

Curriculum Vitae

Jared E. Decker, Ph.D.

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Education

- Ph.D. Genetics, University of Missouri (2012)
Dissertation: Evolutionary relationships and signatures of selection in cattle established using genome-wide single nucleotide polymorphisms
- Ph.D. Minor Statistics, University of Missouri (2012)
- B.S. Animal Science, New Mexico State University (2007)
Graduated with Highest Honors in College of Agriculture
Thesis: The association of scrotal circumference in bulls at the age of 240 days to 365 days
- B.S. Minor Biology, New Mexico State University (2007)

Research Interests

Population genomics, including identification of causal mutations underlying complex phenotypes and diseases, genomic selection, population structure and history, molecular signatures of selection, genome assembly, genome structure, and phylogenomics

Research Experience

- 2013-present Assistant Professor, State Beef Genetics Extension Specialist and Computational Genomicist, Division of Animal Sciences, University of Missouri
- 2012-2013 USDA-NIFA Postdoctoral Fellow, Animal Genomics, Division of Animal Sciences, University of Missouri (Jeremy F. Taylor)
- 2007-2012 Graduate Research Assistant, Animal Genomics, Division of Animal Sciences, University of Missouri (Jeremy F. Taylor)
- 2006-2007 Laboratory worker, Physiological Genetics, Department of Animal Science, New Mexico State University (Milton Thomas)
- 2006 Intern, Miller Summer Internship in the Division of Animal Sciences, University of Missouri (Jeremy F. Taylor)

2002 Laboratory worker, Nutritional Toxicology, Department of Animal Science,
New Mexico State University (James Strickland)

Teaching Experience

2013 Guest Lecturer, Veterinary Cattle Practicum, University of Missouri

2012 Guest Lecturer, Animal Science 9423 Genetics of Populations, University of
Missouri

2012 Guest Lecturer, Veterinary Pathobiology 5579 Veterinary Genomics,
University of Missouri

2010 Teaching Assistant, Animal Science 9423 Genetics of Populations, University
of Missouri

2008 Teaching Assistant, Animal Science/Plant Science 3213 Genetics, University
of Missouri

2008 Teaching Assistant, Animal Science 4323 Applied Livestock Genetics,
University of Missouri

2006-2007 Tutor, Student Support Services, New Mexico State University
Certified Level 1 by College Reading & Learning Association

Scientific Outreach Experience

2011 Article published in Lincoln Red Association newsletter, describing recent
advances in genome research.

2011 Extension presentation at the University of Missouri Thompson Farm Field
Day.

2011 Extension presentation at the Show-Me Shorthorn University.

2011 Extension presentation during University of Missouri Regional Livestock
Extension In-Service.

2010 Extension presentation at the MizzouCentral College of Agriculture, Food
and Natural Resources booth at the Missouri State Fair.

2009 Extension presentation regarding the impact of genomic technologies in
agriculture to the Centralia, Missouri Young Farmers Chapter.

2009 Outreach presentation regarding alternative careers in agriculture to the

Centralia High School Future Farmers of America Chapter.

2009 Judge for Genetics, Environment, and Evolution section, Missouri Life Sciences Week poster competition.

Funding

2013-2016 USDA-NIFA-AFRI. Improving Reference Genomes for Agriculturally Important Animals. Worley K, Dalrymple B, **Decker JE**. \$500,000 (Awarded)

2012-2014 USDA-NIFA-AFRI. Reassembly and quality assessment of the bovine reference genome sequence incorporating next-generation sequencing data. **Decker JE**, Taylor JF, Zimin A, Schnabel RD. \$130,000 (Awarded)

Awards & Honors

1st Place in Biological Sciences category, Graduate Professional Council 29th Annual Research and Creative Arts Forum, University of Missouri 3/2012

Gordon Research Conference on Quantitative Genetics and Genomics Student Travel Award 2/2011

Beef Improvement Federation Student Travel Fellowship 6/2010

MU GSA Outstanding Graduate Student Award for Genetics Area Program 5/2010

1st Place in Biological Sciences category, Graduate Professional Council 26th Annual Research and Creative Arts Forum, University of Missouri 3/2009

Neal A. Jorgensen Genome Bioinformatics Travel Award, Plant and Animal Genome XVII Conference 1/2009

Honorable Mention- Graduate Research Fellowship Program, National Science Foundation 4/2008

1st Place in Genetics, Evolution and Ecology Category of Life Sciences Week Research Competition, Missouri Life Sciences Week, University of Missouri 4/2008

1st Year University of Missouri Life Science Fellowship Travel Award 1/2008

University of Missouri Life Sciences Fellowship 7/2007 through 7/2011

Animal Science Dean's Award of Excellence, New Mexico State University 5/2007

Computer Skills

Systems	Windows, Fedora Linux, OpenSUSE Linux
Languages	R, Perl, Python, SAS, HTML
Databases	MS Access, pgAdmin
Applications	PLINK, GEMMA, EMMAX, GenSel, TreeMix, EIGENSOFT, ADMIXTURE, NextGENe, SOAPdenovo, EDENA, MSR-CA, AMOS, MUMmer, MAUVE, CRIMAP, GridQTL, PHYLIP, PAUP, TNT, SPLITSTREE, NETWORK, Illumina GenomeStudio, VCFtools, MS Office, Adobe Creative Suite, GIMP, Inkscape

Book Chapters

Patterson DJ, Brown DS, Sexten WJ, **Decker JE**, Pooch SE. 2013. Management Strategies for Adding Value to Replacement Beef Heifers: A Working Model. *In* Veterinary Clinics of North America: Food Animal Practice. Elsevier.

Taylor JF, McKay SD, Rolf MM, Ramey H, **Decker JE**, Schnabel RD. 2012. Genomic selection in beef cattle. *In* Bovine Genomics. J.E. Womack Ed., Wiley-Blackwell.

Peer Reviewed Publications

Submitted

Rolf MM, Garrick DJ, Fountain T, Ramey HR, Weaber RL, **Decker JE**, Pollack EJ, Schnabel RD, Taylor JF. (2013) Comparison of some Bayesian models with varying training and validation population sizes for estimating direct genomic values in crossbred and purebred beef cattle. *Genetics Selection Evolution* (under review)

2013

Tizioto P, **Decker JE**, Taylor JF, Schnabel RD, Mudadu M, Silva F, Mourão G, Coutinho L, Tholon P, Sonstegard T, Rosa A, Alencar M, Tullio R, Medeiros S, Nassu R, Feijo G, Silva L, Torres R, Siqueira F, Higa R, Regitano L. (2013) A genome scan for meat quality traits in Nelore beef cattle. *Physiological Genomics* doi: 10.1152/physiolgenomics.00066.2013

Ramey HR, **Decker JE**, McKay SD, Rolf MM, Schnabel RD, Taylor JF. (2013). Detection of selective sweeps in cattle using genome-wide SNP data. *BMC Genomics* **14**:382 doi:10.1186/1471-2164-14-382 arXiv:1212.2300

McTavish EJ, **Decker JE**, Schnabel RD, Taylor JF, Hillis DM. (2013). New World Cattle Show Ancestry from Multiple Independent Domestication Events. *Proceedings of the National Academy of Sciences USA* **110**: E1398-E1406 (15) doi: 10.1073/pnas.1303367110

2012

Sanders DN, Zeng R, Wenger DA, Johnson GS, **Decker JE**, Katz ML, Platt SR, O'Brien DP. (2013). G_{M2} Gangliosidosis Associated with a HEXA Missense Mutation in Japanese Chin Dogs: a Potential Model for Tay-Sachs Disease. *Molecular Genetics and Metabolism* **108**:70-75 (1) doi: 10.1016/j.ymgme.2012.11.008

Decker JE, Vasco DA, McKay SD, McClure MC, Rolf MM, Kim JW, Northcutt SL, Bauck S, Woodward BW, Schnabel RD, and Taylor JF. (2012). A novel analytical method, Birth Date Selection Mapping, detects response of the Angus (*Bos taurus*) genome to artificial selection on complex traits. *BMC Genomics* **13**:606 doi:10.1186/1471-2164-13-606

McClure MC, Ramey HR, Rolf MM, McKay SD, **Decker JE**, Chapple RH, Kim JW, Taxis TM, Weaber RL, Schnabel RD, and Taylor JF (2012). Genome-wide association analysis for quantitative trait loci influencing Warner–Bratzler shear force in five taurine cattle breeds. *Animal Genetics* **43**:662-673 (6) doi: 10.1111/j.1365-2052.2012.02323.x

2011

Saatchi M, McClure MC, McKay SC, Rolf MM, Kim JW, **Decker JE**, Taxis TM, Chapple RH, Ramey HR, Northcutt SL, Bauck S, Woodward B, Dekkers JCM, Fernando RL, Schnabel RD, Garrick DJ, and Taylor JF (2011). Accuracies of genomic breeding values in American Angus beef cattle using K-means clustering for cross-validation. *Genetics Selection Evolution* **43**:40
(6) Citations: 3

Zeng R, Farias FHG, Johnson GS, McKay SD, Schnabel RD, **Decker JE**, Taylor JF, Mann CS, Katz ML, Johnson GC, Coates JR, and O'Brien DP (2011). A truncated retrotransposon disrupts the *GRM1* coding sequence in Coton de Tulear dogs with Bandera's neonatal ataxia. *Journal of Veterinary Internal Medicine* **25**:267-272 (5) Citations: 5

2010

Taylor JF, Chapple RH, **Decker JE**, Gregg SJ, Kim JW, McKay SD, Ramey HR, Rolf MM, Taxis TM, Schnabel RD (2010) Genomic tools for characterizing monogenic and polygenic traits in ruminants-using the bovine as an example. *Soc Reprod Fertil Suppl* **67**:13-28 (4)
Citations: 2

Seabury CM, Seabury PM, **Decker JE**, Schnabel RD, Taylor JF, and Womack JE (2010). Diversity and evolution of 11 innate immune genes in *Bos taurus taurus* and *Bos taurus indicus* cattle. *Proceedings of the National Academy of Sciences USA* **107**:151-156 (3) Citations: 17

2009

Decker JE, Pires JC, Conant GC, McKay SD, Heaton MP, Chen K, Cooper A, Vilkki J, Seabury CM, Caetano AR, Johnson GS, Brenneman RA, Hanotte O, Eggert LS, Wiener P, Kim JJ, Kim KS, Sonstegard TS, Van Tassell CP, Neibergs HL, McEwan JC, Brauning R, Coutinho LL, Babar ME, Wilson GA, McClure MC, Rolf MM, Kim JW, Schnabel RD, and Taylor JF (2009). Resolving the evolution of extant and extinct ruminants with high-throughput phylogenomics. *Proceedings of the National Academy of Sciences USA* **106**:18644-18649 (2) Citations: 52

2008

Decker JE, Luna-Nevarez P, Encinias AM, Enns RM, and Thomas MG (2008). Case Study: Scrotal Circumference in Beef Bulls Prediction of Measures at 365 Days of Age from Measures at 240 Days of Age with Data from the Tucumcari Bull Test. *The Professional Animal Scientist*, **24**:488-493 (1) Citations: 2

Non-Peer Reviewed Publications

2010

Rolf MM, McKay SD, McClure MC, **Decker JE**, Taxis TM, Chapple RH, Vasco DA, Gregg SJ, Kim JW, Schnabel RD, Taylor JF (2010) How the next generation of genetic technologies will impact beef cattle selection. *Proc. Beef Improve. Fed.*, Columbia, MO. 46-56. Citations: 2

Invited Presentations

Decker JE, Noyes H, Kim JW, Babar ME, Reecy JM, Saif-Ur-Rehman M, Götherström A, Praharani L, Sonstegard TS, Hanotte O, Molina A, Seabury CM, Yildiz MA, Heaton MP, Liu W, Schnabel RD, Taylor JF. (2013) Worldwide patterns of divergence, migration, and admixture in domesticated cattle. Gordon Research Seminar on Quantitative Genetics and Genomics (*Oral Presentation*)

Decker JE, Noyes H, Kim JW, Babar ME, Reecy JM, Saif-Ur-Rehman M, Götherström A, Praharani L, Sonstegard TS, Hanotte O, Molina A, Seabury CM, Yildiz MA, Heaton MP, Liu W, Schnabel RD, Taylor JF. (2013) Worldwide patterns of divergence, migration, and admixture in domesticated cattle. Plant and Animal Genome XXI (*Oral Presentation*)

Decker JE, Schnabel RD, Taylor JF (2013). Birth Date Selection Mapping in four *Bos taurus* breeds. Plant and Animal Genome XXI (*Oral Presentation*)

Decker JE, Pires JC, Conant GC, McKay SD, Heaton MP, Vilkki J, Chen K, Cooper A, Seabury CM, Caetano AR, Johnson GS, Brenneman RA, Hanotte O, Eggert LS, Wiener P, Kim JJ, Kim KS, Sonstegard TS, Van Tassell C, Neiberghs HL, Schnabel RD, Taylor JF (2009). Molecular Phylogeny of Pecora and Phylogenetic Relationships of Cattle Breeds. Plant and Animal Genome XVII (*Oral Presentation*)

Contributed Presentations

Decker JE, Schnabel RD, Taylor JF (2013). Birth Date Selection Mapping in four *Bos taurus* breeds. Gordon Research Conference on Quantitative Genetics and Genomics (*Poster Presentation*)

Decker JE, Vasco DA, McKay SD, McClure MC, Rolf MM, Kim JW, Northcutt SL, Bauck S, Woodward BW, Schnabel RD, and Taylor JF. (2012). A novel analytical method detects response of the Angus (*Bos taurus*) genome to artificial selection on complex traits. Missouri Life Sciences Week, University of Missouri (*Poster Presentation*)

Decker JE, Vasco DA, McKay SD, McClure MC, Rolf MM, Kim JW, Northcutt SL, Bauck S,

Woodward BW, Schnabel RD, and Taylor JF. (2012). A novel analytical method detects response of the Angus (*Bos taurus*) genome to artificial selection on complex traits. Graduate Professional Council Research and Creative Arts Forum, University of Missouri (*Oral Presentation*)

Decker JE, McKay SD, Schnabel RD, Taylor JF (2011). Fine mapping a morphometric QTL on BTA7 in Angus cattle. Animal Sciences Graduate Forum, University of Missouri (*Oral Presentation*)

Decker JE, McKay SD, Schnabel RD, Taylor JF (2011). Fine mapping a morphometric QTL on BTA7 in Angus cattle. Advances in Reproductive Biology and Genetics (*Poster Presentation*)

Decker JE, McKay SD, Schnabel RD, Taylor JF (2011). Fine mapping a morphometric QTL on BTA7 in Angus cattle. Gordon Research Conference on Quantitative Genetics & Genomics (*Poster Presentation*)

Decker JE, Vasco DA, McKay SD, Rolf MM, Taxis TM, Chapple RH, Gregg SJ, Kim JW, Schnabel RD, Taylor JF (2010). Effects Of Population Stratification On GWAS In Livestock Populations Assumed To Be Homogenous. Missouri Life Sciences Week, University of Missouri (*Poster Presentation*)

Decker JE, Vasco DA, McKay SD, Rolf MM, Taxis TM, Chapple RH, Gregg SJ, Kim JW, Schnabel RD, Taylor JF (2010). Effects Of Population Stratification On GWAS In Livestock Populations Assumed To Be Homogenous. Plant and Animal Genome XVIII (*Poster Presentation*)

Decker JE, Pires JC, Conant GC, McKay SD, Heaton MP, Vilkki J, Chen K, Cooper A, Seabury CM, Caetano AR, Johnson GS, Brenneman RA, Hanotte O, Eggert LS, Wiener P, Kim JJ, Kim KS, Sonstegard TS, Van Tassell CP, Neibergs HL, Schnabel RD, Taylor JF (2009). High-Throughput Phylogenomics: From ancient DNA to signatures of animal husbandry. Animal Sciences Graduate Forum, University of Missouri (*Oral Presentation*)

Decker JE, Pires JC, Conant GC, McKay SD, Heaton MP, Vilkki J, Chen K, Cooper A, Seabury CM, Caetano AR, Johnson GS, Brenneman RA, Hanotte O, Eggert LS, Wiener P, Kim JJ, Kim KS, Sonstegard TS, Van Tassell CP, Neibergs HL, Schnabel RD, Taylor JF (2009). High-Throughput Phylogenomics: From ancient DNA to signatures of animal husbandry. Graduate Professional Council Research and Creative Arts Forum, University of Missouri (*Oral Presentation*)

Decker JE, Pires JC, Matukumalli LK, Van Tassell CP, Sonstegard TS, Allen MF, Smith TPL, Schnabel RD, Taylor JF (2008). Phylogenomic analysis of 9 Bovinae species including 18 cattle breeds to identify synapomorphic loci. Missouri Life Sciences Week, University of

Missouri (*Poster Presentation*)

Decker JE, Pires JC, Matukumalli LK, Van Tassell CP, Sonstegard TS, Allen MF, Smith TPL, Schnabel RD, Taylor JF (2008). Phylogenomic analysis of 9 Bovinae species including 18 cattle breeds to identify synapomorphic loci. Animal Science Graduate Forum, University of Missouri (*Poster Presentation*)

Abstracts

Hoff J, **Decker JE**, Schnabel RD, Taylor JF. 2013. Identifying Polymorphisms Underlying QTLs in *Bos taurus* using GWAS and Whole Genome Sequence Data. Plant and Animal Genome XXI. San Diego, CA. January 12-16, 2013.

Whitacre L, **Decker JE**, Kim JW, Schnabel RD, Taylor JF. 2013. Kinase Insert Domain Receptor - A Candidate for the Hereford "spotted" Gene. Plant and Animal Genome XXI. San Diego, CA. January 12-16, 2013.

Neibergs H, Seabury CM, Taylor JF, Wang Z, Scraggs E, Schnabel RD, **Decker JE**, Wojtowicz A, Davis J, Lehenbauer T, Van Eenennaam A, Aly SS, Blanchard P, Crossley B, Bovine Respiratory Disease Consortium. 2013. Identification of Loci Associated with Bovine Respiratory Disease in Holstein Calves. Plant and Animal Genome XXI. San Diego, CA. January 12-16, 2013.

Tizioto PC, **Decker JE**, Taylor JF, Schnabel RD, Mudadu MA, Coutinho LL, Mourão GB, Sonstegard T, Rosa AN, Alencar MM, Tullio RR, Medeiros SR, Nassu RT, Feijó GLD, Siqueira F, Regitano LCA. 2013. A Genome-Wide Association Study of Meat Tenderness in Nelore Beef Cattle. Plant and Animal Genome XXI. San Diego, CA. January 12-16, 2013.

Moore JD, Allaby RG, Barker G, Teakle GR, Pires JC, **Decker JE**, Edger P, Arias T, Walley PG, Mayfield DRF. 2013. Insights Into Evolutionary Relationships Among C Genome Wild Species and Crops. Plant and Animal Genome XXI. San Diego, CA. January 12-16, 2013.

Schnabel RD, Mhlanga-Mutangadura T, Gilliam DH, **Decker JE**, O'Brien DP, Coates JR, Taylor JF, Johnson GS. 2013. Application Of Whole Genome Sequencing To Identify Mendelian Disease Candidates In Dogs Using a 1-Case + N-Control Design. Plant and Animal Genome XXI. San Diego, CA. January 12-16, 2013.

Mapholi NO, **Decker JE**, Rolf MM, McKay SD, Yampara-Iquise H, Kim JW, Ramey HR, Chapple RH, Schnabel RD, Dzama K, Maiwashe A and Taylor JF. 2012. Validation of chromosomal positions for genes controlling coat colour and horn/polled traits in Shorthorn cattle using the 50k Bovine SNP Chip. 45th South African Society for Animal Science Congress. East London, Eastern Cape. July 9-12, 2012

Schnabel RD, McKay SD, Kim JW, **Decker JE**, Rolf MM, Chapple RH, Ramey HR, Taylor JF. 2012. Angus Genome Project. Workshop 150. Plant and Animal Genome XX. San Diego, CA. January 14-18, 2012.

Ramey HR, **Decker JE**, McKay SD, Rolf MM, Schnabel RD, Taylor JF. 2012. Validation of Bovine Selective Sweeps Using High Resolution SNP Data. Poster 550, Plant and Animal Genome XX. San Diego, CA. January 14-18, 2012.

Ramey HR, McKay SD, Gregg SJ, Chapple RH, **Decker JE**, Kim JW, Rolf MM, Taxis TM, Schnabel RD, Taylor JF. 2011. Detection Of Selective Sweeps In Cattle Using High-Density And Genome-Wide SNP Data. Poster 517, Plant and Animal Genome XIX. San Diego, CA. January 15-19, 2011.

Schnabel RD, **Decker JE**, Cooper A, Chen K, McKay SD, McClure MC, Taxis TM, Kim JW, Rolf MM, Chapple RH, Vasco DA, Gregg SJ and Taylor JF. 2010. High-throughput genomics: Applications in conservation biology and phylogenomics. Adelaide Phylogenetics Conference, April 12-16, Adelaide, Australia.

Taylor JF, Chapple RH, **Decker JE**, Gregg SJ, Kim JW, McKay SD, Ramey HR, Rolf MM, Taxis TM and Schnabel RD. 2010. Unique aspects of the domestic ruminant genome. Proc. 8th International Ruminant Reproduction Symposium. Sept. 3-7, Anchorage, AK.

Nkrumah JD, Garrick DJ, Fernando RL, Northcutt S, Bowman B, Woodward BW, Bauck SW, Vasco D, Taxis TM, Rolf MA, **Decker JE**, Kim JW, McClure MC, McKay SD, Schnabel RD, Taylor JF. Alternative methods for selecting tagSNP panels from the bovine 50K chip to predict marbling in Angus cattle. Abstract 34819. 2009 Joint Meeting of ADSA, CSAS and ASAS, Montreal, Quebec, Canada July 12-16, 2009.

Rolf MM, Taylor JF, Schnabel RD, McKay SD, Vasco DA, McClure MC, **Decker JE**, Taxis TM, Weaber RL. Evaluation Of Model Predicted Feed Intake Data For Genetic Analysis And QTL Discovery In Beef Cattle. Poster 488, Plant and Animal Genome XVII. San Diego, CA. January 10-14, 2009.

Taylor JF, McKay SD, McClure MC, Kim JW, Vasco DA, **Decker JE**, Rolf MM, Schnabel RD. Prospects For Whole Genome Selection In Beef Cattle. Workshop 080, Plant and Animal Genome XVII. San Diego, CA. January 10-14, 2009.

McClure MC, Kim JW, Morsci NS, McKay SD, Rolf MM, **Decker JE**, Schnabel RD and Taylor JF. Whole Genome Scan in Commercial Angus Cattle for QTL Influencing Carcass Value Traits: Carcass Weight, Fat Thickness, Marbling, and Ribeye Area. Poster 2009, Proceedings of the 31st International Conference on Animal Genetics, ISAG 2008, Amsterdam, Netherlands, July 20-24, 2008.

Rolf MM, **Decker JE**, Bishop JA, McClure MC, Schnabel RD and Taylor JF. Crossing the

breed barrier: Utilization of beef and dairy breeds to cross-validate quantitative trait nucleotides. Poster 520, Plant and Animal Genome XVI. San Diego, CA. January 12-16, 2008.

Professional Organizations

Member, Sigma Xi (5/2009-2012)
Member, The Society of Systematic Biologists (3/2008 - 3/2009)
Member, American Society of Animal Science (2/2007 - 2/2008)

Conferences Attended

National Beef Cattle Evaluation Consortium Symposium 3/2013
Gordon Research Conference on Quantitative Genetics & Genomics 2/2013
Plant and Animal Genome XXI 1/2013
Cold Spring Harbor Laboratory Biology of Genomes 5/2012
Frontiers in Metagenomics 5/2012
Advances in Reproductive Biology and Genetics 5/2011
Gordon Research Conference on Quantitative Genetics & Genomics 2/2011
Beef Improvement Federation Conference 6/2010
Plant and Animal Genome XVIII 1/2010
Statistical Genetics of Livestock in the Post-Genomic Era 5/2009
Plant and Animal Genome XVII 1/2009
9th Genetic Prediction Workshop 12/2008
Ecological Genomics Symposium 11/2008
Plant and Animal Genome XVI 1/2008

Dissertation Committee

Jeremy F. Taylor (chair)	Curators' Professor and Wurdack Chair of Animal Genomics, Division of Animal Sciences, University of Missouri
Robert D. Schnabel	Division of Animal Sciences, University of Missouri
J. Chris Pires	Division of Biological Sciences, University of Missouri
Gavin C. Conant	Division of Animal Sciences, University of Missouri
Lori S. Eggert	Division of Biological Sciences, University of Missouri