

Genetic Parameter Estimates for Growth Traits in Saanen Kids

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Abstract

Genetic parameters of test day (from birth to sixth month) body weight and body size parameters of Saanen kids were estimated by random regression with third order Legendre polynomial. The analyses were applied to 2673 test day records of 382 Saanen kids (Twin = 328; Single = 54; Female = 204; Male = 178) in a private dairy goat farm in Samsun, at the black Sea region of Turkey. Permanent environmental variances were static for height at sacrum, height at withers and chest depth, increased for body weight and body length on time. Heritability values ranged from 0.2679 to 0.6135 for body weight and Height at withers. Genetic correlations changed between 0.725 and 0.979 in all traits. The positive high genetic correlations among traits suggested that selection for any one of these traits would result in considerable positive change in other traits.

Keywords: Saanen kids, Heritability, Growth, Genetic parameters

Saanen Oğlaklarında Büyüme Özellikleri İçin Genetik Parametre Tahminleri

Özet

Saanen oğlaklarının test günü canlı ağırlığı ve vücut ölçülerinin genetik parametreleri random regresyon ile üçüncü dereceden Legendre polinomu kullanılarak tahmin edilmiştir. Analizler, Türkiye'nin Karadeniz bölgesinde, Samsun'daki özel bir süt keçi çiftliğinde yetiştirilen 382 adet Saanen oğlağına (ikiz = 328; Tekiz = 54; Dişi = 204; Erkek = 178) ait 2673 test günü (doğumdan altıncı aya kadar) kayıtlarına uygulanmıştır. Kalıcı çevre varyansları, sağrı yüksekliği, cidago yüksekliği ve göğüs derinliği için durağan iken vücut ağırlığı ve vücut uzunluğu için zamanla yükselmiştir. Kalıtım derecesi değerleri vücut ağırlığı ve cidago yüksekliği için 0.2679 ile 0.6135 arasında değişim göstermiştir. Genetik korelasyonlar tüm özelliklerde 0.725 ile 0.979 arasında değişmektedir. Özellikler arasındaki pozitif yüksek genetik korelasyonlar bu özelliklerden herhangi biri için yapılacak seleksiyonun diğer özellikler için de önemli bir ilerleme sağlanacağını göstermektedir.

Anahtar sözcükler: Saanen oğlağı, Kalıtım derecesi, Büyüme, Genetik parametre

INTRODUCTION

Goats become an alternative livestock animals for farmers in the rugged terrain of the Black Sea region in Turkey. Turkey's goat population is about 8.9 million head and 8.1 million of this population is the native hair goat^[1]. That breed is characterized by low litter size, short lactation period and low milk yield^[2]. To increase goat milk production in these areas, the Saanen breed was introduced as substitute to hair goat for the past 15 years.

Important factors affecting profitability for goat enterprises are early growth traits. The weight and size of kids at birth are determined not only by their genetic potential but also by environment and maternal effects^[3]. When selecting goat breeding stock observing some growth characteristics of the kids may be useful^[2]. Furthermore, recognizing genetic parameters of growth traits may also facilitate the breeding program. Growth traits are economically important for using early breeding of young animals.



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Traditionally, traits that are measured in time are analyzed with a multitrait model, defining the phenotypic values at distinct ages as different traits. One advantage of random regression models over multivariate models is that with random regression models it is possible to calculate (co)variances between or at every age or instance. Random regression models provide a method for analyzing independent components of variation that reveal specific patterns of change overtime^[4].

Random regression (RR) models have become a popular choice for modeling of traits, which are measured repeatedly per individual, but change gradually and continually with time. The RR models have described general shape of growth curve by fixed regression for all dams and the individual genetic deviation from the fixed regressions. Regression coefficients from RR models are generally described by the orthogonal functions such as Legendre polynomials. Coefficients derived from fitting orthogonal functions are very useful for analyzing patterns of genetic variation in the trajectory. Legendre polynomials, a family of the orthogonal functions, are orthogonal and normalized, which results in better converge and more accurate results than the conventional polynomials. Applications in genetic evaluation schemes have been limited to the analysis of test-day records. Genetic merit for growth of meat producing animals is generally assessed treating records taken at different ages, or ranges of ages, as different traits^[5,6].

Zhang et al.^[7] reported that the mean values and standard errors of direct additive heritability estimates calculated with the optimum model were 0.17 ± 0.07 , 0.22 ± 0.08 , 0.07 ± 0.07 , 0.10 ± 0.08 , 0.30 ± 0.12 and 0.08 ± 0.10 for birth weight, body weight at 90 days, average daily gains from birth to 90 days, body weight at 300 days, average daily gains from birth to 300 days and average daily gains from 90 to 300 days, respectively for Boer goat. Janssens and Vandepitte^[8] showed that heritability of body measurements were in the range of 0.26-0.57 and genetic correlations between these traits were high for Belgian Bleu du Maine, Suffolk and Texel sheep. Alade et al.^[9] reported that heritability estimates from sire component were 0.39, 0.47, 0.39, 0.04, 0.03 and 0.22 for litter size, birth weight, pre-weaning gain, weaning weight, post-weaning gain and 9 month body weight, respectively. The corresponding values of repeatability estimates for mentioned study were 0.12, 0.61, 0.37, 0.52, 0.24 and 0.4. Zhang et al.^[3] declared that the mean values and standard error of direct additive heritability estimates for body weight, body length, height and chest depth calculated with REML model were 0.19 ± 0.08 , 0.14 ± 0.07 , 0.24 ± 0.09 and 0.25 ± 0.10 , respectively.

The objective of this study is to estimate the genetic parameters for weight and size including length, height at sacrum and withers and chest girth measures at birth to

six months of age in Saanen goats raised in the Black Sea region of Turkey.

MATERIAL and METHODS

Material

Data was collected at a private dairy goat farm in Samsun, Turkey ($40^{\circ}31'N$, $36^{\circ}53'E$ and 650 m above the sea level), which consisted of 382 Saanen kids (Twin = 328; Single = 54; Female = 204; Male = 178) born from February to March 2013 from 278 does (only the data of lived animals during the experiment were used. Hence, 382 records were used for each time point). 11 bucks were used to impregnate the animals. For the analysis 2673 test day records were recorded. Body weight (BW) and body size parameters; body length (BL), height at sacrum (HS), height at withers (HW) and chest depth (CD) at birth were recorded within 24 h after the birth using the routine method as described by Chen^[10]. These traits were measured monthly from birth to six months of age.

Kids were fed with dam's milk, had free access to alfalfa hay and concentrate after 2nd week under intensive system, Kids weaned at 65-70 days of age.

Methods

In this study, additive genetic and permanent environmental (co)variances and heritability values of the BW, BL, HS, HW and CD were estimated using random regression model with Legendre polynomials. These polynomials were used because they are orthogonal, normalized and resulted in a better convergence and more accurate results as compared to conventional polynomials^[11] and they represent the coefficients most widely used to describe size-age relationships in animals^[12]. Moreover, to model the (co)variance structure of the random components of the data for RRM, third order Legendre polynomial model was preferred due to the best fit^[13-19]. Residual variance was also assumed to be constant. All data were analyzed with the DXMRR option of the DFREML statistical package^[20]. The general random regression model used in this study is as follows:

$$y_{ijkl} = TB_i + S_j + \sum_{m=1}^3 \beta_m \phi_m X_m(t_{ijk}) + \sum_{m=1}^3 \alpha_{jm} \phi_m(t_{ij}) + \sum_{m=1}^3 p_{jm} \phi_m(t_{ijk}) + e_{ijkl} \quad (1)$$

where y_{ijkl} is the i^{th} test day records of the kid k , TB_i is the i^{th} type of birth effect, S is the j^{th} sex effect, b_m is the m^{th} fixed regression coefficients, t_{ijk} is the test day of the kid k , $X_m(t_{ijk})$ is the m^{th} covariate evaluated at t_{ijk} , α_{jm} is the m^{th} additive genetic random regression coefficients for kid k , p_{jm} is the m^{th} permanent environmental random regression coefficients for kid k , ϕ_m is the m^{th} polynomial

evaluated for the age t_{ijk} , and e_{ijkl} is the random residual effect. To calculate phenotypic correlations, canonical correlation [21] was used because of repeated data for each time point belonged to 382 animals.

RESULTS

Means and standard deviations of BW, BL, HS, HW and CD for each time point for birth type and sex were given in [Table 1](#) and [Table 2](#), respectively.

Third order Legendre polynomial model was used for random effects because of best fit. Other attempted models such as linear and quadratic were not argued in this study to avoid confusion. Estimated variance components for test day measurements were given in [Fig. 1](#), [Fig. 2](#) and [Fig. 3](#) for additive genetic variance, permanent environmental variance and heritability estimates, respectively.

Estimates of genetic and canonical phenotypic

correlations among BW, BL, HS, HW and CD traits were given in [Table 3](#).

The estimates of additive genetic variances among traits were not similar. Genetic variances ranged from 0.1424 (BW) to 3.078 (HW), permanent environmental variances ranged from 0.1854 (CD) to 2.365 (HS) and heritability ranged from 0.2679 (BW) to 0.6135 (HW). The highest additive genetic variances were obtained for HS and HW, lowest was for CD. Permanent environmental variance was almost stationary over time for HS, HW, BL and CG, but tended to increase over time for BL. Changes in heritability estimates were compatible with changes in additive genetic variances for all traits. The heritability estimates of all traits were perpetually increased over time. Heritability for BW was the most increasing heritability over time. Strong positive phenotypic and genetic correlations were obtained among all traits showing values greater than 70 percent. All traits had insignificant genetic correlations with BW.

Table 1. Mean and pooled standard deviation of traits on each time point for birth type (n=382)

Tablo 1. Her bir zaman noktasında doğum şekli için özelliklerin ortalaması ve bileşik standart sapması (n=382)

Birth type	Traits	Birth	Month 1	Month 2	Month 3	Month 4	Month 5	Month 6	PSD
Single	BW	4.14	9.92	14.24	18.39	22.82	27.35	31.65	1.57
	BL	38.87	42.71	46.73	49.69	52.26	54.69	56.82	2.00
	HS	40.30	42.92	46.07	49.32	52.35	55.82	60.43	2.01
	HW	40.10	42.94	46.62	50.96	54.55	57.71	60.48	1.77
	CD	12.44	15.98	17.79	19.56	21.12	22.96	25.49	1.24
Twin	BW	2.98	8.24	11.88	15.71	19.43	23.80	27.87	1.29
	BL	37.19	40.83	45.02	47.54	50.08	52.31	54.37	1.86
	HS	38.90	41.50	44.17	47.44	50.54	53.85	57.79	1.88
	HW	38.92	41.44	44.85	48.94	52.50	55.56	58.17	1.44
	CD	11.42	14.87	16.44	18.23	19.58	21.69	24.35	0.90

BW: body weight, BL: body length, HS: height at sacrum, HW: height at withers, CD: chest depth, PSD: pooled standard deviation

Table 2. Mean and pooled standard deviation of traits on each time point for sex (n=382)

Tablo 2. Her bir zaman noktasında cinsiyet için özelliklerin ortalaması ve bileşik standart sapması (n=382)

Sex	Traits	Birth	Month 1	Month 2	Month 3	Month 4	Month 5	Month 6	PSD
Male	BW	4.03	10.30	14.88	19.26	23.26	27.65	31.85	3.12
	BL	38.89	42.68	46.34	50.13	52.58	55.10	57.42	2.18
	HS	39.89	42.76	45.79	49.37	52.47	55.84	60.87	2.41
	HW	39.68	43.00	47.16	50.79	54.61	58.08	61.37	2.53
	CD	12.34	16.24	17.97	20.03	21.42	23.29	25.45	1.42
Female	BW	3.55	8.59	12.29	16.06	20.44	24.99	29.34	2.85
	BL	37.85	41.63	46.06	48.03	50.69	52.92	54.85	2.01
	HS	39.83	42.22	45.19	48.17	51.17	54.68	58.49	2.17
	HW	39.76	42.59	46.33	50.19	52.99	56.03	58.53	2.22
	CD	11.92	15.10	16.83	18.38	19.94	21.92	24.85	1.38

BW: body weight, BL: body length, HS: height at sacrum, HW: height at withers, CD: chest depth, PSD: pooled standard deviation

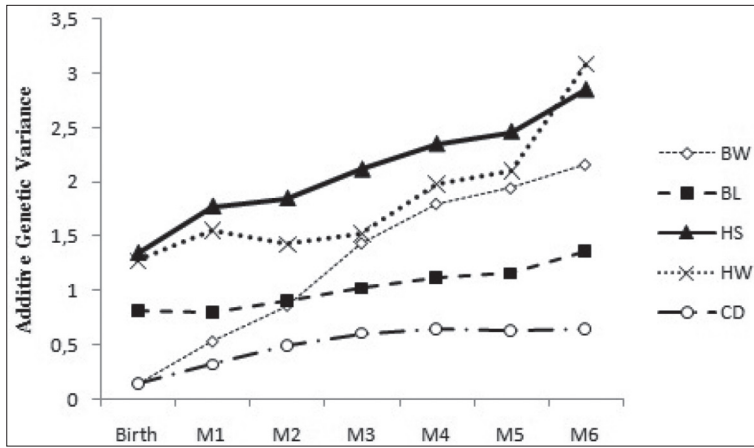


Fig 1. Additive genetic variances for traits of body weight, body length, height at sacrum, height at withers and chest depth of Saanen kids

Şekil 1. Saanen oğlaklarının vücut ağırlığı, vücut uzunluğu, cidago yüksekliği, sağrı yüksekliği ve göğüs derinliği özellikleri için eklemeli genetik varyansları

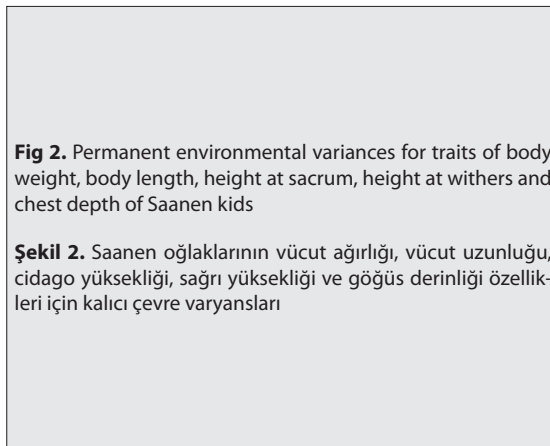


Fig 2. Permanent environmental variances for traits of body weight, body length, height at sacrum, height at withers and chest depth of Saanen kids

Şekil 2. Saanen oğlaklarının vücut ağırlığı, vücut uzunluğu, cidago yüksekliği, sağrı yüksekliği ve göğüs derinliği özellikleri için kalıcı çevre varyansları

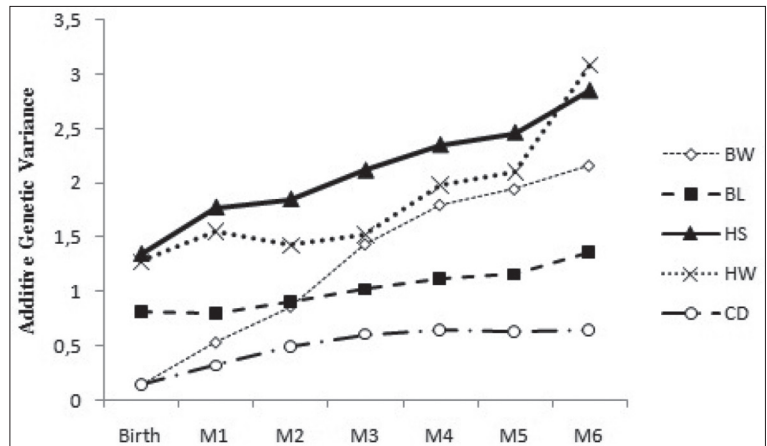


Fig 3. Heritability estimates for traits of body weight, body length, height at sacrum, height at withers and chest depth of Saanen kids

Şekil 3. Saanen oğlaklarının vücut ağırlığı, vücut uzunluğu, cidago yüksekliği, sağrı yüksekliği ve göğüs derinliği özellikleri için kalıtım derecesi tahminleri

DISCUSSION

The mean values of BW, BL, HS, HW and CD traits in Saanen kids raised in Black Sea region of Turkey were similar to values reported by Ocağ et al.^[2] for Saanens in the Cukurova sub-tropical region. Mean values of BW, BL and HS were greater than those reported by Bungsisawat and Tumwasorn^[22] and BW values were greater than those reported by Simsek et al.^[23]. The higher values recorded for these traits may be the result of adaptation to environment or quality of environmental conditions.

For any production objective fixed effects are very important. In this study, fixed effects on growth traits were similar to those reported by Boujenane and El Hazzab^[24], Otuma and Osakwe^[25], Bedhane et al.^[26] and Ocağ et al.^[2]. In all these studies as well as ours growth stages were highly affected by birth type and sex. But the effects of sex factor decreased with age and lost its importance as highlighted by Olfaz et al.^[27].

Variance component estimations are more sensitive to sampling errors. For all interested traits, weight was the most variable trait with a coefficient of variation (CV) of

Table 3. Estimates of genetic (above diagonal) and canonical phenotypic (below diagonal) correlations among traits**Tablo 3.** Özellikler arasındaki genetik (köşegen üstü) ve kanonik fenotipik (köşegen altı) korelasyon tahminleri

Traits	BW	BL	HS	HW	CD
BW		0.827**	0.971**	0.807**	0.979**
BL	0.951**		0.904**	0.936**	0.725**
HS	0.957**	0.953**		0.911**	0.919**
HW	0.973**	0.970**	0.978**		0.726**
CD	0.973**	0.947**	0.953**	0.959**	

BW: body weight, **BL:** body length, **HS:** height at sacrum, **HW:** height at withers, **CD:** chest depth

16%, for the other traits CV was around 5%. A considerable amount of the variation could be explained especially by fixed effect of birth type, similarly with the result of Janssens and Vandepitte [8] and Ocak et al. [2]. Estimates of additive genetic variance were higher than the values from previous studies Bedhane et al. [26], Zhang et al. [3]. Similar additive genetic variance estimates were presented by Schoeman et al. [28]. That was lower than the results of Abbasi and Ghafouri-Kesbi [29] except for HS and HW traits.

The estimates of permanent environmental variances were lower than the values from previous studies Bungsisawat and Tumwasorn [22], Abbasi and Ghafouri-Kesbi [29] and Schoeman et al. [28]. Permanent environmental variances obtained in this study were higher than the study of Zhang et al. [3] with the exception of chest depth. Estimates of heritability were higher for BW, HS and HW than the results presented by Zhang et al. [3] and Bungsisawat and Tumwasorn [22]. Similar heritability estimates obtained for BL and CD with the study of Zhang et al. [3]. Alike heritability estimates obtained for BL with the results presented by Bungsisawat and Tumwasorn [22]. Similar heritability estimates observed for all traits with results of Abbasi and Ghafouri-Kesbi [29]. Estimated genetic correlations for all traits were similar to the results of Zhang et al. [3], Abbasi and Ghafouri-Kesbi [29].

Estimated heritability values indicated that improvement in body weight and body measurements of Saanen kid is possible through selection procedures for using early breeding. The positive high correlations between body weight and body measurements indicate that these traits share a genetic component; therefore, selection for body measurements could possibly lead to improve in body weight and vice versa. The positive high genetic correlations among traits suggested that selection for any one of these traits would result in considerable positive change in other traits. Accurate estimates of genetic parameters are crucial for genetic improvement in livestock. The results obtained in this investigation can be applied for genetic improvement programme of Saanen goats.

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