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Breeding value for type traits in beef cattle in the Czech Republic

Z. Veselá[1], J. Přibyl[1], P. Šafus[1], L. Vostrý[1], K. Šeba[2], L. Štolc[3]

[1]Research Institute of Animal Production, Prague-Uhříněves, Czech Republic
[2]Czech Beef Cattle Association, Prague, Czech Republic
[3]Czech Agricultural University, Prague, Czech Republic

ABSTRACT: The type was evaluated in 5 424 young animals of twelve beef breeds. Ten type traits were evaluated: height at sacrum (HS), body length (BL), live weight (LW), front chest width (CW), chest depth (CD), pelvis (P), shoulder muscling (SM), back muscling (BM), rump muscling (RM) and production type (PT). The traits represent two groups: (1) traits scoring body measurements and body capacity (HS, BL, LW, CW, CD, P) and (2) traits scoring muscling (SM, BM, RM, PT). These fixed effects were included in the model: breed, sex, HYS, mother's age, linear regression on age at evaluation and average gain from birth to evaluation. Fixed effects in the model explained 40% to 60% of variability. The highest values of heritability coefficient were estimated for HS (h^2 = 0.51) and LW (h^2 = 0.50). BL had the lowest values of heritability coefficient (h^2 = 0.25). The values h^2 = 0.25–0.32 were calculated for the traits scoring body capacity (CW, CD, P). The range of values for muscling traits was h^2 = 0.26–0.35. The coefficient of heritability for PT was h^2 = 0.34. All traits scoring muscling and PT showed high genetic correlations (r_g > 0.95). The traits scoring body capacity (P, CW, CD) were highly genetically correlated with muscling r_g > 0.83. Breeding values were determined by a multi-trait animal model. Standard deviations of breeding values were higher in HS (s_{BV} = 0.71) and LW (s_{BV} = 0.84), which was connected with a different method of evaluation of these traits. They were in the range of 0.19 (BL) to 0.30 (RM) in the other traits.

Keywords: animal model; beef cattle; breeding value; genetic correlation; heritability; type traits

Beef cattle production in the Czech Republic is a relatively new industry that has expanded since 1990. In total, twelve beef cattle breeds and their crosses are kept in the Czech Republic. Breeding value for the results of field test in beef cattle (calving ease, birth weight and live weight at the age of 120, 210 and 365 days) has been evaluated by a multi-trait animal model since 2000 (Přibyl et al., 2003). In 2004 estimation of breeding value for the own growth of beef bulls at performance-test stations was introduced (Přibylová et al., 2004; Přibyl et al., 2004).

Evaluation of the type is an integral part of cattle breeding. Objective evaluation of the type in beef cattle is significantly related with the expression of meat performance. An evaluation method is given in methodical instructions for the description and evaluation of the type of beef cattle by Czech Beef Cattle Association (ČSCHMS, 1996).

Scientific papers pay great attention to the method of linear evaluation of the type of dairy cattle (Thomson et al., 1981; Brotherstone et al., 1990) and to its relation to production traits (Meyer et al., 1987; Brotherstone, 1994; Veerkamp and Brotherstone, 1997; Royal et al., 2002) and longevity (Setatti et al., 2004). Genetic parameters for type traits in Czech Piek cattle (dual-purpose type) were estimated by Bouška et al. (1991). The analysis of correlations between type traits of cows and their production traits, considered as important

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background data for effective selection in Czech Fleckvieh cattle, was carried out by Bouška et al. (1999). Evaluation of the type in beef cattle is presented in literature less frequently. Gutiérrez and Goyache (2002) estimated genetic parameters in the beef cattle breed Asturiana de los Valles. They estimated genetic parameters for 10 type traits. They divided the traits into two groups: (1) traits scoring skeletal and muscular development and (2) traits scoring adjustment to the breed standard. Vági (1997) evaluated 27 type traits in Hungarian beef cattle by factor analysis. The relationship between the type and longevity in beef cattle was examined by Forabosco et al. (2004). Gutiérrez et al. (2002) studied genetic relationships between major reproductive traits in beef cattle (calving date, calving interval and age at first calving) and type traits in order to evaluate the usefulness of type classification in predicting reproductive performance in beef cattle.

The objective of this paper was to estimate genetic parameters and breeding values for type traits of young animals of beef cattle breeds in the Czech Republic.

MATERIAL AND METHOD

In the Czech Republic beef cattle are evaluated according to methodical instructions for the description and evaluation of the type of beef breeds of cattle developed by the Czech Beef Cattle Association (ČSCHMS, 1996). Evaluation is based on the scoring of an evaluated trait by 1 (minimum) to 10 (maximum) points within the biological extremes of evaluated breed. Evaluating the scored traits, the classifier takes into account the population mean of evaluated breed and approved breed standard. Therefore the expression of the scoring scale for body traits according to the particular breeds is quite specific. The evaluation of the type involves 10 traits: height at sacrum – HS (measured with a measuring staff), body length – BL, live weight – LW (determined by the weighing of the animal), front chest width – CW (width of the chest base between the front legs front view), chest depth – CD (chest depth behind the blade), pelvis – P (pelvis length and width), shoulder muscling – SM, back muscling – BM, rump muscling – RM and production type – PT (overall thoroughbredness, harmony of body conformation and sex expression). A majority of traits is evaluated subjectively. Height at sacrum and live weight are determined by measuring and weighing, and conversion tables are used to obtain their point scoring while age, sex and breed are respected.

Available were 5 424 records of young animals (descendants of 586 sires) of 12 beef breeds and crosses with dairy and dual-purpose breeds (Aberdeen Angus – 1 156, Belgian Blue-White – 34, Blonde d'Aquitaine – 205, Galloway – 13, Gasconne – 34, Hereford – 496, Highland – 5, Charolais – 1 787, Limousine – 567, Beef Simmental – 970, Piemontese – 144, Salers – 13) evaluated at the age from 180 to 519 days. 84% of the evaluated individuals were purebred animals or with the proportion of beef breed higher than 88%. The other individuals were products of crossing with a higher proportion of beef breeds (at least 50%). The animals were evaluated at the time of weaning at the end of grazing season by one of nine classifiers or by a commission at performance-test stations of beef bulls (64 bulls).

Breeding values and genetic parameters were estimated by a multi-trait animal model.

REMLF90 programme (Misztal, 2002) was used to estimate genetic parameters. After omitting the groups with small numbers of contemporaries and individuals that did not have any sibs in the evaluated set, the sample size for the estimation of genetic parameters was 5 128 individuals with the evaluated type. The total sample size (including three generations of ancestors) was 12 749 individuals.

A total of 17 030 individuals including 4 generations of ancestors was used in the estimation of breeding value. BLUPF90 programme (Misztal, 2002) was used for the estimation of breeding value.

To estimate genetic parameters and breeding value the traits were divided into two groups: (1) traits scoring body measurements and body capacity (height at sacrum, body length, live weight, front chest width, chest depth and pelvis) and (2) traits scoring muscling and overall type (shoulder muscling, back muscling, rump muscling and production type).

For the first group of traits this model equation was used:

$$y_{ijkl} = \mu + HYS_i + S_j + AM_k + aAE_{ijkl} + g_{ijkl} + e_{ijkl} \quad (1)$$

For the second group of traits this model equation was used:

$$y_{ijk} = \mu + HYS_i + S_j + aAE_{ijk} + bDG_{ijk} + g_{ijk} + e_{ijk} \quad (2)$$

where: $y_{ijk(l)}$ = evaluation of the trait
μ = population mean
HYS_i = fixed effect of the group of jointly evaluated animals (herd, year, season)
S_j = fixed effect of the sex of the animal (young bulls, heifers/twins, singles)
AM_k = fixed effect of the age of mother at calving (younger than three years, four years old, five to seven years old, older than seven years and embryo recipients)
$aAE_{ijk(l)}$ = regression on age at evaluation
bDG_{ijk} = linear regression on average daily gain from birth to the date of evaluation
$g_{ijk(l)}$ = breeding value of the animal (random effect) – with the relationship matrix and genetic groups according to the breed
$e_{ijk(l)}$ = random error

Table 1. Basic statistical characteristics of evaluated traits

Evaluated trait	Mean	*s*	Min	Max
HS	5.66	2.17	1	10
BL	6.49	0.97	2	9
LW	6.76	2.65	1	10
CW	5.75	0.99	2	9
CD	6.19	0.98	2	9
P	5.81	0.99	2	9
SM	5.59	0.97	2	9
BM	5.76	0.98	2	9
RM	5.83	1.13	2	9
PT	5.84	1.13	2	9

RESULTS AND DISCUSSION

Table 1 shows basic statistical characteristics of the evaluated type traits. Standard deviations of the scoring of height at sacrum (*s* = 2.17) and live weight (*s* = 2.65) were higher than standard deviations of the scoring of other traits (*s* = 0.97–1.13). It was a result of different methods of evaluation. Height at sacrum and live weight were determined by objective methods (measuring and weighing) and converted to scores according to a conversion table taking into account age, sex and breed. The others traits were evaluated subjectively by a classifier. Figure 1 shows frequencies of distribution according to height at sacrum scoring. It was flat normal distribution. The classes of the extremes (scores 1 and 10) comprised a high number of individuals. On the contrary, the results of live weight did not show normal distribution (Figure 2). Most animals received higher scores in live weight evaluation. In both these traits (HS, LW) the whole scale from 1 to 10 was used for scoring. Figure 3 illustrates frequencies of distribution according to production type scoring. Scores from 2 to 9 were used for this evaluation and the results showed normal distribution. Similar distribution was found out in the other traits evaluated subjectively.

Figure 4 documents numbers of animals according to age at evaluation. A majority of the evaluated animals were at the age of 330 days and younger.

SAS/GLM procedure (SAS, 2004) was applied to test several models that included these fixed ef-

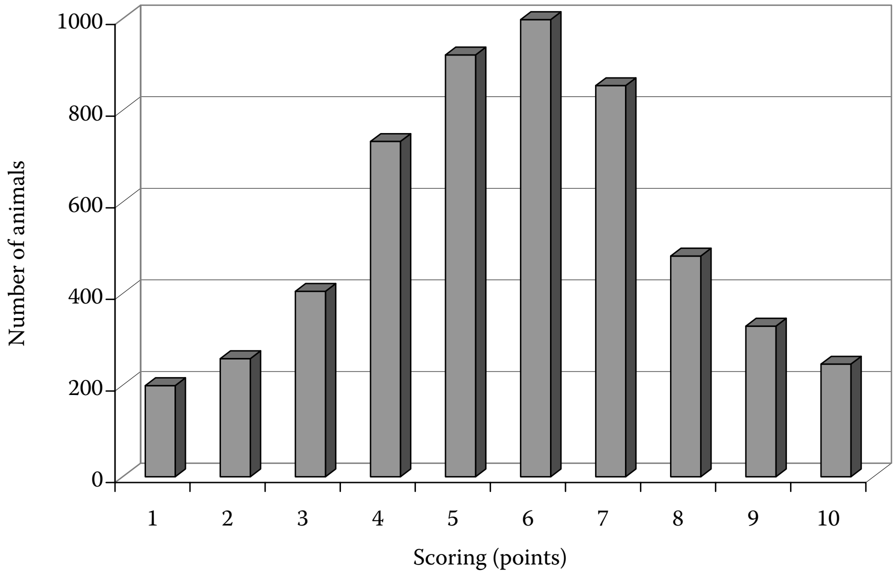

Figure 1. Frequencies according to scoring of height at sacrum

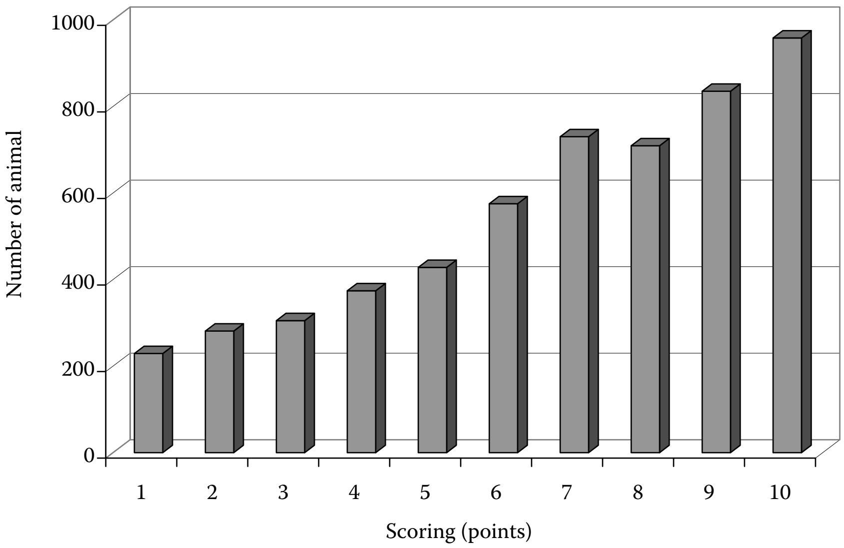

Figure 2. Frequencies according to scoring of weight

fects: sex, group of contemporaries (jointly evaluated animals), mother's age, class of evaluation age (1–10 according to age at evaluation), linear or quadratic regression on age at evaluation and linear regression on average daily gain from birth to evaluation. It was not possible to include the effect of classifier because it overlapped with the effect of the group of contemporaries (HYS). As shown in Table 2, fixed effects in models (1) and (2) explained 40–60% of variability. The group of jointly evaluated animals (HYS) was the most important effect as it explained 28–35% of variability. This effect involves several influences affecting the whole group of animals. All included effects (HYS, sex, mother's age, age at evaluation, gain from birth to evaluation) were statistically significant. The same effects as in models (1) and (2) were included in another suitable model but it comprised quadratic regression on age at evaluation. Fixed effects in this model explained approximately the same variability as models (1) and (2) in HS, LW, CW and SM. In CD, P and BM it explained by 1% of variability more and in BL, RM and PT by 2% more. Figure 5 shows the regression line and curve of production type scoring in relation to the age of evaluation of the animal. The graph was constructed on the basis of regression coefficients estimated by animal model. The other type traits had a similar course of regression. It is obvious from the figure that the quadratic regression curve has an almost linear course approximately until the age of 330 days. As the type of young cattle was evaluated mostly in

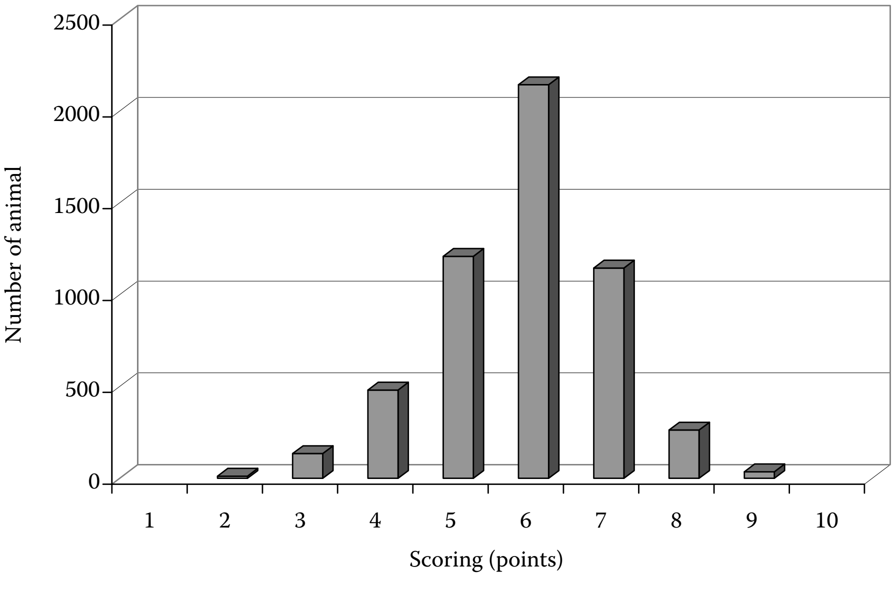

Figure 3. Frequencies according to scoring of production type

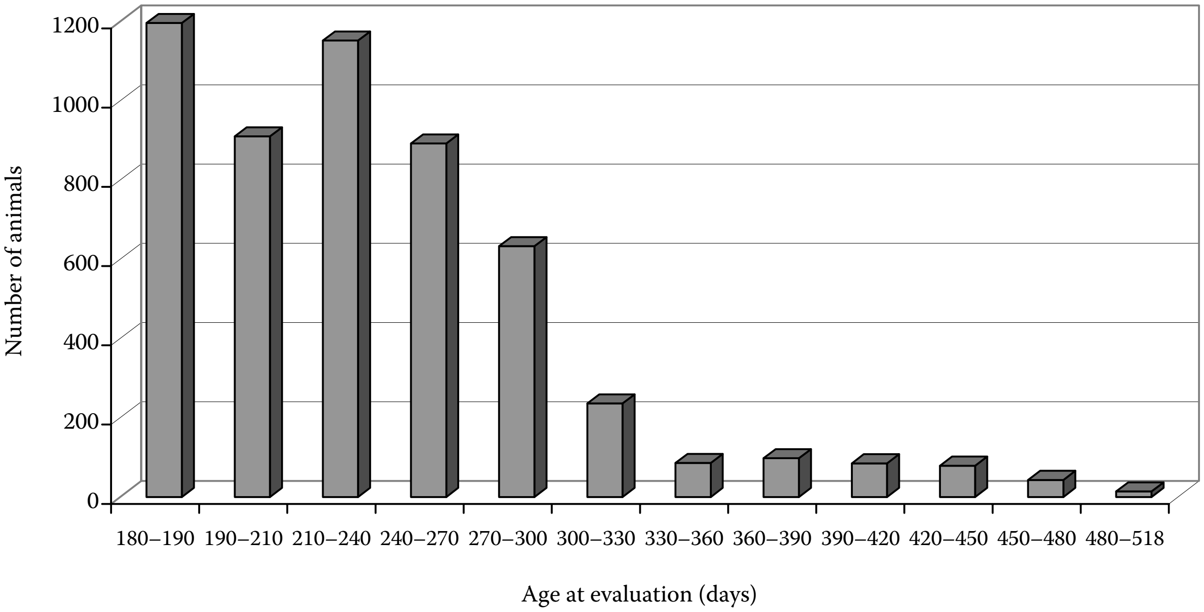

Figure 4. Frequencies according to age at evaluation

animals younger than 330 days (Figure 1), models (1) and (2) involving linear regression were chosen for routine evaluation. Tables 3 and 4 show genetic parameters for models with linear regression on age at evaluation.

Table 3 shows estimated standard deviations (σ_g, σ_e) that were then substituted into the calculation of breeding values. The estimated standard deviations for height at sacrum (σ_g = 1.27, σ_e = 1.25) and live weight (σ_g = 1.58, σ_e = 1.60) are markedly higher; it is a result of different method of evaluation of these two traits.

Coefficients of heritability h^2, phenotypic correlations r_p and genetic correlations r_g calculated from the model with linear regression on age at evaluation are given in Table 4.

The highest values of heritability coefficient (on the diagonal) were calculated for height at sacrum (h^2 = 0.51) and live weight (h^2 = 0.50), but these characteristics do not have a very suitable distribution of frequencies. On the contrary, body length had the lowest values of heritability coefficient (h^2 = 0.25). The coefficients of heritability for traits scoring the body capacity (CW, CD, P) ranged from h^2 = 0.27 (CW) to h^2 = 0.31 (P) and h^2 = 0.32 (CD). As for the traits of muscling, the highest values h^2 were found out for shoulder and

Table 2. Variability explained by fixed effects in total and by the effect of group of contemporaries – HYS (%) in a selected model with linear regression on age at evaluation (Model 1) and in a model with quadratic regression on age at evaluation (Model 2)

	Model 1		Model 2	
	total	HYS	total	HYS
HS	48	35	48	35
BL	40	34	42	35
LW	44	35	44	35
CW	42	35	42	35
CD	40	35	41	35
P	43	33	44	33
SM	57	28	57	28
BM	56	29	57	30
RM	57	28	59	30
PT	60	29	61	30

Table 3. Standard deviations substituted into the estimation of breeding values

	σ_g	σ_e		σ_g	σ_e
HS	1.27	1.25	P	0.46	0.68
BL	0.41	0.71	SM	0.46	0.63
LW	1.58	1.60	BM	0.40	0.68
CW	0.44	0.71	RM	0.52	0.71
CD	0.48	0.69	PT	0.53	0.73

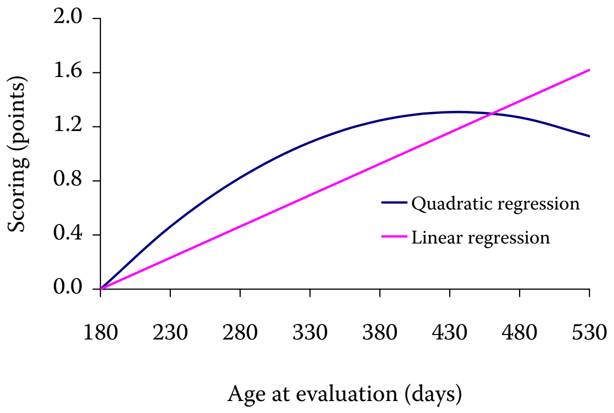

Figure 5. Production type – regression on age at evaluation

rump muscling (h^2 = 0.35) while the value h^2 for back muscling was lower (h^2 = 0.26). A total characteristic – production type reached the values of heritability coefficient h^2 = 0.34.

The calculated values of heritability coefficient correspond to data of other authors. Bouška et al. (1999) reported h^2 = 0.41 for muscling and 0.34 for chest depth in Czech Fleckvieh cattle. Lower coefficients of heritability for muscling were given by Vukašinovič et al. (1994) in Swiss Brown cattle (0.15). In Hungarian beef cattle Vági (1997) reported markedly higher coefficients of heritability for body length (0.70), chest depth (0.63), shoulder muscling (0.71), back muscling (0.44) and rump muscling (0.76). But Vági used a different method to estimate genetic parameters – factor analysis.

The highest phenotypic correlations were determined between the traits of muscling (SM, BM, RM) and production type (r_p = 0.69–0.87). The lowest phenotypic correlations with most traits, particularly with muscling traits (r_p = 0.17–0.21), were calculated for height at sacrum.

The highest genetic correlations (r_g) were found out between back muscling and shoulder muscling, and between back muscling and rump muscling (r_g = 0.98). Production type was in high genetic correlations with almost all scored characteristics except height at sacrum (r_g = 0.24), body length (r_g = 0.43) and live weight (r_g = 0.51). It showed the highest correlations with all three traits of muscling – SM, BM, RM (r_g = 0.96), chest width (r_g = 0.93), pelvis (r_g = 0.92) and chest depth (r_g = 0.87). There existed high genetic correlations of all traits describing muscling of the animal with production type (r_g > 0.95). We also calculated high genetic correlations of muscling with the traits describing body capacity – pelvis shape (r_g > 0.92), chest width (r_g > 0.91) and chest depth (r_g > 0.83).

Table 5 shows coefficients of heritability h^2, phenotypic correlations r_p and genetic correlations r_g calculated from models with quadratic regression on age at evaluation. If quadratic regression on age at evaluation was used, coefficients of heritability of almost all traits were lower than with linear regression. Coefficient of heritability for live weight was identical (h^2 = 0.50). Body length had a markedly lower coefficient of heritability (lower by 0.05). In the other traits the difference between the esti-

Table 4. Coefficients of heritability h^2 (on the diagonal), genetic r_g (above the diagonal) and phenotypic r_p (below the diagonal) correlations calculated from the model with linear regression on age at evaluation

	HS	BL	LW	CW	CD	P	SM	BM	RM	PT
HS	**0.51**	0.70	0.72	0.27	0.28	0.25	0.20	0.17	0.09	0.24
BL	0.43	**0.25**	0.46	0.56	0.56	0.59	0.55	0.54	0.39	0.51
LW	0.54	0.39	**0.50**	0.53	0.51	0.44	0.38	0.41	0.37	0.43
CW	0.28	0.44	0.42	**0.27**	0.96	0.92	0.95	0.95	0.91	0.93
CD	0.27	0.42	0.41	0.59	**0.32**	0.89	0.87	0.89	0.83	0.87
P	0.26	0.43	0.42	0.64	0.58	**0.31**	0.92	0.95	0.92	0.92
SM	0.21	0.39	0.36	0.67	0.59	0.68	**0.35**	0.98	0.95	0.96
BM	0.20	0.38	0.37	0.62	0.57	0.67	0.69	**0.26**	0.98	0.96
RM	0.17	0.34	0.36	0.60	0.56	0.73	0.72	0.72	**0.35**	0.96
PT	0.26	0.42	0.42	0.66	0.62	0.74	0.75	0.74	0.87	**0.34**

Table 5. Coefficients of heritability h^2 (on the diagonal), genetic r_g (above the diagonal) and phenotypic r_p (below the diagonal) correlations calculated from the model with quadratic regression on age at evaluation

	HS	BL	LW	CW	CD	P	SM	BM	RM	PT
HS	**0.50**	0.77	0.72	0.28	0.29	0.26	0.21	0.18	0.09	0.24
BL	0.44	**0.20**	0.52	0.51	0.50	0.55	0.50	0.49	0.35	0.46
LW	0.54	0.40	**0.50**	0.56	0.54	0.46	0.40	0.44	0.38	0.45
CW	0.29	0.43	0.43	**0.25**	0.96	0.91	0.95	0.95	0.90	0.92
CD	0.27	0.41	0.42	0.58	**0.30**	0.88	0.86	0.88	0.82	0.86
P	0.26	0.41	0.43	0.64	0.57	**0.30**	0.91	0.95	0.92	0.92
SM	0.22	0.38	0.37	0.66	0.59	0.67	**0.33**	0.98	0.95	0.95
BM	0.20	0.37	0.38	0.61	0.57	0.67	0.69	**0.25**	0.98	0.95
RM	0.18	0.33	0.37	0.60	0.56	0.72	0.71	0.71	**0.34**	0.96
PT	0.26	0.41	0.43	0.66	0.61	0.73	0.74	0.74	0.87	**0.33**

Table 6. The effect of calf sex (comparison with single bulls)

	Twin bulls	Single heifers	Twin heifers		Twin bulls	Single heifers	Twin heifers
HS	−0.81	1.24	0.09	P	−0.23	−0.08	−0.50
BL	−0.25	−0.01	−0.36	SM	−0.29	−0.06	−0.56
LW	−1.40	−0.77	−1.41	BM	−0.36	−0.05	−0.51
CW	−0.29	−0.09	−0.50	RM	−0.23	−0.07	−0.47
CD	−0.34	−0.02	−0.53	PT	−0.29	−0.04	−0.52

mated coefficients of heritability was 0.01 to 0.02. Genetic correlations (r_g) and phenotypic correlations (r_p) were not markedly different compared to the model with linear regression on age at evaluation. HS and LW were in close genetic correlations with the other traits. On the other hand, genetic correlations were lower in BL.

Animal model provided the results shown in Tables 6–9.

Table 6 documents the effect of calf sex on the type evaluation in comparison with single bulls. Mainly the effect of twins is expressed. The effect of sex is less marked because classifiers take it into account already in the evaluation of animals. In almost all traits bulls and heifers from twins receive lower scores than single bulls and heifers. Higher deviations were found out in height at sacrum and live weight, which is connected with the above-mentioned method of evaluation and distribution of frequencies.

Table 7 shows the effect of mother's age on the results of evaluation of traits scoring body measurements and body capacity. The highest scores in most traits were determined in calves after five- to seven-years old mothers and after mothers seven years old and older.

Table 8 presents regression coefficients of age at evaluation (in years) and of weight gain from the date of birth to evaluation (in kg). Age at evaluation influenced to the largest extent the scoring of

Table 7. The effect of age of mother at calving (comparison with three-year mothers and younger)

	Four years old	Five to seven years old	Eight years old and older
HS	0.60	0.96	0.79
BL	0.12	0.15	0.16
LW	0.50	1.14	0.92
CW	0.07	0.10	0.08
CD	0.07	0.12	0.10
P	−0.01	0.01	0.02

Table 8. Regression on age at evaluation (years) and weight gain from birth to evaluation (kg)

	HS	BL	LW	CW	CD	P	SM	BM	RM	PT
Age at evaluation	0.53	1.44	–1.76	1.66	1.61	1.43	1.66	1.60	1.39	1.69
Weight gain							0.79	0.66	0.78	0.68

live weight (–1.76), production type (+1.69), chest width (+1.66) and shoulder muscling (+0.66). The scoring of height at sacrum was influenced to the smallest extent (+0.53). The relatively markedly different regression coefficients of live weight and height at sacrum are probably influenced by a different method of evaluation from that applied to the other traits. Classifiers consider the effect of age already at the moment of evaluation, nevertheless it is obvious from these regression coefficients that they tend to overestimate older animals in most traits.

Weight gain from birth to the date of evaluation was taken into account in traits scoring muscling (SM, BM, RM) and PT. Regression coefficients were in the range of 0.66 to 0.79 scores per 1 kg weight gain. Weight gain had the lowest effect on back muscling (0.66), on production type (0.68), rump muscling (0.78) and shoulder muscling (0.79).

Standard deviations, minimum and maximum values of breeding values are shown in Table 9. Standard deviations of breeding values were higher in height at sacrum (s_{BV} = 0.71) and live weight (s_{BV} = 0.84). In the other traits standard deviations ranged from 0.19 (BL) to 0.30 (RM). Intrabreed standard deviations were determined by a linear model by one-factor analysis (GLM/SAS procedure). The effect of breed was statistically significant in all traits, but it explained relatively low variability (from 7% to 13%). As shown in the table, intrabreed standard deviations were only a little lower than standard deviations of breeding values including interbreed differences. It is caused by the effect of classifiers again who consider interbreed differences already during the evaluation of animals.

Table 9. Standard deviations, minimum and maximum values of estimated breeding values and standard deviations of breeding values within the breeds

	s_{BV}		Min	Max
	across breeds	within breeds		
HS	0.71	0.66	–3.90	5.67
BL	0.19	0.18	–1.06	0.86
LW	0.84	0.80	–4.17	4.15
CW	0.23	0.22	–1.28	1.05
CD	0.24	0.23	–1.51	1.05
P	0.27	0.25	–2.64	1.36
SM	0.25	0.24	–1.27	1.30
BM	0.23	0.21	–1.64	1.32
RM	0.30	0.28	–2.17	1.59
PT	0.28	0.27	–1.86	1.34

CONCLUSION

We constructed a model for routine estimation of breeding value for a description of the type of young animals of beef cattle. If a majority of animals under evaluation is younger than 11 months, it is possible to use a model with linear regression on age at evaluation; if the range of animal age is wider, it is suitable to apply a model with quadratic regression on age at evaluation. Deviations from normal distribution in the scoring of height at sacrum and live weight document that a different method of evaluation of these two traits should be used that would correspond with evaluation of the other traits. High genetic correlations between some evaluated traits show that the number of evaluated traits may be reduced in practice.

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Corresponding Author

Ing. Zdeňka Veselá, Research Institute of Animal Production, P.O. Box 1, 104 01 Prague 114-Uhříněves, Czech Republic
Tel. +420 267 009 664, e-mail: vesela.zdena@vuzv.cz