Genetic Parameters for Direct and Maternal Effects and Estimation of Breeding Values for Birth Weight in Brown Swiss Cattle

Muammer TİLKİ^{1,*}, Mustafa SAATCI², Mehmet ÇOLAK³

¹Department of Animal Science, Faculty of Veterinary Medicine, Kafkas University, 36300 Kars - TURKEY ²Department of Animal Science, Faculty of Veterinary Medicine, Mehmet Akif Ersoy University, 15100 Burdur - TURKEY ³Bahri Dağdaş International Agricultural Research Institute, Konya - TURKEY

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Abstract: Variance components, genetic parameters, and breeding values for birth weight in Brown Swiss cattle reared in Bahri Dağdaş International Agricultural Research Institute were estimated by REML-BLUP procedures using MTDFREML computer programme. Six different animal models were fitted for the trait ranging from a simple to the most comprehensive model. The most detailed model (model 6) provided the best fit to the used dataset. Heritability was higher in the model without maternal effect. Although maternal effect had a significant place for the data, environmental effect due to dam was not important. Heritability (h²), maternal heritability (m²), and the genetic correlation between these 2 parameters (r_{AM}) were 0.15, 0.06 and 0.92, respectively, according best model (model 6). Breeding values were also calculated for the trait, but no positive or negative change has been observed between years. More detailed accurate data are needed to establish the applied method on the livestock sector in Turkey.

Key Words: Brown Swiss, birth weight, genetic parameters, breeding values, maternal effect

Esmer Irk Sığırlarda Doğum Ağırlığına ait Direkt ve Analık Etkisi Altındaki Genetik Parametreler ve Damızlık Değerlerin Tahmini

Özet: Bu çalışma, Bahri Dağdaş Uluslararası Tarımsal Araştırma Enstitüsünde yetiştirilen Esmer ırk sığırların doğum ağırlıklarının varyans unsurları, genetik parametreleri, ve damızlık değerlerinin tahmini için yapılmıştır. Çalışmada REML-BLUP tekniği kullanılmış, bu amaçla MTDFREML bilgisayar programından faydalanılmıştır. En basit modelden en yoğununa kadar toplam 6 farklı model uygulanmıştır. En uygun modelin, model 6 olduğu belirlenmiştir. Kalıtım derecesi, analık etkisinin olmadığı modelde en yüksek olarak tespit edilmiştir. Analık etkisi çevre faktörleri içerisinde önemli bir yer tutmasına rağmen, anadan kaynaklanan etki önemsizdir. Model 6'ya göre kalıtım derecesi (h^2), analık kalıtım derecesi (m^2) ve bu ikisi arasındaki genetik korelasyon (r_{AM}) sırasıyla 0,15, 0,06 ve 0,92 olarak bulunmuştur. Çalışmada damızlık değerleri de tahmin edilmiştir. Fakat yıllara göre herhangi bir pozitif veya negatif eğilim görülmemiştir. Bu tür çalışmaların Türkiye hayvancılığına uyarlanması için daha detaylı ve uygun verilere ihtiyaç vardır.

Anahtar Sözcükler: İsviçre esmeri, doğum ağırlığı, genetik parametreler, damızlık değerleri, analık etkisi

Introduction

Birth weight (BW) of an animal and its early growth rate, particularly till weaning, are determined not only by its own genetic potential but also by the maternal environment (1). The physiological and physical capacities of a dam and its uterine environment have the influences on fetus and calf as maternal ability (2-5). The genotype of the dam also affects the phenotype of the calf through a sample of half her direct additive genes for growth as well as through her genotype for maternal effects on calf weights (1). Furthermore, birth weight of a calf is a major factor contributing to dystocia and subsequent complication (6). Knowledge of genetic parameters of production traits from birth to slaughter plays an important role in beef production (7,8). Many researchers reported the positive genetic and phenotypic

^{*} Present address: Kafkas University, Faculty of Veterinary Medicine, Department of Animal Science, 36300, Kars - TURKEY E-mail: mtilki@hotmail.com

correlations between BW and several growth traits such as weaning and yearling weight (9,10). Direct heritability for birth weight of calves examined was between 0.18 and 0.40 by Ulutaş (11). The ranges of maternal heritability for birth weight were reported between 0.13 and 0.27 for 5 different cattle breeds (12). Improved computer capability with friendly programs allowed the easy use of restricted maximum likelihood (REML) with several animal models to estimate for both genetic and phenotypic variance components of the traits (13-15).

The aim of this study was to predict (co)variance components due to direct and maternal effects for BW using REML procedures with the data obtained from Brown Swiss cattle herd raised in Bahri Dağdaş International Research Institute, Konya, Turkey.

Material and Methods

Records belonging to the time period between 1981 and 2002 for birth weight (BW) and pedigree information were obtained for Brown Swiss cattle reared in Bahri Dağdaş International Research Institute. Information available for each animal in data set comprised of calf, sire and dam identification, sex (male and female), year, birth type, and dam age. Numbers of records, overall means, and standard deviations with the significance levels of the effects on the trait are presented in Table 1. Additionally, the effect of year and season interaction was tested in a general linear model and found non–significant for birth weight (P > 0.05).

Genetic parameters, (co)variance components, and breeding values of BW were estimated by MTDFREML (6), a set of programs for estimating (co)variance components using animal models and derivative-free restricted maximum likelihood (REML) procedure. The program was rerun with the estimates at previous apparent convergence as initial values until a global minimum of -2 of the log likelihood was found, when -2log of the likelihood did not change to the third decimal after consecutive reruns (16). Six different animal models were used to estimate the parameters as presented in Table 2 (1). Animal was a random factor in the applied models. Models also included the maternal permanent environmental effect, fitted as an additional random effect uncorrelated with all other effects in the model, a maternal common environment effect, an additive maternal effect fitted as a second random effect for each

animal with the same covariance structure as the additive direct effect and a covariance between direct and maternal genetic effects (17). The fixed effects (sex, dam age, etc.) used in the models had been identified in a preliminary analysis of the data (18). Identified non-significant (P > 0.05) fixed effects and covariates removed from the models by backwards-elimination.

The best model for the used data was defined based on the likelihood ratio test, comparing differences between -2 Log L to a critical value from a chi square distribution (19). Breeding values for BW were estimated using the best model. Trends in breeding values were estimated within a year of birth.

Results

The genetic parameters and (co)variance components for the 6 models used are presented in Table 3. Models, which were ignoring additive maternal effects (models 1 and 2), had produced higher h^2 . Similarly models 3 and 5 ignoring the covariance between direct additive and maternal effect tended to generate greater estimates of m^2 . Models 4 and 6 had the lowest -2 Log L value and did not differ significantly from the other models. Model 1 (maternal effect ignored) produced the highest σ^2_{Λ} and h^2 . In model 2 (with maternal environmental effect) a decreasing has been observed in both σ_{A}^{2} and h^{2} compared with model 1 but not with the other models. Including additive maternal effect with no maternal environmental effects in models 3 and 4 resulted smaller σ^2_{A} and h^2 compared to those estimated in models 1 and 2. Letting the covariance between the direct additive and direct maternal effect in model 4 brought about a slight decrease in σ^2_{A} and h^2 . In model 5, additive maternal effect was fitted but $\sigma^{2}_{_{AM}}$ was ignored. In this structure model 5 produced higher σ_{A}^{2} and h^{2} than model 4.

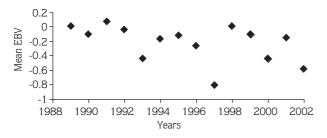
Model 6 was chosen as the best model for the analyzed dataset because of the more detailed parameters and non-significant differences from other models. Obtained h^2 (0.15) in model 6 was same with Model 4 but it was lower than the other models. The breeding values (EBV) were estimated according to the best model (model 6) and the trends in direct breeding values according to years are presented in Figure. No positive or negative trends in direct additive EBVs have been observed among the years.

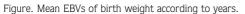
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		Ν	Mean	S. error	Min	Max
		1005	35.45	0.40	18	53
/ear			**			
	1989	68	36.61	0.71 ^a	19	53
	1990	94	35.91	0.65 ^{ab}	18	50
	1991	98	36.56	0.64 ^a	22	52
	1992	86	34.68	0.65 ^{bcd}	19	50
	1993	63	36.29	0.71 ^{ab}	22	50
	1994	52	36.70	0.80 ^a	18	51
	1995	71	33.53	0.71 ^d	19	49
	1996	69	34.94	0.72 ^{bcd}	24	53
	1997	65	34.57	0.72 ^{bcd}	28	51
	1998	80	35.69	0.68 ^{ab}	22	50
	1999	83	35.50	0.66 ^{abc}	23	51
	2000	61	35.47	0.72 ^{abc}	25	53
	2001	65	36.09	0.71 ^{ab}	33	47
	2002	50	33.79	0.79 ^{cd}	26	42
Sex			***			
	Male	519	36.91	0.43	19	53
	Female	486	33.99	0.43	18	50
Dam Age			***			
	2	83	31.11	0.68 ^d	23	46
	3	202	32.78	0.52 ^{cd}	19	49
	4	191	34.99	0.50 ^c	18	53
	5	170	36.49	0.52 ^{ab}	22	52
	6	132	36.81	0.57 ^{ab}	18	53
	7	89	37.22	0.65 ^a	25	52
	8	73	37.78	0.68 ^{ab}	20	53
	9+	65	36.44	0.73 ^{ab}	24	53
Season			*			
	Winter	192	35.02	0.50 ^b	20	53
	Spring	341	36.21	0.45 ^a	18	53
	Summer	268	35.20	0.48 ^b	22	53
	Autumn	204	35.38	0.51 ^{ab}	19	53
Birth type			***			
	Single	962	39.72	0.18	18	53
	Twin	43	31.18	0.77	20	43

Table 1. Effects of year, sex, dam age, calving season, and birth type on birth weight (kg).

 $^{\text{a-d}}$: Means with different superscripts within a column indicate significance (P < 0.05).

*: P < 0.05, **: P < 0.01, ***: P < 0.001





Discussion

Using six different animal models gave an opportunity to employ whole pedigree information in order to estimate genetic parameters and (co)variance components of birth weight for Brown Swiss cattle. Having such parameters and (co)variance components is valuable for the characteristics of breed, because direct and maternal genetic effects and their covariance were

	$\sigma^2_{_A}$	$\sigma^2_{_M}$	$\sigma^2_{_{AM}}$	σ^2_{c}	$\sigma^2_{_E}$	$\sigma^2_{_P}$	h ²	m ²	Γ _{AM}	C^2
Model 1	~				~	~	~			
Model 2	~			~	~	~	~			~
Model 3	~	~			~	~	~	~		
Model 4	V	~	v		~	~	~	~	~	
Model 5	~	~		~	~	~	~	~		~
Model 6	~	~	~	~	~	~	~	~	~	~

Table 2. Used animal models in the analyses.

Table 3. Estimates of (co)variance components and genetic parameters for birth weight of Brown Swiss calf.

	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6
σ^2_A	9.677	6.546	4.316	3.820	4.319	3.819
σ^2_{M}			3.826	2.280	3.822	1.475
σ^{2}_{AM}				2.160		2.373
σ ² c		2.101			0.001	0.001
σ_{E}^{2}	16.164	16.384	17.270	17.120	17.250	17.789
σ ² _P	25.841	25.032	25.413	25.380	25.392	25.457
n ²	0.37	0.26	0.17	0.15	0.17	0.15
(s.e)	(0.080)	(0.086)	(0.081)	(0.072)	(0.082)	(0.072)
m ²			0.15	0.09	0.15	0.06
(s.e)			(0.049)	(0.060)	(0.078)	(0.072)
2 _{AM}				0.085		0.090
R _{AM}				0.73		0.92
C ²		0.083			0.001	0.001
h ² _T	0.37	0.26	0.24,5	0.32	0.25,5	0.32
-2 logL	4156	4151	4149	4147	4149	4147
	9	4	2	0	2	0

 σ_{A}^{2} = direct additive genetic variance; σ_{M}^{2} = maternal additive genetic variance; σ_{AM}^{2} = genetic covariance between direct and maternal effect; σ_{C}^{2} = maternal environmental variance; σ_{E}^{2} = error variance; σ_{P}^{2} = phenotypic variance; h^{2} = direct heritability; m^{2} = maternal heritability; C_{AM} = genetic covariance between direct and maternal effects of proportion $\sigma_{AM}^{2}/\sigma_{P}^{2}$; R_{AM} = direct-maternal genetic correlation; C^{2} = the permanent environmental variance due to the dam as a proportion of the phenotypic variance $\sigma_{C}^{2}/\sigma_{P}^{2}$; h_{T}^{2} = total heritability [(σ_{A}^{2} +0.5 σ_{M}^{2} + 1.5 σ_{AM}^{2})/ σ_{P}^{2}]; -2 log L = log likelihood, s.e = Standard error.

previously established as important for birth weight in cattle (16). Except for models 1 and 2, estimated σ_A^2 and h^2 were close to each other. Because of the similar structure of the models, model 4 and 6 produced similar m^2 while model 3 and 5 generated the same m^2 (Table 3). Allowing for a covariance between direct and maternal genetic effects decreased the σ_A^2 and σ_m^2 in model 6. Very low σ_C^2 in models 5 and 6 reflects that maternal environmental effect is not important for BW as mentioned by Rodríguez-Almeida et al. (20) for MacNay and Rhodes cattle herds. However, the increase in σ_{AM}^2 in

model 6 indicates that relationship between the genetic structure of the calve and genetic structure of the dam has a certain effect on the calve birth weight. While Cantet et al. (21) reported a negative σ^2_{AM} for BW of Hereford cattle, Meyer (1) stated the positive σ^2_{AM} for the BW of Hereford and Angus cattle, which is in line with the outcomes of the present study. Although estimated h^2 in the corresponding study was lower than the h^2 of BW for Angus (0.36) and Hereford (0.40) breeds, m^2 was higher for Brown Swiss compared to both Angus (0.06) and Hereford (0.08) for BW (1). Rodríguez-Almeida et al.

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(20) reported the h^2 of BW for MacNay and Rhodes cattle, which was in agreement with the h^2 of model 1 in the corresponding study but the obtained h^2 from model 6 was lower compared to the reported values. The estimated h^2 of this study was also compared the h^2 of Brown Swiss BW in other studies. According to this comparison, corresponding value was lower than the value (0.36) found by Akbulut et al. (22), higher than the value (0.08) found by Kayqısız (23), but in agreement with the value (0.15) found by Schleppi et al. (24). Estimate of m^2 for BW in this study for Brown Swiss cattle was higher compared to Rhodes cattle but lower compared to MacNay. Rodríguez-Almeida et al. (20) reported the range of estimates of $\sigma^2_{_{AM}}$ from –0.16 to 0.10 for BW, which is lower than the corresponding covariance (1.76-2.53) estimated for Brown Swiss.

According to $-2 \log L$ values models 3-6 are better than models 1 and 2 in terms of fitting to available data. The common difference between these 2 model groups was maternal additive genetic variance ($\sigma^2_{\rm M}$). From the

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reflection of this result, it might be said that $\sigma^2_{_M}$ is essential to deal with the current data set.

Domestic livestock are selected for economically important traits, and the effect of the selection depends on the accurate genetic evaluation. This study presented the components of genetic parameters of BW for the studied Brown Swiss cattle herd. These values might be used to manipulate either BW or possible dystocia. Due to the contribution of maternal effects to the phenotypic variance of BW, those effects should be taken into account in genetic evaluations of the studied Brown Swiss population. Further, intermediate estimate of heritability in BW might be accomplished by selection according to any desired aspect. In order to establish a rearing system to solve the problems with the modern methods such as REML and BLUP, more work is required to determine the genetic correlations between BW and further weight traits. Therefore, full records (not only BW) of an animal may allow an extra opportunity to assess the studied population.

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