

## Rohan L. Fernando

**office:**

Iowa State University  
Department of Animal Science  
225 Kildee Hall  
Ames, IA 50011  
tel: (515) 294-5348  
fax: (515) 294-9150  
email: rohan@iastate.edu  
<http://www.public.iastate.edu/> ans

**home:**

3128 Kingman Road  
Ames, IA 50014  
tel: (515) 296-0126

**Date of Birth:** January 19, 1952

### Academic Positions

- Research Assistant, Department of Animal Science, University of Illinois, 1978–1984.
- Research and Teaching Associate, Department of Animal Sciences, University of Illinois, 1984–1985.
- Assistant Professor of Biometry and Computer Applications, Department of Animal Sciences, University of Illinois, 1985–1991.
- Sabbatical Leave, Department of Biometry and Genetics, Louisiana State University, Medical Center, 1991–1992.
- Associate Professor of Biometry and Computer Applications, Department of Animal Sciences, University of Illinois, 1991–1996.
- Professor of Quantitative Genetics, Department of Animal Science, Iowa State University, 1996–

### Education

- Diploma in Agriculture (First Class Honors) Aquinas College, Colombo, Sri Lanka. 1972–1975 (graduated first in class).
- B.S. (Summa Cum Laude) Agricultural Science with emphasis in animal science, California State University, Fresno. 1976–1978 (graduated first in class).
- M.S. Animal Science, University of Illinois at Urbana-Champaign. 1978–1981.

- Participated in the 3rd International Summer School in Agriculture “Modern Techniques in Animal Breeding”, Dublin, Ireland. June 26 – July 9, 1983.
- Ph.D. Animal Science, University of Illinois at Urbana-Champaign. 1981–1984.

## Publications

\* Indicates the research was directed by Rohan L. Fernando while first author was a graduate student, postdoctoral associate or visiting scientist.

## Chapters in Books

1. Fernando, R. L. and D. Gianola. 1990. Optimal designs for sire evaluation schemes. In “Advances in Statistical Methods for Genetic Improvement of Livestock”. Springer-Verlag, New York.
2. Fernando, R. L. and D. Gianola. 1990. Statistical inferences in populations undergoing selection or non-random mating. In “Advances in Statistical Methods for Genetic Improvement of Livestock”. Springer-Verlag, New York.
3. Gianola, D., S. Im, R. L. Fernando and J. L. Foulley. 1990. Mixed model methodology and the Box-Cox theory of transformations: a Bayesian approach. In “Advances in Statistical Methods for Genetic Improvement of Livestock”. Springer-Verlag, New York.
4. Weller, J. and R. L. Fernando. 1991. Strategies for the improvement of animal production using marker assisted selection. In “Gene Mapping: Strategies, Techniques and Applications”. Marcel Dekker, New York.
5. \*Fernández, S. A., R. L. Fernando and A. L. Carriquiry. 2000. “Analysis in complex pedigrees. Bayesian Case Studies”, pages 307-326. Springer-Verlag.
6. \*Fernández, S. A., R. L. Fernando, A. L. Carriquiry. 2001. An algorithm to sample unobservable genotypes in complex pedigrees. In “Bayesian Methods with Applications to Science, Policy and Official Statistics (Selected papers from ISBA 2000)”, Monographs in Official Statistics, Eurostat, 125-134.
7. Fernando, R.L. and L.R. Totir. 2003. Incorporating Molecular Information in Breeding Programs: Methodology. In “Poultry Breeding and Biotechnology”. CABI Publishing, Cambridge.
8. Fernando, R. L. Kinship and Inbreeding. 2003. In “Encyclopedia of the Human Genome”. Nature Publishing Group, New York.

9. Stricker, C. and R. L. Fernando. 2003. Segregation analysis software. In “Encyclopedia of the Human Genome”. Nature Publishing Group, New York.
10. \*Totir, R. and R. L. Fernando. 2005. Selectia asistată de markeri. In “Programe De Ameliorare Genetică Zootehnie”. Editura Ceres, Bucharest.
11. Abraham, K. J. and R. L. Fernando. 2012. Applications of Graphical Clustering Algorithms in Genome Wide Association Mapping, New Frontiers in Graph Theory, Dr. Yagang Zhang (Ed.), ISBN: 978-953-51-0115-4, InTech.
12. Fernando R.L. and D.J. Garrick. 2013. Bayesian methods applied to GWAS. In “Genome-Wide Association Studies and Genomic Prediction”. Gondro, C., J.H.J. van der Werf and B. Hayes (2013). Springer Series: Methods in Molecular Biology, Berlin.
13. Garrick, D.J. and R.L. Fernando. 2013. Implementing a QTL detection study (GWAS) using genomic prediction methodology. In “Genome-Wide Association Studies and Genomic Prediction”. Gondro, C., J.H.J. van der Werf and B. Hayes (2013). Springer Series: Methods in Molecular Biology, Berlin.
14. Garrick, D.J., R. Fernando, and A. Ruvinsky. 2014. Genomic prediction and genome-wide association studies in beef and dairy cattle. In “The Genetics of Cattle”, Garrick, D.J., and A. Ruvinsky. Second Edition, CABI.
15. Fernando, R. L., D. Habier. Kinship and Inbreeding (version 2) 2017. In “Encyclopedia of the Human Genome”. John Wiley & Sons, Ltd. [www.els.net](http://www.els.net).

### Articles in Journals

1. Fernando, R. L., R. D. Billingsley and D. Gianola. 1983. Effects of method of scaling in heritability estimates and sire evaluations for frame size at weaning in Angus cattle. *J. Anim. Sci.* 56:1047–1056.
2. Rattanaronchart, S., M. Grossman, R. L. Fernando, and R. D. Shanks. 1983. A Monte-Carlo comparison of estimators of average daily gain in body weight. *J. Anim. Sci.* 57:885–891.
3. Fernando, R. L., D. Gianola, and M. Grossman. 1984. Identifying all connected subsets in a two-way classification without interaction. *J. Dairy Sci.* 66:1399–1402.
4. Fernando, R. L., Susan A. Knights and D. Gianola. 1984. On a method of estimating the genetic correlation between characters measured in different experimental units. *Theor. Appl. Genet.* 67:175–178.

5. Fernando, R. L. and D. Gianola. 1984. Rules for assortative mating in relation to selection for linear merit functions. *Theor. Appl. Genet.* 68:227–237.
6. Staples, C. R., R. L. Fernando, G. C. Fahey, Jr, L. L. Berger and E. H. Jaster. 1984. Effect of intake of a mixed diet by dairy steers on digestion events. *J. Dairy Sci.* 67:995–1006.
7. Staples, C. R., R. L. Fernando, G. C. Fahey, Jr., L. L. Berger and E. H. Jaster. 1984. Effects of nutrient additives and sodium hydroxide on ensiling characteristics and in vitro fiber digestion kinetics of dairy cattle waste-energy feedstuff mixtures. *J. Dairy Sci.* 68:1390–1400.
8. Caro, R. F., M. Grossman and R. L. Fernando. 1985. Effects of data imbalance on estimation of heritability. *Theor. Appl. Genet.* 69:523–530.
9. Fernando, R. L. and D. Gianola. 1986. Effect of assortative mating on genetic change due to selection. *Theor. Appl. Genet.* 72:395–404.
10. Fernando, R. L. and D. Gianola. 1986. Optimum properties of the conditional mean as a selection criterion. *Theor. Appl. Genet.* 72:822–825.
11. Gianola, D. and R. L. Fernando. 1986. Bayesian methods in animal breeding theory. *J. Anim. Sci.* 63:217–244.
12. Gianola, D. and R. L. Fernando. 1986. Random effects models for binary responses. *Biometrics* 42:217–218.
13. Gipson, T. A., M. Grossman and R. L. Fernando. 1986. Relationships between predicted difference for milk production traits and buck designation in dairy goats. *J. Dairy Sci.* 69:591–594.
14. Grossman, M., R. L. Fernando, W. A. Mohammed, K. A. Ali and R. D. Shanks. 1986. Correlations between parities for lactation traits in United States dairy goats. *J. Dairy Sci.* 69:1917–1921.
15. Carriquiry, A. L., D. Gianola and R. L. Fernando. 1987. Mixed model analysis of a censored normal distribution with reference to Animal Breeding. *Biometrics* 43(4):929–939.
16. Fernando, R. L. and D. Gianola. 1987. Estimation of heritability by offspring-parent regression when observations do not have a common mean. *Theor. Appl. Genet.* 75:803–806.
17. Merchen, N. R., D. E. Darden, L. L. Berger, G. C. Fahey, Jr., E. C. Titgemeyer and R. L. Fernando. 1987. Effects of dietary energy level and supplemental protein source on performance of growing steers and nutrient digestibility and nitrogen balance in lambs. *J. Anim. Sci.* 65:658–668.

18. Gianola, D., S. Im and R. L. Fernando. 1988. Prediction of breeding value under Henderson's selection model: a revisit. *J. Dairy Sci.* 71:2790–2798.
19. Brown, D. A., P. C. Harrison, R. L. Fernando and T. W. Odom. 1988. Reversal of depressed miduterine arterial flow during hyperthermia induced respiratory alkalosis. *Proc. Soc. Exp. Biol. and Med.* 189:152–157.
20. Grossman, M. and R. L. Fernando. 1988. Covariance between relatives for X-linked loci in a population in disequilibrium. *Theor. Appl. Genet.* 77(3):311–319.
21. Atwell, D. G., E. H. Jaster, K. J. Moore and R. L. Fernando. 1988. Evaluation of high-oil corn and corn silage for lactating cows. *J. Dairy Sci.* 71:2689–2698.
22. Chang, H. L., R. L. Fernando and D. Gianola. 1989. Inverse of an additive x additive relationship matrix due to sires and maternal grandsires. *J. Dairy Sci.* 72:3023–3034.
23. Im, S., R. L. Fernando and D. Gianola. 1989. Likelihood inferences in animal breeding under selection: a missing data theory view point. *Genet. Sel. Evol.* 21:399–414.
24. Fernando, R. L., M. Grossman. 1989. Marker assisted selection using best linear unbiased prediction. *Genet. Sel. Evol.* 21:467–477.
25. Gianola, D., R. L. Fernando, S. Im and J. L. Foulley. 1989. Likelihood estimation of quantitative genetic parameters when selection occurs: models and problems. *Genome* 31:768–777.
26. Long, T. E., D. L. Thomas, R. L. Fernando, J. M. Lewis, U. S. Garrigus and D. F. Waldron. 1989. Estimation of individual and maternal heterosis, repeatability and heritability for ewe productivity and its components in Suffolk and Targhee sheep. *J. Anim. Sci.* 67:1208–1217.
27. Beever, J. E., P. D. George, R. L. Fernando and H. A. Lewin. 1990. Effects of genetic markers on growth and carcass traits in a paternal half-sib family of beef cattle. *J. Anim. Sci.* 68:337–344.
28. Waldron, D. F., D. L. Thomas, J. M. Stookey, T. G. Nash, F. K. McKeith and R. L. Fernando. 1990. Central ram tests in the Midwestern United States: III: Relationship between sire's central test performance and progeny performance. *J. Anim. Sci.* 68:45–53.
29. Gipson, T. A., R. L. Fernando and M. Grossman. 1990. Effects of smoothing data on estimation of parameters for multiphasic lactation curves of dairy goats. *Livest. Prod. Sci.* 24:205–221.

30. Fernando, R. L., M. Grossman. 1990. Genetic evaluation with autosomal and X-chromosomal inheritance. *Theor. Appl. Genet.* 80:75–80.
31. Jaster, E. H., G. C. McCoy and R. L. Fernando. 1990. Dietary fat in milk or milk replacers. *J. Dairy Sci.* 73:1843–1850.
32. McLaren, D. G., R. L. Fernando, H. A. Lewin and L. B. Schook. 1990. Integrated strategies and methodologies for the genetic improvement of animals. *J. Anim. Sci.* 73:2647–2656.
33. Cremin, J. D., D. B. Faulkner, N. R. Merchen, G. C. Fahey, Jr., R. L. Fernando and C. L. Willms. 1990. Digestion criteria in nursing beef calves supplemented with limited levels of protein and energy. *J. Anim. Sci.* 69:1322–1331.
34. Willms C. L., L. L. Berger, N. R. Merchen, G. C. Fahey and R. L. Fernando. 1991. Effects of increasing crude protein level on nitrogen retention and intestinal supply of amino acids in lambs fed diets based on alkaline hydrogen peroxide-treated wheat straw. *J. Anim. Sci.* 69:4939–4950.
35. \*Chang, H. L., R. L. Fernando and M. Grossman. 1991. On the principle underlying the tabular method to compute co-ancestry. *Theor. Appl. Genet.* 81:233–238.
36. Devol, D. L., J. Novakovski, R. L. Fernando and P. J. Bechtel. 1990. Varying amounts of stretch stimulus regulate stretch-induced muscle hypertrophy in the chicken. *J. Compar. Biochem. Physiol.* 100:55–61.
37. \*Perez-Encisco, M. and R. L. Fernando. 1992. Genetic evaluation with uncertain parentage: a comparison of methods. *Theor. Appl. Genet.* 84:173–179.
38. Clamp, P. A., J. E. Beaver, R. L. Fernando, D. G. McLaren and L. B. Schook. 1992. Detection of linkage between genetic markers and genes affecting growth and carcass traits in pigs. *J. Anim. Sci.* 70:2695–2706.
39. \*Cantet, R. J. C., R. L. Fernando and D. Gianola. 1992. Bayesian inference about dispersion parameters of univariate mixed models with maternal effects: theoretical considerations. *Genet. Sel. Evol.* 24:107–135.
40. Wilken, T. M., L. L. Lo, D. G. McLaren, R. L. Fernando, and P. J. Dziuk. 1992. An embryo transfer study of reciprocal cross differences in growth and carcass traits of Duroc and Landrace pigs. *J. Anim. Sci.* 70:2349–2358.
41. Lo, L. L., D. G McLaren, F. K. McKeith, R. L. Fernando, and J. Novakovski. 1992. Genetic analyses of growth, real-time ultrasound, carcass and pork quality in Duroc and Landrace pigs. I. Breed effects. *J. Anim. Sci.* 70:2373–2386.

42. Lo, L. L., D. G McLaren, F. K. McKeith, R. L. Fernando, and J. Novakofski. 1992. Genetic analyses of growth, real-time ultrasound, carcass and pork quality in Duroc and Landrace pigs. II. Heritabilities and correlations. *J. Anim. Sci.* 70:2387–2396.
43. Gianola, D., J. L. Foulley, R. L. Fernando and C. R. Henderson. 1992. Estimation of heterogeneous variances using empirical bayes methods: theoretical considerations. *J. Dairy Sci.* 75:2805–2823.
44. \*Cantet, R. J. C., R. L. Fernando, D. Gianola and I. Misztal. 1992. Genetic grouping for direct and maternal effects with differential assignment of groups. *Genet. Sel. Evol.* 24:211–223.
45. Groeneveld, E., M. Kovac, T. Wang, and R. L. Fernando. 1992. Computing algorithms in a general purpose BLUP package for multivariate prediction and estimation. *Arch. Tierz., Dummerstorf* 35:399–412.
46. van Eijk, M. J., J. A. Stewart-Haynes, J. E. Beever, R. L. Fernando, and H. A. Lewin. 1993. Development of persistent lymphocytosis in cattle is closely associated with DRB2. *Immunogenetics* 37: 64-8.
47. Bunge, R, D. L. Thomas, T. G. Nash and R. L. Fernando. 1993. Performance of hair breeds and prolific wool breeds of sheep in southern Illinois: Effect of breed of service sire on lamb production of Suffolk and Targhee ewes. *J. Anim. Sci.* 71:321-325.
48. Fernando, R. L., C. Stricker, and R. C. Elston. 1993. An efficient algorithm to compute the posterior genotypic distribution for every member of a pedigree without loops. *Theor. Appl. Genet.* 87:89-93.
49. Stricker, C., R. L. Fernando, and R. C. Elston. 1993. Segregation analysis under an alternative formulation for the mixed model. *Genet. Epidemiol.* 10:653–658.
50. \*Lo, L. L., R. L. Fernando, and M. Grossman. 1993. Covariance between relatives in multibreed populations: Additive model. *Theor. Appl. Genet.* 87:423-430.
51. Fernando, R. L., C. Stricker, and R. C. Elston. 1994. The finite polygenic mixed model: an alternative formulation of the mixed model of inheritance. *Theor. Appl. Genet.* 88:573-580.
52. Gianola, D., C. S. Wang, J. L. Foulley and R. L. Fernando. 1994. Bayesian inference about heritability in a linear model with additive genetic effects. *Revista Portuguesa de Zootecnia* 1: 63-86.
53. \*Lo, L. L., R. L. Fernando, R. J. C. Cantet, and M. Grossman. 1995. Theory for modelling means and covariances in a two-breed population with dominance inheritance. *Theor. Appl. Genet.* 90:49-62.

54. Yang Da, V. L. Jarrell, T. Wang, R. L. Fernando, M. B. Wheeler, and H. A. Lewin. 1995. Multilocus analysis for gene-centromere mapping using first polar bodies and secondary oocytes. *Genetics* 139:1091-1097.
55. \*Wang T., R. L. Fernando, S. van der Beek, M. Grossman, and J. A. M. van Arendonk. 1995. Covariance between relatives for a marked quantitative trait locus. *Genet. Sel. Evol.* 27:251-274.
56. Cantet, R. J. C. and R. L. Fernando. 1995. Prediction of breeding values with additive models for crosses originating from two populations. *Genet. Sel. Evol.* 27:323-334.
57. Stricker, C., R. L. Fernando and R. C. Elston. 1995. An algorithm to approximate the likelihood for pedigree data with loops by cutting. *Theor. Appl. Genet.* 91:1054-1063.
58. Stricker, C., R. L. Fernando and R. C. Elston. 1995. Linkage analysis with an alternative formulation for the mixed model of inheritance: the finite polygenic mixed model. *Genetics.* 141:1651-1656.
59. Cisneros, F., M. Ellis, F. K. McKeith, J. Macaw and R. L. Fernando. 1996. Influence of slaughter weight on growth and carcass characteristics, commercial cutting and curing yields, and meat quality of barrows and gilts from two genotypes. *J. Anim. Sci.* 74:925-933.
60. Misztal, I., R.L. Fernando, M. Grossman, T. J. Lawlor and M. Ukaszewicz. 1995. Dominance and epistatic effects in genetic evaluation of farm animals. *Animal Science Papers and Reports* 13:251-266.
61. \*Wang, T., R. L. Fernando, C. Stricker and R. C. Elston. 1996. An approximation to the likelihood for a pedigree with loops. *Theor. Appl. Genet.* 93:1299-1309.
62. Misztal, I., T. J. Lawlor, and R.L. Fernando. 1997. Studies on dominance models by Method R for stature of Holsteins. *J. Dairy Sci.* 80:975-978.
63. \*Lo, L. L., R. L. Fernando and M. Grossman. 1997. Genetic evaluation by BLUP in two-breed terminal crossbreeding systems under dominance inheritance. *J. Anim. Sci.* 75:2877-2884.
64. \*Wang, T., R. L. Fernando and M. Grossman. 1998. Genetic evaluation by BLUP using marker and trait information in a multibreed population. *Genetics* 148:507-515.
65. \*Fernando, R. L., C. Stricker and T. Wang. 1998. Detection and utilization of single genes without DNA assays. *J. Dairy Sci.* 81(2):62-75.
66. \*Totir, L. R. and R. L. Fernando. 1998. The effect of linkage on additive by additive covariance between relatives. *Genet. Sel. Evol.* 30:409-421.



67. Martinez, M. L., N. Vukasinovic, A. E. Freeman and R. L. Fernando. 1998. Mapping QTL in outbred populations using selected samples. *Genet. Sel. Evol.* 30:453-468.
68. Kuhn, M., A. E. Freeman and R. L. Fernando. 1999. Approaches investigated to correct for preferential treatment. *J. Dairy Sci.* 82:181-190.
69. Dekkers, J. C. M., J. Wang, and R. L. Fernando. 1999. QTL mapping using selective DNA pooling data. *Proc. Assoc. Advmt. Anim. Breed. Genet.* 13:223-226.
70. Sorensen, D., R. L. Fernando and D. Gianola. 2001. Inferring the trajectory of genetic variance in the course of artificial selection. *Genetical Research* 77:83-94.
71. \*Fernández, S. A., R. L. Fernando, B. Gulbrandtsen, L.R. Totir, and A.L. Carriquiry. 2001. Sampling genotypes in large pedigrees with loops. *Genet. Sel. Evol.* 33:337-367.
72. Pérez-Enciso, M., R. L. Fernando, J. Bidanel, and P. Le Roy. 2001. QTL analysis in crosses between outbred lines with dominance and inbreeding. *Genetics* 159: 413-422.
73. \*Fernández, S. A., and R. L. Fernando. 2002. Determining Peeling Order Using Sparse Matrix Algorithms. *J. Dairy Sci.* 85:1623-1629.
74. Hakkyo Lee, Jack C.M. Dekkers, M. Soller, Massoud Malek, Rohan L. Fernando, Max F. Rothschild. 2002. Choosing an appropriate error to control in QTL interval mapping: false discovery rate compared to genome-wise type I error rates. *Genetics* 161:905-914.
75. \*Fernández, S. A., R. L. Fernando, B. Gulbrandtsen, C. Stricker, M. Schelling, and A. L. Carriquiry. 2002. Irreducibility and efficiency of ESIP to sample marker genotypes in large pedigrees with loops. *Genet. Sel. Evol.* 34:537-555.
76. Birchmeier A.N., Cantet R.J.C., Fernando R.L., Morris C.A., Holgado F., Jara A., Santos Cristobal M. 2002. Estimation of segregation variance for birth weight in beef cattle, *Lives. Prod. Sci.* 76:27-35.
77. \*Totir, L. R., R. L. Fernando, J.C.M. Dekkers, S.A. Fernandez, and B. Gulbrandtsen. 2003. A comparison of alternative methods to compute conditional genotype probabilities for genetic evaluation with finite locus models. *Genet. Sel. Evol* 35: 585-604.
78. Zhao H, M. F. Rothschild, R. L. Fernando, J. C. M. Dekkers. 2003. Tests of candidate genes in breed cross populations for QTL mapping in livestock. *Mammalian Genome* 14:472-482.

79. \*Totir, L. R., Fernando, R. L., J. C. M. Dekkers, Fernández, S. A. Gulbrandsen, B. 2003. The effect of using approximate gametic variance covariance matrices on marker assisted selection by BLUP. *Genet. Sol. Evol.* 36:29-48.
80. Fernando, R. L., D. Nettleton, B. R. Southey, J. C. M. Dekkers, M. F. Rothschild, M. Soller. 2004. Controlling the proportion of false positives (PFP) in multiple dependent tests. *Genetics* 166: 611-619.
81. \*Grapes, L., J.C.M. Dekkers, M.F. Rothschild, Fernando, R. L. 2004. Comparing linkage disequilibrium-based methods for fine mapping quantitative trait loci. *Genetics* 166: 1561-1570.
82. Jannink, J., R. Fernando. 2004. On the Metropolis-Hastings acceptance probability to add or drop a QTL in MCMC-based Bayesian analyses. *Genetics* 166: 641-643.
83. \*Totir, L. R., R. L. Fernando, J. C. M. Dekkers, S. A. Fernandez. 2004. The effect of the number of loci in finite locus models for genetic evaluation. *Genet. Sel. Evol.* 36: 395-414
84. \*Grapes, L., M. Z. Firat, J. C. M. Dekkers, M. F. Rothschild, R. L. Fernando. 2006. Optimal haplotype structure for linkage disequilibrium-based fine mapping of quantitative trait loci using identity by descent. *Genetics* 172:1955-1965.
85. \*Grapes, L., S. Rudd, R. Fernando, K. Megy, D. Rocha, M. Rothschild. 2006. Prospecting for pig SNPs in the human genome: have we struck gold? *Journal of Animal Breeding and Genetics* 123:145-151.
86. Gianola, D., R. L. Fernando, and A. Stella. 2006. Genomic assisted prediction of genetic value with semi-parametric procedures. *Genetics* 173:1761-1776.
87. Minick, J.A., L. R. Totir, D. E. Wilson, R. L. Fernando. 2006. Conception rate in Angus heifers. *J. Anim. Sci.* 84:2022-2025.
88. \*Abraham, K. J., L. R. Totir, and R. L. Fernando. 2007. Improved techniques for sampling complex pedigrees with the Gibbs sampler. *GSE* 39: 27-38.
89. Zhao, H.H., R.L. Fernando, and J.C.M. Dekkers. 2007. Power and precision of alternate methods for linkage disequilibrium mapping of QTL. *Genetics* 175: 1975-1986
90. \*Habier, D., R.L. Fernando And J.C.M. Dekkers. 2007. The Impact of genetic relationship information on genome-assisted breeding values. *Genetics* 177:2389-3397.

91. Fernando, R.L., D. Habier, C. Stricker, J.C.M. Dekkers, and L.R. Totir. 2007. Genomic selection. *Acta Agriculturae Scandinavica, Section A*, 57:192-195.
92. Piyasatian, N., R. L. Fernando and J. C. M. Dekkers. 2007. Genomic selection for marker-assisted improvement in line crosses. *Theor. Appl. Genet.* 115:665-674.
93. Serenius, T., K. J. Stalder, and R. L. Fernando. Genetic associations of sow longevity with age at first farrowing, number of piglets weaned, and wean to insemination interval in the Finnish Landrace swine population. *J. Anim. Sci.* 2008 86: 3324-3329.
94. Piyasatian, N., R. L. Fernando and J. C. M. Dekkers. 2008. Introgressing multiple QTL in breeding programmes of limited size. *J. Anim. Breed. Genet.* 125:5056.
95. Hassen, A., S. Avendano, W. G. Hill, R. L. Fernando, S. J. Lamont and J. C. M. Dekkers. 2009. The effect of heritability estimates on high-density SNP analyses with related animals. *J. Anim. Sci.* 87: 868-875.
96. \*Ibánñez-Escriche, N., R. L. Fernando, A. Toosi, J. C. M. Dekkers. 2009. Genomic selection of purebreds for crossbred performance. *Genet. Sel. Evol.* 41:12 (<http://www.gsejournal.org/content/41/1/12>).
97. \*Habier, D., R. L. Fernando and J. C. M. Dekkers. 2009. Genomic selection using low-density marker panels. *Genetics* 182: 343-353.
98. Zhong, S., J. C. M. Dekkers, R. L. Fernando, J. Jannink. 2009. Factors affecting accuracy from genomic selection in populations derived from multiple inbred lines: a Barley case study . *Genetics* 182: 355-364.
99. Gianola, D., G. de los Campos, W. G. Hill, E. Manfredi, and R. L. Fernando. 2009. Additive Genetic Variability and the Bayesian Alphabet. *Genetics* 183:347-363.
100. Koltjes, J. E., B. P. Mishra, D. Kumar, R. S. Kataria, L. R. Totir, R. L. Fernando, R. Cobbold, D. Steffen, W. Coppieters, M. Georges and J. M. Reecy. 2009. A nonsense mutation in cGMP-dependent type II protein kinase (PRKG2) causes dwarfism in American Angus cattle *Proc. Natl. Acad. Sci. USA* 106:19250-19255.
101. Coster, A., H. C. Heuven, R. L. Fernando, and J. C. Dekkers. 2009. Haplotype inference in crossbred populations without pedigree information. *Genet. Sel. Evol.* 41:40.
102. \*Legarra, A. and R. L. Fernando. 2009. Linear models for joint association and linkage QTL mapping. *GSE* 41:43.

103. Piyasatian, N., R. L. Fernando and J. C. M. Dekkers. 2009. Models for marker-assisted genetic evaluation with multiple QTL in a crossbred population. *Livest. Sci.* 125:141148.
104. \*Totir, L. R., R. L. Fernando and J. Abraham. 2009. An efficient algorithm to compute marginal posterior genotype probabilities for every member of a pedigree with loops *Genet. Sel. Evol.* 41:52.
105. Abasht, B., E. Sandford, J. Arango, P. Settar, J. E. Fulton, N. P. O'Sullivan, A. Hassen, D. Habier, R. L. Fernando, J. C. M. Dekkers and S. J. Lamont. 2009. Extent and consistency of linkage disequilibrium and identification of DNA markers for production and egg quality traits in commercial layer chicken populations. *BMC Genomics Suppl.* 2:S2.
106. Garrick, D. J., J. F. Taylor and R. L. Fernando. 2009. Deregressing estimated breeding values and weighting information for genomic regression analyses. *Genet. Sel. Evol.* 41:55.
107. \*Toosi, A., R. L. Fernando and J. C. M. Dekkers. 2010. Genomic selection in admixed and crossbred populations. *J Anim. Sci.* 88:32-46.
108. \*Kizilkaya, K., R. L. Fernando and D. J. Garrick. 2010. Genomic prediction of simulated multibreed and purebred performance using observed fifty thousand single nucleotide polymorphism genotypes. *J. Anim. Sci.* 88:544-551.
109. \*He W., Fernando R.L., Dekkers J.C.M., Gilbert H.A. 2010. A gene frequency model for QTL mapping using Bayesian inference. *Genet. Sel. Evol.* 42:21.
110. \*Habier, D., L. R. Totir, R. L. Fernando. 2010. A two-stage approximation for analysis of mixture genetic models in large pedigrees. *Genetics* 185:655-670.
111. \*Kizilkaya, K., Garrick, D., Fernando, R., Mestav, B., Yildiz, M. 2010. Use of linear mixed models for genetic evaluation of gestation length and birth weight allowing for heavy-tailed residual effects. *Genet. Sel. Evol.* 42:26.
112. Wolc, A., C. Stricker, J. Arango, P. Settar, J. E. Fulton, N. P. O'Sullivan, R. Preisinger, D. Habier, R. Fernando, D. J. Garrick, S. J. Lamont, J. C. M. Dekkers. 2011. Breeding value prediction for production traits in layer chickens using pedigree or genomic relationships in a reduced animal model. *Genet. Sel. Evol.* 43:5. <http://www.gsejournal.org/content/43/1/5>.
113. Wolc, A., J. Arango, P. Settar, J.E. Fulton, N.P. O'Sullivan, R. Preisinger, D. Habier, R. Fernando, D. J. Garrick, and J.C.M. Dekkers. 2011. Persistence of accuracy of genomic estimated breeding values over generations in layer chickens. *Genetics Selection Evolution*, 43:23.

114. \*Habier, D., R. L. Fernando, K. Kizilkaya, D. J. Garrick. 2011. Extension of the Bayesian Alphabet for Genomic Selection. *BMC Bioinformatics* 12:186. <http://www.biomedcentral.com/1471-2105/12/186>.
115. Saatchi, M., M. McClure, S. McKay, M. Rolf, J. Kim, J. Decker, T. Taxis, R. Chapple, H. Ramey, S. Northcutt, S. Bauck, B. Woodward, J. Dekkers, R. Fernando, R. Schnabel, D. Garrick, J. Taylor. 2011. Accuracies of genomic breeding values in American Angus beef cattle using K-means clustering for cross-validation. *Genet. Sel. Evol.* 43:40. <http://www.gsejournal.org/content/43/1/40>.
116. Piyasatian, N., R.L. Fernando, J.C.M. Dekkers. 2012. QTL detection and marker-assisted composite line development. *Livestock Science* 143 (2012) 233241.
117. \*Sun, X., L. Qu, R.L. Fernando, D.J. Garrick, and J.C.M Dekkers. 2012. A fast EM algorithm for BayesA-like prediction of genomic breeding values. *PLoS One* 10.1371/journal.pone.0049157
118. Peters, S.O., K. Kizilkaya, D.J. Garrick, R.L. Fernando, J.M. Reecy, R.L. Weaber, G.A. Silver, and M.G. Thomas. 2012. Heritability and Bayesian genome-wide association study of first service conception and pregnancy in Brangus heifers. *Journal of Animal Science*, doi:10.2527/jas.2012-5580.
119. Peters, S.O., K. Kizilkaya, D.J. Garrick, R.L. Fernando, J.M. Reecy, R.L. Weaber, G.A. Silver, and M.G. Thomas. 2012. Bayesian genome-wide association analyses of growth and yearling ultrasound measures of carcass traits in Brangus heifers. *Journal of Animal Science*, doi:10.2527/jas.2011-4507.
120. Resende, M.F.R., P. Munoz, M.D.V. Resende, D.J. Garrick, R.L. Fernando, J.M. Davis, E.J. Jokela, T.A. Martin, G.F. Peter, M. Kirst. 2012. Accuracy of genomic selection models in Loblolly pine. *Genetics*, doi: 10.1534/genetics.111.137026.
121. Wolc, A., J. Arango, P. Settar, J.E. Fulton, N.P. O'Sullivan, R. Preisinger, D. Habier, R.L. 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*, doi 10.1111/j.1365-2052.2012.02381.x
122. Zhao, Y., M. Gowda, T. Wrschum, C. F. H. Longin, V. Korzun, S. Kollers, R. Schachschneider, J. Zeng, R. Fernando, J. Dubcovsky, J. C. Reif. 2013. Dissecting the genetic architecture of frost tolerance in Central European winter wheat. *Journal of Experimental Botany* 64:4453-4460.
123. 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.

124. \*Zeng, J., A. Toosi, R.L. Fernando, J.C.M. Dekkers and D.J. Garrick. 2013. Genomic selection of purebred animals for crossbred performance in the presence of dominance gene action. *Genetics Selection Evolution* 45:11.
125. \*Zhao, Y., J. Zeng, R.L. Fernando, and J.C. Reif. 2013. Genomic Prediction of Hybrid Wheat Performance. *Crop Science* 53:1.
126. \*Zhao, Y., Gowda, M., Wurschum, T., Longin, C.F.H., Korzun, V., Kollers, S., Schachschneider, R., Zeng, J., Fernando, R., Dubcovsky, J., and Reif, J.C. 2013. Dissecting the genetic architecture of frost tolerance in Central European winter wheat. *Journal of Experimental Botany* 64:44534460.
127. Peters, S.O., K. Kizilkaya, D.J. Garrick, R.L. Fernando, E.J. Pollak, M. De Donato, T Hussain, and I.G. Imumorin. 2013. Application of multivariate heavy-tailed distributions to residuals in estimation of genetic parameters of growth traits in beef cattle. *Journal of Animal Science* 91:1552-1561.
128. \*Kizilkaya, K., R. G. Tait, D. J. Garrick, R. L. Fernando and J. M. Reecy. 2013. Genome-wide association study of infectious bovine keratoconjunctivitis in Angus cattle *Journal: BMC Genetics*, 14:23.
129. \*Edriss, V., R.L. Fernando, G. Su, M.S. Lund and B. Guldbbrandtsen. 2013. The effect of using genealogy-based haplotypes for genomic prediction. *Genetics Selection Evolution* 45:5.
130. de Los Campos, G., Vazquez, A., Fernando, R., Klimentidis, Y., and Sorensen, D. 2013. Prediction of complex human traits using the genomic best linear unbiased predictor. *PLoS Genetics*. doi:10.1371/journal.pgen.1003608
131. Wang, C., D. Habier, B.L. Peiris, A. Wolc, A. Kranis, K. Watson, S. Avendano, D. Garrick, R. Fernando, S. Lamont, J. Dekkers. 2013. Accuracy of genomic prediction using an evenly spaced, low-density SNP panel in broiler chickens. *Poultry Science* 92:1712-1723.
132. \*Habier, D., R.L. Fernando and D.J. Garrick. 2013. Genomic-BLUP decoded: a look into the black box. *Genetics* 194:597-607.
133. Wolc, A., J. Arango, P. Settar, J.E. Fulton, N.P. O'Sullivan, R. Presinger, R. Fernando, D.J. Garrick and J.C.M Dekkers. 2013. Analysis of egg production in layer chickens using a random regression model with genomic relationships. *Poultry Science* 92:1486-1491.
134. 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.

135. \*Zhao, Y., J. Zeng, R.L. Fernando, and J.C. Reif. 2013. Genomic Prediction of Hybrid Wheat Performance. *Crop Science* 53:1.
136. Wolc, A., J. Arango, P. Settar, J.E. Fulton, N.P. O'Sullivan, R. Preisinger, D. Habier, R.L. Fernando, D.J. Garrick, J.C.M. Dekkers. 2014. Genome wide association study for egg production and quality in layer chickens. *Journal of Animal Breeding and Genetics* 131:173-182.
137. Peters, S.O., K. Kizilkaya, D.J. Garrick, R.L. Fernando, E.J. Pollak, R. M. Enns, M. De Donato, O.O. Ajayi, I.G. Imumorin. 2014. Use of robust multivariate linear mixed models for estimation of genetic parameters for carcass traits in beef cattle. *Journal of Animal Breeding and Genetics* 2014:1-9, doi: 10.1111/jbg.12093.
138. \*Kizilkaya, K., R.L. Fernando, D.J. Garrick. 2014. Reduction in accuracy of genomic prediction for ordered categorical data compared to continuous observations. *Genetics, Selection, Evolution* 46:37.
139. Garrick, D., J. Dekkers, R. Fernando. 2014. The evolution of methodologies for genomic prediction. *Livestock Science* 166:10-18.
140. Fernando, R.L., J.C.M. Dekkers, 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.
141. Baes, C.F., M.A. Dolezal, J.E. Koltjes, B. Bapst, E. Fritz-Waters, S. Jansen, C. Flury, H. Signer-Hasler, C. Stricker, R. Fernando, R. Fries, J. Moll, D.J. Garrick, J.M. Reecy, B. Gredler. 2014. Evaluation of variant identification methods for whole genome sequencing data in dairy cattle. *BMC Genomics* 15:948.
142. \*Cheng, H., D.J. Garrick, R.L. Fernando. 2015. XSim: Simulation of descendants from ancestors with sequence data. *G3—Genes, Genomes, Genetics*, doi:10.1534/g3.115.016683
143. Wolc, A., H.H. Zhao, J. Arango, P. Settar, J.E. Fulton, N.P. O'Sullivan, R. Preisinger, C. Stricker, D. Habier, R. Fernando, D.J. Garrick, S.J. Lamont, J.C.M. Dekkers. 2015. Response and inbreeding from a genomic selection experiment in layer chickens. *Genetics Selection Evolution* 47:59.
144. \*Cheng, H., L. Qu, D.J. Garrick, R.L. Fernando. 2015. A fast and efficient Gibbs sampler for BayesB in whole genome analyses. *Genetics Selection Evolution* 47:80.
145. Hassani, S., M. Saatchi, R.L. Fernando, D.J. Garrick. 2015. Accuracy of prediction of simulated polygenic phenotypes and their underlying quantitative trait loci genotypes using real or imputed whole-genome markers in cattle. *Genetics Selection Evolution* 47:99.

146. Weng Z-Q, Wolc A., Shen X., Fernando R.L., Dekkers J.C.M., Arango J., Settar P., Fulton J.E., O'Sullivan N.P., Garrick D.J. 2016. Effects of Number of Training Generations on Genomic Prediction for Various Traits in a Layer Chicken Population. *Genetics Selection Evolution* 48:22.
147. Wolc A., Arango J., Settar P., Fulton J.E., O'Sullivan N.P., Dekkers J.C.M., Fernando R., Garrick D.J. 2016. Mixture models detect large effect QTL better than GBLUP and result in more accurate and persistent predictions. *Journal of Animal Science and Biotechnology*. 7:7.
148. \*Karaman, E., Cheng, H., Firat, M., Garrick, D. J., Fernando, R. L. 2016. An upper bound for accuracy of prediction using GBLUP. *PLoS ONE* 11(8): e0161054. doi:10.1371/journal.pone.0161054
149. Heidaritabar M., Wolc A., Arango J., Zeng J., Settar P., Fulton J.E., O'Sullivan N.P., Bastiaansen J.W.M., Fernando R.L., Garrick D.J., Dekkers J.C.M. 2016. Impact of fitting dominance as well as additive effects on accuracy of genomic prediction in layer chickens. *Journal of Animal Breeding and Genetics* 133: 334-346.
150. Abell, C.E., Fernando, R.L., Serenius, T. V., Rothschild, M.F., Gray, K. A., Stalder, K. 2016. Genetic relationship between purebred and crossbred sow longevity. *Journal of Animal Science and Biotechnology* 7:51.
151. \*Sun, X., Fernando, R.L., Dekkers. J.C.M. 2016. Contributions of linkage disequilibrium and co-segregation information to the accuracy of genomic prediction. *Genetics Selection Evolution* 48 (1), 77.
152. Fernando, R.L., Cheng, H., Golden, B.L., Garrick, D.J. 2016. Computational strategies for alternative single-step Bayesian regression models with large numbers of genotyped and non-genotyped animals. *Genetics Selection Evolution* 48: 96.
153. Kramer, L. M., Abdel Ghaffar, M. A., Koltes, J. E., Fritz-Waters, E. R., Mayes, M. S., Sewell, A. D., Weeks, N. T., Garrick, D. J., Fernando, R. L., Ma, L., Reecy, J. M.. 2016. Epistatic interactions associated with fatty acid concentrations of beef from angus sired beef cattle. *BMC Genomics* 17:891.
154. Fernando, R. L., Cheng, H., Garrick, D. J. 2016. An efficient exact method to obtain GBLUP and single-step GBLUP when the genomic relationship matrix is singular. *Genetics Selection Evolution* 48:80.
155. \*Lee, J., Cheng, H., Garrick, D., Golden, B., Dekkers, J., Park, K., Lee, D, Fernando, R. 2017. Comparison of alternative approaches to single-trait genomic prediction using genotyped and non-genotyped Hanwoo beef cattle. *Genetics Selection Evolution* 49: 2.



156. \*Hsu, W.L., Garrick, D.J., Fernando, R.L. 2017. The accuracy and bias of single-step genomic prediction for populations under selection. *G3: Genes, Genomes, Genetics* 7:2685-2694.
157. Fernando, R.L., Cheng, H., Sun, X., Garrick, D.J. 2017. A comparison of identity by descent and identity by state matrices that are used for genetic evaluation and estimation of variance components. *Journal of Animal Breeding and Genetics* 134: 213-223.
158. Fernando, R.L., Toosi, A., Wolc, A., Garrick, D., Dekkers, J. 2017. Application of whole-genome prediction methods for genome-wide association studies: a Bayesian approach. *Journal of Agricultural, Biological and Environmental Statistics* 22: 172-193.
159. \*Cheng, H., Garrick, D.J., Fernando, R.L. 2017. Efficient strategies for leave-one-out cross validation for genomic best linear unbiased prediction. *Journal of animal science and biotechnology* 8:38.
160. \*Toosi, A., Fernando, R.L., Dekkers, J.C.M. 2018. Genome-wide mapping of quantitative trait loci in admixed populations using mixed linear model and Bayesian multiple regression analysis. *Genetics Selection Evolution* 50 (1), 32.
161. \*Zeng, J., Garrick, D., Dekkers, J., Fernando, R. 2018. A nested mixture model for genomic prediction using whole-genome SNP genotypes. *PloS one* 13 (3), e0194683.
162. \*Cheng, H., Kizilkaya, K., Zeng, J., Garrick, J., Fernando, R. 2018. Genomic prediction from multiple-trait Bayesian regression methods using mixture priors. *Genetics*, 209, 89-103.
163. Yang, J., Ramamurthy, R.K., Qi, X., Fernando, R.L., Dekkers, J.C.M., Garrick, D.J., Nettleton, D., Schnable, P.S. and others. 2018. Empirical comparisons of different statistical models to identify and validate kernel row number-associated variants from structured multi-parent mapping populations of Maize. *G3: Genes, Genomes, Genetics*. 8 (11), 3567–3575.
164. Weng, Z., Wolc, A., Su, H., Fernando, R.L., Dekkers, J.C.M., Arango, J., Settar, P., Fulton, J., O’Sullivan, N.P., Garrick, D.J. 2019. Identification of recombination hotspots and quantitative trait loci for recombination rate in layer chickens. *Journal of animal science and biotechnology* 10 (1), 20.
165. Gianola, D., Fernando, R. L., Garrick, D. J. 2019. A certain invariance property of BLUE in a whole genome regression context. *Journal of Animal Breeding and Genetics* 136 (2), 113-117.
166. Westhues, M., Heuer, C., Thaller, G., Fernando, R., Melchinger, A.E. 2019. Efficient genetic value prediction using incomplete omics data. *Theoretical and Applied Genetics* 1-12.

167. Gianola, D., Fernando, R.L., Schoen, C.C. Inferring trait-specific similarity among individuals from molecular markers and phenotypes with Bayesian regression. *Theoretical Population Biology* (2019), <https://doi.org/10.1016/j.tpb.2019.11.008>.
168. Bertolini, F., Chinchilla-Vargas, J., Khadse, J.R., Juneja, A., Deshpande, P. D., Bhave, K., Potdar, V., Kakramkar, P.M., Karlekar, A.R., Pande, A.B., Fernando, R.L., Rothschild, M. F. 2019. Marker discovery and associations with  $\beta$ carotene content in Indian dairy cattle and buffalo breeds. *Journal of dairy science* 102 (11), 10039-10055.
169. Gianola, D., Fernando, R.L. 2020. A multiple-trait Bayesian Lasso for genome-enabled analysis and prediction of complex traits *Genetics* 214 (2), 305-331.
170. Zhao, T., Fernando, R., Garrick, D., Cheng, H. Fast parallelized sampling of Bayesian regression models for whole-genome prediction. *Genet Sel Evol* 52:16, <https://doi.org/10.1186/s12711-020-00533-x>

### Articles in Proceedings

1. Gianola, D., J. L. Foulley and R. L. Fernando. 1986. Prediction of breeding values when variances are not known. *Proc. 3rd Wld. Cong. Genet. App. Liv. Prod.* 12:356–370.
2. Waldron, D. F., D. L. Thomas, J. M. Stookey and R. L. Fernando. 1986. Relationship between growth of Suffolk rams on central performance test and growth of their progeny. *Proc. 3rd Wld. Cong. Genet. App. Liv. Prod.* 9:639–644.
3. Fernando, R. L. 1990. Statistical problems in marker assisted selection for QTL. *Proc. 4th Wld. Cong. Genet. App. Liv. Prod* 13:433–436. Invited paper.
4. Chang H. L., R. L. Fernando and D. Gianola. 1990. An evaluation of maximum likelihood estimators of non-additive genetic variances. *Proc. 4th Wld. Cong. Genet. App. Liv. Prod.* 13:437:440.
5. McLaren, D. G., L. L. Lo, K. K. McKeith and R. L. Fernando. 1990. A preliminary analysis of growth, real-time ultrasound, carcass and pork quality traits in Duroc and Landrace pigs. *Proc. 4th Wld. Cong. Genet. App. Liv. Prod.* 15:497–500.
6. Stricker, C., R. L. Fernando and R. C. Elston. 1994. SALP— Segregation and linkage analysis for pedigrees. *Proc. 5th Wld. Cong. Genet. Appl. Liv. Prod. Prod.* 22:63-64.
7. Stricker, C., R. L. Fernando and R. C. Elston. 1994. Linkage Analysis for Large Pedigrees under Mixed Inheritance. *Proc. 5th Wld. Cong. Genet. Appl. Liv. Prod.* 21:51-54.

8. Fernando, R. L. 1996. Likelihood analysis of extended pedigrees under mixed inheritance. Proc. Annual Meeting of the Biometrics Society, German Region. Invited paper.
9. Fernando, R. L. and M. Grossman. 1996. Genetic evaluation in crossbred populations. Proc. Forty-Fifth Annual National Breeders Roundtable. Invited paper.
10. Stricker, C. and R. L. Fernando. 1998. Some theoretical aspects of finite locus models. Proc. 6th Wld. Cong. Genet. App. Liv. Prod. 26:25-32. Invited paper.
11. \*Southey, B. R. and R. L. Fernando. 1998. Controlling the proportion of false positives among significant results in QTL detection. Proc. 6th Wld. Cong. Genet. App. Liv. Prod. 26:221-224.
12. Fernando, R. L. 1998. Genetic evaluation and selection using genotypic, phenotypic and pedigree information. Proc. 6th Wld. Cong. Genet. App. Liv. Prod. 26:329-336. Invited paper.
13. Schelling, M., C. Stricker, R. L. Fernando and N. Küenzi. 1998. PEDSIM—A simulation program for pedigree data. Proc. 6th Wld. Cong. Genet. App. Liv. Prod. 27:475-476.
14. \*Fernandez, S. A., R. L. Fernando and A. L. Cariquiry. 1999. An algorithm to sample marker genotypes in a pedigree with loops. Proc. Joint Stat. Meet. Baltimore, Maryland.
15. Fernando, R. L. 1999. Analysis of data from crossbred populations. Proc. International Symposium on Animal Breeding and Genetics. Vicoso-MG, Brazil. Invited paper.
16. Fernando, R. L. 1999. Theory for analysis of multi-breed. Proc. 7th Genetic Prediction Workshop of the Beef Improvement Federation. Invited paper.
17. \*Southey, B. R., R. L. Fernando and S. Rodriguez-Zas. 2001. Multipoint linkage analysis in a general population. Proc. Annual Meeting of the Amer. Stat. Assoc.
18. Fernando, R. L. and L. R. Totir. 2002. Advances in genetic and statistical models to predict breeding values. 7th World Congress Genet. Appl. Livest. Prod. CD-ROM Communication *N*<sup>o</sup> 20-01. Invited paper.
19. Chaiwong, J. C. M. Dekkers, R. L. Fernando, and M. F. Rothschild. 2002. Introgressing multiple QTL in backcross breeding programs of limited size. 7th World Congress Genet. Appl. Livest. Prod. CD-ROM Communication *N*<sup>o</sup> 22-08.

20. Fernando, R. L., J. C. M. Dekkers and M. Soller. 2002. Controlling the proportion of false positives (PFP) in a multiple test genome scan for marker-QTL linkage. 7th World Congress Genet. Appl. Livest. Prod. CD-ROM Communication N° 20-01.
21. \*Grapes, L., R. L. Fernando and M. F. Rothschild. 2002. Analysis of methods for fine mapping quantitative trait loci using linkage disequilibrium. 7th World Congress Genet. Appl. Livest. Prod. CD-ROM Communication N° 21-19.
22. Heifetz, E., R. L. Fernando and M. Soller. 2002. Targeted recombinant progeny: a design for ultra high-resolution mapping of QTL using a saturated marker map. 7th World Congress Genet. Appl. Livest. Prod. CD-ROM Communication N° 21-25.
23. Kackman, S. D. and R. L. Fernando. 2002. Analysis of generalized linear models with MATVEC. 7th World Congress Genet. Appl. Livest. Prod. CD-ROM Communication N° 28-04.
24. Stricker, C., M. Schelling, F. Du, I. Hoeschelle, S. A. Fernandez and R. L. Fernando. 2002. A comparison of efficient genotype samplers for complex pedigrees and multiple linked loci. 7th World Congress Genet. Appl. Livest. Prod. CD-ROM Communication N° 21-12. Invited paper.
25. \*Totir, L., R. L. Fernando, J. C. M. Dekkers and S. A. Fernandez. 2002. A strategy to improve the computational efficiency of marker assisted genetic evaluation under finite locus models. 7th World Congress Genet. Appl. Livest. Prod. CD-ROM Communication N° 20-01.
26. Fernando, R. L. 2004. Statistical Issues In Marker Assisted Selection. Proc. 8th Genetic Prediction Workshop of The Beef Improvement Federation. Invited paper.
27. Mishra, B., J. Koltjes, R. Totir, R. Fernando, J. Cavanagh, M. Georges, W. Coppieters, and J. Reecy. 2004. Mapping of the gene causing disproportionate dwarfism in American Angus cattle. Proc. of the International Society of Animal Genetics.
28. Thallman, R. M., D. W. Moser, E. W. Dressler, L. R. Totir, R. L. Fernando, S. K. Kachman, J. M. Rumph, M. E. Dikeman, E. J. Pollak. 2004. Carcass Merit project: DNA marker validation. Proc. 8th Genetic Prediction Workshop of The Beef Improvement Federation. Invited paper.
29. Johnson, D. L., C. Stricker, R.L. Fernando, and B.L. Harris. 2005. Moving from BLUP to marker-assisted BLUP for genetic evaluations. Proc. of the 2005 Interbull meeting. UPPSALA, Sweden.
30. Koltjes, J., R. Totir, R. Fernando, and J. Reecy. Fine-mapping of a 2.8cM region associated with dwarfism in American Angus cattle. 2005. Proc. Of the 3rd symposium of Genet of Anim. Health.

31. Fernando, R.L., L.R. Totir, F.V.C. Pita, C. Stricker, and K.J. Abraham. 2006. Algorithms to compute allele state and origin probabilities for QTL mapping. Proc. 8th World Congress on Genet. Appl. Livest. Prod. Invited paper.
32. Zhao, H.H. J.C.M. Dekkers, and R.L. Fernando. 2006. Power and precision of regression-based linkage disequilibrium mapping of QTL. Proc. 8th World Congress on Genet. Appl. Livest. Prod.
33. Piyasatian, N. R.L. Fernando, and J.C.M. Dekkers. 2006. Genomic selection for composite line development using low density marker maps. Proc. 8th World Congress on Genet. Appl. Livest. Prod.
34. Quaas, R.L., J. Li, R.M. Thallman, A.L. Van Eenennaam, R.L. Fernando, and C. Gill. 2006. Validation of commercial DNA tests for quantitative beef traits. Proc. 8th World Congress on Genet. Appl. Livest. Prod.
35. Serenius, T. K.J. Stalder, and R.L. Fernando. 2006. Genetic associations of length of productive life with age at first farrowing and leg soundness score in Finnish Landrace population. Proc. 8th World Congress on Genet. Appl. Livest. Prod.
36. Dekkers, J.C.M., H.H. Zhao, R.L. Fernando. 2006. Linkage disequilibrium mapping of QTL in livestock. Proc. 8th World Congress on Genet. Appl. Livest. Prod.
37. Koltjes, J.E., L.R. Totir, R.L. Fernando, and J.M. Reecy. 2006. Identification of a putative causal mutation for dwarfism in PRKG2. Plant and Animal Genome meeting XIII proceedings. Proc of Plant and Anim. Genome XIV. p233.
38. \*Ibanez-escriche, N., R. L. Fernando, and J. C. M. Dekkers. 2008. Pueden usarse animales cruzados en seleccion genmica? 2008. ITEA(2008), Vol. 104 (2), 155-159.
39. Thallman, R. M., K. J. Hanford, R. L. Quaas, S. D. Kachman, R. J. Tempelman, R. L. Fernando, L. A. Kuehn, and E. J. Pollak. 2009. Estimation of the proportion of genetic variation accounted for by DNA tests. Proceedings of the Beef Improvement Federation 41st Annual Research Symposium.
40. Gorbach, D., Cai, W., Dekkers, J., Young, J., Garrick, D., Fernando, R., Rothschild, M. 2010. Large-scale SNP association analyses of residual feed intake and its component traits in pigs. Proc. 9th World Congress on Genet. Appl. Livest. Prod. 9:265.
41. \*Habier, D., Fernando, R.L., Kizilkaya, K., Garrick, D.J. 2010. Extension of the Bayesian alphabet for genomic selection. Proc. 9th World Congress on Genet. Appl. Livest. Prod. 9:468.

42. Piyasatian, N., Habier, D., Kranis, A., Watson, K.A., Avendano, S., Fernando, R.L., Dekkers, J.C.M. 2010. Genomic Selection Using Evenly Spaced Low-Density SNPs. Proc. 9th World Congress on Genet. Appl. Livest. Prod. 9:512.
43. Reecy, J., Tait, R., Van Overbeke, D., Garmyn, A., Mateescu, R., Van Eenennaam, A., Duan, Q., Liu, Q.; Schoonmaker, J., Drewnoski, M., Beitz, D., Kizilkaya, K., Fernando, R., Garrick, D. 2010. Use of Genomics to Improve Healthfulness and Quality of Meat. Proc. 9th World Congress on Genet. Appl. Livest. Prod. 9:53.
44. Wolc, A., Stricker, C., Arango, J., Settari, P., Fulton, J.E., O'Sullivan, N., Habier, D., Fernando, R.L., Garrick, D.J., Lamont, S.J., Dekkers, J.C.M. 2010. Breeding Value Prediction For Production Traits In Layers Using Pedigree And Marker Based Methods. Proc. 9th World Congress on Genet. Appl. Livest. Prod. 9:552.
45. Hanford, K., Thallman, M., Kachman, S., Kuehn, L., Quaas, R., Tempelman, R., Fernando, R., Pollak, J. 2010. Estimation of The Proportion of Variation Accounted For By DNA Tests. I. Genetic Variance. Proc. 9th World Congress on Genet. Appl. Livest. Prod. 9:822.
46. \*Habier, D., Fernando, R., Garrick, D. 2010. A combined strategy to infer high-density SNP haplotypes in large pedigrees. Proc. 9th World Congress on Genet. Appl. Livest. Prod. 9:915.
47. Thallman, M., Hanford, K., Kachman, S., Kuehn, L., Quaas, R., Tempelman, R., Fernando, R., Pollak, J. 2010. Estimation of the Proportion of Variation Accounted for by DNA Tests. II. Phenotypic Variance. Proc. 9th World Congress on Genet. Appl. Livest. Prod. 9:918.
48. Andreescu, C., Habier, D., Fernando, R., Kranis, A., Watson, K., Avendano, S., Dekkers, J. 2010. Accuracy of Genomic Predictions Across Breeding Lines of Chickens. Proc. 9th World Congress on Genet. Appl. Livest. Prod. 9:956.
49. \*Sun, X., D. Habier, R. L Fernando, D. J. Garrick, J. C. M. Dekkers. 2011 Genomic breeding value prediction and QTL mapping of QTLMAS2010 data using bayesian methods. BMC Proceedings BMC 2011 5(Suppl 3):S13. (<http://www.biomedcentral.com/1753-6561/5/S3/S13>)
50. \*Kizilkaya, K., R.G. Tait, D.J. Garrick, R.L. Fernando, J.M. Reecy. 2011. Whole genome analysis of infectious bovine keratoconjunctivitis in Angus cattle using Bayesian threshold models. BMC Genomics 5(Suppl 4):S22. <http://www.biomedcentral.com/1753-6561/5/S4/S22>
51. \*Zeng, J., M. Pszczola, A. Wolc, T. Strabel, R.L. Fernando, D.J. Garrick, and J.C.M. Dekkers. 2012. Genomic breeding value prediction and QTL mapping of QTLMAS2011 data using Bayesian and GBLUP methods.

- Proceedings of the 15th QTLMAS workshop. BMC Proceedings 2012, (Suppl 2):S7.
52. Fernando, R.L., D.J. Garrick. 2013. Bayesian regression as an alternative implementation of genomic-enhanced genetic evaluation. Proceedings of the Beef Improvement Federation 10th Genetic Prediction Workshop held in Kansas City 12- 13 December 2103, pages 38-43.
  53. Garrick, D.J., J.C.M. Dekkers, B.L. Golden, R.L. Fernando. 2014. (Invited paper) Bayesian prediction combining genotyped and non-genotyped individuals. Proceedings of the 10th World Congress on Genetics Applied to Livestock Production.
  54. Fernando, R.L., A. Toosi, D.J. Garrick, J.C.M. Dekkers. 2014. (Invited paper) Application of whole-genome prediction methods for genome-wide association studies: a Bayesian approach. Proceedings of the 10th World Congress on Genetics Applied to Livestock Production.
  55. Wolc, A., A. Kranis, J. Arango, P. Settar, J.E. Fulton, N. OSullivan, S. Avendano, K.A. Watson, R. Preisinger, D. Habier, S.J. Lamont, R. Fernando, D.J. Garrick, J.C.M. Dekkers. 2014. (Invited paper) Applications of genomic selection in poultry. Proceedings of the 10th World Congress on Genetics Applied to Livestock Production.
  56. \*Sun, X., R.L. Fernando, D.J. Garrick, J.C.M. Dekkers. 2014. Improved accuracy of genomic prediction for traits with rare QTL by fitting haplotypes. Proceedings of the 10th World Congress on Genetics Applied to Livestock Production.
  57. Weng, Z.-Q., A. Wolc, R.L. Fernando, J.C.M. Dekkers, J. Arango, P. Settar, J.E. Fulton, N.P. OSullivan, D.J. Garrick. 2014. Prediction accuracy of pedigree and genomic estimated breeding values over generations in layer chickens. Proceedings of the 10th World Congress on Genetics Applied to Livestock Production.
  58. Peters, S., K. Kizilkaya, D. Garrick, R. Fernando, J. Reecy, I. Imumorin, M. Thomas. 2014. Genome-wide association study of first service conception rate in Brangus heifers using probit, robit and logit models. Proceedings of the 10th World Congress on Genetics Applied to Livestock Production.
  59. Baes, C.F., M.A. Dolezal, E. Fritz-Waters, J.E. Koltjes, B. Bapst, C. Flury, H. Signer-Hasler, C. Stricker, R. Fernando, F. Schmitz-Hsu, D.J. Garrick, J.M. Reecy, B. Gredler. 2014. Comparison of variant calling methods for whole-genome sequencing data in dairy cattle. Proceedings of the 10th World Congress on Genetics Applied to Livestock Production.
  60. \*Cheng, H., D.J. Garrick, R.L. Fernando. 2014. Parallel computing to speed up whole-genome analyses using independent Metropolis-Hastings

- sampling. Proceedings of the 10th World Congress on Genetics Applied to Livestock Production.
61. Golden, B. L., R. L. Fernando, D. J. Garrick. 2016. Bolt and an alternative approach to genomic EPDs. Proceedings of the Beef Improvement Federation, 102-106.
  62. Garrick, D.J., H. Cheng, B.L. Golden and R.L. Fernando. 2017. Some alternative computational strategies for single-step national genomic evaluations. Association for the Advancement of Animal Breeding and Genetics Conference.
  63. \*Henshall, J., Toosi, A., Fernando, R. L., and Dekkers, J. C. M. 2018. Genome-wide association mapping of quantitative traits loci in admixed populations. Proceedings of the 11th World Congress on Genetics Applied to Livestock Production.
  64. \*Cheng, H., Fernando, R., and Garrick, D. 2018. JWAS: Julia implementation of Whole-genome Analyses Software. Proceedings of the 11th World Congress on Genetics Applied to Livestock Production.
  65. Fernando, R. and Gianola, D. 2018. Bayesian inference of genomic similarity among individuals from markers and phenotypes. Proceedings of the 11th World Congress on Genetics Applied to Livestock Production.

## Reports

1. Goodyear, J. L., D. L. Thomas, J. M. Stookey, R. L. Fernando, J. M. Lewis, F. C. Hinds and M. H. Wallace. 1982. Breed and management system effects on lamb production. University of Illinois Sheep Research Expo., 1982, pp 1-4.
2. Long, T. E., D. L. Thomas, R. L. Fernando, U. S. Garrigus and J. M. Lewis. 1985. Effects of crossbred and backcross matings on ewe productivity in Suffolk and Targhee sheep. Sheep Research Reports, University of Illinois.
3. Thompson, L. H. and Rohan Fernando. 1985. Update on progeny evaluation of boars in Illinois Swine Progeny Testing Program. Swine Research Reports, University of Illinois.
4. Thompson, L. H., D. G. McLaren and R. L. Fernando. 1986. Sire evaluation by progeny from heterospermic litters in field conditions. Swine Research Reports, University of Illinois.
5. Jaster, E. H., G. C. McCoy, R. L. Fernando and M. G. Cameron. 1987. Added fat for dairy calves. Illinois Dairy Report.



6. Beever, J. E., P. D. George, R. L. Fernando and H. A. Lewin. 1988. Genes affecting growth and carcass traits detected in a paternal half-sib family using genetic markers. Illinois Beef Cattle Report.
7. Gipson, T. A., M. Grossman and R. L. Fernando. 1988. Predicted difference and buck designation in dairy goats. Dairy Goat Journal 66(1):41–43.
8. Lo, L. L., and R. L. Fernando, 1994. Effects of multibreed covariance theory on genetic evaluation and selection. Taiwan Sugar 41:28 and 42:17-27.
9. \*Grapes, L., M. Z. Firat, J. C. M. Dekkers, M. F. Rothschild and R. L. Fernando. 2003. Fine-tuning the predicted position of genes associated with economic traits in livestock. Research Reports, Department of Animal Science, Iowa State University.
10. \*Grapes, L., S. Rudd, R. L. Fernando, K. Megy, D. Rocha, M. F. Rothschild. 2004. Searching for mutations in pigs using the human genome. Research Reports, Department of Animal Science, Iowa State University.
11. Garrick, D., R. L. Fernando, K. Kizilkaya, and J. Reecy. 2009. High-density SNP genotypes for predicting genetic merit of beef cattle. Research Reports, Department of Animal Science, Iowa State University.
12. \*Zeng, J, A Toosi, R Fernando, J Dekkers, D Garrick. 2013. Genomic selection of purebred animals for crossbred performance in the presence of dominant gene action. Iowa State University Animal Industry Report 2013, A.S. leaflet R2772. <http://www.ans.iastate.edu/report/air/2013pdf/R2772.pdf>
13. Wang, C, D Habier, A Wolc, DJ Garrick, RL Fernando, SJ Lamont, JCM Dekkers, A Kranis, KA Watson, 2013. Application of genomic selection using an evenly spaced low-density marker panel in broiler chickens. Iowa State University Animal Industry Report 2013, A.S. leaflet R2807. <http://www.ans.iastate.edu/report/air/2013pdf/R2807.pdf>
14. \*Sun, X, R Fernando, D Garrick, J Dekkers. 2013. Genomic prediction using linkage disequilibrium and co-segregation. Iowa State University Animal Industry Report 2013, A.S. leaflet R2818. <http://www.ans.iastate.edu/report/air/2013pdf/R2818.pdf>
15. Fernando, RL, J Dekkers, DJ Garrick. 2014. Bayesian methods for genomic prediction and genome-wide association studies combining information on genotyped and non-genotyped individuals. Iowa State University Animal Industry Report 2014, A.S. leaflet R2865. <http://www.ans.iastate.edu/report/air/2014pdf/R2865.pdf>
16. Yan, J, M Saatchi, H Su, J Lee, R Fernando, DJ Garrick. 2014. Characterization and associations of haplotypes containing PLAG1 in cattle. Iowa State University Animal Industry Report 2014, A.S. leaflet R2851.

17. Weng, Z, A Wolc, R Fernando, J Dekkers, DJ Garrick. 2014. Prediction accuracy and genomic estimated breeding values over generations in layer chickens. Iowa State University Animal Industry Report 2014, A.S. leaflet R2897.
18. Su, H, J Koltes, M Saatchi, J Lee, R Fernando, DJ Garrick. 2014. Characterizing haplotype diversity in ten US beef cattle breeds. Iowa State University Animal Industry Report 2014, A.S. leaflet R2846. <http://www.ans.iastate.edu/report/air/2014pdf/R2846.pdf>.
19. \*Cheng, H, R Fernando, DJ Garrick. 2014. Three different Gibbs samplers for BayesB genomic prediction. Iowa State University Animal Industry Report 2014, A.S. leaflet R2867. <http://www.ans.iastate.edu/report/air/2014pdf/R2867.pdf>
20. Lee, J, M Saatchi, H Su, R Fernando, DJ Garrick. 2014. Genomic prediction using single or multi-breed reference populations in Maine-Anjou cattle. Iowa State University Animal Industry Report 2014, A.S. leaflet R2856.
21. Wolc, A, J Arango, P Settar, JE Fulton, NP OSullivan, R Preisinger, R Fernando, DJ Garrick, J Dekkers. 2014. Genetics of feed efficiency in laying hens. Iowa State University Animal Industry Report 2014, A.S. leaflet R2894. <http://www.ans.iastate.edu/report/air/2014pdf/R2894.pdf>
22. Wolc, A, J Arango, P Settar, JE Fulton, NP OSullivan, R Preisinger, R Fernando, DJ Garrick, J Dekkers. 2014. Application of genomic information to longitudinal traits. Iowa State University Animal Industry Report 2014, A.S. leaflet R2901. <http://www.ans.iastate.edu/report/air/2014pdf/R2901.pdf>
23. J. Lee, H. Su, R.L. Fernando, D.J. Garrick, J. Taylor. 2015. Characterization of the F94L Double Muscling Mutation in Pure- and Crossbred Limousin Animals. Iowa State University Animal Industry Report 2015, A.S. leaflet R2956. [http://lib.dr.iastate.edu/cgi/viewcontent.cgi?article=2065&context=ans\\_air](http://lib.dr.iastate.edu/cgi/viewcontent.cgi?article=2065&context=ans_air)
24. H. Su, R.L. Fernando, D.J. Garrick, B. Golden. 2015. Accuracy of Genomic Predictions for Birth, Weaning and Yearling Weights in US Simmental Beef Cattle. Iowa State University Animal Industry Report 2015, A.S. leaflet R2957. [http://lib.dr.iastate.edu/cgi/viewcontent.cgi?article=2066&context=ans\\_air](http://lib.dr.iastate.edu/cgi/viewcontent.cgi?article=2066&context=ans_air)
25. \*H. Cheng, R.L. Fernando, D.J. Garrick. 2015. GenSim: Simulation of Descendants from Sequenced Ancestors Data. Iowa State University Animal Industry Report 2015, A.S. leaflet R2955. [http://lib.dr.iastate.edu/cgi/viewcontent.cgi?article=2064&context=ans\\_air](http://lib.dr.iastate.edu/cgi/viewcontent.cgi?article=2064&context=ans_air)

26. Z. Weng, A. Wolc, J. Arango, P. Settar, J.E. Fulton, N.P. O'Sullivan, R.L. Fernando, J.C.M. Dekkers, D.J. Garrick. 2015. Estimation of Haplotype Diversity and Recombination Rate on Chromosomes 5 and 15 in Layer Chickens. Iowa State University Animal Industry Report 2015, A.S. leaflet R3001.  
[http://lib.dr.iastate.edu/cgi/viewcontent.cgi?article=2110&context=ans\\_air](http://lib.dr.iastate.edu/cgi/viewcontent.cgi?article=2110&context=ans_air)
27. A. Wolc, J. Arango, P. Settar, J.E. Fulton, N.P. O'Sullivan, T. Jankowski, R.L. Fernando, J.C.M. Dekkers, D.J. Garrick. 2015. Accounting for Complex Population Structure in Pedigree and Genomic Analyses of Laying Chickens. Iowa State University Animal Industry Report 2015, A.S. leaflet R3002.  
[http://lib.dr.iastate.edu/cgi/viewcontent.cgi?article=2111&context=ans\\_air](http://lib.dr.iastate.edu/cgi/viewcontent.cgi?article=2111&context=ans_air)
28. \*X. Sun, R.L. Fernando, D.J. Garrick, J.C.M. Dekkers. 2015. Improved Accuracy of Genomic Prediction for Traits with Rare QTL by Fitting Haplotypes. Iowa State University Animal Industry Report 2015, A.S. leaflet R3032.  
[http://lib.dr.iastate.edu/cgi/viewcontent.cgi?article=2132&context=ans\\_air](http://lib.dr.iastate.edu/cgi/viewcontent.cgi?article=2132&context=ans_air)
29. A. Wolc, A. Kranis, J. Arango, P. Settar, J.E. Fulton, N.P. OSullivan, A. Avendano, K.A. Watson, J.M. Hickey, G. de los Campos, R.L. Fernando, D.J. Garrick, J.C.M. Dekkers. 2016. Implementation of genomic selection in the poultry industry. *Animal Frontiers* 6:23-31.  
<https://www.animalsciencepublications.org/publications/af/articles/6/1/23>
30. \*J. Zeng, D.J. Garrick, J.C. Dekkers, R.L. Fernando. 2016. A Nested Mixture Model for Genomic Prediction Using Whole-Genome SNP Genotypes. *Animal Industry Report* 662 (1), 21.
31. Saatchi, M, Fernando, RL, Hyde, L, Atkins, J, McGuire, S, Shafer, W, Spangler, ML, Golden, B. 2018. Empirical progeny equivalent of genotyped animals in a multi-breed beef cattle genetic evaluation using a single-step Bayesian regression model. *Animal Industry Report* 664 (1) 25.

## Abstracts

1. Fernando, R. L., R. D. Billingsley, D. Gianola and G. E. Ricketts. 1981. Heritability estimates and sire evaluation for frame score at weaning in Illinois Angus cattle. *J. Anim. Sci.* 53 (Suppl. 1):139.
2. Fernando, R, L., D. Gianola and H. W. Norton. 1981. Methods of scaling ordered categories with an underlying genetic component. *J. Anim. Sci.* 53 (Suppl. 1):139.
3. Billingsley, R. D., R. L. Fernando, D. Gianola and G. E. Ricketts. 1981. A possible source of bias in sire evaluation for weaning weight. *J. Anim. Sci.* 53 (Suppl. 1):126

4. Fernando, R. L., M. Grossman and D. Gianola. 1982. An algorithm to identify all connected subsets in a two-way classification. *J. Anim. Sci.* 55 (Suppl. 1):146.
5. Rattanarongchart, S., M. Grossman, R. L. Fernando and R. D. Shanks. 1982. A comparison of estimators of average daily gain in body weight. *J. Anim. Sci.* 55(Suppl. 1):160.
6. Fernando, R. L., R. L. Baker and D. Gianola. 1983. Assortative mating on a linear combination of two traits. *J. Anim. Sci.* 57 (Suppl. 1):150.
7. Goodyear, J. L., D. L. Thomas, J. M. Stookey, R. L. Fernando, J. M. Lewis, F. C. Hinds and M. H. Wallace. 1983. Breed and management system effects on lamb production. *J. Anim. Sci.* 57 (Suppl. 1):83.
8. Knights, S. A., R. L. Fernando, D. Gianola and J. B. Gibb. 1983. Genetic correlations between birth, weaning and yearling weight of bulls, and age at first calving in Angus cattle. *J. Anim. Sci.* 57 (Suppl. 1):80.
9. Fernando, R. L., R. L. Baker and D. Gianola. 1983. Assortative mating and selection: some computer simulation results. 34th Annual Meeting, European Association of Animal Production, Madrid.
10. Caro, R. F., M Grossman and R. L. Fernando. 1984. Effects of data imbalance on estimation of heritability. *Genetics* 107(3,2):s17.
11. Fernando, R. L. and D. Gianola. 1984. Joint effect of assortative mating and selection on genetic progress. *J. Anim. Sci.* 59 (Suppl. 1):82.
12. Carriquiry, A. L., R. L. Fernando, D. Gianola and M. Grossman. 1984. Effect of major genes on response to selection: a computer simulation. *J. Anim. Sci.* 59 (Suppl. 1):82-83.
13. Fernando, R.L. and D. Gianola. 1984 Optimal properties of the conditional mean as a selection criterion. *J. Anim. Sci.* 59 (Suppl. 1):177.
14. Fernando, R. L. and D. Gianola. 1984. An optimal two-stage selection procedure. *J. Anim. Sci.* 59 (Suppl. 1):177.
15. Fernando, R. L. and D. Gianola. 1985. Effect of assortative mating on genetic change due to selection in a finite population. *J. Anim. Sci.* 61 (Suppl. 1):80.
16. Carriquiry, A. L., R. L. Fernando and D. Gianola. 1985. Estimation and prediction from a censored multivariate normal distribution. *J. Anim. Sci.* 61(Suppl. 1):879
17. Gianola, D. and R. L. Fernando. 1985. Inferences about breeding values when the variance-covariance structure is unknown. *J. Anim. Sci.* 61 (Suppl. 1):80.

18. Long, T. E., D. L. Thomas, R. L. Fernando, J. M. Lewis, U. S. Garrigus and H. W. Norton. 1985. Effects of crossbred and backcross matings on reproductive performance in Suffolk and Targhee sheep. *J. Anim. Sci.* 61 (Suppl. 1):78.
19. Fernando, R. L., D. Gianola and C. R. Henderson. 1985. Inferences on breeding values and on genetic and environmental parameters when selection and non-random mating occur. *J. Anim. Sci.* 61 (Suppl. 1):219.
20. Carriquiry, A. L., R. L. Fernando and D. Gianola. 1985. Analysis of multiple traits when one variate is censored. *J. Anim. Sci.* 61 (Suppl. 1):219.
21. Gipson, T. A., M. Grossman and R. L. Fernando. 1985. Relationships between predicted difference for milk production traits and buck designation in dairy goats. *J. Dairy Sci.* 68 (Suppl. 1):219-220.
22. Bechtel, P. J., D. L. DeVol, R. Fernando and J. Novakovski. 1986. Effects of different time periods on passive stretch induced skeletal muscle hypertrophy. Abstracts, 1986, FASEB Annual Meeting.
23. Jones, L. R., S.L. Sphar, H. B. Puckett and R. L. Fernando. 1986. Characterization of real-time milk conductivity data with respect to variability and reliability. *J. Dairy Sci.* 69(Suppl. 1):175.
24. Merchen, N. R. D. E. Darden, L. L. Berger, G. C. Fahey, Jr., E. C. Titgemeyer and R. L. Fernando. 1986. Effects of diet fed the growing period on feed intake and performance of finishing beef cattle. In: *Proc. Symp on Feed Intake in Beef Cattle*, Oklahoma State University Press.
25. Colaco, J. A., R. L. Fernando and D. Gianola. 1987. Variability in milk production among sires, herds and cows in Portuguese dairy cattle. Annual Meeting of the Study Commissions EAAP.
26. Colaco, J. A., R. L. Fernando and D. Gianola. 1987. Estimation and evaluation of age correction factors for milk yield in Portuguese dairy cattle. Annual Meeting of the Study Commissions EAAP.
27. Gianola, D., S. Im, R. L. Fernando and J. L. Foulley. 1987. Transformations in variance component estimation and sire evaluation. *J. Dairy Sci.* 70(Suppl. 1):123.
28. Fernando, R. L. and D. Gianola. 1987. The exact distribution of the offspring-parent regression estimator of heritability. *J. Anim. Sci.* 65(Suppl. 1):98.
29. Jaster, E. J., G. C. McCoy, R. F. Randle and R. L. Fernando. 1987. Added energy for calves in hutches during cold weather. *J. Dairy Sci.* 70(Suppl. 1):146.

30. \*Wang, T., R. L. Fernando, D. G. McLaren and L. H. Thompson. 1988. Field evaluation of heterospermic testing in swine. *J. Anim. Sci.* 66(Suppl. 1):97.
31. Chang, H. L., R. L. Fernando and D. Gianola. 1988. A note on computing additive relationships. *J. Anim. Sci.* 66(Suppl. 1.):99.
32. Fernando, R. L., D. Gianola and S. Im. 1988. Ignorability of selection in estimation of parameters by maximum likelihood. *J. Dairy Sci.* 71(Suppl. 1):261.
33. Im, S., R. L. Fernando and D. Gianola. 1988. Likelihood inferences in animal breeding under selection: a missing data theory view point. *J. Dairy Sci.* 71(Suppl. 1):262.
34. Gianola, D., R. L. Fernando, S. Im and J. L. Foulley. 1988. Maximum likelihood estimation of parameters in a mixed model under Henderson's conditional selection scheme. *J. Dairy Sci.* 71(Suppl. 1)261.
35. Chang, H. L., R. L. Fernando and D. Gianola. 1988. A note on ranking sires for a trait with epistatic genetic variance. *J. Anim. Sci.* 66(Suppl. 1):220.
36. Chang, H. L., R. L. Fernando and D. Gianola. 1988. A computationally efficient method to invert an additive  $\times$  additive relationship matrix. *J. Anim. Sci.* 66(Suppl. 1):220.
37. Beever, J. E., P. D. George, R. L. Fernando, C. J. Stormont and H. A. Lewin. 1988. Genes affecting growth and carcass traits detected in a parental half-sib family using genetic markers. *International Conf. on Animal Blood Groups and Biochemical Polymorphisms.*
38. Gianola, D., R. L. Fernando and S. Im. 1988. Maximum likelihood estimation of quantitative genetic parameters under two selection models. *Genome* 30(Suppl. 1):25.
39. Willms, C. L., L. L. Berger, G. C. Fahey, Jr., N. Merchen and R. L. Fernando. 1988. Effects of dietary crude protein concentration on nitrogen retention and fiber digestibility by lambs fed alkaline hydrogen peroxide-treated wheat straw-based diets fed at 90% of ad libitum intake. *J. Anim. Sci.* 67(Suppl. 2):156.
40. \*Cantet, R. J. C., D. Gianola and R. L. Fernando. 1989. Comparitaison of some designs for estimation of additive direct and maternal genetic parameters. *J. Anim. Sci.* 67(Suppl. 2):85.
41. Beever, J. E., P. D. George, R. L. Fernando, C. J. Stormont and H. A. Lewin. 1989. Genes affecting growth and carcass traits detected in a paternal half-sib family using genetic markers. *J. Anim. Sci.* 67(Suppl. 2):84.

42. Fernando, R. L. and M. Grossman. 1989. Best linear unbiased prediction under autosomal and X-chromosomal inheritance. *J. Anim. Sci.* 67(Suppl. 1):31.
43. Fernando, R. L. and T. Wang. 1989. Marker assisted selection using best linear unbiased prediction. *J. Anim. Sci.* 67(Suppl. 1):31.
44. Gianola, D., J. L. Foulley, R. L. Fernando, and C. R. Henderson. 1989. A bayesian model for estimation of heterogeneous variance. Commission on Animal Genetics, Session VI- Ideas Box.
45. Groeneveld, E., T. Wang, M. Kovac and R. L. Fernando. 1989. PEST - A FORTRAN program for Prediction and ESTimation in multivariate linear models. *J. Anim. Sci.* 68(Suppl. 1):72.
46. Lo, L. L., D. G. McLaren, F. K. McKeith and R. L. Fernando. 1990. Estimation of genetic parameters for growth, carcass and pork quality traits in Duroc and Landrace pigs. *J. Anim. Sci.* 68(Suppl. 1):238.
47. \*Cantet, R. J. C., D. Gianola and R. L. Fernando. 1990. Comparison of quadratic and likelihood estimators of direct and maternal genetic parameters. *J. Dairy Sci.* 73(Suppl. 1):209.
48. \*Wang, T., S. van der Beek, R. L. Fernando and M. Grossman. 1991. Covariance between effects of marked QTL alleles. *J. Anim. Sci.* 69:(suppl. 1):202.
49. Misztal, I. and R. L. Fernando. 1991. Defining unknown-parent groups to minimize sampling variance. *J. Dairy Sci.* 74(Suppl. 1):159.
50. \*Perez-Enciso, M. and R. L. Fernando. 1991. The additive relationship matrix with uncertain parentage 1: Theory.
51. \*Perez-Enciso, M. and R. L. Fernando. 1991. The additive relationship matrix with uncertain parentage: 2: Applications.
52. Clamp, P. A., J. E. Beever, R. L. Fernando, D. G. McLaren, and L. B. Schook. 1991. A study of linkage between four genetic markers and associations with growth and carcass traits in pigs. *J. Anim. Sci.* 69(suppl. 1): 211.
53. \*Lo. L. L., R. L. Fernando, M. Grossman, and R. J. C. Cantet. 1992. Genotypic covariance between relatives in a multibreed population: Additive and dominance models. *J. Anim. Sci.* 70(suppl. 1).
54. Fernando, R. L. 1995. Likelihood analysis of extended pedigrees under mixed inheritance. *Biometrics Bulletin.* 12:5.
55. Jassim, E. W., M. Grossman, W. J. Koops, R. A. J. Luykx, and R. L. Fernando. 1995. Multiphasic analysis of embryo mortality in White Cornish chickens. *Poultry Science* 74(Suppl. 1): 90.

56. Misztal, I, T. J. Lawlor and R.L. Fernando. 1996. The effect of several non-additive models on estimates of variance components obtained by method R for stature in Holsteins J. Dairy Sci. (Suppl. 1) 79:164.
57. Kuhn, M. T., R. L. Fernando and A. E. Freeman. 1977. Response to mass versus quantitative trait locus selection under a finite locus model of inheritance. J. Dairy Sci (Suppl. 1) 80:228.
58. Dekkers, J. C. M., J. Wang and R. L. Fernando. 1999. Quantitative trait locus mapping using selective DNA pooling data. Iowa State University Genetics Visions Conference.
59. \*Southey, B. R. and R. L. Fernando. 1999. Quantitative trait locus mapping with multiple markers in outbred populations. Iowa State University Genetics Visions Conference.
60. \*Guldbrandtsen, B. and R. L. Fernando. 1999. Maximum likelihood parameter estimation in complex pedigrees. Iowa State University Genetics Visions Conference.
61. \*Fernandez, S. A., R. L. Fernando and A. L. Carriquiry. 1999. An algorithm to sample marker genotypes in a pedigree with loops. Iowa State University Genetics Visions Conference.
62. Lee, H.K., Dekkers, J.C.M., Malek, M., Soller, M., Fernando, R.L., and Rothschild, M.F. 2000. Comparison of approaches for determining significance threshold values for QTL detection. J. Anim. Sci. 78 (Suppl. 1):78
63. \*Fernández, S. A., R. L. Fernando and A. L. Carriquiry. 2000. An algorithm to sample unobservable genotypes in complex pedigrees. International Society for Bayesian Analysis (ISBA) 2000. Crete, Greece.
64. \*Perez-Encisco, M. and R. L. 2000. QTL Analysis in crosses between outbred lines allowing for dominance and inbreeding. 51st Annual Meeting of the European Association of Animal Production.
65. Schelling, M., Fernando, R.L., Künzi, N., Stricker, C. (2000) Descent graphs in animal pedigrees. 51<sup>th</sup> EAAP Conference, La Hague, The Netherlands, August 21-25.
66. Fernando, R. L. and S. A. Fernandez. (2001) An algorithm to obtain an irreducible markov chain to sample marker genotypes. Workshop on Statistical Methods, Plant & Animal Genome IX Conference, San Diego, CA.
67. Fernando, R. L. and M. Soller. (2001) An alternative approach to control false positives in QTL scans. Session I: Advances in genetic analysis and evaluation. 52<sup>nd</sup> EAAP Conference, Budapest, Hungary, August 26-29.



68. \*Totir, L.R., R.L. Fernando and J.C.M. Dekkers. 2002. Effect of using approximate gametic variance covariance matrices on marker assisted selection by BLUP. *J. Anim. Sci (Suppl. 2)* 80:35
69. \*Totir, L.R., R. L. Fernando, and J.C.M. Dekkers. 2003. Response to selection by marker assisted BLUP with use of approximate gametic variance covariance matrices. *J. Anim. Sci.* 81 (Suppl. 1)
70. Spike, P.L., R. R. Benson, R. L. Fernando, J. C. M. Dekkers, P. J. Berger, and B. R. Skaar. 2003. A simulation program using .nite loci with infinite possibilities, FLIP. *J. Anim. Sci.* 81 (Suppl. 1): 113
71. Guldbbrandtsen, B., R. Fernando. 2003. Effect of marker assisted selection for mastitis resistance in a real Danish Holstein pedigree. 54<sup>th</sup> EAAP Conference, Rome, Italy.
72. Piyasatian, N., R. Fernando, and J. Dekkers. 2004 Efficiency of selection on multiple QTL in a crossbred population. *J Anim. Sci.* Vol. 82 (Suppl. 1): 377.
73. \*Pita, F., R. Fernando, L. Totir. 2004. An improved approximation of the gametic covariance matrix for marker assisted genetic evaluation by BLUP. *J Anim. Sci.* Vol. 82 (Suppl. 1): 379.
74. \*Gilbert, H., M. Z. Firat, L. R. Totir, J. C. M. Dekkers, and R. L. Fernando. 2004. A new method to fine map a quantitative trait locus using linkage disequilibrium. *J Anim. Sci.* Vol. 82 (Suppl. 1):415.
75. \*Grapes. L., S. Rudd, R. Fernando, K. Megy, D. Rocha, M. Rothschild. 2004. Prospecting for pig SNPs in the human genome: have we struck gold? *J Anim. Sci.* Vol. 82 (Suppl. 1):453.
76. \*Totir, L. R., R. L. Fernando, and J. C. M. Dekkers. 2004. Use of peeling and reverse peeling to estimate the power to map a recessive disease gene. *J Anim. Sci.* Vol. 82 (Suppl. 1):88.
77. Fernando, R. L. 2004. Incorporating molecular markers into genetic evaluation. 55th EAAP Conference, Bled, Slovenia.
78. \*Gilbert, H., M. Z. Firat, L. R. Totir, J. C. M. Dekkers, and R. L. Fernando. 2004. A new method to fine mapping quantitative trait locus using linkage disequilibrium. 55th EAAP Conference, Bled, Slovenia.
79. Mote, B. E., D. Rohan, J. D. Loy, L. R. Totir, R. Fernando, and M. F. Rothsschild. 2005. Combining computational statistics and molecular biology to map the causative mutation associated with a polydactyl phenotype in swine. *Plant & Animal Genome XIII Conference*, San Diego, CA.

80. Piyasatian, N., L. R. Totir, R.L. Fernando, and J.C.M. Dekkers. 2005. Marker-assisted selection on multiple QTL in a crossbred population. 2005. ASAS ADSA Midwest Meeting, Des Moines, Iowa.
81. Zhao, H., R. Fernando, and J. Dekkers. 2006. Power and precision of linkage disequilibrium mapping of QTL in outbred populations. Midwest Animal Science Meeting, Des Moines.
82. Piyasatian, N., L.R. Totir, R.L. Fernando, and J.C.M. Dekkers. 2006. QTL detection and marker-assisted composite line development. Midwest Animal Science Meeting, Des Moines.
83. \*Fernando, R.L., and C. Stricker. 2008. Alternative approaches to whole-genome analyses. Joint biometric conference of the German Region. Munich, Germany.
84. \*Toosi, A., R. Fernando, J. C. M. Dekkers, and R. L. Quaas. 2008. Genomic selection of purebreds using data from admixed populations. *J. Anim. Sci.* Vol. 86, E-Suppl. 2: 362.
85. \*He, W., R. L. Fernando, J. C. M. Dekkers, and D. Gianola. 2008. A gene frequency model to map QTL using Bayesian inference. *J. Anim. Sci.* Vol. 86, E-Suppl. 2: 12.
86. \*Habier, D., J. C. M. Dekkers, and R. L. Fernando. 2008. Genomic selection using low-density SNPs. *J. Anim. Sci.* Vol. 86, E-Suppl. 2: 506.
87. \*Habeir, D., and R. L. Fernando. 2008. A mixture genetic model for whole genome analyses. 59th EAAP Conference, Vilnius, Lithuania.
88. \*Ibanez-Escriche, N., R. L. Fernando, and J. C. M. Dekkers. 2008. Genomic selection of purebreds for crossbred performance using a model with breed-specific SNP effects. 59th EAAP Conference, Vilnius, Lithuania.
89. Fernando, R. L., and C. Stricker. 2008. DNA technology: estimation of genetic merit from large DNA marker panels. *J. Anim. Sci.* Vol. 86, E-Suppl. 2:103.
90. Nkrumah, J. D., D. J. Garrick, R. L. Fernando, S. L. Northcutt, B. Bowman, B. W. Woodward, S. W. Bauck, D. Vasco, S. D. McKay, T. M. Taxis, M. M. Rolf, J. E. Decker, J. W. Kim, M. C. McClure, R. D. Schnabel, J. F. Taylor. 2009. Alternative methods for selecting tagSNP panels from the bovine 50K chip to predict marbling in Angus cattle. *J. Anim. Sci.* Vol. 87, E-Suppl. 2:LB3.
91. Dekkers, J. C. M., C. Stricker, R. L. Fernando, D. J. Garrick, S. J. Lamont, N. P. Oullivan, J. E. Fulton, J. Arango, P. Settar, A. Kranis, J. McKay, K. A. Watson, A. Koerhuis, and R. Preisinger. 2009. Implementation of genomic selection in egg layer chickens. *J. Anim. Sci.* Vol. 87, E-Suppl. 2:LB6.

92. Dekkers, J.C.M., H. H. Zhao, D. Habier, and R. L. Fernando. 2009. Opportunities for genomic detection with redesign of breeding programs. *J. Anim. Sci.* Vol. 87, E-Suppl. 2:312.
93. \*Kizilkaya, K., R. L. Fernando, and D. Garrick. 2009. Simulation of genomic selection in a crossbred beef cattle population. *J. Anim. Sci.* Vol. 87, E-Suppl. 3:52.
94. Abasht, B., E. Beach, J. Arango, P. Settar, J. E. Fulton, N. P. O'Sullivan, A. Hassen, D. Habier, R. L. Fernando, J.C.M. Dekkers, S. J. Lamont. 2009. Extent and consistency of linkage disequilibrium and identification of DNA markers for production and egg quality traits in commercial layer chicken populations. *Plant & Animal Genome XVII Conference*, San Diego, CA. W395.
95. Stricker, C., J. Moll, H. Joerg, D. J. Garrick and R. L. Fernando. 2009. First results on genome-wide genetic evaluation in Swiss Dairy cattle. 60th EAAP Conference, Barcelona 2009.
96. Gorbach, D. M., Cai, W., Dekkers, J. C. M., Young, J. M., Garrick, D. J., Fernando, R. L., Rothschild M. F. 2010. Haplotype analyses of residual feed intake based on genotypes from the PorcineSNP60 BeadChip. 32nd ISAG Conf.
97. Wolc, A, J Arango, P Settar, J Fulton, N Oullivan, R Preisinger, D Habier, D Garrick, R Fernando, S Lamont, J Dekkers. 2011. Persistence of accuracy of estimated breeding values in layers using marker and pedigree based relationship matrices. Abstracts of the Plant & Animal Genome XIX conference, San Diego, P566.
98. Wang, C, D Habier, A Kranis, K Watson, S Avendano, D Garrick, R Fernando, S Lamont, J Dekkers. 2011. Accuracy of genomic EBV using an evenly spaced low density SNP panel in broiler chickens. Abstracts of the Plant & Animal Genome XIX conference, San Diego, P580.
99. \*Zeng, J, A Toosi, RL Fernando, JCM Dekkers, D Garrick. 2011. Genomic selection of purebred animals for crossbred performance under dominance. Abstracts of the Plant & Animal Genome XIX conference, San Diego, P688.
100. \*Sun, X, RL Fernando, DJ Garrick, JCM Dekkers. 2011. An iterative approach for efficient calculation of breeding values and genome-wide association analysis using weighted genomic BLUP. *J. Anim. Sci.* 89, E Suppl.2: 28.  
[http://www.asas.org/abstracts/ASAS\\_2011\\_Sect\\_ABS\\_E-Supplement-2.pdf](http://www.asas.org/abstracts/ASAS_2011_Sect_ABS_E-Supplement-2.pdf).
101. Wolc, A, J Arango, P Settar, JE Fulton, NP Oullivan, R Preisinger, D Habier, R Fernando, DJ Garrick, SJ Lamont, JCM. Dekkers. 2011. Persistence of accuracy of estimated breeding values in layers using marker

- and pedigree based relationship matrices. *J. Anim. Sci.* 89, E Suppl.2: 29.  
[http://www.asas.org/abstracts/ASAS\\_2011\\_Sect\\_ABS\\_E-Supplement-2.pdf](http://www.asas.org/abstracts/ASAS_2011_Sect_ABS_E-Supplement-2.pdf).
102. Wang, C, D Habier, A Kranis, KA Watson, S Avendano, DJ Garrick, R Fernando, SJ Lamont, JCM Dekkers. 2011. Accuracy of genomic EBV using an evenly spaced, low-density SNP panel in broiler chickens. *J. Anim. Sci.* 89, E Suppl.2: 30.  
[http://www.asas.org/abstracts/ASAS\\_2011\\_Sect\\_ABS\\_E-Supplement-2.pdf](http://www.asas.org/abstracts/ASAS_2011_Sect_ABS_E-Supplement-2.pdf).
  103. \*Kizilkaya, K, RL Fernando, D Garrick. 2011. Accuracy of genomic prediction using a threshold model to analyze categorical traits in purebred and crossbred beef cattle populations. *J. Anim. Sci.* 89, E Suppl.2: 31.  
[http://www.asas.org/abstracts/ASAS\\_2011\\_Sect\\_ABS\\_E-Supplement-2.pdf](http://www.asas.org/abstracts/ASAS_2011_Sect_ABS_E-Supplement-2.pdf).
  104. Reecy, JM, RG Tait, DL VanOverbeke, AJ Garmyn, RG Mateescu, AL Van Eenennaam, Q Duan, Q Liu, JP Schoonmaker, ME Drewnoski, DC Beitz, K Kizilkaya, RL Fernando, DJ Garrick. 2011. Use of genomics to improve the fatty acid composition of meat. *J. Anim. Sci.* 89, E Suppl.2: 137.  
[http://www.asas.org/abstracts/ASAS\\_2011\\_Sect\\_ABS\\_E-Supplement-2.pdf](http://www.asas.org/abstracts/ASAS_2011_Sect_ABS_E-Supplement-2.pdf).
  105. Wolc, A., J.M. Hickey, M. Sargolzaei, J. Arango, P. Settar, J.E. Fulton, N.P. Oullivan, R. Preisinger, D. Habier, R. Fernando, D.J. Garrick, C. Wang, and J.C.M. Dekkers. 2011. Comparison of the accuracy of genotype imputation using different methods. P76 in: Proceeding 7th European Symposium on Poultry Genetics.  
<http://www.roslin.ed.ac.uk/7espg/assets/7espg-edited-proceedings.pdf>.
  106. Wolc, A., J. Arango, P. Settar, J.E. Fulton, N.P. Oullivan, R. Preisinger, D. Habier, R. Fernando, D.J. Garrick, C. Wang, and J.C.M. Dekkers. 2011. Accuracy of imputation with low density SNP genotyping of selection candidates and multiple generations of low density genotyped dams. P75 in: Proceeding 7th European Symposium on Poultry Genetics.  
<http://www.roslin.ed.ac.uk/7espg/assets/7espg-edited-proceedings.pdf>.
  107. Wang, C., D. Habier, A. Wolc, A. Kranis, K.A. Watson, S. Avendano, D.J. Garrick, R.S.J. Lamont, and J.C.M. Dekkers. 2011. Accuracy of genomic EBV using an evenly-spaced, low-density, 384-SNP panel in broiler chickens. P73 in: Proceeding 7th European Symposium on Poultry Genetics.  
<http://www.roslin.ed.ac.uk/7espg/assets/7espg-edited-proceedings.pdf>
  108. Saatchi, M, DJ Garrick, RL Fernando, N Boddicker. 2012. Comparison of Different Bayesian Methods for QTL Mapping in Hereford Beef Cattle Using 1 Mb Windows. Abstracts of the Plant & Animal Genome XX conference, San Diego, P0552.  
<http://pag.confex.com/pag/xx/webprogram/Paper3217.html>
  109. Peters, SO, K Kizilkaya, M Thomas, RL Fernando, J Reecy, A Yakubu, M De Donato, I Imumorin. 2012. Whole Genome Linkage Disequilibrium

- Pattern in US Brangus Heifers. Abstracts of the Plant & Animal Genome XX conference, San Diego, P0558.  
<http://pag.confex.com/pag/xx/webprogram/Paper3583.html>
110. Wolc, J. Arango, P. Settar, J.E. Fulton, N.P. Oullivan, R. Preisinger, D. Habier, R. Fernando, D.J. Garrick, and J.C.M. Dekkers. 2012. Genome wide association study for egg defects in layer chickens. Abstracts of the Plant & Animal Genome XX conference, San Diego, W592.  
<http://pag.confex.com/pag/xx/webprogram/Paper2564.html>
  111. Wolc A, J Arango, P Settar, JE Fulton, NP O'Sullivan, R Preisinger, RL Fernando, DJ Garrick, J Dekkers. 2012. Application of a Weighted Genomic Relationship Matrix to Breeding Value Prediction for Egg Production in Laying Hens. Abstracts of the Plant & Animal Genome XXI conference, San Diego, abstract P0639.
  112. Bowerman NC, RL Fernando, C Stricker, DJ Garrick. 2012. Using Genomic Relationships to Identify Haplotypes. Abstracts of the Plant & Animal Genome XXI conference, San Diego, abstract P0532.
  113. Peters SO, K Kizilkaya, IG Imumorin, M Thomas, RL Fernando, JM Reecy, M De Donato, DJ Garrick. 2012. Genome-Wide Linkage Disequilibrium Patterns in 10 Beef Cattle Breeds. Abstracts of the Plant & Animal Genome XXI conference, San Diego, abstract P0530.
  114. \*Habier D, RL Fernando, DJ Garrick. 2012. The three types of quantitative-genetic information in genomic prediction. Abstracts of the Plant & Animal Genome XXI conference, San Diego, abstract W359.
  115. Wolc A, J Arango, P Settar, JE Fulton, NP Oullivan, R Preisinger, D Habier, R Fernando, DJ Garrick and JCM Dekkers. 2012. Genome wide association study for egg production and egg quality in layer chickens. World Poultry Conference held 5-9 August 2012 at Bahia convention center, Brazil.
  116. Saatchi M, RL Fernando and DJ Garrick. 2012. QTL mapping and prediction of direct genomic breeding value using 1 Mb SNP windows and Bayesian inference. Abstract, 16th QTL-MAS workshop held in Alghero, Italy.
  117. Wang C, D Habier, L Peiris, A Wolc, A Kranis, KA Watson, S Avendano, DJ Garrick, RL Fernando, SJ Lamont, and JCM Dekkers. 2012. Identification of genomic regions affecting body weight and hen house production using genomic prediction methods in broiler chickens. Abstract 60,  
<http://adsa.asas.org/midwest/2012/MW2012Abstracts.pdf>
  118. Wolc A, J Arango, P Settar, JE Fulton, NP Oullivan, R Preisinger, D Habier, R Fernando, DJ Garrick and JCM Dekkers. 2012. Analysis of egg production using a random regression model with genomic relationships

- in layer chickens. *J Anim Sci Vol 90 Suppl. 3/J Dairy Sci Vol 95 Suppl 2* : 726.  
<http://www.jtmtg.org/2012/abstracts/686.pdf>
119. Peters, SO, K Kizilkaya, DJ Garrick, RL Fernando, EJ Pollak, M DeDonato, E Chaffee, T Hussain, and IG Imumorin. 2012. Model comparison for genetic parameter estimation of birth and weaning weight traits in beef cattle. *J Anim Sci Vol 90 Suppl. 3/J Dairy Sci Vol 95 Suppl 2*: M35.  
<http://www.jtmtg.org/2012/abstracts/15.pdf>
  120. Wolc, A, J Arango, P. Settar, JE Fulton, NP Oullivan, R Preisinger, D Habier, R Fernando, DJ Garrick, and JCM Dekkers. 2012. Genome wide association study for egg defects in layer chickens. Abstracts of the Plant & Animal Genome XX conference, San Diego, W592.  
<http://pag.confex.com/pag/xx/webprogram/Paper2564.html>
  121. Peters, SO, K Kizilkaya, M Thomas, RL Fernando, J Reecy, A Yakubu, M De Donato, I Imumorin. 2012. Whole Genome Linkage Disequilibrium Pattern in US Brangus Heifers. Abstracts of the Plant & Animal Genome XX conference, San Diego, P0558.  
<http://pag.confex.com/pag/xx/webprogram/Paper3583.html>
  122. Saatchi, M, DJ Garrick, RL Fernando, N Boddicker. 2012. Comparison of Different Bayesian Methods for QTL Mapping in Hereford Beef Cattle Using 1 Mb Windows. Abstracts of the Plant & Animal Genome XX conference, San Diego, P0552.  
<http://pag.confex.com/pag/xx/webprogram/Paper3217.html>
  123. \*Edriss, V, RL Fernando, G Su, Mogens, S Lund, B Guldbrandtsen. 2012. Haplotypes based on local genealogies for genomic prediction. 4th International Conference on Quantitative Genetics. Edinburgh.
  124. Stricker, C. and RL Fernando. 2013. Genauigkeit genomischer Zuchtwerte: Cosegregation or Linkage Disequilibrium? Swiss Association for Animal Production.
  125. Wolc, A., J. Arango, P. Settar, J.E. Fulton, N.P. Oullivan, R. Preisinger, D. Habier, R.L. Fernando, D.J. Garrick, S.J. Lamont, and J.C. Dekkers. 2013. Genomic selection in layer chickens outperforms pedigree-based selection. Proceedings ASAS/ADSA 45th Midwestern sectional scientific sessions and business meeting, abstract O071.
  126. \*Sun, X., R.L. Fernando, D.J. Garrick, and J.C.M. Dekkers. 2013. Accurate prediction of genomic breeding values across families combining linkage disequilibrium and co-segregation. Proceedings ASAS/ADSA 45th Midwestern sectional scientific sessions and business meeting, abstract O181.

127. Fernando, R.L., D. Garrick, J.C.M. Dekkers. 2013. Bayesian regression method for genomic analyses with incomplete genotype data. Abstracts of EAAP, 64th Annual meeting held in Nantes, France, page 225.
128. Su, H., J. Lee, M. Saatchi, R.L. Fernando, D.J. Garrick. 2014. Population structure of ten US beef cattle breeds revealed by principal components analysis on genomic data. Abstracts of the Plant & Animal Genome XXII conference, San Diego, abstract P531.  
<https://pag.confex.com/pag/xxii/webprogram/Paper11207.html>
129. Wolc, A., J. Arango, P. Settar, J.E. Fulton, R.L. Fernando, D.J. Garrick, J. Dekkers, N.P. Sullivan. 2014. Genome wide association study for heat stress mortality in a white egg layer line. Abstracts of the Plant & Animal Genome XXII conference, San Diego, abstract P641.  
<https://pag.confex.com/pag/xxii/webprogram/Paper11328.html>
130. Baes, C.F., M.A. Dolezal, E. Fritz-Waters, J. Koltjes, B. Bapst, C. Flury, H. Signa-Hasler, C. Stricker, R.L. Fernando, J.M. Reecy, D. J. Garrick, R. Fries, B. Gredler. 2014. Comparison of variant calling pipelines for whole-genome sequencing data in dairy cattle. Abstracts of the Plant & Animal Genome XXII conference, San Diego, abstract P1053.  
<https://pag.confex.com/pag/xxii/webprogram/Paper12007.html>
131. Fernando, R.L., H. Cheng, X. Sun. Implications of using identity-by-descent versus identity-by-state matrices in genetic analyses. Abstracts of the Plant & Animal Genome XXII conference, San Diego, abstract W766.  
<https://pag.confex.com/pag/xxii/webprogram/Paper10910.html>
132. Garrick, D.J., J.C.M. Dekkers, R.L. Fernando. 2014. Genomic analysis combining genotyped and non-genotyped individuals. Abstracts of the Plant & Animal Genome XXII conference, San Diego, abstract W766.  
<https://pag.confex.com/pag/xxii/webprogram/Paper10906.html>
133. \*Cheng, H., R.L. Fernando, D.J. Garrick. 2014. A Gibbs sampler for BayesB. Proceedings ASAS/ADSA 46th Midwestern sectional scientific sessions and business meeting.
134. Su, H., J. Koltjes, M. Saatchi, J. Lee, R. Fernando, D.J. Garrick. 2014. Haplotype diversity analysis in ten US cattle breeds. Proceedings ASAS/ADSA 46th Midwestern sectional scientific sessions and business meeting.
135. M. Heidaritabar, A. Wolc, J. Arango, P. Settar, J.E. Fulton, N.P. Osullivan, J.W.M. Bastiaansen, J. Zeng, R. Fernando, D.J. Garrick, J. Dekkers. 2015. Impact of fitting dominance effects on accuracy of genomic prediction in layer chickens. Abstract 259.  
<http://nutrition.ansci.illinois.edu/sites/default/files/EAAP2015abstracts.pdf>

136. Wolc, A., J. Arango, P. Settar, J.E. Fulton, N.P. OSullivan, R.L. Fernando, D.J. Garrick, J.C.M. Dekkers. 2015. Genetics of male reproductive performance in White Leghorns. Proceedings of the EAAP annual meeting. <http://nutrition.ansci.illinois.edu/sites/default/files/EAAP2015abstracts.pdf>
137. S.O. Peters, K. Kizilkaya, D.J. Garrick, R.L. Fernando, I.G. Imumorin, M.G. Thomas. 2015. Use of a robust Bayesian regression model in genome-wide association study of growth traits in Brangus heifers. Abstract T80. Proceedings of the joint meeting of the American Dairy Science Association and the American Society of Animal Science. <http://www.jtmtg.org/JAM/2015/abstracts/341.pdf>
138. Z-Q. Weng, A. Wolc, R.L. Fernando, J.C.M. Dekkers, J. Arango, P. Settar, J.E. Fulton, N.P. OSullivan, D.J. Garrick. 2015. Recombination rates in layer chickens. Proceedings of the joint meeting of the American Dairy Science Association and the American Society of Animal Science. Abstract M70. <http://www.jtmtg.org/JAM/2015/abstracts/32.pdf>
139. \*J. Zeng, D.J. Garrick, R.L. Fernando. 2015. Comparison of a QTL versus marker effects model for genomic prediction with training across families, generations, or breeds. Proceedings ASAS/ADSA 47th Midwestern sectional scientific sessions and business meeting. Abstract 025. [http://www.jtmtg.org/Midwest/Midwest\\_Abstracts-2015.pdf](http://www.jtmtg.org/Midwest/Midwest_Abstracts-2015.pdf)
140. \*X. Sun, R.L. Fernando, D.J. Garrick, J.C.M. Dekkers. 2015. Improved accuracy of genomic prediction combining linkage disequilibrium and cosegregation by fitting haplotypes in addition to SNP genotypes. Proceedings ASAS/ADSA 47th Midwestern sectional scientific sessions and business meeting. Abstract 024. [http://www.jtmtg.org/Midwest/Midwest\\_Abstracts-2015.pdf](http://www.jtmtg.org/Midwest/Midwest_Abstracts-2015.pdf)
141. R. L. Fernando, J. Zeng, H. Cheng, D. Habier, A. Wolc, D. J. Garrick, J. C. M. Dekkers. 2016. Discovery of quantitative trait loci using a quantitative trait loci effects model in a multigenerational pedigree. Proceedings ASAS/ADSA 48th Midwestern sectional scientific sessions and business meeting. *J. of Anim. Sci.* 94, Supplement 2, Abstract 36.
142. R. L. Fernando, D. J. Garrick. 2017. Strategies to improve numerical stability of equations used for genomic prediction of genetic merit. *Plant & Animal Genome XXV conference*, San Diego, abstract W448.
143. Sero, NVL, Gutierrez, NA, Wolc, A, Fernando, RL. 2018. To block or not to block: The tale of initial weight in swine nutrition trials. *J. of Anim. Sci.* 96, Issue suppl2, pp 193-194.



## Theses

1. Fernando R. L. 1981. Scaling ordered categorical variables in relation to sire evaluation for frame score at weaning in Angus cattle. M.S. Thesis. University of Illinois. 116 pp.
2. Fernando, R. L. 1984. Assortative mating and selection. Ph.D. Thesis. University of Illinois. 138 pp.

## Theses Supervised

1. Ang, Iris Hui-Chi. 1990. Comparison of alternative mixed linear model analyses of unbalanced data. M.S. Thesis. 163 pp.
2. Cantet, R. C. 1990. Estimation and prediction problems in mixed linear models for maternal genetic effects. Ph.D. Thesis. 183 pp. (supervised jointly with Dan Gianola)
3. Soto-Murillo, H. W. 1991. Methods for checking the goodness of fit of alternative nonlinear mixed models with an application in fertility traits of beef cows. Ph.D. Thesis. 149 pp. (supervised jointly with Dan Gianola)
4. Lo, L. L. 1993. Genetic evaluation and selection in multibreed populations. Ph.D. Thesis. 168 pp.
5. Wang, T. 1998. Genetic evaluation and parameter estimation using marker and trait information. Ph.D. Thesis. 102 pp.
6. McPherson, S. K. 1999. Estimation of genetic covariances between antibody response and bacterial burden. M.S. Thesis. 47 pp.
7. Santos, N. 2001. Estimation of adjustment factors for 3X milking. Ph.D. Thesis. 186 pp. (supervised jointly with A. E. Freeman)
8. Benson, T. J. 2001. Use of the expected log likelihood to evaluate designs for mapping quantitative trait loci. M. S. Thesis. 96 pp.
9. Fernández, S. A. 2001. An algorithm to sample genotypes in complex pedigrees. Ph.D. Thesis 132 pp. (supervised jointly with Alicia Carriquiry)
10. Totir, L. R. 2002. Genetic evaluation with finite locus models. Ph.D. Thesis. 124 pp.
11. Fonseca, da R. 2003. Use of information on identified genes to reduce the selection bias on genetic evaluation. Ph.D. Thesis. 56 pp. (supervised jointly with Ricardo Euclides).
12. Pita, F. V. da C. 2003. Construction of the gametic covariance matrix for quantitative trait loci analyses in outbred populations. Ph.D. Thesis. 61 pp. (supervised jointly with Paulo Savio Lopes)

13. Grapes, L. 2004. Molecular, bioinformatic and statistical approaches to identify genes underlying complex traits in livestock. Ph.D. Thesis. 118 pp. (supervised jointly with Max Rothschild)
14. He, Wei. 2011. A combined linkage disequilibrium and cosegregation method for fine mapping of QTL and approaches to study the long-term accuracy of genomic selection. Ph.D. Thesis. 183 pp.
15. Zeng, Jian. 2011. Genomic selection of purebred animals for crossbred performance under dominance. M.S. Thesis. 65 pp.
16. Toosi, Ali. 2012. Genome-wide prediction of breeding values and mapping of quantitative trait loci in stratified and admixed populations. Ph.D. Thesis. 208 pp.
17. Sun, Xiaochen. 2014. Genomic prediction using linkage disequilibrium and co-segregation. Ph.D. Thesis. 183 pp.
18. Zeng, Jian. 2015. Whole genome analyses accounting for structures in genotype data. Ph.D. Thesis. 144 pp.
19. Cheng, Hao. 2017. Contributions to improve the accuracy and computational efficiency of genomic prediction. Ph.D. Thesis. 106 pp.

### **Postdoctoral Research Supervision**

1. Bruce Southey. 1996-1998. Research topic: “QTL mapping by pedigree analysis”.
2. Soledad A. Fernandez. 2001 ( 8 months). Research topic: QTL mapping using the IBD approach”, (jointly with Jack Dekkers).
3. Liviu R. Totir. 2002-2005. Research topic: “Use of sampling techniques for refined QTL analysis in complex pedigrees” (jointly with Jack Dekkers)..
4. Mehmet Firat. 2003-2004. Research topic: “QTL detection using linkage and linkage disequilibrium”, (jointly with Jack Dekkers).
5. Helene Gilbert. 2003-2004. Research topic: “Use of linkage-disequilibrium and cosegregation information for marker assisted selection”.
6. Joseph Abraham, 2004-2005. Research topic: “Use of MCMC methods for marker assisted selection”.
7. Tian Kechuan. 2005-2006. Research topic: “Use of marker data for computing gametic relationship matrices”.
8. David Habier. 2006-2008. Research topic: “Improved methods for marker assisted and genomic selection”.

9. Kadir Kizilkaya. 2008-2013. Research topic: “Utilization of natural genomic variation”, (jointly with Dorian Garrick).
10. Mahdi Saatchi. 2012-2014. Research topic: “Factors affecting prediction accuracy of complex human traits and diseases”.
11. Jian Zeng. 2015. Research topic. “Single-step Bayesian method for genomic prediction that combines information from genotyped and non-genotyped animals”
12. Bujun Mei. 2015-2016. Research topic. “Pedigree-free linkage analysis for GWAS”.
13. Wan-Ling Hsu. 2014-2016. Research topic. “Accounting for breed differences in whole-genome analyses that combine information from genotyped and non-genotyped animals”.
14. Joonho Lee. 2016-2017. Research topic. “Single-step Bayesian method for genomic prediction that combines information from genotyped and non-genotyped animals”.

## Courses Taught

Semester-year	Course	Hours	Enrollment
Fall-1985	Advanced Quantitative Genetics	4	6 students about 10 others
Spring-1986	Statistical Methods	4	27 students
Spring-1987	Statistical Methods	4	38 students
	Animal Breeding Seminar	1	16 students
	Research Studies in Animal Science	1	1 student
Spring-1988	Statistical Methods	4	26 students
	Research Studies in Animal Science	1	1 student
Spring-1989	Statistical Methods	4	27 students
Spring-1990	Statistical Methods	4	17 students
	Research Studies in Animal Science	1	1 student
Summer-1990	Research Studies in Animal Science	1	1 student
Spring-1991	Statistical Methods	4	14 students
Fall-1992	Animal Breeding Seminar	1	6 students
Spring-1993	Statistical Methods	4	30 students
	Quantitative Genetics	4	3 students 4 others
Spring-1994	Statistical Methods	4	30 students
	Quantitative Genetics	4	5 students
	Animal Breeding Seminar	1	10 students
Fall-1994	Statistical Methods to Map QTL	4	7 students about 5 others
Spring-1995	Statistical Methods	4	22 students
	Quantitative Genetics	4	5 students
Spring-1996	Quantitative Genetics	4	7 students
Summer-1996	Statistical Methods to Map QTL	3	20 students and others
Fall-1996	Statistical Methods to Map QTL	2	30 students and others
Spring-1997	Population Genetics	3	14 students
Summer-1997	Linear Models in Animal Breeding	4	37 students and others
Fall-1997	Applied Animal Breeding	2	14 students
Spring-1998	Statistical Methods to Map QTL	2	10 students
Fall-1998	Population Genetics	4	14 students
Spring-1999	Statistical Methods to Map QTL	2	15 students 3 faculty
Fall-1999	Population Genetics	4	16 students
Spring-2000	Statistical Methods to Map QTL	2	10 students
Spring-2000	Bioinformatics	2	10 students
Fall-2000	Population Genetics	4	8 students
Fall-2001	Computing Methods for Animal Breeders	2	8 students
Fall-2001	Population Genetics	4	14 students

## Courses Taught (continued)

Semester-year	Course	Hours	Enrollment
Spring-2002	Statistical Methods to Map QTL	2	7 students
	Advance Quantitative Genetics	2	3 students
Fall-2002	Population Genetics	4	13 students
Fall-2003	Computing Methods for Animal Breeders	4	5 students
Spring-2004	Statistical Methods to Map QTL	2	5 students
Summer-2004	QTL Mapping in Complex Pedigrees	2	25 students
Summer-2005	C++ Programming	2	17 students
Fall-2007	Computing Methods for Animal Breeders	2	5 students
Spring-2006	Statistical Methods to Map QTL	2	8 total 2 for credit
Fall-2007	Computing Methods for Animal Breeders	4	2 students
Spring-2008	Statistical Methods to Map QTL	2	6 students 8 total
Summer-2009	Genomic Selection in Livestock		70 participants
February-2010	Armidale, Australia		about 40 participants
Summer-2010			63 participants
Fall-2009	Computing Methods for Animal Breeders	4	2 students
Summer-2011	Genomic Selection Davos, Switzerland		41 participants
	Wageningen, Netherlands		50 participants
Summer-2012	Phoenix, Arizona		about 40 participants
Fall-2011	Computing Methods for Animal Breeders	4	2 student
Spring-2013	Statistical Methods to Map QTL	2	3 students 6 total
Fall-2013	Computing Methods for Animal Breeders	4	3 student
Summer-2013	Genomic Selection Quebec City, Canada		35 participants
	Samsun, Turkey		30 participants
	Davos, Switzerland		20 participants
Fall-2013	Piacenza, Italy		60 participants

## Courses Taught (continued)

Semester-year	Course	Hours	Enrollment
Spring-2015	Statistical Methods to Map QTL	2	1 student
Summer-2015	Genomic Selection Iowa State Davos, Switzerland		70 participants 10 participants
Fall-2015	Computing Methods for Animal Breeders	4	3 student about 3 others
Fall-2015	Genomic Prediction and Genome-Wide Association Studies Palmerston North, New Zealand Hamilton, New Zealand		25 participants 25 participants
Spring-2016	Workshop on Genomic Selection in Livestock Egerton University, Kenya		about 30 participants
Fall-2018	Whole Genome Analyses using Julia Technical University of Munich		about 30 participants
Spring-2019	Statistical Methods to Map QTL	2	3 students
Summer-2019	Modern Programming in Genomic Prediction. UC Davis, CA USA. Bayesian Methods for Genomics China Agricultural University Beijing, China		40 participants 70 participants
Fall-2019	Computing Methods for Animal Breeders	4	3 students

## Description of Courses

**Statistical Methods** I have had primary responsibility for teaching this course for 9 semesters to a total of 231 students. This is a 1-unit course with three one-hour lecture periods and two one-hour lab periods per week. I present the lectures and supervise one or two teaching assistants for the laboratory. This course in applied statistics is aimed at giving students an introduction to the analysis of unbalanced data, using computers. It is taken primarily by graduate students in the College of Agriculture, and it is cross listed with the Departments of Agricultural Engineering and Forestry.

Based on the evaluations of students taking this course, in the Spring of 1991, I was included in the list of teachers ranked excellent by their students.

**Introductory Quantitative Genetics** I have taught this course for 4 semesters to a total of 18 students. This is a 1-unit course with four one-hour lecture pe-

riods per week. This course is aimed at giving students a solid introduction to the fundamentals of Quantitative Genetics. It is taken primarily by graduate students in plant and animal breeding, and it is cross listed with Biology.

Based on the evaluations of students taking this course, in the Spring of 1994, I was included in the list of teachers ranked excellent by their students.

**Advanced Quantitative Genetics** In 1985, co-taught this course, with Dr. Gianola and with guest lectures by several other faculty to a group of about 20 including 8 to 10 faculty members and visiting scholars. I presented and discussed nine out of 37 key papers. Notes were provided for each paper with detailed derivations of formulae.

**Statistical Methods to Map QTL** I taught this course in 1994 to a group of 7 students and several faculty and research associates. This is a 1-unit course with four one-hour lecture periods per week. The material covered included the theory of maximum likelihood estimation, hypothesis testing in relation to linkage analysis, methods for linkage analysis between markers, between markers and QTL in crosses of inbred lines, and between markers and QTL in outbred populations. In the summer of 1996, this course was taught at the University of Wisconsin (Madison) to a group of about 20. In the fall of 1996 part of this material was taught to a group of about 30, including some faculty members, at Iowa State University. This course is offered every other year at ISU. In 1999, I taught some of this material in Argentina and Brazil. In Spring 2002, I introduced the use of Bayesian methods. In 2008, the focus of the course was changed to the analysis to whole-genome data. New material introduced included: 1) theory on the generation of linkage disequilibrium due to genetic drift in finite populations; 2) Bayesian variable selection methods; and 3) whole-genome selection. In 2015, The course material, including programs for analysis of data, were presented in a Jupyter notebook format, using the Julia dynamic programming language.

**Computing Techniques in Animal Breeding** I helped Dr. Groeneveld develop and teach this course for the first time in 1989. I taught about 10 percent of the course. The code that was prototyped during the development of this course led to the package PEST.

**Animal Breeding and Genetics Seminar** I was responsible for organizing this seminar class for three semesters.

**Research Studies in Animal Science** I have directed students in independent research projects in Monte-Carlo simulation studies, estimation of genetic parameters, theory of covariance between relatives, and mitochondrial inheritance.

**Population Genetics** I taught this course for the first time in the Spring of 1997 at Iowa State University. This course is aimed at giving students a solid introduction to the fundamentals of Population and Quantitative Genetics. It is taken primarily by graduate students in Animal Breeding, Plant Breeding and Interdepartmental Genetics. In Fall 1998, this course was expanded to cover some more material relevant to plant breeding and was taught as a four hour course jointly by Jim Holland and me.

**Linear Models in Animal Breeding** I was invited to teach this as Nordic-Ph.D. course in the Summer of 1997 to 37 students and young research scientists. The topics included the theory underlying estimation of fixed effects and hypothesis testing, prediction of random effects, and estimation of variance components using maximum likelihood techniques.

**Applied Animal Breeding** I was responsible for teaching this course through distance learning methods (ICN and video tapes) to 14 students in the Fall of 1998. Half of this two hour course dealt with theory and concepts underlying animal breeding. I gave the lectures on theory and concepts. The second half of the course covered the application of these concepts to genetic improvement in the swine, beef, dairy, poultry, and sheep industries. The lectures on industry applications were given by five others.

**Bioinformatics** This was an informal workshop, organized by ETH, Zurich, Switzerland, to introduce the problems and concepts in the field of Bioinformatics and Computational Biology to Animal Breeders. I taught it once in May, 2000 at St. Moritz, Switzerland, and there were 10 Animal Breeders from Switzerland, Germany, and France. The topics covered included the analysis of biological sequence data, linkage analysis, and molecular phylogeny construction.

**Advanced Computational Methods in Animal Breeding** This course is offered in two modules. In module 1, students learn how to use C++ to solve Henderson's mixed model equations by iterative techniques for very large pedigrees. In Module 2 estimation of parameters is considered. This module was taught for the first time in 2004 and estimation of variance components in mixed linear models by maximum likelihood was considered. Simple models were used to introduce concepts. Subsequently, the models were extended to accommodate multiple traits, correlated random effects, and marker data. In Summer of 2005, module 1 was taught as a two-week short course. In the Fall, I taught the second module where students learned to simulate genomic data and how to modify the mixed model programs to estimate parameters by Bayesian methods. In the Fall of 2009, the course was offered as an online course to students at Iowa State. In Fall of 2015, the course was taught at ISU using the Julia dynamic programming language.



**Genomic Analyses using Julia** A workshop was offered at the Technical University of Munich, December 3–7. Students were introduced to 1) XSim, a package for simulation of genomic data from breeding populations; JWAS, a Julia package for Bayesian analyses of genomic data; use of Julia as a matrix calculator; advanced programming techniques such as the use of recursive functions, associative arrays and sparse matrices.

**Advanced Quantitative Genetics** Advanced linear and non-linear methods for analyses of quantitative traits. In Spring 2002, I taught this course for the first time with Jack Dekkers. My lectures were on the analysis of data from populations undergoing selection and non-random mating and on the theory underlying Markov Chain Monte Carlo methods.

**QTL Mapping in Complex Pedigrees** This course was offered as a summer workshop in 2004. Theory and algorithms were presented for QTL mapping in outbred populations using linear model and mixture model methods. Computer programs for implementing these methods were discussed and made available to the students.

**Use of High-density SNP Genotyping for Genetic Improvement of Livestock** This course focuses on theory and applications related to the use of whole-genome SNP data for genetic improvement of livestock. It has been taught jointly, and my contributions have been on the theory of Bayesian methods and their implementations. Taught Summer 2009 with Jack Dekkers (JD) and Dorian Garrick (DG), February 2010 in Armidale, Australia with DG, Summer 2010 with JD and DG, 2013 with JD and DG in Quebec City, with DG in Samsun, Turkey and Davos Switzerland, by myself in Piacenza, Italy and February 2016 with DG in Njoro, Kenya.

## Honors and Awards

1. Ralph and Mabel Hunter Fellowship, College of Agriculture, University of Illinois. 1978–1979.
2. Jessie E. Hackett Fellowship, College of Agriculture, University of Illinois. 1981–1982.
3. Full Scholarship to participate in the 3rd International Summer School in Agriculture “Modern Techniques in Animal Breeding”, Dublin, Ireland. 1983.
4. Norton Prize in Statistics (for outstanding student contributions to Theoretical or Applied Statistics), Graduate College Statistics Program, University of Illinois. 1985.

5. University of Illinois Teachers Ranked Excellent by Their Students: Statistical Methods–1991, Quantitative Genetics–1994.
6. Over 50 invited lectures in U.S. and 14 foreign countries. 1984–present.
7. Associate editor for Genetics, Selection and Evolution. 1992–1994.
8. Advisory Board, Genetics, Selection and Evolution. 1998–2000.
9. Scientific Program Chair for session on Estimation of Genetic Parameters, 6th World Congr. Genetics Appl. Livest. Prod. Armidale, Australia. 1998.
10. Henderson Lecturer, 1998. Department of Animal Science, Cornell University, Ithaca, New York.
11. Review Panel, USDA Scientific Quality Control. 2002.
12. ASAS travelling fellow to European Association of Animal Production, 2004.
13. Rotary LeClerg Lecture, University of Maryland. 2009.
14. Associate Editor, Frontiers in Livestock Genomics, 2011–
15. Rockefeller Prentice Memorial Award in Animal Breeding and Genetics. American Society of Animal Science. 2012.
16. ASAS travelling fellow to European Association of Animal Production, 2013.
17. AL Rae Centre for Genetics and Breeding Travel Fellowship. Massey University, Palmerston North, New Zealand. 2018.

## Invited Lectures

1. Discussant in symposium, “New Statistical Methods in Animal Breeding and Genetics”, at the American Society of Animal Science Annual Meeting. 1984.
2. Optimum designs for sire evaluation schemes. At the “International Symposium on Advances in Statistical Methods for Genetic Improvement of Livestock”, Armidale, Australia. 1987.
3. Statistical inferences in populations undergoing selection or non-random mating. At the “International Symposium on Advances in Statistical Methods for Genetic Improvement of Livestock”, Armidale, Australia. 1987.

4. Prioritizing Animal Breeding Research for the 90's: Statistics. At the Annual Meeting of the American Society of Animal Science, Midwestern section. 1989.
5. Integrated Strategies and methodologies for the genetic improvement of animals. At the "Symposium on the Role of Animal Breeding in an Age of Molecular and Zygotic Manipulation", at the Annual Meeting of the American Society of Animal Science. 1989.
6. Marker assisted selection. At conference on "Mapping Domestic Animal Genomes: Needs and Opportunities". Allerton Park, IL. 1990.
7. Statistical problems in marker assisted selection for QTL. At workshop on "Genetic Parameter Estimation", 4th Wld. Cong. Genet. App. Liv. Prod., Edinburgh, Scotland. 1990.
8. Best linear unbiased prediction. At the Department of Biometry and Genetics, Louisiana State University, Medical Center. 1991.
9. An alternative formulation of the mixed model of inheritance for segregation and linkage analysis. At E.T.H. Zürich, Switzerland. 1992.
10. Best linear unbiased prediction theory for marker assisted selection. At E.T.H. Zürich, Switzerland. 1992.
11. Statistical problems in marker assisted selection for QTL. At I.N.R.A. Jouy-en-Josas, France. 1992.
12. An alternative formulation of the mixed model of inheritance for segregation and linkage analysis. At I.N.R.A. Jouy-en-Josas, France. 1992.
13. Comparison of alternative approaches for analysis of data with mixed model inheritance. At I.N.R.A. Jouy-en-Josas, France. 1992.
14. Best linear unbiased prediction theory for marker assisted selection. At I.N.R.A. Jouy-en-Josas, France. 1992.
15. Best linear unbiased prediction theory for marker assisted selection. At I.N.R.A. Toulouse, France. 1992.
16. Genetic means and covariances between relatives in crossbred populations under dominance. At the University of Wisconsin, Madison, Wisconsin. 1993.
17. Design of QTL experiments in cattle. At workshop on "The Design of Experimental Populations to Detect and Map Livestock QTL", 5th Wld. Cong. Genet. App. Liv. Prod. Guelph, Canada. 1994.
18. Likelihood analysis of extended pedigrees under mixed inheritance. At Annual Meeting of the International Biometric Society, German Region. Hohenheim University, Stuttgart. Germany. 1995.

19. Theory for genetic evaluation in crossbred populations. At E.T.H. Zürich, Switzerland. 1995.
20. Theory for genetic evaluation in crossbred populations. At Hohenheim University, Stuttgart. Germany. 1995.
21. Statistical methods for marker-QTL studies. At Hebrew University of Jerusalem, Rehovot, Israel. 1995.
22. Theory for genetic evaluation in crossbred populations under dominance inheritance. At University of Guelph, Guelph, Canada. 1995.
23. Genetic evaluation in crossbred populations. At National Breeders Roundtable. 1996.
24. Multiple tests in linkage analysis. At Allerton II: Genetic Analysis of Economically Important Traits in Livestock. 1996.
25. Detection and utilization of single genes without DNA assays. At the "Dairy Cattle Improvement Symposium in Honor of Prof. Charles Smith on Breeding Objectives and Strategies", at the Annual Meeting of the American Dairy Science Association. 1997.
26. Controlling error rates in mapping QTL. At Agricultural University of Norway, Ås, Norway. 1997.
27. Controlling error rates in mapping QTL. At Danish Institute of Animal Science, Tjele, Denmark. 1997.
28. Controlling error rates in mapping QTL. At E.T.H. Zürich, Switzerland. 1997.
29. Genetic evaluation and selection using genotypic, phenotypic and pedigree information, 6th Wld. Cong. Genet. App. Liv. Prod. Armidale, Australia. 1998.
30. Controlling error rates in mapping QTL. At Department of Epidemiology and Biostatistics, Case Western Reserve University, Cleveland, Ohio, 1998.
31. Identification of QTL and ETL. Ensminger International Workshop. Central Agricultural University, Wuhan, China. 1998.
32. Genomics and Computational Biology. Ensminger International Workshop. Central Agricultural University, Wuhan, China. 1998.
33. Genomics and Computational Biology. Ensminger International Workshop. China Agricultural University, Beijing, China. 1998.
34. Genetic Evaluation in Crossbred Populations. Department of Animal Science, Cornell University, Ithaca, New York. 1998.

35. A two-stage test for mapping QTL. University of Wisconsin. Madison, Wisconsin. 1999.
36. An alternative approach to control false discoveries in detecting QTL. Biotechnology Seminar, University of Nebraska, Lincoln, Nebraska. 1999.
37. Analysis of data from crossbred populations. International Symposium on Animal Breeding and Genetics. Federal University of Vicosa, Brazil. 1999.
38. Theory for analysis of data from multibreed populations. Genetic Prediction Workshop of the Beef Improvement Federation. 1999.
39. Controlling the relative frequency of false positives in a multiple test situation. Baker Center for Bioinformatics and Biological Statistics, Iowa State University, Ames, Iowa. 2000.
40. An Algorithm to Obtain an Irreducible Markov Chain to Sample Marker Genotypes. Statistical Methods of Pedigree Analysis Workshop, IX International Plant and Animal Genome Conference. San Diego, California. 2001.
41. An alternative approach to control false positives in QTL scans. Session I: Advances in genetic analysis and evaluation. 512<sup>th</sup> EAAP Conference, Budapest, Hungary. 2001.
42. Controlling the proportion of false positives in genome scans for QTL. NCR-199 Committee Meeting, Cornell University, Ithaca, NY. 2001.
43. Advances in genetic and statistical models to predict breeding values. 7<sup>th</sup> World Congress Genet. Appl. Livest. Prod. France. 2002.
44. Statistical Issues In Marker Assisted Selection. 8<sup>th</sup> Genetic Prediction Workshop of the Beef Improvement Federation. 2003.
45. Use of Linkage Disequilibrium for Fine Mapping Quantitative Trait Loci. Department of Statistics, Iowa State University, Ames, Iowa. 2003.
46. Incorporating molecular markers into genetic evaluation. EAAP Conference, Bled, Slovenia. 2004.
47. Controlling the proportion of false positives in multiple dependent tests. Department of Epidemiology and Biostatistics, Case Western Reserve University School of Medicine, Cleveland, Ohio. 2004.
48. Incorporating Molecular Markers into Genetic Evaluation. Pioneer Hi-Bred International, Johnston, Iowa. 2005.
49. Combining Disequilibrium and Cosegregation Information to Map Quantitative Trait Genes. Department of Epidemiology and Biostatistics, Case Western Reserve University School of Medicine, Cleveland, Ohio. 2005.

50. Theory for genetic evaluation given genotypes at a trait locus. Roslin Institute, Edinburgh, Scotland, UK. 2005.
51. Marker assisted BLUP. Genesis Faraday Symposium on High throughput genotyping, numerical genomics and quantitative genetics in farm animals. Edinburgh, Scotland, UK. 2006.
52. Algorithms to compute allele state and origin probabilities for QTL mapping. 8th World Congress Genet. Appl. Livest. Prod. Brazil. 2006.
53. Genomic selection. Symposium on "Statistics in animal breeding and quantitative genetics: the next 60 years". Sonderborg, Denmark. 2007.
54. Unraveling a paradox in marker assisted selection. Statistical Genomics Workshop, International Plant and Animal Genome Conference XVI. San Diego, California. 2008.
55. Alternative approaches for whole-genome analyses. Joint Biometric Conference of the German Region. Munich, Germany. 2008.
56. Genomic selection of purebreds for crossbred performance. National Breeders Roundtable. 2008.
57. Genomic selection of purebreds for crossbred performance. I.N.R.A. Jouy-en-Josas, France. 2008.
58. Genomic selection of purebreds for crossbred performance. I.N.R.A. Toulouse, France. 2008.
59. DNA technology: estimation of genetic merit from large DNA marker panels. American Society of Animal Science, Annual Meeting. 2008.
60. Controlling Error Rates in QTL Mapping and Marker Assisted Selection. Rotary LeClerg Lecture, University of Maryland. 2009.
61. Genomic Selection in Admixed and Crossbred Populations. Rotary LeClerg Lecture, University of Maryland. 2009.
62. A mixture model for genomic selection. Symposium on Statistical Genetics of Livestock for the Post-Genomic Era. University of Wisconsin, Madison, Wisconsin. 2009.
63. Combining information from genotyped and ungenotyped individuals. Aviagen Advisory Group Meeting. Edinburgh, Scotland, UK. 2009.
64. Accuracy of genomic prediction. Aviagen Advisory Group Meeting. Chicago, Illinois. 2010.
65. Controlling false positives in genome-wide association studies: a Bayesian approach. Department of Biometry, University of Alabama at Birmingham. 2011.

66. Bayesian regression method for genomic analyses with incomplete genotype data. EAAP Conference, Nantes, France. 2013.
67. Bayesian regression as an alternative implementation of genomic-enhanced genetic evaluation. Beef Improvement Federation 10th Genetic Prediction Workshop held in Kansas City. 2013.
68. Implications of using identity-by-descent versus identity-by-state matrices in genetic analyses. Plant and Animal Genome XXII conference, San Diego. 2014.
69. Application of whole-genome prediction methods for genome-wide association studies: a Bayesian approach. 10th World Congress on Genetics Applied to Livestock Production. Vancouver, Canada. 2014.
70. Why Another Programming Language? An Introduction to Julia Rohan L. Fernando February, 10, 2015. Animal Breeding and Genetics Seminar. Iowa State University.
71. Strategies to Improve Numerical Stability of Equations used for Genomic Prediction of Genetic Merit. Plant and Animal Genome XXV conference, San Diego. 2017.
72. Alternative Model for Single-Step Bayesian Regression Analyses. University of Nebraska, Lincoln, Nebraska. 2017.
73. Bayesian Multiple Regression for GWAS. LIC, Hamilton, New Zealand. March, 2018.
74. An introduction to Julia. Technical University of Munich, School of Life Sciences Weihenstephan, Freising, Germany. June, 2018
75. Introduction to genetic evaluation: Fisher to Visscher. Conf. New Frontiers in Genetic Evaluation. Corteva Agriscience, Johnston, Iowa. July, 2018.
76. The evolution of genetic evaluation: Fisher to Visscher. INIA, Madrid, Spain. September, 2018.
77. An algorithm to parallelize empirical BayesA. International Congress on Domestic Animal Breeding, Genetics and Husbandry. Antalya, Turkey. September, 2018.
78. An upper bound for accuracy of prediction using GBLUP. KWS Seeds, Einbeck, Germany. December, 2018.
79. Use of Bayesian Inference for QTL Mapping: Influence of Priors. Plant and Animal Genome XXVII conference, San Diego. 2019.

## Invited Courses

1. Statistical Methods to Map QTL. Summer 1996. University of Wisconsin, Madison Wisconsin.
2. Inter-Nordic Course: Linear Models in Animal Breeding. Summer 1997. Biri, Norway.
3. FOMECA Visiting Professor: Statistical Methods to Map QTL. 1999. University of Buenos Aires, Argentina.
4. Statistical Methods to Map QTL. 1999. Federal University of Vicosa, Brazil.
5. Bioinformatics workshop organized by ETH, Zurich, Switzerland. 2000, St. Moritz, Switzerland.
6. QTL Mapping in Complex Pedigrees. Iowa State University. 2004, Ames, Iowa, USA.
7. C++ Programming for Animal Breeding. Iowa State University. 2005, Ames, Iowa, USA. (taught jointly with Steve Kachman)
8. Use of High-density SNP Genotyping for Genetic Improvement of Livestock. Iowa State University. 2009, Ames, Iowa, USA. (taught jointly with Jack Dekkers and Dorian Garrick)
9. Armidale Animal Breeding Summer Course: Bayesian Methods in Genome Association Studies. University of New England. 2010. Armidale, Australia (taught jointly with Dorian Garrick)
10. Summer Workshop: Genomic Selection of Livestock. Iowa State University. Ames, Iowa, USA. 2010. (taught jointly with Jack Dekkers and Dorian Garrick)
11. Genomic Selection in Livestock. 2011. agn Genetics Davos, Switzerland. (taught jointly with Dorian Garrick)
12. Genomic Selection in Livestock. 2011. Animal Breeding and Genomics Centre, Wageningen, The Netherlands. (taught jointly with Dorian Garrick)
13. Workshop on Genomic Selection in Livestock. 2012. Funded by USDA-NIFA Higher Education Challenge Program. Phoenix, Arizona. (taught jointly with Jack Dekkers and Dorian Garrick)
14. Workshop on Genomic Selection in Livestock. 2013. Funded by USDA-NIFA Higher Education Challenge Program. Quebec City, Canada. (taught jointly with Jack Dekkers and Dorian Garrick)



15. Workshop on Genomic Selection in Livestock. 2013. Samsun, Turkey. (taught jointly with Dorian Garrick)
16. Workshop on Genomic Selection in Livestock. 2013. Davos, Switzerland. (taught jointly with Dorian Garrick)
17. Theory and Methods for Genomic Prediction. 2013. Gen2Farm Winter School. Piacenza, Italy.
18. Genomic Prediction in Livestock. May 11-15, 2015. (taught jointly with Dorian Garrick and Jack Dekkers) Part of the Breeding and Genetics Graduate Education Online program and is partially sponsored by USDA-NIFA grant no. 2011-38411-30551.
19. Genomic Prediction in Livestock. June 19-23, 2015. agn, Davos, Switzerland. (taught jointly with Dorian Garrick)
20. A.L. Rae Centre Workshop on Genomic Prediction and Genome-Wide Association Studies November 9-13, 2015. Palmerston North, New Zealand. (taught jointly with Dorian Garrick).
21. A.L. Rae Centre Workshop on Genomic Prediction and Genome-Wide Association Studies. November 16-20, 2015. Hamilton, New Zealand. (taught jointly with Dorian Garrick).
22. Workshop on Genomic Selection in Livestock. January 31 to February 6, 2016. Egerton University, Njoro, Kenya. (taught jointly with Dorian Garrick).
23. Whole Genome Analyses Using Julia. December 3-7. Technical University of Munich, School of Life Sciences Weihenstephan, Freising, Germany (taught jointly with Christian Stricker).
24. Modern Programming in Genomic Prediction. June 24 to 28, 2019. University of California, Davis. California, USA. (taught jointly with Hao Cheng).
25. Bayesian Methods for Genomics. July 13 to 22, 2019. Summer School on Quantitative Genetics, China Agricultural University. Beijing, China.

## Service

1. Member of the QTL group of the National Consortium for Beef Cattle Evaluation. 2001-2015.
2. Interdepartmental Genetics, Supervisory Committee. 1999-2003.
3. Interdepartmental Genetics, Admissions Committee. 2001.
4. USDA Scientific Quality Control Review Panel. 2002.

5. BCB Admissions Committee 2002,2003,2004,2007, 2008
6. Interdepartmental Genetics and Genomics, Curriculum Committee, 2013, 2014,2015, 2016.

## Areas of Research

- Theory and methods for use of genetic markers in breeding. This includes the development of theory and methods for:
  1. detection of QTL by linkage analysis
  2. linkage disequilibrium methods for fine mapping
  3. estimation of marker-QTL parameters
  4. comparison alternative designs
  5. marker assisted selection
  6. evaluation of the advantage of marker assisted selection
  7. Markov chain Monte Carlo methods
  8. statistical and computational issues related to analysis of whole-genome data
  9. semi-parametric methods for genome assisted selection
  10. use of parallel computing to reduce computing time in whole-genome analyses
- Theory and methods for genetic evaluation of crossbred animals. This includes the development of theory and methods for:
  1. covariance between relatives
  2. estimation of genetic parameters
  3. genetic evaluation and selection
  4. finite locus models using Markov chain Monte-Carlo
  5. comparison of breeding schemes
  6. use of whole-genome data for QTL mapping and prediction of breeding values using crossbreds and mixed breed populations
- Other areas of research include
  1. methodology related to the estimation of genetic parameters and the prediction of genetic merit in populations undergoing selection and non-random mating.
  2. Bayesian methodology for analysis of unbalanced mixed model data
  3. Optimization of breeding programs.
  4. Use of computer simulation to study dynamics of genetic systems.