

Jack C. M. Dekkers

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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%).

Awards and Honors

- LeClerc 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)

Teaching Experience

Undergraduate

- Livestock&Poultry Breeding (1992 – 1997), University of Guelph
- Livestock Improvement Through Animal Breeding (1997), ISU
- Issues Facing Animal Science (2000), ISU
- Academic advisor for 15-20 undergraduate students (1999 - present), ISU

Graduate

- Animal Breeding Strategies (1998, 1999, 2001, 2003, 2005, 2007, 2010, 2013, 2015)
- Advanced Statistical Methods for Animal Breeding, co-instructor (2002)
- Applied Animal Breeding (1999)
- Population&Quantitative Genetics for Breeding: co-instructor '03-'06; sole instructor '06-'14
- Applied Beef and Dairy Cattle Breeding – course coordinator and co-instructor (2012)

On-line Graduate

- Introduction to Marker Association Analysis and QTL Detection. Animal Breeding Online, '13,'14,'15.
- Prediction and Control of Inbreeding in Breeding Programs. Animal Breeding Online, '14

Post-graduate short courses/workshops

- Breeding program design with genomic selection (2014, University of New England, Australia; 2015, Iowa State University) 1-week course, Co-instructor
- Genomic selection in livestock (2013) 1-week course. Quebec City, Canada. Organizer and co-instructor.
- Genomic selection in livestock (2012) 1-week course. ASAS/ADSA. Organizer and co-instructor.
- Genomic selection in livestock (2010, 2012, 2013) 1-week course. Organizer and co-instructor.
- Use of high-density SNP genotyping data for genetic improvement of livestock (2009) 2-week course. ISU. Organizer and co-instructor.
- Quantitative Genetics with Integration of Molecular Genetics (2008) 2-week NOVA course, University of Helsinki, Finland, Instructor
- Design and economic of animal breeding strategies (2003), ISU, Organizer and instructor
- Applied economic aspects of animal breeding programs (2001) Univ. Guelph, Canada, Instructor

- Quantitative genetics for new technologies in animal breeding (1999), University of New South Wales, Australia, co-instructor
- Organizer Animal Breeding and Genetics summer short courses (two in 2004; three in 2005; two in 2007, 2009, 2010), ISU

Industry short courses/workshops

- CPAB industry short courses (1996-1997), co-instructor, University of Guelph.
- Molecular methods in plant breeding (2000-2003) (½ day co-instructor), Agronomy Dept, ISU
- USDA-IFAFS-NSIF Workshop on Molecular Genetics (2003, 1 day), Des Moines, Iowa
- Training Workshop on QTL mapping and marker-assisted selection, Canadian Center for Swine Improvement (2004, 1 day), Ottawa, Canada

Significant Research Contributions

- Methods for economic evaluation of breeding programs in competitive markets
- Methods for simulation of breeding programs that combine stochastic and deterministic models
- Design and evaluation of dairy breeding programs to capitalise on reproductive technologies
- Analytical methods to derive asymptotic responses to selection on BLUP breeding values that account for the effects of selection on genetic variance
- Effects associated with genetic markers under the infinitesimal genetic model
- Genetic analysis and national genetic evaluation systems for somatic cell score, longevity, and dystocia for dairy cattle.
- Derivation of economic values and development of total economic index for dairy bulls in Canada
- Use of random regression models for analysis of test-day data
- Optimal selection on non-linear profit functions over multiple generations through the use of optimal control theory
- Marker-assisted selection and optimal selection to resolve the conflict between short- versus long-term responses with marker-assisted selection
- Statistical methods for QTL mapping and their application to detect genes and QTL in pigs.
- Evaluation of measures of linkage disequilibrium
- Comparison of methods for linkage disequilibrium analysis
- Use of high-density SNP genotyping for genomic selection, including improvement of crossbred performance
- Implementation of genomic selection using low-density SNP panels
- Experimental evaluation of genomic selection in layer chickens
- Selection index methods for evaluation of marker-assisted and genomic selection
- Genetic and biological aspects of residual feed intake in pigs; development of RFI research consortium.
- Genome-wide association study for host response to PRRS in pigs; Discovery of major QTL on chromosome 4.
- Identification of Severe Combined Immuno-Deficiency (SCID) in pigs and development of SCID pigs for biomedical research.

Patents

Dekkers, J.C.M., C.K. Tuggle, E.H. Waide, J.W. Ross, N.M. Ellinwood, and M. Schroyen. 2015. Genetic test and genetic basis for SCID in pigs. US Patent Application # 14/592,586 (pending).

- 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. 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.* (Submitted)
- A.3. 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.4. 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.5. Schroyen, M., J.P. Steibel, J.E. Koltjes, I. Choi, N.E. Raney, C. Eisley, 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.6. 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.7. 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.8. 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.9. Dunkelberger, J.R., N.J. Boddicker, N.V.L. Sero, 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.10. 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.11. 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.12. 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.13. 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.14. Koltjes JE, E Fritz-Waters, CJ Eislely, 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.15. 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.16. 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.17. 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.18. Garrick, D., J. **Dekkers**, and R. Fernando. 2014. The evolution of methodologies for genomic prediction. *Livestock Science* 8: 2905-2921.
- A.19. 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.20. 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.21. 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.22. 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.23. 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.24. 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.25. 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.26. 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.27. 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.28. 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.29. 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.30. 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.31. 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.32. 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.33. 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.34. 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.35. 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.36. 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.37. 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.38. 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.39. 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.40. 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.41. 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.42. 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.43. 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.44. 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.45. 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.46. 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.47. 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.48. 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.49. **Dekkers**, J.C.M., 2012. Application of genomics tools to animal breeding. *Curr. Genomics* 13: 207-212. [7]
- A.50. 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.51. 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.52. 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.53. 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.54. 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.55. 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.56. 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.57. 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.58. 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.59. 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.60. 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.61. 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]
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B. *Books and Book Chapters*

Books

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C. Invited Presentations at (Inter)national Scientific Meetings

- C.1. **Dekkers**, J.C.M. 2015. Genetics of host resistance to PRRS and PCV2. North American PRRS Symposium, Chicago, IL.
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- C.3. **Dekkers**, J.C.M. 2015. Genomic selection for crossbred performance in livestock. Genetics Society 2015 Spring Meeting, Roslin Institute, Edinburgh, Scotland.
- C.4. **Dekkers**, J.C.M. 2014. Genetics of host response to PRRS. North American PRRS Symp., Chicago, IL.
- C.5. **Dekkers**, J.C.M. 2014. Genetic basis or host response to PRRS virus infection in Pigs. 23rd International Pig Veterinary Society Congress, Cancun, Mexico.
- C.6. **Dekkers**, J.C.M., and J.H.J. van der Werf. Breeding goals and phenotyping programs for multi-trait improvement in the genomics era. 10th World Congress on Genetics Applied to Livestock Production, Vancouver, Canada
- C.7. **Dekkers**, J.C.M. 2014. Genomic Prediction Strategy and Applications. W365 Plant and Animal Genome meetings, San Diego.
- C.8. Wolc A., Arango J., Settar P., Fulton J. E., O'Sullivan N. P., Preisinger R., Habier D., Fernando R., Garrick D. J., Lamont S. J., and **Dekkers** J. C. M. 2013. Genomic selection in layer chickens outperforms pedigree-based selection. ASAS/ADSA 45th Meeting Midwestern Sectional Scientific Sessions and Business Meeting. 11-13.03.2013 - Des Moines. USA
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- C.15. **Dekkers**, J.C.M., H.H. Zhao, and R.L. Fernando. 2006. Linkage disequilibrium mapping in livestock. 8th World Congress on Genetics Applied to Livestock Production. Belo Horizonte, Brazil.
- C.16. **Dekkers**, J.C.M. 2006. Strategies for the use of molecular information in breeding programs. British Society of Animal Science Annual Meeting, York, UK.
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- C.35. **Dekkers**, J.C.M. Genetic improvement of dairy cattle for profitability. Canadian Society of Animal Science. 1995, Ottawa, Canada.
- C.36. **Dekkers**, J.C.M. and L.K. Jairath. Requirements and uses of genetic evaluations for conformation and herd life. Proc. 5th World Congr. Genetics Applied to Livestock Production, 1994, Guelph, Canada, Vol. 17:61-68.
- C.37. **Dekkers**, J.C.M. Structure of breeding programs to capitalize on reproductive technology for genetic improvement. A.D.S.A. August 13, 1991, Logan, Utah.