



**HAL**  
open science

## Inbreeding and effective population size on Latxa dairy sheep breed

I. Granado-Tajada, Silvia Teresa Rodríguez-Ramilo, Andres Legarra, E. Ugarte

► **To cite this version:**

I. Granado-Tajada, Silvia Teresa Rodríguez-Ramilo, Andres Legarra, E. Ugarte. Inbreeding and effective population size on Latxa dairy sheep breed. 70. Annual Meeting of the European Federation of Animal Science (EAAP), Aug 2019, Gant, Belgium. hal-02734142

**HAL Id: hal-02734142**

**<https://hal.inrae.fr/hal-02734142v1>**

Submitted on 2 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.

## INBREEDING AND EFFECTIVE POPULATION SIZE ON LATXA DAIRY SHEEP BREED

Granado-Tajada<sup>1</sup>, I., Rodríguez-Ramilo<sup>2</sup>, S.T., Legarra<sup>2</sup>, A. and Ugarte<sup>1</sup>, E.

<sup>1</sup>Departamento de producción animal, NEIKER-Tecnalia, Instituto Vasco de Investigación y Desarrollo Agrario, Campus Agroalimentario de Arkaute s/n, E-01080 Arkaute, Spain. <sup>2</sup>INRA, UMR 1388 GenPhySE, 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 41200 SNPs and 4468 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 is an evident difference 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 Rouse (MTR) has avoided the increase of inbreeding per generation, the estimation of effective population size is 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.

**Keywords:** Inbreeding, Effective population size, ROH, Pedigree, Sheep.