

Genetic evaluation of Hanoverian warmblood horses for conformation traits considering the proportion of genes of foreign breeds

WIEBKE SCHRÖDER, KATHRIN FRIEDERIKE STOCK and OTTMAR DISTL

Institute for Animal Breeding and Genetics, University of Veterinary Medicine Hannover (Foundation), Hannover, Germany

Abstract

Conformation data of in total 29053 Hanoverian warmblood mares were used to determine whether genetic evaluation for conformation in the Hanoverian could benefit from the inclusion of the proportion of genes of foreign breeds in the model. For our analyses, we considered all Hanoverian mares born from 1992 to 2005 with available studbook inspection data. Genetic parameters were estimated univariately for eight routinely scored conformation traits (head, neck, saddle position, frontlegs, hindlegs, type, frame, and general impression and development), and height at withers from studbook inspections, in a linear animal model using Residual Maximum Likelihood (REML). Genetic evaluation was subsequently performed using Best Linear Unbiased Prediction. To investigate the effect of correcting for the proportion of genes of foreign breeds, two different models were used for the analyses. In Model 1, the fixed effect age at studbook inspection, and the random effect date-place interaction were considered. In Model 2, proportions of genes of Thoroughbred, Trakehner and Holsteiner were additionally included as fixed effects. Heritabilities of analyzed conformation traits and withers height ranged in both models between 0.10 and 0.57, with standard errors of ≤ 0.01 . Pearson correlation coefficients determined between breeding values of corresponding traits using Model 1 and 2 were highly positive (>0.99), indicating little effect of the model on the results of genetic evaluation. According to the results using a model which includes the proportion of genes of Thoroughbred, Trakehner and Holsteiner as fixed effects will not relevantly improve genetic evaluation for conformation in the Hanoverian.

Keywords: horse, Hanoverian, genetic parameters, blood proportion, breeding values, conformation, type

Zusammenfassung

Genetische Evaluierung von Exterieurmerkmalen des Hannoveraners unter Berücksichtigung von Fremdgenanteilen

Untersucht wurde, ob die Berücksichtigung von Fremdgenanteilen ein Modell für genetische Analysen von Exterieurmerkmalen verbessern kann. Zu diesem Zweck standen Stutbuchaufnahmedaten von insgesamt 29053 Hannoveraner Stuten der Jahrgänge 1992 bis 2005 des Hannoveraner Verbandes zur Verfügung. Genetische Parameter wurden für

acht, routinemäßig bei Stutbuchaufnahmen beurteilte, Exterieurmerkmale (Kopf, Hals, Sattellage, Vorderhand, Hinterhand, Typ, Rahmen und Gesamteindruck und Entwicklung) sowie die Widerristhöhe univariat in einem linearen Tiermodell mittels Residual Maximum Likelihood geschätzt. Die Zuchtwertschätzung wurde anschließend mittels Best Linear Unbiased Prediction und der geschätzten Varianzen durchgeführt. Um die Auswirkungen einer Berücksichtigung von Fremdgenanteilen auf genetische Analysen prüfen zu können, wurden zwei unterschiedliche Modelle verwendet. In Modell 1 wurde das Alter bei Aufnahme ins Stutbuch als fixer Effekt und die Kombination aus Datum und Ort als zufälliger Effekt berücksichtigt. Ein zweites Modell wurde zusätzlich um die Genanteilklassen von Englischen Vollblut, Trakehner und Holsteiner als fixen Effekten erweitert. Heritabilitäten lagen in beiden Modellen zwischen 0,10 und 0,57 bei Standardfehlern $\leq 0,01$ für die analysierten Exterieurmerkmale sowie der Widerristhöhe. Die Zuchtwerte, geschätzt mit Modell 1 und Modell 2, waren hoch positiv miteinander korreliert (Korrelationskoeffizienten nach Pearson $> 0,99$). Zusammenfassend zeigen die Ergebnisse, dass eine Berücksichtigung von Fremdgenanteilen in einem Zuchtwertschätzmodell für Exterieurmerkmale des Hannoveraners keine wesentlichen Vorteile bringt.

Schlüsselwörter: Pferd, Hannoveraner, genetische Parameter, Blutanteile, Zuchtwerte, Exterieur, Typ

Introduction

Breeding aims of most European warmblood breeds are focused on performance, particularly on performance in dressage and show jumping, with some breeding organizations favouring either of the two riding disciplines (KOENEN *et al.* 2004). The evaluation of conformation traits is the main part of the studbook inspection and registration procedure for brood mares of most warmblood breeding associations. Positive genetic correlations between conformation traits and performance in equestrian sports have been shown in several, although not all genetic studies (e.g. HOLMSTRÖM and PHILIPSSON 1993, KOENEN *et al.* 1995, POSTA *et al.* 2007). Such results supported the common practice of indirect performance selection via selection for functional conformation. However, despite similar breeding aims with regard to performance, conformation is rather characteristic for the individual warmblood breeds. The amount of crossbreeding, with Arabians and Thoroughbreds which are typically used to increase nobility, may be one of the most important factors for breed-specific conformation. Recently, a model including breed classes was recommended for the estimation of breeding values for dressage traits in the horse population of Great Britain (STEWART *et al.* 2009). Because success in dressage is relevantly influenced by type and conformation of a horse (KOENEN *et al.* 1995), genetic evaluation for conformation may also benefit from considering proportions of genes of certain horse breeds. For the Hanoverian warmblood (Hanoverian), Thoroughbred, Trakehner, and the Holsteiner warmblood (Holsteiner) are most common stallions used for crossbreeding Hanoverian mares. Therefore the aim of this study was to determine whether genetic evaluation for conformation in the Hanoverian could benefit from inclusion of the proportion of genes of these three breeds.

Material and methods

Conformation data

Results of studbook inspections (SBI) from 1995 to 2008 of the Hanoverian Studbook Society (HSS), and pedigree information on the evaluated mares were made available by the HSS through the national ownership database (Vereinigte Informationssysteme Tierhaltung w.V., VIT) in Verden at the Aller, Germany.

Data included 29 053 Hanoverian mares, born between 1992 and 2005. At SBI a judging commission scores gaits (walk in hand, correctness as well as impetus and elasticity of gaits in walk and trot in hand) and conformation of the head (Head), the neck (Neck), the saddle position (Sad), the frontlegs (ConFL), the hindlegs (ConHL) as well as the type (Type), the frame (Frame), and the general impression and development (Dev) of the horse presented. Scores on a scale from 0 (not shown) to 10 (excellently shown) were assigned for each of these traits. In addition, height at withers (WH) is measured in cm. In the following, only the eight conformation-related traits and WH will be considered.

In the study period, the number of judged mares per year ranged between 1 773 and 2 222 (mean 2 075). Presented mares had a mean age of 3.79 ± 1.66 years (range 3 to 16). There were 182 places of SBI with on average 11.73 ± 12.44 (range 1 to 83) inspected mares per day and place.

Pedigree data

For the genetic analyses, four ancestral generations of all mares with SBI data were considered. The relationship matrix comprised 80 746 individuals, including 7 486 base animals. The 29 053 mares with SBI data descended from 1 079 sires and 1 706 maternal grandsires. The sires were on average represented by 26.91 ± 63.50 (range 1-998) horses, and maternal grandsires were on average represented by 17.02 ± 12.44 (range 1-704) horses.

The proportion of genes provided by Thoroughbred, Trakehner and Holsteiner stallions were calculated for the Hanoverian population using all available pedigree information. Details are described elsewhere (HAMANN and DISTL 2008). Mean (median) proportions of genes in the conformation evaluated Hanoverian mares were 0.58 (0.59) for the Hanoverian, 0.23 (0.20) for Thoroughbred, 0.07 (0.05) for Trakehner, and 0.05 (0) for the Holsteiner.

Statistical analyses and model development

The following effects were tested for their influence on distribution of conformation traits from SBI: Age at SBI as covariate or fixed effect (3-, 4- or ≥ 5 year old); evaluation year (individual years from 1995-2008), evaluation month (individual months), evaluation season (February through April, Mai through July, August through October, and November through January), and evaluation place (182 places) as fixed effects; combined date-place (2 476 levels) as random effect; proportion of genes (Hanoverian or Thoroughbred, Trakehner and Holsteiner) as covariate or fixed effect (low, moderate, and high proportion of genes of the respective breed).

Simple and multiple analyses of variance (ANOVA) were performed using the procedures GLM and MIXED of SAS, version 9.2, (SAS Institute 2010).

Model choice was based on the model fit test statistics and the significance tests. In the basic model (Model 1) age at SBI was considered as fixed effect, and the combined date-place was considered as random effect. In the extended model (Model 2) the proportions of Thoroughbred, Trakehner and Holsteiner genes in classes were additionally included as fixed effects. Given the uneven representation of breeds, boundaries were set independently for Thoroughbred (≤ 0.13 , > 0.13 and < 0.30 , ≥ 0.30), Trakehner (≤ 0.2 , > 0.2 and < 0.8 , ≥ 0.8), and Holsteiner (0.0, > 0.0 and < 0.3 , ≥ 0.3). Distributions of original trait values and residuals were analyzed including tests for normality using Kolmogorov-Smirnov statistics of the UNIVARIATE procedure of SAS.

Genetic analyses

Genetic parameters were estimated univariately in a linear animal model with REML (Residual Maximum Likelihood) using VCE-5, version 5.1.2 (Variance Component Estimation; KOVAC *et al.* 2003).

$$\text{Model 1: } Y_{imnop} = \mu + AGE_i + date \times place_{mn} + a_o + e_{imnop} \quad (1)$$

$$\text{Model 2: } Y_{ijklmnop} = \mu + AGE_i + TB_j + TRAK_k + HOL_l + date \times place_{mn} + a_o + e_{ijklmnop} \quad (2)$$

where Y_{imnop} is the conformation score or measured WH, μ is the model constant, AGE_i is the fixed effect of the i -th age group at SBI evaluation ($i=1-3$), TB_j is the fixed effect of the j -th class of proportion of Thoroughbred genes ($j=1-3$), $TRAK_k$ is the fixed effect of the k -th class of proportion of Trakehner genes ($k=1-3$), HOL_l is the fixed effect of the l -th class of proportion of Holstein warmblood genes ($l=1-3$), $date \times place_{mn}$ is the random effect of interaction between the m -th date of performance evaluation and n -th place of SBI, a_o is the random additive genetic effect of the individual horse ($o=1-36,441$) and $e_{ijklmnop}$ is the random residual.

Estimates for environmental and genetic effects were obtained under the same models and the specific variances for the respective model using BLUP (Best Linear Unbiased Prediction) with the software PEST (GROENEVELD *et al.* 1990). To study the genetic correlations between analyzed traits and to compare the results of genetic evaluations obtained under the two models, Pearson correlation coefficients between breeding values were calculated using the procedure CORR of SAS.

Results

Statistical analyses

Between 1995 and 2008, 29 053 Hanoverian mares were presented at SBI and having been scored for the eight conformation traits and measured for WH. Means and ranges of SBI scores and WH are shown in Table 1. Average WH of the evaluated mares was 165.5 cm (range 143-185 cm). Mean scores ranged from 6.38 (ConHL) to 7.25 (Head), while scores in general ranged between 3 and the maximum score 10. None of the conformation scores and their residuals was distributed normally ($P < 0.001$). Skewness coefficients ranged between $|s|=0.03$ and 0.43.

Table 1

Mean scores, ranges of scores (on a scale from 0 [not shown] to 10 [excellently shown]), and skewness coefficients of conformation scores and means, ranges, and skewness coefficients of height at withers in 29053 Hanoverian mares evaluated on the occasion of studbook inspection (SBI) of the HSS in 1995-2008

Durchschnittsnoten für Exterieurmerkmale (Notenspektrum) und die Schiefe der Notenverteilung sowie die durchschnittliche Widerristhöhe (Größenspektrum) und die Schiefe der Größenverteilung der Stutbuchaufnahmen von 29053 Hannoveraner Stuten der Geburtsjahrgänge 1992 bis 2005

Trait	Mean (range)	Skewness coefficients
Conformation front legs	6.63 (3-9)	-0.1763
Conformation hind legs	6.38 (3-9)	-0.2785
Height at withers	165.50 (143-185)	0.0313
General impression and development	6.85 (3-10)	-0.4318
Type	7.09 (4-10)	-0.0363
Frame	6.80 (4-10)	-0.1635
Saddle position	7.02 (4-10)	-0.0386
Conformation head	7.25 (4-10)	0.1236
Conformation neck	7.05 (3-10)	0.0375

Analyses of variance and model development

The fixed effects age and class of proportions of genes of Thoroughbred, Trakehner and Holsteiner were significant for all traits as it was the case for the random effect (combined date-place effect). Least square means of conformation scores and WH for the proportions of genes of Thoroughbred, Trakehner and Holsteiner are shown with their standard errors in Table 2. The relation between conformation and the proportion of genes of the considered horse breeds is illustrated in Figures 1-3. Large differences between the upper and lower 10%-quantiles were seen for Head, Type and Sad with respect to Thoroughbred and Trakehner.

Genetic analyses

Results of univariate genetic analyses of conformation traits and WH, estimated using Model 1 and Model 2 are shown in Table 3. The event variances (σ_e^2) were identical for Dev, Type, Sad, Head, and Neck, and varied only slightly by 0.0001 for ConFL, ConHL, and Frame, and by 0.0007 WH. Residual variances (σ_r^2) were slightly higher for all traits in Model 2 than in Model 1, with differences ranging between 0.0005 (Neck) and 0.0041 (Sad). Additive genetic variances were slightly smaller using Model 2 compared to Model 1, with differences ranging between 0.0007 (Neck) and 0.0057 (WH). For conformation trait scores, heritabilities ranged between 0.10 (ConFL, both models) and 0.48 (Head, Model 2) with standard errors of ≤ 0.01 . Higher heritability of 0.57 ± 0.01 was estimated for WH. Comparing heritability estimates from Model 1 and Model 2, only slight differences of 0.0005 (WH) to 0.0101 (Sad) were seen.

Pearson correlation coefficients determined between breeding values for all conformation traits and WH are given in Table 4. All correlations between the scored conformation traits were significantly positive, ranging between 0.27 and 0.79. Correlations between conformation scores and WH were in most cases also positive (range 0.04-0.31). Head was the only trait showing a slightly negative correlation of -0.05 with WH.

Comparison of breeding values estimated in Model 1 and Model 2 for the same traits revealed for all traits Pearson correlation coefficients close to unity ($r \geq 0.99$; results not shown).

Table 2

Least square means (LSM) with their standard errors (SE) of conformation scores evaluated at studbook inspection for the proportion of genes of Thoroughbred, Trakehner and Holsteiner stallions, estimated in 29053 Hanoverian mares born in 1992-2005

Least square-Mittelwerte (LSM) und Standardfehler der bei Stutbuchaufnahmen vergebenen Exterieurnoten und gemessenen Widerristhöhen von 29053 Hannoveraner Stuten der Geburtsjahrgänge 1992 bis 2005 nach Genanteilen von Englischem Vollblut, Trakehner und Holsteiner

Breed	Breedclass	Head	Neck	Sad	ConFL	ConHL
TB	1	7.15 ± 0.01	6.95 ± 0.01	6.82 ± 0.01	6.49 ± 0.01	6.28 ± 0.01
	2	7.20 ± 0.01	6.99 ± 0.01	6.89 ± 0.01	6.52 ± 0.01	6.31 ± 0.01
	3	7.28 ± 0.01	6.93 ± 0.01	7.01 ± 0.01	6.56 ± 0.01	6.28 ± 0.01
Trak	1	7.15 ± 0.01	6.90 ± 0.01	6.88 ± 0.01	6.50 ± 0.01	6.27 ± 0.01
	2	7.18 ± 0.01	6.95 ± 0.01	6.91 ± 0.01	6.52 ± 0.01	6.30 ± 0.01
	3	7.31 ± 0.01	7.02 ± 0.01	6.93 ± 0.01	6.55 ± 0.01	6.30 ± 0.01
Hol	1	7.20 ± 0.01	6.95 ± 0.01	6.97 ± 0.01	6.55 ± 0.01	3.30 ± 0.01
	2	7.24 ± 0.02	6.96 ± 0.02	6.88 ± 0.02	6.53 ± 0.02	6.32 ± 0.02
	3	7.20 ± 0.01	6.96 ± 0.01	6.87 ± 0.01	6.49 ± 0.01	6.24 ± 0.01

		WH	Dev	Type	Frame
TB	1	165.67 ± 0.05	6.68 ± 0.01	6.91 ± 0.01	6.61 ± 0.01
	2	165.80 ± 0.04	6.74 ± 0.01	6.98 ± 0.01	6.68 ± 0.01
	3	165.78 ± 0.05	6.79 ± 0.01	7.06 ± 0.01	6.74 ± 0.01
Trak	1	165.63 ± 0.05	6.69 ± 0.01	6.93 ± 0.01	6.66 ± 0.01
	2	165.76 ± 0.04	6.74 ± 0.01	6.98 ± 0.01	6.68 ± 0.01
	3	165.85 ± 0.05	6.77 ± 0.01	7.04 ± 0.01	6.70 ± 0.01
Hol	1	165.66 ± 0.03	6.74 ± 0.01	6.99 ± 0.01	6.67 ± 0.01
	2	165.65 ± 0.07	6.76 ± 0.02	7.02 ± 0.02	6.72 ± 0.02
	3	165.94 ± 0.05	6.70 ± 0.01	6.96 ± 0.01	6.64 ± 0.01

ConFL conformation of front legs, ConHL conformation of hind legs, WH height at withers, Dev general impression and development, Sad saddle position, TB Thoroughbred (1= ≤ 0.13 , 2= > 0.13 and < 0.30 , 3= ≥ 0.30 of Thoroughbred genes), Trak Trakehner (1= ≤ 0.2 , 2= > 0.2 and < 0.8 , 3= ≥ 0.8 of Trakehner genes), Hol Holsteiner (1=0.0, 2= > 0.0 and < 0.3 , 3= ≥ 0.3 of Holsteiner warm blood genes)

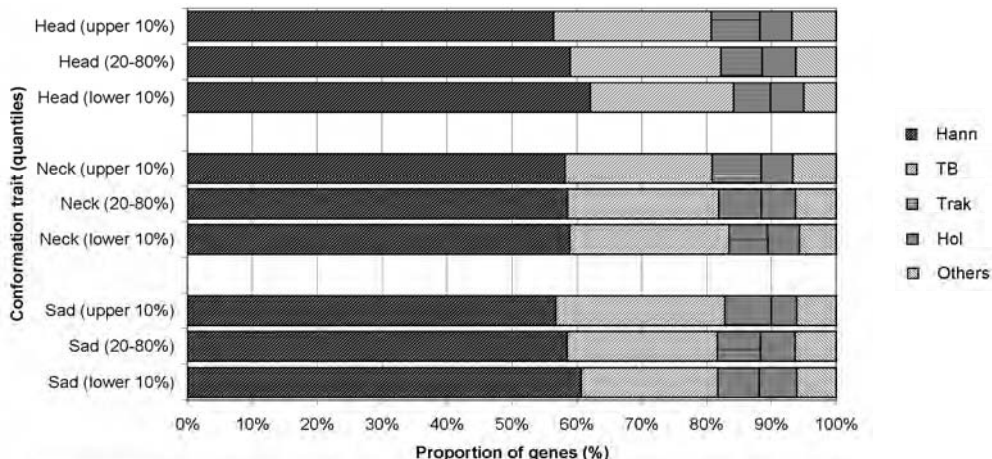


Figure 1

Proportions of genes of Hanoverian warmblood (Han), Thoroughbred (TB), Trakehner (Trak), Holsteiner warmblood (Hol), and other breeds (Others) by quantiles of scores for the head (Head), the neck (Neck), and the saddle position (Sad) evaluated at studbook inspections between 1995 and 2008 in 29031 Hanoverian mares from the birth years 1992-2005 *Verteilung der Genanteile von Hannoveraner (Han), Englischem Vollblut (TB), Trakehner (Trak), Holsteiner (Hol) und sonstiger Rassen (Others) innerhalb von Quantilen für die bei Stutbuchaufnahmen bewerteten Exterieurmerkmale Kopf (Head), Hals (Neck) und Sattellage (Sad) von 29053 Hannoveraner Stuten der Geburtsjahrgänge 1992-2005*

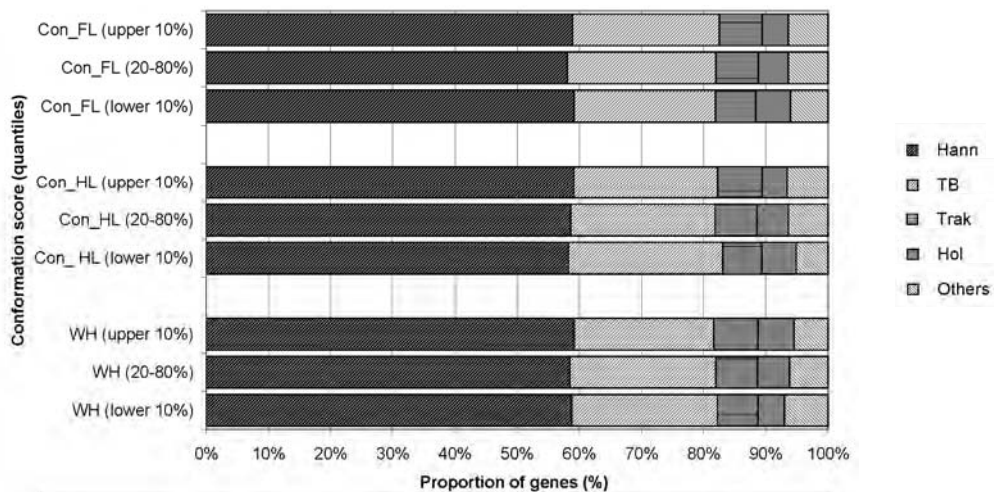


Figure 2
Proportions of genes of Hanoverian warmblood (Han), Thoroughbred (TB), Trakehner (Trak), Holsteiner warmblood (Hol), and other breeds (Others) by quantiles of scores for the conformation of the front legs (ConFL), the conformation of the hind legs (ConHL) and height at withers (WH); evaluated at studbook inspections between 1995 and 2008 in 29 031 Hanoverians mares from the birth years 1992-2005

Verteilung der Genanteile von Hannoveraner (Han), Englischem Vollblut (TB), Trakehner (Trak), Holsteiner (Hol) und sonstigen Rassen (Others) innerhalb von Quantilen für die bei Stutbuchaufnahmen bewerteten Fundamentmerkmale Vorderhand (ConFL) und Hinterhand (ConHL) sowie Widerristhöhe (WH) von 29 053 Hannoveraner Stuten der Geburtsjahrgänge 1992-2005

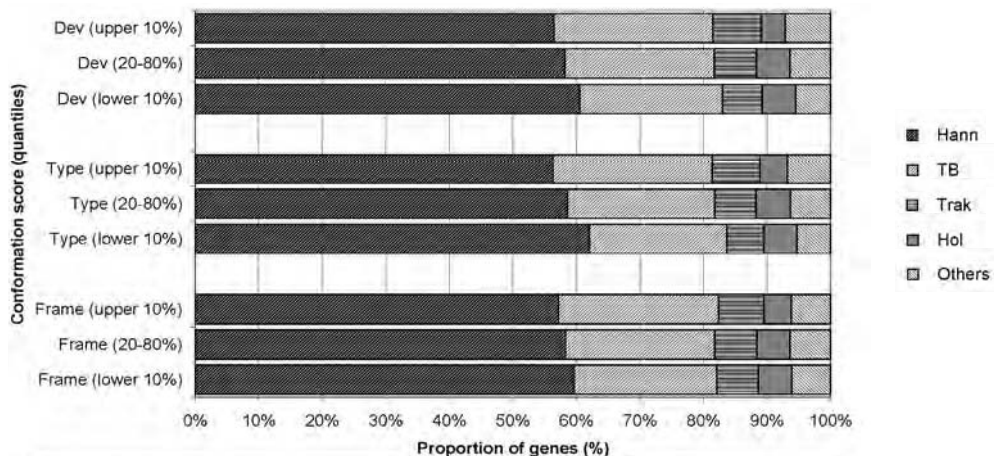


Figure 3
Proportions of genes of Hanoverian warmblood (Han), Thoroughbred (TB), Trakehner (Trak), Holsteiner warmblood (Hol), and other breeds (Others) by quantiles of scores for the general impression and development (Dev), the type (Type), and the frame (Frame) evaluated at studbook inspections between 1995 and 2008 in 29 031 Hanoverians mares from the birth years 1992-2005

Verteilung der Genanteile von Hannoveraner (Han), Englischem Vollblut (TB), Trakehner (Trak), Holsteiner (Hol) und sonstiger Rassen (Others) innerhalb von Quantilen für die bei Stutbuchaufnahmen bewerteten Exterieurmerkmale Gesamteindruck und Entwicklung (Dev), Rahmen (Frame) und Typ (Type) von 29 053 Hannoveraner Stuten der Geburtsjahrgänge 1992-2005

Table 3

Comparison of residual variances (σ_e^2), event variances (σ_r^2), and additive genetic variances (σ_a^2) and of heritabilities (h^2) which were univariately estimated for conformation traits and withers height from studbook inspections of 29 053 Hanoverian warmblood mares from birth years 1992-2005 with Model 1 or Model 2

Vergleich von Residualvarianz (σ_e^2), Veranstaltungsvarianz (σ_r^2) und additiv genetischer Varianz (σ_a^2) sowie der Heritabilität (h^2) von univariat ermittelten Zuchtwerten für Exterieurmerkmale und Widerristhöhe, ermittelt bei Stutbuchaufnahmen von 29 053 Hannoveraner Stuten der Geburtsjahrgänge 1992 bis 2005 mit Modell 1 oder Modell 2

Trait	Model 1				Model 2			
	σ_e^2	σ_r^2	σ_a^2	h^2	σ_e^2	σ_r^2	σ_a^2	h^2
ConFL	0.4318 ±	0.0388 ±	0.0538 ±	0.1027 ±	0.4327 ±	0.0387 ±	0.0526 ±	0.1005 ±
	0.0059	0.0025	0.0060	0.0081	0.0059	0.0025	0.0060	0.0081
ConHL	0.4386 ±	0.0433 ±	0.0651 ±	0.1190 ±	0.4392 ±	0.0434 ±	0.0642 ±	0.1174 ±
	0.0064	0.0026	0.0067	0.0088	0.0064	0.0026	0.0067	0.0088
WH	3.9425 ±	0.3696 ±	5.7387 ±	0.5710 ±	3.9466 ±	0.3689 ±	5.7330 ±	0.5705 ±
	0.0353	0.0069	0.0566	0.0129	0.0353	0.0069	0.0566	0.0129
Dev	0.2802 ±	0.0182 ±	0.1704 ±	0.3634 ±	0.2823 ±	0.0182 ±	0.1669 ±	0.3570 ±
	0.0063	0.0016	0.0085	0.0110	0.0064	0.0016	0.0086	0.0111
Type	0.2958 ±	0.0292 ±	0.1153 ±	0.2618 ±	0.2980 ±	0.0292 ±	0.1118 ±	0.2546 ±
	0.0060	0.0020	0.0078	0.0109	0.0060	0.0021	0.0078	0.0109
Frame	0.3909 ±	0.0382 ±	0.1109 ±	0.2054 ±	0.3933 ±	0.0383 ±	0.1072 ±	0.1990 ±
	0.0066	0.0023	0.0080	0.0103	0.0066	0.0023	0.0080	0.0104
Head	0.3350 ±	0.0168 ±	0.3220 ±	0.4779 ±	0.3367 ±	0.0168 ±	0.3192 ±	0.4746 ±
	0.0076	0.0015	0.0113	0.0110	0.0078	0.0015	0.0119	0.0116
Neck	0.3616 ±	0.0143 ±	0.1616 ±	0.3006 ±	0.3621 ±	0.0143 ±	0.1609 ±	0.2995 ±
	0.0070	0.0015	0.0093	0.0115	0.0067	0.0014	0.0089	0.0110
Sad	0.3134 ±	0.0331 ±	0.1321 ±	0.2758 ±	0.3173 ±	0.0331 ±	0.1268 ±	0.2657 ±
	0.0060	0.0021	0.0081	0.0107	0.0061	0.0020	0.0082	0.0109

ConFL conformation of front legs, ConHL conformation of hind legs, WH height at withers, Dev general impression and development, Sad saddle position

Table 4

Pearson correlation coefficients determined between breeding values which were univariately estimated for conformation traits and height of withers from studbook inspection of 29 053 Hanoverian warmblood mares from birth year 1992-2005 with Model 1 or Model 2

Pearson Korrelationskoeffizienten, berechnet für univariat geschätzte Zuchtwerte für Exterieurmerkmale und Widerristhöhe, ermittelt bei Stutbuchaufnahmen von 29 053 Hannoveraner Stuten geboren zwischen 1992 und 2005 mit Modell 1 oder Modell 2

Model Trait	ConFL	ConHL	WH	Dev	Type	ConT	Head	Neck	Sad
<i>Model 1</i>									
ConFL	1.00	0.52	0.06	0.59	0.59	0.50	0.35	0.49	0.41
ConHL		1.00	0.05	0.57	0.52	0.52	0.27	0.40	0.34
WH			1.00	0.18	0.13	0.25	-0.05	0.13	0.31
Dev				1.00	0.80	0.69	0.52	0.60	0.54
Type					1.00	0.70	0.73	0.71	0.60
Frame						1.00	0.37	0.52	0.60
Head							1.00	0.53	0.33
Neck								1.00	0.41
Sad									1.00
<i>Model 2</i>									
ConFL	1.00	0.51	0.06	0.59	0.59	0.50	0.36	0.47	0.44
ConHL		1.00	0.05	0.55	0.50	0.50	0.27	0.40	0.33
WH			1.00	0.19	0.13	0.25	-0.05	0.13	0.30
Dev				1.00	0.79	0.70	0.53	0.59	0.54
Type					1.00	0.71	0.73	0.69	0.60
Frame						1.00	0.38	0.50	0.59
Head							1.00	0.53	0.34
Neck								1.00	0.38
Sad									1.00

ConFL conformation of front legs, ConHL conformation of hind legs, WH height at withers, Dev general impression and development, Sad saddle position

Discussion

The aim of this study was to investigate, if a model for genetic evaluation for conformation traits of the Hanoverian could benefit from inclusion of the proportions of genes of Thoroughbred, Trakehner and Holsteiner.

Conformation plays an important role for performance and health. In particular dressage performance is significantly positively correlated with most conformation traits (KOENEN *et al.* 1995, VON LENGERKEN and SCHWARK 2002). WELLER *et al.* (2006b) identified certain conformational parameters that were associated with the risk of injury and there are clear relationships between back conformation and movement that may be important to the orthopaedic health, performance and soundness of the horse (JOHNSTON *et al.* 2002). Therefore genetic evaluation for conformation can play an important role in selecting young dressage horses.

The Hanoverian, is primarily bred to be rideable and talented sport horse with good abilities for the disciplines dressage, jumping, eventing, and driving (KOENEN *et al.* 2004). Besides performance, conformation is explicitly stressed in the breeding aim of the HSS. For this purpose,

Thoroughbred and Trakehner stallions are commonly crossbred with Hanoverian mares to make the future progeny nobler, while Holsteiner stallions are mainly used to improve jumping ability.

The Holsteiner society (2010) puts more weight on performance, especially in show jumping. Thoroughbred breeding, however, is primarily focused on speed, and conformation only has to be functional, to allow a fast and efficient gallop (WELLER *et al.* 2006a).

Recently, STEWART *et al.* (2009) recommended the inclusion of breed classes in the model used for genetic evaluation for dressage performance of the sport horse population in the United Kingdom. A potential benefit through inclusion of some breed effects into a model for genetic evaluation for performance could also be shown by VANDERICK *et al.* (2009) for a crossbred dairy cattle population of New Zealand. KOENEN *et al.* (1995) considered the percentage of Thoroughbred for genetic evaluations of conformation traits and their influence on show jumping performance in Dutch warmblood riding horses. However, no results were shown supporting the advantage of considering the percentage of Thoroughbred. The impact of different proportions of genes of foreign horse breeds on conformation or breeding values for conformation has not been investigated yet for the Hanoverian or any other German warmblood breed.

Results of SBI have been used for this study. Because SBI is obligatory for all Hanoverian brood mares, results of this study should be representative for the whole Hanoverian population. Our heritability estimates were negligibly influenced by model choice and agree well with previous findings (STOCK and DISTL 2006, DIETEL *et al.* 2004).

All SBI conformation scores increased during 1995 and 2008, particularly for Head, Neck, and Type, illustrating the breeding process towards a modern, goodlined, and noble horse. Our data supported that higher proportions of genes of Thoroughbred and Trakehner stallions slightly increased most of the conformation scores, while the proportion of Holsteiner genes only marginally affected them. Our results are in line with the current recommendation of the HSS to increase the usage of Thoroughbred stallions for breeding. Accordingly, genetic variances were slightly lower extending the model for routine genetic evaluations by effects correcting for foreign genes. However, decrease of heritabilities was very small, and the impact of genetic evaluation was negligible, indicating that the use of an extended model is not relevant for the identification of genetically favourable individuals.

There is not any previous study analyzing the influence of the proportions of foreign breeds on genetic evaluations for conformation. The Hanoverian population used for the current analyses was large and homogenous, with conformation scores gained under standardized conditions, and comprehensive pedigree information was available. Hence, possible breed-related differences may have been taken into account by the relationship matrix. Therefore, genetic evaluations in the linear animal model without explicit consideration of the proportions of Thoroughbred, Trakehner and Holsteiner genes produced almost identical results as the extended version. Based on these results, we conclude that genetic analyses of conformation data with comprehensive pedigree information, and data collected under same conditions available, will not improve considerably from model extension by breed class effects.

However, for analyses including different breeds from several breeding organisations inclusion of the proportions of genes of foreign breeds may be necessary.

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Received 17 February 2010, accepted 4 May 2010.

Corresponding author:

OTTMAR DISTL

email: ottmar.distl@tiho-hannover.de

Institute for Animal Breeding and Genetics, University of Veterinary Medicine Hannover (Foundation), Bünteweg 17 p, 30559 Hannover, Germany
