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Original study

Genetic evaluations of the German Sport Horse: Population structure and use of data from foal and mare inspections and performance tests of mares

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Abstract

The aim of the study was to characterize the population of the German Sport Horse, a sub-population of the German Riding Horse, in terms of population structure and genetic parameters. Data from 26 490 horses with information from foal inspections (FI; n=17 881), broodmare inspections (BI; n=12 069) and mare performance tests (MPT; n=2 756) from the years 1990-2006 were used for analysis. A total of 21 traits as scored in the three types of performance tests were analysed. Heritability estimates for traits from FIs ranged from 0.24 ± 0.01 (conformation) to 0.50 ± 0.01 (type). For BIs estimates ranged between 0.15 ± 0.02 (forelegs) and 0.50 ± 0.02 (head). Traits evaluated in the MPT showed heritabilities between 0.18 ± 0.02 (rideability) and 0.46 ± 0.02 (trot). Genetic correlations within and across the three tests were all positive. An analysis of the structure of genetic relationships revealed that the population is influenced by different German Riding Horse sub-populations as well as by thoroughbreds. The genetic connectedness within the population is of a complex structure and appeared to be sufficient for genetic analyses. Differences between the genetic parameters estimated in this study for the GSH and those used in the national breeding value estimation system are predominantly insignificant. These results confirm that the GSH is both adequately represented in the national system and that the population itself is a representative part of the entire German Riding Horse population.

Keywords: heritability, genetic correlations, conformation traits, young horses performance tests

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Abbreviations: BB: Berlin-Brandenburg, BI: broodmare inspection, FI: foal inspection, GS: genetic similarity, GSH: German Sport Horse, MPT: mare performance test, NSC: number of stallions in common, PEC: pedigree completeness, SN: Saxony, ST: Saxony-Anhalt, TH: Thuringia, vit: Vereinigte Informationssysteme Tierhaltung

Introduction

In 2010, the breeding stock of German Riding Horses amounted to about 68 000 registered mares and 4 000 stallions (FN 2010). Of these, approximately 5 000 mares and 240 stallions were registered as German Sport Horse (GSH). The GSH is a new horse breed with a common stud book of origin since 2003. It was created by merging the four regional warm-blooded populations of Berlin-Brandenburg, Saxony-Anhalt, Saxony and Thuringia. Horse breeding in these regions is historically closely linked and has developed in close cooperation. The merger of the regional populations and the establishment of a joint breeding programme improved the situation for the breeding organisations with the use of shared resources, providing synergies resulting in a stronger position on the horse market.

The merging of the active breeding populations also leads to a considerably expanded data pool. The GSH is incorporated into the system of integrated breeding value estimation of the German Equestrian Federation, carried out annually by the vit (Vereinigte Informationssysteme Tierhaltung), the central computing centre for genetic evaluations of horses and dairy cattle in Germany. Because the national genetic evaluation system is highly oriented towards sport performance in show jumping and dressage, it was aspired to compare the national system with an internal system focusing on data from foal inspections (FI), broodmare inspections (BI) and mare performance tests (MPT).

The information for the first two data sources is collected at an early stage in the animal's life. It is comprehensively collected with little pre-selection. It focuses on the conformation traits and includes the evaluation of movements presented in hand or free. So far, no genetic analyses had been done on these data for the GSH. However, studies have been undertaken for some of the other sub-populations of the German Riding Horse and the Trakehner breed. Estimates of heritabilities for similar sets of traits showed moderate to high values. As an example, Teegen (2008) found estimates between 0.17 (correctness of legs) and 0.39 (type) for Trakehners. Bösch *et al.* (2000) reported heritabilities of 0.42 (type/conformation) and 0.40 (gait/swing) for Holsteiner foals. Studies on traits for mare inspections already exist for Holsteiner, Mecklenburger, Trakehner and Hanoverian mares.

Genetic parameters from these studies showed a variation between individual populations as well as between studies. Traits describing the overall type predominantly exhibited high heritabilities. Estimates vary between 0.29 for the Mecklenburger population (Dietl *et al.* 2004) and 0.46 for Trakehner mares (Teegen 2008). In contrast, for the trait correctness of legs or the individual traits front and hind limbs mostly low heritabilities in the range of ≤0.20 were found (*e.g.* Bösch *et al.* 2000, Christmann 1996, Dietl *et al.* 2004, Teegen 2008). Traits used to describe the quality of movement vary widely in their estimates of heritability (0.09-0.44). This is partly due to different breeding organisations using different definitions for the traits, particularly in earlier studies. In recent years, criteria have become increasingly uniform. Another point is that under some recording systems the environmental influences are larger than under others. In general, research has shown low heritabilities for correctness of gaits and a moderate to high heritability for trot.

Mare performance test is focused on the horse's dressage and jumping ability and it is also the interface with the national integrated system for breeding value estimation. A MPT can be conducted as a station or a field test and is harmonized in its trait definitions for the traits walk, trot, canter, rideability and free jumping across Germany. Estimates of the MPT traits as found in other sub-populations of the German Riding Horse are shown in Table 1.

Table 1
Estimated heritabilities for traits in the mare performance test as reported in the literature for various sub-populations of the German Riding Horse

Reference	Walk	Trot	Canter	Rideability	Free jumping
Teegen 2008	0.23	0.47	0.22	0.19 (test rider) 0.31 (commission)	0.36
Dietl *et al.* 2005	0.32	0.34	0.40	0.14	0.54
Lührs-Behnke *et al.* 2002	0.27	0.38	0.34	0.29	0.32
Bösch *et al.* 2000	0.31	0.31	0.29	0.32	0.41
von Velsen-Zerweck 1998	0.27	0.36	0.35	0.30	0.35
Christmann 1996	0.27	0.37	0.30	0.30	0.41
Schade 1996	0.27	0.36	0.29	0.29	0.42

Heritabilities in Table 1 range from 0.23 to 0.32 for walk, from 0.31 to 0.47 for trot, from 0.22 to 0.40 for canter, from 0.14 to 0.32 for rideability and from 0.32 to 0.54 for free jumping. For the integrated breeding value estimation, the vit uses genetic parameters of 0.30 (walk), 0.40 (trot), 0.37 (canter), 0.32 (rideability) and 0.34 (free jumping; vit 2010). German Sport Horses are included in the genetic evaluation. However, no genetic-statistical analyses have been carried out yet specifically for the population of the GSH.

Thorén Hellsten *et al.* (2006) compared various tests of young horses from European warm-blooded horse breeding associations. They found a good agreement for results of major horse populations. For the Swedish Warmblood, there are two types of 1-day field tests available for young sport horses. For those tests, genetic parameters have been evaluated in several studies (Thorèn Hellsten *et al.* 2009, Viklund *et al.* 2008, Wallin *et al.* 2003). In these studies, the estimates for heritabilities ranged from 0.24 to 0.53 for conformation traits (excepting leg-traits), from 0.17 to 0.53 for gait traits and from 0.17 to 0.33 for jumping traits.

For Dutch Warmblood horses, Ducro *et al.* (2007) studied the heritabilties of stud book entry traits. In this study, the estimates for the subjective traits were 0.33 for conformation, 0.34 for movement and 0.40 for free-jumping. Koenen *et al.* (1995) estimated heritabilities for the different linear scored traits for Dutch Warmblood horses. They obtained values between 0.16 and 0.21 (for trait group front), 0.15 and 0.28 (for trait group body), 0.09 and 0.23 (for trait group legs) as well as 0.12 and 0.22 (for trait group movement). Linear conformation traits and type traits have been analysed for the Belgian Warmblood horse by Rustin *et al.* (2009). The estimates of heritability for this population were between 0.15 and 0.55 for conformation traits and between 0.33 and 0.52 for gait traits.

The aim of the present study was to characterize the population of the GSH, in particular the population structure and the genetic population parameters. Results from this analysis were regarded as a prerequisite for the development of an internal system of genetic evaluations. Additionally, the analysis was expected to provide information on the question whether the GSH can be regarded as a sub-population of the German Riding Horse and should take part in the national evaluation system. Knowledge about the population parameters and the pedigree structure is also necessary for future research, especially for the development of a system for prediction of genomic breeding values. This study is the first genetic-statistical analysis of the GSH population. It is based on extensively documented performance data and comprehensive pedigree information from the breed associations in Brandenburg-Anhalt and Saxony-Thuringia, which were the partners in this research.

Material and methods

Data were comprised of FIs and BIs as well as MPTs from 1990 to 2006. Foal inspections take place in the first months of the horse's life and are conducted with the foal walking at foot with the mare. Broodmares are mostly inspected at the age of three years, but may also be inspected at a later age. They are presented in hand or running free. The MPT is designed to evaluate three- and four-year-old mares under rider (gaits and rideability) and free running (free jumping). It can be taken as a one-day field test or as a station performance test lasting 14 to 21 days. All three tests are separate evaluations. Foals were inspected independently from their dams.

Edited data consisted of 26 490 animals with records from at least one of the three tests. In total, 1 187 mares were examined in all three tests and 3 842 passed two tests. The most common combination of two records was FI plus BI (2 535 records), followed by BI plus MPT (n=1 250 records) and FI plus MPT (57 records). A total of 87 199 horses were included in the pedigree file with a maximum of 23 generations. A coefficient for pedigree completeness (PEC) was calculated, using the index proposed by MacCluer *et al.* (1983). This index describes the proportion of known ancestors for a certain number of generations. It is calculated separately for paternal and maternal lines. The harmonic mean of the paternal and maternal indices explains the overall completeness index for the pedigree of the individual animal. In the present study, the average PEC over 3 generations was 0.99.

Across all three forms of tests, 21 traits were included in the analysis. All traits were scored on a scale of 1 to 10 with 1 denoting very poor and 10 denoting excellently shown. Use of half-point scores was possible. An overview of the data is given in Table 2.

The number of available records was 17 881 for FI, 12 069 for BI and 2 756 for MPT. Different numbers of observations in BI were caused by the fact that some of the traits were added subsequently to the evaluation scheme.

In the FI, the animal is evaluated for the traits type conformation$_f$ and gait. Broodmare inspections comprise evaluations for seven main traits. The trait conformation$_m$ is generated from the arithmetic mean of the individual traits head, neck, saddle position, frame, forelegs and hind legs. Even though type characteristics are closely related to the conformation, the type is judged separately. For scoring type, appearance, proportions and morphological contours are considered. When judging the conformation, certain points of the six individual traits are examined. The analysis for MPT concentrated on the traits walk, trot, canter, rideability and free jumping.

Table 2
Raw means ($\bar{x}$), standard deviation (s), minima and maxima for foal inspection traits, broodmare inspection traits and mare performance tests traits

		Trait	n	$\bar{x}$	s	Min	Max
FI n=17 881	1	Type	17 881	8.20	0.79	4.0	10.0
	2	Conformation$_f$	17 881	7.42	0.62	5.0	9.5
	3	Gait	17 881	7.74	0.87	4.0	10.0
BI n=12 069	1	Breed and sex type	12 069	7.87	0.85	4.0	10.0
	2	Conformation$_m$	8 224	7.31	0.52	4.8	9.7
	2a	Head	12 067	7.68	0.87	4.0	10.0
	2b	Neck	12 069	7.64	0.84	5.0	10.0
	2c	Saddle position	12 068	7.66	0.82	2.0	10.0
	2d	Frame	12 069	7.40	0.84	2.0	10.0
	2e	Forelegs	8 228	7.03	0.70	4.0	10.0
	2f	Hindlegs	9 002	6.94	0.70	4.0	10.0
	3	Correctness of gaits	12 069	7.12	0.71	4.0	10.0
	4	Walk$_{bi}$	9 686	7.28	0.80	4.0	10.0
	5	Trot$_{bi}$	12 067	7.45	0.88	4.0	10.0
	6	Canter$_{bi}$	2 162	7.28	0.71	5.0	9.5
	7	Overall impression & development	8 045	7.52	0.76	4.0	10.0
MPT n=2 756	1	Walk$_{pt}$	2 729	7.02	0.82	3.0	10.0
	2	Trot$_{pt}$	2 728	6.81	0.82	3.5	9.2
	3	Canter$_{pt}$	2 729	6.90	0.78	4.0	9.5
	4	Rideability	2 699	6.96	0.92	3.5	9.5
	5	Free jumping	2 756	7.12	0.86	3.9	10.0

Range of minima for all traits was between 2.0 to 5.0. For the traits saddle position and frame the minimal score was 2.0. For most of the traits the minimal score was 4.0 or 5.0, and thus reflects the insufficient use of the lower part of the scale. The often criticised subjective nature of horse inspections and scoring also leads to a relative low yet typical level of the standard deviation of score values found in data on horse breeding. In this study, data standard deviations were found in the range from 0.62 for conformation$_f$ to 0.92 for rideability, without consideration of the cumulative grade for conformation$_{bi}$.

Merging and preparation of data as well as editing was performed using the software package SAS 9.1 (SAS Institute Inc., Cary, NC, USA). The software B&S Kinghorn Pedigree Viewer (version 5.3, Kinghorn & Kinghorn 2006) was used for inspections of pedigree links of individual and most influential animals. Merging of performance data files and the pedigree file was done in such a way that only relevant animals were extracted from the pedigree file.

Relevant animals were defined as animals that either had records or if an animal did not have records, provided more than just one link with another animal. This ›pruning‹ of the pedigree data was performed using a Python-based programme. The genetic connectedness within the population was checked using *genetic similarity* (GS) with the help of the genetic similarity formula developed by Rekaya *et al.* (2003) which was already used by Thorén Hellsten *et al.* (2008) to measure connectedness among European sport horse populations.

Genetic similarity is calculated from the ratio between the tested progeny of a sire with progeny in different breeding areas and the total number of tested progeny in the respective area [1]. In addition, an imbalance in the distribution of the progeny can be detected when calculating the contribution of each breeding area to the GS [2]. The use of stallions contributing to connectedness served as a further indicator, which was determined by the *Number of stallions in common* (NSC; used by Thorén Hellsten *et al.* [2008]). This method is derived from the *number of common bulls* (Weigel *et al.* 2000), a measure for genetic connectedness.

$$GS_{ij} = \frac{\sum_{k=1}^{N_{ij}} (n_{ik} + n_{jk})}{\sum_{k=1}^{N_i} n_{ik} + \sum_{k=1}^{N_j} n_{jk}} \tag{1}$$

$$GS = \frac{\sum_{k=1}^{N_i} n_{ik}}{\sum_{k=1}^{N_{ij}} (n_{ik} + n_{jk})} \times 100 \quad [in\ \%] \tag{2}$$

Where N_{ij} is the number of stallions with tested progeny in region *i* and *j*, n_{ik} and n_{ij} are the numbers of tested progeny of stallion *k* in region *i* and *j*, N_i is the number of stallions with tested progeny in region *i* and N_j is the number of stallions with tested progeny in region *j*. In the present study, FI data was used to analyse the genetic connectedness. Data from 17 881 foals descending from 1 329 different stallions was included.

Estimation of variance components were based on the REML-method (Patterson & Thompson 1971) using the software packages VCE version 5.1 (Kovač & Groeneveld 2002) and VCE version 6.0 (Groeneveld *et al.* 2008). The latter was used for the estimation of genetic relationships between traits from BI and MPT. VCE version 5.1 was used for the rest of estimations of variance components. All runs finished with convergence status 1 (*i. e.* save convergence is guaranteed).

The SAS routine Proc Mixed was used to develop the models by testing the significance of fixed effects and evaluating the AIC-value (Akaike 1973). Estimation of genetic parameters was performed with three different mixed linear models. Traits were assigned to one of the three models below depending on the type of performance test:

For foal inspection:

$$(F_{IN}) y_{ijklm} = \mu_i + age_j + sex_k + place\text{-}year_l + animal_m + e_{ijklm} \tag{3}$$

where y_{ijklm} is the phenotypic value of trait l, μ_i is the overall mean, age_j is the fixed effect of age j at performance (j=1-4), sex_k is the fixed effect of sex k (k=1-2), $place\text{-}year_l$ is the fixed effect of combination l of place and year (l=1-47), $animal_m$ is the random effect of the foal m (m=1-17.881) and e_{ijklm} is the random residual effect (0, σ_e^2).

For broodmare inspection:

$$(BM_{IN})\, y_{ijkl} = \mu_i + age_j + place\text{-}year_k + animal_l + e_{ijkl} \tag{4}$$

where y_{ijkl} is the phenotypic value of trait l, μ_i is the overall mean, age_j is the fixed effect of age j at performance (j=1-3), $place\text{-}year_k$ is the fixed effect of the combination k of place and year (k=1-66), $animal_l$ is the random effect of the mare l (l=1-12.069) and e_{ijkl} is the random residual effect (0, σ_e^2).

For mare performance test:

$$(M_{MPT})\, y_{ijklm} = \mu_i + age_j + type\_of\_test_k + place\text{-}year\text{-}season_l + animal_m + e_{ijklm} \tag{5}$$

where y_{ijklm} is the phenotypic value of trait l, μ_i is the overall mean, age_j is the fixed effect of age j at performance (j=1-2), $type\_of\_test_k$ is the fixed effect of type of test k (k=1-2), $place\text{-}year\text{-}season_l$ is the fixed effect of the combination l of place, year and season (l=1-92), $animal_m$ is the random effect of the mare m (m=1-2.756) and e_{ijklm} is the random residual effect (0, σ_e^2).

Overall, it proved to be difficult to define contemporary groups for all three tests. Small test groups are a common problem in equine field data. Small size of groups may cause limited representativeness of the respective group and lead to inadequate connectedness. In this study, alternative definitions of contemporary groups were tested (data not shown) and evaluated, resulting in combinations of place-year and place-year-season which were preferred over the individual test group.

Results

Population structure

Parents of horses that completed at least one of the three tests were analysed (n=26 490). The results exhibited an average number of 10.8 and 2.0 tested progeny per stallion and mare, respectively. Maximum number of progeny was 616 for sires and 12 for dams. Out of the 2 439 stallions, 30 had more than 100, 131 had more than 50 and 583 had more than 10 progeny. Among mares, 29 had at least 10 and 990 had at least 5 tested progeny. An analysis of the stallions with respect to their sub-population of origin showed that 72.8 % of the tested progeny descended from either Hanoverian stallions (18.2 %), Holsteiner (15.7 %), Oldenburger (12.4 %) or Westphalians (11.1 %) and 15.4 % could be traced back to GSH. For GSH, the sub-populations of Berlin-Brandenburg (BB), Saxony-Anhalt (ST), Saxony (SN) and Thuringia (TH) contributed 1 636, 1 264, 739 and 398 stallions, respectively. All stallions of other populations contributed less than five percent of the tested progeny, with the exception of the Trakehner (6 %) and the thoroughbreds (6 %). Dutch stallions were found for 2.4 % of the horses.

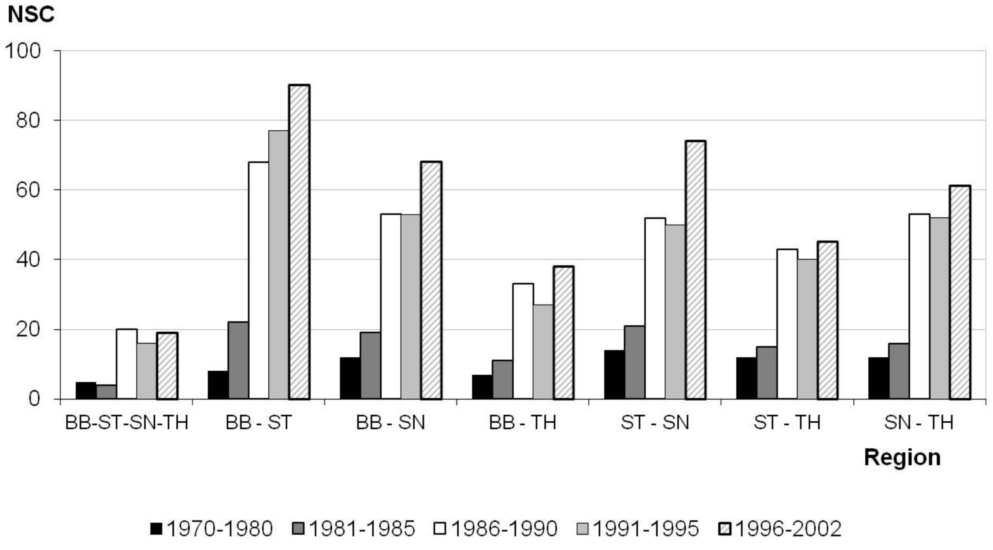
Across all four sub-populations of the GSH (BB, ST, SN, TH), 64 common stallions were found (Table 3). In each of the sub-populations, the stallions that also had been used in all other sub-populations amounted to more than 10 % of all stallions of the respective sub-population. The highest number of common stallions was found for BB and ST (n=267). The frequency of these sires within the two sub-populations is also comparatively high (50.3 % and 44.8 %). The smallest overlap was found between BB and TH with 117 stallions. The contribution of these sires amounted to a relative frequency of 22.0 % and 26.8 %.

The NSC in the GSH sub-populations was determined by dividing the stallions into groups based on their birth year (Figure 1). Across all areas, this value ranges between four (1981-1985) and 20 (1986-1990). The increase in NSC from group I and II (1970-1985) to the following groups (from 1986) indicates a clear increase in the common use of stallions between all sub-population combinations. Genetic similarity across all four sub-populations is 0.19. It is based on the 3 432 foals of the 64 stallions with tested progeny in all sub-populations. The individual combinations have a GS that ranges from 0.26 (BB-TH) to 0.67 (BB-ST). The contributions to GS demonstrate that the distribution of progeny of the common stallions between the sub-populations is equal (Table 4). The maximum difference is 18 % for the combination TH-SN.

Table 3
Number of stallions in common, proportion of common stallions relative to all stallions in the region and number of progeny of the common stallions with tested progeny in foal inspection (n=17 881)

Region	NSC	Proportion of common stallions [%]	Total number of progeny of common stallions
BB - ST - SN - TH	64	12.1 - 10.7 - 11.1 - 14.7	3 432
BB - ST	267	50.3 - 44.8	6 011
BB - SN	208	39.2 - 26.0	4 204
BB - TH	117	22.0 - 26.8	2 011
ST - SN	212	35.6 - 36.7	4 217
ST - TH	155	26.0 - 35.6	3 300
SN - TH	195	33.8 - 44.7	5 366

BB: Berlin-Brandenburg, SN: Saxony, ST: Saxony-Anhalt, TH: Thuringia



BB: Berlin-Brandenburg, SN: Saxony, ST: Saxony-Anhalt, TH: Thuringia

Figure 1
Number of stallions in common between the regions for different birth year groups of stallions with tested progeny in foal inspection (n=17 881)

Table 4
Genetic similarity (after Rekaya *et al.* 2003) between the four regions (above diagonal) and contribution to GS in % [region in rows : region in column], based on stallions with tested progeny in foal inspections (n=17 881)

Region	BB	ST	SN	TH
BB		0.67	0.45	0.26
ST	50.0 : 50.0		0.42	0.38
SN	56.4 : 43.6	56.1 : 43.9		0.61
TH	53.9 : 46.2	50.2 : 49.8	41.0 : 59.0	

BB: Berlin-Brandenburg, SN: Saxony, ST: Saxony-Anhalt, TH: Thuringia

Genetic parameters

Foal and broodmare inspection

Multivariate estimation of variance components for the foal inspection traits resulted in estimated heritabilities of h^2=0.24 for conformation$_f$ to h^2=0.50 for type (Table 5). The genetic correlation between type and conformation$_f$ is high (r_g=0.84). Trait combinations type – gait and conformation$_f$ – gait show an equal genetic correlation of r_g=0.56. Genetic relationships between traits from FI and traits from BI as well as from MPT were estimated in bivariate runs. Estimates range from moderate to high (Table 6), except for the combination gait – free jumping, which has a low estimate of r_g=0.09. With the exception of walk (r_g=0.48), BI traits show high genetic correlation with the FI traits ($0.69 \le r_g \le 0.85$). Individual traits for basic gaits from the MPT range in their genetic correlation to gait from r_g=0.37 (trot$_{pt}$) to r_g=0.46 (walk$_{pt}$).

Genetic analysis for BI included 13 traits. Parameters were estimated in bivariate runs. Resulting estimates for correlations are shown in Table 7. Estimates for heritabilities were averaged over all runs. The estimates demonstrate a wide interval for heritabilities of the BI traits. As expected, type (h^2=0.46), conformation$_m$ (h^2=0.43) and head (h^2=0.50) exhibit all a high heritability. The conformation traits head, neck, saddle position and frame show a moderate level of heritability. Forelegs and hind legs proved to have low heritability with estimates of h^2=0.15 and h^2=0.19. The results for basic gaits range between h^2=0.25 (walk$_{bi}$) and h^2=0.49 (canter$_{bi}$). Genetic correlations are consistently on a moderate to high level. In particular, the traits type conformation$_{bi}$ as well as overall impression and development are very closely related.

Mare performance test

Results from multivariate estimation of variance components MPT traits are shown in Table 8. Estimates of heritability vary between h^2=0.18 (rideability) and h^2=0.46 (trot$_{pt}$). Estimates for basic gaits are on a moderate level and thus emphasize the potential for improvements through genetic selection. Among all traits of the MPT, with the exception of free jumping, all genetic correlations are moderate to high.

Genetic relationships between traits from different tests

The combined analysis of traits from the BI and MPT gives insight into the genetic relationships between traits from both tests. Results in Table 9 are based on bivariate estimation runs. Estimates of heritability were pooled across bivariate estimation runs. Pooled estimates deviate slightly from those shown in Tables 7 and 8 due to different combinations of traits. For walk and trot, estimates of heritability from MPT were found to be higher by 0.05 than compared to BI. However, canter shows a considerably lower heritability. Genetic correlations between basic gaits within the two tests range in intervals of $0.50 \leq r_g \leq 0.65$ (for BI) and $0.56 \leq r_g \leq 0.80$ (for MPT). When comparing the two forms of tests, the respective basic gait traits show a genetic correlation of r_g=0.95 (walk), r_g=0.69 (trot) and r_g=0.83 (canter). It is interesting to note that genetic correlations between free jumping from the MPT and the basic gait traits of BI are higher than those within MPT.

Table 5
Estimates of heritability (on diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal) for foal inspection traits; standard errors in parentheses

Trait (n=17 881)	Type	Conformation$_f$	Gait
Type	0.50 (0.01)	0.84 (0.01)	0.56 (0.01)
Conformation$_f$	0.16	0.24 (0.01)	0.56 (0.02)
Gait	0.15	0.08	0.41 (0.01)

Table 6
Estimates of genetic correlations between foal inspection traits and broodmare inspection traits as well as between foal inspection traits and mare performance tests traits, standard errors: 0.015-0.049

Foal inspection traits	Broodmare inspection traits	Genetic correlation
Type	Breed and sex type	0.85
Conformation$_{f}$	Conformation$_{bi}$	0.82
Gait	Walk$_{bi}$	0.48
Gait	Trot$_{bi}$	0.77
Gait	Canter$_{bi}$	0.69
Foal inspection traits	**Mare performance tests traits**	**Genetic correlation**
Gait	Walk$_{pt}$	0.46
Gait	Trot$_{pt}$	0.37
Gait	Canter$_{pt}$	0.45
Gait	Free jumping	0.09

Table 7
Estimates of heritabilities (on diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal) for broodmare inspection traits; standard errors in parentheses

Trait		(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)	(13)
N		13 562	8 837	13 560	13 562	13 560	13 561	8 848	9 760	13 560	10 783	13 559	2 192	9 060
Breed and sex type	(1)	.46 (.02)	.95	.86	.83	.81	.83	.58	.71	.76	.51	.71	.72	.98
Conformation$_{m}$	(2)	.29	.43 (.02)	.83	.81	.81	.86	.67	.80	.85	.58	.75	.66	.98
Head	(3)	.40	.26	.50 (.02)	.69	.59	.61	.39	.57	.65	.34	.55	.46	.77
Neck	(4)	.34	.25	.29	.36 (.02)	.64	.62	.44	.56	.65	.39	.67	.51	.80
Saddle position	(5)	.26	.22	.15	.20	.28 (.02)	.78	.45	.60	.58	.55	.67	.59	.80
Frame	(6)	.30	.25	.19	.20	.21	.25 (.02)	.62	.75	.70	.56	.74	.74	.92
Forelegs	(7)	.18	.18	.10	.11	.12	.15	.15 (.01)	.73	.78	.48	.52	.35	.71
Hindlegs	(8)	.20	.19	.14	.13	.11	.18	.15	.19 (.02)	.81	.49	.67	.48	.79
Correctness of gaits	(9)	.17	.13	.13	.12	.10	.13	.15	.14	.16 (.01)	.45	.59	.42	.71
Walk$_{bi}$	(10)	.16	.12	.09	.09	.12	.13	.12	.11	.09	.25 (.02)	.61	.50	.60
Trot$_{bi}$	(11)	.26	.17	.18	.19	.19	.21	.13	.13	.16	.20	.42 (.02)	.65	.79
Canter$_{bi}$	(12)	.26	.16	.13	.16	.20	.21	.11	.11	.11	.17	.34	.49 (.04)	.75
Overall impression & development	(13)	.42	.25	.30	.28	.23	.31	.17	.19	.18	.18	.29	.28	.36 (.02)

Table 8
Estimates of heritabilities (diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal) for mare performance tests traits; standard errors in parentheses; standard errors (s.e.) for genetic correlations: 0.024≤s.e.≤0.059)

Trait	Walk$_{pt}$	Trot$_{pt}$	Canter$_{pt}$	Rideability	Free jumping
N	2 729	2 728	2 729	2 699	2 756
Walk$_{pt}$	0.29 (0.02)	0.55	0.62	0.37	0.03
Trot$_{pt}$	0.28	0.46 (0.02)	0.80	0.66	0.08
Canter$_{pt}$	0.24	0.37	0.28 (0.02)	0.73	0.22
Rideability	0.21	0.27	0.31	0.18 (0.02)	0.08
Free jumping	0.09	0.12	0.16	0.13	0.41 (0.02)

Table 9
Estimates of heritabilities (on diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal) for broodmare inspection traits (BI) and mare performance tests traits (MPT); standard errors in parentheses; standard errors (s.e.) for genetic correlations: 0.029≤s.e.≤0.087)

Trait		Walk$_{bi}$	Trot$_{bi}$	Canter$_{bi}$	Walk$_{pt}$	Trot$_{pt}$	Canter$_{pt}$	Rideability	Free jumping
		BI	BI	BI	MPT	MPT	MPT	MPT	MPT
N		9 686	12 067	2 162	2 729	2 728	2 729	2 699	2 756
Walk$_{bi}$	BI	0.25 (0.02)	0.61	0.50	0.95	0.55	0.62	0.50	0.05
Trot$_{bi}$	BI	0.20	0.41 (0.02)	0.65	0.60	0.69	0.71	0.53	0.18
Canter$_{bi}$	BI	0.17	0.34	0.48 (0.04)	0.44	0.51	0.83	0.52	0.50
Walk$_{pt}$	MPT	0.22	0.13	0.12	0.30 (0.03)	0.56	0.65	0.38	0.03
Trot$_{pt}$	MPT	0.12	0.22	0.22	0.28	0.46 (0.03)	0.80	0.65	0.08
Canter$_{pt}$	MPT	0.10	0.18	0.28	0.24	0.37	0.28 (0.03)	0.73	0.17
Rideability	MPT	0.06	0.09	0.15	0.21	0.27	0.31	0.18 (0.03)	0.07
Free jumping	MPT	0.06	0.07	0.13	0.09	0.12	0.16	0.13	0.41 (0.03)

Discussion

The GSH is a relatively new sub-population of the German Riding Horse and itself can be stratified into four regional sub-populations. The analysis presented in this study is the first joint genetic analysis of all four sub-populations and covered an analysis of the population structure as well as an estimation of genetic parameters based on data from FIs, BIs and MPTs. The general breeding programme of the GSH is defined as ›pure-breeding in an open population‹. This strategy is reflected in the structure of the parental generation. Of all tested horses, 15 % descend from stallions of the regional sub-populations (BB, ST, SN, TH). The population is also considerably influenced by Hanoverian, Holsteiner, Oldenburger and Westphalian stallions. All in all, an intensive use of sires from different German breeding areas was observed. This has a considerable influence on the genetic make-up of the GSH population and also ensures a genetic connectedness with the all-German Riding Horse population. Hence, the genetic connectedness of the GSH with the rest of the German Riding Horse population in the national genetic evaluation system is fully established. The GSH population is a representative part of the German Riding Horse population and therefore will be able to contribute valuable data for future research work concerning genomic breeding values and genomic selection.

Data presented in this study show a gender-specific parents-progeny-distribution typical for horse breeding. The genetic connectedness between the four sub-populations is realized solely by the comprehensive use of sires while the maternal side with its low numbers of progeny per mare contributes little to connectedness. The genetic connectedness between the sub-populations is very strong. The NSC as well as the GS reflect an intensive cooperation between the sub-populations of BB and ST as well as SN and TH. The number of common sires across all regions appears to be rather low (n=64). Only a few overall ›link-providers‹ could be detected. Even highly frequented stallions are often underrepresented in one of the sub-populations. The percentage contributions of the individual GS according to formula [2] were fairly even and suggest a mostly balanced distribution of the sires and their progeny across sub-populations. Across time, a continuous exchange of genetic material is observed. The enormous increase of the parameter ›number of stallions in common‹ in the mid-eighties (Figure 1) apparently can be attributed to enhanced opportunities in reproductive biology, especially to the increased use of artificial insemination. Thorén Hellsten *et al.* (2008) also detected an increasing NSC for Hanoverian and Holsteiner sport horse populations. Between these populations, GS was estimated at 15 %.

Germany is the main exporting country for stallions and their genetics in Europe and together with France and the Netherlands, it is considered the most connected country, *i.e.* population (Ruhlmann *et al.* 2009). Studies by Thorén Hellsten *et al.* (2008) show GS values of $0.07 \leq GS \leq 0.31$ for different European riding horse populations. The horses in this study are connected much closer ($0.26 \leq GS \leq 0.67$), which was to be expected since the GSH was formed from closely cooperating sub-populations. The high degree of genetic connectedness is beneficial for an internal system of genetic evaluations as a supplement to the national genetic evaluation system. In summary, the genetic connectedness within the GSH population is not fully balanced. However, it can be considered to be sufficiently strong and complex to enable a reliable estimation of population parameters and breeding values.

The inspection of a foal within the first months of its life provides early indicators of performance for the horse. These data provide a relatively general description of the disposition of the young horse in the traits type, conformation and gait. As expected, the estimation of parameters thus results in a high level of heritability (Table 5). Comparisons with findings of similar studies show values to be predominantly comparable, but the definition of traits is not completely consistent. For Holsteiner foals Bösch *et al.* (2000) determined values of $h^2_{type/conformation}=0.42$ and $h^2_{gait/swing}=0.40$. Teegen (2008) calculated $h^2_{type}=0.39$ and $h^2_{body/legs}=0.27/0.17$ for Trakehner foals with a sire-dam model.

The importance of the FI as an early indicator was examined using the correlation between traits from FI and subsequent trait evaluations in the BI and MPTs. Foal inspection as an early performance appraisal has to be viewed from different perspectives. Traits within the trait group type and conformation exhibit high correlations. The genetic relationship between gait (from FI) and walk from both BI and MPT was very similar (0.48, 0.46). However, the correlation between gait and the other two basic gaits differs substantially. For trot as well as for canter the genetic relationship between foal and mare traits is much higher for BI than for MPT. It may be hypothesized that one reason for this is the different kind of presentation of the horse. For FI and BI the presentation of the animals is very similar: free moving or shown in hand. In contrast, for MPT the mare is presented under saddle and is therefore subject to the direct influence of the rider. Since FI and BI are separate evaluations, they are independently judged. Whether the appearance of the mare has an indirect influence on the scoring of the foal cannot be assessed.

Based on the results of this study, the foal evaluation may be considered as a reliable indicator for type and conformation of subsequent tests. With regard to the adult performance in basic gaits, a distinction must be made between the kind of test (BI or MPT). Inferences on the ability in free jumping based on the FIs are not possible.

Estimated heritabilities of the traits in BI are within the range of values from other studies for German Riding Horse populations. In particular, for the traits breed and sex type, $walk_m$, $trot_m$ and overall impression, the results of this study are almost identical to the values from Teegen (2008) for Trakehner mares. Estimates for forelegs and hind legs as well as the correctness of gaits confirm the apparent low level of heritability, which was also documented for the mare population of Hanoverians (Christmann 1996), Holsteiners (Bösch *et al.* 2000) and Mecklenburgers (Dietl *et al.* 2004).

Estimates of heritabilities for further conformation traits as well as the genetic correlations among them were slightly above the values of comparable analyses. Estimates of genetic correlations were somewhat higher for most of the traits when compared to studies by Christmann (1996) and Dietl *et al.* (2004). However, the estimates almost invariably confirm the trait-specific trend. Very high correlations were found between the characteristics type $conformation_m$, overall impression and development. This finding seems to confirm the existence of suspected autocorrelations between individual traits as presumed by Willms *et al.* (1999).

A strong genetic relationship between fore- and hind legs with correctness of gaits is documented in correlations of r_g=0.81 and r_g=0.78. Considering basic gait traits, genetic relationships appear to be stronger between trot and canter as well as between trot and walk than between canter and walk. Christmann (1996) also found some correlations for BI traits of Hanoverians to be negative. This cannot be confirmed neither for the Mecklenburger population (Dietl *et al.* 2004) nor from the results of this study.

Viklund *et al.* (2008) analysed the Swedish Warmblood Horses using data from the *Young Horse Test* (predominantly 3-year-olds) and from the *Riding Horse Quality Test* (predominantly 4-year-olds). For the young horse test, these authors found heritability estimates of 0.46/0.39 for type, 0.08/0.08 for correctness of gaits, 0.37/0.31 for walk in hand, and 0.45/0.41 for trot in hand. For the riding horse quality test, the authors also studied the basic gaits under rider and estimated heritabilities of 0.38 (walk), 0.48 (trot) and 0.38 (canter). Analogous to this study, the presentation of walk and trot under saddle in the analysis by Viklund *et al.* (2008)

tended to show higher estimates than free-walking or in hand presentation. However, the results of this study show the opposite trend for canter.

Overall, estimates of heritabilities for traits from MPT range within values reported in comparable studies from other German Riding Horse populations (Table 1). Free jumping and trot show high heritabilities. Rideability ranks in the lower range of similar analyses. Huizinga *et al.* (1990), however, found much lower values (h^2=0.03) for the Dutch population and furthermore, also for other traits evaluated in field tests relatively low values were estimated (trot: 0.14, walk: 0.22, canter: 0.18, free jumping: 0.15).

A comparison of the results of this study with the parameters used for the national evaluation system show an almost identical value for walk. For trot and free jumping our estimates are slightly higher than those from the national system. For canter and rideability, the situation is reversed with the highest difference for rideability. A comparison of the genetic correlations estimated in this study with genetic correlations as used for respective traits in the national genetic evaluation system exhibits values and relations between traits largely in a similar range. With the exception of walk : rideability (Δ=0.19) and trot : canter (Δ=0.11) the maximum difference is 10 %.

Thus, with regard to the national breeding value estimation, the parameters used in the national system appear to be in line with the GSH population. Only the trait rideability should be viewed with a critical eye and the cause of the deviation should be subject to further investigations.

In inspections and performance tests of sport horses as well as when assessing prospects for future success in tournaments, rideability and jumping ability play an important role. Besides show jumping and dressage competitions themselves, the MPT provides an opportunity to assess the dressage and jumping ability of the horse.

However, relatively few mares which often have also been pre-selected participate in the MPT. Thus, the correlations with traits from the BI, which has a much higher number of participants, are of interest, in particular the basic gaits which are potential link traits. Genetic relationships of traits from BI and MPT were analysed and the results showed that genetic correlations are on a moderate to high level with the exception of free jumping (Table 9). The three basic gaits are correlated with the respective counterpart with estimates ranging from r_g=0.69 (trot) to r_g=0.95 (walk). Teegen (2008) compared results for traits from BI and MPT as a field test. Compared to our study, genetic correlations between BI and MPT as a field test rank equally but on a lower level of magnitude. Christmann (1996) reported higher values with r_g=1.00 for walk and r_g=0.81 for trot. It is noteworthy that free jumping in MPT is more closely correlated to basic gaits from the BI than to basic gaits of MPT itself. This may be due to the way the horse is presented. Scoring for basic gaits in MPT is under saddle. Broodmare inspection and free jumping in MPT are conducted with the horse in hand or free walking and consequently there is no effect of the rider in both cases.

The analysis of the relationships between traits across tests proved the inherent connection between BI and MPT. Genetic correlations between BI and MPT for basic gaits and for rideability allow a joint use of these complexes. However, walk, trot and canter must be considered as individual traits in each test, as they cannot be regarded as an identical trait genetically.

All in all, traits from mare inspection and MPTs have mostly moderate to high heritabilities and do not reveal any genetic antagonisms. This suggests that the prospects for improvements through genetic selection are very good. As both tests take place at nearly the same time in the mare's life, the estimation of genetic correlation between the traits of both complexes is not hampered by differences in time. Additionally, close genetic relationships between the respective basic gaits from both tests and the quantity of data from BIs allow a prognosis for the future ability and performance in basic gaits under the rider.

For further research, competition traits should also be considered in the analysis. Studies from Aldridge *et al.* (2000), Ducro *et al.* (2007) and Kearsley *et al.* (2008) have shown that the inclusion of such data is useful since highly positive correlations between competition traits and young horse test traits have been found (Wallin *et al.* 2003, Viklund *et al.* 2010).

In conclusion, the data analysed can be considered as suitable for genetic analyses and the estimation of breeding values. A joint use of FIs, BIs and MPTs is a valuable addition to the national system and especially utilizes data from a large number of mares not contained in the sport-oriented national system.

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