

Genetic Parameters for Linear Type Traits in Three Czech Draught Horse Breeds

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Summary

Horse conformation is considered an indicator of performance, which plays an important role in breeding decisions. Genetic parameters were estimated for linear type traits in three draught horse breeds – Czech-Moravian Belgian horse, Silesian Noriker and Noriker. Traits were divided in six groups according to the region of the body. Observations on 946 Czech Moravian Belgian horses, 574 Silesian Norikers and 640 Norikers were analysed using a multi breed multitrait animal model. Fixed effects of sex, age at scoring, breed and contemporary group were considered. Genetic parameters were estimated using restricted maximum likelihood. Estimated heritability ranged from 0.05 to 0.59. Lowest values were estimated for stance of back pasterns and shape of back feet, while highest values were found for body measures. Estimations of genetic correlation between traits ranged from -0.53 to 0.98. The highest correlation was found between length of stride in walk and length of stride in trot. The estimated heritabilities and correlations suggest that a genetic improvement of analysed traits is feasible.

Key words

linear scoring of conformation, cold-blooded horses, genetic parameters

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Received: May 1, 2017 | Accepted: July 31, 2017

ACKNOWLEDGEMENTS

This work was financially supported through a grant from the Ministry of Agriculture of the Czech Republic (Project no. QJ1510141).

Introduction

The Silesian Noriker (SN), Czech-Moravian Belgian (CMB) draught horse breeds, along with the Old Kladruber and Hutsul horse, belong to a group of endangered horse breeds recognized as Genetic Resources in the Czech Republic (CR). Over the last 120 years, the CMB breed was developed in the CR territory primarily using imported Belgian stallions and, to a lesser extent, Walloons. CMB horses have a medium square body shape and mature earlier than other typical draught breeds. The SN breed was developed over the last 100 years from imported Noriker stallions and Bavarian draught stallions. SN horses have a longer than average body shape and are a late maturing individuals. Another draught breed maintained on a large scale in the CR territory is the Noriker (N), which contributed to the generation of the SN breed and has been continuously maintained in the CR territory for 150 years. To a large extent, the SN and CMB breeds have been geographically separated. At the age of three years, stallions and mares are selected based on pedigree information, performance test and conformation. Linear scoring system provides an objective description of an animal's conformation and movement. Information on scoring for different type and conformation traits at the individual itself and related animals can be included into a breeding value prediction, which is an useful selection tool, especially in stallions. For the prediction of breeding values, knowledge of genetic parameters is required.

Linear scoring of conformation and type characteristics is routinely used, mainly in cattle, where a number of analyses were previously carried out (Brotherstone, 1994; Veselá et al., 2005). Body conformation in horses was evaluated by point systems in the past, linear scoring was introduced more recently. The linear scoring of conformation and type characteristics and the description of morphological features in horse breeds were studied for example by Jakubec et al. (2007) in the Old Kladruber horse, Maršálek et al. (1999) in Czech warmblood horse breeds, Zechner et al. (2001) in Lipizzan horses and Molina et al. (1999) in Andalusian horses. 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.

The objective of this study was to estimate genetic parameters for body measures and conformation traits assessed by linear scoring system in three draught horse breeds (Czech-Moravian Belgian, Silesian Noriker and Noriker) kept in the Czech Republic.

Material and methods

A total of 946 individuals of Czech-Moravian Belgian horse, 574 individuals of Silesian Noriker and 640 individuals of Noriker breed scored in the years 1996 – 2014 were included in the analysis. The database has been provided by the Horse Breeder's Association of the Czech Republic (ASCHK, www.aschk.cz). A total of 22 conformation traits have been scored using linear scale from 1 to 9: Type, Body shape, Nobility, Length of the neck, Position of the neck, Length of the withers, Shape of the scapula, Length of the back, Line of the back, Length of the loins, Line of the loins, Length of the croup, Shape of the croup (side view), Shape of the croup (back view), Body width, Shape of front feet,

Stance of front pasterns, Stance of hindlegs, Stance of back pasterns, Shape of back feet, Walk: length of stride, Trot: length of stride. The traits were divided into five groups according to body part (Table 1). Except the above mentioned traits, there were also four body part measures (cm) included in the analysis - withers height (stick), withers height (tape), chest circumference and circumference of front cannon bone.

The DMU computer programme (Madsen and Jansen, 2009) was used for the estimation of the variance-covariance components and their standard errors. Genetic parameters were estimated according to the following model for all breeds:

$$Y_{ijklm} = \mu + \text{SEX}_i + \text{AGE}_j + \text{BREED}_k + \text{CG}_l + a_m + e_{ijklm}$$

where: Y_{ijklm} is record of a linear scored trait, μ is overall mean, SEX_i is fixed effect of the i -th sex (i = stallions or mare), AGE_j is fixed effect of the k -th age of evaluation (in years) ($k=3, \dots, 14$), BREED_k is fixed effect of the k -th breed (k = Czech-Moravian Belgian, Silesian Noriker and Noriker), CG_l is fixed effect of the contemporary group (year of scoring \times place of scoring \times classifier) ($l = 1, \dots, 204$), a_m is random effect of the m -th horse ($m = 7081$) and e_{ijklm} is random residual error.

It is assumed that the effects are mutually independent within the particular traits. It is further assumed that the effects have a normal distribution with zero mean and variance σ^2 : $V(a) = A\sigma_a^2$, $V(e) = I\sigma_e^2$, where σ_a^2 is the additive genetic variance of the direct effect, σ_e^2 is the variance of the effect of residual error, A is the relationship matrix, and I is the identity matrix. The influence of the maternal effect on the body conformation of an individual was not included in the analysis due to the low number of individuals per mare. The pedigree set contained 5 generations of ancestors and 7081 individuals.

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

Results and discussion

Table 1 documents the estimations of genetic parameters. Heritability coefficient value higher than 0.50 was estimated only in 1 out of 26 traits (4%), values from 0.30 to 0.50 in 3 traits (12%) and values from 0.10 to 0.30 were calculated in 18 traits (69%). The highest heritability coefficient values were determined for body measures – withers height (stick), withers height (tape) and circumference of the front cannon bone ($h^2 = 0.59, 0.45, \text{ and } 0.43$ respectively). This illustrates the fact that traits, which are not transformed to the linear scoring scale, are not influenced by subjectivity as is present in scored traits. This subjectivity significantly affects the level of residual errors in estimation of genetic parameters. The lowest heritability coefficient values were found for shape of back feet (0.05) and stance of back pasterns (0.06). With regard to the standard errors of heritability coefficients (Table 1), the estimated values of heritability coefficients showed high statistical significance ($P < 0.05$) for most of the traits except stance of back pasterns and shape

Table 1. Estimation of genetic parameters with standard errors (in brackets)

Trait	σ_a^2	σ_e^2	σ_y^2	h^2
Body measures				
1 Withers height (stick)	8.280 (1.106)	5.817 (0.758)	14.097	0.587 (0.045)
2 Withers height (tape)	7.652 (1.239)	9.354 (0.924)	17.006	0.450 (0.047)
3 Chest circumference	34.120 (6.385)	60.100 (5.063)	94.220	0.362 (0.047)
4 Circumference of the front cannon bone	0.289 (0.047)	0.388 (0.036)	0.678	0.427 (0.046)
Comprehensive characteristics				
5 Type	0.207 (0.064)	1.034 (0.062)	1.242	0.167 (0.044)
6 Body shape	0.104 (0.030)	0.507 (0.029)	0.611	0.170 (0.041)
7 Nobility	0.069 (0.033)	0.748 (0.037)	0.817	0.084 (0.038)
Forehand				
8 Length of the neck	0.085 (0.026)	0.475 (0.026)	0.560	0.152 (0.040)
9 Position of the neck	0.146 (0.034)	0.491 (0.031)	0.637	0.229 (0.043)
10 Length of the withers	0.060 (0.024)	0.539 (0.026)	0.599	0.100 (0.036)
11 Shape of the papula	0.088 (0.035)	0.783 (0.039)	0.871	0.101 (0.036)
Body and hindquarters				
12 Length of the back	0.086 (0.026)	0.475 (0.026)	0.562	0.153 (0.040)
13 Line of the back	0.044 (0.015)	0.342 (0.017)	0.386	0.115 (0.036)
14 Length of the Loir	0.058 (0.018)	0.355 (0.019)	0.413	0.141 (0.039)
15 Line of the loins	0.027 (0.011)	0.225 (0.012)	0.252	0.106 (0.039)
16 Length of the croup	0.092 (0.030)	0.542 (0.030)	0.634	0.145 (0.041)
17 Shape of the croup (side view)	0.094 (0.030)	0.531 (0.030)	0.625	0.150 (0.041)
18 Shape of the croup (back view)	0.073 (0.026)	0.476 (0.026)	0.549	0.133 (0.041)
19 Body width	0.168 (0.051)	0.839 (0.050)	1.008	0.167 (0.043)
Limbs				
20 Shape of front feet	0.061 (0.023)	0.454 (0.024)	0.515	0.118 (0.040)
21 Stance of front pasterns	0.031 (0.015)	0.321 (0.016)	0.352	0.088 (0.038)
22 Stance of hindlegs	0.203 (0.045)	0.580 (0.039)	0.783	0.259 (0.044)
23 Stance of back pasterns	0.019 (0.013)	0.337 (0.016)	0.356	0.053 (0.035)
24 Shape of back feet	0.010 (0.007)	0.185 (0.009)	0.194	0.049 (0.034)
Movement				
25 Walk: length of stride	0.166 (0.046)	0.710 (0.044)	0.876	0.190 (0.043)
26 Trot: length of stride	0.243 (0.054)	0.730 (0.048)	0.973	0.250 (0.043)

σ_a^2 is the additive genetic variance of the direct effect, σ_e^2 is the variance of the effect of residual error, σ_y^2 is the phenotype variance and h^2 is coefficient of heritability

of back feet. Jönsson et al. (2014) in Swedish warmblood horse and Vicente et al. (2014) estimated higher value of h^2 for withers height (0.67 and 0.61) and Jönsson et al. (2014) estimate higher value of h^2 for cannon bone circumference (0.55). Molina et al. (1999) estimated higher value of h^2 for chest circumference (0.48) in Andalusian horse. Jakubec et al. (2009) also calculated similar values of h^2 for conformation and type characteristics in the Old Kladruber horse breed. The differences may be explained by the fact that the traits were evaluated in different breeds and in various countries. The high and intermediate values of heritability coefficients suggest that corrective mating for conformation and type characteristics using genetic information can be very efficient.

In the next step the genetic correlations were estimated between analysed traits (Table 2). Most of the estimated genetic correlations were not statistically different from zero. Strong genetic correlations between body measures were estimated, especially between withers height - stick (WHS) and withers height - tape (WHT). The high value of r_G (0.97) is caused by the fact that WHS and WHT are actually the same traits measured by two different methods. The second highest value of genetic correlation (0.94) was estimated between length of stride in walk and length of stride in trot. On the contrary, the lowest absolute

value of genetic correlation (0.02) was estimated between nobility and length of the loin. The higher value of genetic correlation were estimated within six groups of traits. Lower values of genetic correlation were estimated between these groups. The estimated genetic correlations of traits within and between the described groups of traits correspond to the biological relationships between the traits studied. It can generally be said that estimated genetic correlation showed weak to intermediate as positive or negative dependencies. Only 15% of the genetic correlations showed a value of less than 0.10. 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 characteristics in the Dutch Warmblood Riding Horse population. Van Bergen and Van Arendonk (1993) published higher genetic correlation values for identical traits in Shetland ponies.

Estimations of variance components for linear type traits are needed for breeding values prediction, to set up selection programmes and to improve classification systems. Some traits show high genetic correlations (withers height - stick and withers height - tape or length of stride in walk and length of stride in trot). This fact gives a possibility to reduce the number of traits used as selection criteria. The estimation of genetic parameters

Table 2. Genetic correlations between analysed traits

Traits	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26
1	1	0.979	0.374	0.599	0.146	-0.174	-0.430	0.204	-0.020	0.349	-0.156	0.190	-0.204	0.023	0.227	0.029	-0.062	-0.091	-0.382	-0.135	-0.371	-0.147	-0.015	0.035	0.204	0.363
2		1	0.578	0.650	0.685	-0.252	-0.502	0.010	-0.141	0.196	-0.183	-0.047	-0.164	-0.103	0.273	0.156	-0.188	-0.279	-0.320	-0.187	-0.272	-0.059	0.172	0.226	-0.027	0.256
3			1	0.359	0.444	0.170	-0.310	0.204	0.109	0.209	0.236	-0.517	0.116	0.070	0.570	-0.256	-0.720	-0.031	0.039	-0.134	0.359	0.337	0.630	0.435	-0.458	-0.240
4				1	0.490	0.265	-0.545	-0.212	-0.088	0.005	0.288	0.145	0.292	-0.061	0.514	0.006	0.138	0.363	-0.151	0.051	0.103	-0.013	0.315	0.160	0.150	0.272
5					1	-0.134	0.028	0.153	-0.093	0.424	-0.196	0.167	-0.109	-0.078	0.013	-0.034	0.016	0.118	0.197	-0.293	0.190	-0.242	0.010	0.251	0.312	0.411
6						1	-0.086	0.334	0.102	0.849	0.811	-0.473	0.637	-0.274	0.302	-0.473	0.425	-0.081	-0.071	0.409	0.181	-0.722	0.266	0.007	-0.172	-0.226
7							1	0.630	0.439	0.324	-0.075	-0.222	0.022	0.250	-0.169	-0.512	0.094	-0.180	0.179	-0.308	-0.307	0.077	-0.799	-0.532	0.025	-0.046
8								1	0.086	0.061	0.445	-0.118	0.181	0.493	0.136	-0.469	0.032	-0.261	-0.024	-0.150	0.082	0.328	-0.028	-0.438	0.225	0.229
9									1	0.045	0.153	-0.232	0.674	0.355	0.370	-0.250	0.254	0.250	-0.036	0.171	0.240	0.869	-0.048	-0.062	-0.349	-0.293
10										1	0.214	0.240	0.494	-0.358	0.387	-0.180	0.427	-0.012	-0.517	0.150	0.489	0.443	0.078	0.072	0.518	0.602
11											1	-0.437	0.840	0.042	0.552	-0.516	0.575	-0.223	-0.269	0.361	0.302	-0.525	0.493	0.352	-0.033	-0.160
12												1	-0.321	-0.026	-0.483	0.671	0.294	0.025	0.005	-0.175	-0.116	-0.149	-0.484	-0.286	0.236	0.694
13													1	-0.221	0.424	-0.560	0.560	-0.254	-0.711	0.480	0.056	0.143	0.293	0.013	0.072	-0.105
14														1	0.369	0.388	0.476	0.096	0.748	-0.181	0.836	0.823	0.561	0.055	-0.099	0.163
15															1	-0.464	0.014	-0.022	0.071	0.118	0.073	0.987	0.568	0.187	-0.163	-0.189
16																1	0.332	-0.103	-0.024	0.097	0.111	-0.765	-0.012	0.169	0.252	0.397
17																	1	0.226	0.152	0.139	0.152	-0.294	-0.220	0.398	0.206	0.268
18																		1	0.382	0.426	0.643	0.360	0.390	0.198	-0.411	-0.031
19																			1	0.040	0.397	0.487	0.589	0.292	-0.064	0.146
20																				1	0.270	0.271	0.132	-0.233	0.058	-0.045
21																					1	0.486	0.720	0.272	0.029	-0.020
22																						1	0.392	-0.220	0.073	0.102
23																							1	0.445	-0.317	-0.169
24																								1	-0.021	0.076
25																									1	0.944
26																										1

1 – Withers height (stick), 2 – Withers height (tape), 3 - Chest circumference, 4 - Circumference of the front cannon bone, 5 – Type, 6 – Body shape, 7 – Nobility, 8 - Length of the neck, 9 - Position of the neck, 10 - Length of the withers, 11 – Length of the back, 12 – Line of the back, 13 - Length of the loins, 14 – Line of the loins, 15 – Length of the croup, 16 – Shape of the croup (side view), 17 – Shape of the scapula, 18 - Shape of the front feet, 19 – Stance of front pasterns, 20 – Stance of hindlegs, 21 - Stance of back pasterns, 22 – Shape of back feet, 23 – Body width, 24 – Shape of the croup (back view), 25- Walk: length of stride, 26 - Trot: length of stride

done in this study should be followed by a prediction of breeding values, at least for stallions because they are subjected to strict selection to the largest extent. Furthermore, it can be concluded that the data collected from linear scoring can be used to estimate breeding values for stallions. However, breeding values can be published only for males with a certain number of offspring to guarantee an adequate accuracy of estimates even for traits with low heritability.

Conclusion

Linear scoring of conformation and type traits is an essential in breeding programmes of Czech draught horses to preserve the specificity of the breeds in future generations. Linear scoring is an effective tool to pursue a breeding objective with respect to conformation. The results revealed that the traits of linear scoring in the Czech draught horses showed low to medium heritability. The only exceptions were the withers height – stick, the withers height – tape and the circumference of the front cannon bone ($h^2 = 0.59, 0.45$ and 0.43). It is concluded that the data collected on type and conformation traits can be used to estimate breeding values for stallions. The selection for all 26 correlated traits is likely to be ineffective. The possibility to reduce the number of scored traits to enable effective breeding strategy will be discussed.

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