

ESTIMATION OF GENETIC PARAMETERS AND GENETIC TRENDS FOR REPRODUCTIVE TRAITS IN SAANEN GOATS

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The study was conducted on Saanen goats raised in Croatia. The object of the study was to determine the average litter size (LS), birth weight (BW) and total litter weight (TLW). The study included a total of 2 500 goats among which 1 786 were phenotyped. A total of 6 349 records for BW and 4 256 records for LS and TLW were used in descriptive and inferential statistical analysis. Determined averages for LS, BW and TLW were 1.74 lambs, 3.27 kg and 5.65 kg, respectively. Twinning and tripling rates were 36.9% and 6.2%. Single-trait analysis under 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, while herd-year, additive genetic, permanent environmental and residual were treated as random effects, respectively. Investigated environmental effects significantly affected all reproductive traits ($p < 0.001$). The largest phenotype variability among investigated traits was determined for TLW. Additive genetic effect accounted for 7%, 5% and 4% in total variability for LS, BW and TLW, respectively. Genetic trends of reproductive traits were estimated for the period from year 2000 to 2010. A positive genetic trend was determined for LS, a negative genetic trend for BW and genetic stagnation for TLW.

Key words: genetic trend, goats, heritability, reproductive traits, Saanen breed

INTRODUCTION

There are two major directions of goat farming in Croatia, extensive breeding systems in the karst areas mainly focused on meat production, and semi-intensive breeding systems in continental areas focused on milk production. In order to intensify milk production, a considerable number of Alpine and Saanen goats have been imported in Croatia in the last decade (Mioč *et al.*, 2007). According to Croatian agricultural agency, a total of 9 560 goats are covered by the selection program (HPA, 2011). Saanen breed is second in importance of

allochthonous breeds raised in Croatia. Control of reproductive traits for this breed is performed on the entire registered population. Milk production is the main goal of all farmers who raise this breed and the larger part of produced milk is processed into cheese (Mioč *et al.*, 2008). However, a significant part of income is obtained by selling non breeding kids for meat production. Litter size, birth weight and total litter weight are economically important traits often attributed as reproductive traits when considering dam's production. The majority of goats worldwide are reared in (semi) extensive breeding systems. Recording of productive performances in such conditions is hampered in comparison to intensive production systems. This makes studies conducted on goats often less comprehensive compared to those conducted on cattle and sheep, especially considering the estimation of genetic parameters. Reproductive traits are not important only from the meat production point of view. Their importance in milk production relies in strong the correlation with milk yield, thus different approaches in selection for these traits have been developed by now, worldwide. Nevertheless, there is a common scientific opinion that accuracy in the estimation of genetic parameters is crucial for efficient genetic improvement regardless of the selection method used. In order to achieve this goal, besides quality and quantity of data, appropriateness of analytical procedures are also required. Therefore, great efforts are constantly being made to improve statistical procedures and develop high computational programs for their practical implementation. Analysis of investigated traits and environmental effects affecting their expression is an important step in every inferential analysis, thus it can be considered as an indirect goal of this study. The main goals were to estimate genetic parameters for the aforementioned reproductive traits and to obtain genetic trends out of the predicted breeding values of animals in the last decade. By analysis of genetic trends for reproductive traits we will attempt to determine collateral results of the selection performed on milk productive traits in the aforementioned population.

MATERIALS AND METHODS

Animals

Data records for this study were obtained from the central database of the Croatian Agricultural Agency. Records of reproductive traits (birth weight (BW), litter size (LS) and composite trait of total litter weight at birth (TLW)) for Saanen breed used in this study were collected in the period from year 2000 to 2010. Records of birth date, parity, lambing date and herd for each goat were also taken from the same register. Goats with inconsistent records, goats with parities larger than 9 and those from herds with less than 15 animals were excluded from statistical analysis. Date of mating was calculated by subtracting 150 days from the date of kidding. For the purpose of statistical analysis, mating season was defined as the month within the year. In order to improve frequency distribution, some seasons were joined to the previous or next season. If the litter size was larger than 3, it was set to 3. Statistical analysis was performed on records obtained out of 4 256 parturitions from 1 786 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 2500 animals were included in the relationship matrix.

Statistical analysis and genetic parameter estimation

Data editing, descriptive statistics and inferential statistical analysis (fixed effects), as well as pedigree preparation were performed in SAS program package (SAS, 9.2). Variance components and heritabilities were estimated using the REML procedure applied on single trait repeatability animal model. Fixed part of the model included season (as year-month interaction), age at lambing (as quadratic regression) nested within parity (9 levels) and type of birth effect (3 levels), respectively. Herd-year, additive genetic effect and permanent environmental effects were treated as random. Repeated measurements were considered as expression of the same trait over time. The model assumes genetic correlations between parities and constant phenotype variance for all traits. The full model was used for the weight traits (TLW, BW) while the reduced model (without type of birth effect) was used for litter size. General matrix form of the model was:

$$y = Xb + W_h h + W_p p + Z_a a + e;$$

where y is a vector of phenotype observations (BW, LS, TLW); 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 a vector of residuals; while X , Z_a , W_h and W_p are design matrices linking phenotype records with corresponding parameters. Model assumptions were:

$$E(y) = Xb, h | H \sim N(0, H), p | P \sim N(0, P), a | G \sim N(0, G), e | R \sim N(0, R)$$

where $G = A\sigma_a^2$, $H = I_h\sigma_h^2$, $P = I_p\sigma_p^2$ and $R = I_e\sigma_e^2$. A is the numerator relationship matrix and I_h , I_e and 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. Genetic parameters and breeding values were estimated with software package VCE (Groeneveld *et al.*, 2008). Simultaneous estimates for fixed effects (BLUE) and prediction of random effects (BLUP) were obtained out of the following mixed model equation:

$$\begin{matrix} X^T X & X^T Z_a & X^T W_p & X^T W_h & \hat{b} & & \mathbf{X}^T y \\ Z_a^T X & Z_a^T Z_a & A^{-1} & Z_a^T W_p & Z_a^T W_h & \hat{a} & = & Z_a^T y \\ W_p^T X & W_p^T Z_a & W_p^T W_p & I_2 & W_p^T W_h & \hat{p} & & W_p^T y \\ W_h^T X & W_h^T Z_a & W_h^T W_p & W_h^T W_h & I_3 & \hat{h} & & W_h^T y \end{matrix}$$

where: $\alpha_1 = \sigma_e^2/\sigma_a^2$, $\alpha_2 = \sigma_e^2/\sigma_p^2$, $\alpha_3 = \sigma_e^2/\sigma_h^2$.

Genetic trends were obtained as regression of birth year on the average breeding values.

RESULTS

Single records of litter weight related to the age of mating are presented in Figure 1. Litter weight ranged from 1.5 to 13.5 kg, depending on litter size and individual birth weight of kids. On first sight, a pattern of seasonal mating is easily noticeable. Mating season is marked with dense fields, while blanks in the figure clearly represent periods of anestrus i.e. reduced sexual activity. Figure reveals good frequency distribution of phenotyped goats according to different age and parities. The increase in total litter weight, with the increase in litter size, is also evident. However, it can also be seen that larger litter size does not necessarily imply higher total litter weight.

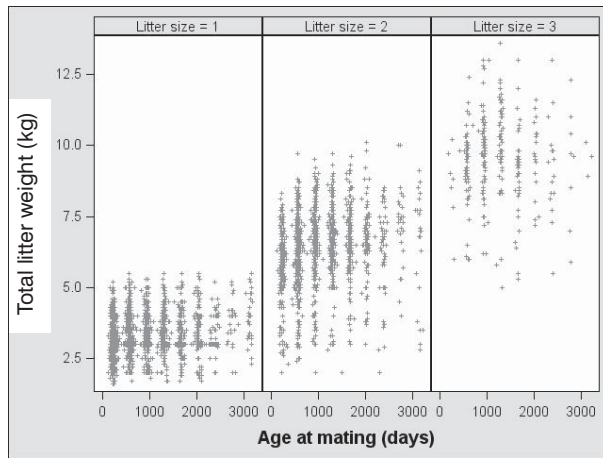


Figure 1. Total litter weights (TLW) obtained in different age of Saanen goats

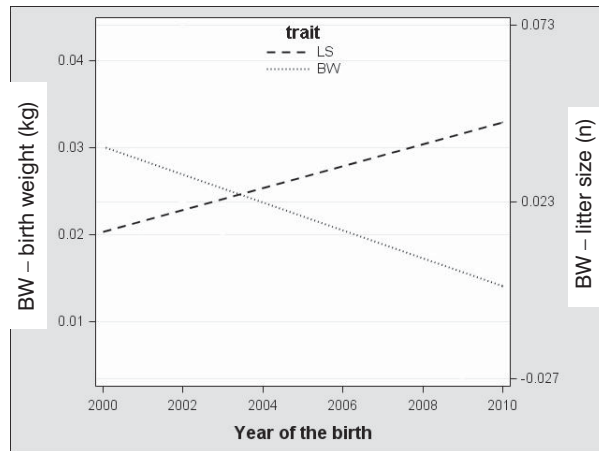


Figure 2. Genetic trends for LS and BW in the period from year 2000 to 2010.

Descriptive statistics of reproductive traits for Saanen goats is presented in Table 1. Average LS, BW and TLW were 1.74 kids, 3.27 kg and 5.65 kg, respectively. Frequencies of kids born as singles, twins and triplets were 38.16, 49.54 and 12.30, respectively. Analogously, 56.9 % of goats had singles, 36.9 % had twins and 6.2 % had triplets. Litter size significantly affected birth weight and total litter weight ($p < 0.001$). The increase in litter size was accompanied by a decrease of individual birth weight of kids. In contrast, a positive effect on total litter weight was detected. Parity significantly affected all investigated traits ($p < 0.001$). Increase for all three traits was detected up to third parity, followed by a gradual decline with further parities.

Table 1. Descriptive statistics of reproductive traits (LS means \pm standard error)

	N	%	LS	BW	TLW
Overall	6349	100	1.74 \pm 0.01	3.27 \pm 0.01	5.65 \pm 0.01
Litter size					
1	2423	38.16	-	3.33 \pm 0.04	3.21 \pm 0.07
2	3145	49.54	-	3.21 \pm 0.04	6.23 \pm 0.07
3	781	12.30	-	3.00 \pm 0.04	9.14 \pm 0.08
Parity					
1	1516	23.88	1.63 \pm 0.05	3.06 \pm 0.04	6.14 \pm 0.07
2	1480	23.31	1.88 \pm 0.03	3.21 \pm 0.03	6.30 \pm 0.05
3	1193	18.79	1.89 \pm 0.02	3.28 \pm 0.02	6.51 \pm 0.03
4	854	13.45	1.78 \pm 0.03	3.24 \pm 0.03	6.37 \pm 0.05
5	627	9.88	1.72 \pm 0.05	3.17 \pm 0.05	6.17 \pm 0.08
6	324	5.10	1.55 \pm 0.07	3.10 \pm 0.07	6.10 \pm 0.11
7	172	2.71	1.53 \pm 0.09	3.07 \pm 0.09	5.98 \pm 0.15
8	101	1.59	1.40 \pm 0.12	3.03 \pm 0.11	6.12 \pm 0.19
9	82	1.29	1.18 \pm 0.15	3.02 \pm 0.14	6.05 \pm 0.24

LS- litter size; BW- birth weight TLW – total litter weight

Estimates of dispersion parameters and heritabilities are presented in Table 2. TLW had the largest phenotype variability among investigated traits. Herd-year, permanent environmental, additive genetic and residual effects respectively accounted for 11%, 16%, 7% and 66% of total phenotype variability in LS.

The same effects accounted for 37%, 3%, 5% and 55% of variability in BW, and 31%, 14%, 4% and 50% of variability in TLW, respectively. A higher proportion of herd-year effect in the total variability was estimated for weight traits in comparison to LS. The heritability estimates for all three traits were anticipated low (4-7%).

Table 2. Variance component estimates and heritabilities for reproductive traits (\pm standard error)

	σ_p^2	σ_a^2	σ_h^2	σ_e^2	σ_{pe}^2	h_a^2
LS	0.261	0.026 \pm 0.009	0.043 \pm 0.008	0.248 \pm 0.005	0.061 \pm 0.008	0.068 \pm 0.023
BW	0.365	0.017 \pm 0.005	0.138 \pm 0.018	0.197 \pm 0.004	0.011 \pm 0.004	0.047 \pm 0.012
TLW	1.046	0.045 \pm 0.016	0.331 \pm 0.047	0.526 \pm 0.011	0.143 \pm 0.015	0.042 \pm 0.016

LS – litter size; BW – birth weight; TLW – 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

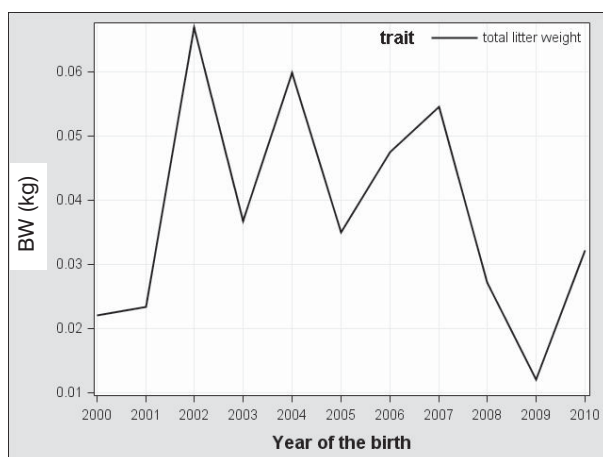


Figure 3. Average breeding values for TLW in the period from year 2000 to 2010.

Genetic trends for LS and BW are presented in Figure 2. Genetic progress of LS and simultaneous genetic decline of BW can be detected. Annual fluctuations of average estimated breeding values for the composite trait TLW in the last decade is presented in Figure 3, which reveals the absence of genetic progress for this trait which is practically the result of the opposite genetic trends of its components i.e. LS and BW.

DISCUSSION

The peak of mating activity in the investigated goats was detected 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 (Mioč and Pavić, 2002; Misztal *et al.*, 2004; Zarazaga *et al.*, 2005). Reproductive traits determined in this study, as well as results of investigated environmental effects were in accordance with some

previous reports for dairy goats (Amoah *et al.*, 1996; Mellado *et al.*, 2011). Also, an almost identical pattern of changes in reproductive traits of sheep with progressing age and parity was reported by Škorput *et al.* (2011) and Maria and Ascaso (1999). Results of our study confirm numerous statements that the ability of multiparous females to produce larger litters is influenced by two factors: age and previous reproductive experience (Amoah and Gelaye, 1990; Awemu *et al.*, 1999; Maria and Ascaso, 1999). Nevertheless, it is always a problem to clearly distinguish between these effects and quantify their contribution in the total variability. Confounding is almost unavoidable here and fitting these effects in statistical models requires special attention. Furthermore, models for the analysis of repeated measurements over time (longitudinal data), require appropriate covariance structures, and, if computationally feasible, the inclusion of non-genetic random effects in the estimation of genetic parameters, as well as in the prediction of breeding values. Our estimates of heritability for LS (7%) are in agreement with those reported by Maghsoudi *et al.* (2009), Rashidi *et al.* (2011), Tesfaye *et al.* (2011) and Mohammadi *et al.* (2011). On the other hand, Bagnicka *et al.* (2007), Zhang *et al.* (2009) and Gunia *et al.* (2011) reported higher estimates in their studies. Estimate of heritability for TLW (4%) was in agreement with estimates reported by Rashidi *et al.* (2011), and lower than those reported by Zhang *et al.* (2009) and Mohammadi *et al.* (2011). The wide range of estimated variance components and genetic parameters between different studies mainly arises because of different analytical approaches (statistical models). By not including additional non-genetic random effects in the statistical models, genetic parameters are often over-estimated. Also, inconsistent data between studies in terms of population size and pedigree structures (linkage of animals) are also important causative factors of this variability. Considerably high ratio of herd-year effect in our study determined for weight traits implicates their high sensibility to different management systems (food supply). In contrast, a smaller contribution of the mentioned effect in variation of litter size indicates lower environmental plasticity of this trait. By the analysis of genetic trends, small genetic progress is determined for litter size. Since reproductive traits weren't the selection target in this population yet, genetic correlation between milk yield and litter size (Komniakis *et al.*, 1998, Ligda *et al.*, 2000) implicate that genetic gain is the collateral result of long term selection on milk yield. Besides the introduction of BLUP for milk yield for dairy goats in Croatia, this progress is partially a result of import of animals with high genetic potential for milk production. Also, the contribution of farmers that select animals according to phenotype must be considered here. In the same period, genetic decline is detected for the birth weight of kids. That is reasonable and somewhat expected, considering the negative correlation between litter size and birth weight (Mioč *et al.*, 2011). Furthermore, decline in BW resulted in absence of genetic progress of TLW despite genetic progress of LS. Low heritability estimates for all investigated traits obtained in this study support numerous statements of non-effective direct selection for reproductive traits. In order to discuss the possibilities of genetic progress for reproductive traits simultaneously with genetic progress for milk yield, multi-trait analysis will be performed in the near future.

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PROCJENA GENETSKIH PARAMETRA I GENETSKIH TRENDOVA ZA REPRODUKTIVNA SVOJSTVA U POPULACIJI SANSKIH KOZA

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SADRŽAJ

Istraživanje je provedeno na populaciji koza sanske pasmine u Hrvatskoj. Istraživanjem je obuhvaćeno ukupno 2 500 koza od kojih je 1 786 koza bilo fenotipizirano. Analizirana su sljedeća svojstva: broj jaradi u leglu, porodna masa jaradi i ukupna masa legla. U deskriptivnoj i inferencijalnoj statističkoj analizi korišćeno je ukupno 6 349 fenotipskih zapisa za porodnu masu jaradi te 4 256 zapisa za broj jaradi u leglu i ukupnu masu legla. Ovim istraživanjem je utvrđeno prosječno 1.74 jaradi u leglu te porodna masa jaradi 3.27 kg i ukupna masa legla 5.65 kg. U istraživanoj populaciji utvrđeno je 36.9% koza koje su ojarile dvojke te 6.2% koza koje su ojarile trojke. Univarijatnom analizom koristeći „animal“ model sa ponovljenim mjerenjima procijenjene su komponente varijance i predviđene uzgojne vrijednosti. Sezona (mjesec unutar godine), starost prilikom jarenja (kao kvadratna regresija) ugniježdjena unutar redoslijeda jarenja te tip jarenja su tretirani kao fiksni, dok su interakcije stado-godina, aditivni genetski efekti te permanentni utjecaj okoline tretirani kao slučajni utjecaji u statističkom modelu. Svi istraživani utjecaji su statistički značajno utjecali na sva reproduktivna svojstva ($P < 0.001$). Najveća fenotipska varijabilnost je utvrđena za svojstvo ukupne mase legla. Aditivnim genetskim efektima objašnjeno je 7%, 5% te 4% ukupne varijabilnosti broja jaradi u leglu, porodne mase jaradi i ukupne mase legla. Genetski trendovi istraživanih svojstava su procijenjeni za razdoblje od 2000. do 2010. godine. Utvrđen je pozitivan genetski trend za broj jaradi u leglu, negativan genetski trend za porodnu masu jaradi te stagnacija u genetskom smislu za svojstvo ukupne mase legla.

