

1 **Improvement in the national genetic evaluation of warmblood riding horses by**
2 **including information from related studbooks**

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8

9 **Abstract**

10 Young horse performance test data from two warmblood riding horse populations, Norwegian Warmblood
11 (NWB) and Swedish Warmblood (SWB), were analysed to examine whether including information from a
12 related studbook would increase the accuracy of the genetic evaluations within a population. Ten
13 conformation and performance traits from 31,588 horses, 774 NWB and 30,814 SWB, were analysed
14 separately and jointly using single trait animal models. Heritabilities were moderate to high, and varied
15 from 0.15 (conformation, joint data) to 0.74 (jumping technique, NWB data). The genetic similarity (GS)
16 between populations was 31%, with the SWB, as expected given the size of the populations, contributing
17 most to the GS (98%). Genetic correlations between the same traits in the two populations were 0.43-0.90
18 but with large standard errors (0.2-0.3). Including information from the other population increased the
19 average accuracy of estimated breeding values for common stallions, on average 4% for SWB and 110%
20 for NWB.

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22 **Keywords: genetic parameters, sport horse, performance test, genetic evaluation, genetic similarity**

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26 **Introduction**

27 Young horse performance testing is used as a tool to predict a horse's potential value as a sport and
28 breeding animal in most studbooks for warmblood riding horses in Europe. Horses are tested at a young
29 age (3-5 years old) and the tests include conformation and performance traits (Thorén Hellsten et al.
30 2006). Heritabilities for traits recorded at these tests are low to moderate (Huizinga et al. 1990; Ducro et al.
31 2007, Viklund et al. 2008). Genetic correlations between performance traits tested on young horses and
32 performance later in life have been shown to be moderate to high (Wallin et al. 2003; Ducro et al. 2007,
33 Viklund et al. 2010). Hence routine genetic evaluations of horses include information from young horse
34 tests as well as performance in competition on a national level. With increasing use of artificial
35 insemination the horse breeding industry has become more international the last 30 years, as semen from
36 breeding stallions are available for mare owners all over the world. The use of stallions in a riding horse
37 population is not equally distributed. Some stallions might cover only a few mares each year, while others
38 might cover a substantial proportion of the mare population. Their offspring will attend performance tests
39 and/or competition only if the breeder/owner is interested in doing so. For many stallions the information
40 available for estimating breeding values might therefore be limited. If data from other related studbooks
41 could be included in the national genetic evaluation, like the international genetic evaluation in dairy
42 cattle provided by Interbull (Philipsson, 2011), one might produce more reliable breeding values for
43 selection purposes within each riding horse population. Including information from other related
44 populations will strengthen the genetic evaluations within a population if the genetic ties between the
45 populations are sufficiently strong (Kennedy & Trus, 1993). Recent studies initiated by Interstallion have
46 revealed strong genetic ties between many of the European riding horse populations (Thorén Hellsten et
47 al. 2008; Ruhlmann et al. 2009). Those studies showed that the Holstein (Holst) and Hannoverian (Hann)
48 populations from Germany and the Royal Dutch Sport Horse (KWPN) from the Netherlands provided
49 large genetic contributions to the Danish (DWB) and Swedish Warmblood (SWB). In a small riding horse

50 population like the Norwegian Warmblood (NWB), Holstein, SWB and DWB have contributed close to
51 50% of the genes (Furre et al. 2010).

52 The aim of this study was to investigate if joint genetic analyses and estimation of breeding values could
53 be feasible for the two warmblood riding horse studbooks, NWB and SWB. Traits recorded at young
54 horse performance tests in SWB and NWB were therefore analysed separately and jointly to compare the
55 accuracy of predicted breeding values for sires with tested offspring in both studbooks. Special emphasis
56 was put on how information from SWB could improve the accuracy of breeding value estimations in the
57 small NWB population.

58 **Material and Methods**

59 *Traits*

60 Data were from the Young Horse Test (YHT) and the Riding Horse Quality Test (RHQT) in NWB and
61 SWB from 1981 to 2010. The YHT is a test for 3-year old horses, while the RHQT is for 4 year old
62 horses. Both tests are field-tests open for stallions, mares and geldings. Mares that had a foal as a 4-year
63 old are allowed to participate in the RHQT the following year.

64 Data from the young horse tests in NWB included horses tested from 2005 to 2010 for YHT, and 1981 to
65 2010 for the RHQT. For conformation the scores for single traits were missing for half of the data (1989-
66 1991 and 1994-2001), and only the overall conformation scores were available. For the year 1992 no data
67 were available. The lack of data for certain years in the NWB is due to inconsistency in the recording of
68 data. Data from SWB comprised horses completing the YHT from 1999 to 2010 and the RHQT between
69 1981 and 2010. A total of 31,588 horses were included in the analyses, the distribution over tests and
70 countries are given in Table I. The data file contained information on the horses that had completed one or
71 both tests, and included their sex, age and the combination of year and test location they were tested.
72 2,799 horses had records from both YHT and RHQT, but no horses had records from both countries. In
73 NWB there was one test location per year, while in SWB the number of test locations per year and type of

74 test ranged from 12 to 20. There are three main elements in both the YHT and the RHQT; the horses'
75 conformation, gaits under rider, and jumping ability (either under rider or as free-jumping). In both
76 countries all traits were scored on a scale from 1 to 10, with 10 as the highest score and 1 the lowest score.
77 For most of the traits, the scoring was carried out by groups of two to five judges, and the record for each
78 trait is the score given by the group. Detailed descriptions of the traits are given in Wallin et al. (2003) and
79 Viklund et al. (2008). Traits included in the present study are given in Table II. In the analyses jumping
80 under rider and free-jumping were considered as one trait as distinguishing between the two methods were
81 troublesome for some years. The correlation between free-jumping and a combination of the two methods
82 of testing the horses jumping capability has been shown to be high, 0.96-0.98 (Viklund et al. 2008).
83 Descriptive statistics of all traits for the NWB, SWB and joint dataset are given in Table III.

84 *Pedigree data*

85 Pedigree data supplied by NWB (19,787 animals) and SWB (227,000 animals) contained all horses in the
86 studbook database also horses that never had participated in any test. A cross-reference file based on the
87 pedigree-file provided by the NWB was created. The file contained the name of the individual horse, birth
88 year when known, Universal Equine Life Number (UELN) if available, and also registration and/or
89 studbook numbers from foreign studbooks, including the same information for ancestors. For horses with
90 data from young horse tests in Norway the corresponding Swedish registration and/or studbook number
91 were included in the cross reference file if available. The cross-reference file was used to combine the
92 pedigree information from both studbooks based on UELN and Swedish registration and/or studbook
93 number. For horses missing this information their name, birth year and parent information were used for
94 combining the pedigree files. For horses missing birth year information in one or both pedigree files, their
95 name and their parents names were used as criteria for matching the files. The initial pedigree file
96 comprised of all horses in both studbooks. The pedigree files used in the analyses were created by tracing
97 the pedigree for each animal with test data as far back as possible in the full pedigree file. The number of
98 animals in the pedigree files used in the analyses were 7,692, 68,392 and 70,702 for NWB, SWB and the

99 joint analyses respectively. The average pedigree completeness value (PEC) is a measure of how complete
 100 the pedigree information is (Maccluer. et al 1983), for the animals with test-data average PEC was 0.47
 101 for NWB, 0.93 for SWB and 0.91 for the joint pedigree file.

102 *Genetic connectedness between populations*

103 The most basic description of the genetic connectedness level between populations is the number of sires
 104 in common, NSC. However this number does not take into account the number of offspring from each
 105 stallion in the different populations. Another method for calculating the genetic connectedness between
 106 populations is the Genetic similarity (GS) which is a measure of the proportion of the populations that has
 107 sires in common. The GS-method was first proposed by Rekaya et al. (1999), and is the proportion of
 108 progeny of common sires in two populations, in relation to the total number of progeny in the two
 109 populations. In this study the progeny is the tested offspring of common stallions in relation to the total
 110 number of tested animals in the populations. This method was also used by Thorén Hellsten et al. (2008).

111
$$GS_{ij} = \frac{\sum_{k=1}^{N_{ij}} (n_{ik} + n_{jk})}{\sum_{k=1}^{N_i} n_{ik} + \sum_{k=1}^{N_j} n_{jk}}$$

112 where N_{ij} is the number of common stallions in population i and j , n_{ik} and n_{jk} is the number of
 113 offspring of stallion k in country i and j . The GS might give a biased picture of the connectedness level
 114 between populations as there might be stallions in the data that have many offspring in one population and
 115 few in another. Therefore the contribution to the GS was estimated to detect potential skewed
 116 contributions in the data. The contribution to the GS is given in following model:

117
$$\text{Contribution to GS in \%} = \frac{\sum_{k=1}^{N_i} (n_{ik})}{\sum_{k=1}^{N_{ij}} (n_{ik} + n_{jk})} \times 100$$

118 where N_i is the number of stallions in common in population i, n_{ik} is the number of offspring of stallion k
119 in population i, n_{jk} is the number of offspring of stallion k in population j, and N_{ij} is the number of
120 stallions in common in the two populations.

121 *Genetic analyses*

122 Data from NWB and SWB were analysed separately and jointly. A univariate linear animal model was
123 used for genetic analyses. The following model was used for all ten traits:

$$124 \quad Y_{ijklm} = sex_i + age_j + event_k + animal_l + e_{ijklm}$$

125 where Y_{ijklm} is the score for the trait for the l^{th} horse; sex_i is the effect of being either male or female
126 ($i=1,2$), age_j is the age of the horse ($j=3,4,5$), $event$ is the combination of test location and year of the test
127 ($k=1,\dots,30$) for the Norwegian data, ($k=1, \dots, 652$) for the Swedish data, and ($k=1, \dots, 682$) for the joint
128 dataset. In the joint analyses Norway was treated as one test location per year within the Swedish system.
129 $Animal_l$ is the random effect of animal, σ_a^2 and e_{ijklm} is the residual. Variance components were estimated
130 and breeding values predicted using the DMUAI routine in the DMU software (Madsen and Jensen,
131 2008). The genetic correlations between the same traits from Norway and Sweden were estimated using a
132 bivariate linear model with the same fixed and random effects as in model above.

133 Accuracy of breeding values is the correlation between the true and estimated breeding value, r_{TI} . The
134 accuracies were calculated as:

$$135 \quad r_{TI} = \sqrt{\frac{1 - PEV}{\sigma_a^2}}$$

136 where PEV is the prediction error variance.

137 **Results and Discussion**

138 *Genetic connectedness between populations*

139 There were 113 stallions in common between NWB and SWB. In the Norwegian data 108 of these
140 stallions had between 1 and 5 offspring with test-data, while four stallions had 6-10 and only one stallion
141 had more than 10 tested offspring in Norway. The stallions had larger progeny groups in Sweden, where
142 28 of them had more than 100 offspring with test-data. The NSC in NWB and SWB were larger than the
143 NSC found between all pairs of studbooks in Thorén Hellsten et al. (2008) where the largest NSC was
144 found between DWB and SWB with 104 stallions in common. The common stallions in their study had
145 mainly either a Danish, Swedish or German (Hannoverian and Holstein) origin, with the contribution from
146 Germany increasing over time. The origin of the stallions in common in NWB and SWB is given in Table
147 IV. The stallions were divided into three birth year groups (1964-1974, 1975-1984 and 1985 to 2002) in a
148 similar manner as the study of Thorén Hellsten et al. (2008) for comparison purposes. Thorén Hellsten et
149 al. (2008) found that the NSC in common between SWB and DWB originated from these two studbooks
150 in the first two time periods, whereas the German studbooks were the main contributors to the NSC in the
151 last time period. The NSC in common in NWB and SWB came mainly from SWB in the first time period
152 (1959-1974). In the second time-period, the SWB still had a large contribution to the NSC, but the
153 Holstein also had a large contribution with 28% of the stallions in common originating from Holstein. The
154 time-period contributing most to the NSC were for stallions born between 1985-1995 with 58% of the
155 stallions in common born within this time period. These stallions were mainly from Holstein, Hannover or
156 KWPN, and these three studbooks contributed with 65% of the stallions in common. In the present study
157 the DWB had only 4 stallions in total contributing to the NSC between NWB and SWB. The DWB has
158 been shown to have a large contribution to the NWB (Furre et al. 2010a), however, this is not reflected in
159 the NSC in this study.

160 The Genetic Similarity (GS) between NWB and SWB was estimated to 31%. The GS found between
161 SWB and four other European studbooks in earlier studies was 18% with DWB, 9% with Hann, 7% with
162 Holst, and 7% with KWPN (Thorén Hellsten et al. 2008). The marginal contribution from the same
163 studbooks in NWB was 60%, based on horses participating in the RHQT in Norway 1996-2006 (Furre et

164 al. 2010). The high GS between NWB and SWB was therefore expected. Ruhlmann et al. (2009) found
165 GS between Sweden and Germany, and Denmark and the Netherlands ranging from 1-16%, thus not
166 discriminating between studbooks within the countries. These two studies concluded that the GS itself is
167 not an optimal method for measuring genetic connectedness as the contribution from different studbooks
168 might not be equally distributed. The contribution to GS by NWB and SWB was 2.2 and 97.8
169 respectively, meaning that almost 98% of the offspring contributing to the GS were found in the Swedish
170 data. Such skewed contributions were also found in the previous mentioned studies and ranged from 63%
171 (DWB-SWB) to 92% (Hann-SWB) (Thorén Hellsten et al. 2008), and from 0% (Belgium-Sweden) to 48%
172 (Germany-Sweden), (Ruhlmann et al. 2009). Thorén Hellsten et al. (2008) concluded that the NSC for the
173 studbooks in her study was sufficient for estimation of genetic correlations between organizations in her
174 the study, as the NSC was larger than the minimum number of 20 suggested by Mark et al. (2005) for
175 dairy bulls. Mark et al. (2005) pointed out that the correlations between traits in two populations is quite
176 unaffected by differences in e.g data, model and method when the number of sires in common is >20. As
177 there were 113 stallions that had offspring with data in both populations, the populations seem sufficiently
178 connected to perform joint genetic analyses for the two populations.

179 *Heritabilities and genetic correlations*

180 Estimated variance components and heritabilities for the ten traits recorded for both NWB and SWB,
181 analysed separately and jointly, are given in Table V. Heritabilities were moderate to high, and varied
182 from 0.15 (conformation, joint data) to 0.74 (jumping technique, NWB data). Heritabilities were in the
183 same range as for similar traits found in previous studies (Huizinga et al. 1990; Ducro et al. 2007, Viklund
184 et al. 2008). NWB had, as expected, larger standard errors of the heritabilities for all traits since this dataset
185 was small. The PEC-value for the NWB was also substantially lower than for SWB and this might also
186 affect the variance component analyses. Heritabilities were high for type, walk and trot in NWB, but these
187 estimates also had the largest standard errors, and must therefore be interpreted with caution. The overall
188 conformation score is an average of all sub-scores for conformation, and might therefore be a less specific

189 score for the horses' conformation than e.g. the type, which is a single score for the horses' appearance.

190 The heritability for type was also high (0.46-0.51).

191 All heritability estimates for the joint dataset were as expected close to or identical to the SWB estimates.

192 The estimates for the joint and SWB datasets also corresponds well with heritability estimates from other

193 studies in the SWB (Wallin et al. 2003, Viklund et al. 2008), although somewhat differently analyzed in

194 this study, where 3-, 4- and 5-year old horse results were considered the same trait, and thus analyzed with

195 repeated measures for some horses.

196 The genetic correlations between similar traits measured in YHT and RHQT in SWB have been shown to

197 be high, 0.83-0.98 (Viklund et al. 2008). The genetic correlation between similar traits measured in

198 Sweden and Norway in this study ranged from 0.43-0.90 (Table VI). However, standard errors were large

199 and hardly any of the correlations were significantly different from unity. The lowest correlation was for

200 the traits related to the horses' temperament. Heritability for the trait temperament in jumping in the

201 Norwegian data was high (0.66), while for the Swedish data the heritability was only slightly higher than

202 that found in other studies (0.26). Temperament is a trait that might be difficult to quantify and measure as

203 the horses' behavior during the tests might be highly influenced by the previous training and experience of

204 the horse. In addition the various sub-traits within the trait "temperament" are not yet clearly defined

205 (Hausberger et al. 2004; Dietl et al. 2005). Still the NWB estimate for this trait was surprisingly high.

206 *Accuracy of EBV*

207 The mean accuracies of EBVs for the 113 common stallions when using information from NWB only

208 ranged from 0.25 to 0.66. The accuracy for trot under rider was the highest (Table VII). The mean

209 accuracy for EBV from SWB was as expected higher (0.72-0.83) reflecting the larger dataset. However,

210 the accuracy of EBV for common stallions increased both for the NWB and the SWB when performing a

211 joint prediction of breeding values. The increase in accuracy for the NWB was as expected the largest as

212 the information on a national level is limited. The average relative gain in accuracy across traits for NWB

213 was 110%, with trot under rider having the lowest relative gain (19%) while trot by hand had the highest
214 relative gain (229%). The average relative gain in SWB was 4%, with type (2%) having the lowest relative
215 gain, and canter under rider and rideability gaits (both 5%) having the highest relative gain. The relative
216 gain in accuracy for the two populations implies that both NWB and SWB will benefit from including
217 information from related studbooks in their genetic evaluation. Despite the limited amount of extra
218 information provided by the NWB into the joint analyses there was a relative gain in accuracy for all traits
219 also for the SWB population suggesting that the potential additional gain might be even higher including
220 information from other, larger, related studbooks into the genetic analyses.

221 For dairy cattle the joint international evaluations (MACE) are based on national EBV for bulls, and the
222 de-regressed proofs of these, where similar traits measured in different countries are treated as different
223 but correlated traits (Philipsson, 2011). In the present study the NWB had no prior EBV:s for their
224 stallions and therefore the phenotypic data had to be used in a similar way as Fikse et al. (2000) did with a
225 small sized Guernsey population. The present approach to international genetic evaluation might not be
226 optimal as reliable genetic correlations between traits across countries are not available. However, the
227 joint prediction of EBVs has proved to be encouraging for use in practice, especially for the small NWB
228 population.

229 **Conclusions**

230 The large increase in accuracy for the breeding values estimates for NWB implies that this population
231 benefits largely from including information from other populations in their breeding value estimations.
232 The accuracy of breeding values increased however also for the SWB and including information from
233 foreign studbooks in breeding value estimations for warmblood riding-horses is thus recommended. The
234 Genetic similarity (GS) and number of common sires between NWB and SWB populations suggest that
235 joint genetic analyses in the two populations are feasible. This conclusion is supported by positive genetic

236 correlations between the same traits scored in the two populations and that heritabilities are of similar
237 magnitude for most traits.

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298 jumping. *Livestock Production Science* 82, 61-71.

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Table I. Number of horses with test-records from young horse tests in Sweden and Norway and the total no of horses with data in the joint analyses.

	Norway	Sweden	Joint
YHT*	110	12,101	12,211
RHQT**	684	19,783	20,486
Total no. animals with data	774	30,814	31,588

*Young Horse Test for 3-year-old mares, geldings, and stallions

**Riding Horse Quality Test for 4- and 5-year old mares, geldings, and stallions

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Table II. Description of traits recorded at young horse tests used in this study.

Trait	Description
Type	The overall type of the horse
Walk	The quality of the walk shown by hand
Trot	The quality of the trot shown by hand
Overall conformation	An average of all sub-scores for conformation, i.e. type, head-neck-body, walk, trot and correctness of legs.
Jumping, technique & ability	The horses technique and capacity, either under rider or free-jumping
Jumping, temperament	The horses attitude during the jumping test, either under rider or free-jumping
Walk under rider	The quality of the walk shown under rider, impulsion, stride etc
Trot under rider	The quality of the trot shown under rider, impulsion, stride
Canter under rider	The quality of the canter shown under rider, impulsion, stride
Rideability gaits	The horses attitude and rideability during the gaits test

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Table III. Number of records (N), mean and standard deviation (SD) for analysed traits in Norwegian Warmblood (NWB), Swedish Warmblood (SWB) and joint data.

Trait	NWB			SWB			Joint		
	N	Mean	S.D	N	Mean	S.D	N	Mean	S.D
Type	329	6.90	1.20	30,787	7.78	0.65	31,116	7.77	0.67
Walk	340	6.75	1.14	28,258	7.33	0.77	28,598	7.33	0.78
Trot	340	6.50	1.18	28,258	7.80	0.83	28,598	7.08	0.84
Overall conformation	742	6.86	0.86	30,787	7.29	0.69	31,529	7.28	0.69
Jumping, technique & ability	717	6.69	1.43	30,814	6.72	1.37	31,531	6.72	1.38
Jumping, temperament	591	6.92	1.52	30,814	6.80	1.50	31,405	6.80	1.50
Walk under rider	682	6.77	1.10	18,713	6.67	1.00	19,395	6.67	1.00
Trot under rider	682	6.57	1.09	18,713	6.34	1.01	19,395	6.35	1.01
Canter under rider	682	6.76	1.15	18,713	6.69	0.99	19,395	6.69	1.00
Rideability gaits	708	6.77	1.14	18,713	6.63	0.97	19,421	6.64	0.98

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Table IV. Studbook of origin of stallions in common in Norwegian Warmblood and Swedish Warmblood and their birth-year group.

Studbook	Birth-year of stallions in common			Total
	1959-1974	1975-1984	1985-2002	
Swedish Warmblood	14	12	7	33
Holstein	2	7	18	27
Hannoverian	2	1	13	16
KWPN	0	1	12	13
Thoroughbred	2	1	4	7
Oldenburg	0	1	5	6
Danish Warmblood	1	1	2	4
Trakhener	1	1	1	3
Brandenburg	0	0	1	1
Belgian Warmblood	0	0	1	1
Selle Francais	0	0	1	1
Westfahlen	0	0	1	1
Total	22	25	66	113

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Table V. Estimated variance components and heritability for traits in the young horse tests in Swedish Warmblood (SWB) and Norwegian Warmblood (NWB) analysed separately and jointly. Standard errors are given in sub-scripts.

Trait	Genetic variance			Residual variance			Heritability		
	NWB	SWB	Joint	NWB	SWB	Joint	NWB	SWB	Joint
Type	0.52 _{0.27}	0.20 _{0.01}	0.21 _{0.01}	0.49 _{0.25}	0.24 _{0.01}	0.24 _{0.01}	0.51 _{0.25}	0.45 _{0.00}	0.46 _{0.01}
Walk	0.58 _{0.29}	0.18 _{0.01}	0.19 _{0.01}	0.46 _{0.27}	0.36 _{0.01}	0.36 _{0.01}	0.56 _{0.26}	0.33 _{0.01}	0.34 _{0.02}
Trot	0.42 _{0.30}	0.27 _{0.01}	0.28 _{0.01}	0.81 _{0.29}	0.34 _{0.01}	0.34 _{0.01}	0.34 _{0.24}	0.44 _{0.01}	0.45 _{0.01}
Overall conformation	0.20 _{0.06}	0.06 _{0.01}	0.06 _{0.01}	0.23 _{0.05}	0.37 _{0.01}	0.37 _{0.01}	0.47 _{0.12}	0.15 _{0.01}	0.15 _{0.01}
Jumping, technique & ability	1.24 _{0.16}	0.45 _{0.02}	0.46 _{0.02}	0.43 _{0.12}	1.25 _{0.02}	1.25 _{0.02}	0.74 _{0.07}	0.26 _{0.01}	0.27 _{0.01}
Jumping, temperament	1.16 _{0.21}	0.44 _{0.03}	0.44 _{0.03}	0.60 _{0.18}	1.66 _{0.02}	1.66 _{0.02}	0.66 _{0.10}	0.21 _{0.01}	0.21 _{0.01}
Walk under rider	0.28 _{0.15}	0.32 _{0.02}	0.32 _{0.02}	0.72 _{0.14}	0.61 _{0.02}	0.61 _{0.02}	0.28 _{0.14}	0.34 _{0.02}	0.34 _{0.02}
Trot under rider	0.44 _{0.13}	0.43 _{0.02}	0.43 _{0.02}	0.57 _{0.12}	0.51 _{0.02}	0.52 _{0.02}	0.44 _{0.12}	0.45 _{0.02}	0.45 _{0.02}
Canter under rider	0.49 _{0.13}	0.35 _{0.02}	0.35 _{0.02}	0.52 _{0.12}	0.57 ^{0.02}	0.57 _{0.02}	0.48 _{0.12}	0.38 _{0.02}	0.38 _{0.02}
Rideability gaits	0.31 _{0.13}	0.29 _{0.02}	0.29 _{0.02}	0.76 _{0.13}	0.55 _{0.02}	0.56 _{0.02}	0.29 _{0.12}	0.34 _{0.02}	0.34 ^{0.02}

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Table V. Estimated variance components and heritability for traits in the young horse tests in Swedish Warmblood (SWB) and Norwegian Warmblood (NWB) analysed separately and jointly. Standard errors are given in sub-scripts.

Trait	Genetic variance		Residual variance
	NWB	SWB	Joint
Type	0.52 _{0.27}	0.20 _{0.01}	0.21 _{0.01}
Walk	0.58 _{0.29}	0.18 _{0.01}	0.19 _{0.01}
Trot	0.42 _{0.30}	0.27 _{0.01}	0.28 _{0.01}
Overall conformation	0.20 _{0.06}	0.06 _{0.01}	0.06 _{0.01}
Jumping, technique & ability	1.24 _{0.16}	0.45 _{0.02}	0.46 _{0.02}
Jumping, temperament	1.16 _{0.21}	0.44 _{0.03}	0.44 _{0.03}
Walk under rider	0.28 _{0.15}	0.32 _{0.02}	0.32 _{0.02}
Trot under rider	0.44 _{0.13}	0.43 _{0.02}	0.43 _{0.02}
Canter under rider	0.49 _{0.13}	0.35 _{0.02}	0.35 _{0.02}
Rideability gaits	0.31 _{0.13}	0.29 _{0.02}	0.29 _{0.02}

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Table VII. Average accuracies of estimated breeding values for the 113 stallions in common in Norwegian Warmblood (NWB) and Swedish warmblood (SWB) when using national information only, and when combining the information in a joint prediction.

Trait	Average accuracy			Relative gain in accuracy in %	
	NWB	SWB	Joint	NWB	SWB
Type	0.31	0.83	0.85	174	2
Walk	0.32	0.79	0.81	149	3
Trot	0.25	0.81	0.84	229	3
Overall conformation	0.44	0.72	0.75	70	3
Jumping, technique & ability	0.53	0.78	0.81	53	3
Jumping, temperament	0.45	0.76	0.78	73	2
Walk u/rider	0.33	0.72	0.76	129	5
Trot u/rider	0.66	0.75	0.79	19	5
Canter u/rider	0.42	0.73	0.77	82	5
Rideability gaits	0.35	0.72	0.76	121	5

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