Estimation of Genotype × Environment Interaction in Beef Cattle in the Czech Republic

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Introduction

The knowledge of genotype × environment interaction is important for an optimum use of the particular genotypes in different production and breeding systems. It is applicable especially to beef cattle that are kept in both intensive and extensive environments. The genotype × environment interaction is defined as a change in the relative value of performance of two or more genotypes in two or more different environments. When comparing two different genotypes, the magnitude and statistical significance of this interaction is related mainly to the distinctness of genotypes or environment. In fact, such an interaction is assumed to exist whenever two or more genotypes occur in two or more environments. The knowledge of animal × 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 hybridization. If existing animal × environment interactions are neglected, great inaccuracies may arise in the breeding of beef cattle.

Material and methods

Estimation of animal × 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 15 years (1990 – 2007). Data for the estimation of animal × environment interaction were provided by the Czech Association of Beef Cattle Breeders (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:

Localities: Environmental conditions in the Czech Republic were classified into three localities according to the evaluation of less-favoured areas (LFA). Locality 1 comprised mountain areas. These areas represent land at of altitudes more than 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.

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

$$\begin{bmatrix} \boldsymbol{y}_i \\ \boldsymbol{y}_j \end{bmatrix} = \begin{bmatrix} \boldsymbol{X}_i & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{X}_j \end{bmatrix} \begin{bmatrix} \boldsymbol{b}_i \\ \boldsymbol{b}_j \end{bmatrix} + \begin{bmatrix} \boldsymbol{Z}_i & \boldsymbol{0} & \boldsymbol{M}_i & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{Z}_j & \boldsymbol{0} & \boldsymbol{M}_j \end{bmatrix} \begin{bmatrix} \boldsymbol{a}_i \\ \boldsymbol{a}_j \\ \boldsymbol{m}_i \\ \boldsymbol{m}_j \end{bmatrix} + \begin{bmatrix} \boldsymbol{W}_i & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{W}_j \end{bmatrix} \begin{bmatrix} \boldsymbol{pe}_i \\ \boldsymbol{pe}_j \end{bmatrix} + \begin{bmatrix} \boldsymbol{e}_i \\ \boldsymbol{e}_j \end{bmatrix}$$

Results and discussion

The results of bivariate analysis for the estimation of genotype × environment interaction in conditions of the Czech Republic are summarized in Table 1.

Table 1: The characteristics of sampling sets

	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
Awerage 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

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) and Waldron et al. (1993), 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 × 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 × 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, resp. 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 percent. 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 directs effect was estimated to be 0.98 (1, 2) and 0.82 (2, 3) resp., and for maternal effects 0.65 (1, 2) and 0.50 (2, 3) resp. 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 × environment interaction for two environments was not biologically significant if the genetic correlation was higher than 0.80 between the some 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 resp.). Considering the standard errors, the estimates of genetic correlation for maternal effect obviously was not statistically significant.

Table 2: Estimated genetic effects for the particular localities

	Localities			
	1 - 2		2 – 3	
h^2_d	0.12 (0.03)	0.26 (0.03)	0.11 (0.03)	0.23 (0.04)
h^2_m	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)	

From these results it can be concluded that weaning weight of beef cattle kept in the Czech Republic is not influenced by animal × 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 × 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 × environment interaction was confirmed.

Conclusion

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 × 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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This work was supported by the Ministry of Education, Youth and Sports of the Czech Republic (Project No. MSM 6046070901).