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Goat genomic selection: Impact of the integration of genomic information in the genetic evaluations of the Spanish Florida goats

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ABSTRACT

Genomic evaluations have been proposed as a mean to improve the reliabilities of the estimation of breeding values. This hypothesis has been tested using 50,649 lactation records from 19,067 Florida goats, daughters of 4397 dams and 500 sires. A sample of 538 dams and 87 sires from the formerly described population were genotyped with the Illumina 55 K Goat Bead-Chip (53,347 SNP). Genetic parameters were estimated using the animal model and REML methodology comparing two approaches: (i) a classical approach with the BLUP methodology; and (ii) a single step (ss) approach with the single step genomic BLUP (ssGBLUP) methodology. The BLUPF90 software was used to obtain the genomic relationship matrix (**G**) and to estimate genetic parameters and breeding values. The results showed a correlation between **A** (pedigree relationship matrix) and **G** matrix of 0.826. When the full studied population was considered, no significant differences were observed between the estimations of the genetic parameters obtained with **A** and combined **A** and **G** matrices. The correlation between the EBV and GEBV was 0.989. An increment of 1.06% in the average reliability of the estimations was observed in the ssGBLUP vs. the traditional BLUP evaluation. When only the EBVs of the animals genotyped were compared, the correlation between the estimates obtained with both approaches decreased to 0.952, but with an increment of 5.86% of the average reliability of the GEBVs.

1. Introduction

The reliabilities of the estimated breeding values (EBV) obtained in the genetic evaluations of milk traits in the Spanish Florida breed of goats are generally low or moderate, mainly due to a sparse relationship matrix that does not allow to recognize connectedness among herds. Genomic evaluation (GE) has been proposed as a mean to improve these reliabilities. GE has been successfully used during the last decade in many of the national genetic evaluations of Holstein Friesian dairy cattle (Hayes et al., 2009) and it has been implemented for the genetic evaluation of other breeds in different species (Ibañez-Escriche and Gonzalez-Recio, 2011), including small ruminants (Shumbusho et al., 2013). Only the results of genomic evaluations carried out in France (Carillier et al., 2013, 2014), United Kingdom (Mucha et al., 2015) and Canada (Vermette et al., 2013) have been published until now.

Meuwissen et al. (2001) demonstrated that the increase in accuracy of genomic estimations of breeding values (GEBV) largely depend on the extent of linkage disequilibrium (LD) between the genes responsible

for the trait and the markers present in the bead-chip. The LD extent depends on when the selection occurred, and the intensity of the process. The regions affected very much depend of the traits under selection.

Thus, the aim of this work is to determine the benefit, of integrating genomic information into the current genetic evaluation of a Spanish goat breed (Florida breed) in terms of reliabilities of the EBVs for milk yield.

2. Material and methods

2.1. Animal material

The Florida is a native Spanish breed of dairy goats distributed mostly in the Centre and South of Spain, raised under a wide variety of systems of production, ranging from semi-extensive to semi-intensive systems. This breed has a census of 24,717 adult animals in 70 herds with 12,758 does in 42 herds in the selection nucleus (SN). The average

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Table 1
Description of the population subjected to genetic and genomic evaluations.

Variable	
N° of lactations:	41746
Does with lactations:	17907
Herds:	32
Does with several lactations:	11363
Bucks sires of does with lactations:	493
Mothers of does with lactations:	3909
Average duration of lactation:	221.8 ± 0.264
Does with lactations and mother known:	7216
Does with lactations and sire known:	8025
Average milk yield per lactation (Kg):	456.3 ± 1.081

milk yield in the SN is 682.7 kg (with 4.8% fat and 3.5% protein) in an average lactation of 271 days (ARCA, 2016).

2.2. Phenotypic and pedigree data

The original data set comprised 50,649 milk yields of complete natural lactations from 19,067 dairy goats of the Florida breed kidding between 1987 and 2013. Lactations longer than 300 days, and those animals that did not contribute to the genetic model (non informative animals) were removed. After data edition, the final data available for the genetic evaluation included 41,746 lactations from 17,907 does, (2.33 average lactations per goat), born out of 4189 mothers and 493 bucks in 32 farms, with 69.4% of them having more than one lactation recorded. Only 37.6% of the animals had both parents known, 37% had only mother known and 4.5% only father known. The total number of animals in the pedigree used for the genetic and genomic evaluations, once non-contributors to the model were pruned, was of 18,763 (Table 1).

2.3. Genotypic data

A sample of 625 animals (538 dams and 87 sires) from 25 flocks of the formerly described population were genotyped with the Illumina 55 K Goat Bead-Chip (53,347 SNP). SNPs with Call Rate < 0.90, monomorphic or with MAF < 0.05 were removed and animals with Call Rate < 0.90, with parent-progeny Mendelian conflicts or which do not contribute to model were eliminated. After the quality control 585 animals (514 dams and 81 sires) and 50,559 SNP per animal were used for the genomic evaluation. The average allele frequencies after quality control were of 0.509 ± 0.0009 with a MAF of 0.32 ± 0.12 .

2.4. Estimation of genetic parameters, breeding values and genomic breeding values

The animal model including herd-year-season and parity number-age at kidding as fixed effects, permanent environmental and additive genetic as random effects and days in milk as a covariate was used to obtain EBV (ACRIFLOR, 2015). Genetic parameters were estimated with REMLF90 of the family of BLUPF90 software (Misztal et al., 2002) using REML methodology. Genetic parameters were re-estimated using a REML under a single step approach and GEBV were obtained with the single step genomic BLUP (ssGBLUP), with the same model and software. The genomic relationship matrix (**G**) was created using Van Raden (2008) approach with preGSf90 program (BLUPF90 software):

$$G = 0.95 \frac{SS'}{2 \sum_{i=1}^n p_i(1-p_i)} + 0.05A$$

where, n is the number of SNP markers and p_i is the allele frequency of marker i , **A** is the pedigree relationship matrix, and **S** is a centered incidence matrix of SNP markers. In this study, an intermediate frequency (p_i) of 0.5 for all markers was used.

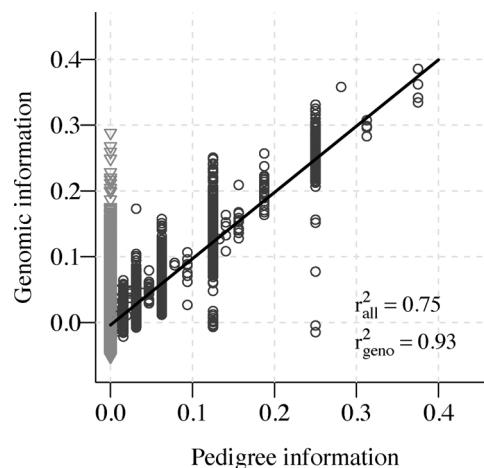


Fig. 1. Relationship between genomic and genealogical in the Florida goat population. Genotyped (black circles) and non-genotyped (light grey triangles) animals are plotted. Correlations between genomic and genealogical kinship for the whole population (r^2_{all}) and genotyped animals (r^2_{geno}) are showed.

3. Results and discussion

The overall correlation between elements of matrices **A** and **G** was 0.826; the correlation between off-diagonal elements 0.943; and the correlation between diagonal elements 0.75. The mean autozygosity estimates by the diagonal elements of **G** matrix (F genomic) was 2% (ranging from 0 to 30.6%). In Fig. 1 the relation between genomic and genealogical kinship is represented. When animals without genealogical information are removed the overall correlation between elements of **A** and **G** rises to 0.934. We can also observe the dispersion of genomic kinships in animals with the same genealogical kinship. As it is well known, **A** represents an expectation depending upon how you can trace back the pedigree. Thus, genealogical kinship measures the identity-by-descent (IBD) while the genomic kinship is a realization and measures the identity-by-state (which includes IBD besides the alleles present at founders level) between each pair of animals.

The present study has addressed, for the first time, a genomic evaluation for milk yield in a Spanish goat breed (the Florida breed), estimating of genetic variance components and comparing breeding values with those obtained with the classical BLUP approach. While no significant differences between the estimations of the genetic parameters derived from the use of the **A** (classical approach) or **G** (single step approach) matrices were observed (Table 2), a moderate increase in the reliabilities of the estimates of breeding values was obtained using the single step genomic evaluation genomic (ssGBLUP), approach.

Table 2

Genetic parameter estimates for milk yield (Kg/lactation) obtained by ssGREML and REML in the whole population of Florida goats.

	ssGREML	REML
AIC	508249.1	508287.9
σ_a^2	2,604.2 ± 19-9.1	2,672.4 ± 201.6
σ_{pef}^2	2,922.8 ± 19-0.1	2,876.6 ± 192.4
σ_{res}^2	9,732.5 ± 88-.2	9,731.1 ± 88.2
h^2	0.171	0.175
t	0.362	0.363

AIC: Akaike Information Criterion.

σ_a^2 : additive genetic variance; σ_{pef}^2 : Permanent environmental variance; σ_{res}^2 : Residual variance.

h^2 : heritability; t: repeatability.

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