

Estimation of animal × environment interaction in Czech beef cattle

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Abstract

The objective was the estimation of animal × environment interaction for weaning weight (WWT) of the most frequent breeds of beef cattle in the Czech Republic. The environment was represented by 3 areas: Mountain (1), Foothills (2) and Lowland (3). A pairwise analysis was carried out between the areas: 1 vs 2 ($n=5149$) and 2 vs 3 ($n=4971$) for the estimation of (co)variance components and genetic correlations between the environments. A multiple-trait animal model was used where weaning weights in different areas were considered as different traits. The direct and maternal heritability estimates of WWT were for area (1): 0.12 (direct) and 0.05 (maternal); for (2): 0.26 and 0.11 (direct), 0.10 and 0.11 (maternal) and for (3): 0.26 (direct) 0.03 (maternal). Direct and maternal genetic correlations were between: 1 and 2 0.98 and 0.65 respectively, with standard deviations 0.03 and 0.37 respectively, and between 2 and 3: 0.82 and 0.50 respectively, with standard deviations 0.12 and 0.31 respectively. The magnitude of the across-areas genetic correlation indicates that the animal by environment interaction was not biologically important and can be ignored in the evaluation of beef cattle in the Czech Republic.

Keywords: cattle, animal model, animal × environment interaction, genetic parameters, weaning weight, REML

Zusammenfassung

Schätzung der Tier-Umwelt-Interaktion bei Fleischrindern in der Tschechischen Republik

Ziel der Arbeit war die Schätzung der Tier-Umwelt-Interaktion für das Absetzgewicht bei den wichtigsten Fleischrinderrassen in der Tschechischen Republik. Die Umwelt wurde in 3 Lokalitäten eingeteilt: Gebirgslagen (1), Gebirgsvorland (2), Niederungen (3). Eine paarweise Analyse zwischen den Lokalitäten wurde: 1 gegen 2 ($n=5149$) und 2 gegen 3 ($n=4971$) für die Schätzung der Varianz und Kovarianzkomponenten und genetischen Korrelationen zwischen den Umwelten durchgeführt. Ein Multiple-Trait-Tiermodell wurde benutzt, wobei die Absetzgewichte in verschiedenen Umwelten als unterschiedliche Merkmale betrachtet wurden. Die direkten und maternalen Heritabilitätsschätzwerte für das Absetzgewicht waren für die Lokalitäten: 1 – 0.12 (direkte) und 0.05 (maternale); 2 – 0.26 und 0.11 (direkte), 0.10 und 0.11 (maternale) und 3 – 0.26 (direkte) 0.03 (maternale). Die direkten bzw. maternalen genetischen Korrelationen waren zwischen: (1) und (2) 0.98 und 0.65 mit Standardabweichungen 0.03 bzw. 0.37 sowie zwischen (2) und (3): 0.82 und

0.50 mit Standardabweichungen 0.12 bzw. 0.31. Diese Werte der genetischen Korrelationen zwischen den Lokalitäten weisen daraufhin, dass Tier-Umwelt-Interaktionen biologisch unbedeutend waren. Beim Vergleich von Fleischrinderrassen in der Tschechischen Republik können Tier-Umwelt-Interaktionen deshalb vernachlässigt werden.

Schlüsselwörter: Fleischrinderrassen, Tiermodell, Tier-Umwelt-Interaktion, genetische Parameter, REML, Absetzgewicht

Introduction

Correct estimation of genetic parameters is the basic step for the estimation of breeding value and subsequent selection of parental pairs. This estimation of genetic parameters is related to the representativeness of the data set and with the appropriate choice of a statistical model. When constructing the model for estimation of genetic parameters, estimation of breeding values of individual animals and genotypic value of populations, which comprises many fixed and random effects, it is assumed in beef cattle breeds that there exist no genotype by environment interactions, i.e. that the reaction of the performance and adaptability of individual animals or breeds to different environmental conditions (nutrition, climate, altitude above sea level, precipitation, temperature, soil structure and quality) is identical. It means that the performance level of breeds in different environmental conditions is not different. However, it follows from the experience gained in the Czech Republic and in other countries that it is not the case because e.g. the animals of breeds of medium-frame beef cattle have optimum performance in mountain locations while the animals of large-frame breeds are better adapted to lowland conditions and animals of some breeds are so adaptable that they have more or less the same performance in any environmental conditions.

According to LIN and TOGASHI (2002) definitions of the animal \times environment interaction can be divided into breed \times environment interaction (between-breed interaction), which was studied e.g. by KRÍŽEK *et al.* (1992), BROWN *et al.* (1993), SANDELIN *et al.* (2002) and VOŠTRÝ *et al.* (2008), and animal \times environment interaction (within breed interaction), which was studied e.g. by NOTTER *et al.* (1992) and DE MATTOS *et al.* (2000).

The knowledge of animal \times environment interaction and its extent in those breeds of beef cattle that are mostly kept under extensive conditions in the Czech Republic is a crucial problem for the estimation of breeding value of animals, genotype value of populations, selection and hybridisation. If existing animal \times environment interactions are neglected, great inaccuracies may arise in the breeding of beef cattle.

The objective of this paper was to test whether there exists any animal \times environment interaction for weaning weight in the main breeds of beef cattle kept under the conditions of the Czech Republic.

Material and methods

Estimation of animal \times environment interaction was performed for the live weight at 210 days of age of beef cattle kept in the Czech Republic during the span of 18 years (1990-2007). Data for the estimation of animal \times environment interaction were provided by the Czech Association of Beef Cattle Breeders (<http://www.cschms.cz>).

Genotypes

Field test data on animals of the following beef cattle breeds were used: meat-type Simmental, Hereford, Aberdeen Angus, Charolais, Blonde d'Aquitaine and Piemontese. Each animal possessed an 88-100% gene share of the breeds concerned. Data were adjusted so that the components of variance among all considered effects would be estimable (VOSTRÝ *et al.* 2007). The data set comprised:

- animals from of sires who had at least 5 offspring with performance testing records and whose offspring were always present in two studied environments,
- animals forming a group of contemporaries that contained 5 animals at least,
- animals from of mothers who had at least two offspring and one half-sister.

The set of pedigrees was formed by attributing two generations of ancestors to the information on animal performance.

Localities

Environmental conditions in the Czech Republic were classified into three localities according to the evaluation of less-favoured areas (LFA) (http://ec.europa.eu/agriculture/consultations/lfa/consultationdoc_en.pdf). Locality 1 comprised mountain areas. These areas represent land at of altitudes more then 500 m above sea level, and with more than 50% of agricultural land on slopes higher than 7 degrees. Locality 2 was described as less-favoured areas, i.e. the territory with a lower production potential. Locality 3 represented intensive production areas with the high production capacity of soil (hereinafter localities 1, 2 and 3) (VOSTRÝ *et al.* 2008). Table 1 shows the characteristics of a sampling set for the particular localities.

Model

The estimation of animal \times environment interaction was done separately between two environments (1×2 , 2×3). To estimate the animal \times environment interaction the same trait in two different environmental conditions it was considered as two traits. The estimation of genotype \times environment interaction was done by a multi-trait animal model (DE MATTOS *et al.* 2000):

$$\begin{bmatrix} \mathbf{y}_i \\ \mathbf{y}_j \end{bmatrix} = \begin{bmatrix} \mathbf{X}_i & 0 \\ 0 & \mathbf{X}_j \end{bmatrix} \begin{bmatrix} \mathbf{b}_i \\ \mathbf{b}_j \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_i & 0 & \mathbf{M}_i & 0 \\ 0 & \mathbf{Z}_j & 0 & \mathbf{M}_j \end{bmatrix} \begin{bmatrix} \mathbf{a}_i \\ \mathbf{a}_j \\ \mathbf{m}_i \\ \mathbf{m}_j \end{bmatrix} + \begin{bmatrix} \mathbf{W}_i & 0 \\ 0 & \mathbf{W}_j \end{bmatrix} \begin{bmatrix} \mathbf{pe}_i \\ \mathbf{pe}_j \end{bmatrix} + \begin{bmatrix} \mathbf{e}_i \\ \mathbf{e}_j \end{bmatrix} \quad (1)$$

where \mathbf{y}_i and \mathbf{y}_j are vectors of the observed values in environments i and j ; \mathbf{b}_i and \mathbf{b}_j are the vectors of fixed effects (combined effect of sex and litter size, effect of mother's age, effect of the group of contemporaries and effect of breed) in environments i and j ; \mathbf{a}_i and \mathbf{a}_j are the vectors of random additive genetic effects in environments i and j ; \mathbf{m}_i and \mathbf{m}_j are the vectors of random additive maternal effects in environments i and j ; \mathbf{pe}_i and \mathbf{pe}_j are the vectors of random effects of mother's permanent environment in environments i and j ; \mathbf{e}_i and \mathbf{e}_j are the vectors of random residual errors in environments i and j ; \mathbf{X}_i , \mathbf{X}_j , \mathbf{Z}_i , \mathbf{Z}_j , \mathbf{M}_i , \mathbf{M}_j , \mathbf{W}_i and \mathbf{W}_j are the known incidence matrices of fixed and random effects in environments i and j .

We assume that random effects show the normal distribution of frequencies with zero average and with the following variance-covariance structure:

$$\mathbf{V} \begin{bmatrix} \mathbf{a}_i \\ \mathbf{a}_j \\ \mathbf{m}_i \\ \mathbf{m}_j \end{bmatrix} = \begin{bmatrix} \sigma_{di}^2 & \sigma_{di,dj} & \sigma_{di,mi} & \sigma_{di,mj} \\ \sigma_{dj,di} & \sigma_{dj}^2 & \sigma_{dj,mi} & \sigma_{dj,mj} \\ \sigma_{mi,di} & \sigma_{mi,dj} & \sigma_{mi}^2 & \sigma_{mi,mj} \\ \sigma_{mj,di} & \sigma_{mj,dj} & \sigma_{mi,mj} & \sigma_{mj}^2 \end{bmatrix} \otimes \mathbf{A} \quad (2)$$

$$\mathbf{V} \begin{bmatrix} \mathbf{e}_i \\ \mathbf{e}_j \end{bmatrix} = \begin{bmatrix} \mathbf{I}\sigma_{ei} & 0 \\ 0 & \mathbf{I}\sigma_{ej} \end{bmatrix}$$

$$\mathbf{V} \begin{bmatrix} \mathbf{pe}_i \\ \mathbf{pe}_j \end{bmatrix} = \begin{bmatrix} \mathbf{I}\sigma_{pei}^2 & 0 \\ 0 & \mathbf{I}\sigma_{pej}^2 \end{bmatrix}$$

where σ_{di}^2 and σ_{dj}^2 are the additive genetic variances of direct effect for environments i and j ; σ_{mi}^2 and σ_{mj}^2 are the additive genetic variances of maternal effect for environments i and j ; $\sigma_{di,mi}$ and $\sigma_{di,mj}$ are the genetic covariance of direct and maternal effect [Cov(d,m)] for environment i and j ; $\sigma_{di,dj}$ and $\sigma_{mi,mj}$ are the covariance between direct or maternal effect for environment i and j ; $\sigma_{di,mj}$ is the covariance between direct effect in environment i and maternal effect in environment j ; $\sigma_{dj,mi}$ is the covariance between direct effect in environment j and maternal effect in environment i ; σ_{pei}^2 and σ_{pej}^2 are the variance of the effects of permanent maternal environment; σ_{ei}^2 and σ_{ej}^2 are the variance of the effect of residual errors; \mathbf{A} is the relationship matrix and \mathbf{I} is the identity matrix.

The computation programme VCE5 (KOVÁČ *et al.* 2002) was used for the estimation of variance and covariance components. The other population parameters were derived from the estimated variance-covariance components (WILLHAM 1979).

Table 1
The characteristics of sampling sets
Die Charakteristik der Selektionsdatei

	Localities					
	1-2		1-3		2-3	
Numbers of animals	2460	2689	686	1546	2350	2621
Numbers of sires	133		52		127	
Numbers of HYS	113	139	45	95	135	145
Average weight (kg)	241.38	271.16	266.19	274.49	282.39	280.74
Standard deviations (kg)	49.51	43.38	44.00	42.55	42.55	44.00

Results and discussion

Table 1 shows descriptive characteristics of sampling sets. The table documents that the data sets for two-trait analyses between localities 1 vs 2 and 2 vs 3 showed approximately identical values in these characteristics. Markedly lower values of localities particular characteristics were computed in the set for the analysis of 1 vs 3. The table also indicates the existence of a marked disproportion among the numbers of animals, sires and groups

of contemporaries in the data set for the analysis of localities 1 and 3. These set showed no meaningful results. This disproportion significantly influenced the estimation of variance components of the given set and that did not make sense. For this reason the analysis between localities 1 vs 3 will not be mentioned any more. The estimations of mean values and standard deviations within the localities were done only in the analyses of 1 vs 2 and 2 vs 3. In a comparison of 1 vs 2 average live weights reached higher values in more favourable localities (locality 2). On the contrary, a higher value was reached by locality 2 in a comparison of localities 2 vs 3. The comparison of standard deviations showed that in localities with lower average live weight locality 1 in the comparison of localities 1 vs 2, or locality 3 in the comparison of localities 2 vs 3, had higher values of variability. Similar values for beef cattle breeds were published e.g. by JAKUBEC *et al.* (2003), VOŠTRÝ *et al.* (2007) and PILARCZYK and WÓJCIK (2008).

The results of bivariate analysis for the estimation of animal \times environment interaction in conditions of the Czech Republic are summarized in Table 2.

Table 2
Estimated genetic effects for the particular localities
Genetische Parameter für die Lokalitäten

	Localities			
	1-2		2-3	
σ_a^2	122.65 (0.59)	262.51 (0.83)	115.27 (0.62)	259.78 (1.04)
σ_m^2	50.54 (0.38)	103.12 (0.65)	115.62 (0.73)	34.66 (0.47)
σ_{am}	22.27 (0.71)	-30.61 (0.53)	26.36 (0.78)	0.66 (0.52)
σ_{pe}^2	159.85 (0.47)	77.95 (0.63)	73.17 (0.86)	60.52 (0.63)
σ_e^2	653.19 (0.42)	602.39 (0.60)	697.41 (0.56)	758.19 (0.75)
σ_y^2	1008.50	1015.36	1027.83	1113.80
h_d^2	0.12 (0.03)	0.26 (0.03)	0.11 (0.03)	0.23 (0.04)
h_m^2	0.05 (0.02)	0.10 (0.03)	0.11 (0.03)	0.03 (0.02)
r_{dm}	0.28 (0.22)	-0.19 (0.12)	0.22 (0.11)	0.01 (0.21)
c^2	0.15 (0.02)	0.08 (0.03)	0.07 (0.03)	0.05 (0.02)
r_d		0.98 (0.03)		0.82 (0.12)
r_m		0.65 (0.37)		0.50 (0.31)

Total phenotypic variance among the particular localities ranged from 1008.50 to 1113.80 when the lowest value was reached in locality 1 and the highest value was computed for locality 3. The values of residual variance showed a similar trend. Locality 2 was the only exception, for which the lowest value of residual variance was estimated (602.39).

The estimates of direct heritability coefficients among the localities amounted to 0.11 to 0.26. The estimates of maternal heritability coefficient were in the same range as the estimates of direct heritability coefficients from 0.03 to 0.11. The coefficients of direct or maternal heritability had similar values like those reported by MEYER (1997), ROBINSON (1996), WALDRON *et al.* (1993) and SZABÓ *et al.* (2007), who estimated heritability coefficients in the range from 0.15 to 0.57 for the direct effect and from 0.16 to 0.4 for the maternal effect. A comparison of the values of standard deviations with the coefficients of direct heritability shows that the estimations of coefficients h_d^2 are statistically significant. The estimates of maternal heritability coefficients reached statistical

significance only in locality 2. VAN VLECK (1963) suggested that significant differences between the heritability coefficients of one trait in two environments might signal the existence of genotype \times environment interaction. A comparison of direct heritability estimates in two-trait analyses revealed pronounced differences (0.12 vs 0.26 and 0.11 vs 0.23). But this considerable variation need not be necessarily caused by the existence of genotype \times environment interaction.

Large variation was also observed in the coefficient of genetic correlation between direct and maternal effect (r_{dm}). Estimation of r_{dm} for localities 1 and 3 resulted in zero to medium positive values, i.e. 0.01 and 0.28, respectively. However, estimation of r_{dm} in locality 2 turned out a negative (-0.19) and a positive (0.22) value. These genetic correlation between direct and maternal effect fitted into estimates the large range of values published by the above-mentioned authors (-0.594 to 0.223). Unlike the other coefficients, the estimates for genetic correlation between direct and maternal effect was not significantly different from zero.

A similar trend as in r_{dm} was observed in the ratio of permanent maternal environmental variance to total phenotypic variance (c^2), in which differences among localities and analyses were smaller than in r_{dm} , but for locality 2 similar values were estimated in both analyses. The values of c^2 in the particular analyses ranged from 5 to 15%. DE MATTOS *et al.* (2000) reported c^2 – estimates in the range of 14 to 17% for the Hereford and DONOGHUE and BERTRAND (2004) computed c^2 – estimates between 7 and 17% for Charolais breed. Similar to direct and maternal heritability estimates of coefficients c^2 were significantly different from zero.

Genetic correlation between localities for direct effect was estimated to be 0.98 (1, 2) and 0.82 (2, 3) respectively, and for maternal effects 0.65 (1, 2) and 0.50 (2, 3) respectively. ROBERTSON (1959) recommended to use a multi-trait model for evaluation of the performance of animals across different conditions when performance in different environment is considered to be a different trait. He also stated that the genotype \times environment interaction for two environments was not biologically significant if the genetic correlation was higher than 0.80 between the same trait in the two different environments. The estimates of genetic correlation for direct effect exceeded this critical value while estimates for maternal effect were lower (0.65 and 0.50 respectively). Considering the standard errors, the estimates of genetic correlation for maternal effect obviously was not statistically significant.

From these results it can be concluded that weaning weight of beef cattle kept in the Czech Republic is not influenced by animal \times environment interaction. Applying the bivariate analysis, DE MATTOS *et al.* (1996) analysed weaning weight in the Hereford breed in different localities in Uruguay, LEE and BERTRAND (2002) and DE MATTOS *et al.* (2000) in USA, Canada and Uruguay. These authors estimated genetic correlations for direct and maternal effects to be 0.80 and higher. They concluded that weaning weight of the Hereford breed was not influenced by the genotype \times environment interaction under their conditions. On the contrary, HYDE *et al.* (1998) estimated the genetic correlation for direct genetic effects between conditions of the USA, Canada, Australia and New Zealand to be 0.70 for the Charolais breed while the significance of genotype \times environment interaction was confirmed.

According to DE MATTOS *et al.* (2000) no papers were published dealing with the animal \times environment interaction in which the efficiency of sire, sire-maternal grandsire and animal models was compared. FERREIRA *et al.* (1999) reported large differences in the estimation of breeding value by different models.

The analysis showed that for weaning weight, considered as a different trait in different environmental conditions, of the beef cattle kept in the Czech Republic the estimates for genetic correlation for direct effect were higher than 0.80. Therefore weaning weight in beef cattle kept under the conditions of the Czech Republic is not influenced the animal \times environment interaction. The magnitude of the across-areas genetic correlation indicates that the animal by environment interaction was not biologically important and can be ignored in the evaluation of beef cattle in the Czech Republic.

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References

- Brown MA, Brown AH, Jackson WG, Miesner JR (1993) Genotype \times environment interactions in postweaning performance to yearling in Angus Brahman and reciprocal-cross calves. *J Anim Sci* 71, 3273-9
- Donoghue KA, Bertrand JK (2004) Investigation of genotype by country interactions for growth traits for Charolais populations in Australia Canada New Zealand and USA. *Livest Prod Sci* 85, 129-37
- De Mattos D, Bertrand JK, Herring Wo, Benyshek LL (1996) Sire and maternal grandsire by environment interaction in Uruguay. *J Anim Sci* 74 Suppl, 106 [abstract]
- De Mattos D, Bertrand JK, Misztal I (2000) Investigation of genotype \times environment interactions for weaning weight for Herefords in three countries. *J Anim Sci* 78, 2121-6
- Ferreira GB, Macneil MD, Van Vleck LD (1999) Variance components and breeding values for growth traits from different statistical models. *J Anim Sci* 77, 2641-50
- Hyde LR, Bourdon RN, Golden BL, Comstok CR (1998) Genotype by environment interaction for growth and milk traits in an international population of Charolais cattle. *J Anim Sci* 76 Suppl, 60 [abstract]
- Jakubec V, Schlote W, Říha J, Majzlík I (2003) Comparison of growth traits of eight beef cattle breeds in the Czech Republic. *Arch Tierz* 46, 143-53
- Kovač M, Groeneveld E, García-Cortes LA (2002) VCE-5 A package for the estimation of dispersion parameters. In: *Proc 7th WCGALP CD ROM Commutation No. 8-06*
- Křížek J, Rais I, Říha M (1992) Genotype \times environment interactions under different conditions of set – stocking in sheep. *Arch Tierz* 35, 619-28
- Lin C Y, Togashi K (2002) Genetic improvement in the presence of genotype by environment interaction. *J Anim Sci* 73, 3-11
- Lee DH, Bertrand JK (2002) Investigation of genotype \times country interactions for growth traits in beef cattle. *J Anim Sci* 80, 330-7
- Meyer K (1997) Estimates of genetic parameters for weaning weight of beef cattle accounting for direct-maternal environmental covariances. *Livest Prod Sci* 52, 187-99
- Notter DR, Tier B, Meyer K (1992) Sire \times herd interactions for weaning weight in beef cattle. *J Anim Sci* 70, 2359-65
- Pilarczyk R, Wójcik J (2008) Comparison of body weight and reproduction performance in cows of various beef breeds managed under equal conditions in West Pomerania. *Arch Tierz* 51, 318-28
- Robertson A (1959) The sampling variance of the genetic correlation coefficient. *Biometrics* 15, 469-85

- Robinson DL (1996) Estimation and interpretation of direct and maternal genetic parameters for weights of Australian Angus cattle. *Livest Prod Sci* 45, 1-11
- Sandelin BA, Brown AH, Brown MA, Johanson ZB, Kellogg DW, Stelzleni AM (2002) Genotype × environmental interaction for mature size and rate of maturing for Angus Brahman and reciprocal-cross cows grazing bermudagrass or endophyte infected rescue. *J Anim Sci* 80, 3073-6
- Szabó F, Lengyel Z, Domokos Z, Bene S (2007) Estimation of genetic parameters and (co)variance components for weaning traits of Charolais population in Hungary. *Arch Tierz* 50, 447-54
- Van Vleck LD (1963) Genotype and environment in sire evaluation. *J Dairy Sci* 46, 983-7
- Vostrý L, Příbyl P, Veselá Z, Jakubec V (2007) Selection of a suitable data set and model for the estimation of genetic parameters of the weaning weight in beef cattle. *Arch Tierz* 50, 562-74
- Vostrý L, Příbyl J, Jakubec V, Veselá Z, Majzlík I (2008) Selection of a suitable definition of environment for the estimation of genotype × environment interaction in weaning weight of beef cattle. *J Czech Anim Sci* 53, 407-17
- Waldron DF, Morris CA, Baker RL, Johanson DL (1993) Maternal effects for growth traits in beef cattle. *Livest Prod Sci* 34, 57-70
- Willham RL (1979) The role of maternal effects in animal breeding: III Biometrical aspects of maternal effects in animals. *J Anim Sci* 35, 1288-93

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