

Jack C. M. Dekkers

C.F. Curtiss Distinguished Professor
Section Leader, Animal Breeding and Genetics
Department of Animal Science



Education

B.Sc.	(1982)	Animal Science	Agricultural University, Wageningen, The Netherlands
M.Sc.	(1985)	Animal Science	Agricultural University, Wageningen, The Netherlands
Ph.D.	(1989)	Dairy Science/ Animal Breeding	University of Wisconsin, Madison, Wisconsin
Post-doc	(1989)	Animal Breeding and Genetics	University of Wisconsin, Madison, Wisconsin

Employment

1985 - 1988	Graduate Research Assistant , Univ. of Wisconsin, Madison (Dr. G. Shook) PhD: Economic evaluation of dairy cattle MOET nucleus breeding programs
1989	Post-doctoral Fellow , University of Wisconsin, Madison, WI (Dr. M. Dentine) Research on QTL mapping under the infinitesimal genetic model.
1989 - 1992	Adjunct Professor of Animal Breeding , University of Guelph, Canada Quantitative genetics and breeding strategies with application to dairy cattle. Undergraduate teaching. Fully supported by Can. dairy cattle breed. industry
1992 - 1995	Assistant Professor of Animal Breeding , University of Guelph, Canada Quantitative genetics and breeding strategies with application to dairy cattle. Undergraduate teaching. Fully supported by Can. dairy cattle breeding industry and the Natural Sciences and Engineering Research Council.
1996	Visiting Scientist , Animal Breeding, Agricultural Univ., Wageningen, NL. Sabbatical (4 mo) supported by NATO Fellowship.
1995 - 1997	Associate Professor of Animal Breeding , University of Guelph, Canada Quantitative genetics and breeding strategies with application to dairy cattle. Undergraduate teaching.
1997 - 2002	Associate Professor of Animal Breeding , Iowa State University, Ames, IA Research on QTL mapping, marker-aided selection, breeding strategies, with applications to swine (75%). Graduate and undergraduate teaching (25%).
2002 - 2013	Professor of Animal Breeding , Iowa State University, Ames, IA Research on QTL mapping, marker-aided selection, breeding strategies (75%). Graduate and undergraduate teaching (25%).
2002 - present	Section leader , Animal Breeding and Genetics, Iowa State University, Ames, IA
2013 - present	C.F. Curtiss Distinguished Professor , Iowa State University, Ames, IA Research (75%) on integration of quantitative genetics and genomics; genetic aspects of feed efficiency and health; breeding strategies. Graduate and undergraduate teaching (25%).

Affiliations

American Society of Animal Science American Dairy Science Association Gamma
Poultry Science Association World Poultry Science Association Sigma Delta

Awards and Honors

- LeClerg Lecturer, University of Maryland (2014)
- C.F. Curtiss Distinguished Professor (2013)
- ISU CALS Team Award for RFI group (group leader) (2012)
- ISU Margaret Ellen White Graduate Faculty Award (2012)
- ISU Gamma Sigma Delta Research Award (2012)
- Rockefeller Prentice Memorial Award in Animal Breeding & Genetics, Amer.Soc.Anim.Sci. (2007)
- A.B. Chapman Lecturer, University of Wisconsin, Madison (2005)
- J. L. Lush Award in Animal Breeding, American Dairy Science Association (2004)
- Outstanding Research Award, College of Agriculture, Iowa State University (2004)
- ADSA/ASAS travelling fellow to European Association of Animal Production (2003)
- Special recognition for quality of promotion dossier, President, Iowa State University (2002)
- Invited paper in Nature Reviews: Genetics (2002, Vol. 3: 22-32).
- Travelling Fellow, Assoc. for Advancement of Animal Breeding and Genetics, Australia (1999).
- NATO Fellowship, Dept. Animal Breeding & Genetics, Agric. Univ., Wageningen (1996)
- New Faculty Support Program Award, Natural Sci. & Engineering Res. Council, Canada (1992)

International Professional Experience

Editorial activities:

- 2012 – present Editor-in-Chief, Genetics Selection Evolution, published by BMC
- 2010 – 2012 Executive Editor, Genetics Selection Evolution, published by BMC
- 2002 – 2006 Section Editor, Animal Science, British Society of Animal Science
- 1992 - present Reviewer of grant proposals to Natural Sciences and Engineering Research Council of Canada, Dairy Cattle Genetics Research and Development Council of Canada, USDA-BARD, USDA-NRI, Biotechnology and Biological Sciences Research Council of the UK
- 1989 - present Peer reviewer of manuscripts for Journal of Animal Science, Journal of Dairy Science, PLoS One, Livestock Science, Genetics, Heredity, Genetical Research, Genetics Selection and Evolution, Animal Genetics, BMC Genomics, and others.

Organization of scientific meetings:

- 2011-2012 Chair Gordon Conference on Quantitative Genetics and Bioinformatics
- 2009-2011 Vice Chair Gordon Conference on Quantitative Genetics and Bioinformatics
- 2008 Co-organizer of the Jay Lush International symposium, Ames, IA, April, 2008
- 1999 Co-organizer for international conference 'From Jay Lush to Genomics: Visions for Animal Breeding and Genetics', Ames, IA, May 16-18.
- 1997 Scientific Program Chair for session at the 6th and 10th World Congress on Genetics Applied to Livestock Production
- 1994 Assist organization 4th Wldl Congr. Genetics Appl. Livest. Prod. Guelph, Canada

International scientific reviews and examinations:

- 2015 Chair of review committee of Animal Genetics Division of INRA, France
- 1999 - present External PhD examiner Australia (4), Canada (1), Netherlands (4), Israel (1), Norway (1).
- 1998 and 2008 Member, Scientific Review Committee, Animal Science Institute ID-DLO, Lelystad, the Netherlands

International Teaching Experience

- Breeding program design with genomic selection (2014) University of New England, Australia, 1-week course, co-instructor.
- Genomic selection in livestock (2013) Quebec City, Canada, 1-week course, Organizer and co-instructor.
- Quantitative Genetics with Integration of Molecular Genetics (2008) 2-week NOVA course, University of Helsinki, Finland, Instructor
- Applied economic aspects of animal breeding programs (2001) University of Guelph, Canada, Instructor
- Quantitative genetics for new technologies in animal breeding (1999), University of New South Wales, Australia, co-instructor

A. *Publications in peer-reviewed scientific journals* H-factor (ISI) = 43. Total number of citations = 5,973 (5,579 excluding self citations). Citations by article in brackets [#]

- A.1. Heidaritabar, M., A. Wolc, J. Arango, J. Zeng, P. Settar, J. E. Fulton, N.P. O'Sullivan, J.W.M. Bastiaansen, R.L. Fernando, D.J. Garrick, J.C.M. **Dekkers**. 2016. Impact of fitting dominance and additive effects on accuracy of genomic prediction of breeding values in egg-laying chickens. *J. Animal Breeding and Genetics* (Submitted).
- A.2. Fernando, R., A. Toosi, A. Wolc, D. Garrick, and J. **Dekkers**. 2016. Application of whole-genome prediction methods for genome-wide association studies: a Bayesian approach. *J. Agricultural, Biological, and Environmental Statistics* (Submitted).
- A.3. Weng, Z., A. Wolc, X. Shen, R.L. Fernando, J.C.M. **Dekkers**, J. Arango, P. Settar, J.E. Fulton, N.P. O'Sullivan and D.J. Garrick. 2016. Effects of Number of Training Generations for Genomic Prediction in Various Traits in a Layer Chicken Population. *Genet. Selec. Evol.* (Accepted)
- A.4. Schroyen M, Eislely C, Koltes JE, Fritz-Waters E, Choi I, Plastow G, Guan L, Stothard P, Bao H, Kommadath A, Reecy JM, Lunney JK, Rowland RRR, **Dekkers JCM**, Tuggle CK. 2016. Bioinformatic analyses in early host response to Porcine Reproductive and Respiratory Syndrome virus PRRSV reveals pathway differences between pigs with alternate genotypes for a major host response QTL. *BMC Genomics* (Accepted).
- A.5. Grubbs, J.K., J.C.M. **Dekkers**, E. Huff-Lonergan, C.K. Tuggle, and S.M. Lonergan Identification of potential serum biomarkers to predict feed efficiency in young pigs. *J. Animal Sci.* (Accepted).
- A.6. Wolc, A., A. Kranis, J. Arango, P. Settar, J.E. Fulton, N.P. O'Sullivan, A. Avendano, K.A. Watson, J.M. Hickey, G. de los Campos, R.L. Fernando, D.J. Garrick, and J.C.M. **Dekkers**. 2016. Implementation of Genomic Selection in the Poultry Industry. *Animal Frontiers* 6:1 doi:10.2527/af.2016-0004
- A.7. Schroyen, M., J.P. Steibel, J.E. Koltes, I. Choi, N.E. Raney, C. Eislely, E. Fritz-Waters, J.M. Reecy, J.C.M. **Dekkers**, R.R.R. Rowland, J.K. Lunney, C.W. Ernst, and C.K. Tuggle. 2015. Whole blood microarray analysis of pigs showing extreme phenotypes after a porcine reproductive and respiratory syndrome virus infection. *BMC Genomics* 16:516.
- A.8. Niederwerder M.C., B. Bawa, N.V.L. Serão, B.R. Tribble, M.A. Kerrigan, J.K. Lunney, J.C.M. **Dekkers**, and R.R.R. Rowland. 2015. Vaccination with a porcine and reproductive and respiratory syndrome (PRRS) modified live virus vaccine followed by challenge with PRRSV and porcine circovirus type 2 (PCV2) protects against PRRS but enhances PCV2 replication and pathogenesis. *Clinical and Vaccine Immunology* 22: 1244-1254.
- A.9. Waide, E.H., J.C.M. **Dekkers**, J.W. Ross, R.R.R. Rowland, C.R. Wyatt, C.L. Ewen, A.B. Evans, D.M. Thekkoot, N.J. Boddicker, N.V.L. Serão, N.M. Ellinwood, and C.K. Tuggle. Not all SCID pigs are created equally: Two independent mutations in the *Artemis* gene cause Severe Combined

- Immunodeficiency (SCID) in pigs. *J Immunol* 195: 3171-3179. [1]
- A.10. Wolc, A., Zhao, H.H., Arango, J., Settar, P., Fulton, J.E., O’Sullivan, N.P., Preisinger, R., Stricker, C., Habier, D., Fernando, R., Garrick, D.J., Lamont, S.J., **Dekkers, J.C.M.** 2015. Response and inbreeding from a genomic selection experiment in layer chickens. *Genet Selec Evolution* 47:59
- A.11. Dunkelberger, J.R., N.J. Boddicker, N.V.L. Serao, J.M. Young, R.R.R. Rowland, and J.C.M. **Dekkers.** 2015. Response of pigs divergently selected for residual feed intake to experimental infection with the PRRS virus. *Livestock Sci.* 177: 132-141. [1]
- A.12. Mpetile, Z., J.M. Young, N.K. Gabler, J.C.M. Dekkers, and C.K. Tuggle. 2015. Assessing peripheral blood cell profile of Yorkshire pigs divergently selected for residual feed intake. *J. Animal Sci.* 93:892-899. [1]
- A.13. Fu, W., J.C.M. **Dekkers**, W.R. Lee, and B. Abasht. 2015. Linkage disequilibrium in crossbred and pure line chickens. *Genet Sel Evol.* 47: 11. [1]
- A.14. Arkfeld, E.K., J.M. Young, R.C. Johnson, C.A. Fedler, K. Prusa, J.F. Patience, J.C.M. **Dekkers**, N.K. Gabler, S.M. Lonergan and E. Huff-Lonergan. 2015. Composition and quality characteristics of carcasses from pigs divergently selected for residual feed intake on high or low energy diets. [1]
- A.15. Ewen, C.L., A.G. Cino-Ozuna, H. He, M.A. Kerrigan, J.C.M. **Dekkers**, C.K. Tuggle, R.R.R. Rowland, C.R. Wyatt. 2015. Analysis of blood leukocytes in a naturally occurring immunodeficiency of pigs shows the defect is localized to B and T cells. *Vet. Immun. Immunopath* 162:174-179. [2]
- A.16. Koltjes JE, E Fritz-Waters, CJ Easley, I Choi, H Bao, A Kommadath, NVL Serão, NJ Boddicker, SM Abrams, M Schroyen, H Loyd, CK Tuggle, GS Plastow, L Guan, P Stothard, JK Lunney, P Liu, S Carpenter, RRR Rowland, JCM **Dekkers**, JM Reecy (2015) Identification of a putative quantitative trait nucleotide in Guanylate Binding Protein 5 (GBP5) for host response to Porcine Respiratory and Reproductive Syndrome (PRRS) virus infection. *BMC Genomics*, 16:412. [1]
- A.17. Grubbs, J.K., C.K. Tuggle, J.C.M. **Dekkers**, N.J. Boddicker, Y.T. Nguyen, E. Huff-Lonergan, D. Nettleton, and S.M. Lonergan. 2015. Investigation of the efficacy of albumin removal procedures on porcine serum proteome profile. *J. Anim. Sci.* 93: 1592-1598.
- A.18. Chen, N., J.C.M. **Dekkers**, C.L. Ewen, R.R.R. Rowland. 2015. Porcine reproductive and respiratory syndrome virus replication and quasispecies evolution in pigs that lack adaptive immunity. *Virus Research* 195:246-249.
- A.19. Serão, NVL, O Matika, RA Kemp, J Harding, SC Bishop, GS Plastow, JCM **Dekkers.** 2014. Genetic analysis of reproductive traits and antibody response in a PRRS outbreak herd. *J. Animal Sci.* 92: 2905-2921. [6]
- A.20. Garrick, D., J. **Dekkers**, and R. Fernando. 2014. The evolution of methodologies for genomic prediction. *Livestock Science* 8: 2905-2921.
- A.21. Wolc, A., J. Arango, T. Jankowski, P. Settar, J.E. Fulton, N.P. O’Sullivan, R. Preisinger, R. Fernando, D.J. Garrick and J.C.M **Dekkers.** 2014. Genome-wide association study for egg production and quality in layer chickens. *J. Anim. Breed. Genet.* 131: 173-182. [9]
- A.22. Grubbs, J.K., E. Huff-Lonergan, N.K. Gabler, J.C.M. **Dekkers**, and S.M. Lonergan. 2014. Liver and skeletal muscle mitochondria proteomes are altered in pigs divergently selected for residual feed intake. *J. Anim. Sci.* 92: 1995-2007. [2]
- A.23. Fernando, R.L., J.C.M. **Dekkers** and D.J. Garrick. 2014. A class of Bayesian methods to combine large numbers of genotyped and non-genotyped animals for whole genome analyses. *Genetics Selection Evolution* 46: 50. [7]
- A.24. Abell CE, Dekkers JC, Rothschild MF, Mabry JW, Stalder KJ. 2014. Total cost estimation for implementing genome-enabled selection in a multi-level swine production system. *Genetics Selection Evolution.* 46:32. [2]
- A.25. Boddicker, N., A. Bjorquist, R.R.R. Rowland, J.K. Lunney, J.M. Reecy, and J.C.M. **Dekkers.** 2014.

- Genome-wide association and genomic prediction for host response to PRRSV infection. *Genetics Selection Evolution*. 46:18. [8]
- A.26. Ros-Freixedes, R., L.J. Sadler, S.K. Onteru, R.M. Smith, J.M. Young, A.K. Johnson, S.M. Lonergan, E. Huff-Lonergan, J.C.M. **Dekkers**, and M.F. Rothschild. 2014. Relationship between gilt behavior and meat quality using principal component analysis. *Meat Sci*. 96: 264-269. [1]
- A.27. Boddicker, N., D.J. Garrick, R.R.R. Rowland, J.K. Lunney, J.M. Reecy, and J.C.M. **Dekkers**. 2014. Validation and further characterization of a major quantitative trait locus associated with host response to experimental infection with porcine reproductive and respiratory syndrome virus. *Animal Genetics*. 45: 48-58. [4]
- A.28. Kim, J.J. and J.C.M. **Dekkers**. 2013. A Least Squares Regression Model to Detect Quantitative Trait Loci with Polar Overdominance in a Cross of Outbred Breeds: Simulation. *Asian-Austr. J. Anim. Sci*. 26: 1536-1544
- A.29. Cheng, Y., S. Rachagani, A. Canovas, M.S. Mayes, G. Tait, J.C.M. **Dekkers** and J.M. Reecy. 2013. Body composition and gene expression QTL mapping in mice reveals imprinting and interaction effects. *BMC Genetics* 14:103. [3]
- A.30. Wolc, A., J. Arango, T. Jankowski, P. Settar, J.E. Fulton, N.P. O'Sullivan, R. Fernando, D.J. Garrick and J.C.M **Dekkers**. 2013. Genome-wide association study for Marek's disease mortality in layer chickens. *Avian Diseases* 57:395-400. [4]
- A.31. Onteru, S.K., D.M. Gorbach, J.M. Young, D.J. Garrick, J. **Dekkers**, and M.F. Rothschild. 2013. Whole Genome Association Studies of Residual Feed Intake and Related Traits in the Pig. *PLOS One* 8(6): e61756. [16]
- A.32. Nielsen, M. K., M. D. MacNeil, J. C. M. **Dekkers**, D. H. Crews, Jr., T. A. Rathje, R. M. Enns, and R. L. Weaber. 2013. Review: Life-cycle, total-industry genetic improvement of feed efficiency in beef cattle: Blueprint for the Beef Improvement Federation. *Professional Animal Scientist*. 2013; 29(6): p. 559-565. [1]
- A.33. Zeng, J., Toosi, A., Fernando, R.L., **Dekkers**, J.C.M., Garrick, D.J., 2013. Genomic selection of purebred animals for crossbred performance in the presence of dominant gene action. *Genet. Sel. Evol.* 45: 11. [20]
- A.34. Wang, C., Habier, D., Peiris, B.L., Wolc, A., Kranis, A., Watson, K.A., Avendano, S., Garrick, D.J., Fernando, R.L., Lamont, S.J., and **Dekkers**, J.C.M.. 2013. Accuracy of genomic prediction using an evenly spaced, low-density single nucleotide polymorphism panel in broiler chickens. *Poultry Sci*. 92: 1712-1723. [6]
- A.35. Wolc, A., Arango, J., Settar, P., Fulton, J.E., O'Sullivan, N.P., Preisinger, R., Fernando, R., Garrick, D.J., **Dekkers**, J.C.M. 2013. Analysis of egg production in layer chickens using a random regression model with genomic relationships. *Poultry Sci*. 92: 1486-1491. [4]
- A.36. Wolc, A., J. Arango, T. Jankowski, P. Settar, J.E. Fulton, N.P. O'Sullivan, R. Fernando, D.J. Garrick and J.C.M **Dekkers**. 2013. Pedigree and genomic analyses of feed consumption, feed conversion ratio and residual feed intake in laying hens. *Poultry Science* 92:2270-2275. [3]
- A.37. Grubbs, J.K., Fritchen, A.N., Huff-Lonergan, E., **Dekkers**, J.C.M., Gabler, N.K., Lonergan, S.M. 2013. Divergent genetic selection for residual feed intake impacts mitochondria reactive oxygen species production in pigs. *J. Anim. Sci*. 91: 2133-2140. [10]
- A.38. Mani, V., Harris, A.J., Keating, A.,F., Weber, T.E., **Dekkers**, J.C.M., Gabler, N.K. 2013. Intestinal integrity, endotoxin transport and detoxification in pigs divergently selected for residual feed intake. *J. Anim. Sci*. 91: 2142-2150. [11]
- A.39. Cruzen SM, Harris AJ, Hollinger K, Punt RM, Grubbs JK, Selsby JT, **Dekkers** JC, Gabler NK, Lonergan SM, Huff-Lonergan E. 2013. Evidence of decreased muscle protein turnover in gilts selected for low residual feed intake. *J. Animal Sci*. 91:4007-4016. [10]
- A.40. Abell, C.E., Mabry, J.W., **Dekkers**, J.C.M., Stalder, K.J. 2013. Relationship between litters per sow per year sire breeding values and sire progeny means for farrowing rate, removal parity and lifetime born

- alive. *J. Anim. Breed. Genet.* 130: 64-71. [1]
- A.41. Harris, A. J., J. F. Patience, S. M. Lonergan, J. C. M. **Dekkers** and N. K. Gabler. 2012. Improved nutrient digestibility and retention partially explains feed efficiency gains in pigs selected for low residual feed intake. *J Anim Sci* 90: 164-166. [9]
- A.42. Rakhshandeh, A., J. C. M. **Dekkers**, B. J. Kerr, T. E. Weber, J. English and N. K. Gabler. 2012. Effect of immune system stimulation and divergent selection for residual feed intake on digestive capacity of the small intestine in growing pigs. *J Anim Sci.* 90 (Suppl. 4): 233-235. [9]
- A.43. Rowland R, Lunney JK, **Dekkers** JCM. 2012 Control of porcine reproductive and respiratory syndrome (PRRS) through genetic improvements in disease resistance and tolerance. *Frontiers in Livestock Genomics*. http://www.frontiersin.org/Livestock_Genomics/10.3389/fgene.2012.00260/
- A.44. Schurink, A., A. Wolc, B.J. Ducro, K. Frankena, D.J. Garrick, J.C.M. **Dekkers** and J.A.M. van Arendonk. 2012. Genome-wide association study of insect bite hypersensitivity in two horse populations in the Netherlands. *Genetics Selection Evolution* 44:31, doi:10.1186/1297-9686-44-31. [10]
- A.45. Wyatt, C.R, A.G. Cino Ozuna, R.R.R. Rowland, J. C. M. **Dekkers**, E.H. Waide, and C.K. Tuggle. 2013. Characterization of a naturally occurring Severe Combined Immunodeficiency in pigs. *J. Immunology* 190:141.24.
- A.46. Cino Ozuna, A.G., R.R.R. Rowland, J.C. Nietfeld, J.C.M. **Dekkers**, and C.R. Wyatt. 2013. Preliminary findings of a previously unrecognized porcine primary immunodeficiency disorder. *Veterinary Pathology* 50: 144-146. [4]
- A.47. Spurlock, D. M.; **Dekkers**, J. C. M.; Fernando, R.; Koltjes, D. A.; Wolc, A. 2012. Genetic parameters for energy balance, feed efficiency, and related traits in Holstein cattle. *J. Dairy Sci.* 95: 5393-5402. [20]
- A.48. Cai, W.; Kaiser, M. S.; **Dekkers**, J. C. M. 2012. Bayesian analysis of the effect of selection for residual feed intake on growth and feed intake curves in Yorkshire swine. *J. Anim. Sci.* 90: 127-141. [1]
- A.49. Wolc, A., J. Arango, P. Settar, J.E. Fulton, N.P. O’Sullivan, R. Preisinger, D. Habier, R. Fernando, D.J. Garrick, W.G. Hill and J.C.M. **Dekkers**. 2012. Genome-wide association analysis and genetic architecture of egg weight and egg uniformity in layer chickens. *Animal Genetics* 47: 87-96. [25]
- A.50. Basel, M.T., S. Balivada, A.P. Beck, M.A. Kerrigan, M.M. Pyle, J.C.M. **Dekkers**, C.R. Wyatt, R.R.R. Rowland, D.E. Anderson, S.H. Bossmann, and D.L. Troyer. 2012. Human Xenografts are not rejected in a naturally occurring immunodeficient porcine line: a human tumor model in pigs. *BioResearch Open Access*. 1: 63-68. [2]
- A.51. **Dekkers**, J.C.M., 2012. Application of genomics tools to animal breeding. *Curr. Genomics* 13: 207-212. [7]
- A.52. Piyasatian, N., R.L. Fernando, and J.C.M. **Dekkers**. 2012. QTL detection and marker-assisted composite line development. *Livestock Sci.* 143: 233-241.
- A.53. Powell, J. E., Kranis, A., Floyd, J., **Dekkers**, J. C. M., Knott, S. and Haley, C. S. 2012. Optimal use of regression models in genome-wide association studies. *Animal Genetics*, 43: 133–143. [5]
- A.54. Wolc, A., J. Arango, P. Settar, N.P. O’Sullivan, V.E. Olori, I.M.S. White, W.G. Hill, and J.C.M. **Dekkers**. 2012. Genetic parameters of egg defects and egg quality in layer chickens. *Poultry Sci.* 91: 1292-1298. [9]
- A.55. Abell, C.E., J.W. Mabry, J.C.M. **Dekkers**, and K.J. Stalder. 2012. Genetic and phenotypic relationships among reproductive and post-weaning traits from a commercial swine breeding company. *Livestock Science* 145: 183-188. [3]
- A.56. Sun, X., Qu, L., Garrick, D.J., **Dekkers**, J.C.M., Fernando, R.L. 2012. A Fast EM Algorithm for BayesA-Like Prediction of Genomic Breeding Values. *PLOS ONE* 7:11 [6]
- A.57. Qu, L., D. Nettleton, and J.C.M. **Dekkers**. 2012. A Hierarchical Semiparametric Model for Incorporating Intergene Information for Analysis of Genomic Data. *Biometrics* 68: 1168-1177. [1]

- A.58. Qu, L., D. Nettleton, and J.C.M. **Dekkers**. 2012. Improved estimation of the noncentrality parameter distribution from a large number of *t*-statistics, with applications to false discovery rate estimation in microarray data analysis. *Biometrics* 68: 1178-1187. [2]
- A.59. Boddicker N, Waide EH, Rowland, RR, Lunney JK, Garrick DJ, Reecy JM, and **Dekkers** JCM. 2012. Evidence for a major QTL associated with host response to PPRS virus challenge. *J. Anim.Sci*, 90:1733-1746 [41]
- A.60. Saatchi, M., M.C. McClure, S.D. McKay, M.M. Rolf, J.W. Kim, J.E. Decker, T.M. Taxis, R.H. Chapple, H.R. Ramey, S.L. Northcutt, S. Bauck, B. Woodward, J.C.M. **Dekkers**, R.L. Fernando, R.D. Schnable, D.J. Garrick, and J.F. Taylor. 2011. Accuracies of genomic breeding values in American Angus beef cattle using K-means clustering for cross-validation. *Genet. Sel. Evol.* 43:40. [55]
- A.61. Cai, W, M.S. Kaiser, and J.C.M. **Dekkers**. 2011. Genetic analysis of longitudinal measurements of performance traits in selection lines for residual feed intake in Yorkshire swine. *J. Anim. Sci.* 89: 1270-1280. [3]
- A.62. Uthe, J.J., Qu, L., Couture, O., Bearson, S.M.D., O'Connor, A.M., McKean, J.D., Nettleton, D., Torres, Y.R, **Dekkers**, J.C.M., Nettleton, D., Tuggle, C.K. 2011 Use of bioinformatic SNP predictions in differentially expressed genes to find SNPs associated with Salmonella colonization in swine. *J. Anim. Breed. Genet.* 128: 354-365. [6]
- A.63. Wolc, A., J. Arango, P. Settar, J.E. Fulton, N.P. O'Sullivan, R. Preisinger, D. Habier, R. Fernando, D.J. Garrick, J.C.M. **Dekkers**. 2011. Persistence of accuracy of genomic estimated breeding values over generations in layer chickens. *Genet. Sel. Evol.* 43:23 DOI: 10.1186/1297-9686-43-23. [28]
- A.64. Boddicker, N., N.K. Gabler, M.E. Spurlock, D. Nettleton and J.C.M. **Dekkers**. 2011. Effects of ad libitum and restricted feed intake on early production performance and body composition of Yorkshire pigs selected for reduced residual feed intake. *Animal* 5: 1344-1353. [11]
- A.65. Cheng Y., S. Rachigani, J.C.M. **Dekkers**, M.S. Mayes, R. Tait, et al. 2011. Mapping genetic loci that interact with myostatin to affect growth traits. *Heredity* 107: 565-573. [2]
- A.66. Peiris, L., Ralph, J., Lamont, S.J. and **Dekkers**, J.C. 2011. Predicting allele frequencies in DNA pools using high density SNP genotyping data. *Animal Genetics* 42: 113-116. [5]
- A.67. Cai, W., H. Wu, and J.C.M. **Dekkers**. 2011. Longitudinal analysis of body weight and feed intake in selection lines for residual feed intake in pigs. *Asian-Aust. J. Anim. Sci.* 24: 17-27 [4]
- A.68. Uthe, J.J., Bearson, S.M.D., **Dekkers**, J.C.M., Qu, L., Nettleton, D., Rodriguez Torres, Y., O'Connor, A.M., McKean, J.D., Tuggle, C.K. 2011. Integrating comparative expression profiling data with association of SNPs to salmonella shedding for improved food safety and porcine disease resistance. *Animal Genetics* 42: 521-534. [8]
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