

FERENC SZABÓ¹, ZOLTÁN LENGYEL¹, ZOLTÁN DOMOKOS², and SZABOLCS BENE¹

Estimation of genetic parameters and (co)variance components for weaning traits of Charolais population in Hungary*

Abstract

Weaning performance of 10 808 purebred offsprings (4991 male and 5817 female) of 80 sires in 13 farms were analysed using animal model. Heritability, breeding value, (co)variance components for weaning weight (WW), preweaning daily gain (PDG), 205-day weight (CWW) were calculated. Farm, parity, year of birth, season of birth, sex were treated as fixed, and the maternal permanent environment was treated as random effects. In case of WW and PDG, the age of the calves at weaning was fitted as a covariant. Data were analyzed with MTDFREML (Boldman et al. 1993) program. The overall mean value and standard deviation of WW, PDG and CWW were 221±47 kg, 1,111±0.21 kg/day and 226±42 kg, respectively. The age of the calves at weaning was 202 days. The direct heritability (h^2_d) of WW and PDG were 0.57±0.08, 0.49±0.07 and CWW was 0.44±0.06, respectively. The maternal heritability (h^2_m) of these traits were 0.32±0.09, 0.33±0.10 and 0.33±0.09, respectively. The direct-maternal correlations (r_{dm}) were strong and negative. The medium heritability estimates for direct effects suggest that progeny tests should be used in this population to increase genetic improvement.

Key Words: beef cattle; genetic parameters; breeding value; Charolais

Zusammenfassung

Titel der Arbeit: Schätzung genetischer Parameter und (Ko) Varianzkomponenten von Absetzergebnissen ungarischer Charolais

Es wurden die Absetzergebnisse von 4991 männlichen und 5817 weiblichen Charolaiskälbern aus 13 Betrieben ausgewertet. Unter Nutzung des Tiermodells wurden die Heritabilität, die Zuchtwerte und die (Ko)Variantenkomponenten der Merkmale Absetzgewicht (WW), tägliche Zunahme vor dem Absetzen (PDG) und das auf 205 Tage korrigierte 205 Tagegewicht (CWW) einbezogen. Im Modell wurden die fixen Effekte Betrieb, Zahl der Abkalbungen, Jahrgang, Jahreszeit und der zufällige Effekt Mutter als Umweltfaktor, bei den Parametern WW und PDG ist das Alter des Kalbes als Kovariante berücksichtigt. Die Daten wurden mit dem Modell MTDFREML (BOLDMANN et al., 1993) ausgewertet. Das durchschnittliche Absetzalter betrug 202 Tage. Die Durchschnittswerte und Standardabweichungen der untersuchten Merkmale lagen bei 221±47 kg für WW, 1,11±0,21 kg/Tag für PDG und 226±42 kg für CWW. Die Schätzwerte für die Heritabilität (h^2_d) betragen für WW, PDG bzw. CWW 0,57±0,08, 0,49±0,07 bzw. 0,44±0,06 und für die mütterliche Heritabilität (h^2_m) in der gleichen Merkmalsfolge 0,32±0,09, 0,33±0,10 bzw. 0,33±0,09. Die direkten maternalen Korrelationen (r_{dm}) zeigten bei allen Merkmalen stark negative Zusammenhänge. Die ermittelten Heritabilitätsschätzwerte lassen, bei Einbeziehung dieser Merkmale in die Nachkommenschaftsprüfung, einen Zuchtfortschritt erwarten.

Schlüsselwörter: Fleischrind, genetische Parameter, Zuchtwert, Charolais

Introduction

Weaned beef calves are the products of beef cattle sector, therefore the results are influenced by weaning weight. On the other hand the weaning weight expresses the calf rearing ability of cows, so changes in weaning weight are important factors at selection. However there are results about variation and genetic parameters of the most important beef traits of dairy and dual purpose breeds (ATIL et al., 2005; JACUBEC

et al., 2003; CANTET et al., 2003; GOYACHE et al., 2002; REINSCH and KALM, 1995) it is important requirement to estimate the breeding value based on weaning results very exactly.

NELSEN and KRESS (1981) found that sex and the age of dam influenced the weaning weight of Aberdeen Angus and Hereford herds ($P < 0.01$). JAKUBEC et al. (2000) showed that year, sex and the age of dam influenced the weaning weight and daily gain of Aberdeen Angus calves ($P < 0.01$). GÁSPÁRDY et al. (1998) analysed the weaning weight of Charolais calves. They found that parity (number of calving) and year of birth had an effect on the adjusted 205-day weight. MASSEY and BENYHSEK (1981) in a crossbreed population showed the effect of dam's age on weaning performance. According to SZABÓ and GAJDI (1993) age of dam, sex, year and season had significant effect on 205-day weight of Hereford calves.

SZABÓ (1993) summarized the results of 35 publications and reported that heritability of calf's daily gain before weaning was 0.27 on average. Heritability of weaning weight was 0.30 on average according to 61 publications. BOURDON and BRINKS (1982) found that heritability of the preweaning daily gain and weaning weight was 0.60 and 0.63, respectively. LEE et al. (1997a) examined the weaning weight of Simmental calves. They found that the direct heritability (h^2_d) of weaning weight was 0.21, maternal heritability (h^2_m) was 0.10. MASSEY and BENYHSEK (1981) found that heritability of the 205-day weight and preweaning daily gain was 0.11 and 0.08, respectively. SZABÓ et al. (2001) showed that heritability of weaning weight was 0.29. DUANGJINDA et al. (2001) examined the heritability value of weaning weight in Charolais herds. They found that direct heritability of weaning weight was 0.33, maternal heritability was 0.15. VAN VLECK et al. (1996) found that direct heritability of weaning weight was 0.16 and maternal heritability was 0.12, respectively. TÓZSÉR et al. (2002) showed that heritability of weaning weight of Limousin calves was 0.14 and CANTET et al. (2003) found $h^2 = 0.32$ in Angus beef cattle.

Correlation between direct genetic and maternal effects (r_{dm}) is different. DODENHOFF et al. (1999) examined the genetic parameters of weaning weight in five different breeds. They found that the direct-maternal correlation varied between -0.10 and -0.37. BASCHNAGEL et al. (1998) found that the direct-maternal correlation was -0.50 for Angus in Sweden. MEYER (1992) showed that the direct maternal correlation of weaning weight was -0.59. NUNEZ-DOMINGUEZ et al. (1993) found high positive direct-maternal correlation ($r_{dm} = +0.63$) in the case of weaning weight. VAN VLECK et al. (1996) showed that the direct-maternal correlation of the weaning weight was 0.40.

There have not been any investigations in connection with covariance and genetic parameter estimation in Hungarian beef population so far. That is the reason why analyses of genetic parameters and breeding value of the Hungarian Charolais population were carried out using animal model.

Material and Methods

Field records were provided by the Association of Hungarian Charolais Breeders. The weaning results of 10808 pure bred calves (4991 male and 5817 female) born from 5388 cows mated with 80 sires were analyzed. 36 of the sires with more than 100

offsprings were presented. There were Hungarian and French origin sires used in this population. Description of the samples is shown in Table 1.

Estimated traits were the weaning weight (WW), preweaning daily gain (PDG) and 205-day weight (CWW).

Table 1

Characteristic of the samples for univariate analyses (Charakteristik der einbezogenen Daten)

Number of animals in total	16117
Number of records in data	10808
Sire	80
Dam	5388
Paternal grand sires	14
Maternal grand sires	25
Grand sires together	39
Paternal grand dams	23
Maternal grand dams	121
Grand dams together	144
Calf without performance	47

Genetic parameters (variance, heritability) and breeding values (EBV= Estimated Breeding Value) were predicted with single-trait animal model, using the following equation:

$$y = \mathbf{Xb} + \mathbf{Zu} + \mathbf{Wm} + \mathbf{Spe} + e$$

where, y is a $N \times 1$ vector of observation, \mathbf{b} denotes the vector of fixed effects (herd, parity, year, season and sex), \mathbf{X} is the matrix that associates \mathbf{b} with y ; \mathbf{u} is the vector of breeding values for direct genetic effects, \mathbf{Z} is the matrix that associates \mathbf{u} with y ; \mathbf{m} is the vector of breeding values for maternal genetic effects, \mathbf{W} is the matrix that associates \mathbf{m} with y ; \mathbf{pe} is the vector of permanent environmental effects contributed by dams to records of their progeny, \mathbf{S} is the matrix that associates \mathbf{pe} with y ; and \mathbf{e} is the vector of random residual effects.

It is assumed that

$$\text{var} \begin{pmatrix} \mathbf{b} \\ \mathbf{m} \\ \mathbf{pe} \\ \mathbf{e} \end{pmatrix} = \begin{pmatrix} \mathbf{g}_{11}\mathbf{A} & \mathbf{g}_{12}\mathbf{A} & 0 & 0 \\ \mathbf{g}_{21}\mathbf{A} & \mathbf{g}_{22}\mathbf{A} & 0 & 0 \\ 0 & 0 & \mathbf{I}\sigma_{pe}^2 & 0 \\ 0 & 0 & 0 & \mathbf{I}\sigma_e^2 \end{pmatrix}$$

where \mathbf{A} is the numerator relationship matrix and the \mathbf{I} are identity matrices of appropriate order.

The levels of fixed effects were as follows: 13 levels for farm, 14 levels for parity, 16 levels for year of birth (1987-2002), 4 levels for season (1, December-February; 2, March-May; 3, June-August; 4, September-November) and 2 levels for sex.

Total heritability (h^2_T) defined as (e.g. WILLHAM, 1972) $h^2_T = (\sigma_d^2 + 0,5\sigma_m^2 + 1,5\sigma_{dm}) / \sigma_p^2$ were calculated.

The genetic parameters, (co)variance components and breeding values were estimated with MTDFREML (BOLDMAN et al. 1993) program. Iteration were stopped when the variance of function values ($-2 \log L$) in the simplex were less than 1×10^{-9} .

Results and Discussion

Genetic parameters and (co)variances

The estimated genetic parameters and (co)variance components of the investigated traits are shown in Table 2.

Table 2

The estimated (co)variance components and genetic parameters ((Ko)Varianzen und genetische Parameter der untersuchten Merkmale)

Parameters	Weaning weight	Prewaning daily gain*	205-day weight
σ^2_d	791	0.0172	680
σ^2_m	438	0.0113	517
σ_{dm}	-558	-0.0131	-574
σ^2_{pe}	73	0.0016	66
σ^2_e	633	0.0179	861
σ^2_p	1377	0.0348	1550
h^2_d	0.57±0.081	0.49±0.076	0.44±0.066
h^2_m	0.32±0.094	0.33±0.10	0.33±0.098
r_{dm}	-0.95±0.07	-0.94±0.083	-0.97±0.080
c^2	0.053±0.05	0.046±0.06	0.043±0.06
e^2	0.46±0.06	0.51±0.06	0.55±0.05
$h^2_{m+c^2}$	0.37	0.38	0.37
h^2_T	0.047	0.092	0.050

σ^2_d , direct genetic variance σ^2_m , maternal genetic variance; σ_{dm} , direct- maternal genetic covariance; σ^2_{pe} , maternal permanent environmental effect; σ^2_e , residual variance; σ^2_p , phenotypic variance; h^2_d , direct heritability; h^2_m , maternal heritability; r_{dm} , direct-maternal genetic correlations; c^2 , the ratio of the permanent environmental variance to the phenotypic variance; e^2 , the ratio of the residual variance to the phenotypic variance; h^2_T , total heritability

* estimated in kg/day

Direct heritability (h^2_d) of weaning weight, preweaning daily gain and 205-day weight were 0.57±0.081, 0.49±0.076 and 0.44±0.066, respectively. High estimates of direct heritability for the investigated traits may be due to the used foreign sires, which are increasing the direct additive genetic variance. Maternal heritability (h^2_m) in the case of these traits were 0.32±0.094, 0.33±0.10 and 0.33±0.098.

Direct- maternal genetic correlations were high and negative (r_{dm} =-0.95±0.07, -0.94±0.083, -0.97±0.080). These data in results were higher than the estimates of DODENHOFF (1999) -0.12, PHOCAS and LALOË (2003) -0.19, and DUANGJINDA et al. (2001) -0.46, but MEYER (1992) in the case of Zebu Cross found that the direct-maternal genetic correlation of weaning weight -0.78.

Total heritability (h^2_T = 0.047, 0.092, 0.050) was low due to the high negative direct -maternal genetic correlation. The ratio of the permanent environmental variance (c^2) was low (4-6%). Similar results were found by BASCHNAGEL et al. (1998) for Angus in Sweden, CARNIER et al. (2000) for Piedmontese in Italy, DUANGJINDA et al. (2001) for Gelbvieh, LEE et al. (1997b) for Simmental and VAN VLECK et al. (1996) for Simmental in USA. The residual variance were similar for the three traits. The ratio to the phenotypic variance (e^2) ranged from 46 to 55 %.

Breeding values

Table 3 shows the breeding values of the 36 examined sires, with more than 100 offsprings. The best sire was the registered by number 32500 (+66.51 kg in weaning weight, +0.304 kg/day in preweaning daily gain and +76.89 kg in 205-day weight). The worst sire was of the number 9823 (-46.1kg, -0.179 kg/day and -42.35 kg in the

case of WW, PDG and CWW). Figure 1 and 2 show the overall breeding values of the Hungarian and French Charolais sires. Direct effect of French sires was higher than that of the Hungarian Charolais sires that explains the relatively high direct additive genetic variance. That means that French Charolais sires are genetically better as for the growing capacity than Hungarian ones. As both French and Hungarian Charolais sires had negative maternal EBV values, maternal genetic effect could be increased in order to make further improvement on the genetic merit of the population values. The medium heritability estimates for direct effects suggest that progeny tests should be used to increase genetic improvement.

Table 3

Estimated breeding values of the investigated traits (Bullenzuchtwerte der untersuchten Merkmale)

Sire	Number of progeny	WW	WW	PDG	PDG	CWW	CWW
		direct	maternal	direct	maternal	direct	maternal
Estimated breeding value							
9707	135	29.48	-14.06	0.121	-0.058	13.46	-6.82
9823	139	-46.10	28.81	-0.179	0.119	-42.35	33.20
10927	115	15.99	-14.62	0.095	-0.090	20.50	-19.36
10932	114	19.35	-12.71	0.107	-0.075	15.53	-12.08
10933	118	8.45	-5.23	0.029	-0.022	7.26	-6.02
11234	127	39.26	-27.70	0.169	-0.129	28.05	-23.67
11235	139	-38.63	27.25	-0.172	0.131	-40.62	34.28
11664	193	-4.02	2.84	-0.003	0.002	-0.38	0.32
11987	224	-19.93	14.57	-0.087	0.069	-23.44	20.00
11988	270	-24.84	20.59	-0.108	0.096	-23.50	21.81
12105	148	33.59	-23.44	0.151	-0.113	29.01	-24.36
12107	216	6.07	-7.22	0.026	-0.036	4.40	-5.57
12241	189	-10.58	7.46	-0.044	0.033	-12.74	10.75
12242	105	-9.31	8.14	-0.067	0.059	-15.70	13.95
12246	124	45.44	-32.06	0.191	-0.146	38.54	-32.52
12394	175	-17.14	11.19	-0.096	0.067	-16.02	12.85
12513	212	-8.50	6.23	-0.039	0.030	-12.61	10.74
12525	116	-26.47	18.34	-0.126	0.092	-28.95	23.91
12612	119	41.28	-29.13	0.191	-0.146	38.23	-32.26
12615	119	33.77	-23.23	0.146	-0.110	29.36	-24.52
12628	191	-7.07	5.32	-0.029	0.023	-12.62	10.86
12865	111	-33.57	25.08	-0.181	0.142	-31.85	27.34
12961	120	3.45	-0.93	-0.003	0.013	-4.96	5.38
13032	108	36.69	-27.36	0.173	-0.142	39.10	-33.90
13200	121	-2.43	1.72	-0.025	0.019	-6.57	5.54
13342	123	33.01	-23.29	0.149	-0.114	21.15	-17.85
13923	172	10.25	-7.23	0.074	-0.057	7.71	-6.50
13924	108	33.22	-21.08	0.171	-0.121	34.48	-28.08
14002	234	11.36	-8.01	0.061	-0.047	8.52	-7.19
14003	298	-1.81	1.28	-0.013	0.010	-5.51	4.65
14334	190	17.99	-12.70	0.066	-0.051	16.59	-14.00
14746	105	0.00	0.00	0.000	0.000	0.00	0.00
14957	475	25.48	-17.74	0.102	-0.078	23.97	-20.22
32000	111	27.73	-23.98	0.100	-0.093	15.38	-15.53
32500	504	66.51	-46.93	0.304	-0.232	76.89	-64.88
33000	1894	-3.75	2.65	-0.024	0.019	-1.34	1.13

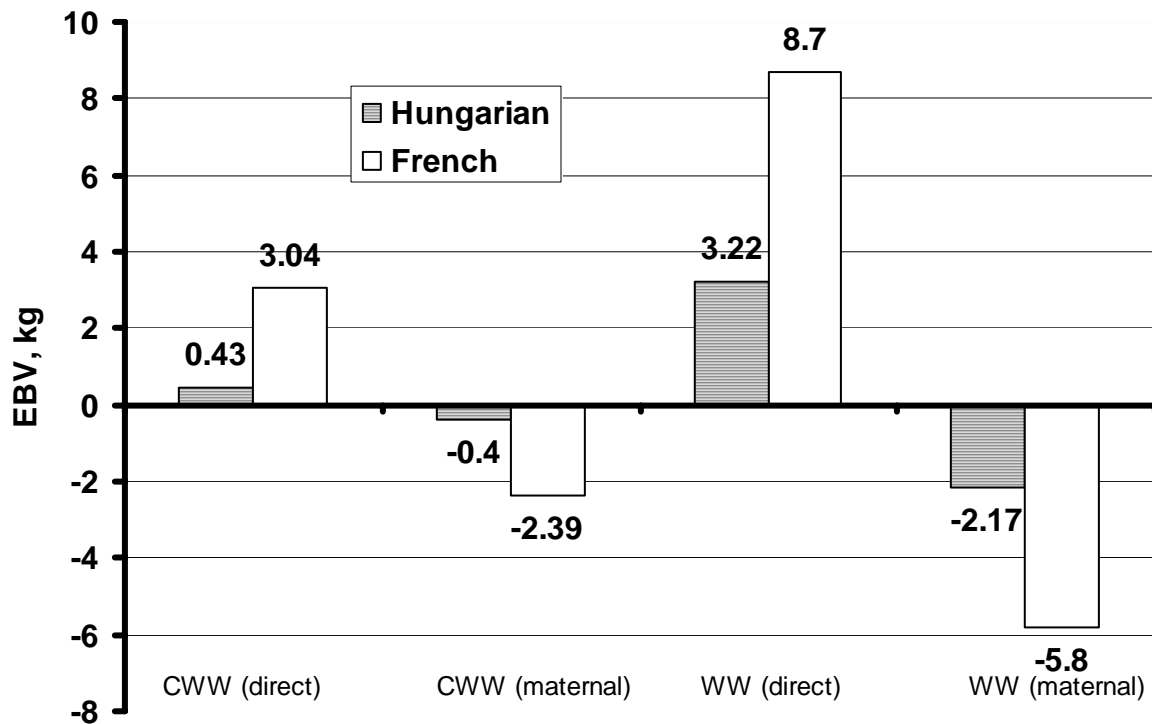


Fig. 1: Overall breeding value of the Hungarian and French Charolais sires in the case of weaning weight (WW) and 205-day weight (CWW) (Zuchtwerte der ungarischen und französischen Charolaisbullen für WW und CWW)

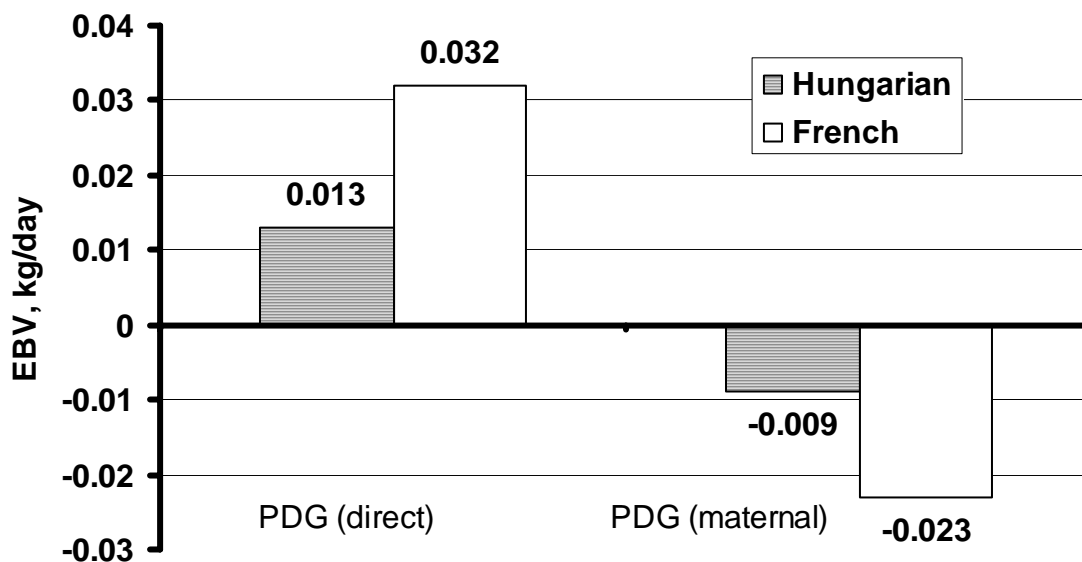


Fig. 2: Overall breeding value of the Hungarian and French Charolais sires in the case of preweaning daily gain (PDG) (Zuchtwerte der ungarischen und französischen Charolaisbullen für PDG)

Based on the results obtained it can be suggested that both the direct and maternal effect, because of the high negative direct and maternal genetic correlation, should be

taken into account during selection. It is assumed that the high genetic variance could contribute to a more successful selection in the future.

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Authors' addresses

FERENC SZABÓ DSc*, ZOLTÁN LENGYEL PhD, SZABOLCS BENE
Department of Animal Science and Production
University of Pannonia, Georgikon Faculty of Agricultural Science
Deák F. str. 16. H-8360, KESZTHELY, HUNGARY

*Corresponding Author

E-Mail: szf@georgikon.hu

ZOLTÁN DOMOKOS

Association of Hungarian Charolais Breeders
Vologda str. 3. H-3525, MISKOLC, HUNGARY