Analyses of performance traits in the Norwegian Warmblood.

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Introduction

Young horse performance testing is highly appreciated and used as a tool for predicting the horses' value as a performance- or breeding animal. Traits included in performance tests are gaits and jumping ability, as well as conformation, health and temperament. The heritability for performance traits from such tests is low to moderate (Huizinga et al 1993, Wallin et al., 2003). Correlations between performance traits tested at young horse tests and performance later in life are moderate to high (Wallin et al., 2003, Ducro et al 2007, Olsson et al 2008). Conformation traits have effect on the horses' performance and health (e.g Holmström et al., 1990, Love et al., 2006, Ducro et al., 2009). A young horse performance test, the Young Horse Quality Test (YHQT) has taken place each year in Norway since 1981. The aim of this study was to analyse performance traits in the Norwegian Warmblood based on records from the YHQT.

Material and method

Traits recorded at the YHQT and analysed in this study are; the overall score for clinical health, conformation and gaits under rider, walk, trot and canter under rider, jumping ability (either as free-jumping or jumping under rider) and temperament during health examination and the jumping ability test. Some traits (walk, trot, canter, overall gaits and jumping under rider) were for some years recorded both by a ground judge and a test rider. All traits were included in the analyses of fixed effects, however only recordings done by the ground judge were included in the genetic analyses. Traits were scored on a scale from 0 to 10. Summary statistics of the data is given in table 1.

Animal material

All 4-year-old horses were allowed to participate in the YHQT as well as 5-year-old mares that had a foal the year before. From 1983-2006 the YHQT was part of the stallion approval system and 5-year-old stallions was also allowed to participate in the test during that time. A total of 584 animals were available for analysis; 102 stallions, 217 mares and 244 geldings, and 21 horses with missing record of their sex. A pedigree-file was constructed based on the pedigree-information of the participating animals, and the pedigree-file consisted of 5884 horses.

Table 1. Summary statistics with number of recordings per trait (N), the mean (M), Standard deviation (SD), and range of the scores for traits presented in this study.

Traits	N	M	SD	Range
Clinical Health [1]	561	8.38	1.20	3-10
Temperament during clinical health examination [1]	514	8.78	1.56	2-10
Conformation [2]	556	6.66	0.82	4-8.8
Walk [2]	519	6.58	1.17	3-10
Trot [2]	519	6.38	1.14	3-10
Canter [2]	519	6.53	1.16	4-10
Gaits [2]	551	6.51	0.95	4.3-9.3
Jumping under rider [2]	439	6.36	1.57	3-10
Temperament jumping under rider [2]	313	6.48	1.76	2-10
Free-jumping [2]	138	6.51	1.70	2-9
Temperament Free-jumping [2]	138	6.98	1.92	3-10
Walk [3]	62	6.87	0.93	5-9
Trot [3]	62	6.42	0.78	5-8
Canter [3]	62	7.18	0.88	5-9
Gaits [3]	62	6.82	0.71	5.0-8.3
Jumping under rider [1]	78	6.44	1.35	4-9

[1] scored by veterinarian, [2] scored by ground-judge, [3] scored by test-rider

Data analyses

General linear model (GLM) analyses in SAS (SAS, 2002) were used to test the significance of fixed effects for each trait. The following model was used for all traits:

$$Y_{ijklm} = \mu + startyear_i + sex_j + birthcountry_k + startgroup_l + e_{ijklm} \qquad \text{(Model I)}$$

where Y_{ijklm} is the score for the recorded trait for animal *m*; μ is the overall mean; $startyear_i$ is the effect of the year the horse was tested (*i* = 1,...,25); sex_j is the effect of the sex (*j* = 1,2,3). The sex of the horse is either stallion, mare or gelding. $birthcountry_k$ is the effect of the country the horse was born in (*k*=1,...,6). The countries were Norway, Sweden, Denmark, Germany and The Netherlands or ‘other’. The ‘other’ group consisted of countries having <10 horses participating in the test; $startgroup_l$ is the start-group the horses’ started in (*l*=1,...,4). Preliminary examinations showed no effect of the horses’ individual starting-order, probably because the number of participating horses varied between the years (from 7 to 34). The horses were therefore divided into four groups according to their starting-order within each year, with the first 25 % of the horses in starting-group 1, the next 25 % in starting group 2, and so on. The residuals were assumed to follow a normal distribution: e_{ijkl} ~N $(0, \sigma_e^2)$.

Univariate linear animal models were used for the genetic analyses. Fixed effects from Model I that were significant ($\alpha < 0.1$) were included in Model II:

$$Y_{ijkl} = \mu + startyear_i + sex_j + birthcountry_k + animal_l + e_{ijkl} \qquad \text{(Model II)}$$

where Y_{ijkl}, μ, startyear, sex, birthcountry and e were defined as in model I, and $animal_l$ is the random effect of animal *l* with the assumed distribution: animal$_l$ ~N(0,**A** σ_a^2). **A** is the additive genetic relationship matrix. The heritability was not estimable for all traits due to few observations for some of the traits (Table 1). Heritabilities were therefore estimated for the main traits clinical health, temperament during clinical health examination, the total conformation score, walk, trot, canter and the total score for gaits. These traits have been recorded in the same way all test-years. Variance components were estimated with the DMUAI routine implemented in the DMU software (Madsen and Jensen, 2008).

Results

Year

There was a significant effect of year implying an increase with time in the overall phenotypic performance for horses in the Norwegian Warmblood Population.

Sex

Stallions got significantly better scores than both mares and geldings for gaits, conformation, jumping and temperament during jumping test, except for the overall gait score where they only scored better than the mares. The stallions had significantly lower scores than mares and geldings for temperament during the clinical health examination. Other studies has defined the sex of the horses as either male or female (Wallin et al., 2001, Holmström & Philipsson 1993), and found that males performed better than females overall.

Starting order

Table 2. LS-means and their standard error (± SE) for the four start groups for some performance traits evaluated and scored in the YHQT.

Traits	LS-means			
	Group 1 $_{\pm SE}$	Group 2 $_{\pm SE}$	Group 3 $_{\pm SE}$	Group 4 $_{\pm SE}$
Temperament [1]	$7.85_{0.21}^{\ d}$	$8.29_{0.21}$	$8.12_{0.21}$	$8.37_{0.23}^{\ a}$
Jumping [2]	$7.05_{0.18}^{\ d}$	$6.93_{0.19}$	$7.00_{0.19}$	$9.59_{0.21}^{\ a}$
Walk [3]	$6.94_{0.25}^{\ c}$	$7.28_{0.30}$	$7.87_{0.36}^{\ a}$	$7.56_{0.34}$
Trot [3]	$6.30_{0.22}^{\ c}$	$6.14_{0.26}^{\ c}$	$7.07_{0.30}^{\ a.b}$	$6.52_{0.30}$
Canter [3]	$7.01_{0.23}^{\ c}$	$7.17_{0.27}^{\ c}$	$8.29_{0.32}^{\ a.b.d}$	$7.40_{0.31}^{\ c}$
Gaits [3]	$6.75_{0.19}^{\ c}$	$6.86_{0.23}^{\ c}$	$7.74_{0.26}^{\ a.b}$	$7.16_{0.26}$

[1] scored by veterinarian, [2] scored by ground-judge, [3] scored by test-rider

$^{a.b.c,d}$ different letters indicating a significant difference between the groups ($p<0.05$).

Table 2 shows that horses starting in the last half of the test had significantly better scores for all traits presented in the table than horses starting in the first half. There was no effect of starting-order on the other traits included in the analyses. Few studies has considered the effect of starting-order, but a German study (Dietl et al 2005) showed differences in the distribution of points given by a judge that had no previous knowledge of a horse and a rider that had trained the same horse for a period of time. It might be assumed that the starting-order effect also includes an effect of the judge and/or test-rider, it was however not possible to include judge/rider as an effect in the analyses,

Country of origin effects

Horses born in Norway had significantly lower scores for gaits and conformation than horses born in Sweden and Denmark, the Danish born horses had also better scores for free jumping than the Norwegian. German born horses were better than the Norwegian ($p<0.05$) for conformation, jumping, temperament during jumping and free-jumping. Dutch born horses were better than Norwegian for jumping and temperament free-jumping. German horses received higher scores than Danish horses for temperament in the jumping test. The observed differences may be because the Norwegian horses represent the average while the foreign horses are selected to Norway due to one or more desirable traits or performance abilities. The effects of country of origin in this study do not imply any ranking of breeding organisations, but rather the specific level of the imported horses. A study by Thorén Hellsten et al (2009) showed that stallions originating from certain breeding associations in Germany, France and

Netherland had significantly higher breeding values for show jumping than Swedish horses implying that there may be genetic differences present as well.

Genetic Analyses

Table 3. Genetic variance, (σ_a^2) residual variance (σ_e^2) with their respective standard errors (± SE), and the corresponding heritability estimates (h^2) for performance traits recorded in the YHQT

Trait	$\sigma_a^2 \pm SE$	$\sigma_e^2 \pm SE$	h^2
Health[1]	$0.04_{0.08}$	$0.60_{0.09}$	0.06
Temperament[1]	$0.20_{0.19}$	$0.94_{0.19}$	0.18
Conformation[2]	$0.13_{0.09}$	$0.37_{0.08}$	0.26
Walk[2]	$0.28_{0.21}$	$0.80_{0.20}$	0.26
Trot[2]	$0.31_{0.17}$	$0.76_{0.17}$	0.29
Canter[2]	$0.17_{0.15}$	$0.83_{0.15}$	0.17
Gaits[2]	$0.22_{0.11}$	$0.44_{0.10}$	0.33

[1] scored by veterinarian, [2] scored by ground-judge

The heritability estimates (table 3) for all traits were low to medium. The highest heritability estimate (0.33) was found for the total score for gaits, and that is also the only significant heritability that was found. Since variance components were estimated based on a small dataset, SE was relatively large and results should be interpreted with caution. However the heritability for conformation, walk, trot and canter are similar to heritabilities found in other studies (Huizinga et al 1990, Wallin et al 2003) and there is reason to believe that these estimates are applicable for further research.

Conclusion

Results obtained in this study suggest that data from the Norwegian Warmblood population is of sufficient quality to allow further statistical analyses. Breeding value estimations for the population can also be performed if additional information is included in the analyses, as is to be done in the ongoing Nordic Interstallion project. This project is aiming at performing joint genetic evaluations in the four Nordic countries, Norway, Finland, Sweden and Denmark.

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