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ESTIMATION OF GENETIC PARAMETERS OF TYPE TRAITS IN BEEF CATTLE IN CZECH REPUBLIC.

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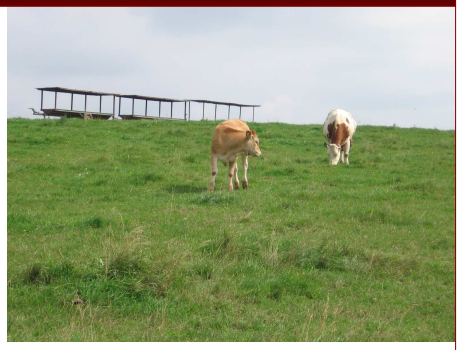
ABSTRACT

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 and 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.

MATERIAL AND METHODS

The evaluation involves 10 traits:

- 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
- Production type - PT



Available were 5 424 records of young animals of 12 beef breeds and crosses with dairy and dual-purpose breeds (Aberdeen Angus – 1 156, Belgian Blue – 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.

Genetic parameters were estimated by a multi-trait animal model.

Model

1.Traits scoring body measurements and body capacity

(HS, BL, LW, CW, CD, P)

$$y_{ijkl} = \mu + HYS_i + S_j + AM_k + aAE_{ijkl} + g_{ijkl} + e_{ijkl}$$

2. Traits scoring muscling and overall type

(SM, BM, RM, PT)

$$y_{ijk} = \mu + HYS_i + S_j + aAE_{ijk} + bDG_{ijk} + g_{ijk} + e_{ijk}$$

where:

- $y_{ijk(l)}$ - evaluation of the trait
- μ - population mean
- HYS_i - fixed effect of the group of jointly evaluated animals
- 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, 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

REMLF90 programme was used to estimate genetic parameters.

RESULTS

Table I. Basic statistical characteristics of evaluated traits

Evaluated trait		Mean	SD	Min	Max
HS	Height at sacrum	5.66	2.17	1	10
BL	Body length	6.49	0.97	2	9
LW	Live weight	6.76	2.65	1	10
CW	Front chest width	5.75	0.99	2	9
CD	Chest depth	6.19	0.98	2	9
P	Pelvis	5.81	0.99	2	9
SM	Shoulder muscling	5.59	0.97	2	9
BM	Back muscling	5.76	0.98	2	9
RM	Rump muscling	5.83	1.13	2	9
PT	Production type	5.84	1.13	2	9

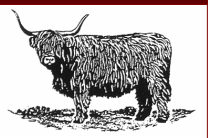
The results of evaluation of height at sacrum showed flat normal distribution. The classes of the extremes (scores 1 and 10) comprised a high number of individuals. On the contrary, the results of live weight did not show normal distribution. Most animals received higher scores in live weight evaluation. In both these traits (HS, LW) the whole scale from 1 to 10 was used for scoring. Scores from 2 to 9 were used for other traits evaluation and the results showed normal distribution.

Table II. Coefficients of heritability h^2 (on the diagonal), genetic r_G (above the diagonal) and phenotypic r_P (below the diagonal) correlations

	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**

CONCLUSION

We constructed a model for estimation of genetic parameters and routine estimation of breeding value for the 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. Deviation 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 a number of evaluated traits may be reduced in practice.



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