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

3

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9

10 **Running head**

11 Long-time horse data for genetic evaluation

12

13 **Abstract**

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

1 Horse Quality Test (RHQT) data of 14 000 horses judged between 1973 and  
2 2007 were used. Genetic correlations of 0.69-1.00 were estimated between traits  
3 recorded in different time periods (RHQT data) or different birth year groups  
4 (competition data). A cross validation study and comparison of BVs using  
5 different sets of data showed that most accurate and similar results were  
6 obtained when BVs were predicted from either the bivariate model or the  
7 univariate model including all data from beginning of recording. We recommend  
8 using all data and applying the univariate model to minimize the computational  
9 efforts for genetic evaluations and for provision of reliable BVs for as many  
10 horses as possible.

11

12

13 **Key words:** Riding Horses, Breeding value, Cross Validation

14

15

## 16 **Implications**

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

1 be used to maximize “unbiasedness” and reliabilities of BVs for as many horses  
2 as possible.

3

4

## 5 **Introduction**

6 Genetic evaluation for Swedish Warmblood sport horses (SWB) is based on a  
7 multiple-trait animal model with results from competitions and young horse  
8 performance tests. Data go back to the beginning of the 1970s. Earlier studies  
9 (Viklund et al., 2008 and 2010) have shown that some of the recorded traits have  
10 not stayed the same throughout the years. The heritabilities and variances  
11 changed over time, and the genetic correlations between traits recorded in  
12 different time periods were sometimes considerably less than unity. For  
13 conformation, gait and jumping traits at Riding Horse Quality Tests for 4-year-  
14 olds (RHQT) heritabilities increased between judging periods 1973-1987 and  
15 1996-2002, mostly due to lower residual variances in the later period (Viklund et  
16 al., 2008). For example, the heritability for canter under rider increased from 0.22  
17 to 0.37, whereas the residual variances decreased from 0.87 to 0.52. The  
18 phenotypic variance decreased for all traits. Genetic correlations between traits in  
19 the different judging periods ranged between 0.48 (correctness of legs) and 0.97  
20 (walk under rider). For dressage competition traits heritabilities decreased slightly  
21 between birth year groups 1953-1983 and 1992-2002 (from 0.18 to 0.14),  
22 whereas they increased slightly for show jumping (from 0.31 to 0.34) (Viklund et  
23 al., 2010). For both disciplines, the phenotypic variances decreased between

1 traits recorded in the early period and late period (0.61 to 0.50 for dressage and  
2 0.61 to 0.47 for show jumping). The genetic correlations between traits in  
3 different birth year periods were 0.71 (dressage) and 0.66 (show jumping). These  
4 changes in genetic parameters were suggested to be caused by expansion of the  
5 sport, changes in scoring of young horses and increased foreign influence on the  
6 horse population as breeding has become internationalised (Viklund et al., 2008  
7 and 2010).

8

9 Accuracy of genetic evaluations depends on how well the assumptions of the  
10 model match the data. Usually, as for the genetic evaluation of SWB, constant  
11 variance of traits recorded across time is assumed, but often this assumption  
12 does not hold. In dairy cattle for example, milk yield has increased over time due  
13 to improvement of management and increased genetic level as a result of  
14 selection. Variances for milk production traits have increased simultaneously with  
15 increasing means (Van Vleck, 1966; Tsuruta et al., 2004). In the Icelandic horse  
16 population, the phenotypic standard deviation as well as the heritabilities  
17 increased considerably between time periods due to a re-definition of traits in  
18 1990 (Árnason & Sigurdsson, 2004). The largest difference in heritabilities  
19 between traits recorded in different judging periods (1979-1989 and 1990-2003)  
20 was found for legs that increased from 0.16 to 0.38, and the largest difference in  
21 phenotypic standard deviation was found for trot (from 0.48 to 0.72). The  
22 correlations between traits in the two different time periods were for many traits

1 significantly deviating from one (0.68-0.94). For other horse populations, changes  
2 in variation of traits over time have not been reported.

3

4 There are different approaches for handling changes in variation over time. One  
5 way is to adjust variances of data from different groups to a common population  
6 variance (e.g. Hill, 1984; Wiggans & VanRaden, 1991; Van der Werf et al., 1994).

7 Another way of handling the problem, suggested by Weigel and Banos (1997), as  
8 regards international dairy sire evaluations, was to discard historical performance  
9 data of bulls from breeds or strains that have been changed by imported stock. A  
10 third approach is to treat traits in different time periods as different traits. In the  
11 Icelandic horse population the traits are regarded as different traits if they are  
12 scored before or later than 1990 (Árnason et al., 2006), and Tsuruta et al. (2004)  
13 handled milk records in every 3-year interval as separate traits.

14

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

21

22

23 **Materials**

1 *Data*

2 The data was provided by the Swedish Warmblood Association and the Swedish  
3 Equestrian Federation. RHQT data comprised 18 216 horses evaluated between  
4 1973 and 2007. The RHQT is a one-day field test, where conformation, gaits,  
5 jumping and rideability are judged on a scale from 1 to 10. The test is open for all  
6 4-year-old SWBs, and for 5-year-old mares that had foaled as 4-year-olds. The  
7 traits studied were type, trot at hand, canter under rider, jumping technique &  
8 ability, and temperament & general appearance for jumping. Competition data  
9 comprised 15 396 horses that had competed in dressage and 29 564 horses that  
10 had competed in show jumping. The horses were born between 1953 and 2002,  
11 and they had competed during the period 1962-2006. Competition results were  
12 recorded as accumulated lifetime upgrading points in show jumping and  
13 dressage, transformed with a logarithm to the basis of ten to a nearly normal  
14 distribution. Show jumping and dressage results were analysed separately. The  
15 data structure is described in more detail by Viklund et al. (2008 and 2010).

16

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

21

22 *Time periods*

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

12

13

## 14 **Methods**

### 15 *Estimation of genetic parameters*

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

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

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

22 UW=Univariate model, all data (whole period),



1 BM=Bivariate model, all data with separate trait definition for early and late time  
2 periods.

3  
4 Additionally, univariate analyses were performed for the whole data sets where  
5 the scores were standardised to a common unity variance. The phenotypic  
6 variance for RHQT traits was adjusted to be equal for all events, whereas the  
7 competition trait variances were adjusted to be equal for all birth years. The  
8 results from these analyses were almost identical to the results from the UW and  
9 are therefore not reported.

10

11 The basic bivariate model (BM) was:

$$12 \begin{pmatrix} y_1 \\ y_2 \end{pmatrix} = \begin{pmatrix} X_1 & 0 \\ 0 & X_2 \end{pmatrix} \begin{pmatrix} \beta_1 \\ \beta_2 \end{pmatrix} + \begin{pmatrix} Z_1 & 0 \\ 0 & Z_2 \end{pmatrix} \begin{pmatrix} a_1 \\ a_2 \end{pmatrix} + \begin{pmatrix} e_1 \\ e_2 \end{pmatrix}$$

13 where  $y_1$  is the observed trait 1 (early period) and  $y_2$  is the observed trait 2 (late  
14 period). The vector  $(\beta_1' \beta_2)'$  contains for RHQT traits the fixed effects of event  
15 (1,...,432), sex (male or female) and age (4 or 5 years of age), and for  
16 competition traits the fixed effects of birth year (1953,...,2002) and sex (male or  
17 female). The  $\mathbf{X}$  and  $\mathbf{Z}$  matrices are incidence matrices relating the observations  
18 to the fixed and random effects, respectively,  $\mathbf{a}$  is a vector of additive genetic  
19 effects of the horses, and  $\mathbf{e}$  is a vector of random residuals:

$$20 \begin{pmatrix} a \\ e \end{pmatrix} \sim N \left[ \begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} G \otimes A & 0 \\ 0 & R \otimes I_n \end{pmatrix} \right]$$

21 where  $\mathbf{G}$  is the additive genetic covariance matrix with the following components:

1 
$$G = \begin{pmatrix} \sigma_{a1}^2 & \sigma_{a1,a2} \\ \sigma_{a2,a1} & \sigma_{a2}^2 \end{pmatrix},$$

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

4 
$$R = \begin{pmatrix} \sigma_{e1}^2 & \sigma_{e1,e2} \\ \sigma_{e2,e1} & \sigma_{e2}^2 \end{pmatrix},$$

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

10

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

14

#### 15 *Index calculation*

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

18

19 
$$BV = \mu + ((BV_u - m_u) / \sigma_a) * s.d.$$

20

1 where BV is the predicted breeding value on the common publication scale,  $\mu$  is  
2 the mean of BV for the reference population equal to 100,  $BV_u$  is the breeding  
3 value on the original scale from the analyses,  $m_u$  is the mean of  $BV_u$  in the  
4 reference population (horses judged in RHQT 1994-2007 or horses born 1989-  
5 2002 with competition results regardless of discipline),  $\sigma_a$ =additive genetic  
6 standard deviation of the trait in the reference population, and s.d. is the desired  
7 genetic standard deviation of BV fixed to 20 units.

8

### 9 *Accuracy of BVs*

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

$$12 \quad r_{TI} = \sqrt{1 - PEV / \sigma_a^2}$$

13

14 where PEV = prediction error variance.

15

### 16 *Comparison of models*

17 *Comparison of BVs.* All comparisons of BVs were performed relative to the BVs  
18 for the late period estimated with the bivariate model, because these were  
19 regarded as the most correct BV for the actual breeding population. Correlations  
20 between BVs predicted in different models were calculated and the average of  
21 the differences (real) and average of the absolute values of the differences  
22 (absolute) between different BVs were investigated. The comparisons were  
23 conducted for different groups of horses, i.e., all horses judged in RHQT and

1 horses in each time period of RHQT, and for all horses with competition results  
2 within a discipline and for horses of each birth year period.

3

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

6

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

19

## 20 **Results**

### 21 *Genetic parameters*

22 In the analyses of RHQT data, heritabilities ranged between 0.08 and 0.38, and  
23 genetic variances ranged between 0.14 and 0.42 (Table 3). For all traits, the

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

15

#### 16 *BVs*

17 The average real differences between BVs for late period in the BM analyses and  
18 the UW analyses were non-existent for either group of traits (Table 6 and 7),  
19 whereas there were some absolute differences between the BVs for horses in  
20 the early period. The correlations between BVs ranged from 0.93 (trot at hand for  
21 horses in early period) to 1.00. The higher correlations between BVs for the  
22 horses in the late period compared to the BVs for horses in the early period

1 showed that those BVs were more closely related to the ones of the whole period  
2 (i.e. in agreement with the absolute difference).

3

4 Comparison between BVs for the late period predicted in the BM and UL  
5 analyses showed no average real differences either. However, there were large  
6 absolute differences in BVs, indicating less reliable BVs for horses from the early  
7 period that were not included with records in univariate analysis (UL) (Table 6  
8 and 7). The largest difference was above 6 index units, corresponding to nearly a  
9 third of the genetic standard deviation. The correlations were moderate to high  
10 (0.72-1.00 for both RHQT and competition data) between the BVs. For horses  
11 with records in the early period the correlations between BVs predicted with late  
12 period data only (UL) and bivariate model (BM) were moderately low (0.72-0.83).

13

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

17

### 18 *Accuracies of BVs*

19 The average accuracies for BVs for the different traits followed the same pattern  
20 as the absolute differences in BVs and are illustrated in Figure 1 (RHQT; trot at  
21 hand) and Figure 2 (competition; show jumping). For horses judged in the later  
22 period of RHQT, both BVs from bivariate analysis (BM, late period) and  
23 univariate analysis with data from the late period (UL) showed high accuracies,

1 closely followed by the univariate analyses with data from the whole period (UW).  
2 For show jumping, similar results were obtained as for the RHQT trait.

3

#### 4 *Cross validation*

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

9

#### 10 **Discussion**

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

23

1 Accumulated life time upgrading points reflect competition performance of a  
2 horse. The equestrian sport has expanded and developed considerably since the  
3 1960s. There are more competitions, more classes, more horses and more riders  
4 that are competing. The horse population has also changed as a result of  
5 selection and importation of breeding stallions. This development explains the  
6 genetic correlations to be less than unity between time periods (0.74 for show  
7 jumping and 0.92 for dressage). It has also led to an increase in the means of  
8 competition traits, but also lower residual variances. The genetic variances were  
9 lower in the late period, especially for dressage, most likely due to inclusion of  
10 younger horses in that data set. These horses have not yet expressed their full  
11 genetic potential due to the longer training period dressage horses require to  
12 achieve results at advanced levels.

13

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

22



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

12

13 Because some of the traits have not stayed the same throughout time, a bivariate  
14 approach (BM) was assumed to give more accurate BVs than a univariate model  
15 including data from the whole period (UW). In the BM analyses the BVs of  
16 interest were based on the most recent data (late period) because it reflected the  
17 current breeding stock. BVs for the older horses were obtained through the  
18 genetic correlations and the performance of relatives. This is similar to the  
19 genetic evaluations for the Icelandic horse population (Árnason et al., 2006).  
20 However, the high correlations between BVs (BM and UW) for the younger group  
21 of horses (0.99-1.00 for both RHQT traits and competition traits from the late  
22 period) indicated that the two models barely differed. The results from the CV  
23 study also showed no difference in predictive ability between the two models. For

1 both models, high accuracies ( $r_{TI}$ ) of BVs were obtained for younger horses  
2 (RHQT and competition traits in the late period), but for older horses (RHQT and  
3 competition traits in the early period) the accuracies were much lower for BVs  
4 from the BM analysis than for BVs from the univariate analysis (UW). In this  
5 study we analysed one trait at a time. In the official breeding evaluation up to 10  
6 traits are included in a multiple-trait analysis. In a bivariate approach with early  
7 and late period traits there will be 20 traits in the genetic evaluations and this can  
8 lead to computational difficulties associated with the large covariance structure  
9 (Árnason et al., 2006). The results show that even if the bivariate approach  
10 theoretically is expected to give more accurate BVs for the breeding stock of  
11 interest, the gain is negligible.

12

13 Another approach to handle heterogeneity in variances over time is to discard  
14 parts of the data as Weigel & Banos (1997) suggested. In international dairy sire  
15 evaluations selection has taken place at different rates among a number of  
16 populations with different base genetic variances. The differences are partly due  
17 to beginning date and rate of importation of stock from other populations, and  
18 how much historical data that is available depending on when the national dairy  
19 database was established (Weigel & Banos, 1997). When performance data from  
20 daughters of sires born before the beginning of importation were discarded, the  
21 estimates of genetic standard deviations became more alike and BVs of elite  
22 bulls were close to true values. The conditions are not the same for national  
23 evaluations of a horse population. In this study, excluding historical data (UL

1 model) negatively affected the accuracies the BVs of the older horses with  
2 recorded traits in the early period. The long generation intervals and overlapping  
3 generations in horse breeding makes it important to correctly predict BVs also for  
4 older animals, even for those that may not belong to active breeding stock.  
5 Therefore, the first period of data cannot be neglected in the genetic evaluation.  
6 This is also appreciated by the breeders who want to see the BVs of horses from  
7 different generations.

8

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

17

18

## 19 **Conclusions**

20 Some traits of riding horses have, except for genetic improvement, changed  
21 considerably over a period of about three decades. Traits from early and late  
22 time periods were considered as genetically different traits and were evaluated in  
23 a bivariate model. Use of all data or exclusion of data from the early time period

1 for univariate analyses showed no difference in BVs of late born horses  
2 compared to BVs from the bivariate model. However, the accuracy of BVs  
3 decreased considerably for older horses when data of the early period was  
4 excluded.

5

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

11

## 12 **Acknowledgement**

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14 acknowledged. The Swedish Warmblood Association, the Swedish Horse Board and  
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16 materials for the study.

17

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15 heterogeneous variance. *Journal of Dairy Science* 74, 4350-4357.

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

Trait and period <sup>1</sup>	No. of horses	Mean	s.d.	Min	Max
<i>Type</i>					
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
<i>Trot at hand</i>					
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
<i>Canter under rider</i>					
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
<i>Jumping, technique &amp; ability</i>					
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
<i>Jumping, temperament</i>					
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

3 <sup>1)</sup> Early period=horses judged 1973-1987; Late period= horses judged 1988-2007; Whole  
 4 period=horses judged 1973-2007.  
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7 Table 2. Description of data used for study of birth period (early – late) based on  
 8 10-log transformed accumulated points at competitions

Discipline and period <sup>1</sup>	No. of horses	Mean	s.d.	Min	Max
<i>Dressage</i>					
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
<i>Show jumping</i>					
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

9 <sup>1)</sup> Early period=horses born 1953-1983; Late period= horses born 1984-2002; Whole period=  
 10 horses born 1953-2002.  
 11  
 12

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

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

4 <sup>1</sup> Early period: horses judged 1973-1987; Late period: horses judged 1988-2007; Whole period =  
 5 horses judged 1973-2007.  
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1 Table 4. Heritabilities ( $h^2$ ), additive genetic ( $\sigma_a^2$ ) and residual ( $\sigma_e^2$ ) variances  
 2 (standard errors as subscripts) estimated in univariate and bivariate analyses for  
 3 10-log transformed accumulated points at competitions for horses born 1953-  
 4 2002

Discipline and period <sup>1</sup>	Type of analysis	$h^2$	$\sigma_a^2$	$\sigma_e^2$
<i>Dressage</i>				
Early period	Univariate (UE)	0.19	0.12 <sub>.02</sub>	0.51 <sub>.02</sub>
Late period	Univariate (UL)	0.14	0.07 <sub>.01</sub>	0.43 <sub>.01</sub>
Whole period	Univariate (UW)	0.15	0.09 <sub>.01</sub>	0.47 <sub>.01</sub>
Early period	Bivariate analysis (BM)	0.18	0.11 <sub>.02</sub>	0.51 <sub>.02</sub>
Late period	Bivariate analysis (BM)	0.14	0.07 <sub>.01</sub>	0.43 <sub>.01</sub>
<i>Show jumping</i>				
Early period	Univariate (UE)	0.29	0.18 <sub>.02</sub>	0.43 <sub>.01</sub>
Late period	Univariate (UL)	0.31	0.16 <sub>.01</sub>	0.36 <sub>.01</sub>
Whole period	Univariate (UW)	0.27	0.15 <sub>.01</sub>	0.41 <sub>.01</sub>
Early period	Bivariate analysis (BM)	0.30	0.19 <sub>.02</sub>	0.43 <sub>.01</sub>
Late period	Bivariate analysis (BM)	0.30	0.16 <sub>.01</sub>	0.36 <sub>.01</sub>

5 <sup>1</sup> Early period: horses born 1953-1983; Late period: horses born 1984-2002; Whole period =  
 6 horses born 1953-2002.  
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10 Table 5. Genetic correlations ( $r_g$ ) (standard error as subscripts) between early  
 11 and late period of Riding Horse Quality Test<sup>1</sup> (RHQT) and competition<sup>2</sup> traits  
 12 estimated in bivariate analyses

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

13 <sup>1</sup> Genetic correlation between trait judged 1973-1987 and trait judged 1988-2007.

14 <sup>2</sup> Genetic correlation for 10-log transformed accumulated points between birth year 1953-1983  
 15 and birth year 1984-2002.  
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1 Table 6. Average real and absolute (abs.) differences, and correlations (corr.) between predicted breeding values for late  
 2 period<sup>1</sup> Riding Horse Quality Test traits in bivariate analysis (BM) and BVs in univariate analysis for whole period<sup>1</sup> (UW),  
 3 early period<sup>1</sup> (UE) and late period<sup>1</sup> (UL)

Trait and group of horses	UW:BM (late)			UE:BM (late)			UL:BM (late)		
	Real	Abs.	Corr.	Real	Abs.	Corr.	Real	Abs.	Corr.
<i>Type</i>									
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
<i>Trot at hand</i>									
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
<i>Canter under rider</i>									
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
<i>Jumping, technique &amp; ability</i>									
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
<i>Jumping, temperament</i>									
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

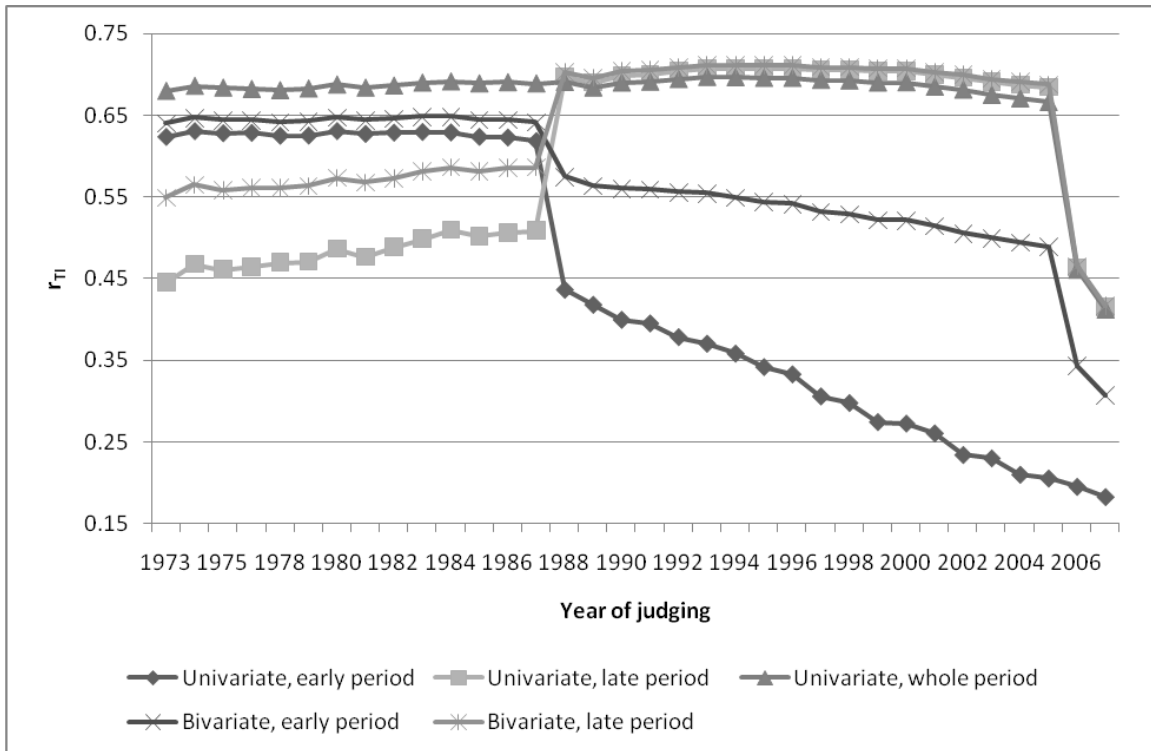
<sup>1)</sup> Whole period = 1973-2007; Early period: trait judged 1973-1987; Late period: trait judged 1988-2007.

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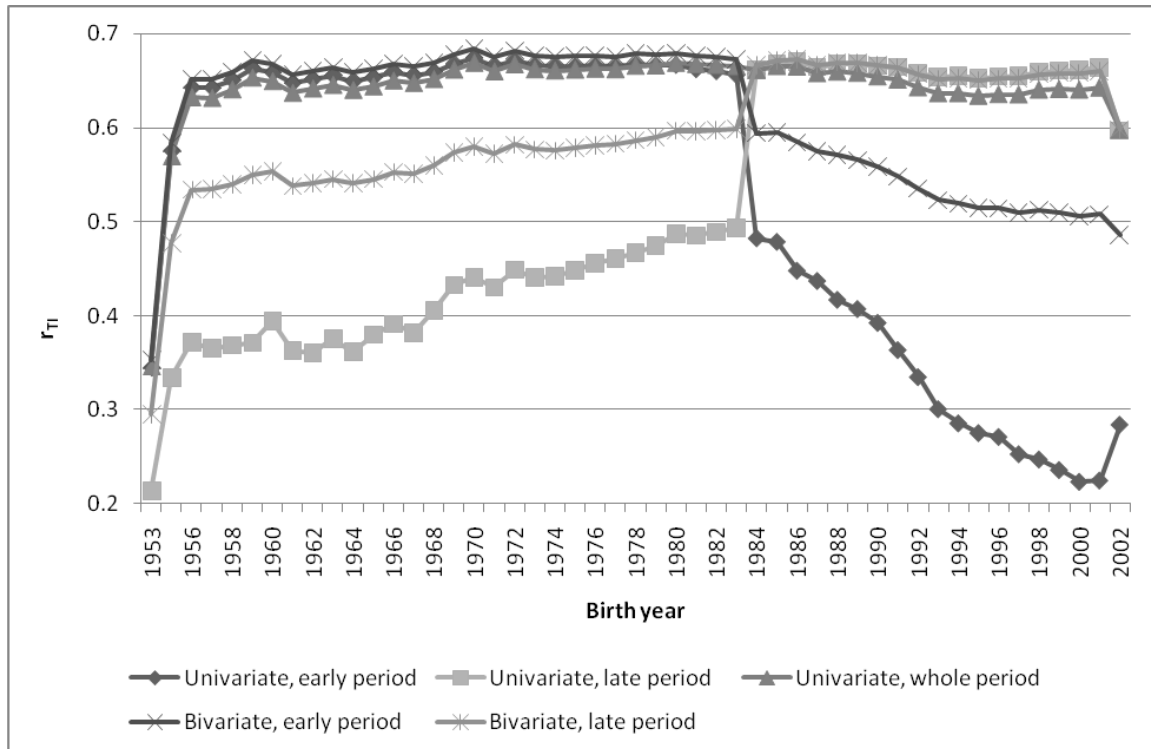
- 1 Table 7. Average real and absolute (abs.) differences, and correlations (corr.) between predicted breeding values for late  
 2 period<sup>1</sup> competition traits in bivariate analysis (BM) and BVs in univariate analysis for whole period<sup>1</sup> (UW), early period<sup>1</sup>  
 3 (UE), and late period<sup>1</sup> (UL)

Trait and group of horses	UW-BM			UE-BM			UL -BM		
	Differences			Differences			Differences		
	Real	Abs.	Corr.	Real	Abs.	Corr.	Real	Abs.	Corr.
<i>Dressage</i>									
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
<i>Show jumping</i>									
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

- 4 <sup>1)</sup> Whole period = horses born 1953-2002; Early period: horses born 1953-1983; Late period: horses born 1984-2002.



**Figure 1.** Average accuracies ( $r_{T1}$ ) 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 ( $r_{T1}$ ) 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

Test data set	UW <sup>1</sup>		UL <sup>2</sup>		BM <sup>3</sup>	
	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

<sup>1</sup>)UW=univariate model, all data (whole period).

<sup>2</sup>)UL=univariate model, only data from late period.

<sup>3</sup>)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

Test data set	UW <sup>1</sup>		UL <sup>2</sup>		BM <sup>3</sup>	
	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

<sup>1</sup>)UW=univariate model, all data (whole period).

<sup>2</sup>)UL=univariate model, only data from late period.

<sup>3</sup>)BM=bivariate model, all data with separate trait definition for early and late time periods.