CURRICULUM VITAE

University of Idaho

NAME: Brenda Mae Murdoch

DATE: January 3, 2018

RANK OR TITLE: Assistant Professor

DEPARTMENT: Animal and Veterinary Sciences

OFFICE LOCATION AND CAMPUS ZIP: Ag Biotech Rm 311

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DATE OF FIRST EMPLOYMENT AT UI: May, 2014

DATE OF TENURE: Untenured

DATE OF PRESENT RANK OR TITLE: November, 2014

EDUCATION BEYOND HIGH SCHOOL:

Degrees:
Doctor of Philosophy, Animal Science, 2010, University of Alberta, Edmonton, AB
Bachelor of Science, Agriculture - Major Animal Science, 1999, University of Alberta, Edmonton, AB

Diploma:
Biological Science Technology, Laboratory and Research, 1989, Northern Alberta Institute of Technology, Edmonton, AB
Biological Science Technology, Biotechnology, 1989, Northern Alberta Institute of Technology, Edmonton, AB

EXPERIENCE:

Teaching, Extension and Research Appointments:

2014–present	Assistant Professor, Department of Animal and Veterinary Science, College of Agriculture and Life Sciences, University of Idaho.
2011–present	Adjunct Faculty member, Center for Reproductive Biology, Washington State University.
2010-2014	Assistant Research Professor, School of Molecular Biosciences, Washington State University.
2010-2014	Affiliate Assistant Professor, Department of Animal and Veterinary Science, College of Agriculture and Life Sciences, University of Idaho.
2007-2010	Imaging Core /Laboratory Manager, School of Molecular Biosciences, Washington State University.
2000-2007	Senior Molecular Genetic Technologist, Alberta Beef Genomics, Department of Agricultural, Food and Nutritional Sciences, University of Alberta.
1996-2000	Senior Molecular Technologist, Dairy Research, Department of Agricultural, Food and Nutritional Sciences, University of Alberta.
1989-1996	Molecular Biology Technologist, Faculty of Medicine, Department of Physiology, University of Alberta.

TEACHING ACCOMPLISHMENTS:

Areas of Specialization: Molecular Genetics/Genomics, Biotechnology

Courses Taught:
Graduate Student Seminar AVS 501, University of Idaho, 2017- present
Critical Evaluation of Scientific Research AVS 504, University of Idaho, 2017-present
Genetics of Livestock Improvement AVS 330 (co-instructor), University of Idaho, 2014-present
Molecular Genetic Tools AVS 502, University of Idaho, 2017
Sheep Genomics AVS 499, University of Idaho, 2017

Molecular Tools AVS 299, University of Idaho, 2017
Molecular Genetic Tools AVS 502, University of Idaho, 2015
Farm Animal Genetics, AVS 299, University of Idaho, 2015
Human Genetics, SMB 423, Washington State University, 2013
Laboratory Molecular Techniques - Graduate, AFNS 570, University of Alberta, 2005
Animal Molecular Biology AFNS 484, University of Alberta, 2005

Students Advised:
Undergraduate Students:
  Advisee - (5-2015, 21-2016, 17-2017 average of 14/year)
  Research - Rebekka (Job) Sawyer (2014-present), Megan Follett (2016-present), Eric Robinson (2016-present), Dominic De La Torre (2017-present), Hannah Jaeger (2016-2017), Taylor Badigian (2016-2017), Chanelle Brusseau (2017), Kim Davenport (2015-2016), and Rebeka Kelly (2015-2016), Jonathan Wait (2015), Miranda Holt (2015), Emily Dyas (2014)

Graduate Students: Advised to completion of degree as major professor
  Kimberly Davenport, Masters of Science, completed Aug 4, 2017
Graduate Students: Currently in progress of degree as major professor
  Kimberly Davenport, Doctorate of philosophy, Commenced Aug 21, 2017
  Anna Rodriguez, Masters of Science, Commenced Aug 22, 2016

Served on graduate committee to completion:
  Breann Sandberg, Masters of Science, University of Idaho, Completed May 19, 2107
Serve currently on graduate committee:
- Rebecca Hiltz, Masters of Science, University of Idaho, 2017
- Justin Galliou, Masters of Science, Washington State University, 2017
- Carmen Willmore, Doctorate of Philosophy, University of Idaho, 2016
- Antonetta Colacchio, Masters of Science, University of Idaho, 2016
- Kelcey McBride, Masters of Science, Washington State University, 2016
- Stephen Tamm, Masters of Science, University of Idaho, 2015

Courses Developed:
AVS 504 Critical Evaluation of Scientific Research, University of Idaho, 2017
AVS 502 Molecular Genetic Tools – Graduate level, University of Idaho, 2017
AVS 499 Sheep Genomics, University of Idaho, 2017
AVS 299 Molecular Tools, University of Idaho, 2017
AVS 502 Molecular Genetic Tools – Graduate level, University of Idaho, 2015
AVS 330 Genetics of Livestock Improvement (partial content), University of Idaho, 2014
AFNS 570 Laboratory Molecular Techniques – Graduate level, University of Alberta, 2005
AFNS 484 Animal Molecular Biology, University of Alberta, 2005

Non-credit Classes, Workshops, Seminars, Invited Lectures, etc.:
Invited Seminars: (presenter underlined)
1. Developing the functional annotation of the sheep genome. **<u>Murdoch BM</u>**, White SN, Mousel MR, Massa AT, Worley KC, Archibald AL, Clark EL, Dalrymple B, Kijas J, Clarke S, Brauning R, Smith TPL, Hadfield T, Cockett N. International Sheep Genomics Consortium. Jan 15, 2018.
2. The Ovine FAANG Project. **<u>Murdoch BM</u>**, White SN, Mousel MR, Massa AT, Worley KC, Archibald AL, Clark EL, Dalrymple B, Kijas J, Clarke S, Brauning R, Smith TPL, Hadfield T, Cockett N. International Sheep Genomics Consortium. Jan 15, 2018.
3. Rambouillet Sheep Genomic Resources. Liu Y, Harris RA., Qin X, Richards S, Rogers J, Han Y, Vee V, Wang M, Meng Q, Heaton MP, Smith T.P.L., Dalrymple B, White SN, **Murdoch BM**, Kijas JW, Cockett N, Muzny DM, Gibbs R, <u>Worley K.</u> International Plant & Animal Genomes XXV Conference, January 14, 2017.
4. Update on the Rambouillet Assembly, the 5.0 Reference, and plans for FAANG RNA Sequencing. Liu Y, Harris RA, Qin X, Richards S, Rogers J, Han Y, Vee V, Wang M, Meng Q, Heaton MP, Smith TPL, Dalrymple B, White SN, **Murdoch BM**, Kijas JW, Cockett N, Muzny DM, Gibbs R, <u>Worley K</u>. International Plant & Animal Genomes XXV Conference, January 16, 2017.

5. Genome-Wide Landscape of Active Enhancers in Sheep Alveolar Macrophages. Massa A, Mousel M, **Murdoch BM**, White S. International Plant & Animal Genomes XXV Conference, January 16, 2017.
6. Understanding the Ramification of Recombination Variation in Sheep. Davenport K and **Murdoch BM.** Plant & Animal Genomes XXV Conference, January 16, 2017.
7. Gene regulation in Sheep Alveolar Macrophages: Genome-Wide Identification of Active Enhancers. Massa A, Mousel M, **Murdoch BM**, White S. 36th International Society of Animal Genetic Conference, Dublin July 20, 2017.
8. Investigating Genetic Associations with Meiotic Recombination in Rams. Davenport K, Rodriguez AM, Sawyer RJ, Badigian TM, Jaeger H, Follet MA, **Murdoch BM.** 36th International Society of Animal Genetic Conference, Dublin July 20, 2017.
9. Strategies to employ molecular markers towards improved prediction of carcass quality. **Murdoch B.** Increased Efficiency of Sheep Production NCERA214 Lansing, Michigan June 11-14, 2017.
10. The Future of Sheep Production: Capturing Genetic Variation. **Cockett N and Murdoch B.** American Sheep Industry. Superior Farms board meeting. Denver, CO January 25-28, 2017.
11. Idaho cow-calf herds; a genetic resource for understanding and improving cow reproduction and calf growth efficiency. **Murdoch B.** NRSP8 Hatch report. San Diego Jan 14, 2017.
12. Ovine FAANG Project. **Murdoch B.** International Sheep Genome Consortium. San Diego Jan 16, 2017.
13. Ovine FAANG progress **Murdoch B.** FAANG consortium International Plant and Animal Genome San Diego Jan 17, 2017.
14. University of Idaho Sheep Center. **Murdoch B.** Tri-State Wool Growers, Sun Valley ID Nov 19, 2016.
15. University of Idaho Sheep Center Research. **Murdoch B.** University of Idaho Sheep Unit advisory board meeting. Moscow, ID Nov 4, 2016.
16. Genetics of Livestock, **Murdoch B.** Montana State University, March 16, 2015.
17. Are heterozygous carriers of cohesin mutations at an increased risk of aneuploidy? **Murdoch BM**, Owen N, Nagaoka SI, Hassold TJ, Hunt PA. Platform oral presentation at the 12th International Congress of Human Genetics/American Society of Human Genetics 61st Annual Meeting in Montreal, Canada, October 11-15, 2011.
18. Understanding the genetics of BSE in Cattle. **Murdoch B.** School of Molecular Biosciences, Seminar series February, 17, 2011.
19. Genetic Variation Association Study for BSE Susceptibility and/or Resistance in Cattle. **Murdoch B.** PrP Canada "Exploring New Terrain", February 18-20, 2007.
20. Understanding the genetics of prion disease in cattle. **Murdoch B.** AVS 501, University of Idaho, 2015
21. Understanding the genetics of prion disease in cattle. **Murdoch B.** Biology 310, University of Idaho, 2013

Honors and Awards:

2017 International Society of Animal Genetic – Domestic Animal Sequencing and Annotation, Elected Committee.
2017 National Animal Genome Research Program – NRSP008 (chair elect 2017, chair 2018).
2017 Graduate student trainee, K. Davenport, 36th International Society for Animal Genetics. Poster Excellence award winner.
2017 Graduate student trainee, K. Davenport, International Society for Animal Genetics. U.S. Graduate Student and Early Career Investigator, Abstract and Travel Award.
2017 Graduate student trainee, A. Rodriguez, International Society for Animal Genetics. U.S. Graduate Student and Early Career Investigator, Abstract and Travel Award.
2017 Graduate student trainee, K. Davenport, Neal A Jorgensen Genome Award to speak at the International Plant and Animal Genome XXV Conference.
2016 Graduate student trainee, K. Davenport, Edward J. and Maud R. Iddings Research Fellowship award.
2016 Graduate student trainee, K. Davenport, International Society for Animal Genetics/International Foundation for Animal Genetics. Abstract and Travel award.
2013 International Young Researcher Nominee, Alberta Prion Research Institute.
2010 Outstanding Achievement award, Journal of Toxicology and Environmental Health and Taylor & Francis Group. PrP Canada. March 8-10, 2010 Ottawa, Ontario.
2009 PrioNet Highly Qualified Personnel Award. Prion 2009. September 23-25, 2009 Porto Carras, Chalkidiki, Greece.
2009 Awarded distinction of "Unanimously exemplary performance" with regards to Ph.D. Comprehensive Candidacy examination- May 01, 2009.

2008 Highly Qualified Personnel, Baden Meeting in Montreal June 13 – 15, 2008.
2007 Highly Qualified Personnel, PrP Canada - Canada's Prion Research Conference "Exploring New Terrain" February 18-20, 2007 Calgary, AB, Canada.
2006 Outstanding Contribution to Science. University of Alberta, 2006.
2006 Mary Louise Imrie Scientific Award University of Alberta, International Scientific Communication.

SCHOLARSHIP ACCOMPLISHMENTS:

Publications, Exhibitions, Performances, Recitals:

Refereed/Adjudicated:

Book Chapter:

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

Peer Reviewed/Evaluated:

Articles in Peer Reviewed Journals:

1. Kalbfleisch TS, **Murdoch BM**, Smith TPL, Murdoch JD, Heaton MP and McKay SD. A SNP resource for studying North American moose. ***F1000 Research*** (2018) 13501.
2. **Murdoch BM**, Murdoch GK, Greenwood S, McKay S. Nutritional influence on epigenetic marks and effects on livestock production. ***Frontiers in Genetics***, (2016) Oct 24;7: 182.
3. **Murdoch BM**, Murdoch GK. Genetics of Prion Disease in Cattle. ***Bioinform Biol Insights*** (2015) Sep 24;9 (suppl 4): 1-10.
4. Chapalamadugu KC, **Murdoch BM**, Robison BD, Hill RA and Murdoch GK. Oncorhynchus mykiss Pax7 sequence variations with comparative analyses against other teleost species. ***SpringerPlus*** (2015), 4: 263.
5. Rowsey R, Kashevarova A, **Murdoch B**, Dickenson C, Woodruff T, Cheng E, Hunt P, Hassold T. Germline mosaicism does not explain the maternal age effect on trisomy. ***Am J Med Genet*** (2013) Oct 161 (10): 2495-2503.
6. **Murdoch B**, Owen N, Stevense M, Smith H, Nagaoka S, Hassold T, McKay M, Xu H, Fu J, Revenkova E, Jessberger R, Hunt P. Altered cohesin gene dosage affects mammalian meiotic chromosome structure and behavior. ***PLoS Genet*** (2013) 9(2): e1003241.
7. Hunt PA, Lawson C, Gieske M, **Murdoch B**, Smith H, Marre A, Hassold T, VandeVoort CA. Bisphenol A alters early oogenesis and follicle formation in the fetal ovary of the rhesus monkey. ***Proc Natl Acad Sci*** (2012) Oct 23: 109 (43): 17525-30.
8. **Murdoch BM**, Murdoch GK, Settles M, McKay S, Williams JL, Moore SS. Genome-wide scan identifies loci associated with classical BSE occurrence. ***PLoS One*** (2011) 6(11): e26819.
9. Lawson C, Giekse M, **Murdoch B**, Ye P, Li Y, Hassold T, Hunt PA. Gene expression in the fetal mouse ovary is altered by exposure to low doses of bisphenol A. ***Biol Reprod*** (2011) Jan 84 (1): 79-86.
10. **Murdoch B**, Owen N, Shirley S, Crumb S, Broman KW, Hassold T. Multiple loci contribute to genome-wide recombination levels in male mice. ***Mamm Genome*** (2010) Dec 21 (11-12): 550-555.
11. Gorbach DM, Makgahlela ML, Reecy JM, Kemp SJ, Balyenweck I, Ouma R, Mwai O, Marshall K, **Murdoch B,** Moore S, Rothschild MF. Use of SNP genotyping to determine pedigree and breed composition of dairy cattle in Kenya. ***J Anim Breed Genet*** (2010) Oct 127 (5): 348-351.
12. **Murdoch BM**, Clawson ML, Yue S, Basu U, McKay S, Settles M, Capoferri R, Laegreid WW, Williams JL, Moore SS. PRNP haplotype associated with classical BSE incidence in European Holstein cattle. ***PLoS One*** (2010) Sept 16: 5(9).
13. **Murdoch BM**, Clawson ML, Laegreid WW, Stothard P, Settles M, McKay S, Prasad A, Wang Z, Moore SS, Williams JL. A 2cM genome-wide scan of European Holstein cattle affected by classical BSE. ***BMC Genet*** (2010) Mar 29 11: 20.
14. Kolbehdari D, Wang Z, Grant JR, **Murdoch B,** Prasad A, Xiu Z, Marques E, Stothard P, Moore SS. A whole genome scan to map QTL for milk production traits and somatic cell score in Canadian Holstein bulls. ***J Anim Breed Genet*** (2009) Jun 126(3): 216-227.
15. Bovine HapMap Consortium, Gibbs RA, Taylor JF, Van Tassell CP, Barendse W, Eversole KA, Gill CA, Green RD, Hamernik DL, Kappes SM, Lien S, Matukumalli LK, McEwan JC, Nazareth LV,

Schnabel RD, Weinstock GM, Wheeler DA, Ajmone-Marsan P, Boettcher PJ, Caetano AR, Garcia JF, Hanotte O, Mariani P, Skow LC, Sonstegard TS, Williams JL, Diallo B, Hailemariam L, Martinez ML, Morris CA, Silva LO, Spelman RJ, Mulatu W, Zhao K, Abbey CA, Agaba M, Araujo FR, Bunch RJ, Burton J, Gorni C, Olivier H, Harrison BE, Luff B, Machado MA, Mwakaya J, Plastow G, Sim W, Smith T, Thomas MB, Valentini A, Williams P, Womack J, Woolliams JA, Liu Y, Qin X, Worley KC, Gao C, Jiang H, Moore SS, Ren Y, Song XZ, Bustamante CD, Hernandez RD, Muzny DM, Patil S, San Lucas A, Fu Q, Kent MP, Vega R, Matukumalli A, McWilliam S, Sclep G, Bryc K, Choi J, Gao H, Grefenstette JJ, **Murdoch B**, Stella A, Villa-Angulo R, Wright M, Aerts J, Jann O, Negrini R, Goddard ME, Hayes BJ, Bradley DG, Barbosa da Silva M, Lau LP, Liu GE, Lynn DJ, Panzitta F, Dodds KG. Genome-wide survey of SNP variation uncovers the genetic structure of cattle breeds. ***Science*** (2009) Apr 24 324(5926): 528-532.

16. Sherman EL, Nkrumah JD, Li C, Bartusiak R, **Murdoch BM**, Moore SS. Fine mapping quantitative trait loci for feed intake and feed efficiency in beef cattle. ***J Anim Sci*** (2009) Jan 87(1): 37-45.
17. Prasad A, Schnabel RD, McKay SD, **Murdoch B**, Stothard P, Kolbehdari D, Wang Z, Taylor JF, Moore SS. Linkage disequilibrium and signatures of selection on chromosomes 19 and 29 in beef and dairy cattle. ***Anim Genet*** (2008) Dec 39(6): 597-605.
18. Kolbehdari D, Wang Z, Grant JR, **Murdoch B**, Prasad A, Xiu Z, Marques E, Stothard P, Moore SS. A whole-genome scan to map quantitative trait loci for conformation and functional traits in Canadian Holstein bulls. ***J Dairy Sci*** (2008) Jul 91(7): 2844-2856.
19. McKay SD, Schnabel RD, **Murdoch BM**, Matukumalli LK, Aerts J, Coppieters W, Crews D, Dias Neto E, Gill CA, Gao C, Mannen H, Wang Z, Van Tassell CP, Williams JL, Taylor JF, Moore SS. An assessment of population structure in eight breeds of cattle using a whole genome SNP panel. ***BMC Genet*** (2008) May 20 9: 37.
20. Sherman EL, Nkrumah JD, **Murdoch BM**, Moore SS. Identification of polymorphisms influencing feed intake and efficiency in beef cattle. ***Anim Genet*** (2008) Jun 39(3): 225-31.
21. Sherman EL, Nkrumah JD, **Murdoch BM**, Li C, Wang Z, Fu A, Moore SS. Polymorphisms and haplotypes in the bovine neuropeptide Y, growth hormone receptor, ghrelin, insulin-like growth factor 2, and uncoupling proteins 2 and 3 genes and their associations with measures of growth, performance, feed efficiency, and carcass merit in beef cattle. ***J Anim Sci*** (2008) Jan 86(1): 1-16.
22. McKay SD, Schnabel RD, **Murdoch BM**, Matukumalli LK, Aerts J, Coppieters W, Crews D, Dias Neto E, Gill CA, Gao C, Mannen H, Stothard P, Wang Z, Van Tassell CP, Williams JL, Taylor JF, Moore SS. Whole genome linkage disequilibrium maps in cattle. ***BMC Genet*** (2007) Oct 25 8: 74.
23. Prasad A, Schiex T, McKay S, **Murdoch B**, Wang Z, Womack JE, Stothard P, Moore SS. High resolution radiation hybrid maps of bovine chromosomes 19 and 29: comparison with the bovine genome sequence assembly. ***BMC Genomics*** (2007) Sep 4 8: 310
24. Iqbal M, Navabi A., Salmon DF, Yang R-C, **Murdoch BM,** Moore SS, Spaner D. Genetic analysis of flowering and maturity time in high latitude spring wheat. ***Euphytica*** (2007) 154: 207-218.
25. Nkrumah JD, Sherman EL, Li C, Marques E, Crews DH Jr, Bartusiak R, **Murdoch B**, Wang Z, Basarab JA, Moore SS. Primary genome scan to identify putative quantitative trait loci for feedlot growth rate, feed intake, and feed efficiency of beef cattle. ***J Anim Sci*** (2007) Dec 85(12): 3170-3181.
26. Snelling WM, Chiu R, Schein JE, Hobbs M, Abbey CA, Adelson DL, Aerts J, Bennett GL, Bosdet IE, Boussaha M, Brauning R, Caetano AR, Costa MM, Crawford AM, Dalrymple BP, Eggen A, Everts-van der Wind A, Floriot S, Gautier M, Gill CA, Green RD, Holt R, Jann O, Jones SJ, Kappes SM, Keele JW, de Jong PJ, Larkin DM, Lewin HA, McEwan JC, McKay S, Marra MA, Mathewson CA, Matukumalli LK, Moore SS, **Murdoch B**, Nicholas FW, Osoegawa K, Roy A, Salih H, Schibler L, Schnabel RD, Silveri L, Skow LC, Smith TP, Sonstegard TS, Taylor JF, Tellam R, Van Tassell CP, Williams JL, Womack JE, Wye NH, Yang G, Zhao S; International Bovine BAC Mapping Consortium. A physical map of the bovine genome. ***Genome Biol*** (2007) 8(8): R165.
27. Marques E, de Givry S. Stothard P, **Murdoch B**, Wang Z, Womack J, Moore S. A high resolution radiation hybrid map of bovine Chromosome 14 identifies scaffold rearrangement in the latest bovine assembly. ***BMC Genomics*** (2007) Jul 26: 8-254.
28. McKay SD, Schnabel RD, **Murdoch BM**, Aerts J, Gill CA, Gao C, Li C, Matukumalli LK, Stothard P, Wang Z, Van Tassell CP, Williams JL, Taylor JF, Moore SS. Construction of bovine whole-genome radiation hybrid and linkage maps using high-throughput genotyping. ***Anim Genet*** (2007) Apr 38(2): 120-125.
29. **Murdoch BM,** Fu A, Meng Y, Li C, Hansen C, Snelling WM, Moore SS. Assignment of the SIAT4A gene to bovine chromosome 14 by linkage mapping of an associated microsatellite. ***Anim Genet*** (2004) 35: 146-147.

30. **Murdoch BM,** Fu A, Meng Y, Li C, Hanse, C, Snelling WM, Moore SS. Identification of three microsatellite loci on bovine chromosome 19. ***Anim Genet*** (2004) 35: 145-146.
31. Kneeland J, Li C, Basarab J, Snelling WM, Benkel B, **Murdoch B,** Hansen C, Moore SS. Identification and fine mapping of quantitative trait loci for growth traits on bovine chromosomes 2, 14, 19, 21, and 23 within one commercial line of *Bos Taurus*. ***J Anim. Sci*** (2004) 82: 3405-3414.
32. Nkrumah JD, Basarab J, Price MA, Okine EK**,** Ammoura A, Guercio S, Hansen C, Li C, Benkel B, **Murdoch B,** Moore SS. Different measures of energetic efficiency and their phenotypic relationships with growth, feed intake, and ultrasound and carcass merit in hybrid cattle. ***J Anim. Sci*** (2004) 82: 2451-2459.
33. Li C, Basarab J, Snelling WM, Benkel B**, Murdoch B,** Hansen C, Moore SS. Assessment of positional candidate gene MYF5 and IGF-1 for growth on bovine chromosome 5 in commercial lines of *Bos Taurus*. ***J Anim Sci*** (2004) 82: 1-7.
34. Nkrumah JD, Li C, Basarab J, Guercio S, Meng Y**, Murdoch B,** Hansen C, Moore SS. Association of a single nucleotide polymorphism in the bovine leptin gene with residual feed intake, feed DM and ME intake, growth traits, feeding behavior and carcass quality and composition. ***Can J of Anim Sci*** (2003) 84: 211-219.
35. Li C, Basarab J, Snelling WM, Benkel B, Kneeland J, **Murdoch B,** Hansen C, Moore SS. Identification and Fine mapping of QTL for backfat on bovine chromosomes 2, 5, 6, 19, 21, and 23 in a commercial line of *Bos taurus*. ***J Anim Sci*** (2003) 82: 967-972.
36. Moore SS, Li C, Basarab J, Snelling WM, Kneeland J, **Murdoch B,** Hansen C, Benkel B. Fine mapping of QTL and identification of positional candidate genes for backfat on bovine chromosome 14 in a commercial line of *Bos taurus*. ***J Anim Sci*** (2003) 81: 1919-1925.
37. Li C, Basarab J, Snelling WM, Benkel B, **Murdoch B**, Moore SS. The identification of common haplotypes on bovine chromosome 5 within commercial lines of *Bos taurus* and their associations with growth traits. ***J Anim Sci*** (2002) 80***:*** 1187-1194.

Articles in Refereed Proceedings:

1. Rodriguez A.M, Davenport K.M, McKay S.D, Gill C, and Murdoch B.M. Meiotic Recombination in Ruminant Livestock. The 11th World Congress on Genetics Applied to Livestock Production. Auckland, New Zealand, (2018) February 11-16.
2. Brooker S, Davenport K, Williams J, Bode L, Foster J, McGuire M, McGuire M, **Murdoch B.** Designer Milk? Signatures of Selection in Human Milk Oligosaccharides. BEACON Congress (2016) Michigan August 9-13.
3. Rowsey R, **Murdoch B**, Hunt P, Dickerson C, Woodruff T, Hassold T. Germline mosacism does not explain the maternal age effect on trisomy. Platform oral presentation at the 13th International Congress of Human Genetics/American Society of Human Genetics 62st Annual Meeting in San Francisco, (2012) November 6-10.
4. **Murdoch BM**, Owen N, Nagaoka SI, Hassold TJ, Hunt PA. Are heterozygous carriers of cohesin mutations at an increased risk of aneuploidy? Platform oral presentation at the 12th International Congress of Human Genetics/American Society of Human Genetics 61st Annual Meeting in Montreal (2011), Canada, October 11-15.
5. Gieske MC, Lawson C, Smith H, **Murdoch B**, VandeVoort C, Hunt PA. Fetal Exposure to Bisphenol A Causes Meiotic Defects and Abnormal Follicle Formation in a Primate Model. 44th Annual meeting of the Society for the Study of Reproduction, Portland Oregon (2011) July 31- August 4.
6. Hassold T, Baier B, Crumb S, Owen N, Shirley S, **Murdoch B.** Identification of factors that influence levels of meiotic crossing-over. 42nd Annual Meeting of Society for the Study of Reproduction, Pittsburgh, Pennsylvania, (2009) July 18-22.
7. Chapalamadugu KC, **Murdoch BM**, Lawson C, Griswold J, Hunt P, Murdoch GK. Maternal Exposure to Bisphenol A Alters Expression of Genes Associated with Carbohydrate Metabolism in Developing Fetal Cardiac Tissue. 42nd Annual Meeting of Society for the Study of Reproduction, Pittsburgh, Pennsylvania, (2009) July 18-22.
8. McKay S, Prasad A, Marques E, **Murdoch B**, Wang Z, Williams J, Moore SS. BAC Contigs Based Radiation Hybrid Maps of Bovine Chromosomes 14 and 19: Tool for Fine Mapping of QTL. *In* "8th World Congress on Genetics Applied to Livestock Production", Belo Horizonte, Brazil (2006)
9. Ferreira Marques E, Li C, Nkrumah JD, McKay SD, **Murdoch B**, Wang Z, Moore SS. Fine Mapping of QTL Affecting Carcass Merit on Bovine Chromosome 14 Using a High Density Marker Set. *In* "8th World Congress on Genetics Applied to Livestock Production", Belo Horizonte, Brazil (2006).

10. Li C, Nkrumah JD, Bartusiak R, Fu A, **Murdoch BM**, Sherman EL, McKay SD, Wang Z, Crews DH, Moore SS. A Genome-wide Scan for Quantitative Trait Loci Affecting Ultrasound and Carcass Backfat Thickness in Beef Cattle. *In* "8th World Congress on Genetics Applied to Livestock Production", Belo Horizonte, Brazil (2006).
11. Prasad A, Nkrumah JD, Li C, **Murdoch B**, McKay S, Wang Z, Moore SS. Identification of Quantitative Trait Loci For Backfat Thickness On Bovine Chromosome 19 In Beef Cattle. *In* "8th World Congress on Genetics Applied to Livestock Production", Belo Horizonte, Brazil (2006).
12. Li C, Basarab J, Snelling WM, Benkel B, **Murdoch B**, Kneeland J, Hansen C, Moore SS. Identical by descent haplotype sharing analysis: application in fine mapping of QTLs for birth weight in commercial lines of *Bos taurus.* 7th World Congress on Genetics Applied to Livestock Production in Montpellier, France, (2002) August 19 – 23.

Abstracts:

1. Davenport KM, Kalbfleisch TS McKay S, Heaton MP, **Murdoch BM.** Characterizing allelic variation in the recombination hotspot mediator gene PRDM9 in U.S. sheep. International Plant & Animal Genomes XXVI Conference, San Diego, CA (2018) Jan 13-17.
2. Massa AT, Mousel MR, **Murdoch BM**, White S. ChIP-Seq genome-wide identification of regulatory elements in sheep alveolar macrophages. International Plant & Animal Genomes XXVI Conference, San Diego, CA (2018) Jan 13-17.
3. **Murdoch B**, White S, Mousel M, Massa A, Worley K, Archibald A, Clark E, Dalrymple B, Kijas J, Clarke S, Brauning R, Smith T, Hadfield T, Cockett N. The Ovine Functional Annotation Project. 36th International Society of Animal Genetic Conference, Dublin, Ireland (2017) July 16-21.
4. Davenport KM, Rodriguez AM, Sawyer RJ, Badigian TM, Jaeger HK, Follett MA, **Murdoch BM.** Investigating genetic associations with meiotic recombination in rams. 36th International Society of Animal Genetic Conference, Dublin, Ireland (2017) July 16-21.
5. Rodriguez A, Davenport K, Jaeger H, Follett M, Badigian T, Sawyer R, **Murdoch B.** Differences in meiotic chromosome pairing characteristics in spermatocytes of hybrid beefalo. 36th International Society of Animal Genetic Conference, Dublin, Ireland (2017) July 16-21.
6. Liu Y, Harris RA, Qin X, Richards S, Rogers J, Han Y, Meng Q, Smith TP, Dalrymple BP, White SN, **Murdoch BM**, Kijas JW, Cockett N, Muzny DM, Worley KC. Rambouillet Sheep Genome and FAANG RNA Resources. 36th International Society of Animal Genetic Conference, Dublin, Ireland (2017) July 16-21.
7. Massa A, Mousel M, **Murdoch B**, White S. Gene regulation in sheep alveolar macrophages: Genome-wide identification of active enhancers. 36th International Society of Animal Genetic Conference, Dublin, Ireland (2017) July 16-21.
8. DeSilva K, Kalbfleisch TS, Robbins CT, Jansen HT, McGuire M, Laegreid WW, Heaton MP, **Murdoch BM**. Rudimentary Genomic Reference for the Grizzly Bear Derived Using Short Read Data from Several Animals. International Plant & Animal Genomes XXV Conference, San Diego, CA (2017) Jan 14-18.
9. Rodriguez AM, Davenport KM, **Murdoch BM**. Understanding Chromosome Pairing and Crossovers in Beefalo Spermatocytes. International Plant & Animal Genomes XXV Conference, San Diego, CA (2017) Jan 14 -18.
10. Liu Y, Harris RA, Qin X, Richards S, Rodger J, Han Y, Vee V, Meng Q, Heaton M, Smith TPL, Dalrymple B, White S, **Murdoch B**, Kijas J, Cockett N, Muzny D, Gibbs R, Worley KC. Rambouillet Sheep Genomic Resources. International Plant & Animal Genomes XXV Conference, San Diego, CA (2017) January 14 -18.
11. Davenport K, **Murdoch B**. Understanding the Ramification of Recombination Variation in Sheep. International Plant & Animal Genomes XXV Conference, San Diego, CA (2017) January 14 - 18.
12. Massa A, Mousel M, **Murdoch BM**, White S. Genome-Wide Identification of Active Enhancers in Sheep Alveolar Macrophages. International Plant & Animal Genomes XXV Conference, San Diego, CA (2017) January 14 - 18.
13. Davenport KM, **Murdoch BM.** Does domestication affect the evolution of meiotic recombination in males differently? BEACON Congress, (2016) August 9-13.
14. Davenport KM, **Murdoch BM**. The Ramification of Meiotic Recombination Differences in Sheep. 35th International Society for Animal Genetics Salt Lake City USA July 23-27, 2016.
15. Prause MR, **Murdoch BM**, Sawyer JE, Williams JL, McKay SD, Gill CA. Analysis of methylation patterns of bovine spermatozoa. 35th International Society for Animal Genetics, Salt Lake City USA (2016) July 23-27.

16. Davenport KM, **Murdoch BM**. Meiotic recombination differences in ruminant livestock species. American Society of Animal Science, Salt Lake City USA (2016) July 19-23.
17. McKay S, Kalbfleisch T, Heaton M, **Murdoch B.** A viewable whole genome resource with four North American Moose mapped to cattle and sheep. International Plant & Animal Genomes XXIV Conference, (2016) San Diego, CA January 8-13.
18. Davenport K, **Murdoch B**. Meiotic recombination crossing-over into livestock species. International Plant & Animal Genomes XXIV Conference, San Diego, CA (2016) January 8-13.
19. K.M. Davenport, J.J. Peak and **Murdoch B.M.** Genomic testing of female Holsteins: a resource for selection and improvement. American Dairy Science Association. Orlando, FL (2015) July 19-23.
20. **Murdoch B**, Settles M, McKay S, Williams J, Moore S (2011) Genome-Wide Association Study Of Classical BSE In European Holstein Cattle. International Plant & Animal Genomes XIX Conference, San Diego, CA January 15-19.
21. **Murdoch B**, Clawson M, Yue S, Basu U, McKay S, Laegreid W, Williams J, Moore S. Prion gene regulatory domain polymorphism associated with incidence of classical BSE in European Holstein cattle. PrP Canada, Ottawa Canada, (2010) March 9-11.
22. Chapalamadugu KC, VandeVoort C, Settles M, Robison B, Hunt P, **Murdoch BM,** Murdoch GK Consequences of Maternal BPA on the primate fetal muscle transcriptome. Center of Reproductive Biology, May, Spokane WA, (2010).
23. **Murdoch B**, Williams JL, Moore S. Genome-wide association study of classical BSE susceptibility or resistance in European Holstein cattle. NeuroPrion, Chalkidiki, Greece (2009) September 23-25.
24. **Murdoch B**, Clawson M, Laegreid W, Heaton M, Stothard P, Kolbehdari D, McKay S, Prasad A, Wang Z, Moore S, Williams J. A Genome scan for classical BSE susceptibility or resistance in European Holstein cattle. NeuroPrion, Madrid, Spain (2008) October 8-10.
25. Prasad A, Kolbehdari D, **Murdoch B**, Wang Z, Grant J, Stothard P, Moore S. Identification of polymorphisms influencing production and functional traits on bovine chromosomes 19 and 29 in Canadian Holstein cattle. 31st International Society of Animal Genetics, Amsterdam (2008).
26. **Murdoch B**, McKay S, Prasad A, Kolbehdari D, Wang Z, Moore S, Williams J. Genome Scan for BSE Susceptibility and/or Resistance in European Holstein cattle. PrP Canada- Canada's Prion Research Conference "Making Tracks" Toronto, ON, Canada, February 3-5, 2008.
27. Grant J, Wang Z, Prasad A, **Murdoch B**, Moon D, Cai Z, Xu J, Lin G, Moore S, Stothard P. A Software Pipeline to Build High-Resolution Radiation Hybrid Maps. International Plant & Animal Genomes XVI Conference, San Diego, CA (2008) January 12-16.
28. **Murdoch B**, McKay S, Prasad, A Marques, E, Kolbehdari D, Wang, Z; Stella A, Clawson M, Heaton M, Laegreid W, Moore S, Williams J. Genome Scan for BSE Susceptibility and/or Resistance in European Holstein Cattle NueroPrion Edinburgh, Scotland, UK (2007) September 26-28.
29. **Murdoch B**, McKay S, Prasad A, Clawson M, Laegreid W, Heaton M, Williams J, Moore S. PrP Canada - Canada's Prion Research Conference "Exploring New Terrain", Calgary, AB, Canada, (2007) February 18-20.
30. Heaton M, Snelling W, Smith T, Keele J, Harhay G, Wiedmann R, Bennett G, Freking B, Van Tassell C, Sonstegard T, Gasbarre L, Moore S, **Murdoch B**, McKay S, Kalbfleisch T, and Laegreid W. A Marker Set for Parentage-Based DNA Traceback in Beef And Dairy Cattle. International Plant & Animal Genomes XV Conference, San Diego, CA (2007) January 13-17.
31. **Murdoch BM**, McKay SD, Wang Z, Williams JL, Moore SS. Polymorphic Information Content Analysis of Genome-Wide Bovine SNPs. 30th Conference of the International Society for Animal Genetics, Porto Seguro, Brazil, (2006).
32. McKay SD, Schnabel RD, **Murdoch BM**, Aerts J, Couppieters W, Crews D, Dias-Neto E, Gao C, Georges M, Gill C, Mannen H, Matukumall LK, Van Tassel CP, Wang Z, Williams JL, Taylor J, Moore SS. A Bovine Whole Genome Linkage Disequilibrium Map. 30th Conference of the International Society for Animal Genetics, Porto Seguro, Brazil, (2006).
33. Marques EF, Li C, Nkrumah D, McKay SD, **Murdoch BM**, Wang Z, Moore SS. Associations Between Single Nucleotide Polymorphism Markers On Bovine Chromosome 14 with Carcass Merit in Beef Cattle. 30th Conference of the International Society for Animal Genetics, Porto Seguro, Brazil, (2006).
34. Prasad A, Nkrumah D, Li C, **Murdoch B**, McKay S, Wang Z, Snelling WM, Moore SS. A Chromosome-wide Scan for Quantitative Trait Loci Affecting Carcass Merit on Bovine Chromosome 19 in Beef Cattle. 30th Conference of the International Society for Animal Genetics, Porto Seguro, Brazil, (2006).

35. Sherman LE, Nkrumah DJ, **Murdoch B**, Changxi Li C, McKay SD, Wang Z, Moore SS. Haplotypes within the bovine GHR, NPY, and UCP genes and their associations with measures of performance and carcass merit in beef cattle. 30th Conference of the International Society for Animal Genetics, Porto Seguro, BraziL, (2006).
36. Mujibi FN, Nkrumah DJ, **Murdoch BM**, Li C, Moore SS. Haplotypes in the bovine leptin gene associated with serum leptin, feeding efficiency, growth and carcass merit. 30th Conference of the International Society for Animal Genetics, Porto Seguro, Brazil (2006).
37. **Murdoch BM**, Marques E, Schimd K, McKay S, Wang Z, Nkrumah D, Gill C, Moore SS. The Comparison of Whole Genome Amplified DNA with Use Of The Illumina Beadstation. International Plant, Animal & Microbe Genomes XIV Conference, San Diego, CA, (2006) January 14-18.
38. Wang Z, **Murdoch B,** McKay S, Li C, Williams J, Gao C, Gill C, Stone R, Hennig S, Marques E, Fu A, Moore SS. Compilation And Construction Of Oligo Pool Assays For Bovine Whole Genome SNP Verification Using The Illumina® Beadstation 500g Genotyping System. International Plant & Animal Genomes XIV Conference, San Diego, CA, (2006) January 14-18.
39. Nkrumah DJ, Li C, Bartusiak R, Sherman LE, **Murdoch B**, McKay SD, Wang Z, Moore SS A Primary Genome-Wide Scan For Quantitative Trait Loci Affecting Feeding Behaviour Traits In Beef Cattle. International Plant & Animal Genomes XIV Conference, San Diego, CA, (2006) January 14-18.
40. Moore SS, Nkrumah DJ, Li C, Bartusiak R, Sherman LE, **Murdoch B**, McKay SD, Wang Z. Genome-Wide Scan For QTL Affecting Feed Intake And Feed Efficiency In Beef Cattle. International Plant & Animal Genomes XIV Conference, San Diego, CA, (2006) January 14-18.
41. Sherman LE, Nkrumah DJ**, Murdoch BM**, Li C, McKay SD, Wang Z, Moore SS Polymorphisms In The GHR, NPY, Ghrelin, And UCP2 Genes And Their Associations With Measures Of Performance And Carcass Merit In Beef Cattle. International Plant & Animal Genomes XIV Conference, San Diego, CA, (2006) January 14-18.
42. Marques EF, McKay SD, **Murdoch BM**, Williams J, Gill C, Moore SS. SNP Detection and Mapping of A Backfat QTL Region On Bovine Chromosome 14. International Plant & Animal Genomes XIV Conference, San Diego, CA, (2006) January 14-18.
43. McKay SD, **Murdoch BM**, Williams JL, Gill C, Aerts J, Law A, Wang Z, Moore SS. An Illumina Based Whole Genome Bovine-Human Comparative Map Constructed With High Throughput Methodology. International Plant & Animal Genomes XIV Conference, San Diego, CA, (2006) January 14-18.
44. McKay SD, **Murdoch BM**, Taylor J, Schnabel R, Gill C, Gao, C Williams JL, Aerts J, Coppieters W, Crews D, Dias Neto E, Georges M, Law A, Mannen H, Wang Z, Moore SS. A Bovine Whole Genome Linkage Disequilibrium Map. International Plant & Animal Genomes XIV Conference, San Diego, CA, (2006) January 14-18.
45. Prasad A, McKay S, **Murdoch B**, Li C, Wang Z, Williams J, Moore SS. Construction Of A Radiation Hybrid Map Of Bovine Chromosome 19. Plant, Animal & Microbe Genomes XIV Conference, San Diego, CA, (2006) January 14-18.
46. McKay SD, Moore SS, **Murdoch BM**, Wang Z, Williams JL. High Throughput Genotyping Enabling Rapid Construction of Whole Genome Radiation Hybrid Maps. International Plant & Animal Genomes XIV Conference, San Diego, CA, (2006) January 14-18.
47. Li C, **Murdoch B,** Stone RT, Wang Z, Moore SS. Massive verification and mapping SNP in cattle using the Illumina Beadstation 500G genotyping system. International Plant & Animal Genomes XIII Conference San Diego, CA, (2005).
48. McKay S, Schnabel R, **Murdoch B,** Gill C, Gao C, Williams J, Aerts J, Coppietiers W, Crews D, Neto E, Georges M, Law A, Mannen H, Wang Z, Kumar L, Tassell C, Taylor J, Moore S. Towards a bovine chromosomal linkage disequilibrium map: An integrated radiation hybrid map of *Bos taurus* chromosome 14. International Plant & Animal Genomes XIII Conference, San Diego, CA (2005).
49. McKay SD, Moore SS, **Murdoch BM**, Wang Z, Williams JL. High throughput genotyping enabling rapid construction of whole genome radiation hybrid maps. European Farm Animal Functional Genomics Conference, Edinburgh, Scotland, (2005).
50. Nkrumah JD, Li C, Basarab J, Guercio S, Men, Y**, Murdoch B,** Hansen C, Moore SS. Association of a single nucleotide polymorphism in the bovine leptin gene with residual feed intake, feed DM and ME intake, growth traits, feeding behavior and carcass quality and composition. Canadian Society of Animal Science Annual Meeting. Saskatoon, Saskatchewan, (2002).
51. Nkrumah JD, Li C, Basarab J, Guercio S, Meng Y**, Murdoch B,** Hansen C, Moore SS. Relationship between residual feed intake, feed intake, growth, feed efficiency, and ultrasound carcass

measurements in young hybrid beef calves. Canadian Society of Animal Science Annual Meeting. Saskatoon, Saskatchewan, (2002).

52. Li C, Basarab J, Snelling WM, Benkel B, Kneeland J. **Murdoch B,** Hansen C, Moore SS. Fine mapping of QTL for backfat on bovine chromosomes 2, 5, 6, 19, 21, and 23 in a commercial line of *Bos taurus*. Canadian Society of Animal Science Annual Meeting. Saskatoon, Saskatchewan, (2002).
53. Kneeland J, Li C, Basarab J., Snelling WM, Benkel B, **Murdoch B,** Moore SS. Identification and fine mapping for growth traits on bovine chromosomes 2, 5, 6, 19, 21, and 23 with one commercial line of *Bos taurus*. Canadian Society of Animal Science Annual Meeting. Saskatoon, Saskatchewan, (2002).
54. Li C, Kneeland J, **Murdoch B,** Benkel B, Basarab J, Snelling W, Moore SS. Mapping QTLs for Back Fat in Commercial Lines of *Bos taurus.* International Plant and Animal Genome Conference X, in San Diego, CA, (2002).
55. Kneeland J, Li C, **Murdoch B**, Basarab J, Snelling W, Benkel B, Moore SS. Distribution of haplotypes in BTA 6, 14, 19 and 21 within one commercial line of *Bos taurus* and their associations with growth traits. 28th International Society of Animal Genetics Conference in Goettingen, Germany, (2002).
56. Li C, Basarab J, Snelling WM, Benkel B, **Murdoch B**, Kneeland J, Hansen C, Moore SS. Identical by descent haplotype sharing analysis: application in fine mapping of QTLs for birth weight in commercial lines of *Bos taurus.* Canadian Society of Animal Science Conference, Quebec, Canada, July 22 – 26 (2002).
57. Li C, Moore, S, Kneeland J, **Murdoch B,** Basarab J, Snelling WM. Distribution of haplotypes within a commercial line of *Bos taurus* cattle and their associations with growth traits. International Plant and Animal Genome IX Conference, San Diego, CA, (2001) January 13-17.

Other: (reports, proceedings, papers, citations and references, performances)

1. GenBank Sequence submission Accession JQ303314: Onocorhychus mykiss paired box protein 7 alpha variant 4 (pax7) mRNA, complete cds, alternatively spliced submitted by: Chapalamdugu, K.C., **Murdoch, B.M.**, Robison, B.D., Hill, R.A. and Murdoch, G.K.
2. GenBank Sequence submission Accession JQ303320: Onocorhychus mykiss paired box protein 7 beta variant 6 (pax7) mRNA, complete cds, alternatively spliced submitted by: Chapalamdugu, K.C., **Murdoch, B.M.**, Robison, B.D., Hill, R.A. and Murdoch, G.K.
3. Sequences from Bos taurus genomic sequence contigs containing highly polymorphic single nucleotide sites. 81 sequences were submitted to and accepted by GenBank database. The sequences were submitted by: Heaton MP, Clawson ML, Snelling WM, Keel JW, Harhay GP, Wiedmann RT, Bennett GT, Smith TPL, Freking BA, Van Tassell CP, Sonstegard TS, Gasgarre LC, Moore SS, **Murdoch B,** McKay SD, Kalbfleisch T, and Laegreid WW.

Article - The Genetics of Prion Disease in *The Prioneer* Issues 3, 2010.

Book Chapter (scheduled for submission)

Sandor Dudas, Stephanie Czub, **Brenda Murdoch.** Prion Diseases in Cattle. Prion Diseases: What we Know and Research Advancements, 2017 Nova Science Publishers, Inc.

Refereed/Adjudicated

1. Davenport K, McKay S, Fahey A, Gill C, **Murdoch BM**. Meiotic recombination differences in rams from three breeds of sheep in the U.S. (submitted to Cytogenetic sand Genome Research).
2. Cantrell B, Lachance H, **Murdoch B**, Funston R, Weaber R, McKay S. Global DNA Methylation of the Limbic System of Cattle with Extreme Measures of Docility. (in review BMC Genomics)
3. Davenport KM, Spencer JA, Peak JJ, Dalton JC, **Murdoch BM**. Genomic testing of female Holsteins: A resource for selection and improvement. (submitted to PAS)
4. Cantrell B, Friedman S, Lachance H, Bernier C, **Murdoch B**, Frattini S, Talenti A, Crepaldi P, McKay S. A novel understanding of global DNA methylation in Bobcat liver. (scheduled to be submitted to Animal Genetics)

Presentations and Other Creative Activities:

1. Jaeger H, Davenport K, Sawyer R, Follett M, Murdoch B. Size matters: Examining the relationship between chromosome length and meiotic recombination in sheep spermatocytes. UI Undergraduate Research Symposium April 24, 2017.
2. Sawyer R, Rodriguez, Davenport K, Glaze B, Murdoch B. UI Undergraduate Research Symposium April 24, 2017.

3. Presented to University of College Dublin and Teagasc Moorepark Ireland (May 02-03, 2016)
4. College of Agriculture and Life Science, Simplot presentation October 16, 2015
5. Invited talk Professional Development for Woman. Sigma Alpha Sorority October 12, 2015
6. B Murdoch laboratory research presentations Oct 9, 2015
7. B Murdoch laboratory research presentations Steve Miller Oct 16, 2015
8. Presented Murdoch Laboratory Research projects November 6, 2015

Professional Meeting Papers, Workshops, Showings, Recitals:

1. Genomes to Phenomes: USDA blueprint workshop. November 15-16, 2017.
2. Livestock high throughput phenotyping and big data analytics workshop. November 13-14, 2017.
3. Tri State Wool Growers convention. Sun Valley, Idaho November 9-11, 2017
4. Washington State Sheep Producer, Pullman Washington October 27-28, 2017.
5. American Society of Animal Science Baltimore, Maryland July 8-12, 2017.
6. NCERA214 Increased Efficiency of Sheep Production East Lansing Michigan, June 11-14, 2017.
7. Increased Efficiency of Sheep Production NCERA214 station report meeting, Lansing Michigan June 11-14, 2017
8. 36th International Society of Animal Genetics meeting, Dublin Ireland, July 16-21, 2017.
9. American Sheep Industry Association, Denver, CO January 25-28, 2017
10. Superior farms sheep genetics talk to cooperative board. American Sheep Industry Conference. Denver Co January 25, 2017.
11. International Plant and Animal Genome XXVI. San Diego, CA, January 14-18, 2017.
12. FAANG consortium - Ovine FAANG project update January 16, 2017
13. NRSP8 Cattle/Swine and Cattle/Sheep/Goat workshops, January 14-15, 2017.
14. NRSP8 Hatch annual meeting, San Diego, January 14, 2017.
15. NRSP8 PD meeting, San Diego, January 13, 2017.
16. University of Idaho Sheep Center talk to Tri-State Wool Growers. Sun Valley ID November 19, 2016.
17. Large Animal Genetic Engineering Summit. Bethesda Maryland, September 18-20, 2016.
18. 35th International Society for Animal Genetics Salt Lake City USA July 23-27, 2016.
19. American Society of Animal Science, Salt Lake City USA (2016) July 19-23.
20. Presentation of Research to University College Dublin and Teagsac Moorepark Dublin, Ireland May 2-5, 2016.
21. International Plant and Animal Genome XXIV Conference. San Diego January 9-13, 2016.
22. NRSP8 Annual meeting, San Diego, January 9-13, 2016.
23. Bio/Computational Evolution in Action Consortium BEACON Congress, Michigan State August 15-17, 2015.
24. Joint American Dairy Science Association and American Society of Animal Science. Orlando, FL July 19-23, 2015.
25. Sheep Genetic Tools Workshop in Lincoln NB, 2014.

Patents:

none

Grants and Contracts Awarded:

Funded

1. The Functional Annotation of the Bovine Animal Genome. (2018- 2022) USDA- NIFA PI: P. Ross co-PI’s: J. Medrano, Z. Huaijun, J. Honglin, M. Rijnkels, C. Gill, J. Reecy, J. Zhihua, L. Wansheng, B. Murdoch, S. McKay, M. Thomas, T. Smith. Awarded $2,500,000.
2. University of Idaho & Washington State University - NSIP Carcass Ultrasound School. (2017-2018) PI Brenda Murdoch. Awarded $4,200.
3. Does Domestication Affect the Evolution of Meiotic Recombination? (2017-2018) IBEST TAG, PI-Murdoch B. Awarded $10,000.
4. Ovine FAANG project. (2017-2020) AFRI NIFA, PI-Murdoch B, Co-PI’s Cockett N, Worley K, White S, Archibald A, Dalrymple B, Clarke S., Kijas J. and Brauning R. Awarded $500,000.

5. Understanding parasite resistance in organic livestock and using a systems approach for control. (2016 (2016-2020) Organic Agriculture Research and Extension (OREI), NIFA PI - Joan Burke, Co–PI's - Bowdridge S., Coffey L., Lewis R., Terrill T. and Murdoch B. Awarded $1,991,149.00.
6. Solving the maturity grade problem through targeted gene analyses. (2016-2017) Idaho Beef Council PI - Murdoch G.K., Co-PI's – Doumit M. and Murdoch B. FY Awarded $23,640
7. Meiotic Recombination: Crossing-over into livestock species. (2016-2017) University of Idaho Seed Grant, PI - Murdoch B. Awarded $12,000.
8. Idaho cow-calf herds; a genetic resource for understanding and improving cow reproduction and calf growth efficiency. National Animal Genome Research Program – NRSP008 - Hatch Grant PI-Murdoch B.
9. Has evolution of human milk sugars responded to a biocultural sweet tooth? (2015) BEACON PI: B. Murdoch co-PI's M. McGuire, J. Foster, M. Settles. Awarded $110,829.
10. The Genetic Evaluation of the University of Idaho Dairy Herd. (2015) Zoetis. Awarded ~$10,000 genetic test Clarifide®.

Unfunded

1. Meiotic recombination variation within and across different breeds of cattle. (2107-2019) USDA-NIFA PI: B. Murdoch ($150,000).
2. Does Domestication Affect the Evolution of Meiotic Recombination? PI – Murdoch B, Co-PI Foster J. BEACON – NSF, (2017) $61,160 *Denied*
3. Whole genome survey in human populations for evidence of evolutionary selection of milk components., PI - Murdoch B., Co-PI's Foster J., Sullivan J., McGuire M. and McGuire M. BEACON – NSF (2017) $76,162.4 *Denied*
4. Whole genome survey in human populations for evidence of evolutionary selection of milk components. PI - Murdoch B., Co-PI's Foster J., Sullivan J., McGuire M. and McGuire M. BEACON – NSF, (2016) 2017 $101,530. *Denied*
5. In-Gene-ious; enhanced genomic screening of livestock for improving production traits and thus economic sustainability. PI-Murdoch B., Co-PI Superior Farms. IGEM $175,428. *Denied by UI.*
6. Genetic contribution to wool growth under two production systems. PI Murdoch B, Co-PI's Glaze B., Murdoch G., Laarman A., Chibisa G. American Sheep Industry "Lets grow" (2016) $32,425 *Denied*
7. Meiotic recombination within and across breeds of cattle. PI Murdoch B, Co-PI Fahey A. USDA AFRI NIFA, (2016) $149,943 *ranked 3rd but Denied.*
8. Engaging Young Scholars in Shaping New Methods for Genomic Selection: Integrating Quantitative and Molecular Genetics Using Sheep as a Model. PI: Ronald Lewis co-PI's: Matthew Spangler and Jessica Petersen. CAP USDA-NIFA. (2016) Amount requested ($2,000,000) *Denied.*
9. Recent changes in human milk oligosaccharides (HMO) driven by maternal genetics? PI: M. McGuire, co-PI's L. Bode, J Foster, M.K. McGuire, B. Murdoch and M. Settles. IBEST, UI (2015) Amount requested Amount requested $150,000 *Denied*.
10. New Research Capacity at the Forefront of Meiotic Recombination in Mammals. PI: B.M. Murdoch UI Seed Grant. (2015) Amount requested $12,000 *Denied.*
11. Murdoch B.M., Ytreberg F.M., Bode L., McGuire M.K., McGuire M.A. Towards an understanding of the complex interactions that determine human milk. CMCI - NSF (2015) $79,353 *Denied.*
12. Murdoch G.K. Murdoch, B.M. Examining genetic contribution to advanced heifer maturity assessed at harvest. Idaho Beef Council (2015) $36,360 *Denied.*
13. Whole Genome Sequencing (WGS) of U.S. Sheep. PI: B.M. Murdoch Collaborators Noelle Cockett, Utah State University, Michael Heaton, USDA/ARS Meat Animal Research Center, Rodney Kott, Montana State University, Michelle Mousel, USDA/ARS Animal Disease Unit, Reid Redden; North Dakota State University, David Thomas, University of Wisconsin, Theodore Kalbfleisch, University of Louisville. National Sheep Industry Improvement Center (NSIIC) (2014) Amount requested $50,000 *Denied*.
14. Idaho Cow-Calf Herds; A Genetic Resource for Understanding and Improving Reproduction and Calf Growth Efficiency in Varied Climates. PI: B.M. Murdoch Co-PI's: J.B. Hall, B.J. Glaze and G.K. Murdoch. USDA AFRI NIFA (2014) Amount requested $149,768 *Denied*.
15. Improving growth of beef cattle through novel regimen of β-agonist administration, enhancing efficiency and carcass quality. (2013) USDA AFRI NIFA PI: Gordon Murdoch co-PI's Matthew Doumit and Brenda Murdoch. Amount requested $498,210 *Denied*.

Pending

1. Multidisciplinary Graduate Training: Sustainable Beef Production-Effect of the Beef Cow Environment (2018- 2023) USDA- NIFA PI: M. Colle co-PI's: J. Hall, M. Ellison, B Murdoch, J. Sprinkle. ($241,000).

Honors and Awards:

- Travel awarded to attend and moderate at Sheep Genetic Workshop in Lincoln NB, 2014.

SERVICE:

Major Committee Assignments:

International

- International Society of Animal Genetic – Domestic Animal Sequencing and Annotation, Organizing Committee (2017 – present)
- Serve on the Functional Annotation of ANimal Genome FAANG Animal Sampling Committee (2015-present)
- Dairy Farmers of Canada, Ad hoc grant reviewer (2016-present)
- International Society of Animal Genetics – (2017- poster judge)

National

- Genome to Phenome: An USDA Blue Print for Animal Production. Writing Committee workshop (2017)
- National Animal Genome Research Program – NRSP008 (chair elect 2017, chair 2018)
- External Reviewer USDA Meat and Animal Research Center - 5 year research plan (2017)
- NCERA214 Increased Efficiency of Sheep Production (2017)
- National Sheep Improvement Program Genomics Technical Committee (2017)
- Sheep Reference Genome FAANG sample collection - Utah State University (April 25-27, 2016)
- Go FAANG workshop (October 7-8, 2015)
- Genetic Tools for Improved Sheep Production workshop (2015)
- National Animal Genome Research Program – NRSP008 member

University

- University of Idaho representative for the Washington State University College of Veterinary Medicine Idaho admissions committee (2015-present)
- University of Idaho Sheep Unit advisory board (2016-present)
- BEACON member – grant reviewer (2014- present)
- Ad hoc BMC Genomics review (2015-present)
- Bioinformatics and Computational Biology (BCB) Faculty Member

College

- Search committee member- Research Scientist, Genome Editing Center IRIC 2017
- Search committee member, UI Animal and Veterinary Science Interim Department head, 2016
- Tenure and promotion committee – Dr. M. Chahine September, 2015.
- UI Beef Program of Distinction (POD) member, 2015 – present

Department

- AVS Research technician, Search committee member July–August, 2017
- AVS Small ruminant food animal medicine, Search committee chair – 2016-2017
- AVS Reproductive physiologist, Search committee member –2016-2017
- AVS Instructor/Advising position, Search committee 2015
- Sheep UI Faculty Advisory member, 2016 - present
- UI Student sheep club, 2016 - present

Professional and Scholarly Organizations
Memberships:

- International Society for Animal Genetics member

- International Sheep Genome Consortium member
- Functional annotation of animal genome (FAANG), Animal Sample Assay (ASA)
- American Sheep Industry (ASI) member
- American Society of Animal Science member
- NRSP8, A National Animal Genome Research Program member
- NCERA, Increased efficiency of sheep production member
- Bioinformatics and Computational Biology (BCB) faculty member
- Center for Reproductive Biology (CRB) faculty member
- University of Idaho Beef Program of Distinction member
- BEACN An NSF Action Center for the Study of Evolution in Action member
- Center for Modeling Complex Interactions (CMCI) member
- The Institute of Bioinformatics and Evolutionary Studies (IBEST) member
- Golden Key International Honor Society
- Networks of Centers of Excellence, Student Young Professionals Association (SYPA) 2006-2011
- Professional Agrologist 2000-2006

Faculty Advisor:
Major advisors for two graduate students, graduate committee member for six graduate students.
Five current undergraduates working in the laboratory and Pre-Vet undergraduate advisees.
University of Idaho Women's Hockey Club, 2015-present.
Faculty advisor and mentor for Sigma Alpha, Women in Agriculture sorority, 2014 - present.

Outreach Service:
- University of Idaho Sheep Club
- Tri State Wool growers, Sun Valley, ID 2016
- University of Idaho Sheep Unit advisory board meeting. Moscow, ID Nov 4, 2016.
- Livestock Genetics presentation at NMCREEC for field day demonstration August 8, 2014.
- Video linked short talk to beef producers at the NMCREEC, September 18, 2014.

Community Service:
Palouse Youth Hockey Association, 2007- 2015
Josephburg Minor Hockey Association, 2005- 2007
4H Leader and riding instructor, Rein Riders 4H club, 2002
University of Alberta Dept. AFNS Equity committee 2001-2003
Alberta Institute Agrologist conference and AGM organizing committee 2001-2002

PROFESSIONAL DEVELOPMENT:

Teaching:
1. The Impactful reporting writing Workshop Aug, 2017
2. Women's Leadership Conference University of Idaho March 30, 2017
3. University of Idaho Compliance trainings, 2017
4. Ethics sensitivity training, Washington State University, 2017

Scholarship:
1. International Society of Animal Genetics meeting, Dublin Ireland, July 16-21, 2017.
2. Increased Efficiency of Sheep Production East Lansing Michigan, June 11-14, 2017.
3. American Society of Animal Science Baltimore, Maryland July 8-12, 2017.
4. Attended American Sheep Industry Association, Denver, CO January 25-28, 2017.
5. Attended International Plant and Animal Genome XXVI. San Diego, CA, January 13 -18, 2017.
6. Sheep Production Researcher invited meeting USDA, Meat and Animal Research Center Clay Center Nebraska November 30- December 2, 2016
7. Large Animal Genetic Engineering Summit, Bethesda Maryland, Sept 18-20, 2016.
8. International Society of Animal Genetics, Salt Lake Utah, July 23-27, 2016
9. American Society of Dairy Science/American Society of Animal Science, Salt Lake Utah, July 19-23, 2016
10. Attended American Sheep Industry Association, Scottsdale AZ, January 27-30, 2016.
11. Attended International Plant and Animal Genome XXV. San Diego, CA, January 9 -13, 2016.

12. ASAS member. Attended ADSA - ASAS joint JAM, Orlando, July 12-16, 2015.
13. Bio/Computational Evolution in Action Consortium BEACON Congress, Michigan State August 15-17, 2015
14. Go Functional Annotation Animal Genome FAANG Washington DC October 7-8, 2015.
15. Attended American Sheep Industry Association. Reno NV, January 28-31, 2015.
16. Attended International Plant and Animal Genome XXIV. San Diego, CA, January 10 -14, 2015.
17. The Institute of Bioinformatics and Evolutionary Studies (IBEST) member and participant in seminar series.
18. Center for Modeling Complex Interactions (CMCI) member and participant in seminar series.
19. Bioinformatics and Computational Biology (BCB) faculty member
20. National Beef Cattle Evaluation Consortium (NBCEC) online brown bagger workshops (2015- present).
21. Attended World Congress on Genetics Applied to Livestock Production. Vancouver, Canada, Aug 17-22, 2014.
22. Sheep Genomics Workshop – Invited moderator November 13, 2014.
23. Attended CRB WSU/UI Annual Meeting/conference, Pullman, WA May 2013.
24. Attended CRB WSU/UI Annual Meeting/conference, Pullman, WA May 2012.
25. Center for Reproductive Biology (CRB) faculty member

Outreach:
Faculty advisor and mentor for Sigma Alpha, Women in Agriculture sorority, 2014 - present.
UI Student Sheep club, 2016-present
University of Idaho Women's Hockey Club, 2015-present.

Administration/Management: