



HAL
open science

A comparison of various methods for the computation of genomic breeding values in French Lacaune dairy sheep breed

Christèle Robert-Granié, Sandrine Duchemin, Helene H. Larroque, Guillaume G. Baloche, Francis F. Barillet, Carole Moreno-Romieux Moreno, Andres Legarra, Eduardo Manfredi

► To cite this version:

Christèle Robert-Granié, Sandrine Duchemin, Helene H. Larroque, Guillaume G. Baloche, Francis F. Barillet, et al.. A comparison of various methods for the computation of genomic breeding values in French Lacaune dairy sheep breed. 62. Annual Meeting of the European Federation of Animal Science (EAAP), Aug 2011, Stavanger, Norway. Wageningen Academic Publishers, Abstract, p. 346, 2011, 978-90-8686-177-4. hal-02802283

HAL Id: hal-02802283

<https://hal.inrae.fr/hal-02802283>

Submitted on 5 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

A comparison of various methods for the computation of genomic breeding values in french lacaune dairy sheep breed

Robert-Granie, C., Duchemin, S., Larroque, H., Baloche, G., Barillet, F., Moreno, C., Legarra, A. and Manfredi, E., INRA, UR631-SAGA, 31326 Castanet-Tolosan, France; christele.robert-granie@toulouse.inra.fr

Genomic selection refers to selection based on genomic breeding values (GEBV), where the genomic breeding values are calculated from marker effects located across the whole genome. This study evaluated several statistical methods for predicting SNP effects for genomic selection. The methods included GBLUP ; a Bayesian approach -BayesC π - used stochastic search variable selection for all SNPs ; the Partial Least Squares (PLS) and Sparse PLS (sPLS) regression, which reduce the number of variables in the final model and select the most important variables for the sPLS. We compared the ability of these methods to accurately predict GEBV in actual dairy sheep data set containing 2,651 AI rams, born between 1998 and 2009 and genotyped for 44,131 SNPs. These approaches were applied to estimate GEBV for milk production traits, somatic cell score and udder morphology traits. Phenotypes used for this study were DYD (Daughter Yield Deviations) corresponding to the average performance of a sire's daughters, adjusted for fixed and non genetic random effects and for the additive genetic value of their dam. DYD were weighted by their variance which is a function of the sire's Effective Daughters Contribution (EDC). Validation populations containing 666 young AI rams born in 2007 and 2008 were used to assess the accuracy of the GEBV by comparing the estimated GEBV with the DYD. The weighted correlation between GEBV and observed DYD was computed using EDC as weights. The genomic approaches tested in this study produced similar accuracies of the GBLUP method (results presented in another French paper and showing a better correlation between GEBV and observed DYD compared with pedigree-based BLUP). The accuracies of the genomic method were not significantly different for most traits.

Implementation of BLUP breeding values estimations into breeding programs for sheep in Slovakia and Czechia.

Milerski, M.¹, Margetin, M.^{2,3} and Oravcová, M.³, ¹Research Institute of Animal Science, Přátelství 815, 104 00 Prague 10 - Uhřetěves, Czech Republic, ²Slovak University of Agriculture in Nitra, Tr. A. Hlinku 2, 949 76 Nitra, Slovakia (Slovak Republic), ³Animal Production Research Centre Nitra, Hlohovecká 2, 951 41 Lužianky, Slovakia (Slovak Republic); m.milerski@seznam.cz

While in the Czech Republic (CR) sheep husbandry is focused mostly on heavy lamb production, in the Slovak Republic (SR) predominantly dairy sheep are kept. Due to different specializations of production also different breeding programs are used in SR and CR. In the SR the highest attention is paid to estimation of breeding values (BVs) for milk yield and milk components. In Improved Valachian and Tsigai populations the BVs are estimated by the multitrait test-day BLUP Animal Model methodology, while in less numerous breeds Lacaune and Eastfriesian and in population of hybrids the single-trait whole lactation approach is applied. Additionally BVs for litter size and lamb weight at weaning are estimated. In the CR breeding values have been estimated by the use of BLUP methodology since 2003. In the year 2010 totally 16 breeds were involved. BVs for lamb weight at the age of 100 days (both direct and maternal genetic effects) and for litter size are estimated for all breeds. Additionally BVs for eye-muscle depth and back-fat thickness measured by ultrasound are estimated for terminal sire breeds (Suffolk, Charollais, Texel, Oxford Down, German Blackhead) and Romney. Program of estimation of BVs for milk traits is being implemented into practice currently. In both countries the main obstacle for the BVs estimations is very low level of AI usage resulting in limited amount of relationship connectedness between flocks. Also lack of links between performance recording databases in different countries and shortage of initial information about breeding animals in a case of their import are considered by sheep breeders as a serious problems especially in dairy sheep.

Book of Abstracts of the 62nd Annual Meeting of the European Federation of Animal Science



**Book of abstracts No. 17 (2011)
Stavanger, Norway
29 August - 2 September 2011**