ANNEXES

Annex 1 – PUBLICATIONS BY RANK

1 – SCIENTIFIC PUBLICATIONS

1.1 – Primary original research articles

1.1.1. In peer-reviewed journals

2001

A. Legarra, E. Ugarte. 2001. Genetic parameters of milk traits in Latxa dairy sheep. *Animal Science,* 73, 407-412.

M. Serrano, E. Ugarte, J.J. Jurado, M.D. Pérez-Guzmán, A. Legarra. 2001. Test-day models and genetic parameters in Latxa and Manchega dairy ewes. *Livestock Production Science*, 67:253-264.

2004

A. Legarra, I. Misztal, J.K. Bertrand. 2004. Constructing Covariance Functions for Random Regression Models for Growth in Gelbvieh Beef Cattle. *Journal of Animal Science,* 82: 1564-1571.

2005

A. Legarra, P. López-Romero, E. Ugarte. 2005. Bayesian model selection of contemporary groups for BLUP genetic evaluation in Latxa dairy sheep. *Livestock Production Science,* 93: 205-212.

A. Legarra, E. Ugarte. 2005. Genetic Parameters of Udder Traits, Somatic Cell Score and Milk Yield in Latxa Sheep. *Journal of Dairy Science,* 88: 2238-2245.

2006

L. Alfonso, A. Parada, A. Legarra, E. Ugarte, A. Arana. 2006. Effects on genetic variability of selection against scrapie sensitivity in the Latxa Black-Faced sheep. *Genetics Selection Evolution,* 38:495-512.

2007

A. Legarra, M. Ramón, E. Ugarte, M.D. Pérez-Guzmán. 2007. Economic weights of fertility, prolificacy, milk yield and longevity in dairy sheep. *Animal*, Vol. 1 (02): 193-203.

A. Legarra, M. Ramón, E. Ugarte, M.D. Pérez-Guzmán, J. Arranz. 2007. Economic weights of somatic cell score in dairy sheep. *Animal*, Vol. 1 (02): 205-212.

E. López de Maturana, A. Legarra, E. Ugarte. 2007. Analysis of Fertility and Dystocia Using Recursive Multivariate Models, Handling Censored and Categorical Data in Holsteins. *Journal of Dairy Science,* 90: 2012-2024.

A. Legarra, J.K. Bertrand, T. Strabel, R. Sapp, J.P. Sanchez, I. Misztal. 2007. Multi-breed genetic evaluation in a Gelbvieh population. *Journal of Animal Breeding and Genetics*, 124: 286-295.

2008

A. Legarra, I. Misztal, 2008. Computing strategies in genome-wide selection. *Journal of Dairy Science*, J. Dairy Sci. 91:360–366.

A. Legarra, C. Robert-Granié, E. Manfredi, J.M. Elsen. 2008. Performance of genomic selection in mice. *Genetics*, 180:611-618.

2009

G. de los Campos, H. Naya, D. Gianola, J. Crossa, A. Legarra, E. Manfredi, K. Weigel, J.M. Cotes. 2009. Predicting Quantitative Traits with Regression Models for Dense Molecular Markers and Pedigrees. *Genetics*, 182: 375–385.

I. David, L. Bodin, A. Legarra, C. Robert-Granié. 2009. Product versus additive threshold models for analysis of reproduction outcomes in animal genetics. *Journal of Animal Science,* 87:2510-2518.

A. Legarra, I. Aguilar, I. Misztal. 2009. A relationship matrix including full pedigree and genomic information. *Journal of Dairy Science*, 92:4656-4663.

I. Misztal, A. Legarra, I. Aguilar. 2009. Computing procedures for genetic evaluation including phenotypic, full pedigree and genomic information. *Journal of Dairy Science,* 92:4648-4655.

A. Legarra, R. Fernando. 2009. Linear models for joint association and linkage QTL Mapping. *Genetics Selection Evolution* 41:43.

2010

I. Aguilar, I. Misztal, D. Johnson, A. Legarra, S. Tsuruta, T. Lawlor. 2010. A unified approach to utilize phenotypic, full pedigree, and genomic information for genetic evaluation of Holstein final score. *Journal of Dairy Science*, 93:743–752.

A. Ricard, A. Legarra, 2010. Validation of models for analysis of ranks in horse breeding evaluation*.* *Genetics Selection Evolution*, 42:3.

M. Ramón, A. Legarra, E. Ugarte, J.J. Garde, M.D. Pérez-Guzmán. 2010. Economic weights for major milk constituents of Manchega dairy ewes. *J. Dairy Sci.* 93:3303–3309

C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estival, N. Oumouhou, B. Mangin. 2010. Does probabilistic modelling of linkage disequilibrium evolution improve the accuracy of QTL location in animal pedigrees? *Genetics Selection Evolution*, 42:38.

2011

A. Legarra, F. Calenge, P. Mariani, P. Velge, C. Beaumont. 2011. Use of a reduced set of SNP for genetic evaluation of resistance to Salmonella carrier state in laying hens. *Poultry Science,* 90:731-736.

A. Legarra, C. Robert-Granié, P. Croiseau, F. Guillaume, S. Fritz. 2011. Improved Lasso for Genomic Selection. *Genetics Research,* 93: 77–87

L. Tusell, A. Legarra, M. García-Tomás, O. Rafel, J. Ramon, M. Piles. 2011. Different ways to model biological relationships between fertility and the pH of the semen in rabbits. *Journal of Animal Science*, 89:1294-1303.

C.Y. Chen, I. Misztal, I. Aguilar, A. Legarra, W.M. Muir. 2011. Effect of different genomic relationship matrices on accuracy and scale. *Journal of Animal Science*, 89:2673-2679.

L. Tusell, I. David, L. Bodin, A. Legarra, O. Rafel, M. López-Bejar, M. Piles. 2011. Using the product threshold model for estimating separately the effect of temperature on male and female fertility. *Journal of Animal Science*, 89:3983-3995.

R. Simeone, I. Misztal, I. Aguilar, A. Legarra. 2011. Evaluation of the utility of diagonal elements of the genomic relationship matrix as a diagnostic tool to detect mislabelled genotyped animals in a broiler chicken population. *Journal of Animal Breeding and Genetics*, 128:386-393.

Z.G. Vitezica, I. Aguilar, I. Misztal, A. Legarra. 2011. Bias in genomic predictions for populations under selection. *Genetics Research*, 93:357-366.

M.A. Toro, L.A. García-Cortés, A. Legarra. 2011. A note on the rationale for estimating genealogical coancestry from molecular markers. *Genetics, Selection, Evolution*, 43:27.

I. Aguilar, I. Misztal, A. Legarra, S. Tsuruta. 2011. Efficient computations of genomic relationship matrix and other matrices used in the single-step evaluation. *Journal of Animal Breeding and Genetics*, 128:422-428.

P. Croiseau, A. Legarra, F. Guillaume, S. Fritz, A. Baur, C. Colombani, C. Robert-Granié, D Boichard, V. Ducrocq. 2011. Fine tuning genomic evaluations in dairy cattle through SNP pre-selection with the Elastic-Net algorithm. *Genetics Research*, 93:409-417.

L. Tusell, A. Legarra, M. García-Tomás, O. Rafel, J. Ramon, M. Piles. 2011. Genetic basis of semen traits and their relationship with growth rate in rabbits. *Journal of Animal Science*, 89(3):669-679.

C. Marie-Etancelin, B. Basso, S. Davail, K. Gontier, X. Fernandez, Z.G. Vitezica, D. Bastianelli, E. Baéza, M.-D. Bernadet, G. Guy, J.M. Brun, A. Legarra. 2011. Genetic parameters of product quality and hepatic metabolism in fattened mule ducks. *Journal of Animal Science*, 89: 669-679.

2012

H. Wang, I. Misztal, I. Aguilar, A. Legarra, W.M. Muir, 2012. Genome-wide association mapping including phenotypes from relatives without genotypes. *Genet. Res., Camb.* 94: 73-83.

C. Colombani, P. Croiseau, S. Fritz, F. Guillaume, A. Legarra, V. Ducrocq, C. Robert-Granié. 2012. A comparison of PLS and sparse PLS regressions in genomic selection in French dairy cattle. *Journal of Dairy Science,* 95: 2120-2131.

S. I. Duchemin, C. Colombani, A. Legarra, G. Baloche, H. Larroque, J-M. Astruc, F. Barillet, C. Robert-Granié, E. Manfredi. 2012. Genomic selection in French Lacaune dairy sheep breed. *Journal of Dairy Science,* 95: 2723-2733.

A. Legarra, V. Ducrocq. 2012. Computational strategies for national integration of phenotypic, genomic and pedigree data in a single-step BLUP. *Journal of Dairy Science,* 95:4629-4645, *featured article*.

D.L. Roldan, H. Gilbert, J. Henshall., A. Legarra, J.M. Elsen. 2012. Fine-mapping quantitative trait loci with a medium-high marker density panel: efficiency of population structures and comparison of linkage disequilibrium linkage analysis models. *Genetics Research*, 94:223-234.

F. Ytournel, S. Teyssèdre, D.L. Roldan, M. Erbe, H. Simianer, D. Boichard, H. Gilbert, T. Druet, A. Legarra. 2012. LDSO: A program to simulate pedigrees and molecular information under various evolutionary forces. *Journal of Animal Breeding and Genetics*, 129: 417-421.

S. Karoui, M.J. Carabaño, C. Diaz, A. Legarra. 2012. Joint genomic evaluation of French dairy cattle breeds using multiple-trait models. *Genetics Selection Evolution*, 44:39.

G. Sallé, P. Jacquiet, L. Gruner, J. Cortet, C. Sauvé, F. Prévot, C. Grisez, J. P. Bergeaud, L. Schibler, A. Tircazes, D. François, C. Pery, F. Bouvier, J.C. Thouly, J.C. Brunel, A. Legarra, J.M. Elsen, J. Bouix, R. Rupp, C.R. Moreno. 2012. A genome scan for QTL affecting resistance to Haemonchus contortus in sheep. *Journal of Animal Science*, 90(13):4690-4705.

2013

C. Colombani, A. Legarra, S. Fritz, F. Guillaume, P. Croiseau, V. Ducrocq, C. Robert-Granie. 2013. Application of Bayesian Lasso and BayesCΠ methods for genomic selection in French Holstein and Montbéliarde breeds. *Journal of Dairy Science*, 96: 575-591.

I. Misztal, S. Tsuruta, I. Aguilar, A. Legarra, P.M. VanRaden, T.J. Lawlor. 2013. Methods to approximate reliabilities in Single-Step genomic evaluation. *Journal of Dairy Science*, 96:647-654.

A. Ricard, A. Legarra, S. Danvy. 2013. Computation of deregressed proofs for genomic selection when own phenotypes exist with an application in French show-jumping horses. *Journal of Animal Science*, 91:1076-1085

I. Misztal, Z.G. Vitezica, I. Aguilar, A. Legarra, A. Swan. 2013. Unknown-parent groups in single-step genomic evaluation. *Journal of Animal Breeding and Genetics,* 130:252-258.

L.A. García-Cortés, A. Legarra, C. Chevalet, M.A. Toro. 2013. Variance and covariance of actual relationships between relatives at one locus. *PLOS One* 8: e57003.

J. Casellas, C. Esquivelzeta, A. Legarra. 2013. Accounting for new additive mutations in genomic prediction models. *Journal of Dairy Science*, 96 (8), 5398-5402.

Z.G. Vitezica, L. Varona, A. Legarra. 2013. On the additive and dominant variance and covariance of individuals within the genomic selection scope. *Genetics*, 195:1223-1230.

2014

F. Assenza, J.M. Elsen, A. Legarra, C. Carré, G. Sallé, C. Robert-Granié, C. Moreno. 2014. Genetic parameters for growth and faecal worm egg count following Haemonchus contortus experimental infestations using pedigree and molecular information. *Genetics, Selection, Evolution*, 46:13.

L.A. Garcia-Cortes, A. Legarra, M.A. Toro. 2014. The coefficient of dominance is not (always) estimable with biallelic markers. *Journal of Animal Breeding and Genetics*, 137:91-104.

G. Baloche , A. Legarra , G. Sallé ,H. Larroque , J.-M. Astruc ,C. Robert-Granié, F. Barillet. 2014. Assessment of accuracy of genomic prediction for French Lacaune dairy sheep. *Journal of Dairy Science,* 97:1-10.

A. Legarra, G. Baloche, F.Barillet, J.M. Astruc, C. Soulas, X. Aguerre, F. Arrese, L.Mintegi, M. Lasarte, F. Maeztu|, I. Beltrán de Heredia, E. Ugarte. 2014. Within and across-breed genomic predictions and genomic relationships for Western Pyrenees breeds of dairy sheep Latxa, Manech and Basco-Bearnaise. *Journal of Dairy Science*, 3200-3212.

I. Misztal, A. Legarra, I. Aguilar. 2014. Using recursion to compute the inverse of the genomic relationship matrix. *Journal of Dairy Science*, 97: 3943-3952.

H. Wang, I. Misztal, I. Aguilar, A. Legarra, R.L. Fernando, Z.G. Vitezica, R. Okimoto, T. Wing, R. Hawken, 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 in Genetics* 5:134.

J. Ertl, A. Legarra, Z.G. Vitezica, L. Varona, C. Edel, R. Emmerling, K.U. Götz., 2014 Genomic analysis of dominance effects in milk production and conformation traits of Fleckvieh cattle. *Genetics Selection Evolution*, 46:40

H. Wang, I. Misztal, A. Legarra. 2014. Differences and fit to theoretical expectations between realized (genomic-based) and expected (pedigree-based) relationships in a chicken population. *Journal of Animal Breeding and Genetics*, 131:445-451.

A, Legarra, O.F. Christensen, I. Aguilar, I. MisztaL. 2014. Single Step, A general approach for genomic selection. *Livestock Science*, 166: 54-65.

2015

A. Legarra, P. Croiseau, M.P. Sanchez, S. Teyssèdre, G. Sallé, S. Allais, S. Fritz, C.R. Moreno, A. Ricard, J.M. Elsen. 2015. A comparison of methods for whole-genome QTL fine mapping using dense markers in four livestock species. *Genetics Selection Evolution*, 47:6

N.S. Forneris, 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

D.A.L. Lourenco, 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. *Journal of Animal Science*. 2015;93(6):2653-62.

B.O. Fragomeni, 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 best linear unbiased predictor (BLUP) with a large number of genotypes. *Journal of Dairy Science*. 2015;98(6):4090-4.

A. Legarra, O.F. Christensen, Z.G. Vitezica, I. Aguilar, I. Misztal. 2015. Ancestral relationships using metafounders: finite ancestral populations and across population relationships. 2015. *Genetics*, 200, 455–468

M. Perez-Enciso, J.C. Rincón and A. Legarra. 2015. Sequence- vs. chip-assisted genomic selection: Accurate biological information is advised. *Genetics Selection Evolution* 47(1):43.

T. Xiang, P. Ma, T. Ostersen, A. Legarra, O.F. Christensen. 2015. Imputation of genotypes in Danish purebred and two-way crossbred pigs using low density panels. *Genetics Selection Evolution* 47:54

D.A.L. Lourenco, B.O. Fragomeni, S. Tsuruta, I. Aguilar, B. Zumbach, R.J. Hawken, A. Legarra and I. Misztal. Accuracy of estimated breeding values for males and females with genomic information on males, females, or both: a broiler chicken example. *Genetics Selection Evolution* 47(1):1-9.

Hans Cheng, Ph.D.; Sudeep Perumbakkam, Ph.D.; Alexis Black Pyrkosz, Ph.D.; John R. Dunn, DVM, Ph.D.; Andres Leggara, Ph.D.; William M. Muir. Fine mapping of QTL and genomic prediction using allele-specific expression SNPs demonstrates that the complex trait of genetic resistance to Marek's disease is predominantly determined by transcriptional regulation. *BMC Genomics, accepted*

A. Legarra, Z.G. Vitezica. Genetic evaluation with major genes and polygenic inheritance when some animals are not genotyped using Gene Content Multiple Trait BLUP. *Genetics Selection Evolution* 47:98

O. F. Christensen, A. Legarra, G. Su, M. S. Lund. 2015. Genetic evaluation for three-way crossbreeding *Genetics Selection Evolution,* 47:89

2016

Pocrnic, I., Lourenco, D.A., Masuda, Y., Legarra, A. and Misztal, I., 2016. The Dimensionality of Genomic Information and its Effect on Genomic Prediction. Genetics, *preview*.

A. Legarra. 2016. Comparing estimates of genetic variance across different models of relationships. *Theoretical Population Biology 107:26-30.*

Z.G. Vitezica, L. Varona, J.M. Elsen,I. Misztal, W. Herring, A. Legarra. Genomic BLUP including additive and dominant variation in purebreds and F1 crossbreds, with an application in pigs. *Genetics Selection Evolution* 48:6

Y Masuda, I Misztal, S Tsuruta, A Legarra, I Aguilar, DAL Lourenco, BO Fragomeni, TJ Lawlor. Implementation of genomic recursions in single-step genomic best linear unbiased predictor for US Holsteins with a large number of genotyped animals. Journal of Dairy Science, 99:1968-1974

Marchal, A., Legarra, A., Tisné, S., Carasco-Lacombe, C., Manez, A., Suryana, E., Omoré, A., Nouy, B., Durand-Gasselin, T., Sánchez, L. and Bouvet, J.M., 2016. Multivariate genomic model improves analysis of oil palm (Elaeis guineensis Jacq.) progeny tests. Molecular Breeding, 36:2.

M. Perez-Enciso, A. Legarra. A combined coalescence gene-dropping tool for evaluating genomic selection in complex scenarios (ms2gs). *Journal of Animal Breeding and Genetics, early view.*

T. Xiang, B. Nielsen, G. Su, A. Legarra and O. F. Christensen. Application of single-step genomic evaluation for crossbred performance in pigs. *Journal of Animal Science*, early view

L. Tusell, H. Gilbert, J. Riquet, M.J. Mercat, A. Legarra, C. Larzul. 2016. Pedigree and genomic evaluation of pigs using a terminal-cross model. *Genetics Selection Evolution* 48:32

Forneris, N.S. Steibel, J.P. Legarra, A, Vitezica, Z.G., Bates, R.O., Ernst, C.W., Basso, A.L., Cantet, R.J.C., A comparison of methods to estimate relationships using pedigree and markers in populations with many ungenotyped animals. Accepted in *Journal of Animal Breeding and Genetics*

Papers in refereed journals (in French)

Robert-Granié C., Legarra A., Ducrocq V., 2011. Principes de base de la sélection génomique. In : Numéro spécial, Amélioration génétique. Mulsant P., Bodin L., Coudurier B., Deretz S., Le Roy P., Quillet E., Perez J.M. (Eds). INRA Prod.Anim., 24, 331-340. (Invited)

Papers in refereed journals (in Spanish)

A. Legarra, E. Ugarte. 2001. Resultados de la aplicación de metodologías de extensión de lactaciones a 120 días en ovejas de la raza Latxa. *ITEA* 97A:104-116.

A. Legarra, E. Ugarte, F. Arrese. 2003. Análisis del progreso genético en el esquema de mejora de la raza Latxa. *ITEA* 99A: 192-202.

Papers presented at Meetings, with reviewing

A. Favier, J.M. Elsen, S. de Givry, A. Legarra. 2010. Optimal haplotype reconstruction in half-sib families, *ICLP-10 workshop on Constraint Based Methods for Bioinformatics*, Edinburgh, UK.

A. Favier, S. de Givry, A. Legarra, T. Schiex. 2011. Pairwise decomposition for combinatorial optimization in graphical models, *Proc. 22th International Joint Conference on Artificial Intelligence (IJCAI'11)*, Barcelona, Spain.

Papers presented at Meetings, with reviewing (in French)

A. Favier, S. de Givry, A. Legarra, T. Schiex. 2011. Décomposition par paire pour l'optimisation combinatoire dans les modèles graphiques. *7èmes Journées Francophone de Programmation par Contraintes*, Lyon, France.

1.1.2. In non-peer-reviewed journals

1.1.3. Theses, doctorates

2002. Ph.D. at Universidad Publica de Navarra, Pamplona, Spain. Title: *"Optimization of the breeding program of the Latxa breed: Analysis of the model of genetic evaluation and introduction of new traits in the breeding objective"*. Supervisor: Dr. Eva Ugarte, NEIKER, Vitoria, Spain.

2012. HDR at Institut National Polytechnique de Toulouse, France. Title: *"De la Latxa à la Manech : au travers les méthodes et applications en amélioration et évaluation génétique"*.

1.1.4. Material presented in conferences and symposia (please specify: extract, synopsis, full text)

Papers presented at Meetings

1999

A. Legarra, F.J. Mendizábal. 2009. Sheep milk quality in the Basque Country Community and Navarra from 1996 to 1998. *Seminar on Production systems and product quality*, Murcia, Spain, September 23-25. FAO-CIHEAM Network on sheeps and goats. *Options Méditerranéennes*, serie A, 46, 145-149.

2001

E. Ugarte, A. Legarra, I. Beltrán de Heredia, J. Arranz. 2001. Udder morphology: a new trait to introduce in the Latxa breeding programme. *52nd Annual Meeting of the EAAP*. Budapest, August 26-29. Abstract.

2002

E. Ugarte, A. Legarra. 2002. Scientific background of the selection program in the Latxa breed. *Proc. of the meeting of the FAO-CIHEAM of Genetic resources of sheep and goats.* Sassari, Italy, May 9-11. Options Méditerranéennes, serie A, 55, 91-98.

E. Ugarte, A. Legarra. 2002. Organisational changes in the Latxa breeding programme to introduce selection for milk quality. *Proc. of the meeting of the FAO-CIHEAM of Genetic resources of sheep and goats*. Sassari, Italy, May 9-11. Options Méditerranéennes, serie A, 55, 141-146.

A. Legarra, P. López-Romero, E. Ugarte. 2002. Bayesian model selection: an application to genetic evaluation of the Latxa dairy sheep. *Proc 7th World Congr. Genet. Appl. Livest. Prod.*, Montpellier, France. CD-ROM communication nº 20-07. Full-text.

2003

A. Legarra, T. Strabel, J.K. Bertrand, I. Misztal. 2003. Setting up the Gelbvieh multiple breed evaluation. ADSA and ASAS joint meeting, Phoenix, EEUU, 2003. *Journal of Dairy Science*, Vol. 86, Suppl.1, p.198. Abstract.

A. Legarra, I. Misztal, J. Jamrozik J. 2003. Plotting covariance functions from random regression models. ADSA and ASAS joint meeting, Phoenix, EEUU, 2003. *Journal of Dairy Science*, Vol. 86, Suppl.1, p.113. Abstract.

2004

K.R. Robbins, I. Misztal, J. K. Bertrand, A. Legarra, S. Tsuruta. 2004. A practical longitudinal model for evaluating growth in Gelbvieh cattle. ADSA and ASAS joint meeting, St Louis, USA, 2004. *J. Anim Sci.*, Vol. 82, Suppl.I, p.243. Abstract.

A. Legarra, E. Ugarte, 2004. A rationale to introduce more traits in the Latxa breeding program. *55th annual meeting of the EAAP.* Book of abstracts, p. 237

2006

A. Legarra, C. Robert-Granié. 2006. Computation of recursive models and an example on fertility traits. *8th World Congress on Genetics applied to Livestock Production*, Belo Horizonte, Brazil, CD-ROM communication 24-07. Full-text.

Z.G. Vitezica, A. Legarra. 2006. Accuracy of genotype estimation using loop breakers. *8th World Congress on Genetics applied to Livestock Production*, Belo Horizonte, Brazil. CD-ROM communication 20-13. Full-text.

E. López de Maturana, A. Legarra, E. Ugarte. 2006. Effects of calving ease on fertility in the basque Holstein population using recursive methodology. *8th World Congress on Genetics applied to Livestock Production*, Belo Horizonte, Brazil. CD-ROM communication 01-23. Full-text.

2007

A. Legarra, C. Robert-Granié, E. Manfredi, J.M. Elsen. 2007. Does genomic selection work in a mice population? Pages 66-74 in XI QTLMAS 2007. Papers and abstracts from the *Workshop on QTL and Marker Assisted Selection (QTLMAS).* March 22-23, Toulouse, France. http://germinal.toulouse.inra.fr/qtlmas/

A. Legarra, E. Manfredi, C. Robert-Granié, J.M. Elsen. 2007. Validation of genomic selection in an outbred mouse. *58th annual meeting of the EAAP*, Dublin, 2007. Book of abstracts, page 162.

2008

H. Garreau, S.J. Eady, J. Hurtaud, A. Legarra. 2008. Genetic parameters of production traits and resistance to digestive disorders in a commercial rabbit population. *Proc. 9th World Rabbit Congress*, Verona, Italy, June 10-13. Full-text.

2009

A. Legarra, R. Fernando, 2009. Joint association and linkage QTL mapping on half-sib families by regression. *13th QTLMAS workshop*, Wageningen, the Netherlands. Abstract.

A. Legarra, I. Aguilar, I. Misztal. 2009. Whole-population relationship matrix including pedigree and markers for genomic selection. *Symposium SGLPGE,* Madison, Wisconsin. Poster.

A. Legarra, I. Aguilar, I. Misztal. 2009. Whole-population relationship matrix including pedigree and markers for genomic selection. *60th Annual Meeting of the EAAP*, Barcelona, Spain. Poster.

I. Misztal, A. Legarra, I. Aguilar. 2009. Computing procedures for genetic evaluation including phenotypic, full pedigree and genomic information. *60th Annual Meeting of the EAAP,* Barcelona, Spain. Oral communication.

J.M. Elsen, O. Filangi, H. Gilbert, A. Legarra, P. Le Roy, C. Moreno-Romieu. 2009. QTLMAP a software for the detection of QTL in full and half sib families. *60th Annual Meeting of the EAAP*, Barcelone, Spain. Session 53, Theatre 13, p.603.

A. Ricard, A. Legarra. 2009. Ranking in competition: an efficient tool to measure aptitude. *60th Annual Meeting of the EAAP*, Barcelone, Spain. Session 19, Theatre 7, p. 216.

I. Misztal, I. Aguilar, D. Johnson, A. Legarra, S. Tsuruta, T.J. Lawlor. 2009. A unified approach to utilize phenotypic, full pedigree, and genomic information for a genetic evaluation of Holstein final score. *Interbull Bulletin* 40. Full-text.

C. Marie-Etancelin, X Fernandez, S. Davail, J.M. André, D. Bastianelli, E. Baéza, M.D. Bernadet, G. Guy, A. Legarra, J.M. Brun. 2009. Genetic parameters of mule ducks' meat and fatty liver performances simultaneously estimated in both parental lines. *IX European Symposium on the Quality of Poultry Meat*, Turku, Finland. Full-text.

I. Aguilar, I. Misztal, A. Legarra. 2009. Computing procedures for genetic evaluation including phenotypic, full pedigree and genomic information. *ADSA and ASAS joint meeting*, Montreal, Canada, 2009. Abstract.

I. Misztal, A. Legarra, I. Aguilar. 2009. Genetic evaluation including phenotypic, full pedigree and genomic information. *ADSA and ASAS joint meeting*, Montreal, Canada. Abstract.

2010

C. Colombani, A. Legarra, P. Croiseau, F. Guillaume, S. Fritz, V. Ducrocq, C. Robert-Granie. 2010. Application of PLS and Sparse PLS regression in Genomic Selection. *9th World Congress on Genetics applied to Livestock Production*, Leipzig, Germany. CD-ROM Communication 0439. Full-text.

L. Tusell Palomero, A. Legarra Albizu, M. García-Tomás, O. Rafel Guarro, J. Ramón Riba, M. Piles Rovira. 2010. Different ways to model the biological relationship between fertility and pH of the semen in rabbits. *9th World Congress on Genetics applied to Livestock Production*, Leipzig, Germany. CD-ROM Communication 0569. Full-text.

I. Misztal, I. Aguilar, A. Legarra, D. Johnson, S. Tsuruta, T. Lawlor. 2010. A unified approach to utilize phenotypic, full pedigree, and genomic information for genetic evaluation. *9th World Congress on Genetics applied to Livestock Production*, Leipzig, Germany. CD-ROM Comm. 0050. Full-text.

A. Legarra, C. Robert-Granié, P. Croiseau, F. Guillaume, S. Fritz, V. Ducrocq. 2010. Aptitude of Bayesian Lasso for genomic selection. *9th World Congress on Genetics applied to Livestock Production*, Leipzig, Germany. CD-ROM Comm. 0118. Full-text.

Z.G. Vitezica, I. Aguilar, A. Legarra. 2010. One-step vs. multi-step methods for genomic prediction in presence of selection. *9th World Congress on Genetics applied to Livestock Production*, Leipzig, Germany. CD-ROM Comm. 0131. Full-text.

A. Favier, J.-M. Elsen, A. Legarra, S. de Givry. 2010. Exact haplotype reconstruction in half-sib families with dense marker maps. *9th World Congress on Genetics applied to Livestock Production*, Leipzig, Germany. CD-ROM Comm. 0260. Full-text.

P. Croiseau, C. Colombani, A. Legarra, F. Guillaume, S. Fritz, A. Baur, R. Dassonneville, C. Patry, C. Robert-Granié, V. Ducrocq. 2010. Improving genomic evaluation strategies in dairy cattle through SNP pre-selection. *9th World Congress on Genetics applied to Livestock Production*, Leipzig, Germany. CD-ROM Comm. 0360. Full-text.

G. Sallé, P. Jacquiet, L. Gruner, J. Cortet, C. Sauvé, F. Prevot, D. François, F. Bouvier, C. Pery, J. Bouix, A. Legarra, R. Rupp, C. Moreno. 2010. Preliminary results of a QTL detection study for resistance to Haemonchus contortus in sheep using the ovineSNP50 Beadchip. *9th World Congress on Genetics applied to Livestock Production*, Leipzig, Germany. CD-ROM Comm. 0463. Full-text.

G. Salle, P. Jacquiet, L. Gruner, J. Cortet, C. Sauve, F. Prevot, F. Bouvier, D. Francois, C. Pery, J. Bouix, A. Legarra, R. Rupp, C.R. Moreno. 2010. Preliminary results of a QTL detection study for resistance to Haemonchus contortus in sheep using the ovineSNP50 Beadchip. *2010 Animal Genomics for Animal Health International Symposium*. 31 May - 2 June 2010 - "Maison de la Chimie", Paris (France). Abstract.

S. Tsuruta, I. Aguilar, I. Misztal, A. Legarra, T. Lawlor. 2010. Multiple trait genetic evaluation of linear type traits using genomic and phenotypic data in US Holsteins. *9th World Congress on Genetics applied to Livestock Production*, Leipzig, Germany. CD-ROM Comm. 0489_PP2-150. Full-text.

I. Aguilar, I. Misztal, A. Legarra, S. Tsuruta. 2010. Efficient computations of genomic relationship matrix and other matrices used in the single-step evaluation. *9th World Congress on Genetics applied to Livestock Production*, Leipzig, Germany. CD-ROM Comm. 0768. Full-text.

S. Tsuruta, I. Aguilar, I. Misztal, A. Legarra, T.J. Lawlor. 2010. Multiple trait genetic evaluation of linear type traits using genomic and phenotypic information in US Holsteins. *ASAS meeting*, July 11-15. Colorado, USA. Abstract.

I. Misztal, I. Aguilar, A. Legarra, T.J. Lawlor. 2010. Choice of parameters for single-step genomic evaluation for type. *ASAS meeting*, July 11-15. Colorado, USA. Abstract.

C. Moreno, J.M. Elsen, A. Legarra, R. Rupp, J. Bouix, F. Barillet, I. Palhière, H. Larroque, D. Allain, D. François, C. Robert, G. Tosser-Klopp, L. Bodin, P. Mulsant. 2010. Searching for genes of interest in sheep. Book of abstracts *EAAP 2010*, p. 116. Heraklion, Greece.

I. Misztal, I. Aguilar, A. Legarra, T.J. Lawlor. 2010. Choice of parameters for single-step genomic evaluation for type. Book of abstracts, *EAAP 2010*, p. 357. Heraklion, Greece.

2011

I. Misztal, C.Y. Chen, I. Aguilar, Z.G. Vitezica, A. Legarra, W.M. Muir. 2011. Effect of different genomic relationship matrices on accuracy and scale. Book of abstracts joint ADSA-ASAS meeting, *J. Anim. Sci.* Vol. 89, E-Suppl. 1/*J. Dairy Sci.* Vol. 94, E-Suppl. 1, p.163. Abstract.

G. Sallé, C.R. Moreno, L. Gruner, J. Cortet, C. Sauvé, F. Prévot, F. Bouvier, D. François, C. Pery, J. Bouix, A. Legarra, R. Rupp, P. Jacquiet. 2011. Genomic Mapping of Resistance to Haemonchus contortus Using the High-density OvineSNP50 Beadchip. *23rd International*

Conference of the World Association for the Advancement of Veterinary Parasitology, August 21-25. Buenos Aires, Argentina. Abstract.

Legarra, A., Misztal, I. and Aguilar, I. 2011. The single step: genomic evaluation for all. Book of abstracts of the EAAP 2011, p. 1. **Invited talk.**

I. Misztal, S. Tsuruta, I. Aguilar, A. Legarra, T.J. Lawlor. 2011. Approximation of genomic accuracies in single-step genomic evaluation. *Interbull Meeting*, Stavanger, Norway. Full-text.

P. Croiseau, C. Hozé, S. Fritz, F. Guillaume, C. Colombani, A. Legarra, A. Baur, C. Robert-Granié, D. Boichard, V. Ducrocq. 2011. Description of the French genomic evaluation approach. Book of abstracts of the *EAAP 2011*, p. 3.

C. Colombani, A. Legarra, P. Croiseau, S. Fritz, F. Guillaume, V. Ducrocq, C. Robert-Granié, C. 2011. Bayes Cpi versus GBLUP, PLS regression, sparse PLS and elastic net methods for genomic selection in french dairy cattle. Book of abstracts of the *EAAP 2011*, p. 7.

J. Casellas, C. Esquivelzeta, A. Legarra. 2011. Genomic BLUP with additive mutational effects. Book of abstracts of the *EAAP 2011*, p. 8.

Z.G. Vitezica, A. Legarra. 2011. How to remove bias in genomic predictions? Book of abstracts of the *EAAP 2011*, p. 31.

M.A. Toro, L.A. Garcia-Cortes, A. Legarra. 2011. Rationale for estimating genealogical coancestry from molecular markers. Book of abstracts of the *EAAP 2011*, p. 175.

I. Beltran De Heredia, E. Ugarte, X. Aguerre, C. Soulas, F. Arrese, L. Mintegi, J.M. Astruc, F. Maeztu, M. Lasarte, A. Legarra, F. Barillet. 2011. Genomia: across-Pyrenees genomic selection for dairy sheep Book of abstracts of the *EAAP 2011*, p. 181.

G. Baloche, H. Larroque, J.M. Astruc, J.M. Babilliot, M.Y. Boscher, P. Boulenc, C. Chantry-Darmon, C. De Boissieu, G. Frégeat, B. Giral-Viala, P. Guibert, G. Lagriffoul, C. Moreno, P. Panis, C. Robert-Granié, G. Salle, A. Legarra, F. Barillet. 2011. Work in progress on genomic evaluation using GBLUP in French Lacaune dairy sheep breed. Book of abstracts of the *EAAP 2011*, p.345.

C. Robert-Granie, S. Duchemin, H. Larroque, G. Baloche, F. Barillet, C. Moreno, A. Legarra, E. Manfredi. 2011 A comparison of various methods for the computation of genomic breeding values in French Lacaune dairy sheep breed. Book of abstracts of the *EAAP 2011*, p. 346.

2012

I. Misztal, H. Wang, I. Aguilar, A. Legarra, W. Muir. 2012. Tools for Genomic Analyses Using Single-Step Methodology. *Plant and Animal Genome* (PAG), San Diego, CA, USA. Abstract.

S. Karoui, M.J. Carabaño, C. Diaz, A. Legarra. 2012. Genomic evaluation combining different French dairy cattle breeds. Book of abstracts of the *EAAP 2012*, p. 128.

G. Baloche, A. Legarra, G. Lagriffoul, H. Larroque, C. Moreno, C. Robert-Granié, B. Giral, P. Panis, J.M. Astruc, F. Barillet. 2012. Comparison of genomic evaluation in Lacaune dairy sheep using single or multiple step GBLUP. Book of abstracts of the *EAAP 2012*, p. 132

I. Misztal, I. Aguilar, S. Tsuruta, A. Legarra. Adaptation of BLUPF90 package for genomic computations. Book of abstracts of the *EAAP 2012*, p. 135.

I. Misztal, H. Wang, I. Aguilar, A. Legarra, W. Muir. Genome-wide association mapping using single-step GBLUP. Book of abstracts of the *EAAP 2012*, p. 304.

A. Ricard, S. Danvy, A. Legarra. 2012. First results on genomic selection in French show-jumping horses. Book of abstracts of the *EAAP 2012*, p. 324.

O. Filangi, N. Bacciu, O. Demeure, A. Legarra, J.M. Elsen, P. Le Roy. 2012. Finding gene to genome epistatic effects. Book of abstracts of the *EAAP 2012*, p. 355.

A. Legarra. 2012. A real data based comparison of methods for whole-genome QTL fine mapping in four livestock species. *25th International Conference "Genetic Days".* Wrocław, Poland, 18 - 20 September. **Invited talk.**

N. Bohossian, M. Saad, A. Legarra, M. Martinez. 2012. Single- and Multi-Marker Mixed Models for Polygenic Score Analysis in Family-Based Data. *Genetics Analysis Workshop.* October 13-17. Stevenson, Washington, USA. Full-text.

N. Bohossian, M. Saad, A. Legarra, M. Martinez. 2012. A Multi-Marker Genome-Wide Association Study: The Story of Bayes Cπ. *21 Annual International Genetic Epidemiological Society.* October 18-20, 2012. Stevenson, Washington, USA. BMC Proceedings 8 (Suppl 1), S63. Full-text.

N. Bohossian, M. Saad, A. Legarra , M. Martinez, M. 2012. Exploring models for simultaneous analysis of all SNPs in genome-wide association data of human complex phenotypes. Annals of Human Genetics, 76 (5). Presented at European Mathematical Genetics Meeting, Göttingen, DEU (2012-04-12 - 2012-04-13). Hoboken, USA : Wiley-Blackwell.

A. Ricard, S. danvy, A. Legarra. 2012. First results on genomic selection in French show-jumping horses. Presented at 33. Conference of the International Society of Animal Genetics ISAG, Cairns, AUS (2012-07-15 - 2012-07-20).

2013

H. Wang, I. Misztal, I. Aguilar, A. Legarra, W. Muir. 2013. Genome-wide association mapping using single-step GBLUP. *Plant and Animal Genome*. San Diego, CA, USA. Abstract.

H. Wang, I. Misztal, I. Aguilar, A. Legarra, W. Muir, R. Fernando, R. Hawken. 2013. Genome-wide association mapping including phenotypes from relatives without genotypes for three traits in broiler chickens. *ADSA-ASAS joint annual meeting.* July 8-12. Indianapolis, Indiana, USA. Journal of Dairy Science, Volume 96, E-Supplement 1, p. 191. Abstract.

I. Misztal, Z. Vitezica, A. Legarra, I. Aguilar, and A. Swan. 2013. Unknown-parent groups and incomplete pedigrees in single-step genomic evaluation. *ADSA-ASAS joint annual meeting.* July 8-12. Indianapolis, Indiana, USA. Journal of Dairy Science, Volume 96, E-Supplement 1, p. 621. Abstract.

I Aguilar, A Legarra, S Tsuruta, I Misztal. 2013. Genetic evaluation using unsymmetric single step genomic methodology with large number of genotypes. *Interbull meeting.* Nantes, France. Interbull Bulletin 47. Full-text.

J. Ertl, A. Legarra, Z.G. Vitezica, L. Varona, C. Edel, E. Reiner, K.U. Götz. 2013. Genomic analysis of dominance effects in milk production and conformation traits of Fleckvieh cattle. *Interbull meeting*, Nantes, France. Interbull Bulletin 47. Full-text.

L.A. Garcia-Cortes, A. Legarra, C. Chevalet, M.A. Toro. 2013. Variance and covariances of actual relationships at one locus. Book of abstracts *EAAP, 2013*. Nantes, France.

F. Assenza, J.M. Elsen, A. Legarra, C. Carre, G. Salle, C. Robert-Granie, C. Moreno. 2013. Genetic parameters of growth and faecal egg count obtained by using pedigree or SNP information. Book of abstracts *EAAP 2013*. Nantes, France.

Z.G. Vitezica, L. Varona, A. Legarra. 2013. Interpretation of dominant and additive variance from genomic models. Book of abstracts *EAAP 2013*. Nantes, France.

I. Misztal, Z.G. Vitezica, A. Legarra, I. Aguilar, A. Swan. 2013. Unknown parent groups and incomplete pedigrees in single-step genomic evaluation. Book of abstracts *EAAP 2013*. Nantes, France.

G. Sallé, C.R. Moreno, J. Ruesche, M. Aletru, J.L. Weisbecker, F. Bouvier, F. Prévot, J.P. Bergeaud, C. Trumel, C. Grisez, D. François, A. Legarra, E. Liénard and P. Jacquiet. 2013. Functional investigation of a QTL affecting resistance to Haemonchus contortus in sheep. Book of abstracts *EAAP 2013*. Nantes, France.

2014

A. Legarra. Applications of (genomic) relationships to Livestock Genetics, International Biometric Conference, Florence, Italy, July 6-11 2014. **Invited talk.**

A. Legarra. A relationship matrix combining pedigree and markers when some individuals are not genotyped. Workshop: Statistical and computational methods for relatedness and relationship inference from genetic marker data. Sep 22, 2014 - Sep 26, 2014. ICMS, Edinburgh. **Invited talk.**

A. Legarra, I. Aguilar, I. Misztal. Single Step Methods with a View towards Poultry Breeding, World Congress on Genetics Applied to Livestock Production, Vancouver, Canada, August 21 2014. **Invited talk.**

H. Larroque, F. Barillet, G. Baloche, J.M. Astruc, D. Buisson, F. Shumbusho, V. Clément, G. Lagriffoul, I. Toward. 2014. Genomic Breeding Programs in French Dairy Sheep and Goats. *10th World Congress on Genetics Applied to Livestock Production*, Vancouver, Canada, August 17-21. Full-text. **Invited talk.**

G. Baloche, J. M. Astruc, P. Boulenc, B. Giral-Viala, P. Guibert, P. Panis, A. Legarra, F. Barillet. 2014. Genomic Selection Experiment in Lacaune Dairy Sheep: Progeny Test Results of Rams Initially Selected either on Parent Average or on Genomic Prediction. *10th World Congress on Genetics Applied to Livestock Production*, Vancouver, Canada, August 17-21. Full-text.

A. Legarra, O.F. Christensen, Z.G. Vitezica, I. Aguilar, and I. Misztal. 2014. Across-Breeds Ancestral Relationships and Metafounders for Genomic Evaluation. *10th World Congress on Genetics Applied to Livestock Production*, Vancouver, Canada, August 17-21. Full-text.

T. Xiang, O.F. Christensen, A. Legarra, and T. Ostersen. Imputation of Genotypes in Danish Two-Way Crossbred Pigs using Low Density Panels. *10th World Congress on Genetics Applied to Livestock Production*, Vancouver, Canada, August 17-21. Full-text.

N.S. Forneris, A. Legarra, Z.G. Vitezica, S. Tsuruta, I. Aguilar, R.J.C. Cantet, I. Misztal. 2014. Quality Control of Genotypes using Heritability Estimates of Gene Content. *10th World Congress on Genetics Applied to Livestock Production*, Vancouver, Canada, August 17-21. Full-text.

L. Varona, Z.G. Vitezica, S. Munilla, A. Legarra. 2014. A general approach for calculation of genomic relationship matrices with epistatic effects. *10th World Congress on Genetics Applied to Livestock Production*, Vancouver, Canada, August 17-21. Full-text.

I. Aguilar, I. Misztal, S. Tsuruta, A. Legarra, H. Wang. 2014. PREGSF90 – POSTGSF90: Computational Tools for the Implementation of Single-Step Genomic Selection and Genome-Wide Association with Ungenotyped Individuals in BLUPF90 Programs. *10th World Congress on Genetics Applied to Livestock Production*, Vancouver, Canada, August 17-21. Full-text.

X. Zhang, D.A.L. Lourenco, I. Misztal, I. Aguilar, A. Legarra. 2014. Weighted Single-Step Genomic BLUP: An Iterative Approach for Accurate Calculation of GEBV and GWAS. *10th World Congress on Genetics Applied to Livestock Production*, Vancouver, Canada, August 17-21. Full-text.

I. Misztal, H. Wang, I. Aguilar, A. Legarra, S. Tsuruta, D.A.L. Lourenco, B. O. Fragomeni, X. Zhang, W. M. Muir, H. H. Cheng, R. Okimoto, T. Wing, R. R. Hawken, B. Zumbach, R. Fernando. GWAS using ssGBLUP. World Congress on Genetics Applied to Livestock Production, Vancouver, Canada, August 21 2014. **Invited talk.**

2015

Y. Masuda, I. Misztal, S. Tsuruta, D.A.L. Lourenco, B.O. Fragomeni, A. Legarra, I. Aguilar and T. J. Lawlor. Single-Step Genomic Evaluations with 570K Genotyped Animals in US Holsteins. Interbull bulletin NO. 49. Orlando, Florida, July 09 - 12, 2015

I. Misztal, B.O. Fragomeni, D.A.L. Lourenco, S. Tsuruta, Y. Masuda, I. Aguilar, A. Legarra, and T. J. Lawlor. Efficient inversion of genomic relationship matrix by the algorithm for proven and young (APY). Interbull bulletin NO. 49. Orlando, Florida, July 09 - 12, 2015.

D.A.L. Lourenco, B.O. Fragomeni, S. Tsuruta, I. Aguilar, B. Zumbach, R.J. Hawken, A. Legarra, and I. Misztal. Accuracy of estimated breeding values for males and females with genomic information on males, females, or both: A broiler chicken example. 2015 ADSA-ASAS Joint Annual Meeting, July 12-16, Orlando, Florida. Abstract M67.

B.D. Fragomeni, D.A.L. Lourenco, S. Tsuruta, Y. Masuda, I. Aguilar, A. Legarra, T.J. Lawlor, and I. Misztal. Use of genomic recursions in single-step genomic BLUP with a large number of genotypes. . 2015 ADSA-ASAS Joint Annual Meeting, July 12-16, Orlando, Florida. Abstract 534.

Y. Masuda, I. Misztal, S. Tsuruta, D.A.L. Lourenco, Breno Fragomeni, A. Legarra, I. Aguilar, and T.J. Lawlor. Genomic predictions with approximated G-inverse for a large number of genotyped animals. . 2015 ADSA-ASAS Joint Annual Meeting, July 12-16, Orlando, Florida. Abstract 535

D.A.L. Lourenco, 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. Large-scale single-step genomic BLUP evaluation for American Angus. 2015 ADSA-ASAS Joint Annual Meeting, July 12-16, Orlando, Florida. Abstract 646.

D.A.L. Lourenco, B.O. Fragomeni, S. Tsuruta, I. Aguilar, B. Zumbach, R. Hawken, A. Legarra and I. Misztal. Realized accuracies for males and females with genomic information on males, females, or both. 66th Annual Meeting of EAAP, Warsaw, 31 August – 4 september 2015. Book of abstracts 247

O.F. Christensen, A. Legarra, M.S. Lund and G. Su. Genetic evaluation for three way crossbreeding. 66th Annual Meeting of EAAP, Warsaw, 31 August – 4 september 2015. Book of abstracts 247

L. Tusell, H. Gilbert, J. Riquet, M.J. Mercat, A. Legarra and C. Larzul.Pedigree and genomic evaluation of pigs using a terminal cross model. 66th Annual Meeting of EAAP, Warsaw, 31 August – 4 september 2015. Book of abstracts 248

T. Xiang, B. Nielsen, G. Su, A. Legarra and O.F. Christensen. Application of single-step genomic evaluation for crossbred performance in pig. 66th Annual Meeting of EAAP, Warsaw, 31 August – 4 september 2015. Book of abstracts 456.

Z.G. Vitezica, J.M. Elsen, I. Misztal, W. Herring, L. Varona and A. Legarra. Genetic parameter estimation in purebred and crossbred swine from genomic models. 66th Annual Meeting of EAAP, Warsaw, 31 August – 4 september 2015. Book of abstracts 460.

I. Misztal, B. Fragomeni, D.A.L. Lourenco, Y. Masuda, I. Aguilar, A. Legarra and T.J. Lawlor. Use of genomic recursions in single-step genomic BLUP with a large number of genotypes. 66th Annual Meeting of EAAP, Warsaw, 31 August – 4 september 2015. Book of abstracts 501

Y. Masuda, I. Misztal, S. Tsuruta, D.A.L. Lourenco, B. Fragomeni, A. Legarra, I. Aguilar and T.J. Lawlor. Genomic predictions with approximated G-inverse from large-scale genotyping data. 66th Annual Meeting of EAAP, Warsaw, 31 August – 4 september 2015. Book of abstracts 502

D.A.L. Lourenco, S. Tsuruta, B.O. Fragomeni, Y. Masuda, I. Aguilar, A. Legarra, J.K. Bertrand, D.W. Moser and I. Misztal. Large-scale single-step genomic BLUP evaluation for American Angus. 66th Annual Meeting of EAAP, Warsaw, 31 August – 4 september 2015. Book of abstracts 502

A. Legarra and Z.G. Vitezica. Prediction with major genes partially genotyped using gene content multiple trait BLUP. 66th Annual Meeting of EAAP, Warsaw, 31 August – 4 september 2015. Book of abstracts 505

2017

AAABG Invited talk

Papers presented at Meetings (in Spanish)

1999

A. Legarra , J. Arranz, I. Beltrán de Heredia, E. Ugarte. 1999. Sistema de calificación de la morfología mamaria en ovejas de Raza Latxa: resultados preliminares. VIII Jornadas de Producción Animal, Zaragoza, Spain, May 11-13. *ITEA* Vol. Extra 20, 345-347.

2000

A. Legarra, E. Ugarte, E. Ruiz de Zárate. 2000. Adecuación de la estructura de datos del caballo de carne en Alava. X Reunión de mejora genética animal, Caldes de Montbui, Barcelona, Spain, June 8-9. *ITEA* 96A:311-317.

2001

A. Legarra, E. Ugarte, I. Beltrán de Heredia, J. Arranz. 2001. Parámetros genéticos y respuestas a diferentes índices de selección de caracteres de morfología mamaria en la raza Latxa. IX Jornadas de Producción Animal, Zaragoza, Spain, April 25-27. *ITEA* Vol. Extra 22, 24-26.

J. Arranz, A. Legarra. 2001. Importancia de la metodología de la toma de muestra en la composición de la leche de oveja. IX Jornadas de Producción Animal, Zaragoza, Spain, April 25-27. *ITEA* Vol. Extra 22, 649-651.

2004

A. Legarra, E. Ugarte, I. Beltrán de Heredia. 2004. Análisis de asociación entre genotipos de PrP y producción de leche en la raza Latxa. XII Reunión nacional de mejora genética animal. Arucas, Las Palmas, Canarias. *ITEA*, 100A, 127-133

E. López de Maturana, A. Legarra, E. Ugarte. 2004. Estudio de la relación genética entre los caracteres facilidad de parto materna y fertilidad de la hembra en el ganado vacuno lechero de la CAPV. XII Reunión nacional de mejora genética animal. Arucas, Las Palmas, Canarias. *ITEA* 100A, 156-166

2005

M. Ramón, A. Legarra, M.D. Pérez-Guzmán, E. Ugarte. 2005. Análisis técnico-económico de ganaderías de raza Latxa y Manchega como paso previo al cálculo de pesos económicos. (Poster). XI Jornadas sobre Producción Animal, Zaragoza, Spain, May 11-12. *ITEA* Vol. Extra 26, 90-92.

E. López de Maturana, A. Legarra, E. Ugarte. 2005. Estudio integral del carácter facilidad de parto en ganado vacuno Frisón de la CAPV. XI Jornadas sobre Producción Animal, Zaragoza, Spain, May 11-12. *ITEA* Vol. Extra 26, 123-125.

M. Ramón, A. Legarra, M.D. Pérez-Guzmán, E. Ugarte. 2005. Obtención de pesos económicos para selección por rentabilidad. XI Jornadas sobre Producción Animal, Zaragoza, Spain, May 11-12. *ITEA* Vol. Extra 26, 129-131.

A. Legarra, M. Ramón, E. Ugarte, M.D. Pérez-Guzmán. 2005. Pesos económicos en ovino lechero en razas Latxa y Manchega. XI Jornadas sobre Producción Animal, Zaragoza, Spain, May 11-12. *ITEA* Vol. Extra 26, 132-134.

2010

A. Legarra, C. Robert-Granié, P. Croiseau, F. Guillaume, S. Fritz. 2010. Lasso Bayesiano Mejorado para selección genómica. *XV Reunión Nacional de Mejora Genética*, Vigo, Spain, June. Invited talk.

2011

M.A. Toro, L.A. García-Cortés, A. Legarra. 2011. Estimación del parentesco molecular mediante marcadores moleculares. *XXXVIII Congreso de la Sociedad Española de Genética*, Murcia, Spain. Abstract.

2013

L.A. García-Cortés, A. Legarra, C. Chevalet, M.A. Toro. 2013. Variance and covariance of kinship at one locus. In *XV Jornadas sobre Producción Animal*, Zaragoza, Spain. May 14-15. pp. 508-510.

A. Legarra, G. Baloche, F. Barillet, J. M. Astruc, C. Soulas, X. Aguerre, F. Arrese et al. 2013. Genomic relationships across dairy sheep breeds in the western Pyrenees: Latxa and Manech. *XV Jornadas sobre Producción Animal*, Zaragoza, Spain. May 14-15. pp. 592-594.

2014

A. Legarra, O.F. Christensen, Z.G. Vitezica, I. Aguilar, I. Misztal. 2014. La huella de los metafundadores. *XVII Reunión Nacional de Mejora Genética Animal*, June 5-6. Bellaterra, Spain. Abstract.

Papers presented at Meetings (in French)

2008

C. Marie-Etancelin, J.M. André, E. Baéza, B. Basso, D. Bastianelli, M.D. Bernadet, J.M. Brun, S. Davail, F. Dubos, X. Fernandez, D. Guémené, K. Gontier, G. Guy, A. Legarra. 2008. Parametres génétiques d'indicateurs du métabolisme hépatique durant le gavage, de la qualité des produits et du taux de corticostérone chez le canard, estimes dans le cadre du programme « GENECAN ». *Journées de la recherche avicole*, October. Abstract.

2009

F. Guillaume, S. Fritz, P. Croiseau, A. Legarra, C. Robert-Granié, C. Colombani, C. Patry, D. Boichard, V. Ducrocq. 2009. Modèles d'évaluation génomique : Application aux populations bovines laitières françaises. *Rencontres Recherches Ruminants*, Paris, France, December 2-3. pp 1-8.

C. Moreno, C. Kopp, P. Mulsant, C. Robert-Granié, R. Rupp, F. Barillet, C. Delmas, J. Bouix, D. Allain, E. Manfredi, L. Bodin, J.M. Elsen, D. Robelin, B. Mangin, T. Faraut, B. Servin, P. Jacquiet, G. Foucras, A. Legarra. 2009. Utilisation d'une puce 60 000 SNP pour cartographier finement des QTL affectant des caractères de production, de résistance aux maladies et de comportement chez les ovins. *16ème Rencontres Recherches Ruminants*, Paris, France. December 2-3. Abstract, 1 p.

2011

A. Ricard, A. Legarra, S. Danvy, C. Guyon, J.C. Meriaux, G. Guèrin. 2011. Peut-on prédire la qualité d'un reproducteur équin pour le CSO à partir de la génomique ? *37ème Journée de la Recherche Equine*, February 24. Abstract.

2012

A. Ricard, A. Legarra, J.C. Meriaux, S. Danvy, G. Guerin. 2012. Résultats mitigés de l'évaluation génomique chez les chevaux de concours hippique. *38ème Journée de la Recherche Equine*, February. Abstract.

J.M. Astruc, G. Baloche, H. Larroque, I. Beltran de Heredia, J. Labatut, G. Lagriffoul, C. Moreno, C. Robert-Granié, M.Y. Boscher, C. Chantry-Darmon, X. Aguerre, P. Boulenc, G. Frégeat, B. Giral-Viala, P. Guibert, P. Panis, C. Soulas, F. Barillet, A. Legarra. 2012. La sélection génomique des ovins laitiers en France : Stratégies, premiers résultats des évaluations génomiques et perspectives. In: 19èmes Rencontres autour des Recherches sur les Ruminants (p. 81-84). Rencontres autour des Recherches sur les Ruminants. Presented at 19. Rencontres Recherche Ruminants, Paris, FRA (2012-12-05 - 2012-12-06). Paris, FRA : Institut de l'Elevage.

2014

F. Barillet, G. Baloche, D. Buisson, G. Lagriffoul, X. Aguerre, P. Boulenc, F.Fidele, G. Fregeat, B. Giral-Viala, P. Guibert, P. Panis, C. Soulas, C. Robert-Granie, H. Larroque, A. Legarra, J.M. Astruc. 2014 Sélection génomique en ovins laitiers en France : principaux résultats et conséquences pour la mise en place de schémas de sélection génomique. Presented at 20. Rencontres Recherche Ruminants, Paris.

1.1.5. Other material

1.2 – Secondary research articles (author)

1.2.1. In peer-reviewed journals

2011

C. Robert-Granié, A. Legarra, V. Ducrocq. 2011. Principes de base de la sélection génomique. *In: Numéro spécial, Amélioration génétique.* Mulsant P., Bodin L., Coudurier B., Deretz S., Le Roy P., Quillet E., Perez J.M. (Eds). INRA Prod.Anim., 24, 331-340. (Invited).

2014

A. Legarra, O.F. Christensen, I. Aguilar, I. Misztal. 2014. Single Step, A general approach for genomic selection. *Livestock Science,* 166: 54-65. (Invited).

1.2.2. In non-peer-reviewed journals

Course Notes: « Basis for Genomic Prediction », 60 pp.
http://nce.ads.uga.edu/wiki/doku.php?id=course_materials_-_from_uga_2014

1.2.3. Chapter of a publication
1.2.4. Publication
1.2.5. Bibliographical theses or doctorates (e.g.: veterinary theses)

1.2.6. Material presented in conferences and symposia (please specify: extract, synopsis, full text)

Invited talks:

At congresses:

2010. Genomic selection (‘Mejora animal mediante selección genómica: nuevos aires para el parecido entre parientes’). XVIII Seminario de Genética de Poblaciones y Evolución. Guitiriz, Spain, 5-7 May. Abstract.

2010. Improved Bayesian Lasso for genomic selection (‘Lasso Bayesiano Mejorado para selección genómica’). XIV Reunión nacional de mejora genética animal. Vigo, Spain, 16-18 June. Abstract.

2011. The Single Step: genomic selection for all. Meeting of the European Association of Animal Production, 28 August. Stavanger, Norway. Abstract.

2012. A real data based comparison of methods for whole-genome QTL fine mapping in four livestock species. 25th International Conference "Genetic Days", September 18 - 20, , Wrocław, Poland. Abstract.

2014. Applications of (genomic) relationships to Livestock Genetics, International Biometric Conference, Florence, Italy, July 6-11. Abstract.

2014. Single Step Methods with a View towards Poultry Breeding, World Congress on Genetics Applied to Livestock Production, Vancouver, Canada, August 21. Full-text.

At workshops:

2007. Genomic selection: Joint seminar of the departments “animal genetics” and “plant genetics” of INRA, Paris, 18 September.

2007. Genomic selection: Seminar of the avian genetic network of INRA, 6 December.

2008. Practical application of Genomic selection: September 7-8 in Salzburg, Austria, University of Natural Resources and Applied Life Sciences.

2009. One-step genetic evaluation including pedigree, genomic, and phenotypic data. Universidad de Zaragoza, Spain, 10 November.

2012. Talk “Renovation of Statistical Genetics”, 15 February, Montpellier SupAgro.

2013. The Single Step GBLUP: a unified framework to combine all phenotypes, pedigrees and markers in genomic prediction. Workshop: Workshop Biometrische Aspekte der Genomanalyse 20-22 Fenruary in the Castle of Rauischholzhausen, Marburg, Germany.

2013. Genomic prediction with all data using the Single Step for very large data sets. 5th Workshop COST action Statseq, 24-26 April, Helsinki, Finland. Abstract.

2014. Statistical and computational methods for relatedness and relationship inference from genetic marker data, ICMS, Edinburgh, 22-26 September.

Seminars given at Universidad de Buenos Aires, at University of Georgia, at Iowa State University.

1.2.7. Other material

2 – TEACHING, DEVELOPMENT, POPULARISATION AND PROMOTION DOCUMENTS and research coordination documents

2.1 – Own work

2.1.1. In peer-reviewed journals
2.1.2. In non-peer-reviewed journals
2.1.3. Chapter of a publication
2.1.4. Publication
2.1.5. Theses or doctorates

2.1.6. Material presented in conferences and symposia

Conseil Régional de Midi Pyrénées (2011).

POCTEFA (European FEDER Funds): GENOMIA project: “Renforcement des schémas de sélection des races ovines laitières locales d’intérêt économique, écologique et social.

2.1.7. Written material (including patents and specialisations)

Software manuals: TM, GS3 (see Software)

Manual for BLUPF90 family of programs
http://nce.ads.uga.edu/wiki/lib/exe/fetch.php?media=blupf90_all1.pdf

Exercises for courses on Genomic Prediction.

2.1.8. Digital or audiovisual work

Software TM (estimation of genetic parameters including threshold and censored traits) and GS3 (genomic evaluation by Bayesian Regression and estimation of parameters), both available at http://genotoul.toulouse.inra.fr/~alegarra .
Software ms2gs (with Miguel Perez-Enciso)

I have contributed to the development of the blupf90 suite of programs: http://nce.ads.uga.edu/wiki ,
to QxPak: http://www.icrea.cat/Web/OtherSectionViewer.aspx?key=485
and to LDSO and QTLMAP: https://qgsp.jouy.inra.fr .
Scientific blog: http://artadia.blogspot.fr

2.2. Oversight of peer work
2.2.1. Editor of group work
2.2.2. Thesis research director
2.2.3. Other

Annex 2 – RESEARCH COORDINATION ACTIVITIES AND ACTIVITIES OTHER THAN SCIENTIFIC PRODUCTION WITHIN PUBLIC SCIENTIFIC AND TECHNOLOGICAL ESTABLISHMENTS (EPST)

(Non-exhaustive list)

1 – JOINT RESEARCH COORDINATION

- Coordination and management of research groups

Financed grants

Coordinator:

INRA (Métaprogramme SELGEN): X-GEN:“Crossbreeding and accuracy in genomic evaluation”. Total budget: 30,000 euros + 3 PhD scholarships. 2013-2015.

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.

Associated to foreign grants

USDA (US): Ignacy Misztal, 2009-2012

Ministerio de Economia (Spain): Miguel Pérez-Enciso, 2015-2017

NIFA (US): Ignacy Misztal, 2014-2018

- Coordination of European Union projects

INRA Coordinator:
POCTEFA (European FEDER Funds): GENOMIA. “Renforcement des schémas de sélection des races ovines laitières locales d’intérêt économique, écologique et social. » Total budget: 650,000 euros. 2010-2013.

- Participation in scientific advisory boards or evaluation committees

Project reviews for the Netherlands Grant System, PERSPECTIEF

Project reviews for INRA metaprogram SelGen

Project reviews for Science Peer Reviewer for the New Zealand Ministry of Business, Innovation & Employment

Project reviews for the International Foundation for Science (Sweden, www.ifs.se)

Project reviews for Research Foundation - Flanders (Fonds Wetenschappelijk Onderzoek - Vlaanderen, FWO), Belgium.

Candidate to vice-president, Genetics commission, EAAP, 2014.

- Edition of collective scientific work, participation in editorial boards

Member of the editorial board of Journal of Animal Science 2005-2007, reviewing about 5 papers a year.

Member of the editorial board of Journal of Dairy Science 2014-, reviewing about 5 papers a year.

Associate editor, Genetics Selection Evolution, since 2012, handling around 10 papers a year.

I review around 15 papers a year, for the journals: Genetics; Genetics, Selection, Evolution; Heredity; Journal of Animal Science; Journal of Dairy Science; Plos ONE; Plos Genetics Jounral of Animal Breeding and Genetics; Animal; 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.

- Team coordination or research centre management

'Animateur' of the group MG2 (Modélisation Génétique et Génomique), GenPhySE unit.

2 – TEACHING AND TRAINING OF JUNIOR SCIENTISTS, EXPERTISE, KNOWLEDGE, TECHNOLOGY AND INNOVATION TRANSFER, PARTNERSHIPS

- Education and vocational training at all levels (Accreditation to supervise research (HDR), training or joint training of junior scientists, ASC, thesis candidates, students), teaching, student evaluation, participation in selection boards for open competitions

Teaching

Official courses, Master level:

2008-2010. 1-day course "Genetic improvement in Animal Science", Master EURAMA, EIP, Toulouse, 17/9/2008; 24/9/2009. 15/9/2010.

Since 2011 : 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). Season 2011-2012, 2012-2013, 2013-2014.

Official courses, PhD level:

2009. 4-day course: "Genome-wide association mapping and genomic selection", Universidad de Buenos Aires, Argentina, 3-7 March.

2012. 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.

2014. 5-day course: “Short course - Programming and computer algorithms with focus on genomic selection in animal breeding”. University of Georgia, Athens, USA, 26-30 May.

2015. 4-day course : “Methods for genomic evaluation”, 7-10 April 2015, Universitat Politècnica de València, Spain

These courses include exercises and notes, e.g.

http://nce.ads.uga.edu/wiki/doku.php?id=course_materials_-_from_uga_2014

https://www.dropbox.com/sh/mcqodzpqfhklzg6/AABh4to7EKKNWDFNn0ZOHXhfa?dl=0

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", June 24-26, 1 day intervention.

Supervision of students

Formal supervision of 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.

Eduardo Nestor Fernandez (2013-2015). 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”.

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.

Visiting Students

Several PhD students supervised by other people have visited me. These visits took 3 to 6 months:

Ll Tusell (IRTA, Barcelona, Spain, supervised by M. Piles): 2009, 2010

S. Karoui (INIA, Madrid, Spain, supervised by MJ Carabaño and C Diaz): 2011, 2012

J. Ertl (Institute of Animal Breeding, Bavarian State Research Centre for Agriculture, supervised by KU Goetz): 2013

N. Forneris (Universidad de Buenos Aires, supervised by RJC Cantet) 2014

C.Garcia-Baccino (Universidad de Buenos Aires, supervised by RJC Cantet) 2015

Collaboration with students

I have worked with other PhD students not supervised by me. This includes E. Lopez de Maturana (Neiker, Espagne, 2007), M. Ramon (INIA, Espagne, 2007), I. Aguilar (UGA, US, 2010), I. David (INRA, 2009), C. Colombani (INRA, 2013), D. Roldan (INRA, 2012), F. Ytournel (INRA, 2009, R. Simeone (UGA, MSc, 2010), S.I. Duchemin (INRA, MSc, 2011).

PhD commitees

(Comité de thèse): D. Roldan, C. Colombani, Chris Hoze, D. Jonas, H. Giraud, Iola Croue, C. Carillier, F Bonnafous.

Member of the Jury

In the PhD dissertations of:

Evangelina López de Maturana, Universidad de Zaragoza, 2007.
Manuel Ramón, Universidad de Castilla La Mancha, 2007.
Llibertat Tusell, Universidad Politécnica de Valencia, 2011.
Bin Yang, Universidad Autónoma de Barcelona, 2011.
Raquel Lavara, Universidad Politécnica de Valencia, 2013.
Thierry Tribout, AgroParisTech, 2013.

In the mid-term dissertation of Hadi Esfandyari (University of Aarhus, Denmark), 2014

Member of the jury for recruitement of Open Research Scientists at INRA, 2012.

Others

"Free" professor (*docente libre*) at the Universidad de Buenos Aires, Argentina.

- Works for the general public: presentations, exhibits, audiovisual work, written documents

- Scientific and technical support functions

Genetic evaluation

During 2003-2005 in NEIKER I was in charge together with Eva Ugarte of the Latxa dairy sheep genetic evaluation in Spain for milk yield and contents and udder morphology, including ~500,000 animals across four breeds and 5 traits.

- Expertise and consultancy

- Science promotion activities (patents, contracts, contribution to data bases, software development, management and promotion of collections or enhanced biological material (lines, varieties, etc.))

International collaborations :

As a Visiting Scientist

2008. Iowa State University, collaboration with Rohan Fernando. 3 weeks, March-April.

2009 -. University of Georgia, collaboration with Ignacy Misztal. Generally 10 days, one month in 2010 and 2014.

2010. NEIKER, Vitoria, Spain, one week.

2012. Instituto Nacional de Investigación Agropecuaria (), collaboration with Ignacio Aguilar, Montevideo, Uruguay. December, one week.

2013 - now. University of Aarhus, Foulum, Denmark. Collaboration with Ole Christensen. 4 days each time.

Visiting scientists for collaborations

2006, 2010, 2012. Ignacy Misztal, University of Georgia. 2006 (one week), 2010 (one week), 2012 (one month).

2008. Rohan Fernando (Iowa State University). One week, June.

2013. Luis Varona (Universidad de Zaragoza). 2013. February, one week.

2014. Rodolfo J.C. Cantet (Universidad de Buenos Aires). February, one month.

2016. Rohan Fernando (Iowa State University). Two weeks, March.

3 – RESEARCH SUPPORT, INSTITUTIONAL SUPPORT, CROSS-CUTTING MISSIONS

- Coordination and management in research units: human resources management, budget preparation, asset management (in particular, innovation development and follow-up)
- Duties in local or national administrative bodies supporting research
- Technical and administrative duties in INRA partner establishments (e.g.: technical institutes, professional organisations, higher education, ministries)