

## Stability of Aberdeen Angus breeding values in the Czech Republic from 1997 to 2007

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**ABSTRACT:** We predict the stability of breeding values (BVs) for direct effect (DE) and maternal effect (ME) for live weights at 210 days of age in the entire population of purebred Aberdeen Angus cattle in the Czech Republic according to an increase of progeny number in performance recording over a period of 11 years (1997 to 2007) and the course of BVs for DE and ME during the years of observation in animals born until 1997. Furthermore we compare genetic trends of BVs for DE and ME among animals born in different years and detect the level and significance of correlation coefficients among predictions of BVs for DE and ME performed during the years of observation. The animal model and the BLUPF90 programme were used for these predictions. The used model included the effects of animal, sex, contemporary group, dam, age of dam, and permanent environment of dam. The variance of BVs ranged from 4.96 to 10.87 depending on the year of evaluation and whether it was related to maternal or direct genetic effect. The animals were initially assigned to groups according to their BV in 1997, and this ranking was not affected by the BVs predicted in subsequent years. The existence of a negative correlation between direct and maternal effects was confirmed. The significant correlations ( $P < 0.0001$ ) demonstrated a strong relationship between the BVs predicted in successive years, e.g. the correlation coefficient for the relationship between BVs for direct effect predicted in the last years of the examined period was above 0.9 and that for maternal effect was above 0.8.

**Keywords:** Aberdeen Angus; breeding value; BLUP, weaning weight; stability of breeding value; direct effect; maternal effect

Beef cattle have been introduced into the Czech Republic only recently. The first evaluation of breeding results was processed and published for the period 1991–1997 (Stádník et al., 1999). Since 2000, breeding values (BVs) have been routinely predicted using a multiple-trait animal model with maternal effects for the results of the field test (calving difficulty, birth weight, weight at 120, 210, and 365 days) (Příbyl et al., 2003). In 2004, the prediction of BVs for bulls' own growth performance at test stations was introduced using a single-trait animal model (Příbylova et al., 2004). Finally, a multiple-trait animal model for the prediction of

BVs for type traits was launched in 2005 (Veselá et al., 2005). Šafus et al. (2006) constructed three selection indexes for bulls of beef cattle. Vostrý et al. (2008) predicted the genetic parameters and the heterosis effect on growth traits in crossbred cattle and Vostrý et al. (2009) predicted genotype × environment interaction in Czech beef cattle. Kamieniecki et al. (2009) detected a significant effect of sire breed on the growth and carcass performance of progeny. Simultaneously, possibilities of the carcass quality classification on live animals were evaluated by Stádník et al. (2009). And, subsequently, the prediction of carcass quality BVs is

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an integral part of beef cattle breeding. Therefore they are soon to be introduced as routinely determined values (Veselá, 2010). Meat quality and nutrient profile as an additional trait of carcass value in cattle (Bartoň et al., 2010; Węglarz, 2010), pigs (Bečková and Václavková, 2010; Rybarczyk et al., 2011), chickens (Straková et al., 2010), and/or sheep and lambs (Kaczor et al., 2010; Xu et al., 2011) is currently studied as well. Animals with high functional longevity and economic weights for functional traits are required (Krupová et al., 2009; Zavadilová et al., 2009). A number of authors investigated economic weights for different traits in other farm animals (Houška et al., 2010). However, similar studies performed in beef cattle are necessary in the future and the growth ability is constantly a basic performance trait.

The BV prediction in beef cattle is affected by a number of factors. The two most important and most frequently indicated genetic factors are the BVs for direct effect (DE) and maternal effect (ME) (Vostrý et al., 2009). Young beef animals are often selected for breeding only on the basis of their own growth performance and the performance of their half-siblings. Therefore, their BVs obtained at the time of selection have only low reliabilities. Genetically evaluated sires with high reliabilities of BVs are used much less frequently. The relationship between real and predicted BVs was examined by Postma (2006), who analysed different aspects associated with the prediction of BVs in cattle, their effect on the population and subsequent genetic trends.

Breeding efforts result in breed improvement expressed by genetic gain, in the consequence of which younger animals are genetically superior to older animals born in previous years. Therefore, it is necessary to upgrade BVs continually on the basis of comparisons with younger animals (Příbýl et al., 2002).

The correlations between BVs predicted during a certain period of animal's life ranged between 0.71 and 0.90 and depended on the trait evaluated and the time span. Repeated prediction only slightly changed the rank of the best sires. Changes occurred only within the group of animals with similar BVs (above average), and thus the stability of predictions over time was demonstrated (Příbýl et al., 2002). An important factor influencing BVs is the negative genetic correlation between DE and ME. The maternal BV can be negative, if a high BV for DE is based on own growth performance records (Schaeffer, 2002).

Genetic trends and genetic parameters for different traits of dairy cows were predicted in a number of previous reports and various discrepancies in BV prediction were detected (Cañon and Muñoz, 1991; Banos et al., 1992; Němcová et al., 2011; Ptak et al. 2011; Zavadilová et al., 2011).

To test the stability of BVs and to validate the genetic trend in dairy cattle, three different methods were developed (Boichard et al., 1995). These methods differed in the number of traits or lactations evaluated, and in the requirement for the access to raw production data, i.e. official evaluation results, which are restrictedly, usually publicly available and can be accessed by anyone. Lee and Freeman (1985) used regression techniques to determine the trends in yearly averages of cow indexes and predicted differences of bulls' BVs for production traits. The stability rate of BVs can be expressed using the correlation coefficient.

However, these analyses have not been performed in beef cattle in the Czech Republic yet. Based on this fact, the prediction of the course and reliability of BVs in Aberdeen Angus cattle is suitable for precision evaluation of performance and next orientation of beef selection and breeding. We hypothesized, according to results detected on the other production types of cattle, that the significant trend of breeding values predicted in particular years will be determined in relation to a higher number of progeny, that the stability of BVs predicted in 1997 will be confirmed during the subsequent years, that the genetic trends of DE and ME will confirm expected relationships between these BVs, and that the significant correlation coefficients will be detected among the years evaluated.

The objective of this study was to determine the course of breeding values (BV) for direct effect (DE) and maternal effect (ME) for live weights at 210 days of age in the purebred population of Aberdeen Angus cattle in the Czech Republic according to an increase in the number of progeny in performance recording over a period of 11 years (1997 to 2007); the second objective was to evaluate the course of BVs for DE and ME during the observed years in animals born until 1997; the third objective was to compare genetic trends of BVs for DE and ME among animals born in different years; and the fourth objective was to detect the level and significance of correlation coefficients among predictions of BVs for DE and ME performed during the years of observation.

## MATERIAL AND METHODS

BVs for live weight at 210 days in the complete population of purebred Aberdeen Angus cattle were predicted using the database of the Czech Beef Breeders Association (CSCHMS, 2009).

A total of 11 subsets of cumulatively increasing size were formed from the database according to the date of prediction (from 1997 to 2007). The used datasets differed in the number of animals in the pedigree, which cumulatively increased from 2385 to 17 173 over the years analysed. This was accompanied by increasing numbers of dams and contemporary groups (HYS). However, in accordance with changes in the entire Aberdeen Angus population which increased because of large imports of purebred animals, the progeny of dams with one contemporary only was deleted from the data set before prediction. Therefore the size of the contemporary groups varied from 2 to 26. The number of levels was the same for the effects of dam and permanent environment of dam. The numbers of levels for different effects in the model used are presented in Table 1.

Processing of the data set was performed using SAS (2004) with SORT, FREQ, and MEANS procedures. The entire cumulative database including data from previous years was estimated each year and the predictions were performed using the BLUPF290 programme (Misztal et al., 2002). The necessary

Table 1. Number of animals included in evaluation in different years

Year	Recorded animals	Animals in pedigree	Dams	Contemporary groups (HYS)
1997	1 834	2 385	849	159
1998	2 591	3 206	1 116	225
1999	3 473	4 124	1 381	288
2000	4 685	5 355	1 768	380
2001	5 959	6 632	2 116	477
2002	7 793	8 473	2 691	601
2003	9 600	10 286	3 185	724
2004	11 161	11 850	3 648	832
2005	12 696	13 389	4 083	933
2006	14 596	15 293	4 653	1 039
2007	16 448	17 173	5 125	1 137

HYS = herd-year-season interaction

variances and co-variances for direct and maternal effects were adopted from a report by Přibyl et al. (2003) and used in data processing for the entire period estimated. This step enables to predict a negative correlation between direct and maternal effects (Schaeffer, 2002) on the level  $r = -0.18$ . Matrices for the effect of sex were 4 columns and 1834 to 16 448 rows, depending on the year of evaluation. Matrices for the effect of HYS had 159 to 1137 columns and 1836 to 16 448 rows, depending on the year of evaluation. Matrices for the effect of maternal age had 5 columns and 1836 to 16 448 rows, depending on the year of evaluation. The matrix for random effect of animal had from 1836 to 16448 columns and rows, depending on the year of evaluation. The random matrix of dam's effect had from 849 to 5125 columns and 1836 to 16 448 rows, depending on the year of evaluation. The random matrix of the effect of dam's permanent environment had the same dimensions as the matrix for the random effect of dam. Subsequently, BVs in different years were determined using the animal model. The BVs predicted by the BLUPF290 programme were consequently analysed using the SAS (2004) procedures SORT, FREQ, MEANS, and CORR.

## Linear animal model

BVs were predicted using the BLUP-AM method with maternal effects and correlations between direct and maternal effects. The model used was as follows:

$$Y = X_1 \text{sex} + X_2 \text{hys} + X_3 \text{age} + Z \text{DE} + W \text{ME} + S \text{ped} + e$$

where:

Y = weight at 210 days of age

$X_1, X_2, X_3$  = experimental design matrices for fixed effects

Z, W, S = design matrices for the effects of animal, dam and permanent environment of dam

sex = vector of fixed effects of sex

hys = vector of fixed effects of contemporary groups

age = vector of fixed effects of dam age

DE = vector of random effects of animals for direct genetic effect

ME = vector of random effects of animals for maternal genetic effect

ped = vector of random effects of permanent environment of dam

e = residual effect (error)

Table 2. Numbers of evaluations in accordance with breeding value in 1997

Group	Bulls			Cows		
	BV (kg)	DE	ME	BV (kg)	DE	ME
1	< -3	263	245	< -4	312	401
2	-3 to 4	239	569	-4 to 8	960	1056
3	4 to 11	201	55	> 8	243	57
4	> 11	168	2			

BV = breeding value, DE = direct effect, ME = maternal effect

The prediction results were analysed as follows:

- (1) Correlations between BVs for the same animal from successive years of evaluation were determined.
- (2) Differences in BVs between different birth years of animals were predicted.
- (3) The following groups of bulls and cows were formed according to their BVs in 1997 and in accordance with the size of the particular groups:

Bulls: Group 1 – BV below 3 kg; Group 2 – BV 3 to 4 kg; Group 3 – BV 4 to 11 kg; Group 4 – BV above 11 kg.

Cows: Group 1 – BV below 4 kg; Group 2 – BV 4 to 8 kg; Group 3 – BV above 8 kg.

Then the development of BVs in different years of prediction was compared within and between groups (mainly convergence and divergence from

average BVs). The numbers in different groups of bulls and cows are shown in Table 2.

## RESULTS AND DISCUSSION

### Database involving all animals available

Table 3 presents descriptive statistics of BVs [number of animals, mean BV ( $\mu$ ), standard deviation (SD), extreme BVs (min and max)] for direct (DE) and maternal (ME) effects. Over time, average BVs for DE increased as well as the range of BVs within a year. The variability expressed by standard deviations also slightly increased, indicating that the reliability of BVs was elevated with time. A more moderate tendency and also a lower variability were observed for ME. Similarly like DE, the variability increased over years as the size of the used database increased. The

Table 3. Mean breeding values for direct and maternal effects over years

Year	Number of animals	DE				ME			
		$\mu$	SD	min	max	$\mu$	SD	min	max
1997	2 385	1.76	8.78	-26.66	35.73	-1.43	5.59	-35.67	22.30
1998	3 206	2.01	8.90	-29.20	38.71	-1.08	5.90	-37.84	23.18
1999	4 124	1.91	9.08	-29.57	38.50	-1.41	6.25	-36.05	23.02
2000	5 355	2.61	9.41	-31.38	39.41	-1.46	6.65	-30.83	24.81
2001	6 632	2.96	9.78	-33.46	38.78	-1.91	7.02	-32.92	27.43
2002	8 473	3.01	9.97	-36.25	39.00	-1.65	6.76	-31.75	29.23
2003	10 286	3.62	10.16	-42.43	55.75	-1.40	7.04	-30.09	30.55
2004	11 850	4.04	10.38	-40.16	62.70	-0.99	7.16	-30.55	30.53
2005	13 389	4.21	10.52	-41.89	69.44	-0.50	7.12	-30.84	34.72
2006	15 293	4.57	10.61	-40.52	62.64	-0.37	7.06	-30.44	32.06
2007	17 173	4.73	10.87	-42.46	60.93	-0.50	7.14	-36.39	31.61

DE = direct effect, ME = maternal effect,  $\mu$  = mean of breeding value, SD = standard deviation

Table 4. Evolution of breeding values for direct and maternal effects over years in animals born until 1997 ( $n = 2385$ )

Year	DE				ME			
	$\mu$	SD	Min	Max	$\mu$	SD	Min	Max
1997	1.76	8.78	–26.66	35.73	–1.43	5.59	–35.67	22.30
1998	1.64	8.86	–29.20	38.71	–1.18	6.22	–37.84	23.18
1999	1.27	8.81	–29.57	38.50	–1.26	6.77	–36.05	23.02
2000	1.68	8.97	–31.38	39.41	–0.66	7.08	–30.83	23.92
2001	1.71	9.16	–33.46	38.78	–0.76	7.53	–32.92	27.29
2002	1.40	9.18	–35.04	37.00	–0.29	7.54	–30.78	27.68
2003	1.67	9.30	–42.43	36.52	0.07	7.66	–30.09	26.41
2004	1.96	9.48	–40.16	37.89	0.64	7.69	–30.55	29.17
2005	2.00	9.50	–39.64	38.68	0.91	7.73	–30.84	34.72
2006	1.81	9.50	–40.52	37.55	1.02	7.53	–29.11	32.06
2007	1.84	9.62	–41.18	38.12	0.90	7.59	–31.88	31.61

DE = direct effect, ME = maternal effect,  $\mu$  = mean of breeding value, SD = standard deviation

comparison of average BVs for DE and ME predicted over years demonstrated that the increased number of available animals resulted in the increased values of DE. The continually increasing BVs for DE indicated that younger generations of animals were genetically superior. This improvement is much smaller for ME due to the preferential selection of breeding bulls according to DE at the expense of ME, as can be seen in the breeding programme for Aberdeen Angus (CSCHMS, 2009). In addition, this result is also associated with a negative genetic correlation between DE and ME (Grotheer et al., 1997; Schaeffer, 2002).

Average BVs for DE over years in animals born until 1997 are given in Table 4. The dataset included all animals born until the end of 1997 ( $n = 2385$ ). The results indicate that the inclusion of new information did not result in any significant

changes in variability and average BVs, but the reliability of BV prediction increased. The development of BVs for DE over time was compared in all available animals and in animals born until 1997 (Tables 3 and 4). The difference is obvious and demonstrates the importance of breeding, since younger animals are on average superior to older generations due to positive selection (Příbyl et al., 2002). This comparison also confirms the stability of BVs estimated in 1997, as the BVs of animals born until 1997 remain similar in successive years of evaluation. Strabel et al. (2001) compared the reliabilities obtained from the inversion matrix for single-trait and multi-trait models. The correlations predicted for weaning weight were 0.94 for DE and 0.98 for ME. The reliability predicted and error covariances computed either by a multi-trait model

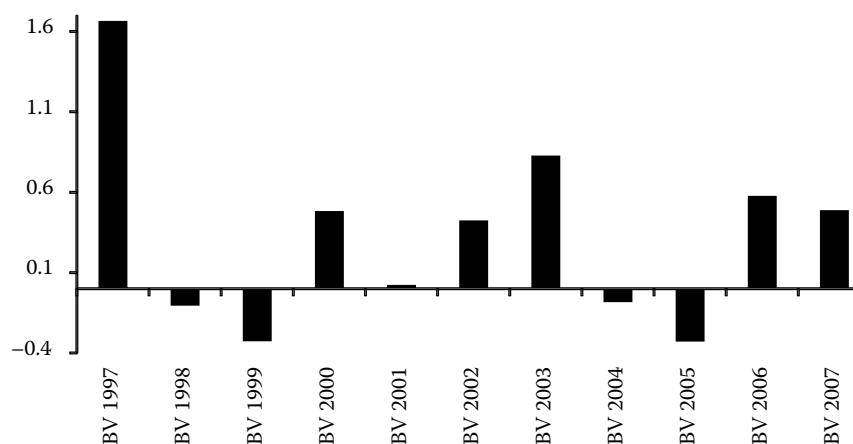


Figure 1. Comparison of genetic trends of breeding values (BV) for direct effect among animals born in different years



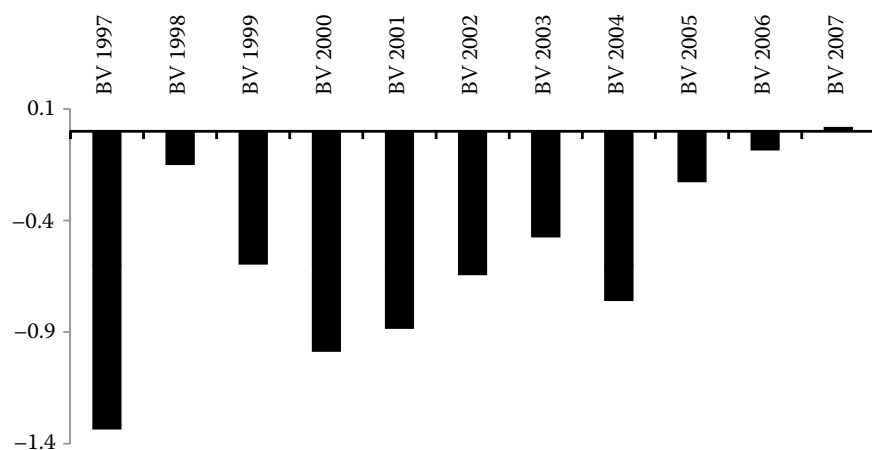


Figure 2. Comparison of genetic trends of breeding values (BV) for maternal effect among animals born in different years

or by a random regression model in beef cattle was also investigated (Tier and Meyer, 2004). Powell et al. (1977) already observed an increasing genetic trend for BV prediction as a result of successfully applied breeding methods. Similarly to our results, they also encountered the variation of BVs or even their slight decrease over several years.

The increasing genetic trend in beef cattle is currently associated mainly with the improvement of animal evaluation, introduction of new breeding approaches and methods of BV prediction (DeGroot et al., 2007). Average BVs for DE in animals born in different years are shown in Figure 1. The BVs were predicted for the latest possible year. The variation of BVs predicted in 2007 depended on the number of animals born in a given year. If a linear curve were applied to the data, a slightly decreasing trend would be obvious.

Average BVs for ME in animals born until 1997 are presented in Table 4. A total of 2385 animals were included in the dataset. There is a slight but quite clear increase of average BVs. The difference

between the trends of BVs for ME predicted for all available animals and for animals born until 1997 is demonstrated in Tables 3 and 4. In the first three years, these trends were quite similar. In subsequent years, however, the BVs for ME predicted for animals born until 1997 increased more rapidly compared to the BVs predicted in all available animals, and the differences between the BVs of both groups gradually became constant. These differences were caused by the preferentially used selection for DE at the expense of ME, which are negatively correlated with each other (Schaeffer, 2002). More intensive selection for DE results in improved growth traits, but due to the existing negative correlation, the economically important maternal characteristics may deteriorate.

When all animals were included, standard deviations of BVs for DE and ME ranged from 8.78 to 10.87 and from 5.59 to 7.16, respectively. When only animals born in 1997 were evaluated, standard deviations of BVs for DE and ME ranged from 8.78 to 9.62 and from 5.59 to 7.59, respectively. It is evident

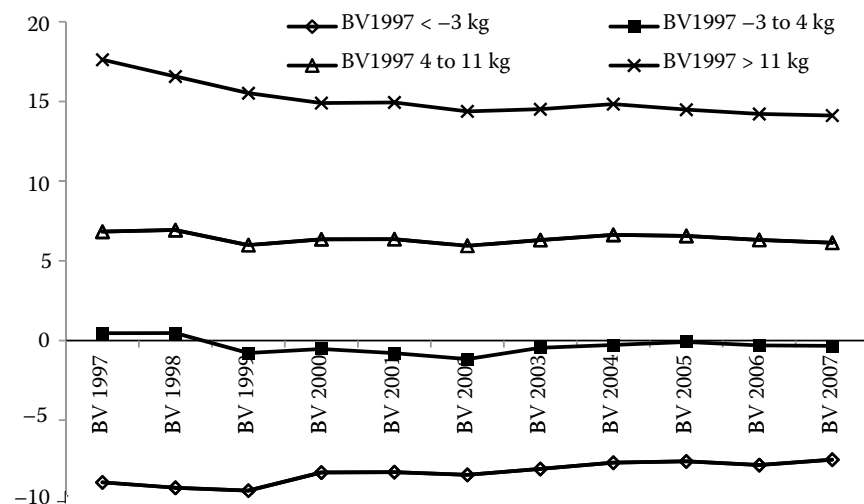


Figure 3. The evolution of breeding values (BV) for direct effect of bull groups with different breeding value estimated in 1997

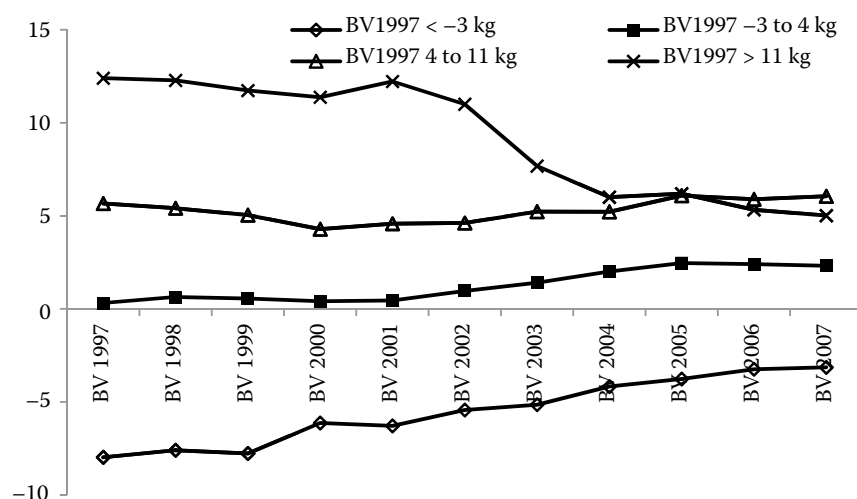


Figure 4. The evolution of breeding values (BV) for maternal effect of bull groups with different breeding value estimated in 1997

that the rate of within-year variation was different neither for DE nor for ME. Greater variation for DE was, however, observed between different years of evaluation. Mrode and Swanson (1996), Carlén et al. (2004) and Wolf et al. (2010) also reported variations of genetic parameters and Liu and Reents (2000) or Samoré et al. (2008) explained significant differences in relation to populations, statistical models and estimation methods.

The animals born until 1997 had higher average BVs for ME compared to the total average. This was probably due to lower BVs for ME in younger animals. With respect to ME, younger animals fell below average, while older animals were superior, both according to the increase of BVs for DE.

Average BVs for ME in animals born in different years are shown in Figure 2. The BVs were predicted for the latest possible year. The average BVs for ME were relatively high at the beginning and at the end of the evaluated period compared to the years in the

middle of the period. The year of evaluation had a significant effect on the variation of BVs. The trend shown in Figure 2 can be explained by a slightly increased focus on the selection for maternal characteristics, or by a lower preference for DE in the breeding plan. It also confirms the efficiency of the selection currently applied within the population of Aberdeen Angus (CSCHMS, 2009).

#### Evaluation of animals grouped according to their BVs and sex

The animals born until 1997 were divided into groups according to their BVs and sex. Higher range and standard deviations of BVs were recorded in bulls, and therefore they were assigned to four groups, while cows only to three groups. This allocation was necessary to obtain balanced groups with similar animal numbers.

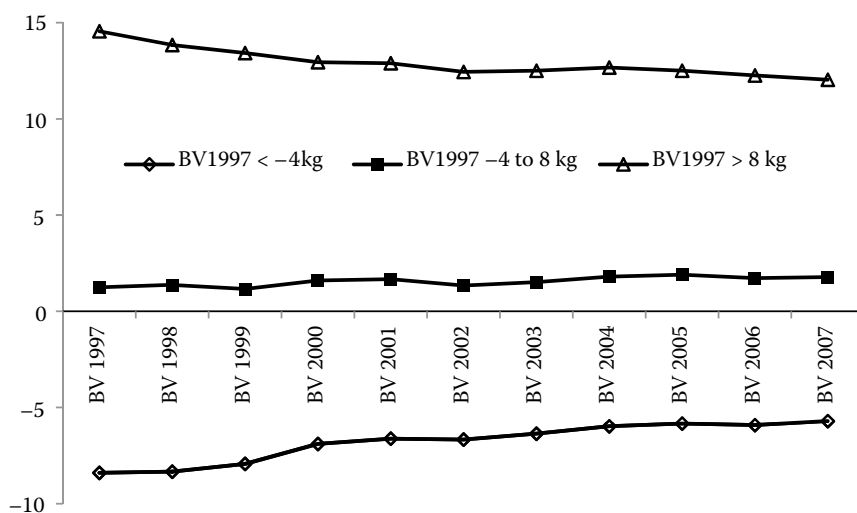


Figure 5. The development of breeding value (BV) for direct effect of cow groups with different breeding value estimated in 1997

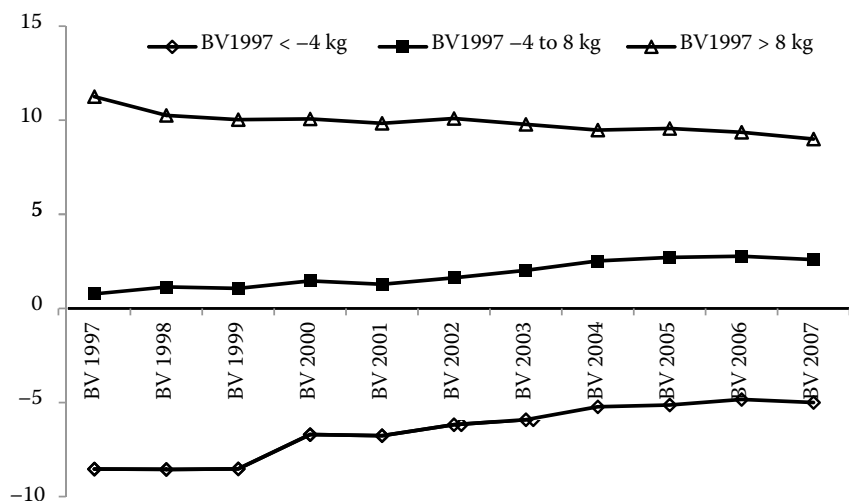


Figure 6. The development of breeding values (BV) for maternal effect of cow groups with different breeding value estimated in 1997

A high stability of BV averages within individual groups was observed. This means that the group of below average animals in 1997 was also below average in the successive evaluations. Similarly, animals above average in 1997 were also above average in the following years. The development of BVs for DE of bull groups with different BVs predicted from 1997 is demonstrated in Figure 3. There was a certain variation within the groups, but the level of each group remained generally constant. The average BVs for DE of the examined groups tended to converge slightly. This fact can be explained by the prediction of BVs over time and by the increasing size of the database used for BV prediction. The development of BVs for ME of bulls born until 1997 is shown in Figure 4. The tendency towards the convergence of average BVs was more explicit. It was related to a lower reliability

of BVs for ME. The two best groups of bulls even switched their order in 2006 and 2007.

The average BVs of cows born until 1997 for DE and ME are shown in Figures 5 and 6, respectively. A high stability of BVs is demonstrated by these figures. Thus, animals with low BVs in 1997 remained below average also in successive predictions. Again, the variation increased over time in accordance with findings of Liu and Reents (2000) or Samoré et al. (2008).

The stability of BVs particularly for ME was higher in cows compared to bulls (Figure 4 vs. Figure 6) as a biological consequence of the expression of maternal effect in females. Lassen et al. (2007) applied three different models for a modelling of genetic gain for the maternal effect of milk production over 16 years and recommended using more complicated multi-trait models.

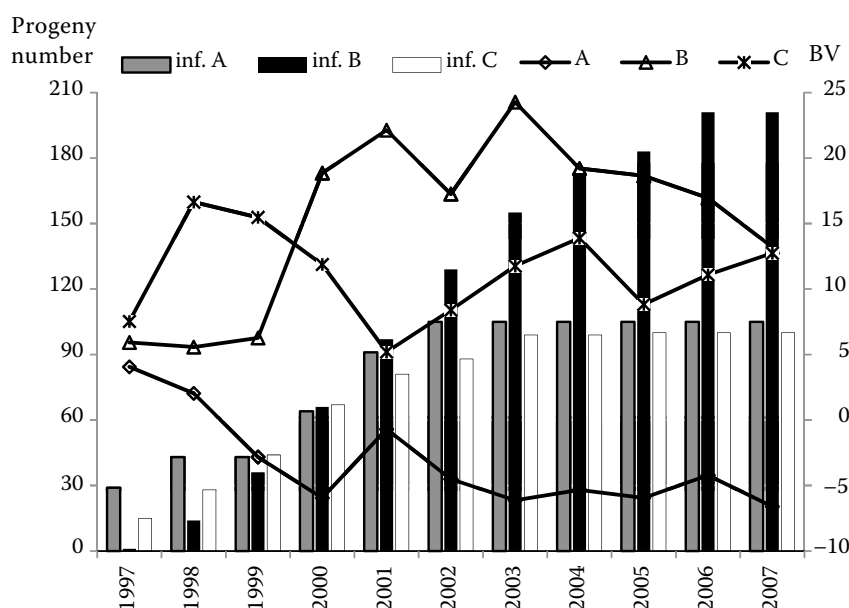


Figure 7. Breeding values (BV) for direct effect in selected bulls (A–C) as affected by the amount of information (inf.A–inf.C)



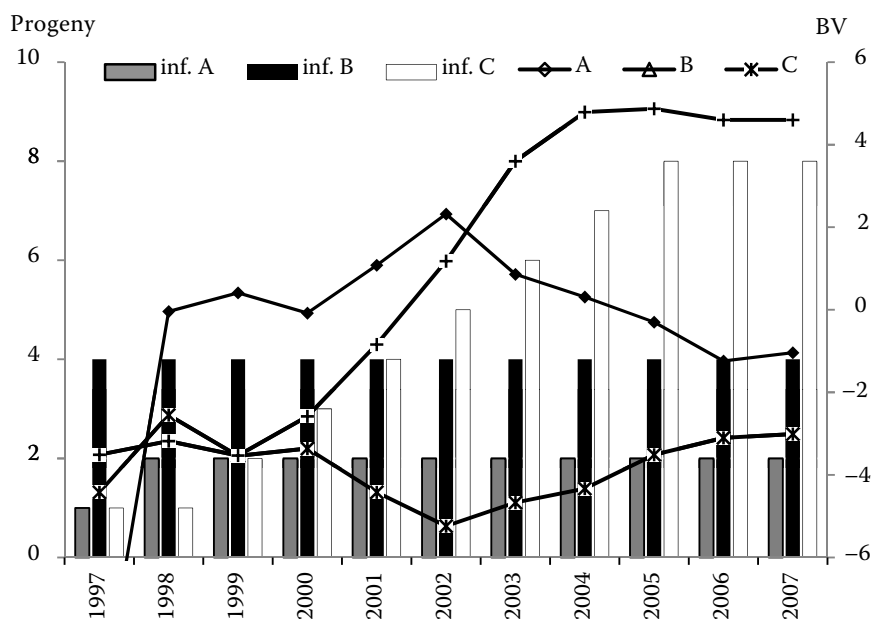


Figure 8. Breeding values for maternal effect in selected cows (A–C) as affected by the amount of information (inf. A–inf. C)

### The relationship between the amount of data and BVs

The analysis revealed the existence of a relationship between BVs and the amount of data on the individual performance of animals and the number of progeny. Figure 7 illustrates the development of BVs for DE in several bulls from 1997 to 2007. The bulls were ranked according to their BVs from the worst to the best animal. Figure 7 shows both BVs predicted in each year for each animal and the amount of information in each year for each animal. Thus, for each of the 3 selected bulls 3 BVs and 3 values

describing the amount of information are shown. The values for the amount of information were predicted from the number of progeny and their own performance records. A similar analysis was also performed for BVs for ME of cows (Figure 8).

The BVs for ME of selected cows tended to increase less rapidly over time. This was due to the amount of information for each cow in different years. It was evident from the comparison in Figure 7 and Figure 8 that the increasing size of the database and the growing amount of information had a more pronounced effect on cows, i.e. on animals with little available information. These findings

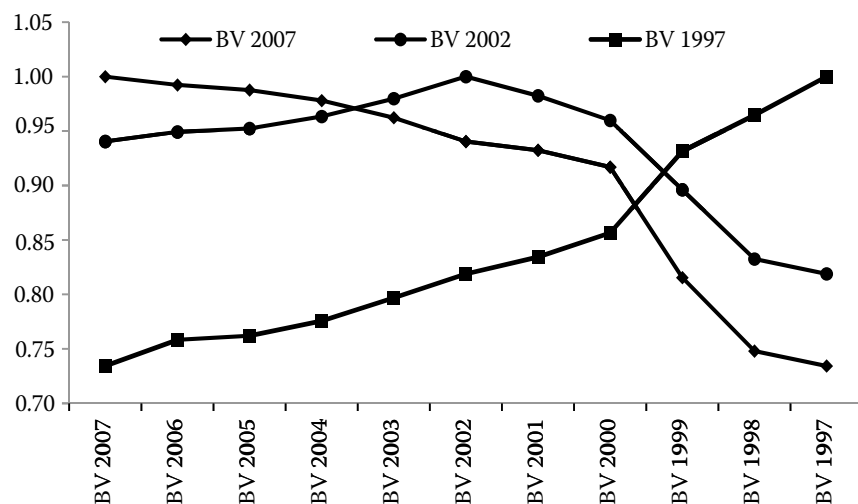


Figure 9. Correlations between breeding values (BV) for direct effect estimated in 1997, 2002, and 2007 in animals born till 1997 ( $n = 2385$ )

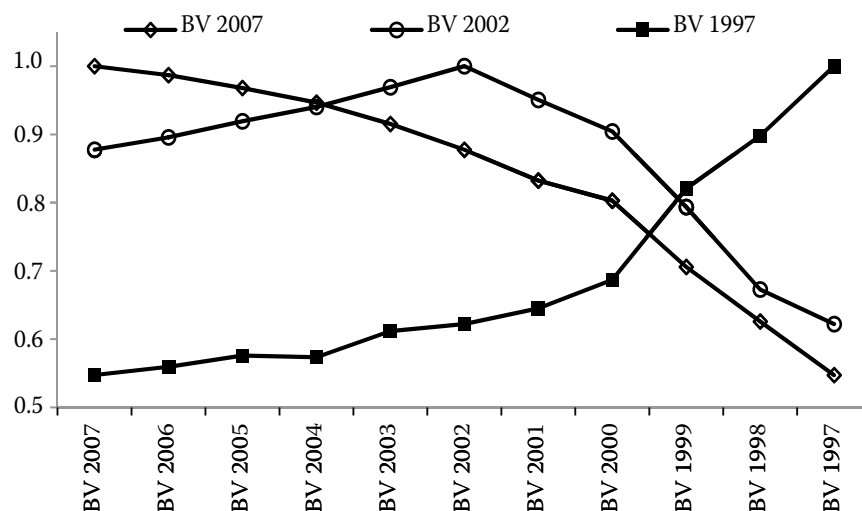


Figure 10. Correlations between breeding values (BV) for maternal effect estimated for 1997, 2002, and 2007 in the animals born until 1997 ( $n = 2385$ )

agree with results of Přibyl et al. (2002) or Cañon and Muñoz (1991).

#### Relationships between BVs in different years of evaluation

In the animals born in 1997, correlation coefficients were predicted for their BVs predicted in different years. The correlations of BVs for DE from 1997 to 2007 are shown in Figure 9. All the correlations were high ( $r = 0.73–0.99$ ) ( $P < 0.0001$ ), and they slightly decreased with the increasing period between the years of evaluation. Correlation coefficients above 0.9 ( $P < 0.0001$ ) were predicted for the relationship between the BVs for DE predicted over the period from 2000 to 2007. In most predictions, tendencies changed to a certain extent in 2000. The correlations between the values predicted before and after 2000 were somewhat lower, but they were above 0.7 ( $P < 0.0001$ ). This threshold point was probably associated with the increasing reliability of BVs and the increasing size of the database due to the expansion of beef cattle breeds by 1997 (CMSCH, 2010) and the larger-scale introduction of beef performance recording. The highest correlations were determined between the adjacent years of evaluation, and they declined with the increasing period between the years of evaluation.

The correlations of BVs for ME for the animals born after 1997 are shown in Figure 10. The tendencies were similar to those for DE, but the correlation coefficients were lower due to lower reliabilities of BVs for ME (Schaeffer, 2002).

#### CONCLUSION

The increased number of Aberdeen Angus animals included in performance recording in the Czech Republic resulted in increased values of BV for DE for live weights at 210 days of age and this improvement is much smaller for BV for ME due to the preferential selection of breeding bulls according to DE at the expense of ME.

A high reliability of BV averages within the particular groups was observed when the group of below- and/or above-average animals in 1997 was also below and/or above average in the following years. The BVs particularly for DE remain approximately similar over time in different groups of animals as well as in the individual animals. The BVs for ME converge more in the groups of both bulls and cows. In spite of that, it is concluded that over the period examined the accuracy of average BVs improved, and only small changes between animal groups were observed. This corresponds with the predicted correlation coefficients for the last years of evaluation, which were above 0.8 ( $P < 0.0001$ ).

With respect to our results describing BVs for DE, younger animals are genetically superior to the older ones. In contrast, younger animals are inferior compared to the older ones in BVs for ME. This may result from the selection pressure currently applied in Aberdeen Angus in the Czech Republic when DE is given priority to ME. Prediction results confirmed the negative correlation between DE and ME. This was apparent from some of the trends for DE and ME depicted in the tables with mutually opposite trends. These findings could be

used subsequently in a scheme of Aberdeen Angus breeding and selection on the level of herds and population as well.

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## REFERENCES

- Banos G., Wiggans G.R., Robinson J.A.B. (1992): Comparison of methods to rank bulls across countries. *Journal of Dairy Science*, 75, 2560–2568.
- Bartoň L., Bureš D., Kudrna V. (2010): Meat quality and fatty acid profile of the musculus longissimus lumborum in Czech Fleckvieh, Charolais and Charolais × Czech Fleckvieh bulls fed different types of silages. *Czech Journal of Animal Science*, 55, 479–487.
- Bečková R., Václavková E. (2010): The effect of linseed diet on carcass value traits and fatty acid composition in muscle and fat tissue of fattening pigs. *Czech Journal of Animal Science*, 55, 313–320.
- Boichard D., Bonaiti B., Barbat A., Mattalia S. (1995): Three methods to validate the estimation of genetic trend for dairy cattle. *Journal of Dairy Science*, 78, 431–437.
- Cañon J., Muñoz A. (1991): Genetic trend for milk production in Spanish Holstein population. *Journal of Animal Breeding and Genetics*, 108, 41–47.
- Carlén E., Strandberg E., Roth A. (2004): Genetic parameters for clinical mastitis, somatic cell score, and production in the first three lactations of Swedish Holstein cows. *Journal of Dairy Science*, 87, 3062–3070.
- CSCHMS (2009): Czech beef breeders association [serial online]. Available from [www.cschms.cz](http://www.cschms.cz) (accessed Feb 28, 2009).
- CMSCH (2010): Czech-Moravian breeders association [serial online]. Available from [www.cmsch.cz/cz/](http://www.cmsch.cz/cz/) (accessed Aug 24, 2010).
- DeGroot B.J., Keown J.F., Van Vleck L.D., Kachman S.D. (2007): Estimates of genetic parameters for Holstein cows for test-day yield traits with a random regression cubic spline model. *Genetics and Molecular Research*, 6, 434–444.
- Grotheer V., Rohe R., Kalm E. (1997): Development of a model for estimation of breeding values for beef cattle in Germany. *Züchtungskunde*, 69, 349–365. (in German)
- Houška L., Wolfová M., Nagy I., Csörnyei Z., Komlósi I. (2010): Economic values for traits of pigs in Hungary. *Czech Journal of Animal Science*, 55, 139–148.
- Kaczor U., Borys B., Pustkowiak H. (2010): Effect of intensive fattening of lambs with forages on the fatty acid profile of intramuscular and subcutaneous fat. *Czech Journal of Animal Science*, 55, 408–419.
- Kamieniecki H., Wójcik J., Pilarczyk R., Lachowicz K., Sobczak M., Grzesiak W., Błaszczyk P. (2009): Growth and carcass performance of bull calves born from Hereford, Simmental and Charolais cows sired by Charolais bulls. *Czech Journal of Animal Science*, 54, 47–54.
- Krupová Z., Huba J., Daňo J., Krupa E., Oravcová M., Peškovičová D. (2009): Economic weights of production and functional traits in dairy cattle under a direct subsidy regime. *Czech Journal of Animal Science*, 54, 249–259.
- Lassen J., Sørensen M.K., Madsen P., Ducrocq V. (2007): A stochastic simulation study on validation of an approximate multitrait model using preadjusted data for prediction of breeding values. *Journal of Dairy Science*, 90, 3002–3011.
- Lee K.L., Freeman A.E. (1985): Estimation of genetic change in the registered Holstein cattle population. *Journal of Dairy Science*, 68, 2629–2638.
- Liu Z., Reents R. (2000): Parameter estimates of a random regression test day model for first three lactations somatic cell scores INTERBULL Bulletin, No. 26, 61–65.
- Misztal I., Tsuruta S., Strabel T., Auvray B., Druet T., Lee D. H. (2002): BLUPF90 and related programs (BGF90). In: 7<sup>th</sup> World Congr. Genetics Applied to Livestock Production, Montpellier, France, Communication No. 28–07.
- Mrode R.A., Swanson G.J.T. (1996): Genetic and statistical properties of somatic cell count and its suitability as an indirect means of reducing the incidence of mastitis in dairy cattle. *Animal Breeding Abstracts*, 64, 847–857.
- Němcová E., Štípková M., Zavadilová L. (2011): Genetic parameters for linear type traits in Czech Holstein cattle. *Czech Journal of Animal Science*, 56, 157–162.
- Postma E. (2006): Implications of the difference between true and predicted breeding values for the study of natural selection and micro-evolution. *Journal of Evolutionary Biology*, 19, 309–320.
- Powell R.L., Norman H.D., Dickinson F.N. (1977): Trends in breeding value and production. *Journal of Dairy Science*, 60, 1316–1326.
- Příbýl J., Šeba K., Misztal I., Příbylová J. (2002): Stability of breeding values for growth in beef cattle. In: 20<sup>th</sup> Genetic Days, Brno, Czech Republic, 190–192.
- Příbýl J., Misztal I., Příbylová J., Šeba K. (2003): Multiple-breed, multiple-traits evaluation of beef cattle in the

- Czech Republic. Czech Journal of Animal Science, 48, 519–532.
- Příbylová J., Vostrý L., Veselá Z., Příbyl J., Bohmanová J. (2004): Breeding value for own growth of beef bulls in performance-test station. *Animal Science Papers and Reports*, 22, 97–103.
- Ptak, E., Jagusiak W., Żarnecki A., Otwinowska-Mindur A. (2011): Heritabilities and genetic correlations of lactational and daily somatic cell score with conformation traits in Polish Holstein cattle. *Czech Journal of Animal Science*, 56, 205–212.
- Rybarczyk A., Pietruszka A., Jacyno E., Dvořák J. (2011): Carcass and meat quality traits of pig reciprocal crosses with a share of Pietrain breed. *Czech Journal of Animal Science*, 56, 47–52.
- Šafus P., Příbyl J., Veselá Z., Vostrý L., Štípková M., Stádník L. (2006): Selection indexes for bulls of beef cattle. *Czech Journal of Animal Science*, 51, 285–298.
- Samoré A.B., Groen A.F., Boettcher P. J., Jamrozik J., Canavesi F., Bagnato A. (2008): Genetic correlation patterns between somatic cell score and protein yield in the Italian Holstein-Friesian population. *Journal of Dairy Science*, 91, 4013–4021.
- SAS (2004): SAS/STAT® 9.1. User's Guide. Cary, NC, SAS Institute Inc. 5121 pp.
- Schaeffer L. (2002): Maternal Effects Models, ANSC637 Set 13 [serial online]. Available from [www.aps.uoguelph.ca/~lrs/ANSC637/LRS13/](http://www.aps.uoguelph.ca/~lrs/ANSC637/LRS13/) (accessed Oct 22, 2008).
- Stádník, L., Louda, F., Dvořák, P., Šeba, K., Řehounek, V. (1999): The results of breeding measures within the population of Charolais cattle in the Czech Republic in 1991–1997. *Czech Journal of Animal Science*, 44, 389–396.
- Stádník L., Ježková A., Louda F., Dvořáková J., Štolc, L. (2009): The relationships among lumbar region width, back muscling and musculus longissimus lumborum et thoracis area in Blonde d'Aquitaine bulls and heifers during rearing period. *Archiv für Tierzucht*, 52, 243–254.
- Strabel T., Misztal I., Bertrand J. K. (2001): Approximation of reliabilities for multiple-trait model with maternal effects. *Journal of Animal Science*, 79, 833–839.
- Straková E., Suchý P., Herzig I., Hudečková P., Ivanko Š. (2010): Variation in fatty acids in chicken meat as a result of a lupin-containing diet. *Czech Journal of Animal Science*, 55, 75–82.
- Tier B., Meyer K. (2004): Approximating prediction error covariances among additive genetic effects within animal in multiple-trait and random regression models. *Journal of Animal Breeding and Genetics*, 121, 77–89.
- Veselá Z., Příbyl J., Šafus P., Vostrý L., Šeba K., Štolc L. (2005): Breeding value for type traits in beef cattle in the Czech Republic. *Czech Journal of Animal Science*, 50, 385–393.
- Veselá Z. (2010): Genetics parameters for evaluation carcass system SEUROP in beef cattle. *Our breeding*, 8/2010, LXX, 34–35.
- Vostrý L., Jakubec V., Schlote W., Bjelka M., Bezdiček J., Majzlík I. (2008): Analysis of population and heterosis effects in crossbred cattle of Czech Fleckvieh and Beef Simmental parentage for growth traits. *Archiv für Tierzucht*, 51, 207–215.
- Vostrý L., Příbyl J., Schlote W., Veselá Z., Jakubec V., Majzlík I., Mach K. (2009): Estimation of animal × environment interaction in Czech beef cattle. *Archiv für Tierzucht*, 52, 15–22.
- Węglarz A. (2010): Meat quality defined based on pH and colour depending on cattle category and slaughter season. *Czech Journal of Animal Science*, 55, 548–556.
- Wolf J., Wolfová M., Štípková, M. (2010): A model for the genetic evaluation of number of clinical mastitis cases per lactation in Czech Holstein cows. *Journal of Dairy Science*, 93, 1193–1204.
- Xu Q.L., Tang G.W., Zhang Q.L., Huang Y.K., Liu Y.X., Quan K., Zhu K.Y., Zhang C.X. (2011): The *FABP4* gene polymorphism is associated with meat tenderness in three Chinese native sheep breeds. *Czech Journal of Animal Science*, 56, 1–6.
- Zavadilová L., Štípková M., Němcová E., Bouška J., Matějčíková J. (2009): Analysis of the phenotypic relationships between type traits and functional survival in Czech Fleckvieh cows. *Czech Journal of Animal Science*, 54, 521–531.
- Zavadilová L., Wolf J., Štípková M., Němcová E., Jamrozik J. (2011): Genetic parameters for somatic cell score in the first three lactations of Czech Holstein and Fleckvieh breeds using a random regression model. *Czech Journal of Animal Science*, 56, 251–260.

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