Publication list NCERA 225

Abdollahi-Arpanahi R, Morota G, and Penagaricano F. Predicting bull fertility using genomic data and biological information. Journal of Dairy Science. Early online

Aguilar-Trejo, C.M., K.M. Valerio-Valle, R.I. Luna-Ramirez, G. Luna-Nevarez, J.R. Reyna-Granados, J.A. Roma, M.A. Sanchez-Castro, X. Zeng, R.M. Enns, S.E. Speidel, M.G. Thomas, and P. Luna-Nevarez. 2017. Validation of candidate markers associated with reproductive performance in PRRSV naturally-infected replacement gilts in Southern Sonora Mexico. J. Anim. Sci. 95(E. Suppl. 4):29.

Aherin, D.G., J.M. Bormann, J.L. Heier Stamm, M.D. MacNeil, and R.L. Weaber. 2017. Decision Making Tools: Stochastic simulation model accounting for the impacts of biological variation on success of bovine embryo transfer programs. Translation Animal Science. Accepted November 2, 2017.

Andonov, S., D.A.L. Lourenco, B.O. Fragomeni, Y. Masuda, I. Pocrnic, S. Tsuruta, and I. Misztal. 2017. Accuracy of breeding values in small genotyped populations using different sources of external information—A simulation study. J. Dairy Sci. 100:395–401.

Bailey, D.W., M.G. Trotter, C.W. Knight, and M.G. Thomas. 2017. Use of GPS tracking collars and accelerometers for rangeland livestock production research. J. Anim. Sci. 95(E. Suppl. 4):360.

Beissinger TM and Morota G. Medical subject heading (MeSH) annotations illuminate maize genetics and evolution. Plant Methods. 13:8.

Boldt, R.J., S.E. Speidel, M.G. Thomas, and L.D. Keenan. 2017. Genetic parameters for carcass traits and stayability in Red Angus Cattle. J. Anim. Sci. 95(E. Suppl. 4):96.

Bradford, H.L., I. Pocrnić, B.O. Fragomeni, D.A.L. Lourenco, and I. Misztal. 2017. Selection of core animals in the Algorithm for Proven and Young using a simulation model. J. Anim. Breed. Genet. 134:(in press; doi: 10.1111/jbg.12276).

Buckley, B.A., S.E. Speidel, R. J. Boldt, R. M. Enns, X. Zeng, M. L. Spangler, J. Lee, and M. G. Thomas. 2017. Genome-wide association study of heifer pregnancy in Red Angus Cattle. J. Anim. Sci. 95: Suppl. 4.

Canovas, A., J. Casellas, M. Thomas, and J.F. Medrano. 2017. Applying new genomic technology to accelerate genetic improvement in beef and dairy cattle. Proc. Assoc. Adv. Anim. Breed. Genet. 2017. 22:to be posted http://www.aaabg.org/aaabghome/AllProceedings.php) July 2-5, 2017.

Canovas, A., M.G. Thomas, J. Casellas, and J.F. Medrano. 2017. Understanding the nature of complex phenotypes in beef cattle using systems biology. J. Anim. Sci. 95(E. Suppl. 4):367.

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.

Cole, J.B., J.M. Bormann, C.A. Gill, H. Khatib, J.E. Koltes, C. Maltecca, and F. Miglior. 2017. Breeding and Genetics Symposium: Resilience of livestock to changing environments. J. Anim. Sci. 95:1777-1779. doi:10.2527/jas.2017.1402.

Crawford, N.F., S.J. Coleman, T.N. Holt, S.E. Speidel, R.M. Enns, J.H. Newman, R. Hamid, and M.G. Thomas. 2017. Genotyping a SNP in the endothelial PAS domain-containing protein 1 (EPAS1) gene: is it associated with mean pulmonary arterial pressures in Yearling Angus cattle? J. Anim. Sci. 95(E. Suppl. 4):87.

Crawford, N. F., R. M. Enns, S. E. Speidel, B. LaShell, T. N. Holt, M. G. Thomas. 2017. Case Study: Factors influencing pulmonary arterial pressure in cattle of the San Juan Basin Research Center 4-Corners Bull test data. PAS. 33:387-392. doi:10.15232/pas.2016-01587.

Culbertson, M.M., M.G. Thomas, L.L. Leachman, R.M. Enns, and S.E. Speidel. 2017. Multivariate analysis of beef cattle pulmonary arterial pressures measured at differing elevations. J. Anim. Sci. 95(E. Suppl. 4):86.

Dias, M. M., A. Canovas, C. Mantilla-Rojas, D. G. Riley, P. Luna-Nevarez, S. J. Coleman, S. E. Speidel, R. M. Enns, A. Islas-Trejo, J. F. Medrano, S. S. Moore, M. R. S. Fortes, L. T. Nguyen, B. Venus, I. S. D. P. Diaz, F. R. P. Souza, L. F. S. Fonseca, F. Baldi, L. G. Albuquerque, M. G. Thomas and H. N. Oliveria. 2017. SNP detection using RNA-sequences of candidate genes associated with puberty in cattle. Genet. Mol. Res. 16(1). doi:10.4238/gmr16019522.

Enns, R.M., T.G. McDaneld, J.W. Keele, R.J. Boldt, T.P. Smith, and L.A. Kuehn. 2017. Genetic markers associated with succeptibility to bovine respiratory disease. J. Anim. Sci. 95(E. Suppl. 4):90.

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.

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.

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.

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.

Fragomeni, B., D. A. L. Lourenco, Y. Masuda, A. Legarra, and I. Misztal. 2017. Incorporation of Causative Quantitative Trait Nucleotides in Single-step GBLUP. Genet. Sel. Evol. 49:59.

Garcia-Baccino, C.A., A. Legarra, O.F. Christensen, I. Misztal, I. Pocrnic, Z.G. Vitezica, and R.J.C. Cantet. 2017. Metafounders are related to Fst fixation indices and reduce bias in single-step genomic evaluations. Genet. Sel. Evol. 49:34.

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.

Id-Lahoucine, S., A. Canovas, C. Jaton, F. Miglior, S.P. Miller, M. Sargolzaei, J.F. Medrano and J. Casellas. 2017. Statistical power of the Bayesian analysis for transmission ratio distortion in cattle. American Dairy Science Association annual meeting, Pittsburgh, PA.

Jennings, K.J., X. Zeng, A. Reverter, T.N. Holt, S.J. Coleman, R.M. Enns, S.E. Speidel, and M.G. Thomas. 2017. Construction of an association weight matrix to identify SNP that play a role in performance of Angus cattle at higher elevations. J. Anim. Sci. 95(E. Suppl. 4):86-87.

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

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.

Krehbiel, B.C., M.G. Thomas, S.E. Speidel, R.M. Enns, and H.D. Blackburn. 2017. Genetic structure of Angus and Salers in relation to SNP associated with pulmonary arterial pressure. J. Anim. Sci. 95(E. Suppl. 4):87.

Kuehn, L. A., S. P. Miller, K. J. Retallick and D. W. Moser. 2017. Comparison of genomic-enhanced EPD systems using an external phenotypic database. J. Anim. Sci. 95(Supp. 4):85.

Kuehn, L. A., and R. M. Thallman. 2017. Across-breed EPD tables for the year 2017 adjusted to breed differences for birth year of 2015. In: Proceeding of the Beef Improvement Federation, Athens, GA. p 112-144.

Kuehn, L. A., and R. M. Thallman. 2017. Mean EPDs Reported by Different Breeds. In: Proceeding of the Beef Improvement Federation, Athens, GA. p 107-111.

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 nongenotyped Hanwoo beef cattle. Genetics Selection Evolution 49: 2.

Lee, J., S. D. Kachman, and M. L. Spangler. 2017. The impact of training strategies on the accuracy of genomic predictors in United States Red Angus cattle1. J. Anim. Sci. 95:3406-3414. doi:10.2527/jas2017.1604

Lourenco, D.A.L., I. Aguilar, and F. Baldi. 2017. Application of single step genomic BLUP under different uncertain paternity scenarios using simulated data. PLoS ONE 12(9): e0181752.

Lourenco, D.A.L., B.O. Fragomeni, H. L. Bradford, I.R. Menezes, J.B.S. Ferraz, S. Tsuruta, I. Aguilar, and I. Misztal. 2017. Implications of SNP weighting on single-step genomic predictions for different reference population sizes. J. Anim. Bred. Genet. 134: (in press; doi: 10.1111/jbg.12288).

Masuda, Y., I. Misztal, A. Legarra, S. Tsuruta, D.A.L. Lourenco, B.O. Fragomeni, and I. Aguilar. 2017. Technical note: Avoiding the direct inversion of the numerator relationship matrix for genotyped animals in single-step genomic best linear unbiased prediction solved with the preconditioned conjugate gradient. J. Dairy Sci. 95:49-52.

Misztal, I. 2017. Breeding and Genetics Symposium: Resilience and lessons from studies in genetics of heat stress. J. Anim. Sci. 95:1780–1787.

Misztal, I., and A. Legarra. 2017. Invited review: Efficient computation strategies in genomic selection. Animal 11:731–736.

Ochsner, K.P., M.D. MacNeil, R.M. Lewis, and M.L. Spangler. 2017. Economic selection index development for Beefmaster cattle I: Terminal breeding objective. J. Anim. Sci. 95:1063-1070.

Ochsner, K.P., M.D. MacNeil, R.M. Lewis, and M.L. Spangler. 2017. Economic selection index development for Beefmaster cattle II: General-purpose breeding objective. J. Anim. Sci. 95:1913-1920.

Oliveira, D.P. F.R. Araújo Neto, R.R. Aspilcueta-Borquis, D.J.A. Santos, L.G. Albuquerque, G.M.F.d Camargo, D.A.L. Lourenco, S. Tsuruta, I. Misztal, H. Tonhati. 2017. Reaction norm for yearling weight by single-step methodology in beef cattle. J. Anim. Sci. (Accepted).

Paz, H.A., K. E. Hales, J. E. Wells, L. A. Kuehn, H. C. Freetly, M. L. Spangler, S. C. Fernando. 2017. Identifying the influence of the rumen microbiome on the feed efficiency phenotype in beef cattle. J. Dairy Sci. 100: Suppl. 2.

Pierce, C.F., M.M. Dias, D.W. Bailey, J.F. Medrano, A. Canovas, S.E. Speidel, S.J. Coleman, R.M. Enns, and M.G. Thomas. 2017. SNP discovery for QTL associated with grazing distribution in Angus cattle using RNA-seq. J. Anim. Sci. 95(E. Suppl. 4):85-86.

Pocrnic,I, D. A. L. Lourenco, H. L. Bradford, C. Y. Chen, and I. Misztal. 2017. Technical note: Impact of pedigree depth on convergence of single-step genomic BLUP in a purebred swine population. J. Animal. Sci. 95: 3391-3395.

Retallick, K. J., J. M. Bormann, R. L. Weaber, M. D. MacNeil, H. L. Bradford, H. C. Freetly, D. W. Moser, W. M. Snelling, R. M. Thallman, and L. A. Kuehn. 2017. Genetic variance and covariance components for feed intake, average daily gain, and postweaning gain to improve feed efficiency in growing cattle. J. Anim. Sci. 95: 1444-1450.

Sanchez-Castro, M.A., R.A. Boldt, M.G. Thomas, R.M. Enns, and S.E. Speidel. 2017. Expected progeny differences for stayability in Angus cattle using a random regression model. J. Anim. Sci. 95(E. Suppl. 4):88.

Seabury, C.M., D.L. Oldeschulte, M. Saatchi, J.E. Beever, J.E. Decker, Y.A. Halley, E.K. Bhattarai, M. Molaei, H.C. Freetly, S.L. Hansen, H. Yampara-Iquise, K.A. Johnson, M. S. Kerley, J. Kim, D.D. Loy, E. Marques, H.L. Neibergs, R. D. Schnabel, D.W. Shike, M.L. Spangler, R.L. Weaber, D.J. Garrick, and J.F. Taylor. 2017. Genome-Wide Association Study For Feed Efficiency and Growth Traits in U.S. Beef Cattle. BMC Genomics 18:386.

Silva, R.M.O., N.B. Stafuzza, B.O. Fragomeni, G.M.F. de Camargo, T.M. Ceacero, J.N.S.G. Cyrillo, F. Baldi, A.A. Boligon, M.E.Z. Mercadante, D.L. Lourenco, I. Misztal, and L.G. Albuquerque. 2017. Genome-wide association study for carcass traits in an experimental Nelore cattle population. PloS One 12:e0169860.

Snelling, W.M., S.D. Kachman, G.L. Bennett, M.L. Spangler, L.A. Kuehn, and R.M. Thallman. 2017. Functional SNP associated with birth weight in independent populations identified with a permutation step added to GBLUP-GWAS. J. Anim. Sci. 95: Suppl. 4.

Snelling, W. M., L. A. Kuehn, B. N. Keel, R. M. Thallman, and G. L. Bennett. 2017. Linkage disequilibrium among commonly genotyped SNP and variants detected from bull sequence. Animal Genetics 48: 516-522.

Spangler, Matt. 2017. How to get the most out of genomic selection. Proceedings: DNA In Beef Cattle: where we've been, where we're at, and where we're going, Clay Center, NE.

Spangler, M.L. 2017. Using Genomics to Affect Cow Herd Reproduction. In Proc. Florida Beef Cattle Shortcourse, Gainesville, FL.

Spangler, Matt, and Alison Van Eenennaam. 2017. Where We Are Going with Genomics and Genetic Improvement. In Proc. Beef Improvement Federation Annual Convention, Athens, GA.

Spangler, M.L., and R.L. Weaber. 2017. Genetic selection vs visual appraisal: Is it a conundrum? In: Proc. Range Beef Cow Symposium XXV, Cheyenne, WY.

Speidel, S.E., B. A. Buckley, R. J. Boldt, R. M. Enns, X. Zeng, J. Lee, M. L. Spangler, and M. G. Thomas. 2017. Genome-wide association study for stayability in Red Angus Cattle. J. Anim. Sci. 95: Suppl. 4.

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 48:77.

Taylor, Jeremy F., Jonathan E Beever, Jared E Decker, Harvey C. Freetly, Dorian J. Garrick, Stephanie L Hansen, Kristen A Johnson, Monty S. Kerley, Daniel D. Loy, Holly L. Neibergs, Mahdi Saatchi, Robert D Schnabel, Christopher M. Seabury, Daniel W. Shike, Matthew L. Spangler and Robert L. Weaber. 2017. The Genetic Improvement of Feed Efficiency in Beef Cattle. J. Anim. Sci. 95: Suppl. 2.

Thomas M.G.,G.M. Krafsur, T.N. Holt, R.M. Enns, S.E. Speidel, F.B. Garry, A. Canovas, J.F. Medrano, R.D. Brown, K.R. Stenmark, and J.M. Neary. 2017. Genetics of brisket disease in beef cattle: a not so high altitude problem. Proc. Assoc. Adv. Anim. Breed. Genet. 22: <http://www.aaabg.org/aaabghome/AllProceedings.php>. Presented July 4, 2017, Townsville AU.

Tsuruta, S. D. A. L. Lourenco, I. Misztal, and T. J. Lawlor. 2017. Genomic analysis of cow mortality and milk production using a threshold-linear model. J. Dairy Sci. 100: 7295-7305.

Wang, L., S. P. Miller, K. J. Retallick, and D. W. Moser. 2017. Genetic parameter estimation for foot structure in American Angus cattle. J. Anim. Sci. 95(Supp 4):100.

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.

Wilson-Wells, Danielle F. and Kachman, Stephen D. (2016). A Bayesian GWAS method utilizing haplotype clusters for a composite breed population, Annual Conference on Applied Statistics in Agriculture.<http://newprairiepress.org/agstatconference/2016/proceedings/2>

Wilson-Wells, Danielle and Stephen D. Kachman. 2017. A Bayesian GWAS Method which utilizes haplotype clusters to make predictions when maternal and paternal breed composition is known. 2017 Joint Statistical Meetings. July 19-Aug 3 3017. Baltimore MD.

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.

Yu H, Spangler ML, Lewis RM, and Morota G. Genomic relatedness strengthens genetic connectedness across management units. G3: Genes, Genomes, Genetics. 10:3543-3556.

Yu, Haipeng, Matthew L. Spangler, Ronald M. Lewis, and Gota Morota. 2017. Genomic relatedness strengthens genetic connectedness across management units. J. Anim. Sci. 95: Suppl. 4.

Zamorano-Algandar, R., J.C. Leyva-Corona, R.I. Luna-Ramirez, G. Luna-Nevarez, G. Rincon, J.F. Medrano, AI. Hernandez, M.A. Sanchez-Castro, R.M. Enns, S.E. Speidel, M.G. Thomas, and P. Luna-Nevarez. 2017. Molecular breeding value prediction using pregnancy rate in Holstein dairy cows managed in a heat-stressed environment using candidate gene SNP. J. Anim. Sci. 95(E. Suppl. 4):84.