

James M. Reecy
Professor

University Address

Department of Animal Science
Iowa State University
2255 Kildee Hall
Ames, IA 50011

Home Address

2135 Stevenson
Ames, IA 50010

Education

Ph.D. PURDUE UNIVERSITY, West Lafayette, IN. December 1995.
Major: Animal Science
M.S. UNIVERSITY OF MISSOURI-COLUMBIA, Columbia, MO, August 1992.
Major: Animal Science (Ruminant Nutrition)
B.S. SOUTH DAKOTA STATE UNIVERSITY, Brookings, SD, May 1990.
Major: Animal Science Minor: Chemistry

Professional Experience

<u>Professor:</u>	July 2010 – Present	Employer:	Iowa State University
<u>Associate Professor:</u>	July 2005 – Present		Dept of Animal Science
<u>Assistant Professor:</u>	February 1999 – June 2005		Ames, IA
<u>Assistant Professor:</u>	Oct. 1998 – Jan. 1999	Employer:	Baylor College of Medicine
<u>Instructor:</u>	Nov. 1997 – Oct. 1998		Dept. of Cell Biology
<u>Post Doctoral:</u>	Jan. 1996 – Nov. 1997.		One Baylor Plaza Houston, TX 77030

Awards

- ISU College of Agriculture, Early Achievement in Research, 2003
- Midwest American Society of Animal Science. Young Researcher Award 2008
- ISU College of Agriculture, Achievement in Research, 2011

LEADERSHIP POSITIONS

National Research Sponsored Program-8 (USDA/CSREES) Database Coordinator.

Dr. Reecy is leading a collaborative effort with Dr. Sue Lamont, Max Rothschild, and Chris Tuggle. This national coordinator position is to promote, develop, and implement bioinformatic and database activities in domestic animal species, such as beef and dairy cattle, sheep, swine, chickens, turkeys, horses, and fish.

Director of the Office of Biotechnology, Iowa State University

Dr. Reecy is the Director of the Office of Biotechnology at Iowa State University. This position is charged with coordination, maintenance and oversight of ISU core facilities (i.e. DNA sequencing, gene expression, flow cytometry, etc.).

Main Research Topics

My main responsibilities in research include both basic and applied research in the areas of livestock growth and development and beef cattle genetics. Specific research objectives include characterization of molecular mechanisms regulating animal growth and development and the identification of molecular markers to improve beef cattle production, with the overall goal of

identifying ways of increasing lean tissue production and meat quality in livestock. Another objective is to develop bioinformatic tools to allow livestock researchers complete genomics research in a timely manner (www.animalgenome.org).

Sample Refereed Research Publications (76 total)

- Hu, Z.-L., A.M. Ramos, S.J. Humphray, J. Rogers, **J.M. Reecy** and M.F. Rothschild. 2011. Use of genomes sequence information for meat quality trait QTL mining for causal genes and mutations on pig chromosome 17. *Frontiers in Genetics* 2:43. doi: 10.3389/fgene.2011.00043
- Boddicker, N., E.H. Waide, R.R. Rowland, J.K. Lunney, D.J. Garrick, **J.M. Reecy**, J.C. Dekkers. 2011. Evidence for a major QTL associated with host response to Porcine Reproductive and Respiratory Syndrome virus challenge. *J Anim Sci.* 90(6):1733-46. Epub 2011 Dec 28.
- Hu, Z.-L., J.E. Koltes, C.A. Park, E.R. Fritz and J.M. Reecy. 2011. Bioinformatics approaches to livestock animal genomics research. *CAB Reviews: Perspectives in Agriculture, Veterinary Science, Nutrition and Natural Resources* 2011 6, No. 044
- Wu, X.-L., D. Gianola, Z.-L. Hu and J.M. Reecy. 2011. Meta-Analysis of Quantitative Trait Association and Mapping Studies using Parametric and Non-Parametric Models. *Journal of Biometrics and Biostatistics* 2011, S1
- Duan, Q., R.G. Tait, Jr, M.S. Mayes, D.J. Garrick, Q. Liu, A.L. Van Eenennaam, R.G. Mateescu, D.L. Van Overbeke, A.J. Garmyn, D.C. Beitz and J.M. Reecy. 2012. Genetic polymorphisms in bovine transferrin receptor 2 (TFR2) and solute carrier family 40 (iron-regulated transporter), member 1 (SLC40A1) gene and their associations with beef iron content. *Animal Genetics* 43(2):115-22.
- Hu Z.L., **Reecy J.M.**, Wu X.L. 2012. Design database for quantitative trait loci (QTL) data warehouse, data mining, and meta-analysis. *Methods Mol Biol.* 2012;871:121-44.
- Mateescu R.G., Garmyn A.J., O'Neil M.A., Tait R.G. Jr, Abuzaid A., Mayes M.S., Garrick D.J., Van Eenennaam A.L., Vanoverbeke D.L., Hilton G.G., Beitz D.C., **Reecy J.M.** 2012. Genetic parameters for carnitine, creatine, creatinine, carnosine, and anserine concentration in longissimus muscle and their association with palatability traits in Angus cattle. *J Anim Sci.* 2012 Sep 5. [Epub ahead of print]
- Hu ZL, Park CA, Wu XL, **Reecy JM.** 2013. Animal QTLdb: an improved database tool for livestock animal QTL/association data dissemination in the post-genome era. *Nucleic Acids Res.* 2013 Jan 1;41(D1):D871-9. doi: 10.1093/nar/gks1150. Epub 2012 Nov 24.
- Groenen MA, Archibald AL, Uenishi H, Tuggle CK, Takeuchi Y, Rothschild MF, Rogel-Gaillard C, Park C, Milan D, Megens HJ, Li S, Larkin DM, Kim H, Frantz LA, Caccamo M, Ahn H, Aken BL, Anselmo A, Anthon C, Auvil L, Badaoui B, Beattie CW, Bendixen C, Berman D, Blecha F, Blomberg J, Bolund L, Bosse M, Botti S, Bujie Z, Bystrom M, Capitanu B, Carvalho-Silva D, Chardon P, Chen C, Cheng R, Choi SH, Chow W, Clark RC, Clee C, Crooijmans RP, Dawson HD, Dehais P, De Sapio F, Dibbits B, Drou N, Du ZQ, Eversole K, Fadista J, Fairley S, Faraut T, Faulkner GJ, Fowler KE, Fredholm M, Fritz E, Gilbert JG, Giuffra E, Gorodkin J, Griffin DK, Harrow JL, Hayward A, Howe K, Hu ZL, Humphray SJ, Hunt T, Hornshøj H, Jeon JT, Jern P, Jones M, Jurka J, Kanamori H, Kapetanovic R, Kim J, Kim JH, Kim KW, Kim TH, Larson G, Lee K, Lee KT, Leggett R, Lewin HA, Li Y, Liu W, Loveland JE, Lu Y, Lunney JK, Ma J, Madsen O, Mann K, Matthews L, McLaren S, Morozumi T, Murtaugh MP, Narayan J, Nguyen DT, Ni P, Oh SJ, Onteru S, Panitz F, Park EW, Park HS, Pascal G, Paudel Y, Perez-Enciso M, Ramirez-Gonzalez R, **Reecy JM**, Rodriguez-Zas S, Rohrer GA, Rund L, Sang Y, Schachtschneider K, Schraiber JG, Schwartz

J, Scobie L, Scott C, Searle S, Servin B, Southey BR, Sperber G, Stadler P, Sweedler JV, Tafer H, Thomsen B, Wali R, Wang J, Wang J, White S, Xu X, Yerle M, Zhang G, Zhang J, Zhang J, Zhao S, Rogers J, Churcher C, Schook LB. 2012. Analyses of pig genomes provide insight into porcine demography and evolution. *Nature* 491(7424):393-8.