The Importance of Genetic Contributions into a Small Warmblood Riding-horse Population.

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Introduction

High accuracy in genetic analyses is achieved by having large number of recordings and complete pedigree information. In some small sport-horse populations however, neither of these prerequisites might be satisfactorily fulfilled. The number of phenotypic recordings in the population might be scarce and pedigree information limited. Genetic connectedness is used in calculation of breeding values across populations for e.g. cattle and sheep (Powell et al. (2000); Kuehn et al (2007)). These studies show that including information from other related populations in prediction of breeding values were valuable if the genetic ties between the different populations are strong enough. All riding-horse populations in Europe today contain genetic material from other populations due to increased international trade with semen and livestock. Germany and France are the main exporting countries (Koenen et al. (2004)), while countries with smaller and more recently established populations, like Norway and Finland, mainly import genetic material. The increased internationalisation of the horse breeding industry lead in 1998 to the formation of 'Interstallion', an organisation aiming at better genetic evaluations and exchange of information on riding-horses between countries.

Recent studies initiated by 'Interstallion' have shown strong genetic ties between many of the European riding-horse populations. The genetic connectedness level between the Danish Warmblood, Swedish Warmblood, Hanoverian, Holstein and KWPN studbooks are sufficient for performing genetic analysis across countries (Hellsten et al. (2008)). Seven European countries (Belgium, Denmark, France, Germany, Ireland, Sweden and the Netherlands) have adequate genetic connectedness for estimates of genetic correlations between traits recorded in these countries (Ruhlmann et al. (2009)). Due to increasing demands from national breeders and internationalisation of the breeding industry, the Norwegian Warmblood association (NWB) has recognized the need of a more professional approach to the breeding work, including the need for estimation of breeding values. NWB is a rather small studbook with ~300 foals born per year. Approximately 100 horses per year have recordings from young-horse performance tests (3-4 yrs), mare-grading shows and the stallion approval test. The NWB has organised a test for young horses, the Young Horse Quality Test (YHQT) over a period of 25 years from 1981 to 2006. The aim of this study was firstly to estimate variance components from traits recorded at the YHQT, and secondly to evaluate the genetic contributions to the NWB in order to investigate the possibility of performing joint breeding value evaluations in the Nordic Countries; the Nordic Interstallion.

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Material and methods

Data and pedigree-information. A total of 584 horses completed the YHQT between 1981 and 2006. Traits recorded were health, temperament, conformation and performance traits such as gaits and jumping ability, all scored on a scale from 1-10 (see Wallin et al. (2001) for detailed description of traits and scoring methods). Average scores for traits used in genetic analyses ranged from 6.38-6.66. A pedigree-file that included up to four generations and consisted of a total of 5884 horses, was created based on pedigree information on the participating horses. There were 295 sires, 473 dams and 362 maternal grandsires represented in the pedigree-file. Among the sires 83 also appeared as maternal grandsires. For 27 horses no pedigree-information was available.

Variance components. Traits recorded at the YHQT with sufficient number of records (N=519-556) for estimation of variance components were walk, trot, canter, gaits and overall conformation. Single trait animal models including fixed effects of year (the year the horse attended the test), sex (stallion, mare or gelding) and birth-country (Norway, Sweden, Denmark, Germany, Netherland or 'other') were used for estimation of variance components. Variance components were estimated using the AI-REML procedure in the DMU package (Madsen and Jensen (2005)).

Genetic contribution. The genetic contributions to the Norwegian population were calculated using the method of Boichard et al. (1997). The reference population from which the contribution was calculated in this analysis were defined as the 192 horses that had attended the YHQT between 2000 and 2006. A SAS-program (SAS 2002-2003) was written for calculation of the marginal genetic contribution. In short, the program identifies the founder that has the largest contribution to the population, the contribution is noted and the founder is removed from the pedigree for the subsequent runs. The procedure is repeated until the marginal contribution estimate from all the founders' sums up to 1. All founders were manually coded to a breeding organisation and/or country of birth based on information from written studbooks, online databases etc.

Results and discussion

Variance component and heritability estimates for chosen traits recorded at the YHQT are given in table 1. Heritabilities ranged between 0.17 and 0.33, and were in agreement with heritabilities for traits calculated from scores recorded at similar young horse tests in other countries (Huizinga et al. (1990); Wallin et al. (2003)). However, the standard errors of the variance component estimates in this study were large (Table 1), due to few observations and incomplete pedigree-information on the tested horses. Including information from other studbooks could have increased the accuracy of the estimates if the studbooks were sufficiently genetically connected.

A total of 161 horses had contributed with information on the genetic variation in the NWB population. For some animals, information on country of birth and/or studbook was not available. The marginal genetic contribution from country of birth and studbook is given in table 2.

Table 1. Estimated genetic (σ_a^2) and residual (σ_e^2) variances with standard error and the corresponding heritability (h^2) for some traits recorded in the YHQT.

Trait	σ_a^2	σ_e^2	h^2
Conformation	.13 ±.09	.37 ±.08	.26
Walk	.28 ±.21	.80 ±.20	.26
Trot	.31 ±.17	.76 ±.17	.29
Canter	.17 ±.15	.83 ±.15	.17
Gaits	.22 ±.11	.44 ±.10	.33

Almost 50 percent of the genetic material in the NWB population originates from Germany (table 2) with Holstein being the second largest studbook contributor after Danish Warmblood. Between 44-75 percent of sires of active stallions in Denmark, Sweden and The Netherlands were of German origin (Koenen et al. (2002)). Hellsten et al. (2008) found that Danish Warmblood and Swedish Warmblood have a considerable amount of stallions in common, these stallions are either of Swedish, Danish or German origin.

Table 2. Genetic contribution from country and studbook in the Norwegian Warmblood population.

Country of birth	Marginal Contribution	
Studbook	Country of birth	Studbook
Germany	0,469	
Holstein		0,169
Hannoverian		0,073
Trakehner		0,062
Oldenburg		0,045
Denmark	0,179	
Danish Warmblood		0,192
Sweden	0,151	
Swedish Warmblood		0,120
The Netherlands	0,081	
KWPN		0,058
Norway	0,036	
Norwegian Warmblood		0,045
France	0,027	
Selle Français		0,022
Anglo-Norman		0,019
Other*	0,057	
Other**		0,058
Thoroughbred		0,137
Total	1,000	1,000

*Poland, Ireland, Great Britain, USA and unknown birth countries

**Shagya Arabians, Whestphalers and Gelderlenders and unknown studbooks.

The Thoroughbred is in this study considered as an international studbook independent of the country-of-birth and this generalization has also been applied in other studies (Ruhlmann et al. (2009)). In the Norwegian Warmblood population approximately 14 percent of the genetic contribution was from Thoroughbred horses. Thoroughbreds might in general provide valuable genetic links between studbooks.

The large portion of genetic contribution (~96 %) from foreign studbooks in the Norwegian Warmblood implies that genetic connectedness estimates between the NWB and other riding-horse populations in order to perform genetic analysis, and estimate breeding values in the population is crucial. Studbooks in the main exporting countries (e.g Germany and France) might be in risk of getting biased breeding value estimates for horses in their populations because additional information on horses from their populations competing in other countries might not be available. International calculations of breeding values for horses, as is in dairy cattle done by 'Interbull' might give a more accurate picture of the genetic level in the different riding-horse populations in Europe. Finnish Warmblood (FWB) is probably, like the NWB, strongly influenced by their neighbouring countries Sweden and Denmark. The genetic connectedness level between Finland and Norway will therefore most likely be attended to through the Swedish and Danish populations who are assumed to be the joint factor in future genetic calculations in these four studbooks.

Conclusion

The results from this study indicates that a small warmblood riding-horse population, like the Norwegian Warmblood, will benefit from including information from other populations in genetic evaluations as long as the genetic connectedness level between populations are strong enough. Joint breeding value evaluation between the Nordic Sport-horse populations should be feasible and lead to improved accuracy in the national as well as international EBVs for all countries included in such joint evaluations.

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