

VITA
Ignacy Misztal

Education

1978 M.S. (Computer Engineering), Warsaw Technical University, Warsaw, Poland
1985 Ph.D. (Technical Sciences), Polish Academy of Sciences, Warsaw, Poland

Academic positions

1981–86	Research Scientist	Warsaw Agricultural University, Poland
1986–88	Research Associate	University of Illinois, Urbana, IL
1988–95	Research Data Analyst	University of Illinois, Urbana, IL
1995–2000	Associate Professor	University of Georgia, Athens, GA
2001–2017	Professor	University of Georgia, Athens, GA
2018–present	D.W. Brooks Distinguished Professor	University of Georgia, Athens, GA
2020- present	Distinguished Research Professor	University of Georgia, Athens, GA

Research interests

Genetic evaluation methodology
Programming algorithms related to animal breeding
Genetics of heat tolerance, fertility, and mortality
Genotype × environment interaction and competition effects
Incorporation of genomic information into genetic evaluations

Sponsors (*total of over \$10 million*)

NIFA/USDA, Holstein Association USA, American Angus Association, Pig Improvement Company, Smithfield, Maschoffs, DNA Genetics, Cobb-Vantress, Zoetis, MethodGenetics,...

Major accomplishments

- Developed computational methodology for national evaluation of dairy cattle based on matrix-free, 2nd-order Jacobi iteration (1987); **applied commercially for U.S. Holsteins for next 20 years.**
- Developed computational methodology for large-scale computations with REML based on properties of traces and sparse inverse (1991); **used worldwide by academic, government and industry researchers.**
- Developed methodology to estimate dominance variance for extremely large data sets using Method R and estimated dominance variance for many species and traits (1995); **still cited in research studies.**
- Pioneered new way to develop software for mixed models and animal genetics ("Complex Models, More Data: Simpler Programming," 1999); **used in thousands of research studies and by all large U.S. animal genetics companies for large-scale genetic/genomic evaluations.**
- Pioneered methodology for studying genetics of heat stress in livestock based on public weather data (2001); **applied to dairy, beef and pigs and used extensively in climate change research worldwide.**
- Developed methodology for genetic evaluation using all genomic, phenotypic, and pedigree information jointly (single-step, 2010); **considered most accurate yet most simple evaluation method in animal genomics.**
- Extended Henderson's algorithm to invert a pedigree relationship matrix to genomic relationship matrices (2014); **allows genomic evaluation using massive data from millions of genotyped animals at extremely low cost but high accuracy and excellent numerical stability. Provides novel insight into genomic selection and is a starting point for many new studies.**

- Demonstrated that 98% of the genomic information across farm species compresses to about 4,000 in pigs and broilers to about 15,000 in Holsteins (2016). **This information helps to determine whether the search for major genes (or causative SNP) could improve the accuracy of genomic selection.**
- Showed that the accuracy of the genomic selection is determined by ability to calculate the largest clusters of the genomic information (singular values of gene content) due to common ancestors (2019). **This explains why accuracy of genomic predictions seem pretty good with small data but rise slowly with large data.**
- Showed that the use of genomic selection over time leads to reduced genetic variance and increased antagonistic correlations across traits. Also, genes that are identified to have large effects despite long selection are likely to exhibit pleiotropy and may not be useful in selection (2020). **Following, the expected gains in animal breeding with the genomic information may not be realized.**
- Determined components of the Manhattan plots: QTN, LD to QTN, relationships and noise. In animal populations, signals due to the relationship dominate. Most of the information due to QTN is from LD to QTN which occurs in wide windows: about 1-2 Mb in cattle and 4-8 Mb in pigs and chicken. **Then the identification of QTN is hard. In large data, GBLUP or ssGBLUP accounts for QTN through QTN profile. This study explains why the impact of the sequence data on accuracy in genomic analyses is small.**
- Found a method to estimate heritabilities and genetic correlations for very large populations in genomic models. The method allows for estimation of every cycle of selection separately. **The method allows to find if some genetic parameters are changing rapidly. If so, a selection index can be modified to avoid undesirable declines of fitness traits.**

Software

BLUPF90 software for variance component estimation based on REML and Bayesian methods and supports wide range of models. Commercial version used for large-scale genetic/genomic evaluation by large U.S. animal genetics companies. See <http://nce.ads.uga.edu/wiki/doku.php>.

Regular courses taught at the University of Georgia

Mixed Models

Computing in Animal Breeding

Advanced Animal Breeding

Graduate student seminar

Short courses

United States:	University of Wisconsin (2000) University of Georgia (2008, 2012, 2014, 2016, 2018, 2022)
Europe:	Poland (1998, 2015) Finland (1999) Norway (1999) Belgium (1999) Italy (2002, 2008, 2013) Spain (2003) Denmark (2004, 2011) France (2006) The Netherlands (2007, 2012) Germany (2014)
Asia:	Japan (1999) India (2023)
Oceania:	Australia (2000)
South America:	Brazil (2001, 2004) Uruguay (2005)

Africa: South Africa(2007, 2016)

Awards

- J. L. Lush Award in Animal Breeding and Genetics, American Dairy Science Association (2002)
Rockefeller Prentice Award in Animal Breeding and Genetics, American Society of Animal Science (2008)
Research Award, National Association of Animal Breeders (2008)
D.W. Brooks Research Award, University of Georgia (2010)
Most Cited Paper, Breeding & Genetics, *Journal of Dairy Science* (2013)
Pioneer Award, Beef Improvement Association (2013)
D.W. Brooks Award for Excellence in Global Programs, University of Georgia (2014)
D. W. Distinguished Professorship, University of Georgia (2017)
Distinguished Research Professor, University of Georgia (2020)

Recent refereed publications (*selected from 284 total*)

- Misztal, I.**, A. Legarra, and I. Aguilar. 2014. Using recursion to compute the inverse of the genomic relationship matrix. *J. Dairy Sci.* 97:3943–3952.
- Lourenco, D.A.L., **I. Misztal**, S. Tsuruta, I. Aguilar, T.J. Lawlor, S. Forni, and J.I. Weller. 2014. Are evaluations on young genotyped animals benefiting from the past generations? *J. Dairy Sci.* 97:3930–3942.
- Tokuhisa, K., S. Tsuruta, A. De Vries, J.K. Bertrand, and **I. Misztal**. 2014. Estimation of regional genetic parameters for mortality and 305-d milk yield of US Holsteins in the first 3 parities. *J. Dairy Sci.* 97:4497–4502.
- Tsuruta, S., **I. Misztal**, D.A.L. Lourenco, and T.J. Lawlor. 2014. Assigning unknown parent groups to reduce bias in genomic evaluations of final score in US Holsteins. *J. Dairy Sci.* 97:5814–5821.
- Wang, H., **I. Misztal**, I. Aguilar, A. Legarra, R.L. Fernando, Z. Vitezica, R. Okimoto, T. Wing, R. Hawken, and W.M. Muir. 2014. Genome-wide association mapping including phenotypes from relatives without genotypes in a single-step (ssGWAS) for 6-week body weight in broiler chickens. *Front. Genet.* 5:134.
- Legarra, A., O.F. Christensen, I. Aguilar, and **I. Misztal**. 2014. Single Step, a general approach for genomic selection. *Livest. Sci.* 166:54–65.
- Dufrasne, M., **I. Misztal**, S. Tsuruta, N. Gengler, and K.A. Gray. 2014. Genetic analysis of pig survival up to commercial weight in a crossbred population. *Livest. Sci.* 167:19–24.
- Wang, H., **I. Misztal**, and A. Legarra. 2014. Differences between genomic-based and pedigree-based relationships in a chicken population, as a function of quality control and pedigree links among individuals. *J. Anim. Breed. Genet.* 31:445–451.
- Fragomeni, B.O., **I. Misztal**, D.L. Lourenco, I. Aguilar, R. Okimoto, and W.M. Muir. 2014. Changes in variance explained by top SNP windows over generations for three traits in broiler chicken. *Front. Genet.* 5:3332.
- Zhang, X., **I. Misztal**, M. Heidaritabar, J.W.M. Bastiaansen, R. Borg, R.L. Sapp, T. Wing, R.R. Hawken, D.A.L. Lourenco, and Z.G. Vitezica. 2014. Prior genetic architecture impacting genomic regions under selection: An example using genomic selection in two poultry breeds. *Livest. Sci.* 171:1–11.
- Forneris, N.S., A. Legarra, Z.G. Vitezica, S. Tsuruta, I. Aguilar, **I. Misztal**, and R.J.C. Cantet. 2015. Quality control of genotypes using heritability estimates of gene content at the marker. *Genetics* 199:675–681.
- Lukaszewicz, M., R. Davis, J.K. Bertrand, **I. Misztal**, and S. Tsuruta. 2015. Correlations between purebred and crossbred body weight traits in Limousin and Limousin-Angus populations. *J. Anim. Sci.* 93:1490–1493.
- Fragomeni, B.O., D.A.L. Lourenco, S. Tsuruta, Y. Masuda, I. Aguilar, A. Legarra, T.J. Lawlor, and **I. Misztal**. 2015. Hot topic: Use of genomic recursions in single-step genomic best linear unbiased predictor (BLUP) with a large number of genotypes. *J. Dairy Sci.* 98:4090–4094.
- Fragomeni, B.O., D.A.L. Lourenco, S. Tsuruta, Y. Masuda, I. Aguilar, and **I. Misztal**. 2015. Use of genomic recursions and algorithm for proven and young animals for single-step genomic BLUP analyses—A simulation study. *J. Anim. Breed. Genet.* 132:340–345.
- Legarra, A., O.F. Christensen, Z.G. Vitezica, I. Aguilar, and **I. Misztal**. 2015. Ancestral relationships using metafounders: Finite ancestral populations and across population relationships. *Genetics* 200:455–468.

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- Lourenco, D.A.L., S. Tsuruta, B.O. Fragomeni, Y. Masuda, I. Aguilar, A. Legarra, J.K. Bertrand, T.S. Amen, L. Wang, D.W. Moser, and **I. Misztal**. 2015. Genetic evaluation using single-step genomic best linear unbiased predictor in American Angus. *J. Anim. Sci.* 93:2653–2662.
- Tsuruta, S., D.A.L. Lourenco, **I. Misztal**, and T.J. Lawlor. 2015. Genotype by environment interactions on culling rates and 305-d milk yield of Holstein cows in three US regions. *J. Dairy Sci.* 98:5796–805.
- Lourenco, D.A.L., B.O. Fragomeni, S. Tsuruta, I. Aguilar, B. Zumbach, R.J. Hawken, A. Legarra, and **I. Misztal**. 2015. Accuracy of estimated breeding values for males and females with genomic information on males, females, or both: A broiler chicken example. *Genet. Sel. Evol.* 47:56.
- Masuda, Y., S. Tsuruta, I. Aguilar, and **I. Misztal**. 2015. Technical note: Acceleration of sparse operations for average-information REML analyses with supernodal methods and sparse-storage refinements. *J. Anim. Sci.* 93:4670–4674.
- Misztal, I.** 2016. Inexpensive computation of the inverse of the genomic relationship matrix in populations with small effective population size. *Genetics* 202:411–409.
- Masuda, Y., **I. Misztal**, S. Tsuruta, A. Legarra, I. Aguilar, D.A. Lourenco, B.O. Fragomeni, and T.J. Lawlor. 2016. Implementation of genomic recursions in single-step genomic best linear unbiased predictor for US Holsteins with a large number of genotyped animals. *J. Dairy Sci.* 99:1968–1974.
- Lourenco, D.A.L., S. Tsuruta, B.O. Fragomeni, C.Y. Chen, W.O. Herring, and **I. Misztal**. 2016. Crossbred evaluations in single-step genomic best linear unbiased predictor using adjusted realized relationship matrices. *J. Anim. Sci.* 94:909–919.
- Vitezica, Z., L. Varona, J.M. Elsen, **I. Misztal**, W. Herring, and A. Legarra. 2016. Genomic BLUP including additive and dominant variation in purebreds and F1 crossbreds, with an application in pigs. *Genet. Sel. Evol.* 48:6.
- Pocrnica, I., D.A.L. Lourenco, Y. Masuda, and **I. Misztal**. 2016. The dimensionality of genomic information and its effect on genomic prediction. *Genetics* 203:573–581.
- Vallejo, R.L., T.D. Leeds, B.O. Fragomeni, G. Gao, A.G. Hernandez, **I. Misztal**, T.J. Welch, G.D. Wiens, and Y. Palti. 2016. Evaluation of genome-enabled selection for bacterial cold water disease resistance using progeny performance data in rainbow trout: Insights on genotyping methods and genomic prediction models. *Front. Genet.* 7:96.
- Silva, R.M.O., B.O. Fragomeni, D.A.L. Lourenco, A.F.B. Magalhães, N. Irano, R. Carvalheiro, R.C. Canesin, M.E.Z. Mercadante, A.A. Boligon, F.S. Baldi, **I. Misztal**, and L.G. Albuquerque. 2016. Accuracies of genomic prediction of feed efficiency traits using different prediction and validation methods in an experimental Nelore cattle population. *J. Anim. Sci.* 94:3613–3623.
- van der Heide, E.M.M., D.A.L. Lourenco, C.Y. Chen, W.O. Herring, R.L. Sapp, D.W. Moser, S. Tsuruta, Y. Masuda, B.J. Ducro, and **I. Misztal**. 2016. Sexual dimorphism in livestock species selected for economically important traits. *J. Anim. Sci.* 94:3684–3692.
- Zhang, X., D. Lourenco, I. Aguilar, A. Legarra, and **I. Misztal**. 2016. Weighting strategies for single-step genomic BLUP: An iterative approach for accurate calculation of GEBV and GWAS. *Front. Genet.* 7:151.
- Bradford, H.L., B.O. Fragomeni, D.A.L. Lourenco, and **I. Misztal**. 2016. Genetic evaluations for growth heat tolerance in Angus cattle. *J. Anim. Sci.* 94:4143–4150.
- Bradford, H.L., B.O. Fragomeni, D.A.L. Lourenco, and **I. Misztal**. 2016. Regional and seasonal analyses of weights in growing Angus cattle. *J. Anim. Sci.* 94:4369–4375.
- Pocrnica, I., D.A.L. Lourenco, Y. Masuda, and **I. Misztal**. 2016. Dimensionality of genomic information and performance of the Algorithm for Proven and Young for different livestock species. *Genet. Sel. Evol.* 48:82.
- Fragomeni, B.O., D.A.L. Lourenco, S. Tsuruta, K. Gray, Y. Huang, and **I. Misztal**. 2016. Modeling response to heat stress in pigs from nucleus and commercial farms in different locations in the United States. *J. Anim. Sci.* 94:4789–4798.
- Andonov, S., D.A.L. Lourenco, B.O. Fragomeni, Y. Masuda, I. Pocrnica, 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.

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- Fragomeni, B.O., D.A.L. Lourenco, S. Tsuruta, H.L. Bradford, K.A. Gray, Y. Huang, and **I. Misztal**. 2016. Using single-step genomic best linear unbiased predictor to enhance the mitigation of seasonal losses due to heat stress in pigs. *J. Anim. Sci.* 12:5004–5013.
- Misztal, I.**, and A. Legarra. 2017. Invited review: Efficient computation strategies in genomic selection. *Animal* 11:731–736.
- 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.
- Silva, R.M.O., N.B. Stafizza, 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.
- 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 F_{st} fixation indices and reduce bias in single-step genomic evaluations. *Genet. Sel. Evol.* 49:34.
- 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:(doi: 10.1111/jbg.12276).
- 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. doi.org/10.3168/jds.2017-12665.
- 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. doi: 10.2527/jas.2017.1581.
- 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.* 49:1. (doi: 10.1186/s12711-017-0335-0).
- 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.* 10.1111/jbg.12288.
- Masuda, Y., P. M. VanRaden, **I. Misztal**, and T. J. Lawlor. 2017. Differing genetic trend estimates from traditional and genomic evaluations for genotyped animals as evidence of pre-selection bias in US Holsteins. *J. Dairy Sci.* 101:1–113. *J. Dairy Sci.* 101:1–13. (doi:10.3168/jds.2017-13310)
- Zhang, X., D. A. L. Lourenco, I. Aguilar, A. Legarra, R. J. Hawken, R. L. Sapp, and **I. Misztal**. Relationships among mortality, performance, and disorder traits in broiler chickens: a genetic and genomic approach. 2018. *Poultry Sci.* pex431, <https://doi.org/10.3382/ps/pex431>
- Guarini, A.. D. A. L. Lourenco, L. Brito, M. Sargolzaei, C. Baes, F. Miglior, **I. Misztal**, and F. Schenkel. 2018. Comparison of genomic predictions for lowly heritable traits using multi-step and single-step genomic BLUP in Holstein cattle. *J. Dairy Sci.* (In Print) <https://doi.org/10.3168/jds.2017-14193>
- Garcia, A., B. Bosworth, G. Waldbieser, **I. Misztal**, S. Tsuruta, and D. Lourenco. 2018. Development of genomic predictions for harvest and carcass weight in channel catfish. *Genet. Sel. Evol.* 50:66. <https://doi.org/10.1186/s12711-018-0435-5>.
- Oliveira, D. P., D. A. L. Lourenco, S. Tsuruta, **I. Misztal**, D. J. A. Santos, F. R. de Araújo Neto, R. R. Aspilcueta-Borquis, F. Baldi, R. Carvalheiro, G. M. F. de Camargo, L. G. Albuquerque, and H. Tonhati. 2018. Reaction norm for yearling weight in beef cattle using single-step genomic evaluation, *J. Anim. Sci.* 96:27–34. <https://doi.org/10.1093/jas/skx006>.
- Cesarani, A., I. Pocrnic, **I. Misztal**, N. Maciotti, and D.A.L. Lourenco. 2018. Bias in heritability estimates from genomic restricted maximum likelihood (GREML) methods under different genotyping strategies. *J. Anim. Breed. Genet.* doi: 10.1111/jbg.12367.

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- Guarini, A.. D. A. L. Lourenco, L. Brito, M. Sargolzaei, C. Baes, F. Miglior, **I. Misztal**, and F. Schenkel. Genetics and genomics of reproductive disorders in Holstein cattle. 2019. J.Dairy Sci. https://doi.org/10.3168/jds.2018-15038.
- Bradford, H. L., Y. M. Masuda, P. M. VanRaden, A. Legarra, and **I. Misztal**. 2019. Modeling missing pedigree in single-step genomic BLUP. J. Dairy Sci. https://doi.org/10.3168/jds.2018-15434
- Fragomeni, B., Y. Masuda, H. L. Bradford, D.A.L. Lourenco, and **I. Misztal**. 2019. International bull evaluations by GBLUP with a prediction population. J. Dairy Sci. https://doi.org/10.3168/jds.2018-15554.
- Bradford, H. L., Y. M. Masuda, J. B. Cole, **I. Misztal**, and P. M. VanRaden. 2019. Modeling pedigree accuracy and uncertain parentage in single-step evaluations of simulated and Holstein datasets. J. Dairy Sci. https://doi.org/10.3168/jds.2018-15419.
- Hinayah, O., D. Lourenco, Y. Masuda, **I. Misztal**, S. Tsuruta, J. Jamrozik, L. Brito, F. Fonseca e Silva, and F. Schenkel. 2019. Application of single-step genomic evaluation using multiple-trait random regression test-day models in dairy cattle. J. Dairy Sci. https://doi.org/10.3168/jds.2018-15466.
- Pocrnici, I., D. A. L. Lourenco, C. Y. Chen, W. O. Herring, and **I. Misztal**. 2019. Crossbred evaluations using single-step genomic BLUP and algorithm for proven and young with different sources of data. J. Anim. Sci.
- Guarini, A.R., D.A.L. Lourenco, L.F. Brito, M. Sargolzaei, C. Baes, F. Miglior, S. Tsuruta, **I. Misztal**, and F. Schenkel. Use of a single-step approach for integration of external information into a national genomic evaluation for Holstein cattle in Canada. J. Dairy Sci.
- Aguilar, I., A. Legarra, F. Cardoso, Y. Masuda, D. Lourenco, and **I. Misztal**. 2019. Frequentist p-values for large-scale single step genome-wide association, with an application to birth weight in American Angus cattle. Genet. Sel. Evol. 51:28. https://doi.org/10.1186/s12711-019-0469-3
- Maiorano, A. M., A. Assen, P. Bijma, C. Y. Chen, J. A. Silva, W. O. Herring, S. Tsuruta, **I. Misztal**, and D. A. L. Lourenco. 2019. Improving accuracy of direct and maternal genetic effects in genomic evaluations using pooled boar semen: a simulation study. J. Anim. Sci. 97:3237-3245. https://doi.org/10.1093/jas/skz207
- Oliveira, H., D. Lourenco, Y. Masuda, **I. Misztal**, S. Tsuruta, J. Jamrozik, L. Brito, F. Fonseca e Silva, Fabyano, J. Cant, and F. Schenkel. 2019. Single-step genome-wide association for longitudinal traits of Canadian Ayrshire, Holstein and Jersey dairy cattle. J. Dairy Sci. 102:9995-10011. https://doi.org/10.3168/jds.2019-16821.
- Oliveira, H.R., D.A.L. Lourenco, Y. Masuda, **I. Misztal**, S. Tsuruta, J. Jamrozik, L.F. Brito, F.F. Silva, and F.S. Schenkel. 2019. Application of single-step genomic evaluation using multiple-trait random regression models in dairy cattle. J. Dairy Sci. 102:2365-2377. https://doi.org/10.3168/jds.2018-15466
- Tsuruta, S., D. Lourenco, Y. Masuda, **I. Misztal**, and T. J. Lawlor. 2019. Controlling bias in genomic evaluations for linear type traits in young genotyped bulls. J. Dairy Sci. 102: 9956-9970. https://doi.org/10.3168/jds.2019-16789.
- Fragomeni, B.O., D.A.L. Lourenco, A. Legarra, P. VanRaden, **I. Misztal**. 2019. Alternative SNP weighting for SSGBLUP evaluation of stature in US Holstein in the presence of selected sequence variants. J. Dairy Sci. https://doi.org/10.3168/jds.2019-16262.
- Steyn, Y., D.A.L. Lourenco, and **I. Misztal**. 2019. Genomic predictions in purebreds with a multibreed genomic relationship matrix. J. Anim. Sci. 97:4418-4427. https://doi.org/10.1093/jas/skz296.
- Andonov, S., C. Costa, A. Uzunov, P. Bergomi, D.A.L. Lourenco, and **I. Misztal**. 2019. Modeling honey yield and defensive and swarming behaviors of Italian honey bees (*Apis mellifera ligustica*) using linear-threshold approaches. BMC Genet. 20(1):78. doi: 10.1186/s12863-019-0776-2.
- Pocrnici, I., D.A.L. Lourenco, K. Y. Masuda, and **I. Misztal**. 2019. Accuracy of genomic BLUP when considering a genomic relationship matrix based on the number of the largest eigenvalues: a simulation study. Genet. Sel. Evol. 51:75. doi/10.1186/s12711-019-0516-0.
- Hidalgo, J., S. Tsuruta, D. A. L. Lourenco, Y. Masuda, Y. Huang, K. A. Grant, and **I. Misztal**. 2020. Changes in genetic parameters of fitness and growth traits in pigs under genomic selection. J. Anim. Sci. 98:1-12. doi: 10.1093/jas/skaa032.

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- Garcia, A. L. S., Y. Masuda, S. Tsuruta, S. Miller, **I. Misztal**, D. A. L. Lourenco. 2020. Indirect predictions with a large number of genotyped animals using the algorithm for proven and young. *J. Animal Sci.*
- Misztal, I.**, D. Lourenco, and A. Legarra. 2020. Current status of genomic evaluation. *J. Animal Sci.* 98:. <https://doi.org/10.1093/jas/skaa101>
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- Bermann, M., A. Legarra, M. K. Hollifield, Y. Masuda, D. Lourenco, and **I. Misztal**. 2020. Validation of single-step GBLUP genomic predictions from threshold models using the linear regression (LR) method: an application in chicken mortality. *J. Anim. Sci.*
- Tsuruta, S., T. J. Lawlor, D. Lourenco, and **I. Misztal**. 2020. Bias in genomic predictions by mating practices for linear type traits in a large-scale genomic evaluation. *J. Dairy Sci.*
- Bermann, M., D. Lourenco, and **I. Misztal**. 2021. Technical Note: Automatic scaling in single-step GBLUP. *J. Dairy Sci.* 104:2027-2031. <https://doi.org/10.3168/jds.2020-18969>
- Steyn, Y., D. A. Lourenco, C. Y. Chen, B. D. Valente, J. Holl, W. O. Herring, and **I. Misztal**. 2021. Optimal definition of contemporary groups for crossbred pigs in a joint pure-and crossbred genetic evaluation. *J. Animal Sci.* <https://doi.org/10.1093/jas/skaa396>
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