Andres Legarra

Brief CV

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Born in Pamplona (Navarra, Spain) in May 10, 1972.

Current position: Senior Geneticist, Council on Dairy Cattle Breeding (CDCB), 4201 Northview Drive, Suite 302, Bowie, MD 20716. https://www.uscdcb.com

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- Webpage: https://alegarra.github.io/
- Scientific blog: http://artadia.blogspot.com
- Google scholar: https://scholar.google.com/citations?user=oMML1K4AAAAJ&hl=fr
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Education

1997. Graduate as Engineer in Agriculture (Ingeniero Agrónomo) at the Universidad Pública de Navarra, Pamplona, Spain.
1998. Ph.D. at Universidad Publica de Navarra, Pamplona, Spain, 2002. Supervisor: Dr. Eva Ugarte, NEIKER, Vitoria, Spain.
1999. Habilitation (HDR), Institut National Polytechnique de Toulouse, France.

Positions

- April 2002 – July 2003: Postdoctoral researcher: University of Georgia (Athens, GA, US) under the supervision of J.K. Bertrand and I.Misztal.
- August 2003 – October 2005: Research scientist: NEIKER (Basque Institute for Agricultural Research, Vitoria, Spain)
- November 2005 – 2014 : Research Scientist : INRA (Institut National de la Recherche Agronomique, Toulouse, France)
- November 2014 – December 2022 : Research Director : INRAE (Institut National de la Recherche Agronomique, Toulouse, France)
- January 2023 - current: Senior Geneticist, Council on Dairy Cattle Breeding.

Responsibilities

- Supervision of PhD students (6 so far).
- Section Editor (2018-2020) and Senior Editor (2021-2023) of Journal of Dairy Science, section of Genetics and Genomics.
- Associate Editor of Genetics Selection Evolution since 2014.
- Team Coordinator at INRA 2014-2022.
- Member of the Scientific committee of the WCGALP 2022 congress.
- Deputy Leader workpackage European H2020 project Smarter (2018-2023).
- Member of the Interbull Technical Committee since 2023

Languages

- Spanish: native language
- English: fluent
- French: fluent
- Italian: usable

- Basque: notions

Major Achievements

2007. Economic weights in dairy sheep
2008. First published evaluation of the quality of genomic prediction using cross-validation

2009. “Single-Step” method for genomic predictions
2010. Non-additive models in genomic predictions
2011. Introduction of genomic selection in French dairy sheep breeding programmes
2012. Notes for Genomic Prediction
2013. Notion of metafounders
2014. Method Linear Regression for bias and accuracy of predictions

Software

2004. TM for variance component estimation
2005. GS3 for genomic predictions
2006. BLUPF90 for “Single Step” (in continuous development).

Other achievements

- Coordinator of the group MG2 (Models for Genetics and Genomics), GenPhySE unit, INRAE, 2014-2022

Invited seminars

- Universidad de Buenos Aires
- Universidad Publica de Navarra
- Universidad Politecnica de Valencia
- Ecole d'Agro Montpellier
- Iowa State University
- University of Georgia

Grants

Coordinator:

- INRA (Métaprogramme SELGEN): X-GEN:"Crossbreeding and accuracy in genomic evaluation". Total budget: 30,000 euros + 3 PhD scholarships. 2013-2015.
- European FEDER: GENOMIA. "Renforcement des schémas de sélection des races ovines laitières locales d'intérêt économique, écologique et social." Total budget: 650,000 euros. 2010-2013.
- European FEDER: ARDI (2018-2021;):. "Ardi is Research, Development, Innovation"Recherche, deeveloppement, innovation dans les brebis laitieres" Total budget: 1155000 euros.

Largely implicated:

- INIA (Spain) : RTA02-002-C2. "Economic weights in Dairy sheep genetic improvement programs". Global budget: 20,000 euros. 2003-2005.
- ANR (France) : SheepSNPQTL. " Utilisation d'une puce 60 000 SNP pour cartographier finement des QTL affectant des caractères de production, de resistance aux maladies de comportement chez les ovins » Total budget: 300,000 euros. 2009-2011.
- ANR (France) : Amasgen. "Methodological approaches and applications of geneomic selection in dairy cattle" Total budget: 300000 euros. 2009-2011.
- ANR (France) : Rules&Tools. "Statistical methods for the dissection of trait variability with SNP chips". Total budget : 400,000 euros. 2010-2013.
- European H2020 Projects: "Smarter": Deputy Leader WP5. Total budget: 7M euros. 2018-2023

Award grants

- Joint exchange grant University of Buenos Aires (Argentina)- University of Toulouse (France), financed by the University of Toulouse, 2015-2016 (6000 euros)
- Joint exchange grant CSIRO Brisbane (Australia) – INRA, 2015-2017 (6000 euros for each partner).
- Grant from SelGen metaprogram for a trip to University of Georgia, 2000 euros, 2014.

- Chateaubriand Fellowship exchange grant for a visit of Matias Bermann (University of Georgia)

Project reviews:

- Netherlands Grant System, PERSPECTIEF
- INRA metaprogram SelGen
- Science Peer Reviewer for the New Zealand Ministry of Business, Innovation & Employment
- International Foundation for Science (Sweden, www.ifs.se)
- Research Foundation - Flanders (Fonds Wetenschappelijk Onderzoek - Vlaanderen, FWO), Belgium.
- Agencia Estatal De Investigación (State Research Agency), Spain
- Netherlands Organisation for Scientific Research (NWO)
- "Ambizione", the Swiss National Science Foundation (SNSF), Switzerland
- Consejo Nacional de Ciencia, Tecnología e Innovación Tecnológica (CONCYTEC), Peru

Editorial work

- Editorial board of Journal of Animal Science 2005-2007
- Editorial board Journal of Dairy Science 2014-2019,
- Section editor Journal of Dairy Science, Genetics and Genomics section 2018-2020
- Senior Editor Journal of Dairy Science, Genetics and Genomics section 2021-2023
- Associate editor, Genetics Selection Evolution, since 2012

Reviewer for the journals: - Nature Reviews Genetics - Genetics - Genetics, Selection, Evolution - Heredity - Journal of Animal Science - Journal of Dairy Science - Plos ONE - Plos Genetics - Journal of Animal Breeding and Genetics - Animal - Mammalian Genome - European Journal of Human Genetics - World Rabbit Science - Canadian Journal of Animal Science - Crop Science - Información Técnico-Económica Agraria (ITEA) - Spanish Journal of Agricultural Research.

Organisation of colloquia and symposia

- Organiser of the XI QTLMAS 2007. Workshop on QTL and Marker Assisted Selection. 22-23 March 2007. Toulouse, France.
- Chairman at the XII QTLMAS (Uppsala, Sweden) and at AIDA 2013 (Zaragoza, Spain).
- Organiser of the INRA "Ecole Chercheur" (Research School) "Sélection Génomique. Théorie et mise en relation avec les programmes d'amélioration" Bruz, France, 23 - 27 September 2013.
- Member of the Scientific Board, World Congress Applied to Livestock Production 2022

- Chairman at World Congress Applied to Livestock Production 2022 (Rotterdam, The Netherlands), session « Improving Genomic Prediction »

Awards

Lush Award, American Dairy Science Association, 2022

Teaching

Official courses, Master level:

- 2008, 2009, 2010. 1-day course "Genetic improvement in Animal Science", Master EURAMA, EIP, Toulouse.
- 2011, 2012, 2013. 6 h of course on "Quantitative Genetics", Master courses, (Master MABS : Microbiologie, Agrobiosciences, Bioinformatique et Biologie des Systèmes, UE : Génomique et Génétique Statistique), University of Paul Sabatier (Toulouse, France).

Official courses, PhD level:

- 2009 4-day course: "Genome-wide association mapping and genomic selection", Universidad de Buenos Aires, Argentina, 3-7 March.
- 2012, 2014, 2016, 2022, 2024. 4-day course: "Short course - Programming and computer algorithms with focus on genomic selection in animal breeding". University of Georgia, Athens, USA, May 28-June 1.
- 2012 5-day course: "Genomic selection in animal and plant breeding", Universidad de Buenos Aires, Argentina, December 17-21.
- 2013 5-day course: "Computer algorithms in animal breeding with special focus on genomic selection", University of Padova, Italy, February 4-8.
- 2015 4-day course : "Methods for genomic evaluation", 7-10 April 2015, Universitat Politècnica de València, Spain

Non-academic courses:

- 2010 3-day course: "Genomic selection with parametric methods", Universidad Autonoma de Barcelona, Spain, 29-20 and 1 October.
- 2012 3-day course: "Genomic selection with parametric methods", Instituto Nacional de Investigación Agraria (INIA), Madrid, Spain 11-13 June.
- 2013 Ecole chercheur 'Sélection Génomique" SelGen INRA, Bruz, France, 23-27 septembre, "Models for Genomic Selection", 1 day intervention.
- 2013 Course "Dissection de la variabilité des caractères complexes à l'aide de puces SNP", 24-26 Juin 2013, Agrocampus-Ouest, Rennes, June 24-26, 1 day intervention.

Supervision of students

Stagiare M2

- Brian Acosta (2020). Co-supervised with Zulma Vitezica, INP-Toulouse. “A posteriori partition of genetic gains in dairy sheep breeding schemes.” INP-Toulouse.

PhD students:

- Aurélie Favier (2010-2012). Co-supervised by Simon de Givry, INRA. « Décompositions fonctionnelles et structurelles dans les modèles graphiques probabilistes appliquées à la reconstruction d’haplotypes » (translation : Fonctional and structural decompositions in probabilistic graphical models, with an application in haplotype reconstruction). Financed by the Animal Genetics and Mathematics and Artificial Intelligence Department, INRA. Aurelie est professeure au Lycee Montesquieu, à Libourne.
- Eduardo Nestor Fernandez (2013-2016). Co-supervised with Manuel Baselga (Universidad Politécnica de Valencia, Espagne) and Juan Pablo Sánchez (IRTA, Espagne). “Estimation of additive and non-additive genetic effects in maternal rabbit lines”. Eduardo was Associate Professor in Universidad Nacional de Lomas de Zamora when he died in April 2021.
- Tao Xiang (2013-2017) Co-supervised with Ole Christensen (University of Aarhus, Denmark). “Genomic evaluation on crossbred and purebred pigs”. Financed by the EGS-ABG Graduate School. Tao is now Associate Professor, Huazhong Agricultural University, Wuhan P.R.China.
- Fernando Macedo Fajardo (2018-2021) “Study of the origin and impact of bias in genetic and genomic national evaluations: the case of the dairy sheep”. Financed by Region Occitanie and Selgen metaprogram (INRA). Fernando is in leave from Universidad de la Republica (Uruguay) and works in Interbull, a structure of the Swedish University of Agricultural Sciences (SLU)
- Marine Wicki (2022-2024) :Etude des plans de connexion entre populations génétiquement proches visant à accroître l’intérêt de la sélection génomique en petits ruminants” Co-supervised with Jerome Raoul. Financed by ApisGene and Institut de l’Elevage

Postdoc:

- Carolina Garcia-Baccino June 2019-June 2021. Financed by H-2020 grant Smarter. She works in Nucleus, a pig breeding company (Le Rheu, France).

Miscellaneus

Interviews

- Interview at “Exploreur”, the scientific magazine of University of Toulouse: https://exploreur.univ-toulouse.fr/quand-la-selection-genetique-conserve-les-traditions
- Interview at Guaixe: https://guaixe.eus/irurtzun/1704989487133-datuak-prozesatu-eta-genetika-ebaluazioak-sortzen-ditugu
- Interview at Universidad Politecnica de Valencia, Spain: https://acteon.webs.upv.es/entrevistas.htm

Deliverables from Smarter EU grant

- D5.1 Method for identifying environmental challenge events and assessment of their value for selection for resilience
- D5.2 A report of an improved method to calculate genomic relationship across individuals of different purebred and crossbred populations

Publications

Book Chapters

Boggio, G. M., Christensen, O. F., Legarra, A., Allain, C., Meynadier, A., & Marie-Etancelin, C. (2022). Rumen bacteria do not provide improved genetic evaluation of dairy traits in sheep. In *WCGALP 2022 programme book*. Wageningen Academic Publishers.

Varona, L., Legarra, A., Toro, M. A., & Vitezica, Z. G. (2022). Correction to: Genomic prediction methods accounting for nonadditive genetic effects. In *Genomic prediction of complex traits: Methods and protocols* (pp. C1–C1). Springer US New York, NY.

Varona, L., Legarra, A., Toro, M. A., & Vitezica, Z. G. (2022). Genomic prediction methods accounting for nonadditive genetic effects. In *Genomic Prediction of Complex Traits: Methods and Protocols* (Nourollah Ahmadi and Jérôme Bartholomé, pp. 219–243). HumanaPress.

Journal Articles

Antonios, S., Rodríguez-Ramilo, S. T., Legarra, A., Astruc, J.-M., Varona, L., & Vitezica, Z. G. (2025). Genetic inbreeding load and its individual prediction for milk yield in French dairy sheep. *Genetics Selection Evolution*, *57*(1), 1. https://doi.org/10.1186/s12711-024-00945-z

Legarra, A., & Aguilar, I. (2025). Tools to refine unknown parent group definitions. *Journal of Dairy Science*, *108*(2), 1747–1756. https://doi.org/10.3168/jds.2024-25408

Tabet, J. M., Lourenco, D., Bussiman, F., Bermann, M., Misztal, I., VanRaden, P. M., Vitezica, Z. G., & Legarra, A. (2025). All-breed single-step genomic

best linear unbiased predictor evaluations for fertility traits in US dairy cattle. *Journal of Dairy Science*, *108*(1), 694–706.

Bermann, M., Legarra, A., Munera, A. A., Misztal, I., & Lourenco, D. (2024). Confidence intervals for validation statistics with data truncation in genomic prediction. *Genetics Selection Evolution*, *56*(1), 18.

Legarra, A., Bermann, M., Mei, Q., & Christensen, O. F. (2024). Estimating genomic relationships of metafounders across and within breeds using maximum likelihood, pseudo-expectation–maximization maximum likelihood and increase of relationships. *Genetics Selection Evolution*, *56*(1), 35.

Legarra, A., Bermann, M., Mei, Q., & Christensen, O. F. (2024). Redefining and interpreting genomic relationships of metafounders. *Genetics Selection Evolution*, *56*(1), 34.

Legarra, A., Bermann, M., VanRaden, P. M., Nicolazzi, E. L., Mota, R. R., Tabet, J. M., Lourenco, D. L., & Misztal, I. (2024). Technical options for all-breed Single-step GBLUP for US dairy cattle. *Interbull Bulletin*, *60*, 143–147.

López-Correa, R., Legarra, A., & Aguilar, I. (2024). Modelling missing pedigree with metafounders and validating single-step genomic predictions in a small dairy cattle population with a great influence of foreign genetics. *Journal of Dairy Science*, *107*, 4685–1692. https://doi.org/10.3168/jds.2023-23732

Mota, R., Sullivan, P., Nicolazzi, E., McWhorter, T. M., Legarra, A., & VanRaden, P. (2024). Genomic validation software: USA update including truncated MACE. *Interbull Bulletin*, *60*, 200–206.

Pardo, A. M., Legarra, A., Vitezica, Z. G., Forneris, N. S., Maizon, D. O., & Munilla, S. (2024). On the ability of the LR method to detect bias when there is pedigree misspecification and lack of connectedness. *Genetics Selection Evolution*, *56*(1), 1–15.

Wicki, M., Brown, D. J., Gurman, P. M., Raoul, J., Legarra, A., & Swan, A. A. (2024). Combined genomic evaluation of merino and dohne merino australian sheep populations. *Genetics Selection Evolution*, *56*(1), 69.

Antonios, S., Legarra, A., Pong-Wong, R., Astruc, J., Rodriguez-Ramilo, S., & Vitezica, Z. (2023). Partitioning of the genetic trends of French dairy sheep in Mendelian samplings and long-term contributions. *Journal of Dairy Science*, *106*(9), 6275–6287.

Bermann, M., Aguilar, I., Lourenco, D., Misztal, I., & Legarra, A. (2023). Reliabilities of estimated breeding values in models with metafounders. *Genetics Selection Evolution*, *55*(1), 6.

Bussiman, F., Chen, C.-Y., Holl, J., Bermann, M., Legarra, A., Misztal, I., & Lourenco, D. (2023). Boundaries for genotype, phenotype, and pedigree truncation in genomic evaluations in pigs. *Journal of Animal Science*, *101*, skad273.

Garcia, A., Aguilar, I., Legarra, A., Tsuruta, S., Misztal, I., & Lourenco, D. (2023). Correction: Theoretical accuracy for indirect predictions based on SNP effects from single-step GBLUP. *Genetics Selection Evolution*, *55*(1), 26.

Id-Lahoucine, S., Cánovas, A., Legarra, A., & Casellas, J. (2023). Transmission ratio distortion regions in the context of genomic evaluation and their effects on reproductive traits in cattle. *Journal of Dairy Science*, *106*(11), 7786–7798.

Legarra, A., & Christensen, O. F. (2023). Genomic evaluation methods to include intermediate correlated features such as high-throughput or omics phenotypes. *JDS Communications*, *4*(1), 55–60.

Legarra, A., Gonzalez-Dieguez, D. O., Charcosset, A., & Vitezica, Z. G. (2023). Impact of interpopulation distance on dominance variance and average heterosis in hybrid populations within species. *Genetics*, *224*(2), iyad059.

Legarra, A., & Van Raden, P. M. (2023). Effect of modelling unknown parent groups and metafounders on the historical genetic trend of fertility traits. *Interbull Bulletin*, *59*, 11–14.

Martinez-Boggio, G., Christensen, O., Legarra, A., Meynadier, A., & Marie-Etancelin, C. (2023). Microbiability of milk composition and genetic control of microbiota effects in sheep. *Journal of Dairy Science*, *106*(9), 6288–6298.

McWhorter, T. M., Bermann, M., Garcia, A. L., Legarra, A., Aguilar, I., Misztal, I., & Lourenco, D. (2023). Implication of the order of blending and tuning when computing the genomic relationship matrix in single-step GBLUP. *Journal of Animal Breeding and Genetics*, *140*(1), 60–78.

Steyn, Y., Lawlor, T., Masuda, Y., Tsuruta, S., Legarra, A., Lourenco, D., & Misztal, I. (2023). Nonparallel genome changes within subpopulations over time contributed to genetic diversity within the US Holstein population. *Journal of Dairy Science*, *106*(4), 2551–2572.

Wicki, M., Raoul, J., & Legarra, A. (2023). Effect of subdivision of the Lacaune dairy sheep breed on the accuracy of genomic prediction. *Journal of Dairy Science*, *106*(8), 5570–5581.

Wicki, M., Raoul, J., & Legarra, A. (2023). Estimation of SNP effects in Lacaune dairy sheep depending on the reference population composition. *Proc. Assoc. Advmt. Anim. Breed. Genet*, *25*, 166–169.

Aguerre, S., Astruc, J.-M., Legarra, A., Bordes, L., Prevot, F., Grisez, C., Vial Novella, C., Fidelle, F., Jacquiet, P., & Moreno-Romieux, C. (2022). Unfavorable genetic correlations between fecal egg count and milk production traits in the French blond-faced Manech dairy sheep breed. *Genetics Selection Evolution*, *54*(1), 14.

Astruc, J. M., Buisson, D., Clément, V., Lagriffoul, G., Larroque, H., Legarra, A., Palhiere, I., Ugarte, E., & Moreno-Romieux, C. (2022). Benefits from recent and on-going projects on adaptation and resilience in French dairy sheep and goats. *Options Mediterraneennes Série A. Séminaires Méditerranéens*, *129*, 41–48.

Bermann, M., Lourenco, D., Forneris, N. S., Legarra, A., & Misztal, I. (2022). On the equivalence between marker effect models and breeding value models and direct genomic values with the Algorithm for Proven and Young. *Genetics Selection Evolution*, *54*(1), 52.

Cesarani, A., Lourenco, D., Tsuruta, S., Legarra, A., Nicolazzi, E., VanRaden, P., & Misztal, I. (2022). Multibreed genomic evaluation for production traits of dairy cattle in the United States using single-step genomic best linear unbiased predictor. *Journal of Dairy Science*, *105*(6), 5141–5152.

Fang, F., Li, J., Guo, M., Mei, Q., Yu, M., Liu, H., Legarra, A., & Xiang, T. (2022). Genomic evaluation and genome-wide association studies for total

number of teats in a combined American and Danish Yorkshire pig populations selected in China. *Journal of Animal Science*, *100*(7), skac174.

Garcia, A., Aguilar, I., Legarra, A., Tsuruta, S., Misztal, I., & Lourenco, D. (2022). Theoretical accuracy for indirect predictions based on SNP effects from single-step GBLUP. *Genetics Selection Evolution*, *54*(1), 66.

Garcia-Baccino, C., Pineda-Quiroga, C., Astruc, J., Ugarte, E., & Legarra, A. (2022). High genetic correlation for milk yield across Manech and Latxa dairy sheep from France and Spain. *JDS Communications*, *3*(4), 260–264.

Legarra, A., González-Diéguez, D., & Vitezica, Z. G. (2022). Computing strategies for multi-population genomic evaluation. *Genetics Selection Evolution*, *54*(1), 10.

Macedo, F., Astruc, J., Meuwissen, T., & Legarra, A. (2022). Removing data and using metafounders alleviates biases for all traits in Lacaune dairy sheep predictions. *Journal of Dairy Science*, *105*(3), 2439–2452.

Mei, Q., Vitezica, Z. G., Li, J., Zhao, S., Legarra, A., & Xiang, T. (2022). Impacts of additive, dominance, and inbreeding depression effects on genomic evaluation by combining two SNP chips in Canadian Yorkshire pigs bred in China. *Genetics Selection Evolution*, *54*(1), 69.

Abdollahi-Arpanahi, R., Lourenco, D., Legarra, A., & Misztal, I. (2021). Dissecting genetic trends to understand breeding practices in livestock: A maternal pig line example. *Genetics Selection Evolution*, *53*, 1–10.

Antonios, S., Rodriguez-Ramilo, S. T., Aguilar, I., Astruc, J., Legarra, A., & Vitezica, Z. (2021). Genomic and pedigree estimation of inbreeding depression for semen traits in the Basco-Béarnaise dairy sheep breed. *Journal of Dairy Science*, *104*(3), 3221–3230.

Bermann, M., Legarra, A., Hollifield, M. K., Masuda, Y., Lourenco, D., & Misztal, I. (2021). Validation of single-step GBLUP genomic predictions from threshold models using the linear regression method: An application in chicken mortality. *Journal of Animal Breeding and Genetics*, *138*(1), 4–13.

Christensen, O. F., Börner, V., Varona, L., & Legarra, A. (2021). Corrigendum to: Genetic evaluation including intermediate omics features. *Genetics*, *219*(4), iyab167.

Christensen, O. F., Börner, V., Varona, L., & Legarra, A. (2021). Genetic evaluation including intermediate omics features. *Genetics*, *219*(2), iyab130.

Garcia-Baccino, C. A., Marie-Etancelin, C., Tortereau, F., Marcon, D., Weisbecker, J.-L., & Legarra, A. (2021). Detection of unrecorded environmental challenges in high-frequency recorded traits, and genetic determinism of resilience to challenge, with an application on feed intake in lambs. *Genetics Selection Evolution*, *53*, 1–14.

González-Diéguez, D., Legarra, A., Charcosset, A., Moreau, L., Lehermeier, C., Teyssèdre, S., & Vitezica, Z. G. (2021). Genomic prediction of hybrid crops allows disentangling dominance and epistasis. *Genetics*, *218*(1), iyab026.

Legarra, A., Garcia-Baccino, C. A., Wientjes, Y. C., & Vitezica, Z. G. (2021). The correlation of substitution effects across populations and generations in the presence of nonadditive functional gene action. *Genetics*, *219*(4), iyab138.

Macedo, F. L., Christensen, O. F., & Legarra, A. (2021). Selection and drift reduce genetic variation for milk yield in Manech Tête Rousse dairy sheep. *JDS Communications*, *2*(1), 31–34.

Rodriguez-Ramilo, S., Reverter, A., & Legarra, A. (2021). Islands of runs of homozygosity indicate selection signatures in Ovis aries 6 (OAR6) of French dairy sheep. *JDS Communications*, *2*(3), 132–136.

Aguilar, I., Fernandez, E. N., Blasco, A., Ravagnolo, O., & Legarra, A. (2020). Effects of ignoring inbreeding in model-based accuracy for BLUP and SSGBLUP. *Journal of Animal Breeding and Genetics*, *137*(4), 356–364.

Druet, T., & Legarra, A. (2020). Theoretical and empirical comparisons of expected and realized relationships for the X-chromosome. *Genetics Selection Evolution*, *52*, 1–17.

González-Diéguez, D., Tusell, L., Bouquet, A., Legarra, A., & Vitezica, Z. G. (2020). Purebred and crossbred genomic evaluation and mate allocation strategies to exploit dominance in pig crossbreeding schemes. *G3: Genes, Genomes, Genetics*, *10*(8), 2829–2841.

Granado-Tajada, I., Legarra, A., & Ugarte, E. (2020). Exploring the inclusion of genomic information and metafounders in Latxa dairy sheep genetic evaluations. *Journal of Dairy Science*, *103*(7), 6346–6353.

Granado-Tajada, I., Rodriguez-Ramilo, S. T., Legarra, A., & Ugarte, E. (2020). Inbreeding, effective population size, and coancestry in the Latxa dairy sheep breed. *Journal of Dairy Science*, *103*(6), 5215–5226.

Legarra, A., Aguilar, I., & Colleau, J. J. (2020). Methods to compute genomic inbreeding for ungenotyped individuals. *Journal of Dairy Science*, *103*(4), 3363–3367.

Lourenco, D., Legarra, A., Tsuruta, S., Masuda, Y., Aguilar, I., & Misztal, I. (2020). Single-step genomic evaluations from theory to practice: Using SNP chips and sequence data in BLUPF90. *Genes*, *11*(7), 790.

Macedo, F. L., Christensen, O. F., Astruc, J.-M., Aguilar, I., Masuda, Y., & Legarra, A. (2020). Bias and accuracy of dairy sheep evaluations using BLUP and SSGBLUP with metafounders and unknown parent groups. *Genetics Selection Evolution*, *52*(1), 47.

Macedo, F., Reverter, A., & Legarra, A. (2020). Behavior of the linear regression method to estimate bias and accuracies with correct and incorrect genetic evaluation models. *Journal of Dairy Science*, *103*(1), 529–544.

Misztal, I., Lourenco, D., & Legarra, A. (2020). Current status of genomic evaluation. *Journal of Animal Science*, *98*(4), skaa101.

Reverter, A., Vitezica, Z. G., Naval-Sánchez, M., Henshall, J., Raidan, F. S., Li, Y., Meyer, K., Hudson, N. J., Porto-Neto, L. R., & Legarra, A. (2020). Association analysis of loci implied in “buffering” epistasis. *Journal of Animal Science*, *98*(3), skaa045.

Sánchez, J. P., Legarra, A., Velasco-Galilea, M., Piles, M., Sánchez, A., Rafel, O., González-Rodriguez, O., & Ballester, M. (2020). Genome-wide association study for feed efficiency in collective cage-raised rabbits under full and restricted feeding. *Animal Genetics*, *51*(5), 799–810.

Varona, L., & Legarra, A. (2020). GIBBSTHUR: Software for estimating variance components and predicting breeding values for ranking traits based on a thurstonian model. *Animals*, *10*(6), 1001.

Aguilar, I., Legarra, A., Cardoso, F., Masuda, Y., Lourenco, D., & Misztal, I. (2019). Frequentist p-values for large-scale-single step genome-wide association, with an application to birth weight in American Angus cattle. *Genetics Selection Evolution*, *51*, 1–8.

Bradford, H. L., Masuda, Y., VanRaden, P. M., Legarra, A., & Misztal, I. (2019). Modeling missing pedigree in single-step genomic BLUP. *Journal of Dairy Science*, *102*(3), 2336–2346.

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