

VITA
Ignacy Misztal

Education

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

Academic positions held

2001-	Professor	University of Georgia
1995-2000	Associate Professor	University of Georgia
1988-1995	Research Data Analyst	University of Illinois, Urbana
1986-1988	Research Associate	University of Illinois, Urbana
1981-1986	Research Scientist	Warsaw Agricultural University, Poland

Research Interests

Methods of Genetic Evaluation, Programming in Animal Breeding, Genetics of Heat Tolerance, Genetics of Fertility, Genetics of Mortality, Genotype x Environment Interaction, Competition effects, Incorporation of genomic information into genetic evaluations.

Sponsors

NIFA/USDA, Holstein Association, Angus Association, Pig Improvement Company, Smithfield, Cobb-Vantress, Zoetis,...

Major accomplishments

1. Developed computational methodology for national evaluation of dairy cattle (1987)– methodology applied commercially for US Holsteins for next 20 years
2. Developed computing methodology for large-scale computations with REML (1991)– methodology used everywhere.
3. Developed methodology for estimation of dominance variance with very large data sets and estimated dominance variance for many species and traits (1995) – studies still cited.
4. Pioneered new way of software development for mixed models and animal genetics with paper “Complex models, more data: simpler programming”- resulting software used by thousands of studies and by all largest animal genetic companies in US for large-scale genetic/genomic evaluations.
5. Pioneered methodology for studying genetics of heat stress in animals based on public data (2001) – used by many grant applications worldwide.
6. Developed methodology for genetic evaluation using all genomic, phenotypic and pedigree information called single-step (2010). Methodology considered most accurate yet most simple in animal genomics.
7. Developed extension of Henderson’s algorithm of inversion a pedigree relationship matrix to genomic relationship (2014). Methodology allows genomic evaluation with millions of genotyped individuals at very low cost but high accuracy and excellent numerical stability. Theory of the algorithm provides novel insight into genomic selection and can be a starting point for many new studies.

Software

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

Regular courses taught at University of Georgia

Mixed models; Computing in Animal Breeding; Advanced Animal Breeding; Graduate student seminar

Recent short courses

Poland (1998), Finland (1999), Japan (1999), Norway (1999), Belgium (1999), USA-Wisconsin (2000), Australia (2000), Brazil (2001), Italy (2002), Spain (2003), Brazil (2004), Denmark (2004), Uruguay (2005), France (2006), Netherlands (2007), South Africa (2007), Italy (2008), USA - GA (2008), Denmark (2011); USA-GA (2012), Netherlands (2012), Italy (2013), USA-UGA (2014), Germany (2014), Poland (2015).

Awards

J. L. Lush Award in Animal Breeding and Genetics, ADSA (2002).
 Rockefeller Prentice Award in Animal Breeding and Genetics, ASAS (2008).
 Research Award, National Association of Animal Breeders (2008).
 D.W. Brooks Research Award, UGA (2010).
 Most Cited Breeding&Genetics paper in Journal of Dairy Science (2013)
 Pioneer Award of the Beef Improvement Association (2013)
 D.W. Brooks Award for Excellence in Global Programs, UGA (2014)

Recent refereed publications (out of 198)

Aguilar, I., I. Misztal, S. Tsuruta, G. R. Wiggans and T. J. Lawlor. 2011. Multiple trait genomic evaluation of conception rate in Holsteins. *J. Dairy Sci.* 94:2621-2624.
 Simeone, R., I. Misztal, I. Aguilar, and A. Legarra. 2011. Evaluation of the utility of genomic relationship matrix as a diagnostic tool to detect mislabeled genotyped animals in a broiler chicken population. *J. Anim. Breed. Genet.* 128(5):386-393.
 Chen, C. Y., I. Misztal, I. Aguilar, A. Legarra, and B. Muir. 2011. Effect of different genomic relationship matrix on accuracy and scale. *J. Anim. Sci.* 89:2673-2679.
 Tsuruta, S., I. Aguilar, I. Misztal, and T. J. Lawlor. Multiple-trait genomic evaluation of linear type traits using genomic and phenotypic data in US Holsteins. *J. Dairy Sci.* 94:4198-4204.
 Vitezica, Z. G., I. Aguilar, I. Misztal, and A. Legarra. Bias in Genomic Predictions for Populations Under Selection. *Genet. Res. Camb.* 93:357-366.
 Perez-Enciso, M., and I. Misztal. 2011. Qxpak.5: Old mixed model solutions for new genomics problems. *BMC Bioinformatics.* 12:202.
 Simeone, R., I. Misztal, I. Aguilar, and A. Legarra. 2011. Evaluation of the utility of genomic relationship matrix as a diagnostic tool to detect mislabeled genotyped animals in a broiler chicken population. *J. Anim. Breed. Genet.* 128(5):386-393.

- Chen, C. Y., I. Misztal, I. Aguilar, A. Legarra, and B. Muir. 2011. Effect of different genomic relationship matrix on accuracy and scale. *J. Anim. Sci.* 89:2673-2679.
- Tsuruta, S., I. Aguilar, I. Misztal, and T. J. Lawlor. 2011. Multiple-trait genomic evaluation of linear type traits using genomic and phenotypic data in US Holsteins. *J. Dairy Sci.* 94:4198-4204.
- Vitezica, Z. G., I. Aguilar, I. Misztal, and A. Legarra. 2011. Bias in Genomic Predictions for Populations Under Selection. *Genet. Res. Camb.* 93:357–366.
- Simeone, R., I. Misztal, I. Aguilar, and Z. Vitezica. 2012. Evaluation of a multi-line broiler chicken population using a single-step genomic evaluation procedure. *J. Anim. Breed. Genet.* 129(1):3–10.
- Bloemhof, S., A. Kaue, E. Knol, J. van Arendonk, and I. Misztal. 2012. Heat stress effects on farrowing rate in sows: Genetic parameter estimation using within-line and crossbred models. *J. Anim. Sci.* 90:2109-2119.
- Wang, H., I. Misztal, I. Aguilar, A. Legarra, and W. M. Muir. 2012. Genome-wide association mapping including phenotypes from relatives without genotypes. *Genet. Res.* 94(2):73-83.
- Misztal, I., S. Tsuruta, I. Aguilar, A. Legarra, P. M. VanRaden, and T. J. Lawlor. 2013. Methods to Approximate Reliabilities in Single-Step Genomic Evaluation. *J. Dairy Sci.* 96:647–654.
- Misztal, I., Z.G. Vitezica, A. Legarra, I. Aguilar, and A.A. Swan. 2013. Unknown-parent groups in single-step genomic evaluation. *J. Anim. Breed. Genet.* doi:10.1111/jbg.12025.
- Tsuruta, S., I. Misztal, and T. J. Lawlor. 2013. Genomic evaluations of final score for US Holsteins benefit from the inclusion of genotypes on cows. 96:3332-3335.
- Misztal, I., S. Aggrey, and B. Muir. 2013. Experiences with a Single-Step Genome Evaluation. *J. Poultry Sci.* 92(9):2530–2534.
- Lourenco, D. A. L., I. Misztal, H. Wang, I. Aguilar, S. Tsuruta, and J. K. Bertrand. 2013. Prediction accuracy for a simulated maternally affected trait of beef cattle using different genomic evaluation models. 2013. *J. Anim. Sci.* 91:4090–4098.
- Dufresne, M., I. Misztal, S. Tsuruta, J. Holl, K. A. Gray, and N. Gangler. 2013. Estimation of genetic parameters for birth weight, preweaning mortality, and hot carcass weight of crossbred pigs. *J. Anim. Sci.* 91:5565–5571.
- Elzo, M. A., C. A. Martinez, G. C. Lamb, D. D. Johnson, M. G. Thomas, I. Misztal, D. O. Rae, J. G. Wasdin, and J. D. Driver. 2013. Genomic-polygenic evaluation for ultrasound and weight traits in Angus–Brahman multibreed cattle with the Illumina3k chip. *Livest. Sci.* 153:39–49.
- Lourenco, D. A. L., I. Misztal, S. Tsuruta, I. Aguilar, E. Ezra, M. Ron, A. Shirak, and J. I. Weller. 2014. Methods for genomic evaluation of a relatively small genotyped dairy population and effect of genotyped cow information in multiparity analyses. *J. Dairy Sci.* 97:1742–1752.
- 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 Three 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. *Frontiers Genet.* DOI=10.3389/fgene.2014.00134.
- Legarra, A., O. F. Christensen, I. Aguilar, and I. Misztal. 2014. Single Step, A General Approach For Genomic Selection. *Livest. Sci.* 166:54-65.
- Dufresne, 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. Animal Breeding Genet.* DOI: 10.1111/jbg.12109
- Fragomeni, B., I. Misztal, D. Lourenco, I. Aguilar, R. Okimoto and W. Muir. 2014. Changes in variance of top SNP windows over generations for three traits in broiler chicken. *Frontiers Genet.* doi: 10.3389/fgene.2014.00332
- Zhang, X., I. Misztal, M. Heidaritabar, J. W. M. Bastiaansen, R. Borg, R. L. Sapp, T. Wing, R. R. Hawken, D. A. L. Lourenco, 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.
- Fornieris, 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.* doi: 10.1534/genetics.114.173559.
- 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. Use of genomic recursions in single-step genomic 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.* doi: 10.1534/genetics.115.177014.
- 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 BLUP 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(8):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. Lourenco, B. Fragomeni and T. L. Lawlor. 2016. Implementation of genomic recursions in single-step genomic BLUP 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, and I. Misztal. 2016. Crossbred evaluations in single-step genomic BLUP using adjusted realized relationship matrices. *J. Animal Sci.* (Accepted)
- 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. *Genetics* (Accepted)

Other selected 2015 papers

- Misztal, I. 2015. Will genomic evaluation mature in 2015? Understanding realized accuracies and eliminating computing limits on the number of genotypes. Experiences with a single-step genomic evaluation (ssGBLUP). *Proc. 64th Annual National Breeders Roundtable.*
- Lourenco, D.A.L., I. Misztal, S. Tsuruta, B. Fragomeni, I. Aguilar, Y. Masuda and D. Moser. 2015. Direct and indirect genomic evaluations in beef cattle. *Interbull Bul.* 49.
- Masuda, Y., I. Misztal, S. Tsuruta, D. A. L. Lourenco, B. O. Fragomeni, A. Legarra, I. Aguilar, and T. J. Lawlor. 2015. Single-step genomic evaluations with 570K genotyped animals in US Holsteins. *Interbull Bul.* 49.
- Misztal, I., B. O. Fragomeni, D. A. L. Lourenco, S. Tsuruta, Y. Masuda, I. Aguilar, A. Legarra, and T. J. Lawlor. 2015. Efficient inversion of genomic relationship matrix by the algorithm for proven and young (APY). *Interbull Bul.* 49.