Expected Selection Responses From Index Selection For Milk Production Traits In Mexican Dairy Goats

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Introduction

In the year 2000 a program of genetic improvement began in the central region of Mexico in 13 dairy flocks with around 1300 goats in production control. Goats are maintained in a stall free feeding system, 80% of them are Saanen and milk is used for making cheese (Valencia et al., 2004). The first genetic evaluation was carried out in 2003 for milk yield, and since 2007, the evaluation also included fat and protein yield.

In France and the United States selection indices has been developed in dairy goats, including production traits and type traits (Wiggans and Hubbard, 2001; Leboeuf et al. 2008). With the aim of propitiate a simultaneous genetic improvement on most economically important traits and to simplify the identification of superior genetic animals, it is necessary to develop multi-trait selection indices. The objective of this study was to predict the annual genetic responses, using multi-traits indices with different relative weights, for milk production (MILK), fat production (FAT) and protein production (PRO) in goats of the central region of Mexico.

Material and methods

Three traits were included in the indices: MILK, FAT and PRO, all measured in kg. Expected selection responses were estimated, using multi-trait indices. In table 1 are presented the descriptive statistics of the traits used in the indices.

Table 1. Descriptive statistics for milk production (MILK), fat production (FAT) and protein production (PRO) (Torres-Vázquez, et al. 2009)**:**

	Average	Phenotypic standard deviation	Genetic standard deviation
MILK (kg)	1095	292	83.03
FAT (kg)	33.5	8.95	2.917
PRO (kg)	28.05	7.10	2.15

Table 2 shows the heritabilities, repeatabilities and genetic and phenotypic correlations used in the indices.

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The objective was to evaluate the annual genetic responses for MILK, FAT and PRO, changing the relative weights of each one in the indices, within reasonable ranges for dairy goats populations (Leboeuf et al. 2009). In the present study were evaluated two types of improvement programs, one based in the use of young males selected by pedigree, and other based in the use of tested males for progeny.

Table 2. Parameters used in the indices for estimate generation genetic responses for milk production (MILK), fat production (FAT) and protein production (PRO) (Torres-Vázquez, et al. 2009)**:**

	MILK	FAT	PRO
MILK	0.17 (0.43)	0.85	0.95
FAT	0.72	0.19 (0.42)	0.88
PRO	0.87	0.80	0.17 (0.42)

Heritabilities on the diagonal; repeatabilities in parenthesis on the diagonal; genetic correlations below diagonal and phenotypic correlations above diagonal.

The expected responses per generation for each index, for each trait, were estimated using the MTINDEX program (Van der Werf, 2007), which is based on selection index methodology. For the calculation of the annual genetic responses was assumed that: a) The best 10% of young males were selected, on basis of information of 2 repeated records from the dam, 5 paternal half sister and 2 full sisters. b) In a second phase of male selection, information of progeny was added, that consisted in 8 daughters per male. It was assumed that the best 50% of tested males were selected for to be used as parents. c) The best 90% of dams for replacement were select, assuming that goat has information of 1 own record and 2 repeated records from his dam. For the improvement program based on progeny testing (PT), was assumed that the proportion of inseminated dams with semen of young males is 40%, and remainder 60% is inseminated with tested males. For the selection program based on the use of young males (YM), it was that 100% of the population is inseminated with young males. Selection intensity for young males, tested males and selected dams were 1.755, 0.798 y 0.195 respectively. Average generation intervals assumed in this study were 2.0 years, 4.5 years and 3.5 years for young males, tested males and for selected dams, respectively.

Annual genetic progress (ΔG) was estimated from the responses for each trait per unit of standard deviation of the index, obtained for the different type of select animals (young males, tested males and dams) with the next equation (Spike and Freeman, 1977):

$$\Delta G = (J * i_J * R_J + (1-J) * (i_J * R_J + i_P * R_P) + i_H * R_H) / (J * L_J + (1-J) * L_P + L_H), \text{ where:}$$

J= proportion of used young males (0.4 o 1.0),
1-J= proportion of tested males (0.6 o 0.0),
i_J= selection intensity of young males (1.755, better 10%),
R_J= is the generational response for the trait, per selection of young males,
i_P= selection intensity of tested males (0.798, better 50%),
R_P= is the generational response for the trait, per selection of tested males,
i_H= selection intensity of selection dams (0.195, better 90%),
R_H= is the generational response for the trait, per selection of dams,

L_J= generation interval of young males (2.0 years),
L_P= generation interval of tested males (4.5 years),
L_H= generation interval in dams (3.5 years),

Results and discussion

The ranges for annual genetic responses of MILK, FAT and PRO per doe were from 14.84 to 22.73 kg, 0.422 to 0.729 kg and 0.367 to 0.496 kg, respectively (tables 3 and 4). Table 3 shown the annual genetic response for MILK, FAT and PRO using progeny testing. The minimum percentage for annual genetic response, with respect to the mean, was obtained for FAT (1.67%), and the highest was for MILK (2.07%), which were in the lower part of the expected responses estimated by Montaldo et al. (1994) for milk production, assuming optimum progeny testing programs in goats and considering higher values for the heritability.

Table 3. Annual genetic responses for milk, fat and protein yield, using indices with different relative weights for each trait and progeny testing.

Relative weights MILK: FAT: PRO	MILK (kg)	FAT (kg)	PRO (kg)
0: 0.1: 0.9	20.84 (1.90%)*	0.694 (2.07%)	0.496 (1.76%)
0 : 0.3: 1	19.73 (1.80%)	0.729 (2.17%)	0.491 (1.75%)
0.1:0.5: 0.9	22.73 (2.07%)	0.561 (1.67%)	0.488 (1.74%)
0.1: 0.6: 1	22.661 (2.07%)	0.573 (1.71%)	0.491 (1.75%)

* = percentage from the mean in parenthesis

Annual genetic responses using only young males, were lower than using progeny tests (table 4), even when these programs are not optimized (Montaldo et al. 1994), but in both programs important response are possible. This suggests that selection programs based on the use of young sires could result attractive for their low cost and absence of complex logistic requirement while it can be developed more sophisticated and effective programs for this population.

Table 4. Annual genetic responses for milk, fat and protein production, excluding the use of tested bucks, using different relative weights on the index using young sires selection.

Relative weights MILK: FAT: PRO	MILK	FAT	PRO
0: 0.1: 0.9	15.69 (1.43%)	0.525 (1.56%)	0.374 (1.33%)
0 : 0.3: 1	14.84 (1.35%)	0.533 (1.65%)	0.392 (1.39%)
0.1:0.5: 0.9	17.172 (1.57%)	0.422 (1.25%)	0.367 (1.31%)
0.1: 0.6: 1	17.108 (1.56%)	0.431 (1.28%)	0.370(1.32%)

* = percentage from the mean in parenthesis

With a selection program based on the use of young sires, the minimum percentage for annual genetic response, with respect to the mean, was obtained for PRO (1.31%), and the highest was for FAT (1.65%).

Using real parameters obtained from a Mexican goat population (Torres-Vázquez, et al. 2009), in selection programs for goats based both in young sires selection or progeny testing resulted in high expected annual genetic responses for all studied traits. The effect of changing the relative weights has a relatively small effect on the selection responses. These responses were higher than the responses estimated for MILK, FAT and PRO in US dairy goats (Wiggans and Hubbard, 2001), and for Mexico as well (unpublished data), close to 3 kg. There are good possibilities to attain annual genetic progress in goats >1.3% of the mean for MILK, FAT and PRO,, using relatively single selection programs, based on recording of milk traits and BLUP methodology.

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