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Statistic and genetic parameters of 205-day weaning weight of beef calves

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Abstract

The aim of the study was to do genetic evaluation of the 205-day weaning weight of pure bred herds of different beef cattle breeds kept in Hungary and supply results for genetic programmes of different breeds.

Population genetic analysis was performed on data from 42 695 purebred beef calves from seven breeds born from 1981 to 2005 in Hungary. Animal model was used for the estimations. Sire, herd, age of dam at calving, birth year, season of birth and sex of calf had significant effects on 205-day calf weaning weight for each breed. Significant breed differences and breed overlaps were found. Direct heritability value estimates were 0.18 to 0.61, the maternal heritability values from 0.07 to 0.38, and the total heritability values were between 0.09 and 0.35. The direct-maternal genetic correlations were high and negative for all the breeds varying from −0.63 to −0.88.

Keywords: beef cattle, breeds, weaning weight, breed differences and overlap, heritability, genetic correlations

Introduction

Weaning weight in beef cattle is a trait of major economic importance because the weaned calf is the end product and almost total output of the cow-calf unit. On the other hand it is a complex trait since it reflects not only the growth ability of calf but also the maternal environment created for the calf by its dam. Moreover weaning weight is influenced by some other effects such as sex of the calf, age of dam, birth year, birth season etc. Weaning weight adjusted to 205 day of age is very important selection criteria in the breeding programs even so, measuring and evaluating of this trait is essential part of performance test and breeding value estimation.

In Hungary only a few beef calves are fattened and slaughtered, most of them are sold abroad, so the country is mostly interested in weaning weight. From this situation one of the aims of different breed associations is to improve the weaning weight of their breed whether it is Hereford or Charolais. For breed decision the weaning weight or 205-day weaning weight of the calves of different cows kept in various environments is very important information.

General practice for appropriate weaning weight evaluation and comparison is adjusting weaning weight to 205 days of age. For the applying breeding programmes we have to know the weaning results, variation, co-variation components and genetic parameters of them. Among genetic parameters heritability is important, measure of the proportion of genetic variation within the total phenotypic variation. Also, correlation between different effects is important for breeding programmes.

There are numerous studies that have examined weaning weight of different beef cattle breeds and the influence of environmental and genetic effects (Minyard & Dinkel 1965, Sellers *et al.* 1970, Smith *et al.* 1976, Notter *et al.* 1978, Pell & Thayne 1978, Gregory *et al.* 1979, Amer *et al.* 1992, Meyer *et al.* 1994, Cundiff *et al.* 1998, Szabó *et al.* 2006, Vergara *et al.* 2009). Also there are data for breed differences breed overlap and genetic trend from North America (Sullivan *et al.* 1999).

While a number of these authors have reported heritability values for weaning weight including data for the maternal effect, according to Meyer *et al.* (1994) and Vergara *et al.* (2009) further research is required to separate the direct and maternal genetic components for better estimation of genetic values in beef cattle populations.

The aim of the study was to do genetic evaluation of the 205-day weaning weight of pure bred herds of different beef cattle breeds kept in Hungary and supply results for genetic programmes of different breeds.

The primary objective of this study, using data from pure bred cattle populations in Hungary, was to evaluate environmental and genetic effects on weaning weight. Also, direct and maternal heritabilities, together with direct-maternal genetic correlations, were estimated.

Material and methods

Population genetic analysis was performed on data from 42 695 purebred beef calves from seven breeds, Hungarian Grey, Limousin, Hereford, Angus, Charolais, Hungarian Simmental and Blonde d'Aquitaine, born between 1981 and 2005 in Hungary. Performance and complete pedigree data were recorded by the breed associations. Practically all records available in the given period for Hungarian purebred beef calves were used for the evaluation. The number of calf records can be seen in Table 1. As it can be seen from the table three generations (progeny, parents, and grand parents) were considered in the study.

The beef herds from which the data originated were all on different farms. Cows were mated using both artificial insemination and natural service to produce straightbred calves. The majority, 70-75 % of calvings took place in spring, 10-15 % of calvings were in winter, 5-10 % was in summer, and 4-8 % was in autumn. The calves remained with their dams on pasture. As creep feeding is not a common practice in beef production in Hungary, data for this effect were not available in the dataset of breed organizations. So, the effect of creep feeding was not taken into consideration during this study. The calves were weighed on the day of birth and at weaning. Weaning weights and corresponding ages were recorded between 150 and 240 days age. Calf weaning weight was adjusted to 205 days of age by linear interpolation from birth weight, weaning weight and age. The calculation of 205 day weaning weight was as follows:

$$A = \frac{B-C}{D} \times 205 + C \qquad (1)$$

where A is 205 days weight (kg), B is the weaning weight (kg), C is the birth-weight (kg), D is the weaning age (days).

Due to the calculation the calf age effect could be eliminated as all calves were considered to be at the same age. During the adjustment only the afterbirth gain was counted that is why difference of weaning weight (B) and birth-weight (C) was taken. This difference was divided by weaning age (D) in order to get daily gain between birth and weaning date. Total gain was adjusted to 205 days of age with multiplying daily gain by 205. Finally birth weight (C) was added to the product, because it is part of the total weaning weight.

Table 1
Summary of data used for genetic evaluation

	HG	HS	AA	HE	CH	BD	LI
Period of records	1984-2004	1981-2003	1989-2002	1990-2002	1990-2005	1993-2005	1992-2005
Number of herds	9	2	2	2	12	2	3
of calves	5 720	7 032	2 451	5 109	13 087	3 250	6 046
of sires	182	232	63	119	146	27	55
of dams	2 638	2 057	933	1 954	6 168	1 173	1 838
of paternal grand sires	35	17	13	18	44	3	8
of maternal grand sires	104	114	19	55	101	20	34
of paternal grand dams	50	24	31	32	69	4	16
of maternal grand dams	702		119	234	990	429	558

HG: Hungarian Grey, HS: Hungarian Simmental, AA: Angus, HE: Hereford, CH: Charolais, BD: Blonde d'Aquitaine, LI: Limousin

However, Rossi *et al.* (1992) suggested the age of calf to be included in the evaluation model as a covariate, according to Hungarian Beef Recording Guideline (1996) weaning weight data were pre-adjusted by linear model to 205 days of age and the adjusted weaning weight data were used in the model applied in this study.

Although Rumph & Van Vleck (2004) suggested quadratic model for some effects mostly for effect of age of dam on weaning weight, moreover separated evaluations for male and female calves. As our previous study did not show significance between linear and quadratic model, furthermore we did not find different maternal effect between male and female calves, linear model was used and male and female calves were evaluated together in this study. Sex of calf was just put as a fixed effect into the model.

There can be many effects on weaning weight, however only some more important ones can be and are registered by breed associations. So, sire, herd, age of cow at calving, birth year, birth season and sex of calves were considered and used in the model as a fixed effects. The number of groups (steps) within each effect was as follows: 27-232 sires, 2-12 herds, 12 (from 2 to 14 years) age groups of cows, 26 (from 1981 to 2005) birth yeas groups, 4 (spring, summer, autumn, winter) birth season groups and 2 (male and female) sex groups by breed.

The random part of evaluation, the maternal permanent environmental effect could be evaluated by the applied model, because all cows involved in the evaluation were recorded and had at least two calves. No significant difference was between breeds by the number of calves per cow.

The effect of contemporary group was not considered, as the evaluation was done separately by breed, however there was a farm where cows of different breeds were kept together and their purebred calves were raised in the common management group.

The 205-day weaning weights were analysed using animal model. The software used to evaluate the significance of environmental and genetic effects was Harvey's (1990) Least Squares Maximum Likelihood, Derivative Free Restricted Maximum Likelihood (DFREML) Computer Program (Meyer 1998). To estimate genetic parameters and breeding values the Multitrate Derivative Free Restricted Maximum Likelihood (MTDFREML) program developed by Boldman *et al.* (1993) was used. This programme can consider the number of generations as well as the existence of genetic associations between different populations of a given breed evaluated.

However MTDFREML is and appropriate method to evaluate the population genetic parameters, but do not inform us about the significance of fixed effects. As we were interested in the significance of mentioned fixed effects, DFREML was used for pre-evaluation.

The animal model was as follows:

$$\hat{\boldsymbol{y}} = \boldsymbol{Xb} + \boldsymbol{Zu} + \boldsymbol{Wm} + \boldsymbol{Spe} + \boldsymbol{e} \qquad (2)$$

where $\hat{\boldsymbol{y}}$ is the vector of observation (trait), $\boldsymbol{X}$ is the matrix of fixed effects, $\boldsymbol{Z}$ is the matrix of random effects, $\boldsymbol{W}$ is the matrix of maternal genetic effect, $\boldsymbol{S}$ is the matrix of maternal permanent environmental effect, $\boldsymbol{e}$ is the residual, $\boldsymbol{b}$ is the vector of fixed effects, $\boldsymbol{u}$ is the vector of random effects, $\boldsymbol{m}$ is the vector of maternal genetic effects, $\boldsymbol{pe}$ is the vector of maternal permanent environmental effects.

Breed differences and breed overlap was evaluated on the basis of breed means and distribution. Genetic trend in breeds was estimated based on the breeding value data supplied by MTDFREML. Overall mean breeding value, which was considered as a zero, was calculated for the whole period of estimation for all seven breeds. A yearly breeding value of a given breed was determined by the deviation of its breeding value from the overall mean value. The genetic trend representing the evaluated breeds was described by lines of yearly changes of breeding value.

Results and discussion

Sire, herd (except for Blonde d'Aquitaine), age of dam at calving, birth year, season and sex of calf all had significant effects ($P \leq 0.05$) on 205-day weaning weight of calves in each breed. These findings correspond to the results of others reported in the literature (Minyard & Dinkel 1965, Sellers *et al.* 1970, Pell & Thayne 1978, Gregory *et al.* 1979, Cundiff *et al.* 1975, 1998, Szabó *et al.* 2006) who also found significant effects of one or more of the factors mentioned on weaning performance.

The statistic for weaning weight by breed can be seen in Table 2, while the distribution of 205-day calf weight of the evaluated breeds is shown in Figure 1.

The breed mean 205-day weaning weight varies between 191-242 kg, while that of the standard deviation between 30-41 kg. Coefficient of variation values are below 20 % in all seven breeds. The rank of breeds according to the increasing mean values of 205-day weaning weigh is: Hungarian Grey, Limousin, Hereford, Angus, Charolais, Hungarian Simmental and

Blonde d’ Aquitaine. Breed data show normal distribution. The range within breeds is higher than the mean values in case of each breed. The difference between the mean values of the bottom Hungarian Grey and the top Blonde d’ Aquitaine is 51 kg, which are approximately quarter of the all breeds mean and one third one sixth of the range observed within breeds. The results are similar to findings of Cundiff *et al.* (1975) who reported that breed differences are generally smaller than the within breed variances.

Table 2
Statistics of 205-day weight data of calves

Breed		HG	HS	AA	HE	CH	BD	LI
Number of calves		5 720	7 032	2 451	5 109	13 087	3 250	6 046
205-day weight, kg								
Mean		191	236	212	204	227	242	203
SE		5.05	3.40	3.61	5.06	8.58	7.95	2.99
SD		30.15	39.48	36.19	38.90	40.87	37.03	35.15
CV, %		16.54	16.30	16.84	18.66	18.01	15.16	16.97
Range		223	250	266	266	299	263	257
Deviation from overall mean value, kg								
Age of dam, year	2	-	–16	–15	–20	–15	-	–18
	3	–5	–7	–5	0	–12	–6	–13
	4	0	8	3	7	–1	–5	–5
	5	2	11	5	15	4	–4	2
	6	1	15	6	15	7	–2	8
	7	5	15	10	12	7	0	8
	8	4	15	6	11	4	0	12
	9	5	12	1	8	6	–1	10
	10	1	10	0	6	8	8	8
	11	3	6	–3	6	2	7	8
	12	–3	–3	–7	0	–1	6	4
	13	2	–1	-	–7	–4	1	3
	14	–6	–5	-	–11	–11	1	0
Birth season	Winter	–3	3	5	–14	–2	9	5
	Spring	7	2	7	–2	–2	7	7
	Summer	14	–6	–6	17	–2	–16	–11
	Autumn	–20	2	–5	-	4	-	–1
Sex of calf	Male	9	8	8	6	7	5	7
	Female	–10	–8	–8	–5	–7	–5	–7

HG: Hungarian Grey, HS: Hungarian Simmental, AA: Angus, HE: Hereford, CH: Charolais, BD: Blonde d’Aquitaine, LI: Limousin

Both the data in the table and the figure show breed overlap. Approximately 50 % cent of 205-day weaning weight data fit to all breeds. 20-30 % of the Hungarian Grey calves are heavier than the average of Hereford, Angus and Limousin and 10-20 % of them are heavier than the bottom 10-20 % of the top Blonde d’ Aquitaine breed’s calves. These results are similar to observation of Sullivan *et al.* (1999) who found that substantial breed overlap exists in many regions of North America. For example 1 % of Angus, 3 % of Limousin and 6 % of Hereford were above the Simmental mean as for the weight gain between birth and weaning in their study.

The variance components and heritability value estimates obtained from the animal model are shown in Table 3.

The standard errors for the estimated heritabilities are rather high in some cases. These results can be explained by the situation that herds of the evaluated breeds were kept not in the same environmental conditions, but rather in different farms. Different farms gave different nutrition, management etc. conditions that resulted high phenotypic variation (phenotypic standard deviation values). The fairly high variance resulted in higher standard errors, than it would be expected in population with herds kept in similar environment. In the relevant literature when the situation is like the present study, there are similarly high standard errors of the heritability values. For example Dodenhoff *et al.* (1999) have reported values of standard error 0.4-0.5 for the heritability values of weaning weight of different beef cattle breeds.

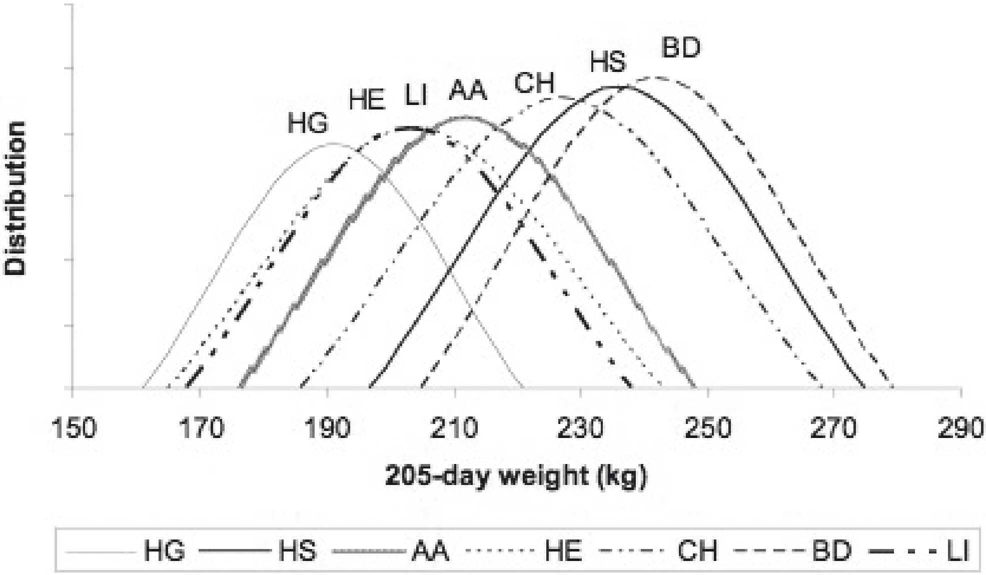


Figure 1
The distribution of 205-day weaning weight of different breeds

HG: Hungarian Grey, HS: Hungarian Simmental, AA: Angus, HE: Hereford, CH: Charolais, BD: Blonde d'Aquitaine, LI: Limousin, The vertical top points in the figure are the mean values (kg) by breeds, while the horizontal ranges are mean values ± s (kg) of breeds.

The direct breed heritability (h_d^2) values ranged 0.18-0.61 across the breeds, lower in case of Hereford and Angus, than that of other breeds. These values are slightly higher than those reported by Meyer *et al.* (1994). Also, they are higher than obtained by Splan *et al.* (2002) who found value 0.14. Maternal heritability value (h_m^2) estimates are less (0.07-0.38) than the direct heritability, and are similar to the finding of Mohiuddin (1993) who reported that the maternal heritability value of weaning weight tended to be lower than the direct heritability value. This result indicates a greater genetic influence of the calf than its dam for the trait. The opposite result was found by Splan *et al.* (2002) whose estimate of maternal heritability was slightly greater (0.19) than the estimate for direct heritability (0.14). The total heritability values (h^2_T) were between 0.09 and 0.35 which are similar to the values obtained by Meyer *et al.* (1994) and Vergara *et al.* (2009).

The direct-maternal genetic correlations (r_{dm}) were high (−0.52 to −0.88) and negative for all breeds. Similar results have been reported by Meyer (1992, 1993) and by Koots *et al.* (1999) who also found strong negative direct-maternal genetic correlations. Several estimates of direct-maternal correlation reported by Mohiuddin (1993) were negative, although they ranged from −0.78 to 0.25. Also, similarly negative, but a somewhat lower correlations were reported by Splan *et al.* (2002) (r_{dm}=−0.18) and Vergara *et al.* (2009), while Sullivan *et al.* (1999) assumed a zero correlation.

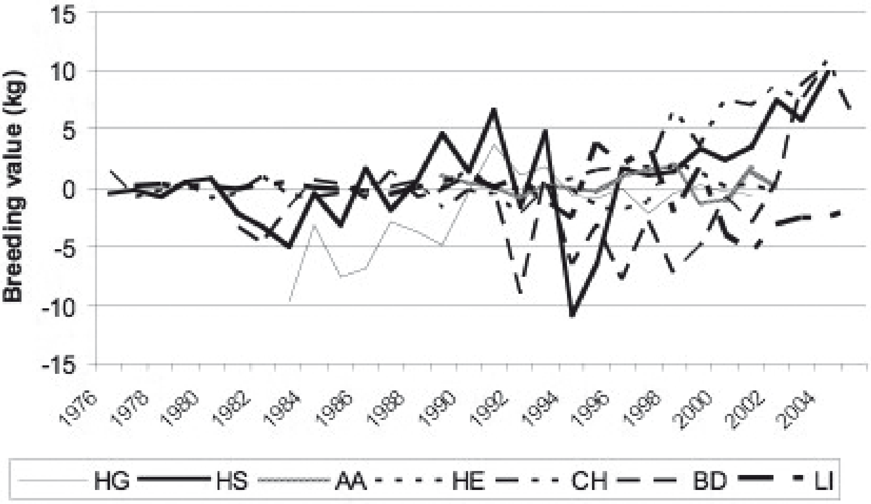
Table 3
Estimated variance and covariance components and heritability values of 205-day weight of calves

	Breed						
Genetic parameters	HG	HS	AA	HE	CH	BD	LI
σ^2_p phenotypic variance	631	1 250	980	1 189	1 515	1 265	871
σ^2_d additive direct genetic variance	384	461	173	224	892	697	302
σ^2_e residual variance	262	768	755	875	626	434	533
σ^2_{pe} maternal permanent environmental effect	42	69	0	80	30	30	72
e^2 the ratio of the residual variance to the phenotypic variance	0.41±0.05	0.61±0.05	0.77±0.05	0.74±0.03	0.41±0.04	0.34±0.11	0.55±0.05
σ^2_m maternal genetic variance	162	89	128	130	569	410	229
σ_{dm} direct-maternal genetic covariance	−219	−137	−77	−120	−602	−307	−165
c^2 the ratio of the maternal permanent environmental variance to the phenotypic variance	0.07±0.03	0.06±0.02	0.00±0.07	0.07±0.05	0.02±0.02	0.02±0.03	0.07±0.03
h^2_d direct heritability	0.61±0.07	0.37±0.06	0.18±0.06	0.19±0.04	0.59±0.06	0.55±0.17	0.31±0.07
h^2_m maternal heritability	0.26±0.05	0.07±0.03	0.13±0.10	0.11±0.08	0.38±0.05	0.32±0.07	0.24±0.05
$h^2_m+c^2$	0.33	0.13	0.13	0.18	0.40	0.32	0.31
h^2_T total heritability	0.22	0.24	0.12	0.09	0.18	0.35	0.19
r_{dm} direct-maternal genetic correlation	−0.88±0.04	−0.68±0.10	−0.52±0.31	−0.70±0.23	−0.84±0.03	−0.57±0.11	−0.63±0.09

HG: Hungarian Grey, HS: Hungarian Simmental, AA: Angus, HE: Hereford, CH: Charolais, BD: Blonde d'Aquitaine, LI: Limousin, e^2, c^2, h^2_d, h^2_m, r_{dm}, ±=standard error (SE)

A difference in the genetic correlation between direct and maternal components of gain from birth to weaning can have several practical consequences. Negative estimates of direct-maternal genetic covariance have been reported for many beef cattle breeds are now included in national genetic evaluations of many breed associations (Splan *et al.* 2002). It is important because a negative genetic correlation between direct and maternal effects will reduce genetic progress (Heydarpour *et al.* 2008). Therefore, consideration of such effect in genetic evaluation requires reliable estimation. It is important to note that one should be careful about interpretation of this correlation estimates, especially in this case, because of small dataset of the evaluated breeds in our study. Covariances are generally more difficult to estimate and the quality of estimation is strongly depend on data structure (Heydarpour *et al.* 2008). According to the mentioned author, the increase of the proportion of cows without records in the population has a negative effect on reliability, increases the standard error and bias of the estimation. As in this study the proportion of cows without records was very low, practically zero, the result can be considered as significant previous data.

The genetic trend, estimated on the basis of breeding value differences from overall mean in a given year by breed are shown in Figure 2. As it can be seen with exception of Hungarian Grey no progress between 1976-88. Unstable genetic trend in most of breeds appeared between 1988-1996 when especially breeding value of Hungarian Grey, Hungarian Simmental and Blonde d'Aquitaine were varying, increasing, and then decreasing.



HG: Hungarian Grey, HS: Hungarian Simmental, AA: Angus, HE: Hereford, CH: Charolais, BD: Blonde d'Aquitaine, LI: Limousin

Figure 2
The genetic trend for 205-day weaning weight of different breeds

After 1996 genetic trends were almost positive, but the magnitudes varied considerably among breeds. Hungarian Simmental, Charolais and Blonde d' Aquitaine had faster genetic trends than the other breeds. These results are different from findings of Cundiff & Van Vleck (1995) and Sullivan *et al.* 1999 who found that lighter breeds generally had faster genetic trends than heavier ones in pre weaning weight gain and weaning weight.

In conclusion, the findings of this study correspond to some other research results that sire, herd, age of dam at calving, birth year, season and sex of calf all have significant effect on 205-day weaning weight of calves in the studied breeds. These effects have to be taken into consideration when evaluating weaning results, doing genetic analyses and breeding value estimation for this trait. Adjustment of weaning weight according to these effects can decrease the bias and may increase the reliability of the genetic analysis.

Breed differences and substantial overlap among breeds seems to exist for weaning performance in beef cattle population in Hungary. These differences can be important because weaned calf market specifications are similar for producers of all breeds, and management have to, therefore, compensate for breed differences.

Variance components, heritability values, and direct-maternal genetic correlations of 205-day weaning weight to some extent were similar for purebred populations of different beef cattle breeds in Hungary, generally corresponding to the results reported by several authors. As using of own heritability values of a given population for a trait, such as weaning weight is basic requirement, these estimates can help to improve the genetic evaluation programmes of different beef cattle breeds in the country. Moreover direct-maternal genetic correlations can be important as many studies suggested that both direct and maternal additive genetic effects should be taken into consideration when setting selection aim.

The results of this study show that genetic trends vary among breeds involved in the evaluation. This fact indicates either that selection objectives or selection efficiencies are variable. The results obtained in genetic trend in the case of different breeds support the opinion that breeders from any breed likely target the average commercial cow.

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