

Linear and linear-threshold model for genetic parameters for SEUROP carcass traits in Czech beef cattle

Z. VESELÁ, L. VOSTRÝ, P. ŠAFUS

Institute of Animal Science, Prague-Uhřetěves, Czech Republic

ABSTRACT: The objective of this study was to estimate genetic parameters for the results of classifying of carcass traits by the SEUROP method in beef cattle in the Czech Republic using linear and linear-threshold models. Genetic parameters were calculated and evaluated in a set of 4276 animals of eleven beef breeds and crosses with dairy and dual-purpose breeds (Aberdeen Angus – 1376, Hereford – 994, Simmental – 651, Charolais – 524, Piemontese – 185, Galloway – 162, Blonde d'Aquitaine – 147, Limousine – 106, Highland – 53, Gasconne – 44, Belgian Blue – 34) in 2005–2008. Aberdeen Angus, Hereford, Charolais and beef Simmental were the most numerous breeds. Fixed effect of a classifier, fixed regression on age at slaughter by means of Legendre polynomial of the second degree separately for the each breed and sex and fixed regression on heterosis coefficient were included in a model equation. Genetic parameters were estimated by a multi-trait animal model using a linear model and a linear-threshold model in which carcass weight (CW) was considered as the linear trait and carcass conformation (CC) and carcass fatness (CF) grading as threshold traits. The heritability coefficient for CW differed only moderately according to the method of the genetic parameter estimation (0.295 in linear model and 0.306 in linear-threshold model). The heritability coefficient for CC was 0.187 in linear model and 0.237 in linear-threshold model. The heritability coefficient for CF grading was 0.089 in linear model and 0.146 in linear-threshold model. Genetic correlation between CW and CC was high (0.823 in linear model and 0.959 in linear-threshold model), the correlation between CW and CF was intermediate (0.332 and 0.328, respectively) and it was low between CF and CC (0.071 and 0.053). If CW was included in the model equation as fixed regression using Legendre polynomial, lower heritability coefficients for CC (0.077 and 0.078) and CF (0.086 and 0.123) were calculated and the correlation between CC and CF was negative (–0.430 and –0.429).

Keywords: genetic parameters; heritability; genetic correlation; REML; EUROP

Since 2000 in the Czech Republic the breeding value for field test (calving ease, birth weight and live weight at 120, 210 and 365 days of age) has been estimated in beef cattle by a multi-trait animal model with maternal effect (Příbyl et al., 2003). The estimation of breeding value for the own growth of bulls at performance-test stations was introduced in 2004 (Příbylová et al., 2004) and since 2005 the breeding value for the type description

of young beef cattle has been estimated (Veselá et al., 2005). An integral part of beef cattle breeding is the classification of carcass quality by the SEUROP method and the estimation of genetic parameters and breeding values for these traits.

Many scientific papers were aimed at the estimation of heritability coefficients for slaughter weight and other measured carcass traits (Rios-Utrera and Van Vleck, 2004). Kamieniecki et al.

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(2009) carried out the analysis of growth and carcass performance in Charolais beef cattle and in Charolais crossbreds with Hereford and Simmental cattle. Weglarz (2010) evaluated the slaughter quality of young cattle according to the post-slaughter EUROP classification and assessed the meat quality considering the season of slaughter. However, relatively only few papers focused on the estimation of genetic parameters for subjectively evaluated traits were published using the (S)EUROP system. This system implements a scale for grading the conformation and another scale for grading the fat cover of the carcass as a basis for grading carcass quality. The system was set up to take into account carcass quality factors in addition to carcass weight. The conformation and fat cover scores are furnished by slaughterhouse personnel who have been suitably trained in the grading of beef carcasses with the aid of the photographic patterns employed in the SEUROP system (Oliver et al., 2010). Eriksson et al. (2003) estimated genetic parameters for these traits by a linear animal model in beef breeds Charolais, Hereford and Simmental in Sweden. Parkkonen et al. (2000) studied the estimation of genetic parameters for carcass traits in Finnish Ayrshire and Holstein-Friesian cattle. They used a linear animal model, linear sire model and linear sire maternal grandsire model for estimations. Hickey et al. (2007) estimated genetic parameters for eight beef breeds, dairy breeds and their crossbreds in Ireland. They used the linear animal model respectively by sire breeds. The traits of carcass conformation and carcass fatness classified by the (S)EUROP system are categorical traits that are usually analysed by a threshold model (Wright, 1934; Dempster and Lerner, 1950; Gianola, 1982). Threshold models assume the existence of an underlying, unobservable normal variable that is categorized through a fixed threshold (Misztal et al., 1989). The threshold model approach has been applied in many cases to evaluate calving ease (Wang et al., 1997; Wiggans et al., 2003). Jamrozik et al. (1991) used a threshold model for the estimation of genetic parameters for conformation traits in dairy cattle. The results of the threshold model were compared with the results of a classical linear model. There was no advantage in the threshold model compared to a conventional linear animal model, mainly due to a wide range of categories observed on the real scale. Varona et al. (2009) compared the results from threshold model and linear model for carcass conformation and carcass fatness classification by (S)EUROP system in

Pirenaica beef cattle. The differences between such results were also very small.

The objective of our study was to estimate genetic parameters for the results of carcass trait classification using the SEUROP method in beef cattle in the Czech Republic and to compare the results obtained from linear and linear-threshold models.

MATERIAL AND METHODS

Data on 11 578 animals of twelve beef breeds and crosses with dairy and dual-purpose breeds were available. Animals were the offspring of 2117 sires (on average 5.5 offspring per sire), they came from 1322 herds (8.7 animals per herd), they were slaughtered in 87 abattoirs and were evaluated by 139 classifiers. They were evaluated in 2005 to 2008. Aberdeen Angus, Hereford, Charolais and Simmental breeds were the most numerous breeds (Aberdeen Angus 2747, Hereford 2617, Charolais 2433, Beef Simmental 1377, Limousine 623, Piemontese 564, Blonde d'Aquitaine 513, Galloway 433, Gasconne 132, Highland 129, Belgian Blue 82). 56% of the evaluated animals were purebreds or individuals with the proportions of beef breeds above 88%. The other animals were products of crossing with a higher proportion of beef breeds (at least 50%). Animals came from herds included in the performance testing system for the national genetic evaluation. It means that their pedigrees were relatively highly reliable. Figure 1 illustrates the frequencies of slaughtered animals by age at slaughter in years. The graph shows a very wide range of the age of animals slaughtered at abattoirs. The youngest animal was slaughtered at 252 days of age while the oldest at 21 years of age. In our study we were interested in genetic parameters for animals designed for fattening and slaughter at abattoir, therefore only the animals slaughtered by two years of age were included in the calculation of genetic parameters, i.e. 52% of the whole set (6152 animals). The data set was provided by the Czech Beef Breeders Association (ČSCHMS).

The classification of carcass traits by the SEUROP method is based on 3 traits: (1) carcass weight, (2) carcass conformation score and (3) carcass fatness score. The carcass conformation is evaluated by a six-class scale (S, E, U, R, O, P) from the best carcass conformation – S to the worst – P. For the purposes of calculations, the grading was transformed to a numerical scale from 1 (for P) to 6

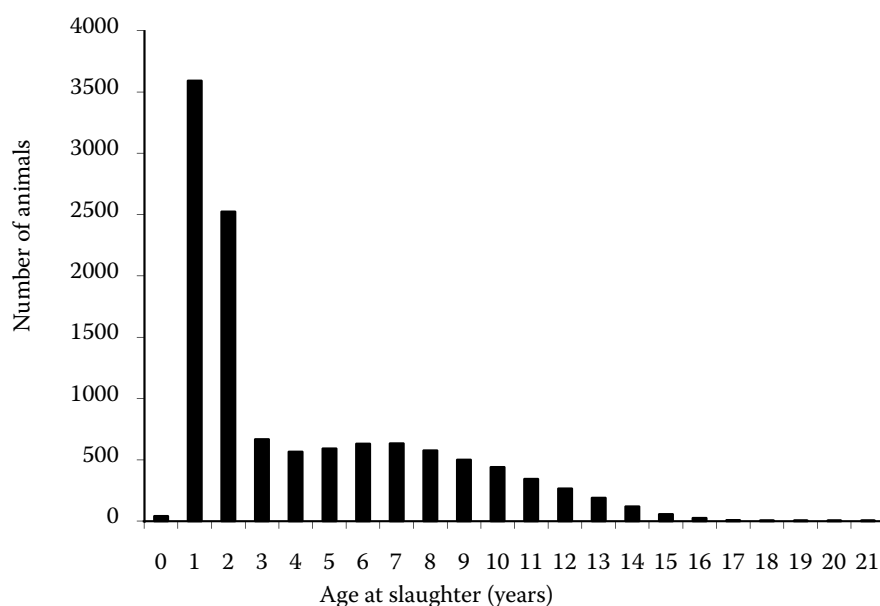


Figure 1. Frequencies of slaughtered animals by age at slaughter in years

(for S). The carcass fatness is evaluated by a five-class scale from 1 (the lowest carcass fatness) to 5 (the highest carcass fatness).

The set for the estimation of genetic parameters was subjected to the checking of data correctness. Animals with daily carcass weight gain that was lower or higher than 3 standard deviations from the mean within groups by slaughter age and sex were discarded from the set for the estimation of genetic parameters. Animals having less than 2 mates within herd, year, season, abattoir group, animals evaluated by a classifier who classified less than 4 animals and animals having in the set less than 3 half-sibs after sire were also discarded from the set for the estimation of genetic parameters.

The resultant set for the estimation of genetic parameters was composed of 4276 animals with results of carcass trait classification. These animals were the offspring of 422 sires (on average 10.1 offspring per sire), came from 239 herds (19.7 animals per herd), were slaughtered in 62 abattoirs and evaluated by 94 classifiers. The set comprised 3513 young bulls and 763 heifers. Table 1 shows the numbers of animals by breed in the set for the estimation of genetic parameters.

We tested several models comprising fixed effects: sex, age of dam, herd (from which the animal came to abattoir), abattoir, classifier, castration, age at slaughter, heterosis coefficient, herd year season – HYS, herd year season abattoir – HYSa, regression on age at slaughter (linear, quadratic and Legendre polynomial). The significance of effects

was tested by hypothesis test for significance in MIXED procedure using the method of restricted maximum likelihood (REML) in SAS analytical software (SAS, 2004). Suitability of the model was tested by Akaike information criterion (Akaike, 1973), which is defined as:

$$AIC = -2 \log(Li) + 2t_i \quad (1)$$

This model equation was used for the estimation of genetic parameters:

Table 1. Numbers of animals by breed in the data set for the estimation of genetic parameters

Breed	Proportion of breed (%)	
	88–100	50–87
Aberdeen Angus	990	386
Beef Simmental	230	421
Belgian Blue		34
Blonde d'Aquitaine	45	102
Charolais	248	276
Galloway	109	53
Gasconne		44
Hereford	693	301
Highland	38	15
Limousine	78	28
Piemontese	68	117
Overall	2499	1777

$$y_{jklmno} = \mu + hysa_j + breed_k + sex_l + \sum_{i=0}^2 z_i age + b_m het + clas_n + g_{jklmno} + e_{jklmno} \quad (2)$$

where:

y_{jklmno} = evaluation of evaluation of carcass weight, carcass conformation class and carcass fatness class

μ = overall mean

$hysa_j$ = random effect of the group of jointly evaluated animals j (herd year season abattoir)

$breed_k$ = fixed effect of the breed k

sex_l = fixed effect of the sex l (male or female) of the animal

$\sum_{i=0}^2 z_i age$ = Legendre polynomial of the second degree for age at slaughter

$b_m het$ = fixed regression of the heterosis coefficient (from 0 to 1)

$clas_n$ = fixed effect of the classifier n

g_{jklmno} = breeding value of the animal (random effect)

e_{jklmno} = the residual error

Parameters of Legendre polynomial were computed according to the method described by Přibyl et al. (2007). Legendre polynomials were calculated separately by breed and sex of animals.

To estimate genetic parameters for carcass conformation and carcass fatness classification with inclusion of carcass weight as fixed effect the regression on carcass weight expressed by Legendre polynomial of the second degree was added to equation (2).

Table 2. Basic statistical characteristics of evaluated traits

	Mean	SD	Min	Max
Carcass weight	330.92	83.61	150	971
Carcass conformation	2.94	0.86	1	6
Carcass fatness	2.2	0.72	1	5

Genetic parameters were estimated by multi-trait animal model. Two methods for the estimation of genetic parameters were used. Firstly, it was a linear model in which linear continuity and normal distribution were assumed in all three evaluated traits. The variance components were estimated by the restricted maximum likelihood – REML using REMLF90 program (Misztal et al., 2002). Secondly, a linear-threshold model was used where carcass weight was a linear trait and the other two traits (carcass conformation classification and carcass fatness classification) were considered as categorical (threshold) traits. A model equation for linear-threshold model was identical to that for linear model (2). The analysis was carried out using Bayesian approach with Gibbs sampling and using the programme THRGIBBS1F90 (Misztal et al., 2002), which is a programme to estimate (co)variance components and genetic parameters as well as solutions for fixed and random effects in the threshold animal mixed model, which allows for any combination of categorical and continuous traits (Lee et al., 2002). The analysis was run as a

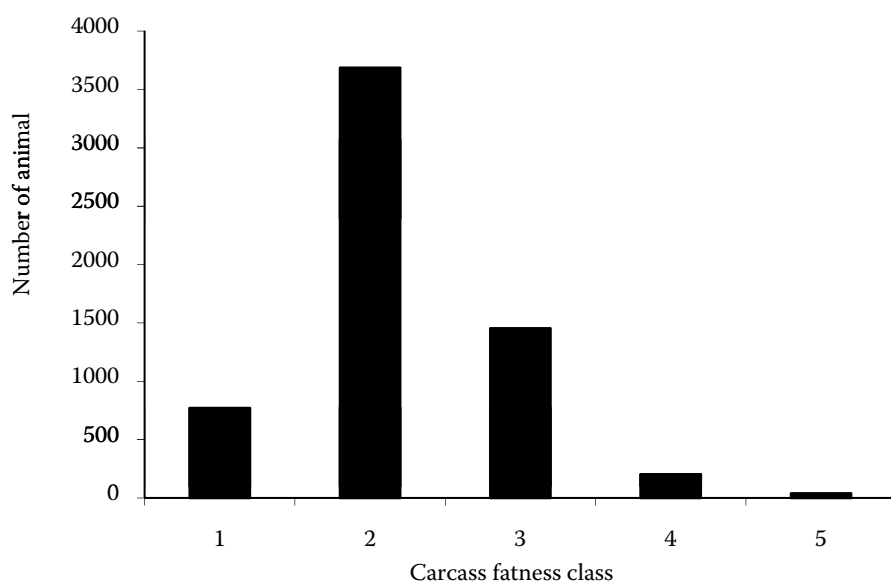


Figure 2. Numbers of animals according to carcass conformation class

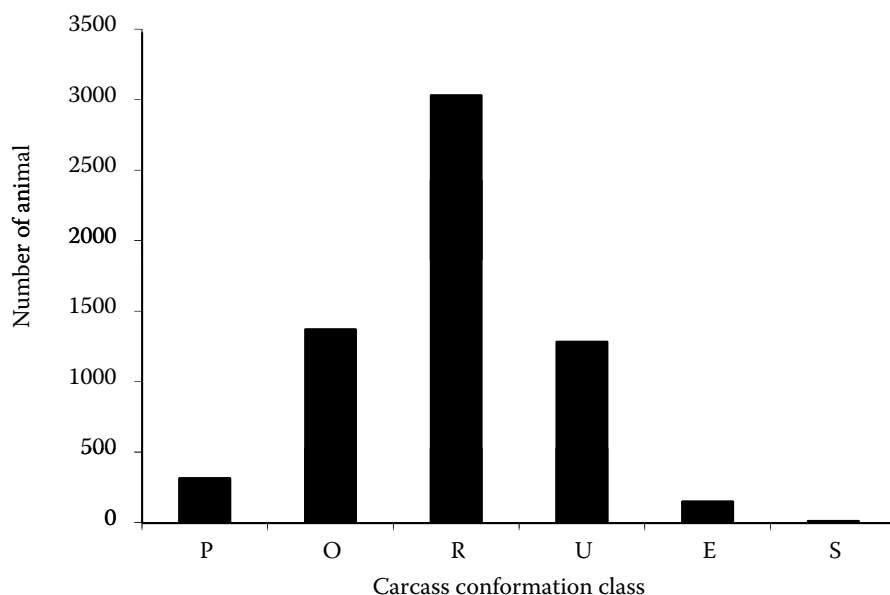


Figure 3. Frequencies of animals according to carcass fatness class

single chain of 200 000 iterations with a burn-in period of the first 30 000, at which a stationary stage was confirmed by graphical inspection. Every 10th sample was stored thereafter to compute posterior means and standard deviations. Post Gibbs analyses were done using POSTGIBBSF90 (Misztal et al., 2002).

RESULTS AND DISCUSSION

Table 2 shows the basic statistical characteristics of evaluated traits. The average carcass weight was 330.92 kg with standard deviation 83.61 kg. The average carcass conformation class was 2.94 scores (it is approximately R class in the SEUROP system) with standard deviation 0.86. The numbers of animals according to carcass conformation class are represented in Figure 2. The graph and basic statistics show that the carcass conformation class tended to lower values; nevertheless, the graph represents the normal distribution of frequencies quite satisfactorily. Only 10 animals were included by the carcass conformation in superior class S. The highest number of animals (3030) was included in R class. The average carcass fatness class was 2.2 scores with standard deviation 0.72. The frequencies of animals according to the carcass fatness class are documented in Figure 3. The graph shows that the majority of the animals received scores for lower carcass fatness, because these were only young animals of beef breeds.

The results of hypothesis test for significance of effects from MIXED procedure in SAS and Akaike information criterion for the most promising tested models are shown in Table 3. The effect of castration in males was found statistically insignificant in all tested models. It was probably so because the whole set comprised only 34 steers. The effect of dam age was also statistically insignificant. The reason is that animals older than 250 days were included in the calculation. The marked influence of the effect of dam age that can be assumed in young animals is a part of model equations for the estimation of breeding values for the growth of young beef cattle – a field test (Příbyl et al., 2003). Czech beef cattle population is small, therefore we used a multiple-breed estimation including all breeds and their crosses with breed as one of the fixed effects in the model equation (Příbyl et al., 2003). The effect of breed was significant in all tested models. We chose model V (2) with a low AIC and with all effects which were highly significant.

The effect of HYSA was considered as random in model (2) because of the high number of levels of these effects. The second reason for the treatment of HYSA effects as random was to ensure the convergence when threshold models based on likelihood methods were used for the parameter estimation (Kadarmideen et al., 2000). The threshold model has problems in the estimation of variance components and prediction of breeding values when the number of fixed effects is high (Misztal et al., 1989; Hoeschele and Tier, 1995; Moreno et al.,

Table 3. Hypothesis test for significance of effects and Akaike information criterion for tested models

	Sex	Breed	AGD	Herd	Abat	Clas	Age	Age ²	Het	HYS	HYSA	P ₁	P ₂	P ₃	Cast	AIC
Model I	< 0.0001	< 0.0001	0.05	< 0.0001	< 0.0001	< 0.0001	< 0.0001	0.0006	< 0.0001						0.08	41 260.9
Model II	< 0.0001	< 0.0001	0.06		0.70	< 0.0001	< 0.0001	< 0.0001	< 0.0001	< 0.0001					0.08	38 068.4
Model III	< 0.0001	< 0.0001	0.06			< 0.0001	< 0.0001	< 0.0001	< 0.0001		< 0.0001				0.07	37 900.6
Model IV	< 0.0001	< 0.0001	0.06			< 0.0001			< 0.0001		< 0.0001	< 0.0001	< 0.0001	0.001	0.07	37 847.1
Model V	< 0.0001	< 0.0001				< 0.0001			< 0.0001		< 0.0001	< 0.0001	0.0001			37 887.3

Sex = sex of animal, Breed = breed of animal, AGD = age of dam, Herd = herd, Abat = abattoir, Clas = classifier, Age = age at slaughter, Het = heterosis coefficient, HYS = herd year season, HYSA = herd year season abattoir, P₁–P₃ = parameters of Legendre polynomial for age at slaughter, Cast = castration, AIC = Akaike information criterion

1997). As comparable models are necessary for a comparison of the results of linear-threshold and linear model, the effect of HYSA was also considered as random in the linear model.

Table 4 shows genetic, residual and phenotype variances and variances in the random effect of HYSA estimated from the linear model and from the linear-threshold model. Differences between phenotype variances obtained by the particular methods were small in carcass weight, which was considered as a linear trait in both methods. Phenotype variance calculated by linear-threshold model ($\sigma_p^2 = 2549.5$) was slightly higher than in linear model ($\sigma_p^2 = 2517.2$). As for carcass conformation and carcass fatness classification, lower phenotype variance was calculated by linear-threshold model ($\sigma_p^2 = 0.254$ for carcass conformation and $\sigma_p^2 = 0.347$ for carcass fatness) compared to linear model ($\sigma_p^2 = 0.32$ for carcass conformation and $\sigma_p^2 = 0.384$ for carcass fatness). Genetic variance was identical in both methods for carcass conformation ($\sigma_a^2 = 0.06$). For carcass weight it was slightly higher in linear-threshold model ($\sigma_a^2 = 780.0$) than in linear model ($\sigma_a^2 = 742.4$). The carcass fatness genetic variance calculated by linear-threshold model was markedly higher ($\sigma_a^2 = 0.051$) compared to linear model ($\sigma_a^2 = 0.034$). Residual variance was lower in the linear-threshold model for all three traits. The most marked difference was determined in carcass conformation ($\sigma_e^2 = 0.097$ in linear-threshold model and $\sigma_e^2 = 0.168$ in linear model) and also in carcass fatness ($\sigma_e^2 = 0.118$ in linear-threshold model and $\sigma_e^2 = 0.188$ in linear model). A difference in residual variance for carcass weight was smaller according to the method ($\sigma_e^2 = 780.8$ in linear-threshold model and $\sigma_e^2 = 803.2$ in linear model). The variance of random effect of HYSA was slightly higher in all three traits in linear-threshold model. There was only a minimum difference for carcass weight and carcass conformation while a difference for carcass fatness was larger. Differences in the estimated components of variance in relation to the method of estimation were more pronounced for carcass conformation and carcass fatness grading, which were considered as threshold traits in linear-threshold model. Smaller differences were observed in carcass weight, which was considered as a linear trait in both methods.

Table 5 shows coefficients of heritability h^2 (on diagonal), genetic r_g (above diagonal) and phenotype r_p (below diagonal) correlations calculated by linear model and by linear-threshold model.

Table 4. Genetic (σ_a^2), residual (σ_e^2), phenotype (σ_p^2) variances and variances in the random effect of HYSA (σ_{hysa}^2)

	Linear model				Linear-threshold model			
	σ_a^2	σ_e^2	σ_p^2	σ_{hysa}^2	σ_a^2	σ_e^2	σ_p^2	σ_{hysa}^2
Carcass weight	742.4	803.2	2517.2	971.6	780.0	780.8	2549.5	988.7
Carcass conformation	0.060	0.168	0.322	0.094	0.060	0.097	0.254	0.096
Carcass fatness	0.034	0.188	0.384	0.161	0.051	0.118	0.347	0.178

Table 5. Coefficients of heritability h^2 (on diagonal), genetic r_g (above diagonal) and phenotype r_p (below diagonal) correlations calculated by linear model and linear-threshold model

	Carcass weight	Carcass conformation	Carcass fatness
Linear model			
Carcass weight	0.295	0.823	0.332
Carcass conformation	0.316	0.187	0.071
Carcass fatness	0.143	0.099	0.089
Linear-threshold model			
Carcass weight	0.306	0.959	0.328
Carcass conformation	0.372	0.237	0.053
Carcass fatness	0.164	0.126	0.146

Heritability coefficient for carcass weight differed only slightly in relation to the chosen method. This trait was included in both models as a linear trait. Heritability coefficient was 0.295 for linear model while it was higher (0.306) for threshold model, which was probably connected with the correlation of carcass weight with traits that were considered as threshold traits in linear-threshold model.

Heritability coefficient for carcass conformation was 0.187 in linear model and 0.237 in linear-threshold model, where carcass conformation was considered as a threshold trait. Heritability coefficient for carcass fatness was significantly lower than heritability coefficient for carcass conformation. It was 0.089 and 0.146 in the linear and linear-threshold model, respectively.

According to the chosen method of the estimation of genetic parameters heritability coefficients for carcass conformation and carcass fatness were different more markedly than heritability coefficient for carcass weight while in all three carcass traits these higher heritability coefficients were estimated by linear-threshold model compared to linear model. The difference in carcass fatness

was larger than that in carcass conformation. The larger difference in heritability coefficients for carcass fatness can probably be explained by the worse approximation of the normal distribution of frequencies of carcass fatness classification results (Figure 3) than in carcass conformation classification (Figure 2). Another explanation will probably be the lower number of carcass fatness classes (5 classes) compared to carcass conformation classes (6 classes). In comparison with carcass fatness carcass conformation grading is moderately more suitable for the potential inclusion of this trait as a linear trait.

Many studies have been aimed at the estimation of heritability coefficient for carcass weight. In their review Utrera et al. (2004) stated that in literary sources there existed a high variability among the estimated coefficients of heritability. The values ranged from 0.09 (Johnson et al., 1992) to 0.92 (Blackwell et al., 1962). The average value of heritability coefficients in literature was 0.42 (Utrera et al., 2004). However, the above-mentioned papers and also the papers cited by Utrera et al. (2004) in their review did not present the estimations of

genetic parameters for carcass traits evaluated by the relatively new SEUROP method. Eriksson et al. (2003) reported the value of heritability 0.21–0.39 for carcass weight in beef cattle in Sweden. These authors also reported somewhat higher values of heritability coefficient for carcass conformation classification ($h^2 = 0.21–0.39$) and significantly higher heritability coefficients for carcass fatness classification ($h^2 = 0.23–0.45$) compared to our study. They estimated genetic parameters for each breed separately and only young bulls were evaluated. This could be the reason for higher heritability coefficients in their study. Parkkonen et al. (2000) calculated considerably lower values of heritability coefficient ($h^2 = 0.07–0.14$) for carcass weight in dairy cattle in Finland. Their heritability coefficients for carcass conformation ($h^2 = 0.16–0.31$) and carcass fatness ($h^2 = 0.08–0.16$) were comparable with our values. It shows the lower variability of carcass weight in dairy cattle than in beef cattle. Hickey et al. (2007) reported average heritability coefficient 0.26 for carcass weight in cattle in Ireland, and 0.17 for carcass conformation and carcass fatness. They estimated genetic parameters separately for 8 sire breed groups and their results show that genetic variances and consequently heritability for SEUROP carcass traits are different in different breeds of cattle. Markedly higher heritability coefficients for carcass weight ($h^2 = 0.59$), carcass conformation ($h^2 = 0.79$) and carcass fatness ($h^2 = 0.63$) were determined by Pabiou et al. (2008), who however estimated genetic parameters in a relatively low number of evaluated animals, which could influence their results. Varona et al. (2009) reported heritability coefficient 0.23–0.26 for carcass conformation grading in Pirenaica beef cattle according to the chosen method and model of estimation; their coefficient for carcass fatness grading was 0.13–0.16.

Veselá et al. (2005) estimated heritability coefficients for the evaluation of muscling as traits describing conformation in live animals that will

be used for breeding in the future; muscling was obtained in the evaluation of the type of young animals of beef cattle in the Czech Republic. Those heritability coefficients were higher than the heritability coefficients calculated in our study for carcass conformation of slaughtered animals, and they were in the range of 0.25–0.35. The higher coefficients may be explained by the fact that it was a more compact set and so it was easier to adjust it for systematic effects. Another reason may be the worse level of the results of carcass trait classification by the SEUROP method.

Genetic correlation between carcass weight and carcass conformation estimated in the present study was quite high. The genetic correlation calculated by linear model was 0.823 while that obtained by linear-threshold model was still considerably higher 0.959. Genetic correlation between carcass weight and carcass fatness grading was intermediate and it differed only moderately by the chosen calculation method. In linear model genetic correlation was 0.332 while in linear-threshold model it was moderately lower 0.328. Genetic correlation between carcass conformation grading and carcass fatness grading was very low. A weak genetic correlation 0.071 was estimated in linear model and a still lower genetic correlation ($r_g = 0.053$) was calculated by linear-threshold model. It means that a minimum genetic correlation between carcass conformation and carcass fatness classification was determined in young animals of beef cattle. Parkkonen et al. (2000) reported a high genetic correlation ($r_g = 0.38–0.66$) between carcass weight and carcass conformation grading in dairy cattle. Similarly like in our study, these authors determined a zero genetic correlation between carcass conformation and carcass fatness. On the contrary, Hickey et al. (2007) reported a relatively high positive genetic correlation ($r_g = 0.44$) between carcass conformation and carcass fatness in the Holstein sire breed group in Irish cattle. But genetic correlation between carcass weight and carcass conformation grading was quite low ($r_g = 0.11$)

Table 6. Residual correlations calculated by linear model (above diagonal) and by linear-threshold model (below diagonal)

	Carcass weight	Carcass conformation	Carcass fatness
Carcass weight		0.302	0.226
Carcass conformation	0.331		0.179
Carcass fatness	0.292	0.320	

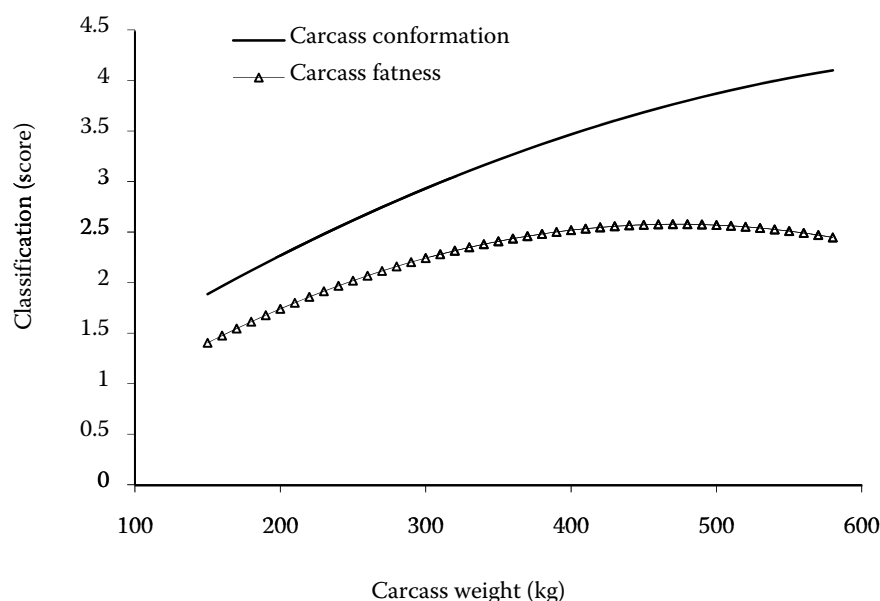


Figure 4. Regression curves for carcass conformation and fatness classification in relation to carcass weight

in their study. It could be caused by different genetic determination of carcass conformation and fatness in dairy cattle than in beef cattle.

Table 6 shows residual correlations calculated by linear model (above diagonal) and by linear-threshold model (below diagonal). The correlations obtained by linear-threshold model were higher than those from linear model. The most marked difference was determined for the correlation between carcass fatness and carcass conformation ($r_e = 0.179$ from linear model and $r_e = 0.320$ from linear-threshold model) and also between carcass fatness and carcass weight ($r_e = 0.226$ from linear model and $r_e = 0.292$ from linear-threshold model). The difference in residual correlation between carcass conformation and carcass weight was smaller ($r_e = 0.302$ from linear model and $r_e = 0.331$ from linear-threshold model). The lowest residual correlation between carcass conformation and carcass fatness was calculated by linear model. In linear-threshold model the values of residual correlations among all traits were almost identical.

As shown in Table 5, a high correlation was calculated between carcass weight and carcass conformation classification. In a further calculation of genetic parameters only for carcass conformation and carcass fatness classification regression on carcass weight by means of Legendre polynomial was included as fixed effect in the model equation. Figure 4 shows the curves plotted from linear model. Obviously, the correlation between carcass conformation and carcass weight has an almost

linear course. The higher the carcass weight, the higher the carcass conformation score. The score of carcass fatness increases approximately to carcass weight of 450 kg, and with a further increase in carcass weight the carcass fatness grading does not markedly change any more. Genetic correlations shown in Table 5 correspond to this result. While there is a high correlation between carcass weight and carcass conformation, the correlation between carcass weight and carcass fatness is much lower. Taking into account the regression curve of carcass fatness it is to assume that the correlation between carcass weight and carcass fatness will be much higher in the set of younger animals with lower carcass weight. Accordingly, it is possible to expect higher heritability coefficient for carcass fatness grading in the set of younger animals.

Table 7 shows variance components, heritability coefficients and genetic correlations calculated by the model with fixed regression on carcass weight. It is evident that compared to the model without regression on carcass weight the changes in carcass conformation were more pronounced than in carcass fatness. In carcass conformation, first of all there was a marked reduction in genetic variance. Residual variance and variance of random effect of HYSA were reduced only slightly. Due to these changes the significantly lower heritability coefficient ($h^2 = 0.077$ in linear model and $h^2 = 0.078$ in linear-threshold model) was determined in carcass conformation compared to the model without regression on carcass weight

Table 7. Genetic parameters for carcass conformation (CC) and carcass fatness (CF) by the model with fixed regression on carcass weight

	Linear model	Linear-threshold model
CC	σ_a^2	0.020
	σ_e^2	0.154
	σ_p^2	0.256
	σ_{SRO}^2	0.082
	h^2	0.077
CF	σ_a^2	0.030
	σ_e^2	0.176
	σ_p^2	0.352
	σ_{SRO}^2	0.146
	h^2	0.086
	r_g	–0.430
	r_e	0.101
	r_p	0.021

($h^2 = 0.187$ and 0.237). These results demonstrate a significant share of carcass weight in the results of carcass conformation classification. In genetic parameters for carcass fatness the changes in estimated variances were smaller. Heritability coefficients ($h^2 = 0.086$ in linear model and $h^2 = 0.123$ in linear-threshold model) were only slightly lower in comparison with the model without regression on carcass weight ($h^2 = 0.089$ and 0.146). The results of genetic correlation between carcass conformation classification and carcass fatness classification were largely different. If regression on carcass weight was included in the model equation, an intermediate negative correlation ($r_g = -0.430$ and -0.429 , respectively) between these two traits was determined. Residual and phenotype correlations were also considerably lower. If carcass weight was included as regression, an almost zero phenotype correlation between carcass conformation and carcass fatness was obtained.

The parameters we estimated in this study were rather different in relation to the method of estimation. Linear-threshold model provided higher heritability coefficients for all traits as well as higher genetic correlation between carcass weight and carcass conformation classification. Varona et al. (2009) compared the results from threshold model

and linear model for the estimation of genetic parameters for carcass fatness and carcass conformation grading. They observed only small differences between the estimated coefficients of variance and heritability. However, in their study the animals were evaluated using a wide range of 16 categories for carcass conformation (P– to S+) and 17 categories for carcass fatness. Many authors compared linear and threshold models for genetic evaluation of calving ease. A scale with 4 or more calving ease scores tends to rank animals similarly using linear and threshold models (Varona et al., 1999; Ramirez-Valverde et al., 2001; Lee et al., 2002). Although the threshold model is considered as more suitable for the estimation of genetic parameters in discontinuous traits, its time consumption is much higher than in the linear model (Kadarmideen et al., 2000). Furthermore, the threshold model has problems in the estimation of variance components and prediction of breeding values when the number of fixed effect is high (Misztal et al., 1989). This problem can be solved by high information content for fixed effect and by inclusion of the effect of herd as random effect (Varona et al., 1999).

CONCLUSION

In the present study genetic parameters for the classification of carcass traits by the SEUROP method were estimated in Czech beef cattle. These estimated parameters differed according to the model, either linear or linear-threshold one, used for their estimation. The most pronounced differences were determined in genetic parameters for carcass conformation and carcass fatness that were considered as threshold traits in linear-threshold model. In linear-threshold model markedly higher heritability coefficients were calculated for these two traits compared to the linear model.

Genetic correlation between carcass weight and carcass conformation classification is high while the correlation between carcass weight and carcass fatness classification is intermediate. These high correlations result in higher heritability coefficients and zero correlation between carcass conformation and carcass fatness classification. If carcass weight is included in the model equation as fixed effect, significantly lower heritability coefficient for carcass conformation and negative correlation between carcass conformation and carcass fatness classification will be obtained. The scores

for carcass conformation are strongly predetermined by carcass weight. Muscling is reflected in the scores to a substantially lesser extent. If the genetic evaluation of animals by a classical model without inclusion of carcass weight as fixed effect is used, breeding values for carcass weight and carcass conformation classification are almost the identical parameter. Taking into account carcass weight as fixed regression, genetic evaluation will be obtained only for pure carcass conformation, which however brings about a decrease of heritability and reliability of the estimation of breeding value.

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Corresponding Author

Ing. Zdenka Veselá, Ph.D., Institute of Animal Science, Přátelství 815, 104 00 Prague-Uhřetěves, Czech Republic
Tel. +420 267 009 664, e-mail: vesela.zdenka@vuzv.cz
