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Summary
(home)

I am Assistant Professor in the Section on Statistical Genetics (**SSG**) in the Biostatistics Department at the University of Alabama at Birmingham (**UAB**). I was previously a Postdoctoral Fellow at the SSG. I received my PhD degree and a MS in the Dairy Science Department at the University of Wisconsin-Madison (**UW-Madison**). I also have a Certificate in Bioinformatics from UW-Madison, and an Agronomy degree from Universidad de la República-Uruguay. My current research focuses on (a) the development and use of genomic-based statistical methods for human health complex traits, including cancer, obesity and heart health traits in a Bayesian context; (b) the incorporation of biological information in models used for the analysis of microarray gene expression data. My previous research included studies with generalized linear mixed models (**GLMM**) with correlated random effects, from which I co-authored an R-package that fits such models.

References
(home)

- Dr. D.B. Allison. University of Alabama-Birmingham.
  e-mail: DAllison@ms.soph.uab.edu, Phone: (205) 975-9169.
- Dr. D. Gianola. University of Wisconsin – Madison.
  e-mail: gianola@ansci.wisc.edu, Phone: (608) 265-2054.
- Dr. G.J.M. Rosa. University of Wisconsin – Madison.
  e-mail: grosa@wisc.edu, Phone: (608) 265-8617.
- Dr. K.A. Weigel. University of Wisconsin – Madison.
  e-mail: kweigel@wisc.edu, Phone: (608) 263-4321.

Education
(home)

Doctor of Philosophy (2008-2010).

Dairy Science, UW-Madison.

Advisers: Dr. Guilherme Rosa, Dr. Daniel Gianola and Dr. Kent Weigel.

Dissertation: *Statistical Modeling of Genomic Data: Applications to Genetic Markers and Gene Expression.*

High-throughput technologies for genomics produce massive amounts of information on each individual assayed, giving raise to severe dimensionality issues with a much larger number of parameters (*p*) than replicates (*n*). Deriving useful inferences and predictions from this "*large-p small-n*" information constitutes a major challenge. The dissertation develops and evaluates statistical tools for genomic information on quantitative traits. (Publications 4 to 12; Abstracts 8, 11 to 16 and 26).

I have completed (including MS and PhD) 132 graduate credits, 55 in research and 77 in several departments (mathematics, statistics, biology and computer sciences), with a GPA of 3.75.

Bioinformatics Certificate (2007-2008).

Biostatistics and Medical Informatics, UW-Madison.

Master of Science (2004-2007)

Dairy Science, UW-Madison.

Advisers: Dr. Daniel Gianola and Dr. Kent Weigel.

Dissertation: *Analysis of number of episodes of clinical mastitis in Norwegian Red and Holstein cows with Poisson and categorical data mixed models.*

> I used GLMM (Poisson, probit, logit and linear) and ordinal threshold models with correlated random effects to study the genetics of clinical mastitis in dairy cattle in two populations. In this context, I co-authored an R-package (*pedigreemm*) with Dr. D.M. Bates that fits GLMM models including pedigrees (Publications 12 to 15 and 20; Abstracts 18 to 21).

Undergraduate Studies (1994-2001).

Universidad de la República, Montevideo-Uruguay.

Major: Plant and Animal Sciences.

Adviser: Dr. Graciela Quintans.

Dissertation: *Effects of the early weaning and body condition on the reproductive performance of primiparous cows* (Publications 17 and 18, 21).

Short Courses.

- *Population Genetic Data Analysis*. Instructors: Drs. Bruce Weir and Jérome Goudet, European Institute in Statistical Genetics, Institute of Evolutionary Biology, University of Edinburgh, Edinburgh, 6/2012.
- *Statistical Learning and Data Mining III*. Instructors: Drs. Trevor Hastie and Robert Tibshirani, Stanford University, Boston, MA, 9/2011.
- *Genomic Selection in Livestock*. Instructors: Drs. Dorian Garrick, Rohan Fernando and Jack Dekkers, Iowa State University, 6/2010.
- *Computational Approaches to Analyzing Microarray Data*. Instructors:

Drs. Karin Borgh, *et al.*, University of Wisconsin Biotechnology Center Promega Corporation, Madison, Wisconsin, 7/2008.

- *QTL Mapping, MAS, and Genomic Selection*. Instructor: Dr. Ben Hayes, Iowa State University, 2007.
- *Fortran Programming and Bayesian Implementation via MCMC Techniques*. Instructors: Drs. Ignacy Misztal and Romdhane Rekaya, University of Georgia, 2005.
- *Bayesian Modeling, Inference and Prediction*. Instructor: Dr. David Draper. University of California, Chicago, 2005.
- *XI International Course on Animal Breeding*, National Institute of Agricultural Research, Spain-Madrid, 10/2001.
- *The evaluation process in the classroom.* Instructor: Ms. Maria Camino Trapero. Universidad de la Republica. Montevideo-Uruguay, Aug.-Sep., 2001.

Programming Skills and Software Development (home)

I do most of my programming in R and Java, and use SAS sporadically. I am fluent in Unix and I have basic knowledge of Fortran and WinBugs.

R package *pedigreemm* (Version 0.2-4 and *in development*).

Authors: Dr. D.M. Bates and **A.I. Vazquez**.

The *pedigreemm* R package extends *lme4*, allowing fitting mixed models with correlated random effects for Gaussian, binary and counting responses. Estimation methods available in *pedigreemm* include: Maximum Likelihood, REML, and penalized quasi-likelihood methods (Publication 13; Abstracts 19 y 20).

Languages (home)

I am fluent in Spanish and English and have basic knowledge of Portuguese.

Professional Experience
(home)

Assistant Professor (Oct 2012, up to date).

Institution: Section of Statistical Genetics at UAB.

Areas of study: My current research centers on (a) the development and use of genomic-based statistical methods for human health complex traits in a Bayesian context; and (b) understanding the complex biological systems behind these traits. My areas of application include height, blood pressure, cancer, obesity, and body composition traits.

Postdoctoral Fellow (2011-2012).

Institution: Section of Statistical Genetics at UAB.

Advisers: Dr. David B. Allison and Dr. Nengjun Yi.

Areas of study: My research addressed the development and use of genomic-based statistical methods for human health-related traits including cancer, obesity and heart health traits in a Bayesian context (Publications 1 to 4 and 6; Abstracts 8 to 12).

Consultant (2011 - 2012).

Institution: Aviagen.

Development of a pipeline of programs to normalize and perform heterozygous correction of pooled genotyping data, estimate allele frequencies, variances, perform chi-squared tests and outcome summaries.

Statistician (2010).

Institution: Section of Statistical Genetics at UAB.

Principal investigators: Dr. David B. Allison and Dr. Christine Duarte.

Activities: Analysis of biomedical data in several areas of application addressing problems of human genomics mostly in mortality, obesity and cardiovascular traits. (Publications 2 to 5, 8 and 9).

Research and Teaching Assistant (2004-2009).

Institution: Dairy Science Department, UW-Madison.

Advisers: Dr. Guilherme Rosa, Dr. Daniel Gianola and Dr. Kent Weigel.

Teaching activities: T.A. of the Following Courses,

- Introduction to Animal and Veterinary Genetics. Animal Science 361, (2008 and 2009, Dr. Rosa and Dr Thomas).
- Principles of Animal Breeding, Animal Science 363, (2008 and 2009, Dr. Rosa and Dr Thomas).
- Design & Analysis of Microarray Experiments in Agriculture. (2009, Dr. Rosa).
- Introduction to Statistical Analysis with R (2009, Xiao-lin Wu).

Research activities: Related to the MS and PhD programs (Publications 1 and 4 to 17; Abstracts 11 to 21).

Internship in Animal Reproduction (2003).

Institution: Dairy Science Department, UW-Madison.

Advisor: Dr. Milo Wiltbank.

Activities in projects related to reproduction in dairy and beef cattle.

Research Assistant in Animal Reproduction (2002).

Institution: National Institute of Agricultural Research (INIA), Uruguay.

Advisor: Dr. Graciela Quintans.

Activities: Support in beef cows and sheep research. (Publications 17 and 18; Abstracts 22 to 26; Extension publications 1 to 9).

Teaching Assistant in Animal Reproduction (2002).

Course: *Reproductive techniques in sheep and cattle.*

Institution: Universidad de la República-Salto, Uruguay.

Advisor: Dr. Daniel Fernandez-Abella.

Teaching and Research Assistant in Animal Breeding (1999-2001).

Institution: Universidad de la República, Uruguay.

Supervisors: Dr. Jorge Urioste and MS. Diego Gimeno.

Activities: T.A. in Animal Breeding course and support in Cross Breeding project (Extension publication 10).

Funding and Awards
(home)

ARVALIS. Models and Software Development for Incorporation of Genetic by Environmental Interactions in Whole Genome Regression Models. Fund: U$S 110,000/year. Period 2013/2014. PI: Gustavo de los Campos and Ana I. Vazquez.

2012- Pilot/Feasibility Study Opportunities offered by the Nutrition Obesity Research Center, at UAB. Awarded project “Statistical Methods for Multivariate Genome Wide SNPs: Developments for Obesity, Body Composition and Bone Health”. Principal Investigator: Ana I. Vazquez, Senior mentors: David Allison and Molly Bray. Fund: U$S 25.000.

2012- 4th Annual Public Health Research Day, First Place in Post Doctoral/Fellow Category. School of Public Health, UAB.

2011- Career Enhancement Awards. Office of Postdoctoral Education, UAB. Award U$S 1,500.

2011- The Seng-jaw Soong Award for Excellence in Biostatistics Research. Comprehensive Cancer Center Retreat, UAB. Award U$S 500.

Funding (Pending)

R21 PA-10-26. “Comprehensive Risk Assessment Model to Predict Breast Cancer Progression”. Institution: National Health Institute, Budget: U$S 404,250. Period: 2 years. Principal Investigator: Ana I. Vazquez.

Supplement Award. “Genetics of Obesity-related and Metabolic traits Discovery Study”. Institution: National Health Institute. Budget: U$S 200,000. Period: 2 years. R01, Principal Investigator: Molly Bray.

Reviewer
(home)

Journal of Animal Breeding and Genetics,
The Journal of the American Medical Association,
Journal of Clinical Oncology,
PLoS Genetics,
Human Heredity,
Genetics Research,
International Journal of Obesity,
Obesity,
Journal of Dairy Science,
Journal of Animal Science,
Animal,
African Journal of Agricultural Research,
Research in Veterinary Science, and
Project evaluation for Agencia Nacional de Investigación e Innovación (ANII), 2010 and 2012, Uruguay.

Tutoring
(home)

- Maggie Delgado, Internship: Genomic predictors of Body Mass Index (BMI) in relation to longevity. Mentors: David B. Allison, Ana I. Vazquez, Gustavo de los Campos. Section on Statistical Genetics. University of Alabama, Birmingham. June-July, 2010.

- Maxine González, Internship: Genomic predictors of Body Mass Index (BMI) *vs*. Family history predictors. Mentors: **Ana I. Vazquez** and David B. Allison. Section on Statistical Genetics. University of Alabama, Birmingham. June-July, 2011.

- Wilnerys Colberg Hernández, Internship: Clinical Utility of Whole Genome Prediction. Mentors: Emily Dhurandhar, **Ana I. Vázquez**, David B. Allison. Section on Statistical Genetics. University of Alabama, Birmingham. June-July, 2012.

- Izel Sorensen, Visiting Scholar. Project: "Pharmacogenetic effects of “candidate gene complexes” on cardiovascular disease outcomes in response to antihypertensive treatments in the GenHAT study". Mentors: **Ana I. Vázquez**, and Marguerite Ryan. Section on Statistical Genetics. University of Alabama, Birmingham. March-May, 2013.

- Dayanara Lebron, Internship: “Genome-Enabling Models for Type 2 Diabetes Risk Assessment”. Mentors: **Ana I. Vázquez**, Emily Dhurandhar, Paulino Perez, David B. Allison. University of Alabama, Birmingham. June-July, 2013.

- Alessandro Ferragina, Visiting Scholar. Project: “Multivariate analysis of complex traits”. Mentors: Alessio Cecchinato, Ana I. Vazquez, Gustavo de los Campos. University of Alabama, Birmingham. Sep-Feb, 2013/2014.

- Yogasudha Veturi, directed studies. “Statistical Methods for Multivariate Genome Wide SNPs, developments for obesity and body composition”. Mentors: Ana I. Vazquez, Sep-Dec, 2013.

Publications Peer Reviewed (pending)

J.A. Dawson, E.J. Dhurandhar, **A.I. Vazquez**, D.B. Allison, Propagation of Obesity Across Generations: The Roles of Differential Realized Fertility and Assortative Mating by Body Mass Index. Human Heredity, Ms No.: 201303002. *In Press*.

S. Aslibekyan, H.W. Wiener, G. Wu, D. Zhi, S. Shrestha, G. de los Campos, **A.I. Vazquez**, Estimating Proportions of Explained Variance: a Comparison of Whole Genome Subsets, In: The Genetic Analysis Workshops 18, 2013. *In Press*.

G. de los Campos, **A.I. Vazquez**, R. Fernando, Y.C. Klimentidis and D. Sorensen, Prediction of Complex Human Traits Using the Genomic Best Linear Unbiased Predictor, PLoS Genetics, 2013, *In Press*.

Y.C. Klimentidis, **A.I. Vazquez**, G.de los Campos, D.B. Allison, M. Dransfield, V.J. Thannickal. Heritability of pulmonary function estimated from pedigree and whole-genome markers. *Submitted.*

E.J. Dhurandhar, **A. I. Vazquez**, G. Argyropoulos, and D.B. Allison. Prediction of Complex Traits With Genetic Information: Even Modest Prediction Accuracy Can Have Substantial Utility. *Submitted.*

A.I. Vazquez, E.J. Dhurandhar, Y.C. Klimentidis, G. de los Campos, V. Srinivasasainagendra, D.B. Allison, P. Perez. Model Evaluation for Whole Genome Prediction of Diabetes. *In preparation.*

Y.C. Klimentidis, **A.I. Vazquez**, G.de los Campos, Z. Chen, F. Martinez, D.B. Allison. High-dimensional genetic prediction of type-2 diabetes susceptibility. *In preparation.*

Publications: Peer Reviewed (home)

1. **A.I. Vazquez**, G. de los Campos, Y.C. Klimentidis, G.J.M. Rosa, D. Gianola, N. Yi, and D.B. Allison, 2012. A comprehensive genetic approach for improving prediction of skin cancer risk in humans, Genetics, Vol. 192, 1493–1502, [doi:10.1534/genetics.112.141705]. [PMID: 23051645].

2. M.A. Pérez-Cabal, **A.I. Vazquez**, D. Gianola, G.J.M. Rosa and K.A. Weigel, 2012. Accuracy of genome enabled prediction in dairy cattle

and wheat populations using different cross-validation designs, Frontiers in Livestock Genomics, 3 (00027), ISSN:1664-8021, doi: 10.3389/fgene.2012.00027.

3. R. Makowsky, N.M. Pajewski, Y.C. Klimentidis, **A.I. Vazquez**, C.W. Duarte, D.B. Allison and G. de los Campos, 2011. Beyond missing heritability: Prediction of complex traits, PLoS Genetics, 7(4): e1002051. doi:10.1371/journal.pgen.1002051.

4. G. de los Campos, Y.C. Klimentidis, **A.I. Vazquez** and D.B. Allison, 2012. Prediction of expected years of life using whole-genome markers, PLoS ONE, 7(7):e40964. doi:10.1371/journal.pone.0040964.

5. **A.I. Vazquez**, M.A. Perez-Cabal, B. Heringstad, M. Rodrigues-Motta, G.J.M. Rosa, D. Gianola and K.A. Weigel, 2011. Predictive ability of alternative models for genetic analysis of clinical mastitis. Journal of Animal Breeding and Genetics, J. Animal Breeding and Genetics, doi: 10.1111/j.1439-0388.2011.00950.x

6. **A.I. Vazquez**, G.J.M. Rosa, K.A. Weigel, G. de los Campos, D. Gianola and D.B. Allison, 2010. Predictive ability of subsets of SNP with and of parent average for several traits in US Holsteins. J. Dairy Sci., 93: 5942-5949.

7. K.A. Weigel, G. de los Campos, **A.I. Vazquez**, G.J.M. Rosa, D. Gianola and C.P. Van Tassell, 2010. Accuracy of direct genomic values derived from imputed single nucleotide polymorphism genotypes in Jersey cattle. J. Dairy Sci., 93: 5423-5435, doi:10.3168/jds.2010-3149.

8. **A.I. Vazquez**, G.J.M. Rosa, K.A. Weigel, D. Gianola, D.B. Allison, 2010. SNP Selection for low-density assays for genomic-enabled predictions using parent averages. Proceedings of the 9th World Congress on Genetics Applied to Livestock Production # 540 and book of abstracts, p 145. August 1-6, Leipzig, Germany.

9. G. de los Campos, D. Gianola, G.J.M. Rosa, K.A. Weigel, **A.I. Vazquez** and D.B. Allison, 2010. Semi-parametric marker-enabled prediction of genetic values using Gaussian processes. Proceedings of the 9th World Congress on Genetics Applied to Livestock Production # 520 and book of abstracts, p 131. August 1-6, Leipzig, Germany.

10. M.A. Pérez-Cabal, **A.I. Vazquez**, D. Gianola, G.J.M. Rosa, and K.A. Weigel, 2010. Accuracy of genomic predictions in USA Holstein cattle from different training-testing designs. Proceedings of the 9th World Congress on Genetics Applied to Livestock Production # 563 and book of abstracts, p 150. August 1-6, Leipzig, Germany.

11. K.A. Weigel, G. de los Campos, **A.I. Vazquez**, C.P. Van Tassell, G.J.M. Rosa, D. Gianola, J.R. O'Connell, P.M. VanRaden and G.R. Wiggans, 2010. Genomic selection and its effects on dairy cattle breeding programs. Proceedings of the 9th World Congress on Genetics Applied to Livestock Production # 119 and book of abstracts, p 19. August 1-6, Leipzig, Germany.

12. G.J.M. Rosa and **A.I. Vazquez**, 2009. Integrating biological information into the statistical analysis and design of microarray experiments. Animal Journal, 4: 165-172.

13. **A.I. Vazquez**, D.M. Bates, G.J.M. Rosa, D. Gianola and K.A. Weigel, 2010. Technical note: An R package for fitting generalized linear mixed models in animal breeding. J. Anim. Sci., 88: 497-504.

14. **A.I. Vazquez**, K.A. Weigel, D. Gianola, D.M. Bates, M.A. Perez-Cabal, G.J.M. Rosa, and Y.M. Chang, 2009. Poisson *versus* threshold models for genetic analysis of clinical mastitis in US Holsteins. J. Dairy Sci., 92:5239-5247.

15. **A.I. Vazquez**, D. Gianola, D.M. Bates, K.A. Weigel, and B. Heringstad, 2009. Assessment of Poisson, logit and linear models for genetic analysis of clinical mastitis in Norwegian Red Cows. J. Dairy Sci., 92: 739-748.

16. M.A. Perez-Cabal, G. de los Campos, **A.I. Vazquez**, D. Gianola, G.J.M. Rosa, K.A. Weigel and R. Alenda, 2009. Genetic evaluation of susceptibility to clinical mastitis in Spanish Holstein cows. J. Dairy Sci., 92: 3472-3480.

17. G. Quintans, **A.I. Vazquez** and K.A. Weigel, 2009. Effect of suckling restriction with nose plates and premature weaning on postpartum anoestrous interval in primiparous cows under range conditions. Animal Reproduction Science, 116: 10-18.

18. F. Dutra, **A.I. Vazquez,** G. Banchero and G. Quintans, 2003. Perinatal lesions in the central nervous system in twin lambs. *In*: XXXI Jornadas Uruguayas de Buiatría, pp 133-137.

Publications, Non-peer reviewed, Dissertations and Thesis
(home)

1. **A.I. Vazquez**, 2010. *Statistical Modeling of Genomic Data: Applications to Genetic Markers and Gene Expression.* Doctor of Philosophy Dissertation, University of Wisconsin – Madison, 109 pp.

2. **A.I. Vazquez**, 2007. *Analysis of Number of Episodes of Clinical Mastitis in Norwegian Red and Holstein Cows with Poisson and Categorical Data Mixed Models*. Master of Science Thesis. University

of Wisconsin – Madison, 162 pp.

3. **A.I. Vazquez** and P. Lacuesta, 2001**.** *Effect of the Early Weaning and Body Condition on the Reproductive Performance of First Calf Cows*. Thesis of Universidad de la República. Montevideo, Uruguay. INIA Uruguay p.91-124.

Abstracts
(home)

1. **A.I. Vazquez**, G. de los Campos, Y.C. Klimentidis, D.B. Allison, 2012. Whole-genome enabled prediction in moderately heritable complex human traits. 4th International Conference of Quantitative Genetics: Understanding Variation in Complex Traits. P-146, Edinburgh, U.K., 6/2012.

2. **A.I. Vazquez**, E.J. Dhurandhar, M.S. Bray, G. de los Campos, Y.C. Klimentidis, D.B. Allison, G. Argyropoulos, M.N. Gonzalez. Genetic predisposition to obesity predicted with thousands of single nucleotide polymorphisms. Obesity Society Meeting, San Antonio, Texas, Control id: 1375685, 9/2012.

3. **A.I. Vazquez**, G. de los Campos, Y.C. Klimentidis, G.J.M. Rosa, D. Gianola, N. Yi and D.B. Allison, 2011. Whole genome-enabled prediction of skin cancer liability *vs*. family-based prediction. UAB SOPH, Research Day, Birmingham, AL, 4/2012; Awarded: First Place Post Doctoral/Fellow Category.

4. Y.C. Klimentidis, **A.I. Vazquez**, G. de los Campos. Prediction of human height with large panels of SNPs – insights into genetic architecture. American Society of Human Genetics, San Francisco, 11/2012.

5. E.J. Dhurandhar, **A.I. Vazquez**, D.B. Allison. Clinical utility of whole genome prediction for personalized obesity treatment. Obesity Society Meeting, San Antonio, Texas, 9/2012.

6. G. de los Campos, Y.C. Klimentidis, **A.I. Vazquez** and D.B. Allison. Prediction of Life Expectancy Using Whole-Genome Regression Methods, Research Day SOPH, UAB, Birmingham, AL, 4/2012.

7. G. de los Campos, **A.I. Vazquez**, Y.C. Klimentidis, and D. Sorensen. Whole-genome regression and prediction of human complex traits using data from related and unrelated individuals. 4th International Conference of Quantitative Genetics: Understanding Variation in Complex Traits. O-24. Edinburgh, U.K, 6/2012.

8. **A.I. Vazquez**, G. de los Campos, Y.C. Klimentidis, G.J.M. Rosa, D. Gianola, N. Yi, and D.B. Allison. Whole-genome enable prediction of

skin cancer liability, Comprehensive Cancer Center 14th Annual Research Retreat and Research Competition., Birmingham, AL, 10/2011; Awarded: *The Seng-jaw Soong Award for Excellence in Biostatistics and Bioinformatics Research*.

9. R. Makowsky, N. M. Pajewski, Y. C. Klimentidis, **A.I. Vazquez**, C. W. Duarte, D. B. Allison, G. de los Campos. Beyond missing heritability: prediction of complex traits. Eastern North American Region, Miami, FL, Spring 2011, book of abstracts, p 202.

10. G. de los Campos, Y.C. Klimentidis, R. Makowsky, **A.I. Vazquez**, N.M. Pajewsky, C.W. Duarte and D.B. Allison. Predicting complex human traits using whole-genome markers: proof of principle with human height and human longevity. Joint Statistical Meetings, Miami, 2011.

11. **A.I. Vazquez**, G. de los Campos, G.M.J. Rosa, D. Gianola, Y.C. Klimentidis and D.B. Allison. Whole genome enabled prediction of liability to cancer related outcomes, Eastern North American Region, Miami, FL, Spring 2011, book of abstracts, p 202.

12. **A.I. Vazquez**, K.A. Weigel, G.J.M. Rosa, D. Gianola and D.B. Allison. Visualization of associations between single nucleotide polymorphisms and economically important dairy traits using biplot analysis ADSA. J. Anim. Sci., 89, E-Suppl. Pp 166. Abstract #39 p.4. July 10-14, 2011, New Orleans, Louisiana.

13. **A.I. Vazquez**, G. de los Campos, K.A. Weigel, G.J.M. Rosa and D. Gianola. Selection of SNPs for an optimal low-density assay for genomic prediction of transmitting abilities. Abstract # 32384. ASAS ADSA CSAS, Meeting, July 12-16, 2009, Montreal, Canada.

14. **A.I. Vazquez**, G.J.M Rosa, G. de los Campos, D. Gianola and K.A. Weigel. Use of biologically informed models for microarray gene expression data analysis. Abstract, p.37. SGLPGE Symposium, May 4-6, 2009, UW-Madison, Wisconsin (Abstract and poster).

15. G.J.M. Rosa and **A.I. Vazquez**. Utilizing biological information to model heterogeneous variability and co-expression in microarray experiments. International Biometric Society, December 2010, Brazil.

16. G. de los Campos, G.J.M. Rosa, D. Gianola, K.A. Weigel, **A.I. Vazquez**, J. Crossa and J.M. Cotes. Choosing regularization parameters in marker-assisted prediction of genetic values: cross-validation versus Bayesian methods. Abstract, p.7. SGLPGE Symposium, May 4-6, 2009, UW-Madison, Wisconsin (Abstract and poster).

17. M.F. Grunwald, J.J. Parrish and **A.I. Vazquez**. Environmental and Genetic Factors Affecting Bull Sperm Shape Using Fourier Harmonic Analysis. ASAS, 2010 ASAS/ADSA. Abstract and Poster #37, Location 206. Midwest Meeting March 15 - 17, 2010, Des Moines, IA.

18. **A.I. Vazquez**, B. Heringstad, M. A. Perez-Cabal, M. Rodriguez-Motta, K. A. Weigel, D. Gianola, G.J.M. Rosa and Y.M. Chang. 2010. Zero Inflated Poisson, threshold and linear models for genetic analysis of mastitis in Norwegian Red cattle. 61st Annual Meeting of the EAAP, Heraklion, Greece, August 23-27. Book of abstracts No 16: 84.

19. **A.I. Vazquez**, D.M. Bates, D. Gianola, K.A. Weigel, and G.J.M. Rosa. An R package for fitting generalized linear mixed models in animal breeding. Abstract # 32394. ASAS ADSA CSAS, Meeting, Montreal, Canada, 7/2009.

20. **A.I. Vazquez** , K.A. Weigel, G.J.M Rosa, D.M. Bates, D. Gianola and J. Crossa. Using the R package *pedigremm* for traditional genetic evaluations and for evaluations using high density genetic markers: An application to a wheat population. Abstract, p. 36. SGLPGE Symposium, May 4-6, 2009, UW-Madison, Wisconsin (Abstract and poster).

21. **A.I. Vazquez**, K.A. Weigel, D. Gianola, D.M. Bates, and B. Heringstad. Poisson versus logit models for genetic analysis of mastitis in Norwegian cattle. Abstract 233. *In:* Breeding and Genetics-Livestock and Poultry: Dairy Cattle I. Abstracts. P195. ASDA. Joint Annual Meeting. San Antonio, TX, July 8-12, 2007.

22. G. Quintans, C. Jimenez and **A.I. Vázquez**. Suckling control in primiparous beef cows under range conditions. *In:* European Symposium in Domestic Animal Reproduction (abstract P 193), Murcia, Spain (Poster), 2005.

23. G. Quintans, J.M. Straumann, W. Ayala and **A.I. Vazquez**. Effect of winter management on the onset of puberty in beef heifers under grazing conditions. *In:* 15th International Congress of Animal Reproduction, (Abstract no. 22), Porto Seguro, Brazil, 2004.

24. G.E. Banchero, **A.I. Vázquez** and G. Quintans. Can a short grazing period of lotus maku increase the ovulation rate in corriedale ewes? *In:* 12th World Corriedale Congress, 9/2003, Uruguay (RP 02), pp 111

25. G. Quintans, L. Blanco, G. Montedónico, **A.I. Vázquez** and G. De Nava. Effect of different suckling control treatments on reproductive performance in beef cows in commercial conditions. *In:* Proceedings of IX World Conference on Animal Production, Porto Alegre, Brazil,

10/2003, pp 219.

26. G. Quintans and **A.I. Vazquez**. Effect of premature weaning and suckling restriction with nose plates on the reproductive performance of primiparous cows under range conditions. *In:* Proceedings of the Sixth International Symposium in Domestic Ruminants, Crieff, Scotland (Abstract no. A65), 2002.

Extension Publications
(home)

1. G.E. Banchero, J. Milton, D. Lindsay, A. La Manna, **A.I. Vázquez** and G. Quintans, 2003. How to increase ovulatory rate in Correidale ewes. *In*: Producción Animal: Unidad Experimental Palo a Pique, Actividades de Difusión 332, INIA Treinta y Tres, pp. 53-57.

2. L. Blanco, G. Montedónico, G. de Nava, **A.I. Vázquez** and G. Quintans, 2003. Evaluation of three weaning techniques in commercial conditions. *In*: Producción Animal: Unidad Experimental Palo a Pique, Actividades de Difusión 332, INIA Treinta y Tres, pp. 34-44.

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