

The ARDI2 project: harmonisation and cooperation toward a cross-border breeding programme involving Latxa and Manech dairy sheep breeds

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Latxa and Manech, each one with their black and red variation, are similar dairy sheep breeds raised in the Spanish (Latxa Cara Negra/LCN and Latxa Cara Rubia/LCR) and French (Manech Tête Noire/MTN and Manech Tête Rousse/MTR) Basque country. Their breeding programs have been run separately until now. However, increasing exchanges of germplasm, insemination doses in majority, have occurred over the last 20 years, mainly from France to Spain. ARDI2 is an INTERREG project (EFA032/01), which intends to harmonise the genetic tools across Latxa and Manech and aims at creating a common selection program between these breeds. A recent previous project (ARDI, EFA208/16) led to the creation of the so-called ARTALDEAN European Economic Interest Grouping cross-border organisation, whose purpose is to discuss the breeding decisions and selection objectives of both populations.

The ARDI2 project (2024-2026) develops several tasks targeting a greater harmonisation and cooperation between Latxa and Manech selection programs. The consolidation of ARTALDEAN to move towards a greater integration of these programs is grounded on increasing the professional and technical relationships, strengthening the genetic connections between populations and harmonising the standard and udder morphology criteria. An international genomic evaluation will be tested and deployed as a major step toward a common breeding program. Besides, management of existing genetic variability will be strengthened through the development of new tools valorising genomic data. New sustainability related traits, relevant in the context of climate change, will be studied for future incorporation in the breeding schemes (methane emissions, thermotolerance, longevity). A last task is dedicated to support the incorporation of innovations and the incorporation of new technologies and societal requirements into the improvement programs.

The across-country genomic evaluation task will extend the work accomplished in the SMARTER project (H2020-no.772787). It will be developed for milk, fat and protein yield and content and udder morphology traits. A bi-trait model will be applied to the raw phenotypes, each country keeping its own model for the fixed effects. The genetic connection between countries is based on 452 and 1,274 common animals present in the pedigree of both countries, in LCN/MTN and LCR/MTR respectively. Genotypes from 813 LCN, 1,075 MTN, 1,982 LCR, and 6,605 MTR obtained from Illumina and

Abstract

Affymetrix platforms will be aligned and cleaned at Interbull Centre through the GenoEx platform, which has been adapted to sheep in the framework of ARDI2. Interbull Centre will also provide genotypes ready for genetic evaluation through the adaptation of existing pipelines for the imputation stage. Hence, this project displays a good example of the extension of common tools built within ICAR/Interbull to other species than cattle.

Keywords: dairy sheep, international genomic evaluation, novel traits, Latxa breed, Manech breed, Interbull Centre.

Introduction

Dairy sheep farming has an undeniable economic, social and environmental value in Spanish and French Pyrenees. Latxa and Manech breeds, each one with their black and red variation, are similar dairy sheep breeds raised in the Spanish (Latxa Cara Negra/LCN and Latxa Cara Rubia/LCR) and French (Manech Tête Noire/MTN and Manech Tête Rousse/MTR) Basque country. Due to historical, geographical and administrative barriers, their breeding programmes have been run separately until now. However, increasing exchanges of germplasm, insemination doses in majority, have occurred over the last 20 years, mainly from France to Spain. A recent previous project (ARDI, EFA208/16, 2018-2021) was dedicated to start building tools to move towards a unification of the breeding programmes and led to the creation of the so-called ARTALDEAN European Economic Interest Grouping cross-border organisation, whose purpose is to discuss the breeding decisions and selection objectives of both Latxa and Manech populations. ARDI2 is a current Interreg POCTEFA project (EFA032/01, 2024-2026), which intends to continue the harmonisation of genetic tools across Latxa and Manech and aims at creating a common selection programme between these breeds.

Different tasks to harmonise selection tools in Latxa and Manech breeds

The aim of ARDI2 is to provide ARTALDEAN with materials and tools and make it a benchmark in the implementation of Latxa and Manech improvement programmes in the Navarra, Euskadi and Aquitaine regions covering the Basque territory and to optimise the common management methodology of these programmes. To this end, new international genomic evaluation models is defined, designing new protocols based on those existing in cattle, and new methodologies are proposed to analyse how genetic exchanges through artificial insemination have influenced the genetic variability of the breeds and to include new traits that improve the sustainability of the dairy sheep systems. In addition, new digital technologies are incorporated and implemented within the selection schemes to increase the competitiveness of the farms and the agroecological characteristics of the breeding programme are studied.

To achieve these objectives, the ARDI2 project (2024-2026) develops several tasks targeting a greater harmonisation and cooperation between Latxa and Manech selection programmes (Figure 1).

The consolidation of ARTALDEAN to move towards a greater integration of the selection programmes is grounded on favouring and increasing the relationships between Latxa and Manech breeders and technicians, strengthening the genetic connections between populations and harmonising the standard of the breeds and the udder morphology criteria.

An international genomic evaluation will be tested and deployed as a major step toward a common breeding programme. Besides, management of existing genetic variability will be strengthened through the development of new tools valorising genomic data.

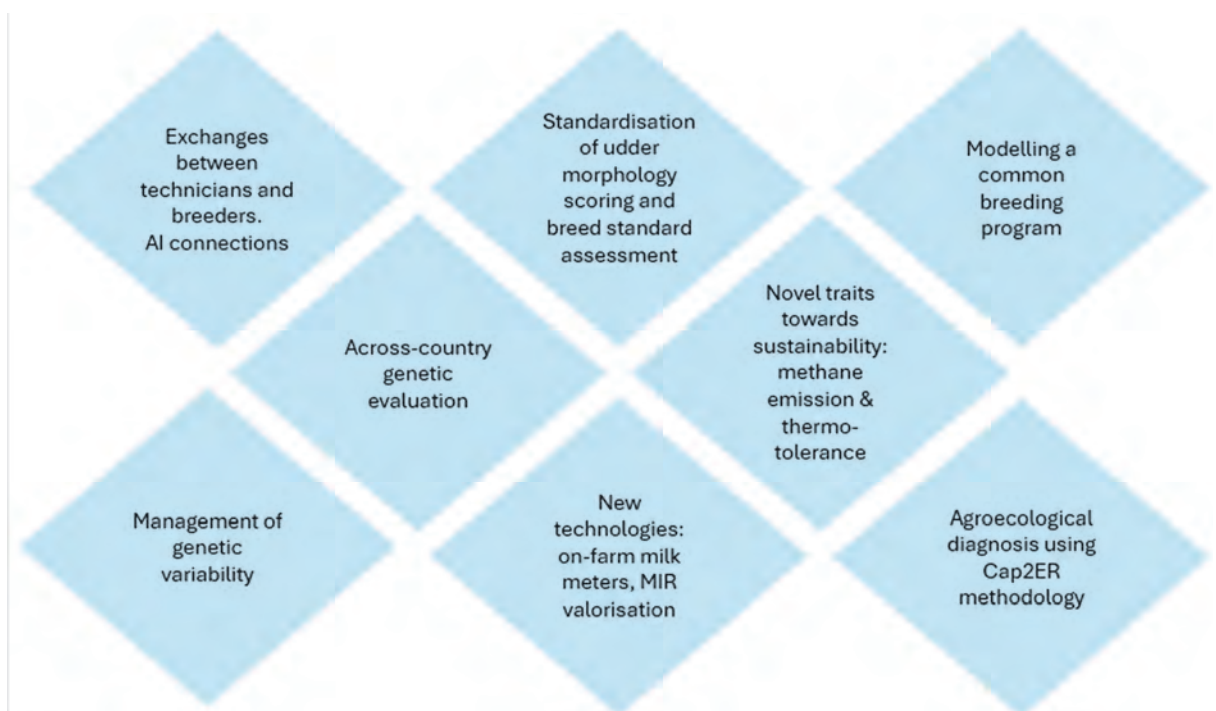


Figure 1. The different tasks addressed in ARD12

New sustainability-related traits, relevant in the context of climate change, will be studied for future incorporation in the breeding schemes (methane emissions, thermotolerance, longevity).

A last task is dedicated to support the incorporation of innovations and the integration of new technologies and societal requirements into the improvement programmes.

Among the tasks undertaken in ARD12, 4 are closely related to ICAR topics of interest:

- The across-country evaluation between Latxa and Manech will be addressed below.
- Measurement of methane emission is tackled with the purpose of merging in the future Spanish and French phenotypes. In Latxa breed, methane emissions are measured with sniffers whereas in Manech breed, greenhouse gases emissions are measured with portative accumulation chambers (PAC). The aim is to make measurement on the same day on the same animals both with the sniffers and the PAC to compare both measurements and assess whether it will be possible to mix the French and Spanish measurements in a transnational evaluation.
- Daily measures of milk yield using the ARG1 milk meter, recently certified by ICAR for sheep and goats (in high line), will be studied. The objective is to use the data for milk recording but also to assess resilience of sheep by discovering challenges along the milking period and identifying the ewes that better cope with the challenge.

- The MIR spectra valorisation. A reference population has been built in France from French breeds milk samples (MIR spectra and reference analyses) to predict fine components and more complex phenotypes. The objective is to strengthen the reference population by adding more milk samples from Latxa breed to improve the accuracy of the predictions with a greater variability of milk. Meanwhile, this task allows to involve the Spanish laboratories and breeding organisations in the different steps of valorisation of MIR spectra (extraction, storage and standardisation of MIR spectra, engineering of prediction).

Towards a transnational genomic evaluation

The across-country genomic evaluation task will extend the work accomplished in the SMARTER project (H2020-no.772787) (Garcia-Baccino *et al.*, 2022). It will be developed for milk, fat and protein yield and content and udder morphology traits. A bi-trait model will be applied to the raw phenotypes, each country keeping its own model for the fixed effects. The genetic connection between countries is based on 452 and 1,274 animals present in the pedigree of both countries, respectively in LCN/MTN and LCR/MTR. Genotypes from 813 LCN, 1,075 MTN, 1,982 LCR and 6,605 MTR obtained from Illumina and Affymetrix platforms will be aligned and cleaned at Interbull Centre through the GenoEx platform, which has been adapted to sheep in the framework of ARDI2. Interbull Centre will also provide genotypes ready for genetic evaluation through the adaptation of existing pipelines for the imputation stage (see section below).

Regarding genotypes, a specific work was realised to identify the correspondence between SNP names of Illumina and Affymetrix. This comparison was done between the Illumina OvineSNP50 Beadchip v1 (54,241 SNP) and the Affymetrix Axiom™ Ovine Genotyping Array 50K. As all other arrays are from Illumina, it was decided to keep the Illumina SNP names. As a result, a list of 38,516 SNPs of the Affymetrix chip was found having a clear correspondence with the Illumina nomenclature. These 38,516 SPNs were used as the “customised Manifest File” uploaded to GenoEx platform.

Regarding phenotypes and pedigree, we will use the format files produced by the SMARTER project and based on the international ID defined by Interbull (breed on 3 digits + country on 3 digits + sex on 1 digit + animal ID on 12 digits). The pedigree file includes the animal, sire and dam international IDs, the birth date, and the animal, sire and dam corresponding national IDs. The phenotype file (one line per animal x trait) includes the following data: trait name, breed, international ID, flock, dependent variable, weight of performance, list of the recoded levels of the environmental effects. We also produce a parameter file that describes, for each trait and breed, the heritability, the animal permanent environmental effect, the number of environmental effects included in the national model, the environmental effects recoded and the type of effects (contemporary group, fixed, covariate, random).

Sheep GENOEX: a useful tool illustrating the possible extension of Interbull to other species than cattle

Within the ARDI2 project, we set up a cooperation with Interbull Centre to use the tools already developed in cattle to store, clean, align and impute genotypes from different countries and different platforms of genotypings. Interbull Centre therefore provides a genotype file ready to be used for the transnational evaluation in ARDI2. For this purpose, the GenoEx platform was adapted to sheep as a “Sheep GenoEx” that allowed to upload all the Manech and Latxa genotypes. Latxa genotypes comes from both by Illumina and Affymetrix platform (mid density chips), while Manech genotypes only comes from by Illumina platform (low and mid density chips). The Manifest File of the

Affymetrix chip was uploaded on Sheep GenoEx with the SNP names of the Illumina chips to have an unequivocal correspondence across all chips.

A reference map is being proposed, based on the Illumina 50K v1. As allele frequencies obtained for Latxa breed are expected to be similar across SNPs panels (Illumina and Affymetrix), a simple comparison by plotting allele frequencies allowed to detect some SNPs with unusual behaviour across panels, that will not be included in the reference map for imputation. The final choice of the reference map panel should be made in autumn 2025 to provide the imputed file.

In addition, the IDEA (Interbull Data Exchange Area) platform was also adapted to sheep to permit uploading Manech and Latxa pedigrees related to the uploaded genotypes. The pedigrees will also be used for the imputation phase.

The imputation pipeline currently used in the Interbull InterGenomics service has been adapted to accommodate sheep data. The programme used for imputation is Findhap (created by Paul vanRaden at USDA). The pipeline has been made flexible to adapt the reference map as desired. The preliminary results of the imputation of sheep genotypes gave accurate results, the final file to be used for genomic evaluation should be released by September 2025.

This project displays a good example of the extension of common tools built within ICAR/Interbull to other species than cattle. The adaptation of GenoEx to sheep and the use of the imputation pipeline in sheep might be useful in the future for other sheep breeds interested in sharing genotypes for an multi country genomic evaluation or other species such as goats.

The results of ARDI2 will strengthen the dairy sheep farming sector on both sides of the border and will allow both sheep farmers and the territory itself to benefit from improvements in the competitiveness of the indigenous Latxa and Manech breeds. It also constitutes a good example of convergence of across-country breeding programmes in sheep, with the required convergence of breeding tools such as phenotyping designs and calculation, and genetic evaluation. Moreover, the know-how acquired, and tools developed should ease the inclusion of other phenotypes of interest.

Various results from ARDI2 might be valorised within the ICAR community: measurement of methane emission, building of a multi country reference population for MIR spectra valorisation in sheep, use of daily milk yield data from on-farm milk meters, across-country evaluation. The task on across-country evaluation is an opportunity to adapt tools to other species than cattle in Interbull (sheep GenoEx, imputation pipeline). These tools could be used by other breeds / species in the future, provided that an economic model is defined. The establishment of a reference centre dedicated to small ruminants that might be constructed in the next years should help such initiative.

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Conclusion and perspectives regarding ICAR

Acknowledgements

List of references

Garcia-Baccino CA, Pineda-Quiroga C, Astruc JM, Ugarte E, Legarra A.
High genetic correlation for milk yield across Manech and Latxa dairy sheep
from France and Spain. JDS Commun. 2022 May 21;3(4):260-264. doi: 10.3168/
jdsc.2021-0195. PMID: 36338014; PMCID: PMC9623675