

**In breeding, effective population size and coancestry on Latxa dairy sheep breed***I. Granado-Tajada<sup>1</sup>, S.T. Rodríguez-Ramilo<sup>2</sup>, A. Legarra<sup>2</sup> and E. Ugarte<sup>1</sup>**<sup>1</sup>NEIKER-Tecnalia, Basque Institute of Agricultural Research and Development, Department of Animal production, Agrifood Campus of Arkaute s/n, E-01080 Arkaute, Spain, <sup>2</sup>INRA, UMR 1388 GenPhySE, Chemin de Borde Rouge, 31326 Castanet Tolosan, France; [igranado@neiker.eus](mailto:igranado@neiker.eus)*

Traditionally, inbreeding estimates have been estimated based on pedigree information. However, in sheep there is a considerable proportion of unknown pedigree due to natural mating and limited use of paternity analysis. Therefore, there is an under estimation of inbreeding coefficients based on pedigree. In the genomics era, genomic information can be used to estimate inbreeding. In this study, three different inbreeding estimation methods were assessed (a pedigree-based methodology, a single SNP-based approach and a method based on runs of homozygosity, (ROH) to analyse the genetic diversity of three populations of Latxa dairy sheep: Latxa Cara Rubia (LCR) and Latxa Cara Negra from Euskadi (LCNEUS) and from Navarre (LCNNAF). A total of 981 animals were genotyped with the Illumina OvineSNP50 BeadChip, bringing around 41,200 SNPs and 4,468 animals in pedigree. The results found for LCNEUS and LCNNAF showed an effective population size ( $N_e$ ) below 100 when inbreeding coefficients were estimated based on pedigree or ROH:  $N_e$  PED=64,  $N_e$  ROH=86 for LCNEUS, and  $N_e$  PED=53,  $N_e$  ROH=66 for LCNNAF. Nevertheless, SNP based estimations yielded higher values:  $N_e$  SNP=282 and 153 for LCNEUS and LCNNAF, respectively. LCNEUS showed a higher genetic diversity than LCNNAF in any of the evaluated methods. There were differences between pedigree and ROH based results and the SNP based ones, possibly due to the reduced number of genotyped animals. In the case of LCR, which historical importation of semen from the French Manech Tête Rousse (MTR) has avoided the increase of inbreeding per generation, the estimation of effective population size was meaningless. For this breed a study of coancestry between the two breeds has been done, based on pedigree and genomic data, to analyse the evolution of genetic variability. Both methods have reflected, as expected, the important effect on inbreeding and genetic variability of introducing animals from another close breed.

**Bias, slope and accuracies of genetic evaluation of milk yield in Manech dairy sheep***F.L. Macedo<sup>1,2</sup> and A. Legarra<sup>2</sup>**<sup>1</sup>FVet-UdelaR, Lasplacas 1550, 11600, Uruguay, <sup>2</sup>INRA, UMR 1388 GenPhySE, 31326 Castanet Tolosan, France; fernando.macedo@inra.fr*

The recently presented method Linear Regression (LR), was proposed to benchmark models in genetic selection schemes. The principle of the method is to estimate biases and accuracies comparing estimated breeding values (EBVs) obtained from a partial data set (with old records, EBVp) and from a whole data set (with the addition of new records, EBVw). In this study, we estimate  $\mu_{wp}$  (the bias or difference between average EBVp and TBV, with an expected value of 0),  $b_{wp}$  (the slope of regression of TBV on EBVp, with an expected value of 1) and  $\rho_{pw}$  (inversely proportional to increase in accuracy from 'partial' to 'whole') for Manech Tete Rousse dairy sheep. Pedigree contains 540,986 individuals born from 1950 to 2017 and the phenotypic data file includes milk production of 1,842,295 lactations. No marker data was used. The model used to estimate breeding values includes five fixed effects as well as the permanent effect for milk production. The heritability used was 0.30. The model takes account of heterogeneous residual variances and genetic groups. The comparisons involved parent average EBV of rams born from 2005 to 2015 (as EBVp) and results from first daughters (as EBVw). Finally, we obtained statistic from 11 pairs of EBVp-EBVw. The mean (mean  $\pm$  standard error) of  $\mu_{wp}$ , expressed in genetic standard deviation of trait, was  $0.26 \pm 0.03$  and the mean of  $b_{wp}$  was  $0.80 \pm 0.09$ , indicating a larger bias. On other hand, the mean of  $\rho_{pw}$  was  $0.51 \pm 0.04$ ; in other words, accuracy doubles with first progeny performance. As conclusion, Manech Tete Rousse parent average EBVs are over dispersed for unknown reasons. Work financed by the ARDI project of Poctefa program (European Union FEDER funds), Metaprogram GENSEL (INRA) and La Region Occitanie.

**Is it worth to change from lactational to test-day genetic evaluation model in Latxa dairy sheep?***C. Pineda-Quiroga and E. Ugarte**NEIKER-Tecnalia, Basque Institute of Agricultural Research and Development., Animal Production, Agrifood Campus of Arkaute s/n, E-01080 Arkaute, Spain; cpineda@neiker.eus*

Genetic evaluation for milk production and composition in the Latxa breed has been based on 120-days standardized lactation records so far. This methodology requires at least three morning test day records (TD) per ewe taken at different lactation stages, the first of which must have been taken 70 d or less after lambing. A time interval between TD shorter than 35 d is also needed. Otherwise, lactation is not calculated and genetic evaluation of ewes that do not meet these requirements is lost. In the case of the Latxa sheep, these losses represent around 25% on average per year. In contrast, every TD record on each ewe is directly used in TD model analysis after filtering abnormal measures, regardless the recording schemes, making it possible to predict the genetic merit of a greater number of animals. The current study aims at comparing the Estimated Breeding Values (EBV) obtained under lactational (LC) and TD models for milk yield, protein and fat percentage and yield of Latxa Cara Rubia (LCR), Latxa Cara Negra from Euskadi (LCNEUS) and from Navarre (LCNNAF), as well as the reliability ( $r$ ) of EBV. To do so, 120-day standardized lactational data and TD records from LCR and LCNEUS were collected between 2000 and 2017, while LCNNAF comprised years 2002 to 2017. For TD, milk recordings were considered as a repeated measure of the same trait. The contemporary group herd-year-month of lambing (HYM) and herd-test day (HDT) were respectively fitted for LC and TD models. As expected, TD allowed the evaluation of fairly more animals than LC model: 4.469 additional ewes in LCR, 9.368 in LCNEUS and 1.259 in LCNNAF. As regards EBV, Pearson correlation showed a significant correlation between models for all evaluated traits ( $R^2 > 0.95$ ,  $P < 0.001$  in all ecotypes), indicating that estimated values of both models are highly comparable. It was also noted an increase of about 9% in  $r$  of fat percentage, and 4% of protein percentage in both LCR and LCNEUS when TD was tested. In light of the present findings, we might infer that it is suitable to implement the TD model in Latxa genetic evaluations.

**Heat stress response in sheep populations under different climatic and productive schemes**

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One of the challenges of the project 'Innovation for sustainable sheep and goat production in Europe (iSAGE)' is to deal with extreme weather events. In particular, heat stress is expected to have a growing negative impact on sustainability because of climate change. In this study, we aimed at the quantification of response to extreme weather events in three dairy sheep breeds, raised under different climatic conditions and productive systems in Spain. Historic milk recording and AI results data (from 10+ years) provided by Assaf (As), Latxa (Lx) and Manchega (Mn) breed associations were joined with weather information from close to farms weather stations. Statistical models used to quantify productive and reproductive response to extreme thermal loads (TLs) included cubic regressions of daily milk yields or AI results on the date of recording and environmental noise effects (Flock and year of lambing, parity number and lactation stage at recording and prolificacy). Comfort regions differed for breeds from temperate vs warmer climate conditions and across traits. Heat stress thresholds were highest for milk yield and for Mn and As breeds (25 °C in Mn and Ass vs 20 °C in Lx) and lowest for fat yield (22 °C for Mn vs 18 °C in Lx). For the heat stress region, maximum losses for milk/fat/protein yields ranged from -22/-3/-2 g/day and °C over max daily TL (30 °C) for the highest producing, intensively raised As breed to -6/-1.1/-0.3 g/day and °C above max daily TL (25 °C) for Lx local sheep breed raised under semi-extensive conditions. Fertility loss was around -1.6% unit of AI success/°C above max TL for both As and Mn breeds. Both productive level and climate conditions of origin of the breed seem to determine the response to high heat loads in sheep breeds.