Analysis of Czech cold-blooded horses: genetic parameters, breeding value and the influence of inbreeding depression on linear description of conformation and type characters

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ABSTRACT: Genetic parameters, breeding values and inbreeding depression for 22 linear type description of conformation and type characters and 4 body measurements were evaluated in a group of 1744 horses of three original cold-blooded breeds in the Czech Republic in a long period of 18 years (1990–2007). Based on the values of Akaike's information criterion, residual variance and heritability coefficient, a model with fixed effects (sex, year of description, breed, and classifier) and with a random effect (animal) was selected. Heritability coefficients for the particular traits were in the range of 0.11 to 0.55 and genetic correlations ranged from –0.63 to 0.97. Inbreeding depression, expressed as coefficients of regression on one percent of inbreeding, was in the range of –0.0992 to 0.0242 points for the particular traits. The inclusion of inbreeding depression in the model resulted in a moderate change in h^2 in one-third of the traits. In two-thirds of traits, the value of r_G increased or decreased by 0.01. Standard deviations of the breeding values for linear type description of conformation and type characters were in the range of 0.30 to 0.72 and 0.62 to 6.18 for body measurement traits. Among breeding values estimated by a model without inbreeding depression and a model with inbreeding depression, Spearman's rank correlation coefficient values for the particular traits were 0.916–0.999 (sample of all horses), 0.710–0.992 (10% of the best horses) and 0.827–0.998 (10% of the worst horses). If the average value of the inbreeding coefficient is low (0.03), then it is not necessary to include the influence of inbreeding depression in the model for the genetic evaluation of individuals of original cold-blooded horses kept in the Czech Republic.

Keywords: breeding value; inbreeding depression; linear description of conformation; cold-blooded horses

The populations of cold-blooded horses in the Czech Republic are few, which has led to an increase in inbreeding coefficient in the populations of these breeds. This was particularly true during the nineties when populations of these breeds were secluded from other populations. The increase in inbreeding coefficient could bring about undesirable inbreeding depression that is manifested in characteristics associated with fitness and reproduction or characteristics closely related with them Maiwashe et al. (2008).

Cold-blooded horse breeds like Silesian Noriker (SN), Noriker (N), Czech-Moravian Belgian hor-

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se (CMB), along with Old Kladruber Horse and Hucul horse, belong to the group of genetic resources in the Czech Republic. In the last approximately 120 years, the CMB has been formed in the Czech Republic utilising imports of mainly original Belgian stallions and to a lesser extent, Walloon stallions. The CMB is a horse with a medium square frame and earlier maturity. The active population of CMB is composed of 50 stallions and 369 mares. SN originated in the last approximately 100 years from imports of original Noriker stallions and Bavarian cold-blooded stallions. SN is a horse with a longer frame and later maturity. The active population consists of 40 stallions and 350 mares. The N breed was originally used for the formation of the SN breed and has been kept in the Czech Republic territory for approximately 150 years. These two breeds were geographically separated. The breeds SN and CMB were recognised as independent breeds in 1991 and have been included in the group of genetic resources. The linear type description of conformation and type characters was introduced in the above-mentioned horse breeds in 1996.

Linear description of conformation and type characters is routinely used, mainly in cattle, where a number of analyses were previously carried out (Brotherstone, 1994; Veselá et al., 2005; Zavadilová et al., 2009a,b). Body conformation in horses was primarily evaluated by a scoring system and then the linear type description of conformation and type characters was introduced later. The linear description of conformation and type characters and the description of morphological features in horse breeds were studied by Jakubec et al. (1999, 2007) in the Old Kladruber horse, Maršálek et al. (1996, 1999) in Czech breeding horse, Pretorius et al. (2004) in Friesian horses, Zechner et al. (2001) and Baban et al. (1998) in Lipizzan horses, Molina et al. (1999) in Andalusian horses, Samoré et al. (1997) in Haflinger horses, Hartman et al. (1994) in riding horses, and by Van Bergen and Van Aredonk (1993) in Shetland ponies. Koenen et al. (1994) investigated a relationship between body conformation and performance in Dutch warm-blooded horses. Schlote et al. (2002) studied the development of the type evaluation and standardisation in horse breeds using computer technology.

Inbreeding depressions are more likely to occur in traits that are closely associated with the reproduction and fitness of an animal, whereas in traits connected with morphological features, such as body measurements, the influence of inbreeding depression is smaller. Nevertheless, the influence of inbreeding depression was observed in morphological characteristics (Gandini et al., 1992; Sierszchulski et al., 2005; Gómez et al., 2009). Analla et al. (1999) reported that the influence of inbreeding depression need not always show a linear course, but Sierszchulski et al. (2005) determined that there is a linear relationship with inbreeding depression in body conformation traits.

Our aim was to choose a suitable model for the estimation of genetic parameters including breeding value and to determine the influence of inbreeding depression on the formation of linear type description of conformation and type characters in three cold-blooded horse breeds in the Czech Republic – Czech and Moravian Belgian horses, Silesian Noriker and Noriker horse breeds.

MATERIAL AND METHODS

Applying the linear descriptive method to cold-blooded horses, 22 traits in 5 groups described identical parts of the body, and each trait was evaluated in each horse:

- 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)

Four body measurements were also included in the analysis: withers height, as measured with a measuring stick (WHS), withers height, as measured with a tape (WHT), chest circumference (CC) and front cannon bone circumference (CBC). A 1 to 9 linear scale was used for the trait description. Data sets were provided by the Horse Breeders Association (www.aschk.cz). The linear type description of conformation and type characters is performed when the horse is listed in the Stud Book at 3 years of age. The dataset was comprised of 1744 purebred horses (373 SN horses, 574 N horses and 794 CMB horses) over an interval of 13 years (1996–2008). The number of offspring

Table 1. Average inbreeding coefficients for cold-blooded horses in 1990 and 2007 (Vostrý et al., 2011b)

Breed	1990		2007		Difference F_x	Min. F_x*	Max. F_x*
	n	average F_x	*n*	average F_x			
CMB	61	0.0254	107	0.0355	0.0101	0.00	0.1523
SN	33	0.0201	65	0.0323	0.0122	0.00	0.1155
N	70	0.0116	69	0.0151	0.0035	0.00	0.1302

*refers to values in 2007

from 227 stallions ranged from 3 to 44, with each stallion having 17 offspring on average. The age of evaluated animals ranged from 2 to 10 years with an average of 3.5 years and standard deviation 1.5 years. The pedigree set for estimation of genetic parameters comprised 5 generations of ancestors for a total of 6464 horses. Table 1 shows the structure and population size of the particular breeds. Means in the particular traits were in the range from 4.64 scores (NL) to 6.67 scores (SC) (Table 2). The smallest standard deviations for body conformation traits were calculated for LF (0.49) while the largest values of standard deviation were determined for TY (1.15).

The selection of a suitable multi-trait BLUP animal model for the estimation of genetic parameters and breeding value was conducted in several steps. In the first step, the choice of the suitable model for the estimation of genetic parameters and inbreeding depression verification was tested for each trait by the REML method and single-trait animal models were based on the preceding analysis (Vostrý et al., 2009). The tested models are shown in Table 3.

Although Torzyński et al. (2005) stated that maternal genetic effect should be included in the analysis of body conformation, the influence of maternal effect on body conformation was not included because of the low number of horses per mares. Live weight, which probably influences body conformation to the largest extent, was not included in the analysis either because it was not determined for the linear type description of conformation and type characters.

The VCE 5.1 computer programme (Kovač et al., 2002) was used for the estimation of the variance-covariance components and their standard errors.

Suitability of the models was tested on the basis of residual variance (σ_e^2) values and Akaike's information criterion (AIC), (Bozdogan, 2000).

$$\mathrm{AIC} = -2\log L(\theta) + 2d$$

where:

$\log L(\theta)$ = logarithm of the value of likelihood function

d = number of free parameters in the model

In the second step, based on the choice of the most suitable model, the influence of inbreeding depression on the formation of linear type description of conformation and type characters was estimated according to the following model for all breeds:

$$y_{ijklmno} = \mu + \mathrm{Sex}_i + \mathrm{Year}D_j + \mathrm{Age}D_k + \mathrm{Breed}_l + \mathrm{Clas}_m + bFx_n + a_n + e_{ijklmno}$$

where:

μ = general mean

Sex_i = fixed effect of the i-th sex

$\mathrm{Year}D_j$ = fixed effect of the j-th year of description

$\mathrm{Age}D_k$ = 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

b = fixed regression coefficient

F_x = effect of the inbreeding coefficient of the n-th horse

a_n = random effect of the n-th horse, and e is the residual error

Only a linear relationship between the linear description of conformation and type characters and the inbreeding level was considered in the model. F_x values for individual horses entering in the analysis were obtained from Vostrý et al. (2011b).

In the third step, genetic correlations among the particular traits were estimated. Due to a small number of horses and a large number of traits, genetic correlations among traits were estimated by a two-trait animal model. Based on the estimated variance-covariance components, genotype

Table 2. Descriptive characteristics

Trait	Characteristic	Mean	SD	Used score
Body measures				
WHS	withers height – stick	159.88	3.70	–
WHT	withers height – tape	171.63	4.26	–
CC	chest circumference	204.53	10.43	–
CBC	cannon bone circumference	23.17	0.96	–
Comprehensive character				
TY	type	6.17	1.15	8.00
FR	frame	5.77	0.88	7.00
NO	nobility	5.26	1.01	8.00
Forehand				
NL	neck length	4.64	0.85	6.00
NS	neck setting	5.90	0.98	7.00
WL	withers length	4.69	0.93	7.00
SB	shoulder blade	5.35	1.11	6.00
Body and hindquarters				
TL	topline length	5.63	0.78	5.00
TF	topline form	4.54	0.65	6.00
LL	loin length	5.45	0.66	5.00
LF	loin form	4.89	0.49	5.00
BW	body width	6.19	1.05	7.00
CL	croup length	5.29	0.94	7.00
CS	croup slope	6.01	0.86	7.00
SC	shape of croup	6.67	0.86	9.00
Limbs				
FO	foretoes	5.19	0.73	7.00
FH	forehoof	4.85	0.60	8.00
HLP	hind limbs posture	5.45	0.95	7.00
FT	fetlock	5.17	0.62	7.00
BH	back hoof	4.97	0.47	5.00
Movement				
LW	length of walk	6.19	1.12	7.00
LT	length of trot	6.15	1.09	6.00

and phenotype variance-covariance matrixes were constructed and subjected to the weighted bending method (Jorjani et al., 2003).

Breeding values were estimated for the linear type description of conformation and type characters by the BLUP multi-trait animal model using the BLUPF90 computer programme (Misztal et al., 2002). Rank correlations among the estimated breeding values were calculated with and without the inclusion of inbreeding depression. The influence of inbreeding depression was expressed as the regression coefficient value, which showed the influence of the coefficient F_x on the formation of morphological traits in cold-blooded horses.

Table 3. Models

	Sex	Year*B*	Year*D*	Age*D*	Breed	Clas	*lin*	*a*
Model 1	F	F		F	F	F	R	R
Model 2	F	F		F	F	F		R
Model 3	F		F	F	F	F		R

Sex = the effect of sex, Year*B* = the effect of year of birth, Year*D* = the effect of year of description, Age*D* = the effect of age at description, Breed = the effect of breed, Clas = the effect of classifier, *a* = the effect of animal, F = fixed, R = random

RESULTS AND DISCUSSION

Inbreeding

For all individuals tested, full pedigrees were determined up to generation 8. Table 1 shows the average value of F_x for Czech Cold-Blooded Horses. The inbreeding coefficient values were as follows: $F_x = 0$ for 23.68% of horses, $0 < F_x < 0.0625$ for 70.01% of horses, $0.0625 < F_x < 0.125$ for 5.79% of horses and $F_x > 0.125$ for 0.52% of horses. The first two groups ($F_x < 0.0625$) included 93.69% of all horses (Vostrý et al., 2011b).

Choice of a suitable model

The values of AIC, σ_e^2 and h^2 estimated by the tested models are shown in Table 4. Because different fixed effects were included in Model 3 and Models 1 and 2, it is possible to use AIC to choose a suitable model only between Model 1 and Model 2.

Out of the total number of 26 studied traits of the linear type description of conformation and type characters and body measurements identical and lower values of AIC were estimated in Model 2 compared to Model 1. These lower and identical values for AIC in Model 2, which did not include the random effect of sire line, demonstrated the higher suitability of Model 2 in comparison with Model 1. By comparison of the values of σ_e^2 estimated by Models 1 and 2, lower values for the 22 linear descriptive conformation and type characters and body measurements were estimated by Model 2. In addition, the estimated values of variability for the effect of line were low in all traits (approximately 0.001). A comparison of the values of AIC and σ_e^2 between Models 1 and 2, where Model 1 included more effects – sire line, and the estimated low variance values for the effect of line indicate the higher suitability of Model 2 for the estimation of genetic parameters, which did not include the random effect of sire line. These results were in agreement with the conclusions published by Vostrý et al. (2011a). Vostrý et al. (2011a) showed that disparity between sire lines was not from obvious genetic factors.

The inclusion of the fixed effect of year of description (Model 3) versus the fixed effect of year of birth (Model 2) resulted in a decrease in the value of σ_e^2 for the 22 linear type descriptions of conformation and type characters. The lower values of σ_e^2 indicated again a higher suitability of the fixed effect of year of description. Moreover, testing Model 3 there was an increase in h^2 in a half of the studied traits (13 out of 26). However, in the remaining 13 traits there was a decrease in h^2 in comparison with Model 2. Overestimation and/or underestimation of the values of h^2 should occur in Model 2 under the influence of the higher values of σ_e^2 estimated by Model 2. These conclusions demonstrate that Model 3 is the most suitable for the estimation of genetic parameters and for testing the influence of inbreeding depression on linear description of conformation and type characters. For these reasons, Model 3 will be used for a further analysis.

Heritability coefficients

Table 5 documents the estimations of variance components obtained by Model 3, which was chosen in the preceding analyses as the most suitable model for the estimation of genetic parameters.

Heritability coefficient values higher than 0.50 were estimated in 3 out of 26 traits (12%), higher than 0.30 in 5 traits (19%) and values lower than 0.20 were calculated in 7 traits (27%). The highest heritability coefficient values were determined for the traits of body conformation measurements WHS, WHT and CBC (h^2 = 0.55, 0.54, and 0.55, respectively). This illustrates that the measured values of these traits are not transformable to the linear descriptive scale, which reduces the environmental influence. As stated in Table 5 and by Vostrý et al. (2009), the entire scoring scale (1–9) was not used for the linear type description of conformation and type characters of cold-blooded horses, which might decrease the variability in the other described traits. The lowest heritability coefficient values were found in the traits FH (0.10) and FO (0.11).

Table 4. The values of AIC, residual variance and heritability coefficients

Trait	Characteristic	Model 1			Model 2			Model 3		
		AIC	σ_e^2	h^2	AIC	σ_e^2	h^2	AIC	σ_e^2	h^2
Body measures										
WHS	withers height – stick	5179	5.780	0.588	5178	5.777	0.593	5199	6.231	0.550
WHT	withers height – tape	5176	8.141	0.556	5175	8.148	0.561	5201	8.359	0.544
CC	chest circumference	5220	67.196	0.360	5225	67.061	0.380	5242	68.454	0.355
CBC	cannon bone circumference	4867	0.345	0.561	4865	0.344	0.565	4906	0.351	0.554
Comprehensive character										
TY	type	5117	1.014	0.215	5115	1.014	0.215	5107	0.997	0.209
FR	frame	5036	0.561	0.221	5036	0.562	0.229	5034	0.547	0.234
NO	nobility	5250	0.770	0.215	5250	0.764	0.229	5246	0.747	0.228
Forehand										
NL	neck length	5213	0.560	0.176	5211	0.560	0.180	5194	0.541	0.182
NS	neck setting	5038	0.552	0.352	5039	0.543	0.378	4990	0.529	0.358
WL	withers length	5194	0.630	0.224	5199	0.613	0.266	5012	0.552	0.242
SB	shoulder blade	5099	0.741	0.331	5105	0.736	0.360	5104	0.713	0.366
Body and hindquarters										
TL	topline length	5271	0.499	0.156	5269	0.499	0.156	5257	0.470	0.185
TF	topline form	5265	0.357	0.132	5263	0.355	0.140	5294	0.354	0.138
LL	loin length	5258	0.353	0.150	5257	0.352	0.159	5250	0.341	0.163
LF	loin form	5296	0.207	0.128	5294	0.207	0.128	5260	0.198	0.136
BW	body width	5227	0.775	0.287	5225	0.773	0.291	5245	0.773	0.283
CL	croup length	5149	0.555	0.329	5148	0.546	0.350	5132	0.528	0.352
CS	croup slope	5243	0.535	0.262	5243	0.534	0.271	5220	0.502	0.293
SC	shape of croup	5245	0.595	0.176	5245	0.595	0.175	5264	0.584	0.184
Limbs										
FO	foretoes	5293	0.484	0.080	5295	0.475	0.110	5334	0.474	0.112
FH	forehoof	5274	0.314	0.100	5272	0.314	0.101	5295	0.312	0.100
HLP	hind limbs posture	5190	0.564	0.371	5188	0.564	0.371	5193	0.555	0.369
FT	fetlock	5177	0.324	0.138	5177	0.321	0.155	5198	0.319	0.158
BH	back hoof	5140	0.222	0.181	5138	0.182	0.181	5167	0.181	0.185
Movement										
LW	length of walk	5005	0.836	0.244	5011	0.824	0.277	5012	0.801	0.281
LT	length of trot	5045	0.829	0.245	5049	0.814	0.278	5027	0.789	0.274

Table 5. Estimations of variance components by Model 3 without and with inclusion of inbreeding depression

Trait	Characteristic	Model without F_x				Model with F_x			
		σ_a^2	σ_e^2	h^2	s_h^2	σ_a^2	σ_e^2	h^2	s_h^2
Body measures									
WHS	withers height – stick	7.62	6.23	0.55	0.05	7.63	6.23	0.55	0.05
WHT	withers height – tape	9.96	8.35	0.54	0.05	10.06	8.28	0.55	0.05
CC	chest circumference	37.74	68.45	0.36	0.05	37.87	68.14	0.36	0.05
CBC	cannon bone circumference	0.44	0.35	0.55	0.05	0.44	0.35	0.55	0.05
Comprehensive character									
TY	type	0.26	1.00	0.21	0.04	0.27	1.00	0.21	0.04
FR	frame	0.17	0.55	0.23	0.04	0.17	0.55	0.24	0.04
NO	nobility	0.22	0.74	0.23	0.04	0.22	0.75	0.23	0.04
Forehand									
NL	neck length	0.12	0.54	0.18	0.03	0.12	0.54	0.18	0.03
NS	neck setting	0.30	0.52	0.36	0.04	0.30	0.53	0.36	0.04
WL	withers length	0.18	0.55	0.24	0.03	0.17	0.56	0.24	0.03
SB	shoulder blade	0.41	0.71	0.36	0.04	0.41	0.71	0.37	0.04
Body and hindquarters									
TL	topline length	0.11	0.47	0.19	0.04	0.11	0.47	0.19	0.04
TF	topline form	0.06	0.35	0.14	0.03	0.05	0.36	0.13	0.03
LL	loin length	0.07	0.34	0.16	0.04	0.07	0.34	0.16	0.04
LF	loin form	0.03	0.20	0.14	0.03	0.03	0.20	0.14	0.03
BW	body width	0.30	0.77	0.28	0.05	0.29	0.78	0.27	0.05
CL	croup length	0.29	0.53	0.35	0.04	0.30	0.52	0.37	0.04
CS	croup slope	0.21	0.50	0.29	0.04	0.21	0.50	0.29	0.04
SC	shape of croup	0.13	0.58	0.18	0.04	0.12	0.59	0.17	0.04
Limbs									
FO	foretoes	0.06	0.47	0.11	0.03	0.06	0.47	0.11	0.03
FH	forehoof	0.03	0.31	0.10	0.03	0.03	0.31	0.10	0.03
HLP	hind limbs posture	0.32	0.55	0.37	0.04	0.33	0.55	0.37	0.04
FT	fetlock	0.06	0.32	0.16	0.03	0.06	0.32	0.16	0.03
BH	back hoof	0.04	0.18	0.19	0.03	0.04	0.18	0.19	0.03
Movement									
LW	length of walk	0.31	0.80	0.28	0.04	0.31	0.80	0.28	0.03
LT	length of trot	0.30	0.78	0.27	0.04	0.30	0.78	0.28	0.04

With regard to the standard error of heritability coefficient (s_h^2) (Table 5), the estimated values of the heritability coefficients showed high statistical significance ($P < 0.01$). The high and intermediate values of the heritability coefficients document that correction breeding for linear type description of conformation and type characters using genetic information can be very efficient. Molina et al. (1999)

estimated an identical value of h^2 for WHS (0.58) but a higher value of h^2 for BW (0.56) in Andalusian horses. Zechner et al. (2001) also estimated similar values for heritability coefficients for WHS (0.58) in Lipizzan horses but a lower value of h^2 for NL (0.05) and CC (0.25). Similarly to the preceding authors, Baban et al. (1998) calculated lower heritability coefficient values for CC (0.18) and WHS (0.25). Fioretti et al. (2005) reported lower values of h^2 for NS (0.22) in Bardigiano horses, but they estimated a higher value of h^2 for HW (0.64). Van Bergen and Van Arendonk (1993) published identical values of h^2 for SLW (0.27). Jakubec et al. (2009) also calculated identical values of h^2 for linear description of conformation and type characters in the Old Kladruber horse breed. However, Samoré et al. (1997) reported lower values of h^2 for SLW (0.19). These differences may be explained by the fact that the traits were evaluated in different breeds and in various countries.

Table 6 shows that the inclusion of inbreeding depression led to an insignificant change in σ_a^2 for 10 traits. There was a decrease in σ_a^2 for 5 traits, and there was an increase in σ_a^2 for another 5 traits. In the remaining 16 traits, the inclusion of fixed regression on F_x did not influence the value of σ_a^2. Similarly to σ_a^2, there was a minimum change in σ_a^2 for 9 traits and a moderate change in h^2 for 8 traits. A decrease in the value of σ_a^2 was determined in 3 traits while σ_a^2 increased in the remaining 6 traits. The value of h^2 also decreased in 3 traits and increased in 5 traits. The increase in h^2 was caused by a decrease in σ_a^2 and a simultaneous increase in σ_a^2. Because the influence of inbreeding depression on the estimation of σ_a^2 and σ_a^2 was minimal, it was not necessary to include it in the model.

Table 6. The influence of inbreeding depression with 1% increase in F_x

Traits	Characteristic	F_x
Body measures (cm)		
WHS	withers height – stick	–0.0250
WHT	withers height – tape	–0.0992
CC	chest circumference	–0.0255
CBC	cannon bone circumference	–0.0044
Comprehensive character (points)		
TY	type	0.0008
FR	frame	0.0232
NO	nobility	–0.0219
Forehand		
NL	neck length	0.0063
NS	neck setting	0.0004
WL	withers length	0.0134
SB	shoulder blade	0.0036
Body and hindquarters		
TL	topline length	0.0032
TF	topline form	0.0030
LL	loin length	–0.0018
LF	loin form	–0.0035
BW	body width	–0.0191
CL	croup length	–0.0340
CS	croup slope	0.0175
SC	shape of croup	–0.0193
Limbs		
FO	foretoes	–0.0050
FH	forehoof	–0.0029
HLP	hind limbs posture	0.0242
FT	fetlock	0.0133
BH	back hoof	–0.0083
Movement		
LW	length of walk	–0.0226
LT	length of trot	–0.0313

Genetic correlations

Table 7 shows genetic correlations (r_G) among all evaluated traits (26). First, genetic correlations within the six groups of traits were described including body measurements, comprehensive character, forehand, body and hindquarters, limbs and movement. Next, correlations among traits from different groups were presented.

Strong genetic correlations among the measurements were estimated for the group of body measurements, especially between WHS and WHT (0.97). This high value of r_G is caused by the fact that WHS and WHT were two expressions of the same trait: height at withers expressed by two different methods. No correlation was determined in the comprehensive character traits with the exception of RA and NO (r_G = –0.02 and 0.03). A weak genetic correlation was estimated (r_G = 0.20) for the

Table 7. The genetic correlation matrix estimated by a model without inbreeding depression (above diagonal) and by a model with inbreeding depression (below 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	–	0.97	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	0.98	–	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	0.70	0.76	–	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	0.68	0.67	0.53	–	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	0.61	0.66	0.47	0.46	–	−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	−0.14	−0.29	−0.14	0.12	−0.02	–	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	−0.11	−0.20	−0.11	−0.21	0.04	0.20	–	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	0.11	0.26	0.53	−0.01	0.28	0.46	0.16	–	−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	−0.17	−0.19	−0.21	0.06	−0.03	0.34	−0.05	−0.27	–	−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	0.40	0.36	0.38	0.27	0.38	0.41	−0.13	0.45	−0.02	–	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	0.02	0.06	−0.02	0.09	0.20	0.38	−0.46	0.29	0.37	0.44	–	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	0.11	−0.09	0.01	0.29	0.01	0.81	0.01	0.35	0.30	0.46	0.53	–	−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	0.55	0.51	0.27	0.28	0.70	−0.23	−0.25	0.60	−0.28	0.56	0.47	−0.16	–	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	0.02	0.12	0.10	0.37	0.31	0.47	−0.49	0.41	0.37	0.62	0.66	0.71	0.20	–	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	0.39	0.28	0.13	−0.08	0.26	−0.48	−0.34	0.19	0.07	0.20	0.37	−0.16	0.65	0.33	–	0.37	0.34	0.13	−0.37	0.11	0.43	0.14	0.63	0.92	−0.27	−0.02
BW	0.18	0.38	0.56	0.34	0.62	−0.18	−0.34	0.05	0.08	0.14	0.24	0.04	0.29	0.22	0.41	–	0.26	−0.21	0.58	0.09	0.21	0.16	0.21	0.26	−0.24	−0.13
CL	0.20	0.15	0.22	0.38	0.12	0.41	−0.32	0.32	0.39	0.44	0.70	0.41	0.37	0.38	0.34	0.26	–	0.18	0.13	−0.32	0.59	0.46	0.23	0.33	−0.25	−0.13
CS	−0.13	−0.06	−0.29	0.04	−0.40	−0.03	−0.18	−0.46	0.25	−0.09	0.27	−0.13	−0.07	−0.31	0.12	−0.19	0.17	–	−0.08	0.26	0.17	0.39	0.23	−0.27	−0.05	0.15
SC	0.11	0.27	0.59	0.36	0.36	0.21	0.41	0.14	0.03	−0.05	0.18	0.28	−0.13	−0.30	−0.33	0.55	0.15	−0.05	–	0.06	−0.01	0.09	−0.08	−0.63	0.26	0.26
FO	0.08	−0.12	−0.06	0.14	0.22	−0.28	−0.03	−0.55	0.39	−0.15	−0.16	−0.35	−0.43	−0.21	0.11	0.11	−0.29	0.25	0.08	–	−0.19	0.25	0.85	0.06	−0.27	−0.03
FH	−0.01	0.03	−0.08	−0.11	0.22	0.32	−0.40	0.56	0.18	0.52	0.72	−0.06	0.56	0.30	0.43	0.23	0.57	0.17	0.01	−0.19	–	0.08	0.41	0.64	−0.40	0.07
HLP	0.22	0.16	0.11	0.39	−0.04	0.35	−0.34	0.11	0.28	0.18	0.26	0.46	0.06	0.38	0.13	0.17	0.44	0.39	0.11	0.24	0.08	–	0.45	0.23	0.07	0.03
FT	−0.25	−0.26	−0.02	−0.05	0.06	0.04	−0.52	−0.08	0.38	0.12	0.24	0.40	0.23	0.31	0.60	0.24	0.21	0.22	−0.06	0.84	0.41	0.45	–	0.56	−0.34	−0.26
BH	−0.01	0.12	0.24	−0.05	0.40	−0.14	−0.44	0.52	0.14	0.41	0.42	0.07	0.33	0.61	0.93	0.28	0.33	−0.28	−0.63	0.06	0.64	0.22	0.56	–	−0.67	−0.47
LW	0.16	0.03	−0.03	−0.03	−0.01	0.15	0.63	0.06	−0.46	−0.27	−0.33	0.02	−0.10	−0.30	−0.26	−0.25	−0.23	−0.05	0.28	−0.26	−0.40	0.07	−0.34	−0.66	–	0.83
LT	0.14	0.06	−0.13	−0.02	0.11	−0.01	0.32	0.05	−0.35	−0.04	−0.05	−0.19	0.14	−0.20	0.01	−0.12	−0.11	0.15	0.30	−0.01	0.07	0.03	−0.27	−0.45	0.83	–

traits FR and NO. A higher occurrence of strong correlations (absolute value > 0.5) was determined for the forehand traits compared to the comprehensive character traits. The highest genetic correlation value in the forehand traits was estimated between NL and WL (0.46) and WL and SB (0.44) while the lowest value was calculated between NL and NS (–0.27). Intermediate and higher genetic correlation values were also found in the body and rear traits. The highest value was estimated between LL and TL ($r_G = 0.70$). The lowest value was estimated between CS and TF ($r_G = –0.40$). For the body and rear traits, r_G mostly assumed intermediate absolute values. In the limbs trait, similarly to the body and rear traits, low to intermediate genetic correlation values were determined. The highest genetic correlation value in the legs trait was estimated between FT and FO ($r_G = 0.85$). The high value of r_G (0.83) between the movement traits [length of walk (LW) and length of trot (LT)] is of physiological origin because horses with spaciousness of pace usually have spaciousness of gallop.

Genetic correlations among the body measurement traits and other groups, with the exception of TY, showed an intermediate level of correlations. The traits of different groups showed weak to intermediate genetic correlations between other groups for most traits.

A high incidence of correlation among the particular traits (absolute value of $r_G > 0.5$) in linear type description of conformation and type characters was recorded in 42 cases (13%). The highest values were determined primarily in body measurements, specifically between WHS and WHT (0.97). A high value of r_G was also observed between BH and LF (0.92), FT and FO (0.85), SLT and SLW (0.83) and TL and FR (0.82). Intermediate values of r_G (absolute value $0.5 > r_G > 0.3$) were estimated for 84 traits of linear type description of conformation and type characters (27%). The lowest r_G value was determined between SLW and BH (–0.67). Estimations of genetic correlations among the described traits corresponded to biological relationships among the studied traits. The estimated high and intermediate values of r_G in a large number of described traits (40%) could be used as a strong metric for the definition of selection criteria because of the possibility for indirect improvement in correlated traits without direct inclusion of the traits in a selection programme. Genetic correlations for identical traits were often studied in the other breeds of horses. Koenen et al. (1995) estimated similar relationships among the linear type descriptions of conformation and type characters in the Dutch Warmblood Riding Horse population. Van Bergen and Van Arendonk (1993) published higher genetic correlation values in identical traits in Shetland ponies. These differences may be caused by the fact that the traits were evaluated in different breeds and in various countries.

The inclusion of the inbreeding depression effect in the model resulted in a minimal increase in the value of r_G in 34% of traits, and a minimal decrease in r_G among the traits in 35% (by approximately 0.01).

Inbreeding depression

The regression coefficient values for the influence of inbreeding on the linear description of conformation and type characters estimated by the BLUP animal model are shown in Table 6. Data in the table documents that insignificant values of inbreeding depression were estimated for all traits. For all body measurements the influence of inbreeding depression led to an insignificant decrease in the value of the studied traits. The highest absolute value was recorded in WHT. In this trait, in comparison with WHS, not only the proper height of the animal is considered but also the chest circumference. That is why both factors are measured in this trait. In linear type description of conformation and type characters, a minimal influence of inbreeding depression was observed for 50% of the traits describing lower development, while in 50% of the traits a minimal influence of inbreeding depression was observed for higher development. The highest number of traits with a lower score on the scale was recorded in the groups of traits for body and back, legs and mechanics of movement. In contrast, the influence of inbreeding depression on the traits with higher scores was dominant in the front and comprehensive character traits. Inbreeding depression had the greatest influence on the linear type description of conformation and type characters of body measurements, FR and mechanics of movement. These results confirm that inbreeding depression mostly influences the traits of body morphology rather than the traits describing the particular body parts. The estimated insignificant values of inbreeding depression indicate that the traits of body measurements and linear type description of conformation and type characters may be influenced by inbreed-

Table 8. Breeding values and Spearman's rank coefficient of correlation among the breeding values of all horses, 10% of the best and 10% of the worst horses as estimated by models with and without inbreeding depression

Traits	Breeding values without F_x			Breeding values with F_x			Correlation between models with and without F_x			
	SD	min.	max.	SD	min.	max.	all	10% of		animals with F_x > 0.1 and with measurement
								best	worst	
Body measures										
WHS	2.58	–13.35	12.94	2.58	–13.45	12.66	0.983	0.988	0.983	0.927
WHT	2.94	–11.29	13.51	2.94	–11.37	13.83	0.976	0.965	0.969	0.997
CC	6.18	–25.83	28.12	6.13	–22.65	27.84	0.987	0.968	0.956	0.964
CBC	0.62	–1.66	2.66	0.63	–1.66	2.70	0.995	0.992	0.992	0.997
Comprehensive character										
TY	0.72	–4.62	7.65	0.72	–4.64	6.49	0.989	0.953	0.979	0.998
FR	0.57	–2.28	8.12	0.56	–2.23	7.16	0.991	0.968	0.966	0.997
NO	0.51	–2.30	1.65	0.52	–2.26	1.72	0.982	0.973	0.963	0.995
Forehand										
NL	0.46	–1.96	1.52	0.45	–1.94	1.53	0.998	0.986	0.985	0.996
NS	0.63	–2.37	2.64	0.63	–2.32	2.63	0.999	0.991	0.984	0.997
WL	0.52	–1.91	3.02	0.52	–1.84	3.06	0.997	0.987	0.982	0.983
SB	0.71	–1.39	3.47	0.71	–1.41	3.45	0.997	0.997	0.994	0.999
Body and hindquarters										
TL	0.41	–2.19	1.90	0.41	–2.18	1.90	0.999	0.990	0.994	0.999
TF	0.33	–1.78	1.55	0.32	–1.78	1.55	0.998	0.983	0.989	0.998
LL	0.34	–1.65	1.75	0.35	–1.63	1.76	0.997	0.981	0.962	0.997
LF	0.24	–1.80	1.55	0.24	–1.79	1.54	0.995	0.964	0.983	0.994
BW	0.62	–3.48	2.38	0.62	–3.55	2.06	0.983	0.830	0.856	0.990
CL	0.61	–3.66	2.05	0.59	–3.52	2.36	0.987	0.951	0.966	0.994
CS	0.48	–2.45	1.67	0.48	–2.50	1.55	0.995	0.953	0.980	0.997
SC	0.44	–2.36	1.80	0.43	–2.33	1.82	0.988	0.944	0.958	0.999
Limbs										
FO	0.37	–3.02	2.16	0.37	–2.94	2.22	0.992	0.971	0.977	0.998
FH	0.30	–1.57	2.18	0.29	–1.55	2.18	0.994	0.995	0.998	0.999
HLP	0.58	–2.67	2.57	0.57	–2.94	2.56	0.993	0.970	0.979	0.997
FT	0.42	–6.88	6.95	0.41	–6.91	6.41	0.993	0.975	0.974	0.996
BH	0.32	–4.30	1.71	0.27	–3.25	1.79	0.916	0.710	0.827	0.902
Movement										
LW	0.64	–2.29	2.32	0.64	–2.26	2.29	0.991	0.954	0.963	0.996
LT	0.59	–2.75	2.48	0.60	–2.79	2.49	0.993	0.919	0.964	0.997

ing depression, but in this analysis, it produces only a minimal influence. However, this inconsiderable influence may be caused by the low F_x coefficient value in this analysed population of cold-blooded horses because the average F_x value within breeds was estimated for the year 2007 in the interval of 1.5% to 3.5% (Vostrý et al., 2011b).

Studies describing a significant influence of inbreeding depression on traits that are not associated with fitness and/or reproduction are scarce. Similarly to this study, Curik et al. (2003) in the Lipizzan breed and Wolc and Balińska (2010) in the Polish Konik breed did not find any influence of inbreeding depression on the morphological traits of horses. However, a significant influence of inbreeding depression on morphological traits was observed in Italian Haflinger horses (Gandini et al., 1992), in Polish Arabian stallions (Sierszchulski et al., 2005) and in Spanish Andalusian horses (Gómez et al., 2009). The significant influence of inbreeding depression reported by the latter author (Gandini et al., 1992; Gómez et al., 2009) maybe due to a higher number of horses included in the analysis.

Breeding value

Subsequently, breeding values were estimated for the linear description of conformation and type characters. Table 8 documents standard deviations, minimums and maximums of the particular breeding values of linear description of conformation and type characters. The standard deviations for breeding values ranged from 0.24 (LF) to 0.72 (TY). The standard deviations for body measurements ranged from 0.62 (CBC) to 6.18 (CC). The variability of breeding values corresponded to h^2 values. The lowest variance in breeding values was determined in traits with low h^2 values. On the other hand, the highest variances in breeding values were calculated for traits with the highest h^2 value. Maximum and minimum breeding values corresponded to these relationships. Similar standard deviations of breeding values for morphological traits in the Haflinger breed were reported by Samoré et al. (1997). As shown in Table 8, the inclusion of inbreeding depression in the model did not significantly influence the estimated breeding values. If inbreeding depression was taken into account, a minute change occurred in the standard deviation and minimum and maximum value of breeding values for only 10 traits.

Breeding values for the linear type description of conformation and type characters estimated by a model without and with inbreeding depression were compared on the basis of Spearman's rank correlation coefficients. When all horses were included, the correlation coefficients showed high correlation values (0.97–0.99). The trait SB was an exception, in which a lower correlation coefficient was estimated (0.92). However, lower correlation coefficient values were estimated in a subpopulation sample of the best and the worst 10% of horses based on the breeding value estimation. In the sample of the 10% of the best horses, correlation coefficients were in the range of 0.71–0.99. More pronounced differences were observed in the sample of the 10% of the worst horses. In this group, no pronounced decrease in the correlation coefficient values was estimated, but a decrease was determined for the majority of the linear type description of conformation and type characters. The lower correlation coefficient in both groups was recorded again in the traits that were influenced by inbreeding depression to a greater extent when compared to other traits (WHT, CC, FR, SLW and SLT). Although some changes in the estimation of breeding value were revealed by correlation analysis with the inclusion of inbreeding depression, these changes were not significant. Most values of the rank correlation coefficient were higher than 0.95. Corresponding rank correlation values were also estimated in the group of horses in which the F_x value was higher than 10% (Table 8). The majority of all correlations (98%) showed a value higher than 0.99. The lowest correlation coefficient values were calculated for BH, but this trait was not the trait with the lowest influence of inbreeding depression (Table 5). These conclusions demonstrated that inbreeding depression did not have a significant influence on the ranking of horses for the estimation of breeding value.

CONCLUSION

The results document that Model 3, which did not incorporate the random effect of the line and contained the fixed effect of year of description, was found to be the most suitable for the estimation of genetic parameters and breeding value for the linear description of conformation and type characters. The linear description of conformation and type characters showed low to intermediate values for heritability.

Inbreeding depression does not influence the morphological features of the body of cold-blooded horses. The inclusion of inbreeding coefficient of a horse in the model did not markedly influence the ranking of horses in the estimation of breeding value. The inclusion of inbreeding depression in the model did not contribute to any significant changes in the values of genetic parameters. For these reasons, it is not necessary to include the influence of inbreeding depression in the model for the genetic evaluation of horses of cold-blooded breeds kept in the Czech Republic.

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