ESTIMATES OF ENVIRONMENTAL EFFECTS, GENETIC PARAMETERS AND GENETIC TRENDS FOR REPRODUCTIVE TRAITS IN ALPINE GOATS

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ABSTRACT

Study of litter size (LS), birth weight (BW) and litter weight (LW) over successive parities was conducted on diary Alpine goats reared in Croatia. Statistical analysis was performed on records obtained out of 46 722 parturitions from 18 546 goats of different ages and parities. Twining and tripling rates were 27% i.e. 1%. Unadjusted averages for LS, BW and LW were 1.46 lambs, 3.29 kg, and 4.75 kg, respectively. Univariate analysis (repeatability animal model) was used in estimation of variance components and prediction of breeding values. Season (as year-month interaction), age at lambing (as quadratic regression) nested within parity and type of birth were treated as fixed, and herd-year, additive genetic, permanent environmental and residual were treated as random effects, respectively. All investigated effects were statistically significant (P < 0.001). Heritability estimates were 0.039, 0.036, and 0.023 for LS, BW, and LW, respectively. Herd-year affected BW (46%) and LW (40%) much more than LS (12%). Average breeding values by year of the birth in the last decade oscillated between investigated years. Positive genetic trends of all investigated traits were determined only after year 2007.

Key words: goats/Alpine breed/reproductive traits/heritability/genetic trends/environmental effects

1   INTRODUCTION

Goat farming in Croatia is organized in two major directions, extensive breeding systems in the Karst areas mainly based on autochthonous breeds and semi-intensive breeding systems in continental areas based exclusively on foreign diary breeds. In both systems, there is a common practice that all non-breeding kids (male and female) are used for the meat production. Alpine breed accounts for about 80% of total number of goats under selection program in Croatia. The breed is mainly raised in counties of Međimurje and Varaždin. Control of reproductive traits is performed on entire registered population of 7 590 goats and 5 821 goats are under milk control (HPA, 2011). Majority of goats worldwide are reared in (semi) extensive breeding systems, therefore, studies conducted in goats are often limited in number

and quality of data used in inferential statistical analysis. Generally speaking, studies conducted in sheep and cattle are more numerous and comprehensive, especially concerning estimation of genetic parameters. Litter size, birth weight, and total litter weight are often attributed as reproductive traits when considering dam's production performances. Different approaches in selection for these traits have been developed by now worldwide. But, there is a general opinion between all researchers that accuracy in estimation of genetic parameters is crucial for implementation of selection programs and efficient genetic improvement regardless of target trait. For this purpose, quality and quantity of data and appropriateness of analytic procedures are required. Respecting aforementioned, analysis of environmental effects and their proper inclusion in statistical models for genetic evaluation of reproductive traits of goats were indirect objectives of

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this work. The main goal of this study was actually to estimate genetic parameters for aforementioned reproductive traits and to obtain genetic trends out of predicted breeding values of animals in the last decade.

2   MATERIALS AND METHODS

Data records for this study were obtained from the central database of Croatian agricultural agency. Records were collected in the period from 1998 to 2010. The objects of our analysis were birth weight (BW), litter size (LS), and composite trait of litter weight at birth (LW). Goats with inconsistent records and goats from herds with less than 15 animals were deleted. Records obtained after ninth parity were also deleted, so final statistical analysis was performed on records obtained out of 46 722 parturitions from 18 546 goats. Pedigree file was created using all available relationship information between phenotyped animals and their ancestors. After elimination (tree cut) of non-informative animals from pedigree, a total of 23 280 animals were included in relationship matrix. Mating season was defined as month-year interaction. Seasons with less than 20 animals were joined to the previous or next season to improve data structure. Repeated measurements were considered as expression of the same trait over time. Predictions of breeding values were obtained with the same models as applied for estimation of variance components. Following (full) model was used for BW and LW while reduced model (without type of birth) was used for LS:

$$y_{ijklmn} = \mu + P_i + S_j + N_k + b_{1i}(x_{ijklmn} - \bar{x})^2 +$$
$$b_{2i}(x_{ijklmn} - \bar{x})^2 + h_l + p_m + a_{n} + e_{ijklmn},$$

where: y_{ijklmn} is phenotype for BW, LW and LS, P_i parity, S_j mating season, N_k number of kids in the litter, b_{1i} *and* b_{2i} linear and quadratic regression coefficients for age at mating nested within parity, x_{ijklmn} age at matting, h_l herd-year effect, p_m permanent environmental effect, a_n direct additive genetic effect and e_{ijklmn} residual term. Herd year, permanent environmental and additive genetic were treated as random effects. Model assumes genetic correlations between parities and constant phenotype variance for all traits. General matrix form of the model was:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z_h h} + \mathbf{Z_p p} + \mathbf{Z_a a} + \mathbf{e},$$

where **y** is a vector of observations (BW, LS, LW); **b** is a vector of unknown parameters for fixed effects (season, age within parity and type of birth); **h**, **p**, and **a** are vectors of unknown parameters for herd-year, permanent

environmental, and additive genetic effect, respectively; **e** is vector of residuals; while **X**, $\mathbf{Z_h}$, $\mathbf{Z_p}$, and $\mathbf{Z_a}$ are incidence matrices linking phenotype records with corresponding parameters. Model assumptions were:

$$E(\mathbf{y}) = \mathbf{Xb}, \quad \mathbf{h} \mid \mathbf{H} \sim N(\mathbf{0}, \mathbf{H}), \quad \mathbf{p} \mid \mathbf{P} \sim N(\mathbf{0}, \mathbf{P}),$$
$$\mathbf{a} \mid \mathbf{G} \sim N(\mathbf{0}, \mathbf{G}), \quad \mathbf{e} \mid \mathbf{R} \sim N(\mathbf{0}, \mathbf{R})$$

where $\mathbf{G} = \mathbf{A}\sigma_a^2$, $\mathbf{H} = \mathbf{I_h}\sigma_h^2$, $\mathbf{P} = \mathbf{I_p}\sigma_p^2$ and $\mathbf{R} = \mathbf{I_e}\sigma_e^2$. **A** is numerator relationship matrix. Unknown parents represented a base population which entails that these animals were sampled from a single population with average breeding value of zero and common variance. $\mathbf{I_h}$, $\mathbf{I_e}$ and $\mathbf{I_p}$ are identity matrices for corresponding random effects. Parameters σ_a^2, σ_h^2, σ_p^2, and σ_e^2 denote direct additive genetic, herd-year, permanent-environmental, and residual variances, respectively. Data editing, descriptive statistics, inferential statistical analysis for fixed effects and pedigree preparation were performed in SAS program package (SAS, 2009). Variance components were estimated using REML procedure applied on single trait repeatability animal model with software package VCE (Groeneveld *et al.*, 2008).

3   RESULTS AND DISCUSSION

Peak of mating activity for investigated goats was determined in September, although a considerable portion of goats was mated in June and October. Although the extent of this seasonal restriction varies within breeds, geographical location and livestock management, this confirms a well-known fact that goats are seasonally polyestrous (Misztal *et al.*, 2004, Zarazaga *et al.*, 2005). Figure 1 presents single records of litter weights related to the age of mating. Mating period is marked with dense fields while blanks in the figure represent periods of anestrous i.e. reduced sexual activity. Annual matting pattern of investigated goats can be detected from the figure. Furthermore, good frequency distribution of phenotyped goats according to age at mating is noticeable.

Descriptive statistics of reproductive traits is presented on Table 1. Among total of 46 722 litters, moderate rate of twining (27%) and low rate of tripling (1%) were recorded. Frequencies of kids born as singles, twins, and triplets were 56.33%, 41.18%, and 2.49%, respectively. Mellado *et al.* (2011) reported practically identical results in their study conducted on five diary breeds of goats. Averages of LS, BW, and LW were 1.46 lambs, 3.2 kg and 4.75 kg, respectively (Table 1). Dependency between LS and BW of kids is in accordance with previous reports for goats (Amoah *et al.*, 1996; Mellado *et al.*,
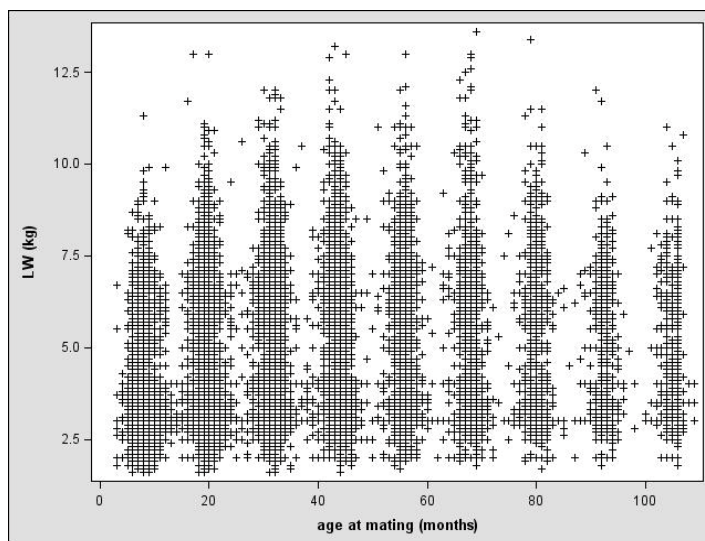
Figure 1: Litter weights (LW) obtained at different age in Alpine goats

2011). As expected, higher averages LW were determined for larger litters (Table 1).

Direction and intensity of changes in reproductive traits over parities can be followed on figure 2. Considerable increase in litter size and consequently in LW can be detected up to fourth parity. It is consistent with numerous statements that litter size is influenced by parity (Amoah and Gelaye, 1990; Awemu *et al.*, 1999; Maria and Ascaso 1999, Škorput *et al.*, 2011). Although insufficiently visible from the graph, parity significantly (P < 0.001) affected BW. The largest difference was determined between first and second parity. Discrepancy in birth weight between the first and subsequent parities supports reports of Luther *et al.* (2007) about conflict of fetal with maternal nutritional requirements in primiparous goats that did not reach their mature bodyweight. All aforementioned factors significantly affected investigated reproductive traits (P < 0.001). It was also the case with the influence of season, which confirms previous reports that reproduction performances can be influenced by different forage availability, photoperiod and temperature (Misztal *et al.*, 2004, Markley *et al.*, 2006, Zarazaga *et al.*, 2005).

Estimates of variance components and direct heritabilities are presented in Table 2. Herd-year, permanent-environmental, and additive genetic effects accounted for 12%, 16%, and 4% of variability in LS, 46%, 2%, 2% of variability in BW and 40%, 10%, and 4% of variability in LW, respectively. The heritability estimates for all three traits were anticipated low (2–4%). Heritability estimates for LS (0.04) are in general agreement with those reported in previous studies for different goat breeds (Maghsoudi *et al.*, 2009; Rashidi *et al.*, 2011; Tesfaye *et al.*, 2011; Mohammadi *et al.*, 2012). On the other hand, Bagnicka *et al.* (2007); Zhang *et al.* (2009) and Gunia *et al.* (2011) reported higher estimates. Our estimate of heritability for LW (0.02) was in agreement with that reported by Rashidi *et al.* (2011), and lower than those reported by Zhang *et al.* (2009) and Mohammadi *et al.* (2012). Besides the different analytical approaches in estimation of genetic parameters, inconsistent structure of data between different studies in terms of population size and pedigree structures (genetic ties within population), are major sources of this variation. Ratio of herd year effect in total phenotype variability was higher for BW and LW in comparison to LW. It indicates their high sensibility to

Table 1: Descriptive statistics of reproductive traits for different type of births (unadjusted means ± standard deviations)

	N	%	LS	BW	LW
Overall	58651	100.00	1.46 ± 0.54	3.29 ± 0.64	4.75 ± 1.52
Singles	32856	56.33	-	3.32 ± 0.65	3.32 ± 0.65
Twins	24334	41.18	-	3.25 ± 0.62	6.43 ± 1.21
Triplets	1461	2.49	-	3.05 ± 0.61	9.02 ± 1.73

LS- litter size; BW- birth weight LW- litter weight
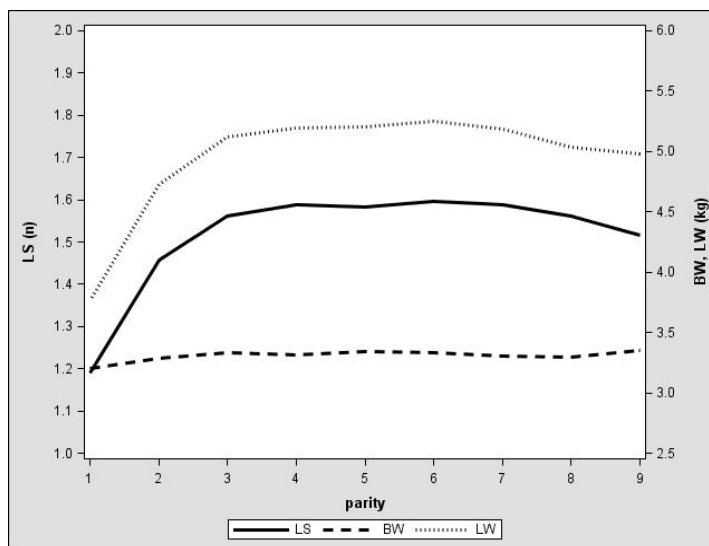
Figure 2: Unadjusted means of birth weight of kids (BW), litter size (LS), and litter weight (LW)

distinct environmental conditions. This primarily refers to the forage availability caused by different climate conditions. Average breeding values by year of the birth for both, male and female goats are presented in Fig. 3. Fluctuations in the average breeding values in the last decade indicate absence of linear genetic trend.

Selection for traits studied was performed only lately, therefore, such fluctuations in genetic trends are somehow anticipated. However, selection performed by breeders themselves according to animal phenotype can not be completely ignored. Small but consistent genetic progress of all traits was detected only after year 2007. Genetic gain of composite trait LW is practically a cumulative result of the genetic progress of its components LS and BW. It is considered that this genetic gain is associated with import of 15 bucks with high genetic potential from Austria in 1996. These bucks were mated to the most productive diary goats and the best of their progeny was left for replacement and further augmentation of herds.

According to the information of Croatian Agricultural agency and some our preliminary analysis for dairy traits, spread of mentioned genetic material increased milk production in a number of herds that are covered by the selection program. Genetic correlation between milk yield and reproductive traits is reported in many studies (Komniakis *et al.*, 1998; Ligda *et al.*, 2000). Taking into account this established scientific facts, we consider that realized genetic progress determined in our study is collateral result of the improvement of dairy traits. Recently, BLUP procedure for dairy traits was introduced in the population of Saanen and Alpine goats in Croatia. Selection, based on BLUPs should provide further improvement not only for milking, but also for reproductive traits. In order to obtain more precise estimates of genetic parameters, models with genetic groups for imported animals will be applied in further analysis. Additionally, comparison of phenotypic, environmental and genetic trends will be done to derive more precisely conclusions about direction and intensity of selection in this population.

4   CONCLUSIONS

Increase in litter size had negative effect on birth weight of kids and positive effect on litter weight. Age, parity, and season influenced litter size, birth weight of

Table 2: Variance component estimates and heritabilities for reproductive traits (± corresponding standard errors)

	σ_p^2		σ_a^2	σ_h^2	σ_e^2	σ_{pe}^2	h_a^2
LS	0.261	-	0.009 ± 0.001	0.031 ± 0.001	0.178 ± 0.001	0.043 ± 0.002	0.036 ± 0.005
BW	0.419	-	0.009 ± 0.001	0.195 ± 0.007	0.207 ± 0.001	0.008 ± 0.001	0.023 ± 0.003
LW	0.912	-	0.035 ± 0.004	0.371 ± 0.016	0.412 ± 0.003	0.093 ± 0.004	0.039 ± 0.005

LS – litter size; BW – birth weight; LW – total litter weight; σ_p^2, σ_a^2, σ_h^2, σ_{pe}^2, σ_e^2 – phenotype, additive genetic, herd-year, permanent-environmental and residual variance, respectively; h_a^2 – direct heritability;
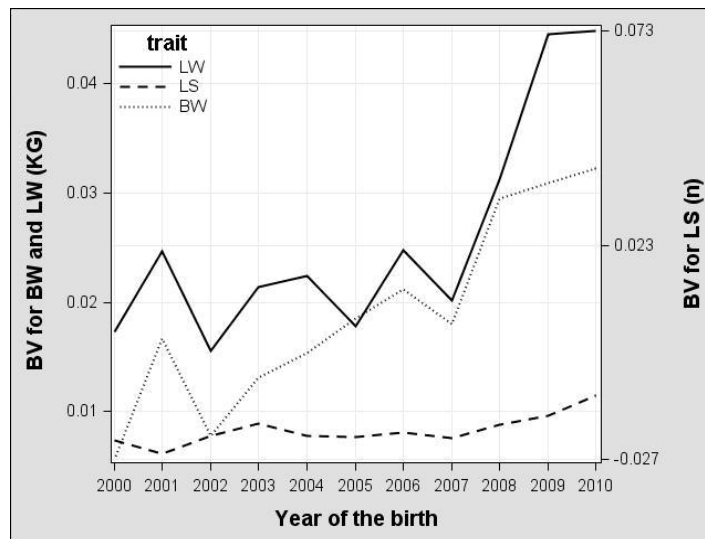
Figure 3: Average breeding values of reproductive traits by year of birth

kids and litter weight. Appreciation of mentioned environmental effects is necessary in statistical models for estimation of genetic parameters and genetic evaluation of goats for these traits. Considerable oscillations of average breeding values were determined in the last decade. Genetic progress in this population is determined after import of bucks for improving milking performances of goats. More genetic progress in existing herds could be expected without further import of sires if selection on milk yield would be based on BLUPs.

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