Genomic selection in Spanish dairy sheep breeds

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Abstract

This paper presents the situation of the implementation of genomic selection in Spanish dairy sheep breeds, both native and foreign. Although in all cases the methodology used is the same (ssGBLUP) and an increase in the reliability of the estimates is observed, the work shows the existing variability in the dimension of this increase (15-60 %), in the criterion of genotyping used in each of them (sex, number and type of animal) and in the characters and models used. Likewise, a reflection is made on the transfer of these results to farmers and on the expectations, contributions and methodological and organizational challenges associated with the implementation of genomic selection.

Introduction

With the development of molecular techniques, bioinformatics and evaluation methodologies, the implementation of genomic selection in breeding programs has been widespread, although at variable rates depending on the species and breed (Ibañez-Escriche and Gonzalez-Recio, 2011; Jonas and de Koning, 2015; Meuwissen *et al.,* 2016).

The International Sheep Genomic Consortium (ISGC, 2002) has facilitated the development of genomic tools in ovine, among them the OvineSNP50 BeadChip (Illumina Inc., San Diego, CA, USA) was released in 2009, bringing new perspectives for genomic selection implementation in sheep breeding programs. In comparison with dairy cattle, dairy sheep breeding has several differences that should be considered. The presence of a wide range of breeds, with environmentally adapted production systems, small population sizes, very heterogeneous data recording systems and a lower economic value per individual are some intrinsic characteristics that influence the implementation of genomic selection in sheep breeding programs (Ibanez-Escriche and Simianer, 2016).

Regarding Spanish dairy sheep breeds, in 2018 studies to assess the state of GS implementation were started in four breeding programs: Assaf, Churra, Manchega and Latxa (National Institute for Agricultural and Food Research and Technology or INIA, 2020). These works focused on analysing the selection criteria to make up the genotyped population and the development and implementation of genomic schemes. Among these breeds, three of them are autochthonous, being the Manchega breed the one with the bigger population (135.000 ewes), followed by Latxa breed (70.000 ewes) and Churra breed (23.000 ewes). Meanwhile, Assaf is a foreign breed that currently has 100.000 ewes. The main objective of this work is to gather the results obtained during the last lustrum among these breeds regarding the implementation of genomic selection, such as the variability in terms of prediction reliability, the genotyping criterion used and the selection objectives considered.

Material and methods

The genomic information available in these dairy sheep breeds has been funded by a project of the Spanish Ministry of Agriculture (2018-2022), regional projects and individual initiatives of breeder's associations. All the breeds have genotyped with the AxiomTM Ovine Genotyping Array (Thermo Fisher Scientific Inc., Waltham, MA, USA), and the Latxa breed also has some individuals genotyped with the OvineSNP50 BeadChip (Illumina Inc., San Diego, CA, USA). The Assaf breeds has the biggest genotyped population (more than 12.000 animals), followed by Manchega breed (6.000 animals), Latxa breed (3.700 animals) and Churra breed (3.000 animas). The distribution of these animals across sexes and presence/absence of phenotypic data is shown in Table 1.

Regarding the selection objectives considered by each breed, Assaf has implemented genomic selection for milk yield (120-d standardized lactation), milk quality (fat and protein), udder morphology and cell score. Latxa breed has implemented for milk yield (120-d standardized lactation), milk quality (fat and protein), and udder morphology; and Manchega for milk yield (test day) and udder morphology. Currently, the Churra breed carries on genotyping, but they has not jet implemented a genomic selection scheme. Besides, we are going to focus on the results obtained for milk yield in Assaf, Latxa and Manchega breeds.

The genomic evaluations of the three breeds are done with the single step genomic BLUP (ssGBLUP) methodology (Aguilar *et al.,* 2010; Christensen and Lund, 2010), performed using the BLUPf90 software suite (Misztal *et al.,* 2002).

Results and discussion

Among the studies done to assess the inclusion of genomic information in genetic evaluations, prediction accuracy of classic and genomic evaluations has been considered, the results for the three dairy sheep breeds are shown in Table 2. Assaf and Latxa show higher prediction accuracies because their selection criterion is milk yield in 120 days of lactation, while Manchega breed considers test day data. Comparing the two methodologies show in all cases that genomic evaluation is more accurate, so that including genomic information increases prediction accuracy from 3 to 14 %.

Furthermore, the reliability of classic and genomic evaluations has been analysed and mean results by sex, availability of phenotypic data and genomic information, and breed can be found in Table 3. The mean values are higher for Manchega breed, as a results of the selection criterion used, as previously described. Comparing both methodologies, reliability values of genomic evaluation are in all cases or similar or higher than pedigree evaluations. This difference is noticeable when the animals are genotyped, but it is especially relevant when the genotyped animals have not progeny data (young rams) or their own phenotypic data (young ewes).

Table 1. Distribution of genotyped individuals by sex and type, for Assaf, Churra, Latxa and Manchega breeds at June 2022.

	Assaf	Churra	Latxa	Manchega
Rams with progeny	3.034	272	1.593	1.902
Ewes with lactations	3.640	2.960	1.483	988
Young rams	4.749	95	592	3.093
Young ewes	927	37	46	57
Total	12.350	3.154	3.714	6.040

Table 2. *Prediction accuracy of milk yield pedigree and genomic evaluation and their difference (genomic-pedigree, G-P) for Assaf, Latxa (Cara Negra from Euskadi population) and Manchega breeds.*

	Assaf	Latxa	Manchega
Pedigree	0.77	0.57	0.54
Genomic	0.79	0.65	0.59
G-P	0.02 (3 %)	0.08 (14 %)	0.05 (9 %)

Table 3. *Prediction reliability of milk yield pedigree and genomic evaluation by sex and availability of phenotypic data and genomic information for Assaf, Latxa (Cara Negra from Euskadi population) and Manchega breeds.*

	Assaf		Latxa		Manchega	
	Pedigree	Genomic	Pedigree	Genomic	Pedigree	Genomic
Rams with progeny	56	56	63	64	70	70
Rams with progeny + geno	62	70	77	79	87	89
Ewes with lactations	43	43	63	63	60	60
Ewes with lactations + geno	50	61	72	75	63	66
Young rams	30	30	27	41	30	30
Young rams + geno	30	48	52	60	35	48
Young ewes	30	30	23	35	30	30
Young ewes + geno	30	49	53	58	30	40

Obtaining evaluations with higher prediction reliabilities allows taking selection decisions when rams have a lower number of progeny and ewes have less lactation data. For instance, to achieve 60 % reliability based on classic evaluation a mean of 14 progeny data per ram or 5/6 lactations per ewe are needed, while with genomic evaluations rams with 5 progeny data and ewes with 2/3 lactations already achieve that reliability value. Therefore, selection decisions are taken earlier, as can be easily seen in the age of the proved rams used in 2019 and in 2022: 56 and 46 months old, respectively. This decrease in the generation interval makes possible a quicker genetic progress and a higher genetic gain. In addition, when the genomic information is included in evaluations, as the Mendelian segregation is considered, it is possible to distinguish full sibs with the same pedigree index by classic evaluation, and thus more informed breeding decisions could be taken.

Future perspectives and challenges

Among the implementation challenges, here some of the methodological issues that have been identified:

- Mistakes in genealogy: Based on genomic information (SNPs) pedigree mistakes from microsatellites analysis could be revealed. Which should be the inconsistency threshold allowed?

- Modelling missing pedigree: Unknown parent groups work well on classic BLUP evaluations, but they are more problematic in genomic BLUP evaluations.

- Direct genomic values: Based on the pedigree index and the estimated SNP effects from genomic evaluations it is possible to estimate a direct genomic value, but how reliable are these values?

- Inflation of genomic values: It has been found especially in selection candidates, and has been already described (Harris *et al.,* 2011). The cause is not known, and currently it is being managed by the scaling of G and A matrixes (Martini *et al.,* 2018).

- Imputation from low density platforms to medium and high density, It is based on the existence of linkage disequilibrium (LD) between SNPs. In sheep breed the LD is very low, thus the imputation is highly inefficient

There are also some other points related with the profitability of the breeding program that have to be considered regarding the change to genomic selection:

- The cost of genotyping platforms could be profitable to continue genotyping at this scale?

- Do the increase in genetic gain make up for the genotyping cost?

- Low density platforms are more economical, it would be worth to genotyped some animals by this option?

- Genotyping platforms that allow unifying several analyses like filiation, scrapie and genomic evaluation could be useful to reduce costs.

- Incorporation of new characters (fertility, illness resistance, longevity, rusticity, adaptation to global warming, etc.) which improvement could make profitable the cost of genotyping platform.

Finally, the implementation of a genomic scheme implies several organizational matters that have to be reflexed to take decision from year to year:

- The maintenance of the reference population: It should be updated every year, but how much animals and what type of animals should be genotyped?

- When there are changes on the selection objectives, to select animals to enter the artificial insemination centre more animals have to be genotyped and phenotyped for the new characters?

- How would be possible to combine the genotyping for the program and for de farmer?

- It is highly relevant to organize the time, chronology and speed in obtaining genotyping results with technicians, farmers and laboratory routines.

Last but not least, it is essential to advice and explain technicians and farmers about the functioning of their genomic scheme to understand the relevance of their work and how important is the involvement of all the agents to achieve good result.

Conclusions

The inclusion of genomic information in Spanish dairy sheep routine genetic evaluations brings an important gain in prediction accuracy and the reliability of genetic values is higher than the obtained with classic evaluations. Moreover, taking more informed

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selection decisions earlier in the lives of animals gives the possibility to accelerate the genetic progress of the breeding program. There are some economic and organizations issues that have to be considered, but genomic selection is an interesting tool for Spanish dairy sheep breeds that will bring advantageous results and keep this breeds at the forefront of innovation.

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