63rd Annual Meeting EAAP 2012
August 27th - 31st, 2012
Bratislava, SLOVAKIA

CZECH UNIVERSITY OF LIFE SCIENCES PRAGUE

GENETIC PARAMETERS ESTIMATION FOR LINEAR TYPE TRAITS DESCRIBED IN THE CZECH DRAFT BREEDS OF HORSES

Luboš Vostrý, Barbora Hofmanová, Zuzana Čapková and Ivan Majzlík
Czech University of Life Sciences Prague, Kamýcká 129, 165 21 Prague 6, Czech Republic, e-mail: hofmanova@af.czu.cz

OBJECTIVE

The aim of this study was to estimate genetic parameters and predict breeding values for described traits and body measurements.

MATERIAL AND METHODS

1 744 purebred horses (373 *SN*, 574 *N* 794 *CMB*) were described in the interval of 18 years (1990 – 2007).

Described traits (22) were divided into 5 groups:

- ***comprehensive character***: type (**TY**), frame (**FR**), nobility (**NO**),
- ***forehand***: neck length (**NL**), neck setting (**NS**), withers length (**WL**), shoulder-blade (**SB**),
- ***body and hindquarters***: topline length (**TL**), topline form (**TF**), loin length (**LL**), loin form (**LF**), body width (**BW**), croup length (**CL**), croup slope (**CS**), shape of croup (**SC**),
- ***limbs***: foretoes (**FO**), forehoof (**FH**), hind-limbs posture (**HLP**), fetlock (**FT**), back hoof (**BH**),
- ***movement*** : length of walk (**LW**), length of trot (**LT**)

A 1 to 9 degrees of linear scale was used for above-mentioned traits description.

Body measurements (4) included in the analysis were:

- withers height measured with a measuring stick (**WHS**),
- withers height measured with a tape (**WHT**),
- chest circumference (**CC**)
- front cannon bone circumference (**CBC**).

Data sets were provided by the Horse Breeders Association (www.aschk.cz)

Genetic parameters were estimated by computer programme VCE 5.1 (Kovač et al., 2002). The pedigree set for estimation comprised 5 generations of ancestors (6 464 horses).

Model used:

$$y_{ijklmno} = \mu + Sex_i + YearD_j + AgeD_k + Breed_l + Clas_m + a_n + e_{ijklmno}$$

where: μ – general mean, Sex_i – fixed effect of the i-th sex, $YearD_j$ – fixed effect of the j-th year of description, $AgeD_k$ – fixed effect of the k-th age at description, $Breed_l$ – fixed effect of the l-th breed, $Clas_m$ – fixed effect of the m-th classifier, a_n – random effect of the n-th horse, e – residual error.

Breeding values were predicted for linear described traits by BLUP multi-trait animal model using the BLUPF90 computer programme (Misztal et al., 2005).

INTRODUCTION

The cold-blooded breeds Silesian Noriker (***SN***), Noriker (***N***) and Czech-Moravian Belgian Horse (***CMB***) belong to the group of genetic resources in the Czech Republic.
Population size: ***SN*** (43, 464), ***N*** (68, 967), ***CMB*** (61, 1012).
CMB has been formed in the CR territory on the basis of Belgian and Walloon stallions.
SN has originated from imports of original Noriker and Bavarian cold-blooded stallions.
N was originally used for the formation of SN breed, these two breeds were further separated geographically and in 1991 were recognized as separate breeds.

CONCLUSION

The values of heritability coefficient higher than 0.50 were estimated in three out of 26 traits (12 %), higher than 0.30 in 5 traits (19 %) and the values lower than 0.20 were calculated in 7 traits (27 %).

- **The high and intermediate values of heritability coefficient document that correction breeding on the basis of genetic information on linear description traits can be very efficient.**
- **Estimations of genetic correlations among the described traits correspond to biological relations.**

The values of standard deviations for breeding values ranged from 0.24 (LF) to 0.72 (TY). The values of standard deviations for body measurements were in the range from 0.62 (CBC) to 6.18 (CC).
The lowest values of variance in breeding values were determined in traits with low h^2 values and vice versa.

- **The breeding values could be used for more effective selection of typical conformation traits in the Czech cold-blooded breeds of horses.**

Heritability coefficients (diagonal) and genetic correlations (above diagonal)

	WHS	WHT	CC	CBC	TY	FR	NO	NL	NS	WL	SB	TL	TF	LL	LF	BW	CL	CS	SC	FO	FH	HLP	FT	BH	LW	LT
WHS	**0.55**	0.97	0.75	0.70	0.63	-0.11	-0.09	0.35	-0.08	0.40	0.03	-0.04	0.53	0.04	0.37	0.18	0.22	-0.08	0.14	0.08	-0.01	0.19	0.25	-0.07	0.15	0.15
WHT		**0.54**	0.76	0.69	0.67	-0.28	-0.18	0.28	-0.12	0.36	0.07	-0.06	0.48	0.15	0.25	0.40	0.17	-0.02	0.31	-0.10	0.03	0.14	-0.26	0.06	0.03	0.06
CC			**0.36**	0.55	0.48	-0.10	-0.06	0.35	-0.10	0.35	0.01	0.06	0.20	0.13	0.08	0.60	0.26	-0.28	0.65	-0.06	-0.07	0.08	-0.07	0.16	-0.04	-0.12
CBC				**0.55**	0.47	0.12	-0.17	0.01	0.11	0.27	0.09	0.32	0.26	0.39	-0.11	0.35	0.40	0.05	0.40	0.12	-0.12	0.35	-0.07	-0.10	-0.03	-0.01
TY					**0.21**	-0.02	0.03	0.28	-0.03	0.11	0.20	0.01	0.69	0.30	0.26	0.61	0.10	-0.39	0.34	0.21	0.23	-0.04	0.07	0.40	-0.02	0.10
FR						**0.23**	0.20	0.47	0.34	0.41	0.38	0.82	-0.21	0.47	-0.46	-0.18	0.43	-0.03	0.19	-0.28	0.32	0.35	0.05	-0.13	0.15	-0.01
NO							**0.23**	0.15	-0.05	-0.13	-0.46	0.01	-0.26	-0.49	-0.35	-0.33	-0.34	-0.18	0.40	-0.04	-0.40	-0.34	-0.52	-0.45	0.63	0.32
NL								**0.18**	-0.27	0.46	0.29	0.35	0.61	0.41	0.20	0.02	0.33	-0.43	0.10	-0.54	0.56	0.12	-0.07	0.52	0.05	0.05
NS									**0.36**	-0.02	0.37	0.30	-0.27	0.38	0.07	0.09	0.41	0.25	0.04	0.39	0.18	0.27	0.37	0.15	-0.46	-0.35
WL										**0.24**	0.44	0.46	0.57	0.59	0.21	0.09	0.43	-0.06	-0.11	-0.15	0.51	0.19	0.14	0.41	-0.27	-0.05
SB											**0.36**	0.53	0.46	0.66	0.37	0.23	0.72	0.27	0.17	-0.16	0.72	0.26	0.24	0.42	-0.34	-0.05
TL												**0.19**	-0.15	0.70	-0.16	0.02	0.42	-0.12	0.25	-0.35	-0.06	0.46	0.40	0.06	0.02	-0.20
TF													**0.14**	0.18	0.66	0.23	0.36	-0.40	-0.19	-0.41	0.54	0.07	0.25	0.32	-0.11	0.12
LL														**0.16**	0.32	0.22	0.38	-0.31	-0.28	-0.21	0.30	0.38	0.31	0.61	-0.30	-0.21
LF															**0.14**	0.37	0.34	0.13	-0.37	0.11	0.43	0.14	0.63	0.92	-0.27	-0.02
BW																**0.28**	0.26	-0.21	0.58	0.09	0.21	0.16	0.21	0.26	-0.24	-0.13
CL																	**0.35**	0.18	0.13	-0.32	0.59	0.46	0.23	0.33	-0.25	-0.13
CS																		**0.29**	-0.08	0.26	0.17	0.39	0.23	-0.27	-0.05	0.15
SC																			**0.18**	0.06	-0.01	0.09	-0.08	-0.63	0.26	0.26
FO																				**0.11**	-0.19	0.25	0.85	0.06	-0.27	-0.03
FH																					**0.10**	0.08	0.41	0.64	-0.40	0.07
HLP																						**0.37**	0.45	0.23	0.07	0.03
FT																							**0.16**	0.56	-0.34	-0.26
BH																								**0.19**	-0.67	-0.47
LW																									**0.28**	0.83
LT																										**0.27**

Standard errors of heritability coefficient s (s_h^2) ranged from 0.03 to 0.05

High positive or negative genetic correlations $|r_G| \geq 0.50$

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