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Performance of pedigree- and genome-based coancestries on selection programmes

Silvia Teresa Rodríguez-Ramilo, L. A. Garcia-Cortès, M. A. R. de Cara

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Organising Committee

**66th EAAP Annual Meeting
Warsaw, 2015**

e-mail: info@eaap2015.org



PARTICIPATION CONFIRMATION

The Organising Committee of the 66th Annual Meeting of the European Federation of Animal Production confirm, that

SILVIA TERESA RODRIGUEZ RAMILO from SPAIN

attended the EAAP Annual meeting from August 31st 2015 till September 4st in Warsaw (Poland).

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Book of Abstracts of the 66th Annual Meeting of the European Federation of Animal Science



Book of abstracts No. 21 (2015)
Warsaw, Poland
31 August - 4 September 2015

Scientific Programme EAAP 2015

Monday 31 August 8.30 – 12.30	Monday 31 August 14.00 – 18.00	Tuesday 1 September 8.30 – 12.30	Tuesday 1 September 14.00 – 18.00
<p>Session 1 Climate smart cattle farming and breeding – Part 1: general overviews (in cooperation with EU projects METHAGENE, RUMINOMICS, OPTIBARN) Chair: O. Vangen/M. Klopčič</p> <hr/> <p>Session 2 Strategies of national gene banks for AnGR in Europe for long term conservation purposes and to support in situ conservation of endangered breeds Chair: S.J. Hiemstra</p> <hr/> <p>Session 3 Feasible solutions to reducing tail biting in commercial settings + rearing entire pigs Chair: A. Velarde</p> <hr/> <p>Session 4 Correctly reporting statistical genetics results in the genomic era Chair: G. Pollott</p> <hr/> <p>Session 7 Nutritional and management strategies in animal disease prevention Chair: G. Savoini</p>	<p>Session 8 Climate smart cattle farming and breeding – Part 2: genetic and nutritional aspects (in cooperation with EU projects METHAGENE, RUMINOMICS, OPTIBARN) Chair: Y. de Haas/C. Thomas</p> <hr/> <p>Session 9 How can we tip the balance between market and non-market outputs from livestock farming systems Chair: M. Zehetmeier/C. Ligda</p> <hr/> <p>Session 10 Young train session – Dairy innovative research and extension Chair: P. Aad/A. Kuipers</p> <hr/> <p>Session 11 Integrating biological knowledge into genetic studies Chair: T. Suchocki</p> <hr/> <p>Session 12 ATF Precision livestock farming</p> <hr/> <p>Session 13 Pork carcass; meat quantity or meat quality? Chair: S. Millet</p> <hr/> <p>Session 14 Customised nutrition taking into account the health status of farms and individual animals Chair: E. Tsiplakou</p> <hr/> <p>Session 15 Poultry husbandry: welfare, breeding and nutrition Chair: G. Das</p>	<p>8.30 – 9.30</p> <p>Welcome Ceremony</p> <p>9.30 – 10.30</p> <p>Session 16 Discovery plenary session part I Chair: P. Chemineau</p> <p>11.00 – 11.30</p> <p>Leroy presentation</p> <p>11.30 – 12.30</p> <p>Session 16 Discovery plenary session part II Chair: P. Chemineau</p>	<p>Session 17 Equine production, management and welfare Chair: K. Potočník</p> <hr/> <p>Session 18 Using electronic identification (EID) and other technological advances in small ruminant farming Chair: C. Morgan-Davies</p> <hr/> <p>Session 19 Efficiency, multifunctionality and tradeoffs in livestock production Chair: R. Ripoll-Bosch</p> <hr/> <p>Session 20 Genetics free communications Chair: E. Wall</p> <hr/> <p>Session 21 Beef production, supply and quality from farm to fork Chair: J.F. Hocquette/K. De Roest</p> <hr/> <p>Session 22 Genomic selection in practice Chair: I. Misztal</p> <hr/> <p>Session 23 Non-human-edible by-products: use and added value as feed material Chair: S. De Campeneere</p> <hr/> <p>Session 24 Success factors for careers in the livestock industry – Industry / Young Scientists Club Chair: P. Aad/C. Lambertz/A. Smetko</p> <hr/> <p>Session 25 Ways of improving udder health and fertility in cattle Chair: B. Fuerst-Waltl/M. Klopčič</p>
	<p>19.00 – 21.00</p> <p>Poster Session (part I), Award Ceremony, Welcome Reception</p>		

	Wednesday 2 September 8.30 – 11.30	Wednesday 2 September 14.00 – 18.00	Thursday 3 September 8.30 – 11.30	Thursday 3 September 14.00 – 18.00
	<p>Session 26 Innovation and research for developing the horse sector – Equine practice in Science – Part 1 Chair: A.S. Santos/P. Lekeux</p> <hr/> <p>Session 27 New sources of phenotypes in cattle production – Part 1 (with ICAR) Chair: G. Thaller/ C. Egger-Danner</p> <hr/> <p>Session 28 Integration of new technologies in livestock farming systems Chair: N. Hostiou</p> <hr/> <p>Session 29 Genetics commission early career scientist competition – Part 1 Chair: C. Pfeiffer</p> <hr/> <p>Session 30 New developments, techniques and research in cattle housing systems Chair: Y. Bewley/P. Galama</p> <hr/> <p>Session 31 Breeding for better health and welfare Chair: L. Boyle</p> <hr/> <p>Session 32 Towards a framework for multifunctional feeding systems Chair: J. Van Milgen</p> <hr/> <p>Session 57 EU project GPLUSE: Technical, economic, societal and environmental issues associated with highly productive dairy cows Chair: M. Crowe</p>	<p>Session 33 Innovation and research for developing the horse sector – Equine practice in Science – Part 2 Chair: A. Stojanowska/ D. Lewczuk</p> <hr/> <p>Session 34 All aspects of automatic milking including combination with grazing (in cooperation with EU project Autograssmilk) Chair: A. Van Den Pol-Van Dasselaar/C. Foley</p> <hr/> <p>Session 35 Future challenges and strategies for smallholders Chair: S. Oosting</p> <hr/> <p>Session 36 Genetics commission early career scientist competition – Part 2 Chair: H. Mulder</p> <hr/> <p>Session 37 New sources of phenotypes in cattle production – Part 2 (with ICAR) Chair: G. Thaller/C. Egger-Danner</p> <hr/> <p>Session 38 Applying physiology – improvements in animal productivity, water efficiency, welfare and behaviour Chair: C.H. Knight</p> <hr/> <p>Session 39 Role of plant bioactive compounds in animal nutrition Chair: E. Auclair/E. Apper</p> <hr/> <p>Session 40 Animal behaviour Chair: K. O'Driscoll</p>	<p>Session 41 Optimising breeding programmes in the genomic era Chair: T.H.E. Meuwissen/ A. de Vries</p> <hr/> <p>Session 42 In the age of genotype, the breeding objective is queen (joint session with INTERBULL) Chair: M. Coffey/R. Reents</p> <hr/> <p>Session 43 Free communications animal nutrition Chair: G. Van Duinkerken</p> <hr/> <p>Session 44 Genetics and genomics in horses Chair: K. Stock</p> <hr/> <p>Session 45 Health and welfare free communications Chair: M. Pearce</p> <hr/> <p>Session 47 Livestock farming systems free communications: livestock sustainability Chair: M. Tichit</p> <hr/> <p>Session 48 Sheep and goats free communications Chair: T. Ådnøy</p> <hr/> <p>Session 49 Nutrient sensing and metabolic signaling plus free communications – Physiology Chair: H. Sauerwein</p>	<p>Session 50 Efficient computation strategies in genomic prediction (joint session with Interbull) Chair: Z. Liu</p> <hr/> <p>Session 51 Biotechnological and genomic advances in small ruminant production Chair: R. Rupp</p> <hr/> <p>Session 52 Data in livestock farming systems : does the science supply meet farmers' needs? Chair: S. Ingrand</p> <hr/> <p>Session 53 Cattle herd management and health Chair: B. Fuerst-Walt/ W. Jagusiak</p> <hr/> <p>Session 54 Cellular physiology of the reproductive processes Chair: C.C. Perez-Marin</p> <hr/> <p>Session 55 Effects of neonate and early life conditions on robustness and resilience in later life Chair: H. Spoolder</p>
	11.30 – 12.30	14.00 – 17.00	11.30-12.30	Friday 4 September 8.30 – 18.00
	Poster Session (part II)	Session 6 Feeding the gestating and lactating sow. Chair: G. Bee	Commission business meetings	Session 56 Local industry day Chair: Z.M. Kowalski/I. Misztal
		17.00 – 18.00 Pig Commission Business meeting	Session 46 8.30 – 12.30 Pig genetics Chair: E. Knol	

Performance of Nelore steers in different Brazil livestock grazing systems <i>R.R.S. Corte, S.L. Silva, A.F. Pedroso, T.C. Alves and P.P.A. Oliveira</i>	244
Bayesian analysis for detection of signatures selection in Spanish autochthonous beef cattle breeds <i>A. González-Rodríguez, S. Munilla, E.F. Mouresan, J.J. Cañas-Álvarez, J.A. Baro, A. Molina, C. Díaz, J. Piedrafitá, J. Altarriba and L. Varona</i>	245

Session 22. Genomic selection in practice

Date: 1 September 2015; 14:00 – 18:00 hours
Chairperson: I. Misztal

Theatre Session 22

invited Challenges in dairy breeding under genomic selection <i>T.J. Lawlor, I. I. Misztal, Y. Masuda and S. Tsuruta</i>	245
Accuracy of genomic prediction using whole genome sequence data in White egg layer chickens <i>M. Heidaritabar, M.P.L. Calus, H.-J. Megens, M.A.M. Groenen, A. Vereijken and J.W.M. Bastiaansen</i>	246
Usage of genomic information to distinguish between full sibs in layer breeding schemes <i>M. Erbe, D. Caverro, R. Preisinger and H. Simianer</i>	246
Realized accuracies for males and females with genomic information on males, females, or both <i>D.A.L. Lourenco, B.O. Fragomeni, S. Tsuruta, I. Aguilar, B. Zumbach, R. Hawken, A. Legarra and I. Misztal</i>	247
Genetic evaluation for three way crossbreeding <i>O.F. Christensen, A. Legarra, M.S. Lund and G. Su</i>	247
Pedigree and genomic evaluation of pigs using a terminal cross model <i>L. Tusell, H. Gilbert, J. Riquet, M.J. Mercat, A. Legarra and C. Larzul</i>	248
Comparison of different Marker-Assisted BLUP models for a new French genomic evaluation <i>P. Croiseau, A. Baur, D. Jonas, C. Hozé, J. Promp, D. Boichard, S. Fritz and V. Ducrocq</i>	248
Genomics, sexed semen: changes in reproduction choices in French dairy herds <i>P. Le Mézec, M. Benoit, S. Moureaux and C. Patry</i>	249
Validation of single step genomic BLUP in field data <i>S. Wijga, A.M.F.M. Sprangers, R. Bergsma and E.F. Knol</i>	249
Approaches to improve genomic predictions in Danish Jersey <i>G. Su, P. Ma, U.S. Nielsen, G.P. Aamand and M.S. Lund</i>	250
Genotyping of cows improves the accuracy of genomic breeding values for Norwegian Red cattle <i>Ø. Nordbø, T.R. Solberg and T. Meuwissen</i>	250
Genomic testing of cows and heifers: An industry perspective <i>S.A.E. Eaglen, G.C.B. Schopen, L.I. Stoffelen, C. Schrooten, M.P.L. Calus, A.P.W. De Roos and C. Van Der Linde</i>	251
Overview of beef cattle national genomic evaluation in France <i>R. Saintilan, T. Tribout, M. Barbat, M.-N. Fouilloux, E. Venot and F. Phocas</i>	251

Poster Session 22

- Genome-wide association study for carcass traits in Nellore cattle 252
G.C. Venturini, R.M.O. Silva, D.G.M. Gordo, G.A. Fernandes Junior, B.O. Fragomeni, D.F. Diercles, F. Baldi, R. Espigolan, J.N.S.G. Cyrillo, M.E.Z. Mercadante and L.G. Albuquerque
- Genome wide association study of reproductive traits in Nellore heifers using Bayesian inference 252
R.B. Costa, G.M.F. Camargo, I.D.P.S. Diaz, N. Irano, M.M. Diaz, R. Carvalheiro, A.A. Boligon, F. Baldi, H.N. Oliveira, H. Tonhati and L.G. Albuquerque
- Genomic evaluation of milk production and fertility traits in Russian Holstein cattle 253
A.A. Sermyagin, E.A. Gladyr, S.N. Kharitonov, A.N. Ermilov, I.N. Yanchukov, N.I. Strekozov and N.A. Zinovieva
- Comparison of simulated dairy cattle breeding schemes for residual feed intake 253
S.E. Wallén and T.H.E. Meuwissen
- Predictability of parametric and semi-parametric models for meat tenderness in Nellore cattle 254
R. Espigolan, D.A. Garcia, D.G.M. Gordo, R.L. Tonussi, A.F.B. Magalhães, T. Bresolin, C.U. Braz, G.A. Fernandes Júnior, W.B.F. Andrade, R.M.O. Silva, L. Takada, L.A.L. Chardulo, R. Carvalheiro, F. Baldi and L.G. Albuquerque
- Genome-wide association study for carcass weight in Nelore cattle 254
G.A. Fernandes Júnior, R.B. Costa, D.A. Garcia, R. Espigolan, R. Carvalheiro, F. Baldi, G.J.M. Rosa, G.M.F. Camargo, D.G.M. Gordo, R.L. Tonussi, A.F.B. Magalhães, T. Bresolin, L.A.L. Chardulo and L.G. Albuquerque
- Identification of genomic regions associated with reproductive traits in Holstein-Friesian bulls 255
T.R. Carthy, K.E. Kemper, D.P. Berry, R.D. Evans and J.E. Pryce
- Analyses on the impact of foreign breed contribution on genomic breeding value estimation 255
A. Bunz, G. Thaller and D. Hinrichs
- GWAS on conception rate and milk production in different stages of lactation for first three parities in US Holsteins 256
S. Tsuruta, D.A.L. Lourenco, I. Aguilar and I. Misztal
- Database management of single nucleotide polymorphisms for use in Polish genomic evaluation 256
K. Żukowski, J. Makarski, K. Mazanek and A. Prokowski
- Performance of pedigree- and genome-based coancestries on selection programmes 257
S.T. Rodríguez-Ramilo, L.A. García-Cortés and M.A.R. De Cara
- Identification of epistasis by comparing SNP effects estimated based on EBVs and on phenotypes 257
T. Suchocki, A. Zarnecki and J. Szyda
- Strategies to reduce the bias of model reliability in genomic prediction 258
P. Ma, G. Su and M.S. Lund
- Implementation of a genomic selection program for Australian Merino Breed in Uruguay 258
G. Ciappesoni, F. Macedo, V. Goldberg and E.A. Navajas
- Impact of fitting dominance effects on accuracy of genomic prediction in layer chickens 259
M. Heidaritabar, A. Wolc, J. Arango, P. Settar, J.E. Fulton, N.P. O'sullivan, J.W.M. Bastiaansen, J. Zeng, R. Fernando, D.J. Garrick and J. Dekkers

- Genetic parameters for carcass and meat traits using genomic information in Nellore cattle 259
D. Gordo, R. Espigolan, R. Tonussi, A. Magalhães, G.A. Fernandes Júnior, T. Bresolin, W. Andrade, F. Baldi, R. Carvalheiro, L. Chardulo and L. Albuquerque

Session 23. Non-human-edible by-products: use and added value as feed material

Date: 1 September 2015; 14:00 – 18:00 hours

Chairperson: S. De Campeneere

Theatre Session 23

- invited* Animal feed and human food: competition and synergies 260
H. Steinfeld and A. Mottet
- How much meat should we eat – the environmental benefit of feeding food waste to pigs 260
H.H.E. Van Zanten, B.G. Meerburg, P. Bikker, H. Mollenhorst and I.J.M. De Boer
- Updating and renovating the INRA-AFZ multispecies feed tables 261
G. Tran, V. Heuzé, P. Chapoutot and D. Sauvant
- Protein digestion in broiler: what are the specificities induced by the protein source in the diet? 261
E. Recoules, H. Sabboh-Jourdan, A. Narcy, M. Lessire, G. Harichaux, M. Duclos and S. Réhault-Godbert
- Yield and amino acid composition of pulp and protein extracted and recovered from legumes and grass 262
V.K. Damborg, L. Stødkilde-Jørgensen, S.K. Jensen and A.P.S. Adamsen
- Nonstarch polysaccharide composition influences the energy value of grains and co-products 262
N.W. Jaworski and H.H. Stein
- Alternative protein sources for monogastrics: composition and functional assessment 263
S.K. Kar, A.J.M. Jansman, L. Kruijt, E.H. Stolte, N. Benis, D. Schokker and M.A. Smits
- Nutritional value of seaweed for ruminants 263
M.R. Weisbjerg, M.Y. Roleda and M. Novoa-Garrido
- Are byproduct feed systems appropriate for high producing dairy cows? 264
M. March, M.G.G. Chagunda, J. Flockhart and D.J. Roberts
- Testing a moist co-product for dairy cows consuming grass silage based diets 264
A.S. Chaudhry
- Systool Web, a new one-line application for the French INRA 265
P. Chapoutot, O. Martin, P. Nozière and D. Sauvant
- Recovery of cheese whey, a by-product from the dairy industry for use as an animal feed 265
E. El-Tanboly and M. El-Hofy

Poster Session 23

- Prediction of cold-pressed rapeseed cakes chemical composition using NIRS 266
I. Zubiria, E. Alonso, A. Garcia-Rodriguez and L. Rincón
- Insect or legume based protein sources to replace soybean cake in a broiler diet 266
F. Leiber, T. Gelencsér, H. Ayrle, Z. Amsler, A. Stamer, B. Früh and V. Maurer

Performance of pedigree- and genome-based coancestries on selection programmes*S.T. Rodríguez-Ramilo¹, L.A. García-Cortés¹ and M.A.R. De Cara²**¹Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria, Departamento Mejora Genética Animal, Crta. A Coruña Km. 7,5, 28040 Madrid, Spain, ²Museum National d'Histoire Naturelle, Laboratoire d'Eco-anthropologie et Ethnobiologie, 17 place du Trocadéro, 75116 Paris, France; rodriguez.silvia@inia.es*

Estimated breeding values (EBVs) obtained from high-density SNP chips have a higher accuracy than EBVs obtained from pedigree information. Additionally, these genome-based EBVs lead to lower increases in inbreeding compared with EBVs based on pedigree information. Using simulated data, we performed a pedigree-based BLUP and genomic BLUPs based on three different genomic coancestries: firstly, an estimate based on shared segments of homozygosity; secondly, an approach based on SNP-by-SNP count corrected by allelic frequencies; and thirdly, we used the identity by state methodology. We simulated a truncation selection scheme involving different population sizes, different number of genomic markers and different heritabilities for a quantitative trait. The performance of the four measures of coancestry is evaluated in terms of genetic gain, changes in coancestry and maintained diversity. Our results show that the genetic gain is very similar for all evaluated coancestries. However, genomic-based BLUPs are superior to BLUP based on pedigree information in terms of maintaining diversity. Furthermore, the coancestry measure based on shared segments seems to provide slightly better results in terms of genetic gain under some scenarios and the increase in inbreeding and loss in diversity is only slightly larger with selection based on this coancestry measure than in the other genome-based measures. Our results show that genome-based information can maintain more diversity without losing genetic gains, and thus secure the future success of selection programmes.

Identification of epistasis by comparing SNP effects estimated based on EBVs and on phenotypes*T. Suchocki¹, A. Zarnecki² and J. Szyda¹**¹Wroclaw University of Environmental and Life Sciences, Department of Genetics, Koźuchowska 7, 51-631 Wroclaw, Poland, ²National Research Institute of Animal Production, Institute of Animal Breeding and Genetics, Krakowska 1, 32-083 Kraków, Poland; tomasz.suchocki@up.wroc.pl*

In genomic selection of dairy cattle pseudo-phenotypes in form of deregressed breeding values are widely used for the estimation of SNP effects. From the nature of the dependent variable use in the model, SNP estimates largely express the additive genetic contributions of the genomic regions marked by them, which is plausible from the breeding perspective. However, from the genetic perspective, such estimates are biased since they lack the dominance and epistatic components. A reliable detection of dominance and epistasis using conventional statistical models suffers from lack of power and a very high dimensionality due to a very large number of possible SNP pairs (in case of a two-locus epistasis) to consider. Therefore, the major goal of this study is the comparison of SNP effects estimated for the Polish Holstein-Friesian dairy cattle using bulls' EBVs and using cows' phenotypes. Differences in effects estimated by both data sets indicate the presence of dominance and/or epistasis within the genomic regions, which can then be formally tested using model comparison criteria. The data set consisted of 3,438 proven bulls and 2,172 cows. Each animal was genotyped using 54K Illumina Bead Chip. Genotypic data was edited based on technical quality of the chip by removing single nucleotide polymorphisms with call rate lower than 95%. In our analysis milk, fat and protein yield, somatic cell score and the non-return rate of heifers were considered. To estimate of the additive effects of SNPs a SNP-BLUP model was used. Using this model two evaluations separately for bulls and cows were carried out. Finally, statistical significance of the particular SNP estimates and genomic region estimates were compared between these two data sets in order to detect regions of nonadditive contribution to the analysed phenotypes.