal Genetics. 2020. Responsible for development of the course, development of lectures, homework and assessments (quizzes and exams). (junior level, class size = 60)
- **Instructor:** Animal Science 210 Career Preparation in Animal Science. Spring, Fall 2018 and 2019 (4 semesters). Co-instructor 3 semesters (lead instructor Fall 2018.) Responsible for coordinating lectures/ speakers, grading and reviewing two drafts of resumes and cover letters as well as providing writing workshops and lectures. (sophomore level, class size = 110-130)
- **Instructor:** Animal Science 568 Animal Breeding and Genetics Seminar. Fall 2018. Coordinated students and guest speakers. (Graduate students, class size = 4)
- **Guest lecturer:** Animal Science 556 Current Topics in Genome Analysis. Spring 2018, 2020. Lectured on topics including bioinformatics, use of computing in biology, re-use of public data. (Two 90-minute lectures and a computer demo: graduate course, class size = 7)
- **Guest lecturer:** Biology/Genetics 313 Principles of Genetics. Fall 2018. Assisted in the development of a lab section, provided 3 lectures. (sophomore level, class size = 35)
- **Guest lecturer:** Animal Science 235 Dairy Cattle Science. Fall 2017, 2018. Presented one lecture on dairy cattle genetics & genomics. (October 2017: undergraduate course, class size = 100)

University of Arkansas

- **Instructor:** Animal Science 3133 Animal Breeding & Genetics. Spring 2016 to present. All basic topics of breeding and genetics including introductory population and quantitative genetics are introduced in this course. Class size = 32-55. (undergraduate course)
- **Guest lecturer:** Animal Science 5901: Graduate Seminar. Discussion will include basics of critical literature review (2 lectures). Fall 2016. Class size = 17.
- **Tutorial Instructor:** Introduction to Bioinformatics for Next-Generation Sequencing Analysis. Spring 2016 (April- May). Instructed participants on basic Unix, Perl, R, and command line driven NGS software for gene expression analysis. Class participants included faculty, research scientists, post-docs and students from Animal and Poultry Science. Class size = 16 participants.
- **Guest lecturer:** Animal Science 4452 Dairy Capstone. Spring 2016, 2017. Presented three lectures on dairy cattle genetics & genomics and its impact on the dairy industry. (April 2016: undergraduate course, class size = 20)
- **Guest lecturer:** Animal Science 5747 Advanced Analytical Methods in Animal Science. Fall 2016: Topics will include DNA analysis methods, Next Generation Sequencing (NGS) (6 lectures), and basics of data visualization with R software, Fall 2015: introduction to NGS technology, application and research in the Animal Sciences. (Class size = 15)

Instruction as a Post-Doctoral Fellow at Iowa State University

- **Guest lecturer:** Animal Science 556 Current Topics in Genome Analysis/ Evolutionary, Ecology and Organismal Biology 561X. Spring 2014. Lectured on topics including transcriptomics, RNAseq analysis methods, co-expression analysis, and systems genetics. (Two 90-minute lectures and a computer demo: graduate course, class size = 25)
- **Tutorial Instructor:** Introduction to Bioinformatics for Next-Generation Sequencing Analysis. Fall 2013. I developed a 10-week course for visiting scientists, post-docs and graduate students to instruct participants on basic Unix, Perl, R, and command line driven NGS software. Topics covered included basic programming for bioinformatics, sequence alignment, sequence assembly, SNP calling, RNA-seq analysis, data visualization with R, variant annotation, iPlant/ iAnimal analysis. This class was co-taught with Eric Fritz. Class size = 18 (voluntary participants)
- **Instructor:** Animal Science 352 Animal breeding and genetics. Mentored by: Dr. Diane Spurlock, Fall 2011. Responsibilities included: presenting 6 lectures, weekly quizzes, teaching 4 labs with 3 sections (12 total), developing one exam and meeting weekly to evaluate material and progress with Dr. Spurlock. Class size = 87 (undergraduates)
- **Instructor:** Animal Science 345 Animal growth and development. Mentored by: Dr. Ted Huiatt, Spring 2011. Responsibilities included: presenting lectures, developing weekly quizzes, wrote one full exam and helped develop, proctor and evaluate all exams, met regularly with Dr. Huiatt to discuss teaching topics, grading, etc. I also developed learning materials on bone growth and develop for this course related to my PhD work on dwarfism. Class size = 24 (undergraduates)

Instruction as a PhD student at Iowa State University

- **Lecturer:** Animal Science 345 Animal growth and development along with Dr. Reecy, 2007; guest lecturer, 2006, 2007. (undergraduates)
- **Guest lab instructor:** Animal Science 360 Fresh meats: muscle growth and development (2006, 2002) (undergraduates)
- **Teaching assistant:** Animal Science 352 Livestock improvement through animal breeding (2004)

Teaching experience as an undergraduate at the University of Wisconsin-Madison

- **Teaching assistant:** Farm and Industry Short Course Genetic Improvement of Dairy cattle (2001)
- **Guest lecturer:** Dairy Science 272 Pre-capstone seminar: Internship experience in animal genetics (2000)

Training

- Howard Hughes Medical Institute teaching workshop. UW-Madison. Fall 2009

Undergraduate Student Mentor:*Iowa State University*

As Faculty (September 2017 to present)

Undergraduate students: Emma Persoon (2019), Aaron Geurts (2018), ;2 lab meeting students, Kendra Spier (2018), Aaron Gerdts (2018-present), Kayla Lucas (2018-2019), Alyssa Lehman (2018-2019), Emma Persoon (2018-2020), Leonora James (2020-present), Jenna Trenhaile (2020-present), Katrina Lee (2020), Kristi Mensen (2020)

University of Arkansas

As Faculty (July 2015 to July 2017)

Undergraduate students: Dayanera Ward (2016), Julie Atchley (2016-2017), Abby Ratton (2016-2017), Lauren Zell (2017).

As student and post-doc at Iowa State University (August 2010 to June 2015)

Undergraduate Students: Aracely Acevado, Julie Collins, Brandon Cornilieu, Andrea Moe, Nicole Rutscher. High School Student: Jessica Frerichs

Undergraduate Honors Theses Advised**University of Arkansas**

Name	Thesis Topic	Date Completed
Julie Atchley	RNA-seq analysis of whole blood in cattle	4/2/18
Abby Ratton	Vaginal microbiome analysis in cattle	8/2/18

Undergraduate Advising

Advising Undergraduate Students (currently 29) August 2017 to Present

PRESENTATIONS & INVITED SEMINARSPresentations**37 total seminars presented (16 invited talks)**

1. PASE successes around the US. 2020 Iowa State Precision Animal Science and Engineering (PASE) virtual organizational meeting. (December 15, 2020)
2. **Invited Talk:** What's new in the December 2020 Dairy Genetic Evaluations. ISU Dairy Extension Monthly Webinar. (virtual presentation: December 8, 2020)
3. **Invited Talk:** US FAANG: Next steps and collaborative opportunities. 2020. FAANG-EU Shared Workshop: Foundation for the Future. Wellcome Genome Campus, Hinxton, Cambridge, UK (February 26, 2020)
4. **Invited Talk:** Application of Genomics and Sexed Semen to Maximize Profits. Dairy Discussions 2019: Making Genetic Decisions Profitable. Orange City, IA (ISU Dairy Extension program; December 3, 2019)
5. Automated collection and processing of precision livestock data for use in animal breeding. Animal Breeding and Genetics Seminar, ISU (November 22, 2019)
6. **Invited Talk:** Precision dairy is here to stay. World Dairy Expo, Madison, WI October 1, 2019
7. **Invited Talk:** Automated collection and processing of data in livestock farms. Within the session, Advancing Artificial Intelligence in Dairy farms at ADSA Cincinnati, OH June 2019.
8. Preliminary Evaluation of Sensor data as Proxies for Efficiency and Health Traits in Holstein Dairy Cattle. 1st Annual Precision Livestock Farming meeting, Ames, IA. (December 6, 2018)
9. Investigation of breed effects and novel phenotypes impacting fescue toxicosis in beef cattle. Animal Breeding and Genetics Seminar, ISU (Fall 2018)
10. Investigating Host-Genetic Mechanisms Associated with Fescue- and Heat-Stress Tolerance in Cattle. Plant and Animal Genome XXVI. (2018)
11. Interaction between the host and microbiome in pigs: Is it epigenetic? Animal Breeding and Genetics Seminar, ISU (Fall 2017)
12. **Invited Talk:** Automated collection of heat stress data in livestock: new technologies and opportunities. National Animal Science Meeting new technologies session. USA. Baltimore, MD, USA (July 2017)
13. **Invited Talk:** Interaction between host and microbiome and epigenetic communication between the two in pigs. Workshop on OMICS strategies applied to livestock science. Hosted by ESALQ/University of San Paolo: Piracicaba, Brazil (April 24-28, 2017)
14. **Invited Talk:** Can nurture modify nature? Investigating the impact of omega3 fatty acids on DNA methylation in pigs. Workshop on OMICS strategies applied to livestock science. Hosted by ESALQ/University of San Paolo: Piracicaba, Brazil (April 24-28, 2017)
15. **Invited Talk:** Efforts to develop genetic & genomics strategies to improve fescue tolerance in cattle. Division of Agriculture/ University of Arkansas Livestock and Forestry Research Station Field Day. Batesville, AR. (April 18, 2017)
16. **Invited Talk:** In search of novel phenotypes and biomarkers associated with tall fescue and heat tolerance in crossbred beef cattle. Presented at the Animal Genomics and Adaptation to Climate Change workshop of Plant and Animal Genome XXIV. (January 18, 2017)

17. Genes in cattle, genes in humans, understanding the complexities of iron regulation. Sigma Xi lecture to the University of Arkansas. October 28, 2016
18. **Invited Talk:** Opportunities for genomics to improve beef cattle profitability. Arkansas Cattleman's Association. Ft. Smith AR. (Aug. 12th, 2016.)
19. **Invited Talk:** Mining functional genomics and epigenetics data with livestock EpiDB. The 35th International Society of Animal Genetics. Salt Lake City, USA. (2016)
20. **Invited Talk:** Current tools in beef cattle breeding: what's worth the money? Division of Agriculture/ University of Arkansas Livestock and Forestry Research Station Field Day. Batesville, AR. (2016)
21. **Invited Talk:** Leveraging genetics, genomics, and epigenetics to advance animal breeding. Plant Pathology Seminar, University of Arkansas. (2016)
22. **Invited Talk:** EpiDB: An omics data resource for cattle. Plant and Animal Genome XXIV. (2016)
23. Nurture modifies nature: Investigating the impact of omega3 fatty acids on DNA methylation. Animal Breeding and Genetics Seminar, ISU (2013)
24. Accelerating livestock genomics with iAnimal. Plant and Animal Genome XXI. (2013)
25. Design of a Buffalo SNP panel. Plant and Animal Genome XXI. (2013)
26. **Invited Talk:** A systems-genetics analysis of bovine skeletal muscle iron content. National Animal Science Meeting Animal Breeding and Genetics section on systems biology, Phoenix, AZ, USA. (2012)
27. Investigating the role of maternal nutrition on fetal growth in beef cattle using transcriptional profiling. Animal Breeding and Genetics Seminar, ISU (2012)
28. VCM3.0: a comparative genetics viewer designed to transfer annotation, QTL and biological information across species. Plant and Animal Genome XX. (2012)
29. A comparison of the transcriptomes of extreme animals for bovine skeletal muscle iron content. Iowa State Illumina Sequencing Workshop. (2011)
30. Exploring the genetics of iron content in beef: implications for Hemochromatosis? Department of Animal Science Seminar. Iowa State University. (2011)
31. Virtual Comparative Map: A comparative genomics viewer & database designed to facilitate genomic discovery. Plant and Animal Genome XIX. (2011)
32. Discovery and Characterization of a causative mutation for bovine dwarfism in cyclic-GMP-dependent, type II, protein kinase (PRKG2). Dairy Science Department Seminar. University of Wisconsin-Madison. (2010)
33. Discovery and Characterization of a causative mutation for bovine dwarfism in cyclic-GMP-dependent, type II, protein kinase (PRKG2). CIBM seminar. University of Wisconsin-Madison. (2010)
34. Molecular dissection of dwarfism in American Angus. Interdepartmental Genetics Seminar. Iowa State University, Ames. (2005)
35. Fine-mapping of the genomic region associated with disproportionate dwarfism in Angus cattle. Interdepartmental Genetics Seminar. Iowa State University, Ames. (2004)
36. Fine-mapping of the locus associated with dwarfism in Angus cattle. Animal Breeding & Genetics Seminar. Iowa State University, Ames. (2004)

37. Report on the stillbirth QTL mapping project in Holsteins at ISU. NC State S1008 Dairy cattle survival meeting. Raleigh, NC (2003)

LEADERSHIP & SERVICE

Professional Service

USDA National Animal Genome Research Program (NAGRP) Livestock Joint-Bioinformatics Coordinator (October 2018 – October 2023)
Role: joint-coordinator with Drs. Fiona McCarthy and Jim Reecy.

Co-organizer of the Precision Animal Science and Engineering virtual meeting (December 2020). Role: Involved in securing funding, helping to organize the meeting and organizing with Drs. Ken Stalder and Anna Johnson. The objective of the meeting was to help foster the development of interdisciplinary research teams studying the use of precision technologies for phenotyping and management for research and application.

FAANG coordination with EU- February 2020 trip to Hinxton, UK. (February 2020). Role: Represented the US FAANG project to provide updates on US FAANG projects and foster collaborations between US and EU research groups.

Organization of the USDA Genome to Phenome Blueprint Meeting (January 2020)
Role: Involved in the organization of the USDA animal genetics blueprint meeting at PAG 2020 to help identify priorities for funding and discuss NRSP8 priorities in the development of a new NRSP8 program for animal genetics research.

Invited as delegate for NIH-NHGRI Strategic Planning Workshop: Perspectives in Comparative Genomics and Evolution. (August 2019-present)
Role: Moderated a session on systems biology and participated in discussions on make non-model organisms (including livestock) more competitive for NIH funding. Participation in the meeting was intended to generate ideas for joint grant proposals and prioritizing funding opportunities for comparative genomics research jointly for NIH, NSF and USDA-NIFA. I was also asked to help write a whitepaper in response to the meeting. (Funded- NSF travel grant.)

NRSP8 future proposal planning committee. (January 2019 – present)
Role: Involved in planning and writing a new national animal genome research program multistate grant to develop community bioinformatics and genomics resources for livestock.

Precision Livestock Farming (PLF) Workshop planning committee member (August- December 2018)
Role: Involved in organizing the Iowa State PLF meeting at the intersection of academia and industry in Ames, IA on December 6, 2018 at the Scheman building.

Co-organizer of USDA research planning conferences: (1) Livestock High-throughput phenotyping (HTP) and Big Data meeting; and (2) USDA Blueprint: Genome to Phenome meeting (November 2017)

Role: Involved in securing funding and helping to run and organize the meeting (for more details, see grant funding description above.) Both meetings were held in Beltsville, MD with the goal of developing new research priorities and goals in Animal Breeding and Genetics and precision livestock applications across all disciplines in the animal sciences.

Midwest Animal Science Meeting Committee Member (March 2017-March 2019)

Role: Involved in organizing the Animal Breeding and Genetics Program for the Midwest meeting (Omaha, NE). Responsibilities included providing ideas for session topics, reviewing abstracts, moderating sessions and organizing and chairing a session on FAANG in March 2019.

National Animal Science Meeting Breeding & Genetics Committee Member:

(August 2016-August 2019)

Role: Responsibilities included identifying session speakers, reviewing abstracts and chairing meeting sessions.

Member of the Functional Annotation of Animal Genomes Consortium

(January 2015-present)

Role: I am a member of the gene expression (RNA-seq.), methylation, long non-coding RNA, and ChIP-seq. analysis groups as well as the bioinformatics/ data analysis sub-committees.

Associate Chair, Gordon Research Seminar on Quantitative Genetics and Genomics

(December 2011- March 2013)

Role: Helped to organize student and keynote speakers for the GRS, reviewed participant abstracts, assisted in writing a USDA grant for the GRC/GRS and chaired sessions at the GRS and GRC.

Service to Professional Societies

Manuscript Reviewer for:

- Animals 2020
- Animal Genetics 2006, 2010, 2013, 2016, 2017, 2018
- Animal Journal 2010-2012
- BMC Genetics 2011
- BMC Genomics 2013, 2015, 2017, 2018, 2019, 2020
- Domestic Animal Endocrinology 2015
- Frontiers in Genetics 2019, 2021
- Frontiers in Physiology 2017
- G3 2019
- Genes 2019, 2020
- Genome Biology 2012
- Journal of Agriculture and Food Research 2020
- Journal of Animal Science 2013, 2016, 2017, 2018, 2020
- Journal of Dairy Science 2015, 2016, 2018, 2021
- Mammalian Genome 2006
- Marine Biotechnology 2014
- Meat Science 2017, 2018

- Plant Physiology 2012
- Poultry Science 2017, 2019
- PLOS One 2015, 2016
- Scientific Reports 2018, 2019

Animal Industry Reports Reviewer 2021

Peer Reviewer for USMARC journal articles 2015

Text Book reviewer: Molecular and Quantitative Genetics, edited by Hasan Khatib.
Role: Edited one chapter. 2013

Grant Reviewer for:

Mitacs (Canada)
ISU PIRI/PIRS
USDA AFRI
BARD

Scientific Advisory Board Member:

1. NSF funded FAANGmine project December 2019 - present
2. USDA-FACT Coordinated Innovation Network Committee for Developing a Dairy Brain:
The Next Big Leap in Dairy Farm Management Using Coordinated Data Ecosystems.
October 2019 – present

Service to the Department of Animal Science at Iowa State University

- ISU Dairy Advisory Group 2020
- **Hiring committee** for ISU Assistant Professor of Dairy Teaching 2020
- **Chair** Departmental IT committee (2017 to present)
- **Chair** Departmental IT working group (transitioning departmental IT to college/university IT systems) (2017 to present)
- Departmental seminar committee (2017 to present)
- Departmental hiring committee, IT staff (2018)

University Service: High Performance Computing Committee (2018 to present)

CALS College Service: panel member on, “the job hunt and roles of a new assistant professor,” to graduate students as part of a CALS graduate student services workshop (February 2018)

Service to the Department of Animal Science, University of Arkansas

- Arkansas High Performance Computing Center (AHPCC) steering committee member (2015 - 2017)
- University of Arkansas Division of Agriculture (AGRI) High Performance Computing Committee (2015 - 2017)
- Departmental facilities planning committee (2015 - 2017)

- Departmental internship committee (2016 - 2017)
- Assisted with Undergraduate Academic Quadrathlon (2015 - 2016)
- Undergraduate Academic Advisor (2015 - 2017)