Citation for the published paper:
Viklund, Å., Näsholm, A., Strandberg, E., Philipsson, J. (2010) Effects of long-time series of data on genetic evaluations for performance of Swedish Warmblood riding horses. *Animal*. Volume: 4 Number: 11, pp 1823–1831.
http://dx.doi.org/10.1017/S1751731110001175

Effects of long-time series of data on genetic evaluations for performance of Swedish Warmblood riding horses

Å. Viklund, A. Näsholm, E. Strandberg and J. Philipsson

Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, SE-750 07 Uppsala, Sweden

Corresponding author: Åsa Viklund. E-mail: Asa.Viklund@hgen.slu.se

Running head

Long-time horse data for genetic evaluation

Abstract

For Swedish Warmblood sport horses (SWB), breeding values (BVs) are predicted using a multiple-trait animal model with results from competitions and young horse performance tests. Data go back to the beginning of the 1970s, and earlier studies have indicated that some of the recorded traits have changed throughout the years. The objective of this study was to investigate the effects of including all performance data or excluding the older ones compared to a bivariate model considering performance traits in early and late periods as separate traits. The bivariate approach was assumed to give the most correct BVs for the actual breeding population. Competition results in dressage and show jumping for almost 40 000 horses until 2006 were available. For Riding

Horse Quality Test (RHQT) data of 14 000 horses judged between 1973 and 2007 were used. Genetic correlations of 0.69-1.00 were estimated between traits recorded in different time periods (RHQT data) or different birth year groups (competition data). A cross validation study and comparison of BVs using different sets of data showed that most accurate and similar results were obtained when BVs were predicted from either the bivariate model or the univariate model including all data from beginning of recording. We recommend using all data and applying the univariate model to minimize the computational efforts for genetic evaluations and for provision of reliable BVs for as many horses as possible.

Key words: Riding Horses, Breeding value, Cross Validation

Implications

Performance data for Swedish Warmblood horses used for genetic evaluation go back to the early 1970s. Some of the recorded traits have changed considerably over the years. To estimate accurate and reliable breeding values it was important to investigate how the long-time series of data should be handled in the genetic evaluations. Different models were compared regarding their predictive ability, and differences and accuracies of predicted breeding values (BVs) were investigated. The study showed that all data from the beginning of recording can be used to maximize “unbiasedness” and reliabilities of BVs for as many horses as possible.

Introduction

Genetic evaluation for Swedish Warmblood sport horses (SWB) is based on a multiple-trait animal model with results from competitions and young horse performance tests. Data go back to the beginning of the 1970s. Earlier studies (Viklund et al., 2008 and 2010) have shown that some of the recorded traits have not stayed the same throughout the years. The heritabilities and variances changed over time, and the genetic correlations between traits recorded in different time periods were sometimes considerably less than unity. For conformation, gait and jumping traits at Riding Horse Quality Tests for 4-year-olds (RHQT) heritabilities increased between judging periods 1973-1987 and 1996-2002, mostly due to lower residual variances in the later period (Viklund et al., 2008). For example, the heritability for canter under rider increased from 0.22 to 0.37, whereas the residual variances decreased from 0.87 to 0.52. The phenotypic variance decreased for all traits. Genetic correlations between traits in the different judging periods ranged between 0.48 (correctness of legs) and 0.97 (walk under rider). For dressage competition traits heritabilities decreased slightly between birth year groups 1953-1983 and 1992-2002 (from 0.18 to 0.14), whereas they increased slightly for show jumping (from 0.31 to 0.34) (Viklund et al., 2010). For both disciplines, the phenotypic variances decreased between traits recorded in the early period and late period (0.61 to 0.50 for dressage and 0.61 to 0.47 for show jumping). The genetic correlations between traits in different birth year periods were 0.71 (dressage) and 0.66 (show jumping). These changes in genetic parameters were suggested to be caused by expansion of the sport, changes in scoring of young horses and increased foreign influence on the horse population as breeding has become internationalised (Viklund et al., 2008 and 2010).

Accuracy of genetic evaluations depends on how well the assumptions of the model match the data. Usually, as for the genetic evaluation of SWB, constant variance of traits recorded across time is assumed, but often this assumption does not hold. In dairy cattle for example, milk yield has increased over time due to improvement of management and increased genetic level as a result of selection. Variances for milk production traits have increased simultaneously with increasing means (Van Vleck, 1966; Tsuruta et al., 2004). In the Icelandic horse population, the phenotypic standard deviation as well as the heritabilities increased considerably between time periods due to a re-definition of traits in 1990 (Árnason & Sigurdsson, 2004). The largest difference in heritabilities between traits recorded in different judging periods (1979-1989 and 1990-2003) was found for legs that increased from 0.16 to 0.38, and the largest difference in phenotypic standard deviation was found for trot (from 0.48 to 0.72). The correlations between traits in the two different time periods were for many traits significantly deviating from one (0.68-0.94). For other horse populations, changes in variation of traits over time have not been reported.

There are different approaches for handling changes in variation over time. One way is to adjust variances of data from different groups to a common population variance (e.g. Hill, 1984; Wiggans & VanRaden, 1991; Van der Werf et al., 1994). Another way of handling the problem, suggested by Weigel and Banos (1997), as regards international dairy sire evaluations, was to discard historical performance data of bulls from breeds or strains that have been changed by imported stock. A third approach is to treat traits in different time periods as different traits. In the Icelandic horse population the traits are regarded as different traits if they are scored before or later than 1990 (Árnason et al., 2006), and Tsuruta et al. (2004) handled milk records in every 3-year interval as separate traits.

The objective of this study was to investigate how the long-time series data of SWB horses should be handled in the genetic evaluation to estimate accurate and reliable breeding values (BVs). Univariate models including all performance data or excluding data from the early period were compared to a bivariate model where performance traits were considered as different traits in early and late period.

Materials

Data

The data was provided by the Swedish Warmblood Association and the Swedish Equestrian Federation. RHQT data comprised 18 216 horses evaluated between 1973 and 2007. The RHQT is a one-day field test, where conformation, gaits, jumping and rideability are judged on a scale from 1 to 10. The test is open for all 4-year-old SWBs, and for 5-year-old mares that had foaled as 4-year-olds. The traits studied were type, trot at hand, canter under rider, jumping technique & ability, and temperament & general appearance for jumping. Competition data comprised 15 396 horses that had competed in dressage and 29 564 horses that had competed in show jumping. The horses were born between 1953 and 2002, and they had competed during the period 1962-2006. Competition results were recorded as accumulated lifetime upgrading points in show jumping and dressage, transformed with a logarithm to the basis of ten to a nearly normal distribution. Show jumping and dressage results were analysed separately. The data structure is described in more detail by Viklund et al. (2008 and 2010).

For both RHQT and competition data a pedigree database including seven ancestral generations was used to create the corresponding additive relationship matrix **A** for the genetic analyses (45 811 ancestors for RHQT data and 81 103 ancestors for competition data).

Time periods

Following Viklund et al. (2008) the RHQT data were divided into two test time periods, early period (1973-1987) and late period (1988-2007). The competition data were divided into two corresponding periods by birth year, early period (1953-1983) and late period (1984-2002), as recommended by Viklund et al. (2010). The cut points were chosen to coincide with a break-point in annual genetic progress, measured by the trends in BLUP-index of tested horses. For horses born until 1983 this progress was modest. Because horses are 4 or 5 years of age at RHQT, the cut point 1987 for RHQT data corresponds to birth year 1983 for competition data. The distribution of horses judged or competing in different time periods, means and standard deviations for RHQT and competition traits are presented in Table 1 and 2.

Methods

Estimation of genetic parameters

The RHQT and competition data were analysed separately. Genetic parameters and BVs were obtained by using the DMU package for analysing multivariate mixed models (Jensen & Madsen, 1997). For each trait four analyses were performed according to the following type of model and data included:

UE=Univariate model, only data from the early period,

UL=Univariate model, only data from the late period,

UW=Univariate model, all data (whole period), BM=Bivariate model, all data with separate trait definition for early and late time periods.

Additionally, univariate analyses were performed for the whole data sets where the scores were standardised to a common unity variance. The phenotypic variance for RHQT traits was adjusted to be equal for all events, whereas the competition trait variances were adjusted to be equal for all birth years. The results from these analyses were almost identical to the results from the UW and are therefore not reported.

The basic bivariate model (BM) was:

$$\begin{pmatrix} y_1 \\ y_2 \end{pmatrix} = \begin{pmatrix} X_1 & 0 \\ 0 & X_2 \end{pmatrix} \begin{pmatrix} \beta_1 \\ \beta_2 \end{pmatrix} + \begin{pmatrix} Z_1 & 0 \\ 0 & Z_2 \end{pmatrix} \begin{pmatrix} a_1 \\ a_2 \end{pmatrix} + \begin{pmatrix} e_1 \\ e_2 \end{pmatrix}$$

where y_1 is the observed trait 1 (early period) and y_2 is the observed trait 2 (late period). The vector $(\beta_1 ' \beta_2 ')'$ contains for RHQT traits the fixed effects of event (1,...,432), sex (male or female) and age (4 or 5 years of age), and for competition traits the fixed effects of birth year (1953,...,2002) and sex (male or female). The **X** and **Z** matrices are incidence matrices relating the observations to the fixed and random effects, respectively, **a** is a vector of additive genetic effects of the horses, and **e** is a vector of random residuals:

$$\begin{pmatrix} a \\ e \end{pmatrix} \sim N\left[\begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} G \otimes A & 0 \\ 0 & \mathrm{R} \otimes I_n \end{pmatrix} \right]$$

where **G** is the additive genetic covariance matrix with the following components:

$$G = \begin{pmatrix} \sigma^2_{a1} & \sigma_{a1,a2} \\ \sigma_{a2,a1} & \sigma^2_{a2} \end{pmatrix},$$

$\otimes$ is the Kronecker product, **A** is the additive genetic relationship matrix and **R** is the residual dispersion matrix and has following components:

$$\mathrm{R} = \begin{pmatrix} \sigma^2_{e1} & \sigma_{e1,e2} \\ \sigma_{e2,e1} & \sigma^2_{e2} \end{pmatrix},$$

where σ^2_{e1} is the residual variance for trait 1 (data from late period is missing); σ^2_{e2} is the residual variance for trait 2 (data from early period is missing); and $\sigma_{e1,e2}$ and $\sigma_{e2,e1}$ are the covariances between early and late period. Because a horse could not have observations from both periods, those covariances are not estimable and were set to zero.

The same model was used in the univariate analyses (UW, UE and UL) with the simplification of including only one trait and the corresponding rows and columns of R and G deleted.

Index calculation

The predicted breeding values from the analyses were transformed to the common publication scale as follows:

$BV=\mu+((BV_u – m_u)/\sigma_a)*s.d.$

where BV is the predicted breeding value on the common publication scale, μ is the mean of BV for the reference population equal to 100, BV_u is the breeding value on the original scale from the analyses, m_u is the mean of BV_u in the reference population (horses judged in RHQT 1994-2007 or horses born 1989-2002 with competition results regardless of discipline), σ_a=additive genetic standard deviation of the trait in the reference population, and s.d. is the desired genetic standard deviation of BV fixed to 20 units.

Accuracy of BVs

Accuracies defined as the correlation between true and estimated BV (r_{TI}), were calculated as

$r_{TI}=\sqrt{1-PEV/\sigma_a^2}$

where PEV = prediction error variance.

Comparison of models

Comparison of BVs. All comparisons of BVs were performed relative to the BVs for the late period estimated with the bivariate model, because these were regarded as the most correct BV for the actual breeding population. Correlations between BVs predicted in different models were calculated and the average of the differences (real) and average of the absolute values of the differences (absolute) between different BVs were investigated. The comparisons were conducted for different groups of horses, i.e., all horses judged in RHQT and horses in each time period of RHQT, and for all horses with competition results within a discipline and for horses of each birth year period.

Comparison of r_{TI}. For each judging year (RHQT) or each birth year (competition) the average r_{TI} was calculated for BVs predicted in the different models.

Cross validation. A cross validation (CV) study was performed for one trait from each data set to compare the predictive ability of the models. The chosen traits trot at hand from RHQT data and 10-log accumulated points in show jumping, had shown the lowest genetic correlations between time periods in the earlier studies by Viklund et al. (2008 and 2010). The late period of the data was divided into five equal test data sets within event for RHQT data and within birth year for competition data. All test data sets had the same number of horses and the same distribution of fixed effects. The UL, UW and BM analyses were performed leaving out one test data set at a time. For the test data set left out the expected phenotypic values of the horses were calculated from the estimates from the analyses and compared to the real phenotypic values by the correlation and the root mean squared error (RMSE).

Results

Genetic parameters

In the analyses of RHQT data, heritabilities ranged between 0.08 and 0.38, and genetic variances ranged between 0.14 and 0.42 (Table 3). For all traits, the heritabilities were largest in late period (UL and BM). The genetic variances were highest in late period (UL and BM) for all traits, except for type, but there were no large differences compared with the univariate analysis using all data (UW). The residual variances were lowest for all traits in the late period (UL and BM). For competition traits, heritabilities ranged between 0.14 and 0.31, and genetic variances ranged between 0.07 and 0.19 (Table 4). For dressage, the heritabilities were highest for the early period (UE and BM). For show jumping there was no difference between early and late period (UE, UL and BM). The genetic variances, as well as the residual variances, were highest in the early period for both dressage and show jumping. The genetic correlations between traits recorded in different time periods (RHQT) or different birth year groups (competition) showed that most traits had not been the same throughout the years, especially trot at hand judged at RHQT (0.69) and show jumping (0.74) (Table 5).

BVs

The average real differences between BVs for late period in the BM analyses and the UW analyses were non-existent for either group of traits (Table 6 and 7), whereas there were some absolute differences between the BVs for horses in the early period. The correlations between BVs ranged from 0.93 (trot at hand for horses in early period) to 1.00. The higher correlations between BVs for the horses in the late period compared to the BVs for horses in the early period showed that those BVs were more closely related to the ones of the whole period (i.e. in agreement with the absolute difference).

Comparison between BVs for the late period predicted in the BM and UL analyses showed no average real differences either. However, there were large absolute differences in BVs, indicating less reliable BVs for horses from the early period that were not included with records in univariate analysis (UL) (Table 6 and 7). The largest difference was above 6 index units, corresponding to nearly a third of the genetic standard deviation. The correlations were moderate to high (0.72-1.00 for both RHQT and competition data) between the BVs. For horses with records in the early period the correlations between BVs predicted with late period data only (UL) and bivariate model (BM) were moderately low (0.72-0.83).

There were large average differences, both real and absolute, between the model with data from the early period only (UE) and the bivariate model (BM). The correlations were low to moderate (0.15-0.89).

Accuracies of BVs

The average accuracies for BVs for the different traits followed the same pattern as the absolute differences in BVs and are illustrated in Figure 1 (RHQT; trot at hand) and Figure 2 (competition; show jumping). For horses judged in the later period of RHQT, both BVs from bivariate analysis (BM, late period) and univariate analysis with data from the late period (UL) showed high accuracies, closely followed by the univariate analyses with data from the whole period (UW). For show jumping, similar results were obtained as for the RHQT trait.

Cross validation

In Table 8 (RHQT; trot at hand) and 9 (competition; show jumping) the correlation and RMSE between the real and estimated phenotypic scores in each test data set are presented. There were no differences between the three compared models for any of the traits studied (UW, UL and BM).

Discussion

To achieve genetic progress in sport horse breeding it is essential to have a reliable genetic evaluation of the horses. In this study we have investigated three different models of using data from long periods of time in the genetic evaluation. The heritabilities and variances were at the same level as earlier estimated by Viklund et al. (2008 and 2010). The judging of horses at RHQT has improved over the years. This was indicated by the lower residual variances and higher heritabilities for the late period. The test is regulated and performed in the same way at all different locations, and the judges have to participate regularly at courses to harmonise the judging. The larger genetic variances for the late period, especially for jumping traits, may be explained by the importation of stallions included in SWB breeding and the increased specialisation for either jumping or dressage, thus contributing to a larger total variation in jumping traits.

Accumulated life time upgrading points reflect competition performance of a horse. The equestrian sport has expanded and developed considerably since the 1960s. There are more competitions, more classes, more horses and more riders that are competing. The horse population has also changed as a result of selection and importation of breeding stallions. This development explains the genetic correlations to be less than unity between time periods (0.74 for show jumping and 0.92 for dressage). It has also led to an increase in the means of competition traits, but also lower residual variances. The genetic variances were lower in the late period, especially for dressage, most likely due to inclusion of younger horses in that data set. These horses have not yet expressed their full genetic potential due to the longer training period dressage horses require to achieve results at advanced levels.

Trot at hand was obviously evaluated in a different way in the late period than in the early period (genetic correlation of 0.69 between traits separately defined by time period). This may be primarily related to the change of judges, which in the early period were dominated by cavalry officers who have been replaced by dressage riders and trainers with a different view on movements of sport horses. Overall, the genetic correlations between traits in the two time periods were in the same range as Árnason & Sigurdsson (2004) estimated for traits evaluated in Icelandic horses before and after 1990 (0.68-0.94).

Adjusting the scores to the same variance per event or birth year did not affect the genetic parameters. Hill (1984) concluded also that scaling by the sample deviation seemed to be a robust procedure, but he stated that it was not obviously the best way to deal with heterogeneity of variance in a BLUP analysis where homogeneity of variance is assumed. Van der Werf et al. (1994) used an animal model and showed that the simple method for standardisation of variances within herd-year reduced biases of breeding values by about 20%. Wiggans and Van Raden (1991) also used an animal model and concluded that the standardisation of variance for yield traits in US dairy cattle generally improved the evaluations but that future research would probably reveal better methods.

Because some of the traits have not stayed the same throughout time, a bivariate approach (BM) was assumed to give more accurate BVs than a univariate model including data from the whole period (UW). In the BM analyses the BVs of interest were based on the most recent data (late period) because it reflected the current breeding stock. BVs for the older horses were obtained through the genetic correlations and the performance of relatives. This is similar to the genetic evaluations for the Icelandic horse population (Árnason et al., 2006). However, the high correlations between BVs (BM and UW) for the younger group of horses (0.99-1.00 for both RHQT traits and competition traits from the late period) indicated that the two models barely differed. The results from the CV study also showed no difference in predictive ability between the two models. For both models, high accuracies (r_{TI}) of BVs were obtained for younger horses (RHQT and competition traits in the late period), but for older horses (RHQT and competition traits in the early period) the accuracies were much lower for BVs from the BM analysis than for BVs from the univariate analysis (UW). In this study we analysed one trait at a time. In the official breeding evaluation up to 10 traits are included in a multiple-trait analysis. In a bivariate approach with early and late period traits there will be 20 traits in the genetic evaluations and this can lead to computational difficulties associated with the large covariance structure (Árnason et al., 2006). The results show that even if the bivariate approach theoretically is expected to give more accurate BVs for the breeding stock of interest, the gain is negligible.

Another approach to handle heterogeneity in variances over time is to discard parts of the data as Wiegel & Banos (1997) suggested. In international dairy sire evaluations selection has taken place at different rates among a number of populations with different base genetic variances. The differences are partly due to beginning date and rate of importation of stock from other populations, and how much historical data that is available depending on when the national dairy database was established (Weigel & Banos, 1997). When performance data from daughters of sires born before the beginning of importation were discarded, the estimates of genetic standard deviations became more alike and BVs of elite bulls were close to true values. The conditions are not the same for national evaluations of a horse population. In this study, excluding historical data (UL model) negatively affected the accuracies the BVs of the older horses with recorded traits in the early period. The long generation intervals and overlapping generations in horse breeding makes it important to correctly predict BVs also for older animals, even for those that may not belong to active breeding stock. Therefore, the first period of data cannot be neglected in the genetic evaluation. This is also appreciated by the breeders who want to see the BVs of horses from different generations.

In a successful breeding programme with large genetic progress, the selection of breeding stock takes place among rather young horses. Therefore, it is most important that these horses are correctly evaluated. However, as stated above, the older horses also contribute important information. In the official BV prediction today, all data are used and no corrections are made to take into account that the traits have changed over time. The results in this study show that this is probably the best compromise to get the most accurate BVs for all horses of interest with limited computational efforts.

Conclusions

Some traits of riding horses have, except for genetic improvement, changed considerably over a period of about three decades. Traits from early and late time periods were considered as genetically different traits and were evaluated in a bivariate model. Use of all data or exclusion of data from the early time period for univariate analyses showed no difference in BVs of late born horses compared to BVs from the bivariate model. However, the accuracy of BVs decreased considerably for older horses when data of the early period was excluded.

The most accurate way to predict BVs for all SWB horses is either by a bivariate model, where the traits are considered genetically different between time periods, or by a univariate model including all data from beginning of recording. We recommend use of the univariate model in the genetic evaluations due to less complex calculations to achieve practically the same results.

Acknowledgement

Financial support from the Swedish Foundation for Equine Research is gratefully acknowledged. The Swedish Warmblood Association, the Swedish Horse Board and the Swedish Equestrian Federation are gratefully acknowledged for providing materials for the study.

References

Árnason T and Sigurdsson A 2004. International genetic evaluation of the Icelandic horse. Conference at the 55th Annual Meeting of the European Association for Animal Production, 5-8 September 2004, Bled, Slovenia, 17pp.

Árnason T, Sigurdsson Á and Lorange L B 2006. Global genetic evaluations of the Icelandic horse and genetic connectedness between countries. Proceedings of the 8th World Congress on Genetics Applied to Livestock Production, 13-18 August 2006, Belo Horizonte, Brazil, paper 24-16.

Hill W G 1984. On selection among groups with heterogeneous variance. Animal Production 39, 473-477.

Jensen J and Madsen P 1997. A User's Guide to DMU. A Package for Analyzing Multivariate Mixed Models. National Institute of Animal Science, Foulum, Denmark. 19 pp.

Tsuruta S, Misztal I and Lawlor T J 2004. Genetic correlations among production, body size, udder, and productive life traits over time in Holsteins. Journal of Dairy Science 87, 1457-1468.

Van der Werf J H J, Meuwissen T H E, De Jong G. Effects of correction for heterogeneity of variance on bias and accuracy of breeding value estimation for Dutch dairy cattle. Journal of Dairy Science 77, 3174-3184.

Van Vleck L D 1966. Change in variance components associated with milk records with time and increase in mean production. Journal of Dairy Science 49, 36-40.

Viklund Å, Thorén Hellsten E, Näsholm A, Strandberg E and Philipsson J 2008. Genetic parameters for traits evaluated at field tests of 3- and 4-year-old Swedish Warmblood horses. Animal 12, 1832-1841.

Viklund Å, Braam Å, Näsholm A, Strandberg E and Philipsson J 2010. Genetic variation in competition traits at different ages and time periods and correlations with traits at field tests of 4-year-old Swedish Warmblood horses. Animal, doi:10.1017/S1751731110000017.

Weigel KA and Banos G 1997. Effect of time period of data used in international dairy sire evaluations. Journal of Dairy Science 80, 3425-3430.

Wiggans GR and VanRaden PM 1991. Method and effect of adjustment for heterogeneous variance. Journal of Dairy Science 74, 4350-4357.

Table 1. Description of data used for study of judging period (early - late) of Riding Horse Quality Test for four-year-old horses

Trait and period[1]	No. of horses	Mean	s.d.	Min	Max
Type					
Early period	4237	7.72	0.81	4	10
Late period	13 979	7.80	0.61	4	10
Whole period	18 216	7.78	0.67	4	10
Trot at hand					
Early period	4237	7.45	0.83	4	10
Late period	12 988	7.11	0.81	4	10
Whole period	17 225	7.20	0.83	4	10
Canter under rider					
Early period	4198	6.58	1.12	1	10
Late period	14 006	6.69	0.97	1	10
Whole period	18 204	6.66	1.01	1	10
Jumping, technique & ability					
Early period	4237	6.65	1.52	1	10
Late period	14 006	6.67	1.39	1	10
Whole period	18 243	6.66	1.42	1	10
Jumping, temperament					
Early period	4237	6.92	1.68	1	10
Late period	14 006	6.75	1.53	1	10
Whole period	18 243	6.79	1.57	1	10

[1)] Early period=horses judged 1973-1987; Late period= horses judged 1988-2007; Whole period=horses judged 1973-2007.

Table 2. Description of data used for study of birth period (early – late) based on 10-log transformed accumulated points at competitions

Discipline and period[1]	No. of horses	Mean	s.d.	Min	Max
Dressage					
Early period	7467	0.74	0.82	0	3.80
Late period	7929	1.23	0.72	0	4.10
Whole period	15 396	0.99	0.81	0	4.10
Show jumping					
Early period	13 245	0.88	0.80	0	3.72
Late period	16 319	1.30	0.75	0	4.08
Whole period	29 564	1.11	0.80	0	4.08

[1)] Early period=horses born 1953-1983; Late period= horses born 1984-2002; Whole period= horses born 1953-2002.

Table 3. Heritabilities (h^2), additive genetic (σ_a^2) and residual (σ_e^2) variances (standard errors as subscripts) estimated in univariate and bivariate analyses for traits evaluated at Riding Horse Quality Tests 1973-2007

Trait and period[1]	Type of analysis	h^2	σ_a^2	σ_e^2
Type				
Early period	Univariate (UE)	0.30	$0.18_{.03}$	$0.42_{.02}$
Late period	Univariate (UL)	0.36	$0.14_{.01}$	$0.24_{.01}$
Whole period	Univariate (UW)	0.33	$0.14_{.01}$	$0.29_{.01}$
Early period	Bivariate analysis (BM)	0.32	$0.20_{.03}$	$0.41_{.02}$
Late period	Bivariate analysis (BM)	0.36	$0.14_{.01}$	$0.24_{.01}$
Trot at hand				
Early period	Univariate (UE)	0.28	$0.17_{.03}$	$0.44_{.02}$
Late period	Univariate (UL)	0.37	$0.22_{.02}$	$0.38_{.01}$
Whole period	Univariate (UW)	0.34	$0.21_{.02}$	$0.40_{.01}$
Early period	Bivariate analysis (BM)	0.29	$0.18_{.03}$	$0.44_{.02}$
Late period	Bivariate analysis (BM)	0.38	$0.23_{.02}$	$0.37_{.01}$
Canter under rider				
Early period	Univariate (UE)	0.17	$0.19_{.04}$	$0.93_{.04}$
Late period	Univariate (UL)	0.38	$0.32_{.03}$	$0.55_{.02}$
Whole period	Univariate (UW)	0.34	$0.32_{.02}$	$0.62_{.02}$
Early period	Bivariate analysis (BM)	0.23	$0.26_{.04}$	$0.88_{.04}$
Late period	Bivariate analysis (BM)	0.38	$0.33_{.03}$	$0.54_{.02}$
Jumping, technique & ability				
Early period	Univariate (UE)	0.14	$0.30_{.07}$	$1.78_{.07}$
Late period	Univariate (UL)	0.23	$0.41_{.04}$	$1.37_{.03}$
Whole period	Univariate (UW)	0.21	$0.39_{.04}$	$1.46_{.03}$
Early period	Bivariate analysis (BM)	0.16	$0.33_{.07}$	$1.75_{.07}$
Late period	Bivariate analysis (BM)	0.23	$0.42_{.04}$	$1.36_{.03}$
Jumping, temperament				
Early period	Univariate (UE)	0.08	$0.19_{.07}$	$2.25_{.07}$
Late period	Univariate (UL)	0.19	$0.42_{.05}$	$1.81_{.04}$
Whole period	Univariate (UW)	0.17	$0.38_{.04}$	$1.91_{.04}$
Early period	Bivariate analysis (BM)	0.09	$0.23_{.06}$	$2.22_{.07}$
Late period	Bivariate analysis (BM)	0.19	$0.42_{.05}$	$1.81_{.04}$

[1)] Early period: horses judged 1973-1987; Late period: horses judged 1988-2007; Whole period = horses judged 1973-2007.

Table 4. Heritabilities (h^2), additive genetic ($\sigma^2_{a)}$ and residual (σ^2_e) variances (standard errors as subscripts) estimated in univariate and bivariate analyses for 10-log transformed accumulated points at competitions for horses born 1953-2002

Discipline and period[1]	Type of analysis	h^2	σ_a^2	σ_e^2
Dressage				
Early period	Univariate (UE)	0.19	$0.12_{.02}$	$0.51_{.02}$
Late period	Univariate (UL)	0.14	$0.07_{.01}$	$0.43_{.01}$
Whole period	Univariate (UW)	0.15	$0.09_{.01}$	$0.47_{.01}$
Early period	Bivariate analysis (BM)	0.18	$0.11_{.02}$	$0.51_{.02}$
Late period	Bivariate analysis (BM)	0.14	$0.07_{.01}$	$0.43_{.01}$
Show jumping				
Early period	Univariate (UE)	0.29	$0.18_{.02}$	$0.43_{.01}$
Late period	Univariate (UL)	0.31	$0.16_{.01}$	$0.36_{.01}$
Whole period	Univariate (UW)	0.27	$0.15_{.01}$	$0.41_{.01}$
Early period	Bivariate analysis (BM)	0.30	$0.19_{.02}$	$0.43_{.01}$
Late period	Bivariate analysis (BM)	0.30	$0.16_{.01}$	$0.36_{.01}$

[1)] Early period: horses born 1953-1983; Late period: horses born 1984-2002; Whole period = horses born 1953-2002.

Table 5. Genetic correlations (r_g) (standard error as subscripts) between early and late period of Riding Horse Quality Test[1] (RHQT) and competition[2] traits estimated in bivariate analyses

Trait	r_g
Riding Horse Quality Test	
Type	$0.84_{.06}$
Trot at hand	$0.69_{.08}$
Canter under rider	$0.91_{.05}$
Jumping, technique & ability	$0.87_{.08}$
Jumping, temperament	$1.00_{.09}$
Competition	
Dressage	$0.92_{.08}$
Show jumping	$0.74_{.06}$

[1)] Genetic correlation between trait judged 1973-1987 and trait judged 1988-2007.

[2)] Genetic correlation for 10-log transformed accumulated points between birth year 1953-1983 and birth year 1984-2002.

Table 6. Average real and absolute (abs.) differences, and correlations (corr.) between predicted breeding values for late period[1] Riding Horse Quality Test traits in bivariate analysis (BM) and BVs in univariate analysis for whole period[1] (UW), early period[1] (UE) and late period[1] (UL)

	UW:BM (late)			UE:BM (late)			UL:BM (late)		
	Differences			Differences			Differences		
Trait and group of horses	Real	Abs.	Corr.	Real	Abs.	Corr.	Real	Abs.	Corr.
Type									
Horses in early period	0.53	3.45	0.97	7.07	7.67	0.89	0.04	5.94	0.72
Horses in late period	0.10	1.13	0.99	1.31	10.45	0.15	-0.03	0.86	0.99
All judged horses	0.20	1.67	0.98	2.65	9.81	0.36	-0.02	2.04	0.95
Trot at hand									
Horses in early period	-0.11	3.76	0.93	7.82	9.14	0.78	0.14	4.54	0.83
Horses in late period	0.03	1.07	1.00	1.66	11.45	0.33	-0.03	0.64	1.00
All judged horses	0	1.69	0.98	3.09	10.91	0.41	0.01	1.54	0.98
Canter under rider									
Horses in early period	0.25	3.08	0.96	9.82	10.10	0.84	0.15	5.36	0.75
Horses in late period	0.07	0.98	1.00	1.89	12.00	0.18	-0.06	0.81	1.00
All judged horses	0.11	1.47	0.99	3.73	11.56	0.34	-0.01	1.87	0.97
Jumping, technique & ability									
Horses in early period	-0.16	2.24	0.97	7.26	7.84	0.84	0.40	4.60	0.81
Horses in late period	0.02	0.77	1.00	1.34	11.14	0.31	-0.01	0.92	1.00
All judged horses	-0.02	1.11	0.99	2.72	10.38	0.43	0.08	1.77	0.98
Jumping, temperament									
Horses in early period	-0.14	1.64	0.98	6.07	6.60	0.83	0.49	4.39	0.78
Horses in late period	-0.01	0.65	1.00	1.10	10.15	0.28	0	1.04	0.99
All judged horses	-0.04	0.88	1.00	2.25	9.32	0.40	0.12	1.82	0.97

[1)] Whole period = 1973-2007; Early period: trait judged 1973-1987; Late period: trait judged 1988-2007.

Table 7. Average real and absolute (abs.) differences, and correlations (corr.) between predicted breeding values for late period[1] competition traits in bivariate analysis (BM) and BVs in univariate analysis for whole period[1] (UW), early period[1] (UE), and late period[1] (UL)

	UW-BM			UE-BM			UL -BM		
	Differences			Differences			Differences		
Trait and group of horses	Real	Abs.	Corr.	Real	Abs.	Corr.	Real	Abs.	Corr.
Dressage									
Horses in early period	0.03	1.18	0.99	3.25	3.82	0.95	0.33	6.17	0.72
Horses in late period	0.04	0.68	1.00	0.76	7.52	0.61	-0.68	2.10	0.97
All competing horses	0.03	0.92	1.00	1.97	5.73	0.79	-0.19	4.08	0.87
Show jumping									
Horses in early period	0.30	3.47	0.94	7.59	8.12	0.87	0.82	5.73	0.74
Horses in late period	0.14	1.40	0.99	0.07	12.12	0.50	-0.10	1.10	1.00
All competing horses	0.21	2.33	0.98	3.44	10.33	0.64	0.31	3.17	0.95

[1)] Whole period = horsed born 1953-2002; Early period: horses born 1953-1983; Late period: horses born 1984-2002.

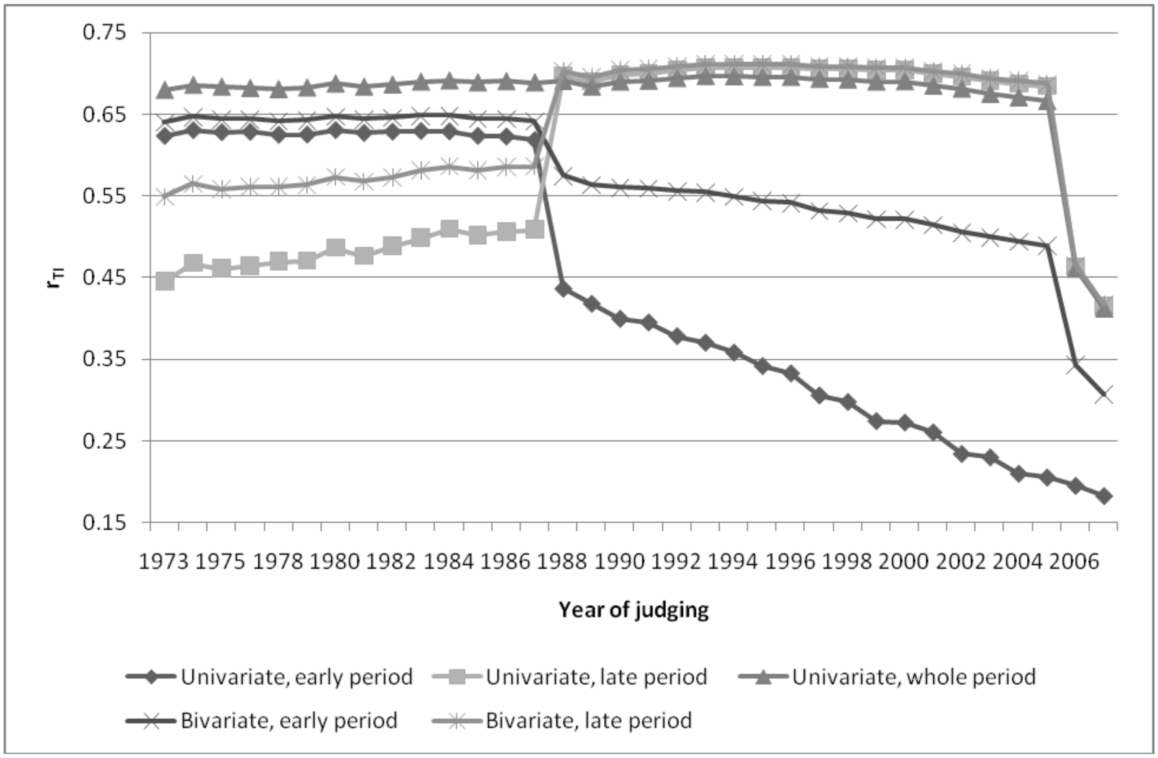

Figure 1. Average accuracies (r_{TI}) of predicted breeding values for trot at hand judged at Riding Horse Quality Test (RHQT) in univariate or bivariate analyses with data from different time periods (Whole period=judging years 1973-2007, Early period=judging years 1973-1987, Late period=judging years 1988-2007).

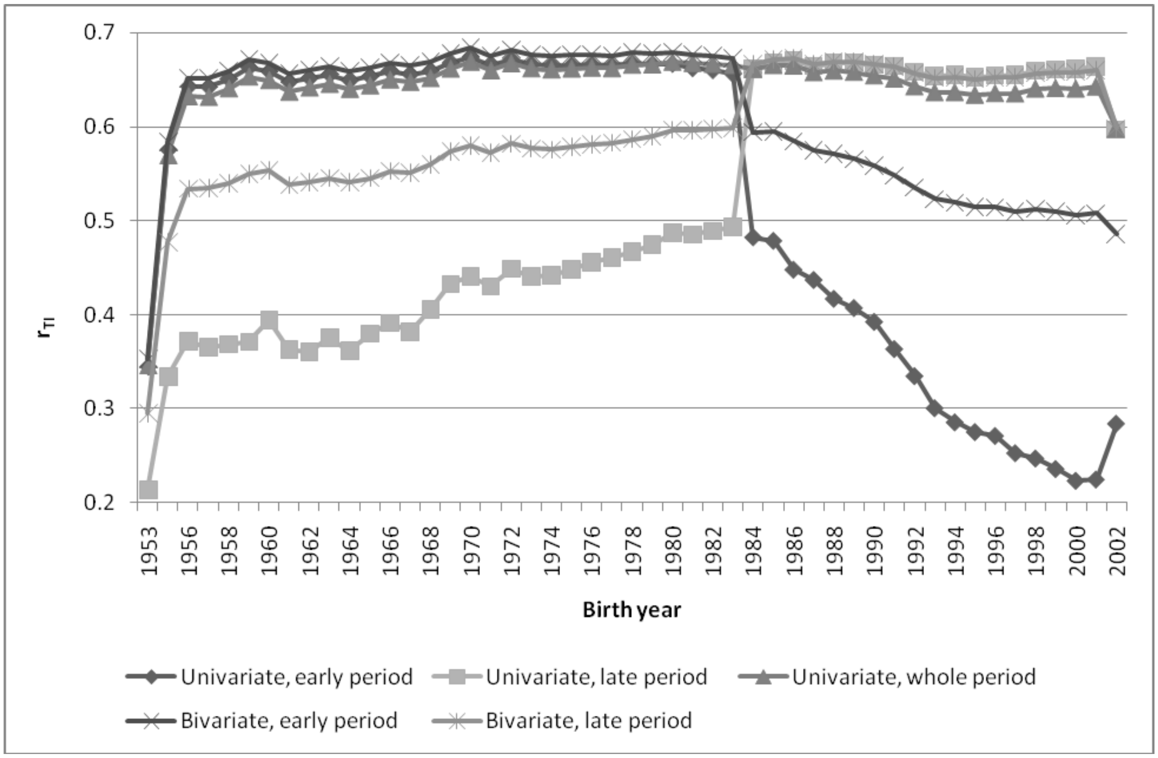

Figure 2. Average accuracies (r_{TI}) of predicted breeding values for show jumping in univariate or bivariate analyses with data from different birth year periods (Whole period=birth years 1953-2002, Early period=birth years 1953-1983, Late period=birth years 1984-2002) for different birth years of competing Swedish Warmblood horses.

Table 8. Correlations (Corr.) and root mean squared errors (RMSE) between predicted and true phenotype for the trait trot at hand at Riding Horse Quality Test for the different test data sets in the cross validation

	UW[1]		UL[2]		BM[3]	
Test data set	Corr.	RMSE	Corr.	RMSE	Corr.	RMSE
1	0.41	0.75	0.41	0.75	0.41	0.75
2	0.38	0.73	0.38	0.73	0.37	0.73
3	0.37	0.73	0.38	0.73	0.42	0.72
4	0.42	0.74	0.42	0.74	0.42	0.74
5	0.42	0.72	0.41	0.73	0.38	0.75
Average	0.40	0.73	0.40	0.74	0.40	0.74

1)UW=univariate model, all data (whole period).
2)UL=univariate model, only data from late period.
3)BM=bivariate model, all data with separate trait definition for early and late time periods.

Table 9. Correlations (Corr.) and root mean squared errors (RMSE) between predicted and true phenotype for the trait accumulated points in show jumping for the different test data sets in the cross validation

	UW[1]		UL[2]		BM[3]	
Test data set	Corr.	RMSE	Corr.	RMSE	Corr.	RMSE
1	0.36	0.70	0.36	0.70	0.37	0.70
2	0.38	0.68	0.38	0.68	0.38	0.68
3	0.37	0.69	0.36	0.69	0.37	0.69
4	0.36	0.70	0.36	0.70	0.36	0.70
5	0.38	0.68	0.38	0.68	0.38	0.70
Average	0.37	0.69	0.37	0.69	0.37	0.69

1)UW=univariate model, all data (whole period).
2)UL=univariate model, only data from late period.
3)BM=bivariate model, all data with separate trait definition for early and late time periods.