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Genetic associations among traits from foals' and mares' evaluations with regard to optimizing the breeding program in the Trakehner Population

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Abstract

The objective of this study was to estimate genetic parameters of traits from the conformation tests of foals and mares in the Trakehner breed. The data analyzed consisted of 6447 records of foals and 4287 records from mare conformation tests. Heritabilities for traits in the foals' evaluations ranged from 0.20 ('correctness of legs') to 0.46 ('type') calculated with an animal model and ranged from 0.18 ('correctness of legs') to 0.37 ('type') when derived from the sire component of a sire-dam model. In the mares' evaluations the heritabilities for the traits ranged from 0.32 ('correctness of legs') and 0.70 ('overall impression') analyzed with the animal model and ranged from 0.23 ('correctness of legs') to 0.49 ('type') derived from the sire component of the sire-dam model. Highest genetic correlations in both models were found between the trait 'overall impression' and the 'conformation of the body' (foals: 0.85) and between the trait 'overall impression' and the gaits (mares: 0.90; 0.89). Genetic correlations between corresponding traits from foals' and mares' tests were high (0.68-0.93). The results indicate that the information from the foals might be of some value in a general breeding framework, if some emphasis is on conformation traits. Estimates for the additive genetic variances are higher for the animal model than for the sire-dam model. Possible reasons for a higher dam variance component could be herd effects, line breeding and the knowledge of genetic background of an animal during evaluation.

Introduction

The Trakehner breed can be traced back to the year 1732 to the first foundation of a herd book society in Trakehnen (East Prussia). The breeding association is nowadays fragmented into 10 regions in Germany which are managed centrally. The Trakehner warm blood breed is a partially closed population. It is particularly demanding to centrally manage a large fragmented breeding population. Unintentional and unfavorable consequences for an effective and sustainable breeding work might be a consequence. We estimated genetic parameters of traits from the conformation tests of foals and mares in the Trakehner breed as a first step of a more comprehending research project initiated to optimize the breeding scheme.

A systematic use of information from foal evaluation tests could be of some value in the selection of breeding animals. This information is available early in life and stems from virtually unselected animals. Furthermore, in the Trakehner breeding association *all* foals of a breeding season are routinely evaluated by the commission.

Materials and methods

The data analyzed consisted of 6447 records of foals and 4287 records from mare conformation tests of the years 1994-2005. For the data preparation the statistic software program R (R DEVELOPMENT CORE TEAM, 2004) was used.

Evaluated traits in the conformation tests of foals and mares are identically named: type, conformation of the body, correctness of the legs, walk, trot, canter and overall impression. These traits are subjectively scored using a grading from 1 to 10 by judges who are representatives of the breeding associations. An evaluation only using full steps in the scale was recently enhanced and now half points of increment are allowed since 2002 and 2004 for foals and mares, respectively.

In the evaluation test foals are presented together with their mothers. Mares are evaluated free running and guided at a central mare grading.

Variance components were estimated by a restricted maximum likelihood (REML) (VCE 5.1.2, KOVAČ, M.; GRONEVELD E**.,** 2003). Due to general problems with convergence we estimated the complete covariance structure using bivariate runs. Estimates for the diagonal elements were pooled subsequently. We used an animal model (a) and alternatively a sire-dam model (b). This was motivated by the fact that we had no herd effect in the model and we assumed this to be a relevant non-genetic cause of resemblance between dams and their offspring (that are more often members of the same herd than not). The models used were:

a) $y_{ijklm} = \mu_i + T_j + A_k + B_l + a_m + e_{ijklm}$

b) $y_{ijklmn} = \mu_i + T_j + A_k + B_l + s_m + d_n + e_{ijklmn}$

where $y_{...}$ is the trait score; μ is the population mean of the *ith* trait; T_j is the fixed effect of the *jth* combination of date and judge (date * judge), *(foals: j = 1-695, mares: j = 1-188)*; A_k is the fixed effect of the *kth* class of age *(k = 1-6, foals only)*; B_l is the fixed effect of the *lth* class of birth month (l = 1-3); a_m is the additive genetic effect of the *mth* animal; s_m is the effect of the *mth* sire (correlated effects); d_n is the effect of the *nth* dam (treated independently); $e_{...}$ is the random residual effect. It seemed to be a natural assumption for us that there is no non-genetic covariance between a sire and his offspring.

The fixed effect of the combination of date and judge was highly significant for foal and mare evaluation traits. The age of the foals was allowed to be between 10 to 365 days and was separated into six classes with a class width of thirty days. For the genetic analysis we considered only fillies in order to increase the reliability. The three classes of birth months were arranged into the early season (October, November, December, January, February), the main season (March, April, May) and the post season (June, July, August, September) for foals and mares.

Results

The judges do not use the whole range of the scoring scale (Table 1 and 2). The traits walk and canter were not evaluated consistently in the foals' evaluation. 18% and 13% of the scores for these traits were missing.

Table 1: Means ($\bar{x}$), standard deviations (s), standard errors (SE) and minimum-, maximum-values for foal traits (n = 6447)

Foal traits	n	$\bar{x}$	s	SE	min	max
Type	6446	7.873	0.724	0.000	5	10
Conformation of body	6445	7.577	0.610	0.000	5	10
Correctness of legs	6394	7.143	0.598	0.000	4	9
Walk	5305	7.433	0.618	0.000	5	10
Trot	6447	7.654	0.793	0.000	5	10
Canter	5587	7.384	0.656	0.000	5	10
Overall impression	6447	7.578	0.629	0.000	5	10

Table 2: Means ($\bar{x}$), standard deviations (s), standard errors (SE) and minimum-, maximum-values for mare traits (n = 4287)

Mare traits	n	$\bar{x}$	s	SE	min	max
Type	4286	7.539	0.758	0.000	5	10
Conformation of body	4286	7.254	0.661	0.000	5	9
Correctness of legs	4284	6.816	0.607	0.000	4	8.5
Walk	4275	7.130	0.749	0.000	5	9
Trot	4277	7.529	0.808	0.000	5	10
Canter	4275	7.066	0.714	0.000	5	9.5
Overall impression	4286	7.309	0.698	0.000	5	9

As expected there is a seasonal trend of reproduction observable, 74% of the foals are born during the main season (March, April, May). The mean value of the age of foals on evaluation day is 90 days. Since the conformation tests are clustered seasonally, there is also a discrete distribution of the age of mares. The mean value of the age for the mares on evaluation day is 3.6 years.

In the final model to estimate variance components for the mares we did not correct for the fixed effect of age. Defining the age of the mares into five classes, we found that there is a strong decrease of the average mean value with growing age (Figure 1).

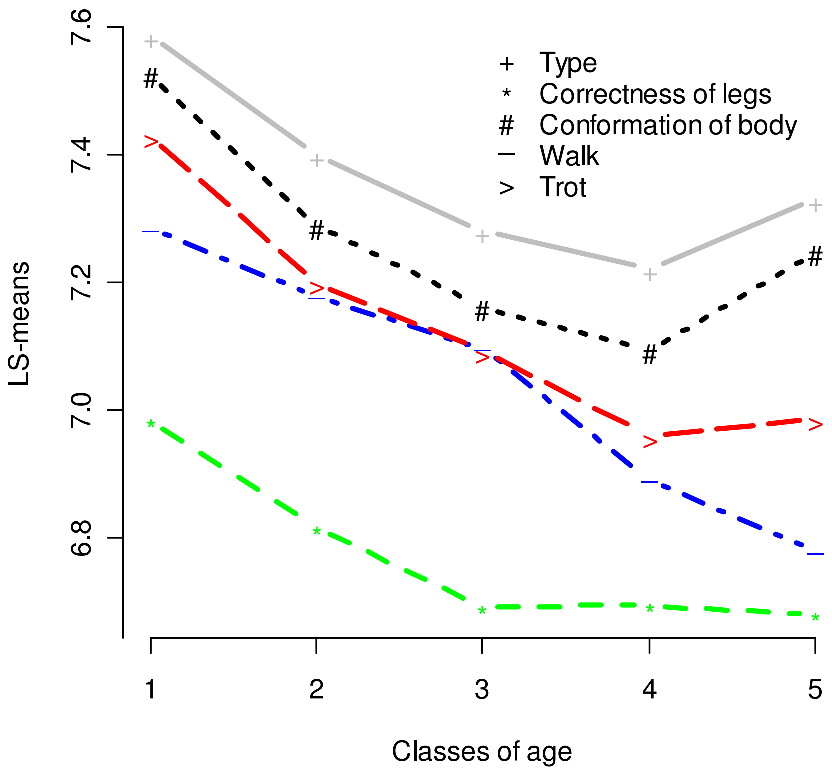

Figure 1: LS-Means for some mare traits per age classes

This is not in accordance with the general expectation that an older animal should, on average, perform better because of ongoing maturity. Additionally, there is some empirical evidence that mares with a higher genetic potential are brought earlier to the evaluation test than otherwise. These mares are of particular interest for breeders, because they are candidates for the status of being a premium mare. Consequently, we assumed an intentional pre-selection as the main source of this unexpected result and did not correct for the effect in the further investigation (CHRISTMANN, 1996).

Estimates for heritability of conformations traits of foals ranged from $h^2 = 0.20$ for ‘correctness of legs’ to $h^2 = 0.46$ for the trait ‘type’ (Table 3) calculated with the animal model. Genetic correlations between traits of foal evaluations ranged from $r_g = 0.31$ (‘correctness of legs’ and ‘canter’) to 0.90 (‘conformation of body’ and ‘overall impression’).

Table 3: Estimates of heritability (h^2; diagonal) and genetic correlations (r_g) for traits of the foal evaluations calculated with the animal model (n = 6447)

Foal traits		1	2	3	4	5	6	7
Type	(1)	*0.46*	0.67	0.43	0.34	0.57	0.45	0.72
Conformation of body	(2)		*0.29*	0.62	0.51	0.62	0.72	0.90
Correctness of legs	(3)			*0.20*	0.51	0.61	0.31	0.71
Walk	(4)				*0.25*	0.70	0.57	0.72
Trot	(5)					*0.42*	0.72	0.85
Canter	(6)						*0.28*	0.82
Overall impression	(7)							*0.40*

The heritabilities derived from the sire component of the sire-dam model (Table 4) are lower comparing to in the animal model. The estimates for heritability range here from $h^2 = 0.18$ for 'correctness of the legs' to $h^2 = 0.39$ for 'trot'. The genetic correlations between the foal traits in the sire-dam model were also high.

Table 4: Estimates of heritability (h^2; diagonal) and genetic correlations (r_g) for traits of the foal evaluations calculated with the sire-dam model (n = 6447)

Foal traits		1	2	3	4	5	6	7
Type	(1)	*0.37*	0.63	0.37	0.44	0.46	0.37	0.65
Conformation of body	(2)		*0.25*	0.46	0.57	0.53	0.52	0.85
Correctness of legs	(3)			*0.18*	0.40	0.52	0.01	0.50
Walk	(4)				*0.19*	0.73	0.50	0.73
Trot	(5)					*0.39*	0.52	0.87
Canter	(6)						*0.19*	0.61
Overall impression	(7)							*0.24*

The results for the heritabilities for the foal traits are comparable with results from JĘDRUCH (2005) calculated from a subset of the same data we used.

The estimates of heritability for the conformation traits of mares ranged from $h^2 = 0.32$ for 'correctness of legs' to $h^2 = 0.70$ for 'overall impression' (Table 5) calculated with the animal model. Genetic correlations for mare evaluation traits ranged from $r_g = 0.43$ ('type' and 'walk') up to $r_g = 0.90$ ('canter' and 'overall impression').

Table 5: Estimates of heritability (h^2; diagonal) and genetic correlations (r_g) for traits of the mare evaluations calculated with the animal model (n = 4287)

Mare traits		1	2	3	4	5	6	7
Type	(1)	*0.58*	0.76	0.62	0.43	0.63	0.55	0.78
Conformation of body	(2)		*0.47*	0.79	0.62	0.66	0.74	0.89
Correctness of legs	(3)			*0.32*	0.54	0.70	0.77	0.85
Walk	(4)				*0.41*	0.68	0.65	0.76
Trott	(5)					*0.64*	0.83	0.87
Canter	(6)						*0.41*	0.90
Overall impression	(7)							*0.70*

There is an apparent difference between the heritability results from the animal model and the results derived from the sire-dam model for the mare evaluation traits. The estimates for heritability derived from the sir component range here from $h^2 = 0.18$ for 'correctness of the legs' to $h^2 = 0.39$ for 'trot' (Table 6). The genetic correlations differ hardly for both models. These results are higher estimates of heritability for mare evaluation traits comparing with the literature (PREISINGER et al., 1991; JĘDRUCH, 2005).

Table 6: Estimates of heritability (h^2; diagonal) and genetic correlations (r_g) for traits of the mare evaluations calculated with the sire-dam model (n = 4287)

Mare traits		1	2	3	4	5	6	7
Type	(1)	*0.49*	0.68	0.60	0.42	0.53	0.47	0.71
Conformation of body	(2)		*0.36*	0.57	0.62	0.59	0.70	0.80
Correctness of legs	(3)			*0.23*	0.55	0.70	0.71	0.72
Walk	(4)				*0.32*	0.61	0.64	0.71
Trott	(5)					*0.48*	0.81	0.89
Canter	(6)						*0.36*	0.85
Overall impression	(7)							*0.44*

Genetic correlations between corresponding traits from foal and mare evaluation test were high for both models ($r_g = 0.68\text{-}0.93$).

Summary and discussion

Comparing the variance components for the sire- and the dam-effect yielded a substantially higher dam component. Both components are compounded in the estimate of the animal model. Dams and their offspring usually are members of the same herd and we assume this additional non- genetic covariance between dams and their offspring to be the main reason for this effect. Although in general there might be some impact of higher selection intensities in sires, we think that this is of no great importance with respect to the phenotypic variance in the subjectively grading of offspring. Since the herd effect could not be modeled (it is not recorded routinely), we assume that the sire-component in our case is somewhat closer to an unbiased estimate.

There might be some additional reasons for the high dam variance component. Line-breeding with respect to the dam-line is a prominent strategy in the Trakehner breed. The knowledge of the genetic background of the animals and presenting foals together with their mothers can also introduce non-genetic covariances between dams and their offspring (KOENEN et al., 1995).

The results indicate that the information from the foals might be of some value in general breeding framework, if some emphasis is put on conformation traits. This is not only because of high genetic correlations but also because this information is available early in life and is recorded even on animals not entering the breeding scheme later. However, the true value of this information can only be appreciated in the context of optimizing the breeding strategy in the Trakehner breed.

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