

STEPHANIE DAWN MCKAY

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EDUCATION

- 2003-2007 University of Alberta (Edmonton, AB, Canada)
Ph.D. Animal Science November 2007
Department of Agriculture Food and Nutritional Sciences
- 1999-2002 Texas A&M University (College Station, Texas)
M.S. Veterinary Pathobiology August 2002
Department of Veterinary Pathobiology
- 1993-1999 Texas A&M University (College Station, Texas)
B.S. Biochemistry May 1999
B.S. Genetics May 1999

RESEARCH AND PROFESSIONAL EXPERIENCE

- 2018-pres. Associate Professor of Genetics and Genomics, University of Vermont,
Department of Animal Science and Veterinary Sciences, Burlington, VT
- 2012-2018 Assistant Professor of Genetics and Genomics, University of Vermont,
Department of Animal Science and Veterinary Sciences, Burlington, VT
- 2007-2012 Postdoctoral Fellow with Drs. Robert Schnabel, Kristen Taylor and
Jeremy Taylor, University of Missouri, Division of Animal Sciences,
Columbia, Missouri
- 2003-2007 Graduate Student with Dr. Stephen Moore, University of Alberta,
Department of Agriculture Food and Nutritional Sciences,
Edmonton, Alberta, Canada
- 2002-2003 Biological Technician II for Dr. Tim King, U.S. Geological Survey
Leetown Science Center's Aquatic Ecology Laboratory,
Kearneysville, WV
- 1999-2002 Research Assistant for Dr. James E. Womack, Texas A&M
University, Department of Veterinary Pathobiology,
College Station, Texas

PROFESSIONAL DEVELOPMENT

- Leadership in Bioscience Workshop, Cold Spring Harbor, NY (February 2013): This in an interactive workshop designed for new investigators in which participants develop the skills necessary to become an effective and productive leader and manager in the scientific workplace.
- Entering Mentoring, University of Missouri (Spring 2011): Training workshop aimed at accelerating the process of learning to be a mentor. Topics included learning to communicate, goals and expectations, identifying challenges and issues, resolving challenges and issues, elements of good mentoring, and developing a mentoring philosophy.
- Grantmanship Training, University of Missouri Seminar Series (September 2008 – April 2009): Monthly topics focused on key aspects of preparing and submitting grants including grants from ground zero, getting above the payline, why is the budget important, tips and tricks to make your proposal shine, tackling the outreach and evaluation sections of your proposal, and writing basics for grant communication.

PROFESSIONAL SOCIETIES

- Texas Genetics Society
- International Society of Animal Genetics
- Graduate Women in Science
- American Association of Animal Science

SERVICE ACTIVITIES

JOURNAL REVIEW: Animal Biotechnology, Animal Genetics, BMC Genomics, BMC Biology, Genetics, Genetics and Molecular Biology, GigaScience, Heredity, Journal of Animal Breeding and Genetics, Journal of Animal Science, Livestock Science, Mammalian Genome, Molecular Ecology, PLoS ONE

INTERNATIONAL

1. Moderator/Chair Biology/Epigenetics session for World Congress on Genetics Applied to Livestock Production, 2018
2. Chair of the Animal Epigenetics Workshop for the International Society of Animal Genetics 2016-2020

NATIONAL

1. Accepted invitation to participate in a two-day workshop and subsequent generation of a follow-up report on Genome to Phenome: A USDA Blueprint for Animal Production (2018 – 2027). This report is a vision to serve as a guide to intra- and extramural research programs at USDA and the broader community, November 2017

2. Co-Chair Cattle Research Coordination Meeting. NSF funded Animal Genome to Phenome Research Coordination Network Sponsored Functional Annotation of Animal Genomes (FAANG) Meeting, January 2017
3. USDA National Animal Genome Research Program chair of cattle organizing committee 2015
4. USDA National Animal Genome Research Program chair-elect of cattle organizing committee 2014

UNIVERSITY

1. Member of Premedical Enhancement Program Committee, University of Vermont, January 2017 to present
2. Member of the Fulbright Fellowship interview committee, University of Vermont, September 2013-2016
3. Member of the Academic Integrity Council, University of Vermont, September 2013 to present

COLLEGE

1. Member of HATCH Grant Review Committee, University of Vermont, 2013 to 2016 and 2018-present
2. Faculty Marshall for College of Agriculture and Life Sciences Graduation, May 2015
3. Member of CALS Curriculum Committee, University of Vermont, Spring 2016

DEPARTMENT

1. Member of ASCI Graduate Program Committee, University of Vermont, 2018-present
2. CALS/Department of Animal and Veterinary Sciences Open House Event, Fall 2014-2016
3. Summer Orientation for Incoming Animal Science Students, Summer 2013 and 2014

GRANT REVIEWS

1. National Institutes of Food and Agriculture, USDA, 2018
2. Dairy Farmers of Canada, 2017
3. Natural Sciences and Engineering Research Council of Canada (NSERC), 2016
4. Alberta Livestock and Meat Agency Ltd (ALMA), October, 2014
5. Binational Agricultural Research and Development Fund (BARD), September 2013
6. International Foundation for Science, 2013

ABSTRACT REVIEWS

1. American Dairy Science Association, Abstract Reviewer for Breeding and Genetics Section, February, 2017

2. Conference Proceedings Reviewer: MidSouth Computational Biology & Bioinformatics Society (MCBIOS), 2016
3. Joint Annual Meeting of ASAS, ADSA[®], and CSAS, Growth and Development Section, February, 2014

HONORS AND AWARDS

- Laboratory Safety Award, The University of Vermont, Department of Risk Management & Safety, Awarded April 2014.
- Douglas D. Randall Young Scientist travel award for travel to Plant & Animal Genome XX Conference, San Diego, California. Awarded February 2012
- International Society for Animal Genetics award for having the second most cited manuscript published in Animal Genetics in the year 2007. Awarded July 2010.
- Accepted into *FIRST IV: Faculty Institutes for Reforming Science Teaching* NSF CCLI - Phase III (DUE 618501), 2009-2012. Diane Ebert-May (PI), Terry Derting (co-PI). Professional development program for teaching and learning in undergraduate biology; participants are postdoctoral scholars in the biological sciences and a selected team of biology faculty who lead the professional development workshops. Postdocs leave the program having designed a complete introductory biology course based on the principles of scientific teaching. Awarded April 2009.

COURSES TAUGHT

- ANFS 395. Doctoral Seminar. Credit 1. 2015- 2018
- ASCI 168. Animal Genetics. Credit 3. Molecular genetics, Mendelian genetics, Population genetics, Quantitative genetics and Genomics University of Vermont. Taught Annually in Spring Semester (2013 to present).
- AS 3001 Applied Livestock Genomics. Credit 2. Introduction to genomics, whole genome sequencing, quantitative traits and marker assisted selection. University of Missouri. Taught Annually (2010 & 2011)

GUEST LECTURER:

- ASCI 001 Introduction to Animal Science. Credit 3. University of Vermont
 - Topic lectured: Livestock genetics (2018)
- ASCI 122 Animal Welfare. Credit 3. University of Vermont
 - Topics lectured: Welfare of Animal Models of Disease; Transgenics and Selection (2016, 2017)
- ASCI 135 CREAM. Credit 4. University of Vermont.
 - Topics lectured: Bovine Genomics (2013, 2014 and 2017)

- AS 3213 Genetics of Agricultural Plants and Animals. Credit 3. University of Missouri.
 - Topics lectured: Biotechnology (2008-2011), Quantitative Genetics (2010)
- AS 4323 Applied Livestock Genetics. Credit 2. University of Missouri.
 - Topics lectured: Marker Assisted Selection (2009)
- AS 4975 Beef Production. Credit 3. University of Missouri.
 - Topics lectured: Genomics (2010)
- AS 8415 Epigenetics. Credit 3. University of Missouri.
 - Topics lectured: Quantitative Epigenetics (2011)

GRANT SUPPORT

- 2017- 2021: USDA NIFA AFRI. 2017-05218. “Functional Annotation of the Bovine Genome.” \$2,500,000 PI: P. Ross CO-PIs: J. Medrano, H. Zhao, H. Jiang, M. Rijnkels, C. Gill, J. Reecy, Z. Jiang, W. Liu, B. Murdoch, S. McKay, M. Thomas, T. Smith.
- 2017-2020: USDA Hatch. VT-H02407MS. “Profiling 5-Hydroxymethylcytosine in the brains of steers with extreme measures of docility.” \$64,500. SD McKay.
- 2017-2018: Select Sires. “Investigation of genetic variation in global DNA methylation in bull semen and its relationship with semen quality and fertility parameters.” \$24,450. C Maltecca (PI), S McKay (Co-PI), A Canovas (Co-PI).
- 2016-2019: USDA Hatch. VT-H02301MS. “Harnessing Chemical Ecology to Address Agricultural Pest and Pollinator Priorities.” \$64,500. PI: Y. Chen and CO-PI: S. McKay
- 2016-2018: College of Agriculture and Life Sciences, University of Vermont. “Facilitating the Generation of a Bovine Methylation Array” \$40,000. SD McKay.
- 2016-2018: USDA NIFA AFRI. 2016-67016-24766. “Facilitating the Generation of a Bovine Methylation Array” \$150,000. SD McKay.
- 2015-2016. The University of Vermont REACH. “How do insect pests rapidly evolve on the Pesticide Treadmill?” PI: Y Chen, CO-PI: S McKay \$40,000.
- 2014-2015: GenHome Dream Project. “Working towards a Bovine bisulfite sequence reference assembly.” SD McKay. €25,000 (~\$31,000).
- 2014: American Simmental Association, Dr. Robert Walton Award. “Characterizing the brain methylome in steers with extreme measures of docility.” SD McKay. \$3,000.
- 2013-2016: USDA Hatch. VT-H02017MS. “Characterizing the brain methylome in steers with extreme measures of docility.” SD McKay. \$79,500.
- 2012-2013: USDA Hatch. “Characterizing the Bovine Epigenome.” SD McKay. \$10,000.

- 2010-2011: Missouri Research Board. “An epigenetic and transcriptomic approach to the dissection of a complex trait.” SD McKay and JF Taylor. \$38,000. 02/01/2010-01/31/2011.
- 2010-2012: USDA NIFA AFRI. 2010-65205-20414. “Exploration of the bovine epigenome: A genome-wide methylation survey and characterization of regions with tissue-specific methylation.” \$130,000. SD McKay, KH Taylor, CW Caldwell, JF Taylor. 01/01/10-12/31/11. *This proposal was reviewed with grants by established PIs, ranked 2nd overall and was scored outstanding.

RESEARCH GIFTS AND IN-KIND SUPPORT

- 2016: American Holstein Association. “An RNA-Seq investigation of Digital Dermatitis in Holstein cattle”. SD McKay \$12,000 (Gift)
- 2016. NeuroScience Associates. Neurohistology of the Bovine Brain and 3D Reconstruction. Bonnie Cantrell and Stephanie McKay. \$108,023 (In-Kind Support)

INVITED PRESENTATIONS

1. McKay, SD. 2018. Profiling Conservation of DNA Methylation in Cattle. American Society of Animal Science and the Canadian Society of Animal Science Meeting, Vancouver, B.C., Canada.
2. McKay, SD, TS Kalbfleisch, BM Murdoch, TPL Smith, JD Murdoch and MP Heaton. 2018. A SNP Resource for Studying North American Moose. 74th Annual Northeast Fish & Wildlife Conference, Burlington, VT
3. Betancourt, F., S. Friedman, S. Perlee, H. Lachance and S.D. McKay*. 2018. Examining conserved DNA methylation in the bovine 5’ AMPK gene family. International Plant & Animal Genome XXVI, San Diego, California.
4. McKay, SD. 2018. Facilitating the Generation of a Bovine Methylation Array. International Plant & Animal Genome XXVI, San Diego, California.
5. McKay, SD. 2017. Profiling Epigenetic Modifications in the Limbic System of the Bovine Brain. Leibniz institute for Farm Animal Biology in Dummerstorf, Germany
6. McKay, SD, GE Liu, Y Zhou, R Tearle, M Del Corvo, E Capra, B Cantrell, B Rosen, JL Williams, P Ajmone Marsan and A Stella. 2017. Whole Genome Bisulfite Sequencing of Three Tissues Related to the Bovine Reference Genome. International Plant & Animal Genome XXV, San Diego, California.
<https://pag.confex.com/pag/xxv/meetingapp.cgi/Paper/26225>
7. Friedman, S and SD McKay. 2016. Global DNA Methylation in the Liver of Vermont Bobcat (*Lynx rufus*). University of Vermont Student Research Conference, Burlington, Vermont.

8. McKay, SD. 2016. The Journey Towards Determining the Extent to which DNA Methylation Affects Variation in Cattle Possessing Extreme Phenotypes for Residual Feed Intake. University of Guelph, Guelph, ON, Canada.
9. McKay, SD. 2015. To What Extent Does DNA Methylation Affect Phenotypic Variation in Cattle? Veterinary and Animal Science Days 2015 , University of Milan. Milan, Italy.
10. McKay, SD. 2015. DNA Methylation Affects Phenotypic Variation in Cattle Possessing Extreme Phenotypes for Residual Feed Intake. Plant & Animal Genome XXIII Conference, San Diego, California
11. Benjamin, AL, WJ Weber, SD McKay, BA Crooker and DE Kerr. 2014. Investigating innate immune response differences between Angus and Holstein cattle with the dermal fibroblast model. Joint ADSA-ASAS Annual Meeting, Kansas City Missouri
12. Green, BB, SD McKay and DE Kerr. 2014. Age dependent changes in heifer fibroblast DNA methylation and LPS-induced gene expression. Joint ADSA-ASAS Annual Meeting, Kansas City Missouri
13. McKay, SD. 2014. Genetics of Feed Efficiency and Applications for the Dairy Industry. Herd Health and Nutrition Conferences, East Syracuse , New York and West Lebanon, New Hampshire.
14. McKay, SD. 2014. DNA Methylation Affects Phenotypic Variation in Animals Possessing Extreme Phenotypes for Feed Efficiency. Plant & Animal Genome XXII Conference, San Diego, California
15. McKay, SD. 2013. Trends in Bovine Epigenomics. Marvin Seminar Series, Department of Plant Biology, University of Vermont.
16. McKay, SD. 2013. RNAseq data handling and experiments' interpretation. Sao Paulo School of Advanced Science in Animal Functional Genomics. Aracutuba, Sao Paulo, Brazil.
17. Kerr, DE, BB Green and SD McKay. 2013. Individual differences in bovine fibroblast DNA methylomes may cause variation in their innate response to LPS. 10th International Veterinary Immunology Symposium. Milan, Italy.
18. Dolezal, MA, D Kedra, G Bussotti, H Tafer, S McKay, Z Qu, JW Kim, D Adelson, R Schnabel, JF Taylor, C Notredame, R Guigo, A Bagnato, E Lipkin, M Soller and J Herrero. 2012. Overlap of constrained GERP elements by protein coding and ncRNA genomic functional elements in the autosomal bovine genome. Livestock Genomics Meeting, Hinxton, UK.
19. McKay SD, KD Wells, JW Kim, RH Chapple, RD Schnabel, CW Caldwell, JF Taylor and KH Taylor. 2012. Feed Efficiency in cattle: An epigenetic perspective. Plant & Animal Genome XX Conference, San Diego, California.
20. McKay SD, JW Kim, RH Chapple, MM Rolf, D Keisler, J Garbe, S Fahrenkrug, C Notredame, R Guigo, D Kedra, I Erb, D Adelson, Z Qu, KH Taylor, CW Caldwell, KD Wells, RD Schnabel and JF Taylor. 2012. Differential gene expression detected

via transcriptome sequencing in Angus steers differing for feed efficiency. Plant & Animal Genome XX Conference, San Diego, California.

21. McKay SD. 2012. Exploration of the Bovine Epigenome: A genome-wide methylation survey and characterization of regions with tissue-specific methylation. USDA-NIFA Animal Genetics, Genomics and Breeding Program Annual Investigator Meeting, San Diego, California.
22. Schnabel, RD, SD McKay, JW Kim, JE Decker, MM Rolf, RH Chapple, HR Ramey and JF Taylor. 2012. Angus Genome Project. Plant & Animal Genome XX Conference, San Diego, California.
23. McKay SD. 2011. Bovine Genomics. Life Sciences Undergraduate Research Opportunity Program. University of Missouri, Columbia, Missouri.
24. McKay SD. 2011. Active Learning in Science. Division of Animal Science Teaching Retreat. University of Missouri, Columbia, Missouri.
25. McKay SD, KD Wells, KH Taylor, CW Caldwell, RD Schnabel, JF Taylor and JW Kim. 2011. Detection of differentially expressed genes in three tissues among cattle divergent for residual feed intake. Plant, Animal & Microbe Genomes XIX Conference, San Diego, California.
26. Schnabel RD, JE Decker, A Cooper, K Chen, SD McKay, MC McClure, TM Taxis, JW Kim, MM Rolf, R Chappel, DA Vasco, S Gregg and JF Taylor. 2010. High-throughput genomics: Applications in conservation biology and phylogenomics. Adelaide Conference on Phylogenetics and Phylogenetics Workshop. The University of Adelaide, Adelaide, Australia.
27. Nkrumah JD, DJ Garrick, RL Fernando, S Northcutt, B Bowman, BW Woodward, SW Bauck, D Vasco, TM Taxis, MM Rolf, JE Decker, JW Kim, MC McClure, SD McKay, RD Schnabel and JF Taylor. 2009. Alternative methods for selecting tagSNP panels from the bovine 50K chip to predict marbling in Angus cattle. Joint ADSA-CSAS-ASAS Annual Meeting, Montreal, Quebec, Canada.
28. Taylor JF, JE Decker, J Kim, MC McClure, SD McKay, MM Rolf, T Taxis, D Vasco and RD Schnabel. 2009. Prospects for genomic selection in beef cattle. Proceedings of the 41st Annual research symposium and annual meeting, Beef Improvement Federation, Sacramento, California.
29. Taylor JF, SD McKay, MC McClure, JW Kim, DA Vasco, JE Decker, MM Rolf and RD Schnabel. 2009. Prospects for whole genome selection in beef cattle. Plant, Animal & Microbe Genomes XVII Conference, San Diego, California.
30. Decker JE, JC Pires, GC Conant, SD McKay, MP Heaton, J Vilkki, K Chen, A Cooper, CM Seabury, AR Caetano, GS Johnson, RA Brennehan, O Hanotte, LL Coutinho, ME Babar, LS Eggert, P Wiener, JJ Kim, KS Kim, TS Sonstegard, CP Van Tassell, HL Neibergs, RD Schnabel and JF Taylor. 2009. Divergence times and signatures of selection from phylogenomic analysis of pecoran species. Plant, Animal & Microbe Genomes XVII Conference. San Diego, California.

31. Vasco DA, D Lee, SD McKay, RD Schnabel and JF Taylor. 2009. Computational strategy for the estimation of population genetic parameters using genomic data. Plant, Animal & Microbe Genomes XVII Conference. San Diego, California.
32. Sonstegard, TS, P Vanraden, G Wiggans, R Schnabel, G Liu, LK Matukumalli, MV Silva, S McKay, SG Schroeder, LC Gasbarre, JF Taylor and CP Van Tassell. 2008. Applied Bovine Genomics: Chipping away at the genetics underlying disease traits. 3rd International Symposium of Animal Functional Genomics. Edinburgh, UK
33. McKay SD. 2006. Linkage disequilibrium: Why do we care and now what? 30th Conference of the International Society for Animal Genetics. Porto Seguro, Brazil.
34. McKay SD. 2006. A bovine whole genome linkage disequilibrium map. Plant, Animal & Microbe Genomes XIV Conference. San Diego, California.
35. McKay SD and SS Moore. 2005. How to map a genome in 12 days. The International Workshop on Bovine Genomics: The Next Phase. Houston, Texas.
36. McKay SD. 2002. The bovine 5`-AMP activated protein kinase gene family in cattle: Mapping and single nucleotide polymorphism detection. Department of Veterinary Pathobiology. Texas A&M University, College Station, Texas.
37. McKay SD. 2002. The AMPK gene family in Cattle: Mapping and SNP detection. Texas Genetics Society. South Padre, Texas.

CORRESPONDENCE

1. Marina Kvaskoff and Stephanie D. McKay, "Education: Scientists need leadership training," *Nature* 506 (7487), 159-159 (2014).

BOOK CHAPTERS

1. McKay SD and RD Schnabel. 2011. History of linkage mapping the bovine genome. In Bovine Genomics. JE Womack Ed., Wiley-Blackwell.
2. Taylor JF, JE Decker, SD McKay, HR Ramey, MM Rolf and RD Schnabel. 2011. Genomic selection in beef cattle. In Bovine Genomics. JE Womack Ed., Wiley-Blackwell.

PROCEEDINGS

1. Rodriguez, AM, KM Davenport, SD McKay, CA Gill and BM Murdoch. 2018. Meiotic Recombination in Ruminant Livestock Species. Proceedings of the 11th World Congress on Genetics Applied to Livestock Production, Auckland, New Zealand.
2. Rolf MM, JF Taylor, RD Schnabel, SD McKay, MC McClure, SL Northcutt, MS Kerley and RL Weaber. 2010. Use of the BovineSNP50 assay for feed efficiency selection decisions in Angus Cattle. Proceedings of the Beef Improvement Federation, Columbia, MO.

3. Rolf MM, SD McKay, MC McClure, JE Decker, TM Taxis, RH Chapple, DA Vasco, SJ Gregg, JW Kim, RD Schnabel and JF Taylor. 2010. How the next generation of genetic technologies will impact beef cattle selection. Proceedings of the Beef Improvement Federation, Columbia, MO.
4. Ferreira Marques E, C Li, JD Nkrumah, SD McKay, B Murdoch, Z Wang and SS Moore. 2006. Fine mapping of QTL affecting carcass merit on bovine chromosome 14 using a high density marker set. Proceedings of the 8th World Congress on Genetics Applied to Livestock Production, Belo Horizonte, Brazil.
5. Li C, JD Nkrumah, R Bartusiak, A Fu, BM Murdoch, EL Sherman, SD McKay, Z Wang, DH Crews and SS Moore. 2006. A genome-wide scan for Quantitative Trait Loci affecting ultrasound and carcass backfat thickness in beef cattle. Proceedings of the 8th World Congress on Genetics Applied to Livestock Production, Belo Horizonte, Brazil.
6. McKay SD, A Prasad, E Marques, B Murdoch, Z Wang, J Williams and SS Moore. 2006. BAC contig based radiation hybrid maps of bovine chromosomes 14 and 19: Tool for fine mapping of QTL. Proceedings of the 8th World Congress on Genetics Applied to Livestock Production, Belo Horizonte, Brazil.
7. Prasad A, JD Nkrumah, C Li, B Murdoch, SD McKay, Z Wang and SS Moore. 2006. Identification of Quantitative Trait Loci for backfat thickness on bovine chromosome 19 in beef cattle. Proceedings of the 8th World Congress on Genetics Applied to Livestock Production, Belo Horizonte, Brazil.

PUBLISHED ABSTRACTS

1. Betancourt, F., S. Friedman, S. Perlee, H. Lachance and S.D. McKay. (2016). P2014 Examining conserved DNA methylation in the bovine 5' AMPK gene family. *Journal of Animal Science* 94(7supplement4), 44-45. doi: 10.2134/jas2016.947supplement444a.
2. Cantrell, B.A., R.L. Weaber, R.N. Funston, H. Lachance and S.D. McKay. (2016). P2011 Novel analysis of global DNA methylation in the limbic system of the bovine brain. *Journal of Animal Science* 94(7supplement4), 43-43. doi: 10.2134/jas2016.947supplement443x.
3. Prause, M.R., B.M. Murdoch, J.E. Sawyer, J.L. Williams, S.D. McKay and C.A. Gill. (2016). P2023 Analysis of methylation patterns in bovine spermatozoa. *Journal of Animal Science* 94(7supplement4), 48-48. doi: 10.2134/jas2016.947supplement448x.
4. Frattini, S., E. Capra, B. Lazzari, B. Coizet, D. Groppetti, A. Pecile, P. Riccaboni, S. Arrighi, S. Chessa, B. Castiglioni, A. Giordano, A. Talenti, J.L. Williams, S.D. McKay, P. Crepaldi, A. Stella, and G. Pagnacco. 2016. The methylome of the hypothalamus of prepubertal and pubertal goats. *International Journal of Health, Animal Science and Food Safety*. 3.

5. McKay, S. (2015). To What Extent Does DNA Methylation Affect Phenotypic Variation in Cattle? *International Journal of Health, Animal Science and Food Safety* 2(1s).
6. Farias FHG, GS Johnson, DP O'Brien, FA Wininger, R Zeng, SD McKay, RD Schnabel, JF Taylor, C Wade and K Lindblad-Toh. (2011). A Mutation in ATP13A2 Causes Adult-Onset Neuronal Ceroid Lipofuscinosis in Tibetan Terriers. *Journal of Veterinary Internal Medicine* 25 (3), 763-764. doi: 10.1111/j.1939-1676.2011.0726.x.

PUBLICATIONS

1. Cantrell, B.A., H. Lachance, B. Murdoch, R.N. Funston, R.L. Weaver, and S.D. McKay. 2018. Global DNA Methylation within the Limbic System of the Bovine Brain. *Frontiers in Genetics*. In Review
2. Kalbfleisch TS, BM Murdoch, TPL Smith, JD Murdoch, MP Heaton and SD McKay. 2018. A SNP resource for studying North American moose. *F1000Research*. 7(40). DOI: 10.12688/f1000research.13501.1
3. Brevik, K, L Lindstrom, SD McKay and Y Chen. 2018. Transgenerational effects of insecticides – implications for rapid pest evolution in agroecosystems. *Current Opinion in Insect Science*. DOI: 10.1016/j.cois.2017.12.007
4. Davenport, KM, S McKay, A Fahey, C Gill and BM Murdoch. 2018. Meiotic Recombination Differences in Rams from three U.S. Breeds of Sheep. *Cytogenetic and Genome Research*. In press
5. Frattini, S., E. Capra, B. Lazzari, S.D. McKay, B. Coizet, A. Talenti, D. Groppetti, P. Riccaboni, A. Pecile, S. Arrighi, S. Chessa, B. Castiglioni, J.L. Williams, G. Pagnacco, A. Stella, and P. Crepaldi. 2016b. Genome-wide analysis of DNA methylation in hypothalamus and ovary of *Capra hircus*. *BMC Genomics*. 18 (1), 476
6. Murdoch, B., G. Murdoch, S. Greenwood and S. McKay. (2016). Nutritional Influence on Epigenetic Marks and Effect on Livestock Production. *Frontiers in Genetics* 7(182). doi: 10.3389/fgene.2016.00182.
7. Benjamin, A.L., B.B. Green, B.C. Crooker, S.D. McKay, and D.E. Kerr. 2016. Differential responsiveness of Holstein and Angus dermal fibroblasts to LPS challenge occurs without major differences in the methylome. *BMC Genomics*. 17(1):1-14
8. Almamun, M., B.T. Levinson, A.C. van Swaay, N.T. Johnson, S.D. McKay, G.L. Arthur, J.W. Davis, and K.H. Taylor. 2015. Integrated methylome and transcriptome analysis reveals novel regulatory elements in pediatric acute lymphoblastic leukemia. *Epigenetics*. 10:882-890.
9. Burmeister DW, EL Hoffman, RT Cristel, SD McKay, GL Arthur, W Davis and KH Taylor. 2015. The expression of RUNDC3B is associated with promoter methylation in lymphoid malignancies. *Hematological Oncology*. DOI: 10.1002/hon.2238

10. Green BB, SD McKay and DE Kerr. 2015. Age dependent changes in the LPS induced transcriptome of bovine dermal fibroblasts occurs without major changes in the methylome. *BMC Genomics*. 16(1):30.
11. Rolf, MM, JE Decker, SD McKay, PC Tizioto, KA Branham, LK Whitacre, JL Hoff, LCA Regitano and JF Taylor. 2014. Genomics and the Beef Industry. *Livestock Science*. 166:84-93.
12. Decker, JE, SD McKay, MM Rolf, JW Kim, A Molina Alcala, TS Sonstegard, O Hanotte, A Gotherstrom, CM Seabury, L Praharani, ME Babar, L Correia de Almeida Regitano, MA Yildiz, MP Heaton, WS Liu, CZ Lei, JM Reecy, M Saif-Ur-Rehman, RD Schnabel, and JF Taylor. 2014. Worldwide patterns of ancestry, divergence, and admixture in domesticated cattle. *PLoS Genet*. 10:e1004254.
13. Ramey HR, JE Decker, SD McKay, MM Rolf, RD Schnabel and JF Taylor. 2013. Detection of selective sweeps in cattle using genome-wide SNP data. *BMC Genomics*. 14:382. DOI:10.1186/1471-2164-14-382 (highly accessed).
14. Chapple, RH, PF Tizioto, KD Wells, SA Givan, JW Kim, SD McKay, RD Schnabel and JF Taylor. 2013 A characterization of the rat developmental liver transcriptome. *Physiological Genomics*. 45:301-11
15. Decker JE, DA Vasco, SD McKay, MC McClure, MM Rolf, JW Kim, SL Northcutt, S Bauck, B Woodward, RD Schnabel and JF Taylor. 2012. A novel analytical method, Birth Date Selection Mapping, detects response of the Angus (*Bos taurus*) genome to selection on complex traits. *BMC Genomics*. 13:606
16. Rolf MM, JF Taylor, RD Schnabel, SD McKay, MC McClure, SL Northcutt, MS Kerley and R L Weaber. 2012. Genome-wide association analysis for feed efficiency in Angus cattle. *Anim. Genet*. 43:367-374. DOI: 10.1111/j.1365-2052.2011.02273.x.
17. McClure MC, HR Ramey, MM Rolf, SD McKay, JE Decker, RH Chapple, JW Kim, TM Taxis, RL Weaber, RD Schnabel and JF Taylor. 2012. Genome wide association analysis for quantitative trait loci influencing Warner Bratzler shear force in five taurine cattle breeds. *Anim Genet* 43(6):662-73
18. Madhi S, MC McClure, SD McKay, MM Rolf, JW Kim, JE Decker, TM Taxis, RH Chapple, HR Ramey, SL Northcutt, S Bauck, B Woodward, JCM Dekkers, RL Fernando, RD Schnabel, D Garrick and JF Taylor. 2011. Accuracies of genomic breeding values in American Angus beef cattle using K-means clustering for cross-validation. *Genetics Selection Evolution* 43:40 (highly accessed).
19. Murdoch, BM, GK Murdoch, M Settles, SD McKay, JL Williams and SS Moore. 2011. Genome-wide scan identifies loci associated with classical BSE incidence. *PLoS ONE* 6(11):e26819.
20. Farias, FH, R Zeng, GS Johnson, FA Wininger, JF Taylor, RD Schnabel, SD McKay, DN Sanders, H. Lohi, EH. Seppälä, CM Wade, K Lindblad-Toh, DP O'Brien, and ML Katz. 2011. A truncating mutation in ATP13A2 is responsible for adult-onset neuronal ceroid lipofuscinosis in Tibetan terriers. *Neurobiology of Disease* 42:468-74.

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