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Genetic progress attained in the selection program of Florida breed of goats in Spain

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Abstract. The objective of this work was to estimate the genetic progress reached with the breeding program of the Florida breed of goats. The genetic progress attained has been estimated analysing a data base containing 273,600 test day records of dairy traits (milk, fat and protein yield) and a pedigree data base with 17,991 records, both registered in 27 herds from January 2003 until March 2012. A random regression model was used for the analysis. A large heterogeneity of the genetic covariance components of the previous traits was observed throughout the lactation curve. The estimated breeding values (EBV) obtained for the animals born each year were used to compute the genetic progress. A significant positive genetic tendency was observed for all traits studied. Animals born in 2010 have an average EBV for fat plus protein yield in 245 days lactation (the main selection objective in this breed) 4.05 kg higher than that of the animals born in 1999. This figure is equivalent to the fat plus protein yield cumulated during 21 days.

Keywords. Dairy goat – Genetic trends – Selection – Regression analysis.

Le progrès génétique atteint dans le programme de sélection de la race caprine Florida en Espagne

Résumé. *L'objectif de ce travail était de vérifier le progres génétique obtenus dans le programme de sélection de la race caprine Florida. La Florida est une race autochtone située dans le sud-ouest de la péninsule ibérique avec un recensement de 19.418 femelles reproductrices. Le progrès génétique obtenu a été estimé a travers l'analyse d'une base de données contenant 273.600 données du jour de contrôle des traits laitiers (rendement du lait, de la graisse et des protéines) et une base de données généalogique avec 17.991 enregistrements, les deux enregistrés dans 27 troupeaux du démarrage du programme de sélection de la race en Janvier 2003 à Mars 2012. Un modèle de régression aléatoire a été utilisé pour l'analyse. Une grande hétérogénéité des composantes de covariance génétique de la forme de la lactation l'avant mentionné traits a été observée tout au long de la courbe de lactation. Une importante composante génétique de la forme de la courbe de lactation (en particulier la persistance de la lactation) a été, donc, détecté. Les valeurs génétiques estimées (EBV) obtenus pour les animaux nés chaque année ont été utilisés pour calculer le progrès génétique de. Une tendance génétique positive significative a été observée pour tous les caractères étudiés. Les animaux nés en 2010 ont en moyenne EBV pour le rendement de la graisse plus les protéines en 245 jours de lactation (l'objectif principal de sélection dans cette race) +4,05 kg plus élevés que ceux des animaux nés en 1999. Ce chiffre équivalent à la production de matière graisse, plus de protéines accumulées pendant 21 jours.*

Mots-clés. *Chèvres laitières – Tendance génétique – Sélection – Analyse de régression.*

I – Introduction

Florida breed is a native dairy goat that was created crossing Nubian goats with local goats of the Pyrenean trunk in the Guadalquivir River Basin (Sánchez and Herrera, 1990). The breed had from its birth until relatively recently a small census and a narrow geographical distribution. Actually, it has been considered in risk of extinction until 2011. The expansion of the breed coincides with the official recognition of the Herd Book, the start of the official milk recording in 2003 and the progeny testing of A.I sires in 2005. Nowadays, Florida breed is distributed in a wide region in the Southwest of the Iberian Peninsula with a census of 19,418 breeding females in 62 herds.

The selection nucleus is constituted by a large part of the total census of the breed (60.2%) distributed in 29 herds Every year, goats with the best genetic index (8.3%) are inseminated with semen from tested sires (6) or from young males being tested (12). Parental assignment of all animals in the selection nucleus is confirmed with DNA exclusion methods since 2007.

Cheese manufacture is the main destination of goat milk in Spain and most cheese industries pay farmers for the amount of fat plus protein supplied. Therefore, this is the main selection objective of this breed. Breeding values for this trait, as well as for linear type traits, are being estimated twice a year analyzing test day records with a random regression model (RRM). This model has been applied to the genetic evaluation of other dairy breeds of goats (Zumbach *et al*., 2004; Menéndez-Buxadera *et al*., 2010 ; Andonov *et al*., 2013).

The objective of this work was to estimate the genetic parameters of the dairy traits throughout the lactation, to describe the different types of response of the estimated breeding values along the lactation curve and to estimate the genetic progress attained in the selection program of the Florida breed of goats from 1999 to 2010.

II – Material and methods

1. Production records

A total of 273,600 monthly records (TD) of daily milk yield (DMY), daily protein yield and percentage (DPY and DPP), daily fat yield and percentage (DFY and DFP) and daily fat plus protein yield (DFPY), recorded between 2003 and 2012 in 28 herds, were provided by the National Breeders Association of Florida Goats. Raw data were thoroughly edited and validated, excluding lactations with only one TD, records collected during the first 10 days after kidding and those recorded after 450 days. Finally, 272,195 production records from 17,543 goats, offspring of 2,841 does and 316 bucks, in 27 flocks, were analyzed. Herds were connected through 6 A.I. and 20 natural service bucks.

A data file with 272,195 production records from 17,543 goats in 27 herds and a kinship matrix with 17,987 animals were used for the analyses.

2. Statistical analysis

A general linear model (SAS, 1996) was used to determine the significant fixed factors. The model included lactation number (L): 1^{st} to 4^{th}, number of milkings per day (M): 1 or 2, week of lactation (W): maximum of 63 weeks per lactation (with 65 to 9,970 TD per level, average 4,320) and the herd-test day (HTD), with 1,546 levels (with 15 to 1,009 TD per level).

The ASREML 3.0 software (Gilmour *et al*., 2009) was used to estimate the genetic (co)variance components (VC) and the breeding values (EBV) along the trajectory of weeks of lactation were independently estimated for each trait using the following random regression model (RRM):

Where Y_{ijklm} is the n_{th} dependent variable recorded in the i_{th} level of HTD, the j_{th} lactation and the k_{th} number of milkings per day (M); β_{lr} is a fixed Legendre polynomial regression coefficient for weeks (W) within l_{th} lactation; a_r is the additive genetic effect associated with the r_{th} Legendre coefficient for the m_{th} animal in the pedigree; p_r is the permanent environmental effect associated with the r_{th} Legendre coefficient for the n_{th} animal with record; e_{ijklmn} is the residual random term. VC are estimated by:

Where, K_a and K_p are the genetic and permanent environmental (co)variances matrices, respectively; A is the numerator relationship matrix between the animals; I is the identity matrix for permanent environmental effects; R is the residual random variance; $\otimes$ is the Kronecker product. The variance structure contains functions of the intercept (σ^2_{a00} and σ^2_{p00}) and the slope (σ^2_{a11}; σ^2_{a22} and σ^2_{p11}; σ^2_{p22}) of the genetic and the environmental effects, respectively. The terms σ^2_{a01}; σ^2_{a12} and σ^2_{p01}; σ^2_{p12} are the respective covariances. The heritability (h^2) and genetic correlations (r_g) for each trait and for all points along W can b estimated following the procedure of Jamrozik and Schaeffer (1997). The EBV of each animal j in the i week of lactation was computed as $EBV_j^i = \phi_j^i a_l'$, is a vector a_l' with the solutions for the additive genetic random regression coefficients and vector ϕ_j^i contains the second-order Legendre polynomial coefficients. The EBV for cumulative productions was computed as $EBV_n = \sum_{i=1}^{n} EBV_n$. Following the proposal of Jamrozik *et al.* (1997), the EBV for persistence of milk yield between two points of the lactation curve can be estimated as the area of a triangle of which the height is de difference between both.

The genetic progress was estimated as lineal regression coefficients for EBV on year of birth of the animals, weighted by the accuracy of the EBV estimation.

III – Results and discussion

Descriptive statistics for dairy traits in Florida breed are presented in Table 1. The average daily milk yield was 2.22 kg. This yield was higher than those of the Spanish breeds Murciano-Granadina and Payoya (2.06 and 1.89, respectively) reported by Menéndez-Buxadera *et al*. (2012). The average contents of milk components were higher than those reported for Alpine and Saanen breeds (Stark, 1988; Brito *et al*., 2011), while Menéndez-Buxadera *et al.* (2010, 2012) founded higher DFP and DPP for Murciano-Granadina breed. An important variability, which can be used for selection purposes, was observed for all traits.

Table 1. Descriptive statistics for milk traits in Florida goats (2003-2012)

Trait	Nº of records	Mean	Standard dev.	Min.	Max.
Lactation period (days)	272,098	136	86	10	450
DMY (Kg)	272,098	2.22	1.12	0.20	9.90
DFP (%)	257,324	5.11	1.32	2.00	9,90
DPP (%)	258,774	3.43	0.52	2.00	9.87
DFY (g)	257,324	112.00	52.20	6.00	577.60
DPY (g)	258,774	76.20	34.40	5.20	524.20
DFPY (g)	257,178	188.30	83.28	12.50	933.20

Figure 1 show the estimated trajectories of heritability over the weeks of lactation for the studied traits. The curves of the heritabilities for yield traits (DMY, DFY, DPY and DFPY) show all the same pattern, in contrast with the results reported by Andonov *et al*. (2013) who found a peak of the estimated h^2 of DMY in mid lactation. The heritabilities of content traits (DFP and DPP) were higher at the end of lactation, as has been reported in previous studies on dairy goats (Breda *et al*., 2006; Zumbach *et al*., 2008; Menedez-Buxadera *et al*., 2010).

Fig. 1. Estimated trajectories of heritability over weeks of lactation for dairy traits in Florida goats.

The estimated genetic correlations between the values at different points of the lactation curve are plotted in Fig. 2. Correlations are higher between adjacent points of the lactation curve, but they are over 0.5 even for distant points, which prove that selection for a single TD will render a positive response for the rest. Similar pattern of correlations was observed by Andonov *et al*. (2013).

Different patterns in the trajectories of the EBV throughout the lactation curve were observed for different animals. In order to classify these patterns, the trajectories of the EBV along the lactation curve from the best 9 bucks, selected according to their EBVs for the cumulated production of fat plus protein in 245 days, were plotted in Fig. 3. Some animals had a more or less stable EBV throughout the lactation curve (stable persistence), others showed their EBV declining with the lactation curve (poor persistence) and for a third group EBV increased through lactation (good persistence).

The genetic trends from 1999 to 2010 were estimated for DFPY at different weeks of lactation: W = 1, W = 10, W = 20, W = 30, W = 40 and W = 50, (Fig. 4). Two different stages can be distinguished. The first period, from 1999 to 2004, show a slight positive response to selection changing the average EBV for 245 days lactation cumulated fat plus protein yields of -0.39 kg in 1999 to 0.29 kg in 2004. The second period (2005-2010) show a high difference between the mean EBV for the same trait of animals born in 2005 and those born in 2010, changing from 1.49 to 3.64 Kg. The use of AI for testing bucks and diffusing genes of the best sires, which started in 2005, has been the key to this result.

The annual genetic progress for the whole period was 1.44%, similar to that reached in the French breeding programs for goats (Montaldo and Manfredi, 2002). This means that animals born in 2010 have an average EBV for fat plus protein yield in the whole lactation 4.05 kg higher than that of the animals born in 1999. This figure is equivalent to the fat plus protein yield cumulated during 21 days.

Fig. 2. Estimated Genetic correlations between different weeks of lactation (W) for DMY, DFPY, DPY and DFY.

Fig. 3. Estimated breeding values along the lactation curve of the 9 best bucks selected by daily fat plus protein yield.

Fig. 4. Genetic trends from 1999 to 2010 for DFPPY at different points of the lactation.

IV – Conclusions

Enough genetic variation to be used for the genetic improvement of dairy traits was observed in the Florida breed of goats. Using test day records with random regression models to estimate breeding values of sires and dams allows for a more effective selection of the animals with the best performances both for lactation yield and persistence, thus contributing to a higher genetic progress in the breeding program.

The annual genetic progress attained during the last six years have been as high as that of other goat breeding programs thoroughly recognized as efficient, which credits the work done by the National Breeders Association of Florida Goats.

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