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Designing Selection Indices for the Florida Dairy Goat Breeding Program

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Abstract: The aim of this study was to compare selection indices for important traits in intensive Spanish goat breeds in four economic scenarios, using the Florida as most representative breed of this production system in Spain. For this analysis, we considered the following traits: milk yield (MY), fat plus protein yields (FPY), casein yield (CY), somatic cell score (SCS), reproductive efficiency (RE), litter size (LS), mammary system (MS), final score (FS), body capacity index (BCI), and length of productive life (LPL). We estimated the genetic parameters and EBVs of most of these traits with REML methodology, while LPL was modeled through survival analysis. Four scenarios were proposed, depending on the overall objective for improvement: (1) milk production, (2) milk production and cheese extract, (3) cheese extract, and (4) milk production, cheese extract and sale of animals. Then, within each scenario, three different types of indices were designed using the different primary and secondary objectives/criteria considered suitable to improve the overall objective. The results indicated that selecting only for primary traits yielded the highest genetic response for all the scenarios. Including secondary traits led to positive correlated responses in those traits, but a decrease in the responses in the primary criteria.

Keywords: heritability; genetic response; index theory

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1. Introduction

The Florida breed is a native Spanish breed of dairy goats that is distributed over several regions of Spain, but mostly in the Andalusian region of southern Spain. This breed is considered to be the prototype for the Spanish breeds exploited in intensive or semi-intensive conditions; it is also present in other countries, such as Portugal, France and Greece.

The Florida breeding program is currently focused on milk production and composition traits [1]. However, there are other economically important traits, and genetic evaluations have been carried out on morphological, reproductive traits [2–4], somatic cell score [5], and more recently, longevity [6]. The greatest challenge in this breed is to find a procedure that can select for a group of economically important traits while considering the economic conditions of the different livestock farms.

For this purpose, selection indices that include the economic weights of important traits for dairy goats may be a good way to simultaneously improve group traits.

The selection index has been used extensively in a wide range of livestock species, such as dairy cattle [7–9], beef cattle [10,11], dairy goats [12,13], meat goats [14], and meat sheep [15]. The classic methodology of selection indices was reformulated by Gutiérrez et al. [16] to overcome its limitations, thus allowing direct work with EBVs instead of phenotypes. Recently, it began to be applied in the Florida Spanish goat breed for female fertility [2] and the Pura Raza Español horse for morphological traits [17].

Therefore, the aim of this study was to assess selection indices for socio-economically relevant traits in intensive Spanish goat breeds by considering different economic scenarios and combining and weighting the traits involved.

2. Materials and Methods

2.1. Phenotypic Data and Pedigree

The data set was provided by the National Association of Florida Goat Breeders (ACRIFLOR) and included records on traits related to milk production, fertility, prolificacy, type, and longevity, in addition to the genealogical information. The following traits were considered in this study as production traits: milk yield (MY), fat plus protein yields (FPY), casein yield (CY), and somatic cell score (SCS), which is a logarithmic transformation of the somatic cell count as an indicator of mastitis. Female fertility was represented as reproductive efficiency (RE), calculated as the deviation between the optimal and real parity number of females at each age. Litter size (LS) was included as a measure of prolificacy, estimated as the total number of kids born per kidding. The following type traits were considered: mammary system (MS), final score (FS), body capacity index (BCI), and the length of productive life (LPL) as a measure of female longevity. After data editing, the final datasets contained: 907,159 test-day records for production traits, 158,579 records for SCS, 138,139 records for RE, 130,849 records for LS, 10,192 records for type traits and, 15,888 records for LPL.

The pedigree was traced back for as many generations as were available in the breed herd book, being 7.3 equivalent generations and including 56,901 animals (1772 sires and 20,035 dams).

2.2. Statistical Analysis

The evaluation process of milk yield traits (MY, FPY and CY) was carried out using a test-day model (TDM) [18] with the following model:

$$y = LP3 + Xb + Zu + Wpe + e$$

where y is the vector of observations of each trait; LP3 is the covariable of the 3^d order of Legendre polynomials measured at days in milk; b is the vector of fixed effects, including the interaction herd-day of control (4597 levels), combined effect of number of lactation*age at kidding (8 levels), and control method (3 levels); u is the random additive genetic effect, pe is the random permanent environmental effect of the female, and e is the random residual effect. X, Z, and W are incidence matrices relating observations to fixed and random effects.

The type traits: mammary system (MS), final score (FS) and body capacity index (BCI) were analysed [18] with a repeatability model as follows:

$$y = Xb + Zu + e$$

where y is the vector of observations of each trait; b is the vector of fixed effects including the combination herd-visit-qualifier (327 levels), the interaction between number of lactation*age of the doe at classification (12 levels), and days in milk at moment of qualification (14 levels); u is the random additive genetic effect, and e is the random residual effect. X and Z are incidence matrices relating observations to fixed and random effects.

Reproductive efficiency and LS were also modelled, fitting a repeatability model:

$$y = Xb + Zu + Wpe + e$$

where y is the vector of observations of each trait; b is the vector of fixed effects including the contemporary group effect of herd-year-season of kidding (1260 levels for RE and

1087 levels for LS) and female age (7 levels for RE and LS); u is the random additive genetic effect, pe is the random permanent environmental effect of the female, and e is the random residual effect. X, Z, and W are incidence matrices relating observations to fixed and random effects.

The length of productive life was evaluated by survival analysis, using a Cox's proportional hazards model that can be described as follows:

$$\lambda(t) = \lambda_0(t)\exp\Big\{\mathrm{agefirst}_i + \mathrm{birth\_herd} * \mathrm{year} * \mathrm{season}_j + \mathrm{kidding\_herd} * \mathrm{year} * \mathrm{season}_k + \mathrm{age}_l + \mathrm{levelprod}_m + \mathrm{lactation\ number} * \mathrm{duration\ of\ lactation}_n + g_o\Big\}$$

where λ(t) is the hazard function (current probability of culling) of the doe t days after its first kidding, λ0(t) is the baseline hazard function t days after the most recent kidding; agefirsti is the time-independent effect of age i at first kidding (monthly intervals from 12 to 15; >15 to 19 and >19 to 24); birth_herd*year*seasonj is the time-independent effect of herd j combined with the year and season of birth of the doe (667 levels); kidding_herd*year*seasonk is the time-dependent effect of herd k combined with the year and season of kidding (829 levels); agel is the time-dependent effect of age l at kidding (monthly intervals from 15 to 19; >19 to 24; >24 to 36; >36 to 48; >48 to 60 and >60 mo); levelprodm is the time-dependent effect of the within-herd class of milk production deviation m (four classes); the time-dependent effect was calculated as the annual deviation of milk production for each doe with respect to the average production of its herd; and lactation number*duration of lactationn is the time-dependent effect of lactation number n (1–6), combined with duration of lactation (1–4), with the classes of lactation duration defined by cut-off points empirically as follows: 90d to 210d; >210d to 240d; >240d to 300d, and 300d to 400d; finally, go is the random additive genetic value of animal o in the pedigree.

A univariate model with the Restricted Maximum Likelihood procedure was used to estimate genetic parameters for all the traits with the REMLF90 version 1.82 software [19], except for longevity, which was modelled through survival analysis using the Survival Kit version 6 software [20]. Genetic correlations between the different traits were estimated following the adjustment procedure for reliabilities devised by Calo et al. [21].

2.3. Expected Genetic Responses

The genetic responses using different selection objectives/criteria were computed and compared in the Florida breed according to the classic selection index theory [22] that was reformulated by Gutiérrez et al. [16] to use genetic parameters rather than phenotypic performances. Briefly, weights in vector $\mathbf{f'}$ to be used for weighting the expected breeding values (EBVs) on v were calculated by $f' = p'C'G^{-1}$, where C' is the covariance matrix between the objectives in vector u and the EBV used as the criteria in vector v, and G^{-1} is the inverse of the (co)variance matrix for the selection criteria v. Matrices C' and G were obtained from the genetic parameters by assuming all the additive genetic variances to be standardized $\left(\sigma^2_{u_1} = \sigma^2_{u_2} = \sigma^2_{u_3} \cdots = \sigma^2_{uk} = 1\right)$, where σ^2_{uk} is the additive genetic variance of trait k: as a result, all of them were on the same genetic scale. When considering the different objectives and/or criteria, the coefficients in f' varied, and matrices C and G also changed. When the objective and criteria are the same traits, the (co)variance matrix between the objectives and criteria C becomes a genetic additive (co)variance matrix, in which the diagonals are equal to one [17]. Off-diagonal elements are the additive genetic correlations between objectives and criteria, given that $r_{ukul} = \frac{\sigma_{ukul}}{\sqrt{\sigma^2_{uk}\sigma^2_{ul}}}$, where r_{ukul} is the additive genetic correlation between traits k and l and $\sigma^2_{uk} = 1$ for any trait, thus becoming $\sigma_{ukul} = r_{ukul}$ and C':

$$C' = \mathrm{Var}(u) = \begin{bmatrix} \sigma^2_{u_1} & \sigma_{u_1u_2} & \sigma_{u_1u_3} & \cdots & \sigma_{u_1u_m} \\ \sigma_{u_2u_1} & \sigma^2_{u_2} & \sigma_{u_2u_3} & \cdots & \sigma_{u_2u_m} \\ \cdots & \cdots & \cdots & \cdots & \cdots \\ \cdots & \cdots & \cdots & \cdots & \cdots \\ \sigma_{u_mu_1} & \sigma_{u_mu_2} & \sigma_{u_mu_3} & \cdots & \sigma^2_{u_m} \end{bmatrix} = \begin{bmatrix} 1 & r_{u_1u_2} & r_{u_1u_3} & \cdots & r_{u_1u_m} \\ r_{u_2u_1} & 1 & r_{u_2u_3} & \cdots & r_{u_2u_m} \\ \cdots & \cdots & \cdots & \cdots & \cdots \\ \cdots & \cdots & \cdots & \cdots & \cdots \\ r_{u_mu_1} & r_{u_mu_2} & r_{u_mu_3} & \cdots & 1 \end{bmatrix}$$

As G and C′ are directly dependent on the genetic parameters, these matrices can be derived directly from genetic parameters to build the desired index. Next, the genetic responses for each trait were obtained by weighting all the responses obtained in the correlated selected traits, including the direct genetic response to itself. Thus, assuming the EBVs are known and applying the assumption given above about all the additive genetic variances being one, the direct genetic response would be the selection intensity (i) reduced by the accuracy of the EBV. The correlated response would be the additive genetic correlation times the selection intensity reduced by the accuracy of the EBV. Gathering this information into a matrix expression, the cumulated genetic responses will be obtained by:

$$t = b'Ti = b\prime \begin{bmatrix} h_1 & h_1r_{u_1u_2} & h_1r_{u_1u_3} & \cdots & h_1r_{u_1u_k} \\ h_2r_{u_2u_1} & h_2 & h_2r_{u_2u_3} & \cdots & h_2r_{u_2u_k} \\ \cdots & \cdots & \cdots & \cdots & \cdots \\ \cdots & \cdots & \cdots & \cdots & \cdots \\ h_kr_{u_ku_1} & h_kr_{u_ku_2} & h_kr_{u_ku_3} & \cdots & h_k \end{bmatrix}$$

where each t_k in t is the cumulated genetic response in trait k and h_k the squared root of the heritability of trait k. Finally, to compare the expected responses, a constant selection intensity of one was assumed, leading to comparable relative results. Details about the different scenarios and traits used as objectives/criteria in the selection indices are provided in Table 1.

Table 1. Summary of the different selection scenarios and the traits used as objective/selection criteria in the Florida goat breed.

	Scenario I	Scenario II	Scenario III	Scenario IV
MY	x	x	x	x
FPY		x	x	x
CY			x	
SCS	x	x	x	x
RE	x	x	x	x
LS				x
MS	x	x	x	x
FS				x
BCI	x	x	x	x
LPL	x	x	x	x

MY: milk yield (grams); FPY: fat plus protein yield (grams); CY: casein yield (grams); SCS: somatic cell score ($\times 10^3$); RE: reproductive efficiency (probability); LS: litter size (number of kids); MS: mammary system (score from 0 to 90 points); FS: final score (score from 0 to 90 points); BCI: body condition index (score from 0 to 90 points); LPL: length of productive life (days).

Four economic scenarios were proposed, depending on the economic objectives and the sources of income of Spanish dairy farms: milk production exclusively; milk production and cheese production; cheese production exclusively; and milk production, cheese extract, and sale of breeding animals. Within each scenario, three different indices have been designed: in the first one, the main objective has been considered as the primary goal and criterion; in the second, the main objective was considered alongside other secondary objectives, with equal economic weighting; and finally, index three was identical to index two, except that different weights were assigned to the various selection objectives. The economic weight is the value of one unit of superiority of a trait when all the other traits in the aggregate genotype remain constant [23].

In this study, the economic weighting of the characters studied was provided by the National Association of Florida Goat Breeders (ACRIFLOR).

3. Results and Discussion

The greatest challenge in this study was to assess a combined index that allowed us to simultaneously improve a group of criteria with the least possible penalization, and the responses obtained in others, under four different economic scenarios related to the main sources of income on goat farms (milk production exclusively; milk and cheese production; cheese production exclusively; and milk production, cheese extract and sale of breeding animals).

For this purpose, the first step was to calculate the genetic parameters, estimated breeding values (EBVs) and reliabilities for the study traits. Next, the genetic selection indices were estimated, as detailed in the Section 2.

3.1. Phenotypic Parameters

The basic descriptive statistics for the traits studied in the Florida breed are presented in Table 2.

Table 2. Descriptive statistics of the traits studied in the Florida goat breed.

	n	**Mean ± s.d**	**Min**	**Max**	**CV (%)**
MY	907,159	2.82 ± 1.58	0.11	11.99	56.02
FPY	907,159	0.23 ± 0.13	0.007	1.62	56.52
CY	907,159	0.099 ± 0.051	0.003	0.59	51.51
SCS	158,579	6.60 ± 0.95	0.69	10.52	14.33
RE	138,139	102.47 ± 18.83	31.83	190.94	18.37
LS	130,849	1.62 ± 0.61	1.0	6.0	37.77
MS	10,192	76.09 ± 2.97	63	84	3.9
FS	10,192	80.21 ± 1.84	70	86	2.29
BCI	10,192	83.47 ± 3.15	64	90	3.77
LPL	15,888	704.88 ± 427.47	163	3091	60.64

s.d: standard deviation; CV: coefficient of variation; MY: milk yield; FPY: fat plus protein yield; CY: casein yield; SCS: somatic cell score; RE: reproductive efficiency; LS: litter size; MS: mammary system; FS: final score; BCI: body condition index; LPL: length of productive life.

The daily averages for milk traits were 2.82 ± 1.58, 0.23 ± 0.13 and 0.099 ± 0.051 for MY, FPY and CY, respectively. For MY, female Florida production was similar to figures for Alpine and Saanen breeds [24], US goat breeds [25] and Polish breeds [26]. Our average of MY was much higher than those of the Spanish Payoya breed [27] and Nigerian Dwarf goats [28], which could be due to the differences in nutritional and management conditions. The means of FPY and PY were in agreement with that observed in Nigerian Dwarf goats [28] and lower than the averages for Alpine and Saanen breeds [24].

Average SCS values have been calculated in other studies using different logarithmic transformations, including $\log_2$, $\log_{10}$, or natural logarithms. In this study, the SCS was calculated using natural logarithm transformation with an average SCS of 6.6 ± 0.95 and similar to that obtained in Polish breeds by the natural logarithm for SCS (6.62 ± 1.25; [26]). The average milk SCS in Florida was higher than that of other dairy breeds (New Zealand mixed-breed dairy goats [29]; Hungarian breeds [30]; and Nigerian Dwarf goats [28] in).

Worldwide phenotypic values for RE are not available in dairy goats since this character has been analysed only in the Florida and Payoya breeds. The average RE value was lower in Payoya than in Florida, indicating that most Payoya females start their reproductive life late since they are reared in a more extensive production system [3].

The average LS obtained in this study, 1.62, was higher than the values of 1.4 and 1.33 observed in Saanen and Alpine goats [31] and in the local Tunisian breed [32], respectively, and similar to that of French Alpine, Saanen, and Toggenburg, with an average litter size of 1.7, 1.7, and 1.6, respectively [33].

The average of FS obtained in the Florida breed was similar to the values estimated in Saanen and Alpine goats (81.5 ± 4.7; [31]), US dairy goats (83.79 ± 4.11; [34]) and Nigerian Dwarf goats (84.1 ± 3.26; [28]). Mellado et al. [31] reported values of 1.8 ± 0.8 and 3.4 ± 1.1 for mammary system, body size, and capacity, respectively, using a 5-point scale.

Earlier studies with different definitions of longevity in dairy goats produced an average of 625 d for productive life at 72 months in US breeds [34], 1726 d for length of true life in UK dairy goats [35], 967 d for functional longevity in Saanen, and 1007 d in Alpine goats [36].

The lowest coefficient of variation was found for FS (2.29%) and the highest for LPL (60.64%), indicating that, except for type traits, there is an important phenotypic variation for the analysed traits in the Florida population, especially for milk production and longevity.

3.2. Genetic Parameters

Estimates of the heritabilities (h^2) and genetic correlations (r_g) for the evaluated traits are summarized in Table 3. Heritabilities ranged between 0.03 for LS and 0.58 for LPL. In general, the estimated h^2 were therefore considered suitable for genetic evaluations and selection for these traits.

Table 3. Estimated heritabilities (diagonal) and genetic (above diagonal) correlations of the traits studied in the Florida goat breed.

	MY	FPY	CY	SCS	RE	LS	MS	FS	BCI	LPL
MY	0.19	0.76	0.90	0.088	0.309	0.029	0.003	0.026	0.073	−0.20
FPY		0.17	0.81	−0.063	0.420	−0.074	0.106	0.103	0.066	−0.21
CY			0.16	−0.01	0.297	0.00	0.06	0.07	0.11	−0.20
SCS				0.20	−0.068	0.148	−0.175	−0.096	0.078	0.090
RE					0.27	−0.084	0.175	0.115	−0.010	−0.142
LS						0.03	−0.220	−0.165	0.013	0.043
MS							0.16	0.731	−0.018	−0.068
FS								0.19	0.463	−0.056
BCI									0.16	−0.026
LPL										0.58

MY: milk yield; FPY: fat plus protein yield; CY: casein yield; SCS: somatic cell score; RE: reproductive efficiency; LS: litter size; MS: mammary system; FS: final score; BCI: body condition index; LPL: length of productive life.

Milk production traits have been widely studied in dairy goats and there is abundant information about their genetic parameters. Our heritabilities for MY, FPY, and CY are within the range of values estimated in other dairy goat populations (Saanen [37]; Alpine and Saanen breeds [24]; and New Zealand goats [38,39]) and lower than the values reported by Mucha et al. [40] in their meta-analysis. The h^2 estimates for SCS reported in other breeds covered a wide range of values, from 0.09 ± 0.03 in the Alpine breed [41] to 0.32 ± 0.095 in Nigerian Dwarf goats [28]. Our estimate was in agreement with the 0.15 estimated in French Alpine goats [42] and the 0.21 values reported in the meta-analysis by Mucha et al. [40] that included twenty-six breeds worldwide, and Bagnicka et al. [26] in Polish breeds.

The heritability estimate for RE in this study was moderate and clearly higher than the estimates for the classical fertility criteria in both Florida and Payoya breeds [3], and in other dairy goat breeds in the world [43]. It is difficult to compare this figure with other estimates in the literature because of the lack of studies about female fertility, as defined in this study and in our previous work in Florida and Payoya breeds [3]. Litter size is not very heritable, which indicates a low possibility of achieving rapid genetic progress through direct selection. Our estimate was in agreement with the low previous estimations (close to zero) in different goat breeds (0.068 in Saanen goats [44]; 0.08 in the local Tunisian breed [32]; and 0.002 in Markhoz goats; [45]).

The type traits recorded and their definitions differ between countries, which makes them difficult to compare. Our estimates were in the range of values reported by Massender et al. [46] for Canadian Alpine and Saanen breeds. Estimations of h^2 of several type traits in Nigerian Dwarf goats ranged between 0.003 for dairyness and 0.71 for stature [28].

Any comparison of the h^2 estimates of longevity from this study with other estimates from other studies of goat is further complicated by the different definitions of longevity and statistical models. To date, except for the Florida breed, the h^2 values for longevity in dairy goats are available using linear models and were clearly lower than ours, ranging between 0.07 and 0.46 (US breeds [34]; UK dairy goats [35]; Saanen and Alpine breeds [36]; German breeds [47]).

Regarding the genetic correlations between the traits analysed, these covered a wide range of magnitudes and values, between −0.21 for FPY-LPL and 0.90 for MY-CY. In this study, the values of genetic correlations between milk yield traits were high, as is typical in dairy goats (Nigerian Dwarf goats [28] and New Zealand breeds [38]).

In general, the information about r_g between milk production traits and SCS in dairy goats was limited, with considerable controversy over its sign and magnitude. Previous studies reported positive r_g between these traits, varying between 0.06 and 0.59 (Alpine breed [24]; Polish breeds [26]; Nigerian Dwarf goats [28]; and New Zealand breeds [38]). In contrast, Rupp et al. [24] observed negative r_g between SCS and FY, and PY (−0.13 and −0.04, respectively) in the French Saanen breed.

In our study, the r_g between milk yields and reproductive efficiency were moderate to high, in contrast with the unfavourable estimations observed in other breeds and species (dairy sheep [48]; dairy goat [49]; dairy cattle [50]). This fact could be due to the definition of reproductive efficiency used in this study. An increase in RE means that the female is kidding at the optimum age, and consequently producing higher milk yields.

A wide range of r_g values was observed between type traits in comparison with others in the literature because the studies used different conformation measures. Valencia-Posadas et al. [28] calculated r_g among 14 type traits, and their estimations oscillated between −0.57 for rear udder height–medial suspensory ligament and 0.55 for stature–rump width. Our estimates of r_g in the Florida breed between milk traits and type traits were low (0.003 to 0.11, Table 3). Manfredi et al. [51] found negative correlations ranging from −0.51 to −0.19 when estimating correlations between udder traits and milk yield in Saanen and Alpine French breeds. The values estimated by Valencia-Posadas et al. [28] ranged between 0.01 to 0.88 in Nigerian Dwarf goats.

Genetic correlations involving SCS and type traits were generally low and in agreement with our estimates. Rupp et al. [24] observed low correlations ranging from -0.27 ± 0.034 to 0.34 ± 0.030 in Alpine and from -0.19 ± 0.036 to 0.15 ± 0.030 in Saanen.

Valencia-Posadas et al. [28] also reported correlations between −0.16 and 0.22 in Nigerian Dwarf goats. Because of the negative or low r_g between SCS and type traits in our study, the options for indirect selection are limited; however, given the relatively high magnitude of h^2 for SCS (0.20), direct selection for this trait may be successful.

Palhiere et al. [36] estimated r_g of functional longevity with production traits, SCC, and udder type traits in French dairy goats; they obtained low values from −0.06 to 0.28 for milk yield, close to zero for fat and protein yields, negative values from −0.29 to −0.35 for SCS, and positive values for udder floor position and rear udder attachment (r_g from 0.17 to 0.29). Castañeda-Bustos et al. [52] in US dairy goats observed a positive r_g for longevity in milk yields ranging between 0.23 and 0.39 and a low r_g for female fertility. Wolber et al. [47] also observed positive genetic correlation of 0.30 for LPL in milk yield in German goat breeds.

Estimation studies of r_g for LS for other traits are scarce. Mourad [53] found a higher r_g than ours (0.029, Table 3) between LS and MY for the last three months of lactation (0.23, 0.43, and 0.48, respectively), as well as total lactation milk (0.91) in Egyptian Alpine goats.

3.3. Expected Genetic Responses

Tables 4–7 showed the expected direct and correlated genetic responses for each of the four scenarios and three selection indices type in the Florida breed. The breeding objectives and selection criteria included actual traits used in the breeding program of the Florida breed, as well as possible traits which are not used at present but could be used for selection, for which genetic parameters are available.

Table 4. Expected genetic responses for Scenario I (overall objective = milk production) in the Florida goat breed.

		Objectives					
Index		**MY**	**MS**	**BCI**	**RE**	**SCS**	**LPL**
1. MY	weight (%)	100	0.00	0.00	0.00	0.00	0.00
	response	0.268	0.001	0.014	0.047	0.010	−0.033
2. MY, MS, BCI, RE, SCS, LPL	weight (%)	16.66	16.66	16.66	16.66	−16.66	16.66
	response	0.043	0.035	0.026	0.035	−0.018	0.033
3. MY, MS, BCI, RE, SCS, LPL	weight (%)	40.00	10.00	5.00	5.00	−10.00	30.00
	response	0.083	0.015	0.010	0.019	−0.004	0.069

MY: milk yield; MS: mammary system; BCI: body condition index; RE: reproductive efficiency; SCS: somatic cell score; LPL: length of productive life.

Table 5. Expected genetic responses for Scenario II (overall objective = milk and cheese production) in the Florida goat breed.

		Objectives						
Index		**MY**	**FPY**	**MS**	**BCI**	**RE**	**SCS**	**LPL**
1. MY, FPY	weight (%)	50.00	50.00	0.00	0.00	0.00	0.00	0.00
	response	0.230	0.202	0.010	0.013	0.054	0.002	−0.033
2. MY, FPY, MS, BCI, RE, SCS, LPL	weight (%)	14.30	14.30	14.30	14.30	14.30	−14.30	14.30
	response	0.065	0.069	0.033	0.024	0.038	−0.016	0.024
3. MY, FPY, MS, BCI, RE, SCS, LPL	weight (%)	25.00	25.00	10.00	5.00	5.00	−10.00	20.00
	response	0.100	0.094	0.022	0.011	0.031	−0.009	0.037

MY: milk yield; FPY: fat plus protein yield; MS: mammary system; BCI: body condition index; RE: reproductive efficiency; SCS: somatic cell score; LPL: length of productive life.

Table 6. Expected genetic responses for Scenario III (overall objective = cheese production) in the Florida goat breed.

		Objectives							
Index		**MY**	**FPY**	**CY**	**MS**	**BCI**	**RE**	**SCS**	**LPL**
1. FPY	weight (%)	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00
	response	0.193	0.226	0.207	0.019	0.012	0.061	−0.007	−0.033
2. MY, FPY, CY, MS, BCI, RE, SCS, LPL	weight (%)	12.50	12.50	12.50	12.50	12.50	12.50	−12.50	12.50
	response	0.084	0.082	0.091	0.030	0.023	0.039	−0.014	0.017
3. MY, FPY, CY, MS, BCI, RE, SCS, LPL	weight (%)	15.00	20.00	25.00	10.00	5.00	5.00	−10.00	10.00
	response	0.128	0.117	0.137	0.026	0.015	0.037	−0.012	0.006

MY: milk yield; FPY: fat plus protein yield; CY: casein yield; MS: mammary system; BCI: body condition index; RE: reproductive efficiency; SCS: somatic cell score; LPL: length of productive life.

In Scenario I, where the overall objective was the optimization of milk yield, the highest genetic response was obtained when the primary objective (milk yield) was included as a unique selection objective/criterion (Index 1, Table 4). Regarding the correlated responses, a low, favourable response was observed in MS, BCI and RE. However, in somatic cell score and length of productive life, there was a small, unfavourable response (increase in RCS and decrease in LPL). By including secondary traits (MS, BCI, RE, SCS and LPL, Index 2, Table 4) and assigning them the same economic weight as the primary ones, a small improvement can be observed in their responses, except for RE. However, this causes the response in the primary trait (MY) to be reduced by approximately six-fold. In the third index, which gave more weight to the primary trait and different weights to the secondary ones according to their relative importance in MS, RE, and BCI, there were hardly any changes. In SCS and LPL, there were favourable responses, but given their very low magnitude, the significant decrease in the response of MY may not be compensated (Index 3, Table 4).

Table 7. Expected genetic responses for Scenario IV (overall objective = milk yield, fat plus protein yield and litter size) in the Florida goat breed.

		Objectives								
Index		**MY**	**FPY**	**MS**	**FS**	**BCI**	**RE**	**LS**	**SCS**	**LPL**
1. MY, FPY, LS	weight (%)	33.33	33.33	0.00	0.00	0.00	0.00	33.33	0.00	0.00
	response	0.154	0.133	0.001	0.004	0.009	0.034	0.018	0.003	−0.021
2. MY, FPY, MS, FS,	weight (%)	11.11	11.11	11.11	11.11	11.11	11.11	11.11	−11.11	11.11
BCI, RE, LS, SCS, LPL	response	0.051	0.055	0.039	0.050	0.029	0.031	−0.004	−0.015	0.017
3. MY, FPY, MS, FS,	weight (%)	20.00	15.00	10.00	10.00	5.00	5.00	0.00	−10.00	10.00
BCI, RE, LS, SCS, LPL	response	0.077	0.074	0.036	0.043	0.019	0.028	−0.009	−0.013	0.012

MY: milk yield; FPY: fat plus protein yield; MS: mammary system; FS: final score; BCI: body condition index; RE: reproductive efficiency; LS: litter size; SCS: somatic cell score; LPL: length of productive life.

In Scenario II, as in the previous one, the improvement in the overall objective (milk and cheese production) could be achieved by selecting only for the MY and FPY primary traits. In the other criteria, there were no correlated responses, except a slight decrease in RE and LPL, respectively (Index 1, Table 5). By incorporating secondary traits into the index, the responses in MY and FPY decreased to less than half (Indices 2 and 3, Table 5), and no significant changes were observed in them, except with RCS and LPL, where slightly favourable responses were observed (Indices 2 and 3, Table 5).

Scenario I has been the most applied in this breed until now. Although there are more farms where milk has been used for cheese extract (fat plus protein yield), farmers do not pay attention to this criterion because, generally, a higher level of milk production allows a greater production of fat plus protein yield. Also, taking into account the feeding management, it is possible to maintain the fat content relatively high even with high production levels.

As with the two previous scenarios, for Scenario III, the greatest response in the primary trait FPY, which is directly related to cheese production, was obtained when it was included as a single selection objective and criterion (Index 1, Table 6). In addition, this index produced the best responses in MY and CY due to their high genetic correlations with FYP. In the other criteria, there were favourable correlated responses, except for LPL (Index 1, Table 6). In the combined indices with primary and secondary criteria, there were favourable responses in all the secondary ones, except for RE. Nevertheless, there was a reduction of almost half in the primary traits (Indices 2 and 3, Table 6). This scenario could be interesting for those farmers who transform their own milk, but they represent a minority within the ACRIFLOR association (in general, for the Spanish dairy goat breeds), and the majority of them do not even process their entire production.

A few years ago, there were proposals by the cheese sector to subsidize the protein yield and even its quality for cheese production, but the current circumstances of the market and the current strong competition for milk production between the different industries have left these aspects aside for now. Under the actual circumstances, and with a clear decreasing trend in milk production in the Florida breed, Scenario I will continue to be applied.

In the last scenario, the index including only the MY, FPY, and LS primary traits (index 1, Table 7) allowed for greater responses. Indices 2 and 3 provided positive responses in the secondary traits, except for RE, although it cannot be guaranteed that this fact would be linked to maximum economic performance. Practically, all Florida farmers sell animals for life, including females that are not left for replacement, and also a significant number of reproductive males. This sale is an important part of the farm's revenues since it can represent between 10 and 20% of the farm's total incomes.

The theory of selection index has been used previously in the Florida breed to estimate direct and correlated genetic responses for classic female fertility traits [2]. The highest genetic response was obtained when the interval between all kiddings was included in the index as a selection criterion. Nevertheless, given its low heritability and late expression in the female's life, it cannot be recommended as early selection criteria. As an alternative, reproductive efficiency has been proposed, which has demonstrated a high h^2, in addition to being easily evaluated and understood by the breeders [3].

In all the scenarios, the use of Index 1 led to the highest genetic responses in the primary traits, which will produce a faster improvement in the overall objectives than Indices 2 and 3. The inclusion of secondary traits in the selection index led to positive correlated responses in those traits but was accompanied by a decrease in the responses in the primary criteria. Here, special attention should be paid to the relationships between some of the traits and their economic weights, as any selection made with the aim of improving one particular group may adversely affect others.

The choice of suitable selection criteria is one of the most important decisions made by dairy goat breeders [20] and varies between the different dairy goat systems [54,55]. In Spain, milk yield and cheese extract constitute the main source of revenues for dairy goat farms through the sale of milk or cheese, or both, in addition to subsidies granted by the government. In the particular case of the Florida breed, the main selection objective of its breeding program is milk production. Milk solids traits therefore showed higher economic values when compared to others, and Index 1 had the best results, as it included the highest weighting for these traits. Also, in the indices applied in other dairy breeds, a greater economic weight has been assigned to milk or its solids in dairy goats [13] and in dairy cattle [56]. Morphological traits are the second selection objectives after milk production in this breed. The MS is interesting for the facility and milking speed (in addition to the obvious relationship between the morphology of the udder and the amount of milk produced), and the possibility of installing automatic milking machines in the milking parlors, which is only useful if there is acceptable mammary conformation of the doe. This point is highly valued by farmers since it means saving many labour hours that would be used for milking. The BCI is related to good body capacity, especially abdominal capacity, and therefore a greater intake capacity of the animals, which will allow greater production, and especially the use of rations with a higher proportion of forages that are cheaper and much healthier for the animal. On the other hand, FS reflects the general dairy morphotype of the animal, closely related to the previous aspects since both weigh 60% in this final score. Furthermore, these morphological aspects are appreciated by dairy farmers, so they can ultimately be very interesting aspects for the issue of animals for sale, which will have a higher price. This last aspect is closely related to LS and RE which, if they increase, will allow farmers to have a greater number of young offspring for sale as breeding animals, a very important aspect for the ACRIFLOR dairy farms.

Nevertheless, apart from milk solids, morphology and reproductive aspects, there are other traits which have an economic impact on livestock production, such as udder health. Several authors have proposed the use of somatic cell count as an indicator of mastitis [57–59]. The negative weight assigned to SCS can result in selection for animals resistant to mastitis, especially in highly productive breeds subjected to high productive stress. This trait is of utmost importance for the udder health in the Florida breed although farmers still do not give it the importance it has, since although they know that it is related to udder health, they generally do not yet have any subsidies or penalties in this regard in the price they receive for their milk, since there are no official limits in the EU for goat milk. In fact, Index 1 in Scenario III (Table 6) and Indices 2 and 3 in all the scenarios (Tables 4–7) showed a reduction in the genetic response of the somatic cell score, which means they could be suitable for the genetic improvement of resistance to mastitis in this breed.

Finally, selecting for productive life of a doe is very interesting, since with the current high feed prices and the costs of keeping females in the herd, the amortization cost per litre of milk produced can be of 15–25% of the total cost of production of a litre of milk. Furthermore, in this breed, a decrease in longevity has been observed, and the average longevity is a little more than two lactations.

4. Conclusions

This study is the first to assess selection indices for economically important traits for the dairy goat industry using four economic scenarios. The results indicate that selecting only for primary traits provides the highest genetic response directly related to the overall objective in all the scenarios. However, including secondary traits in the selection index leads to positive correlated responses in those traits, although this was accompanied by a decrease in the responses in the primary criteria. Further economic evaluations are therefore required to determine whether incorporating secondary traits in the selection index is economically advantageous or not.

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