Sport status and the genetic evaluation for show jumping in Belgian sport horses

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Abstract

Breeding values for show jumping horses in Belgium are based on performances in competition. However, some horses never enter jumping competitions which may point at preselection and this may bias ebv’s or make selection inefficient. The objective was to investigate sport status in the framework of show jumping for Belgian warmblood horses. Pedigree data from the studbooks BWP and sBs were integrated and made uniform (unique horse numbers). Performance data on show jumping were obtained from 2 riding organizations in Belgium and were treated as 2 traits: JN is performance at national level (KBRSF) and JR is at recreational level (LRV). Sport status (ST) was defined as a binary variable (at least one record in competition vs. no performance present in the data).

Genetic parameters were obtained in a Bayesian framework using the Gibbs sampler. Posterior means of heritabilities were 0.10 (JR), 0.08 (JN) and 0.71 (ST). Genetic correlations were approx. 0.68 (JR,JN), 0.14 (JR, ST) and 0.43 (JN,ST). The results indicate that status is highly heritable and moderately positively correlated with performance at national but not at recreational level. Correlations between ebv’s obtained in models with and without ST were high: 0.90 (all horses) and 0.95 (stallions).

Introduction

The selection of show jumping horses in Belgium is currently supported by estimated breeding values (ebv) based on performances in competition. This approach has the advantage that ebv’s are based on a relatively large sample of horses from the Warmblood population. Moreover, the procedure includes horses from 2 studbooks of warmblood horses (Studbook of Belgian Sporthorse, sBs; Belgian Warmblood Horse, BWP) and ebv’s are computed on a national level. Both characteristics should guarantee the representativeness of the published ebv’s. It has been noted however that from all foals registered in the studbooks, only a fraction is entered in jumping competition. Also, differences exist between stallions with regard to the proportion of progeny that competes in show jumping. This may point at a mechanism of “preselection” of the horses, before the age of 4 years. If preselection on jumping capacity exists, than a non-random sample of horses is used in the genetic evaluation and this may reduce heritability estimates and/or result in biased estimated breeding values. In both cases, selection will be inefficient. In trotters, it has been shown that racing status was a valuable trait to remove bias in breeding value estimation (Arnason, 1999; Langlois and Vrijenhoek, 2004, Bugislaus et al. 2005). Racing status was genetically correlated to the traits under selection (placements, earnings etc.) and not considering this information resulted in a different ranking of sires.

The objective of this study was to investigate the trait “sport status” in Belgian warmbloods with respect to jumping performance.

Materials and methods

Complete pedigree data were obtained from the studbooks BWP and sBs. Because of different identification numbers in each studbook, identification numbers were recoded to obtain an integrated pedigree file with unique horse numbers.

Performance data on show jumping were provided by two horse riding organizations in Belgium (Royal Belgian Federation for Equestrian Sports (KBRSF) for national level competitions and Rural Riding Association (LRV) for recreational level competitions). Data from the two organizations were treated as two separate traits, the same way as in the current genetic evaluation system. JN refers to jumping performances at national level, JR to performances in LRV. The reason for using a bivariate model was a genetic correlation between JN and JR of 0.63.

Performance in show jumping was expressed as the ranking of individual horses in separate competitions. Rankings in each separate competition were transformed using the BLOM-score (Reilly et al., 1998). Performance data were available from 1992 to 2006.

Sport status (ST) was defined for all horses in the pedigree file with birth year between 1988 and 2002 and its value depended on the presence of a record in the dataset of show jumping performances. Only the earliest performance of a horse was retained in the analysis of ST. Horses born before 1988 and later competition results were not included in the data for ST.

Table 1 **Descriptive statistics for performance traits and for sport status in Belgian warmblood horses.**

Trait	Definition	Effects in the model (number of levels)	Obs.	Mean	SD
JR Jumping recreational	Ranking of individual horse in LRV jumping in the period 1992-2006	F: sex (2), age (15), competition (6967) R: permanent (32938)	251560	0.00149	1.59
JN Jumping National	Ranking of individual horse in KBRSF jumping in the period 1992-2006	F: sex (2), age (15), competition (3745) R: permanent (32938)	253582	0.0000	1.61
ST Sport status	Horses registered in Belgium born from 1988 - 2002	F: year of birth (15), sex (2)	87435	0.383	0.486
	Total pedigree		179996		
	Sires (perf. horses)		4679		

The model for JN and JR corresponded to the current model for genetic evaluation including fixed effects for age of the horse, sex and competition (see table 1). A random permanent environmental effect linked to each performing horse was also fitted. For ST, year of birth and sex of the horse were fitted as fixed effects. In total, 179 996 horses and 592 577 performances were included in the computations. From the 4679 sires, about one third had progeny for all three traits. Only 384 sires were included with exclusively non performing horses. There were on average about 8 progeny per sire and over 17 performances per competing horse.

Since an analysis of ST with a linear model is not optimal, a threshold model was fitted. Threshold models assume an underlying continuous distribution for an observed trait having only a limited number of distinct phenotypes (ST in this study has 2 classes). Threshold - linear models have been studied in a Bayesian framework, using the Gibbs sampler (e.g. Van Tassell et al., 1998, Janssens and Vandepitte, 2006). In the 3 trait model, 12 parameters were studied namely, 7 variances, 5 co-variances and one threshold (the variance of the binary trait was set=1). Inference on variances and co-variances was made from the posterior distributions of the different parameters.

Chains were generated with different sets of prior distributions (table 2) in order to evaluate the dependency of posterior distributions on the prior information and to assess convergence. The residual covariance between ST and the two linear traits was restricted to zero because horses with ST=0 (no performances) always had missing observations for JN and JR. Posterior distributions of variance ratio's and of correlations were evaluated using descriptive statistics such as mean, standard deviation and 95% highest posterior region (HPR95).

Breeding values were estimated by Gauss-Seidel-iteration using the mean of the variance components in chain A. These values were compared to ebv's obtained with the routine genetic evaluation model (traits JR and JN only). Correlation coefficients between estimates were computed for all animals and for stallions. The highest 15% and 5% ranking animals were compared and the number of animals dropping out was evaluated.

Results

The proportion of progeny with performances varies between sires. With increasing numbers of progeny, this proportion seems to stabilize at around 0.40.

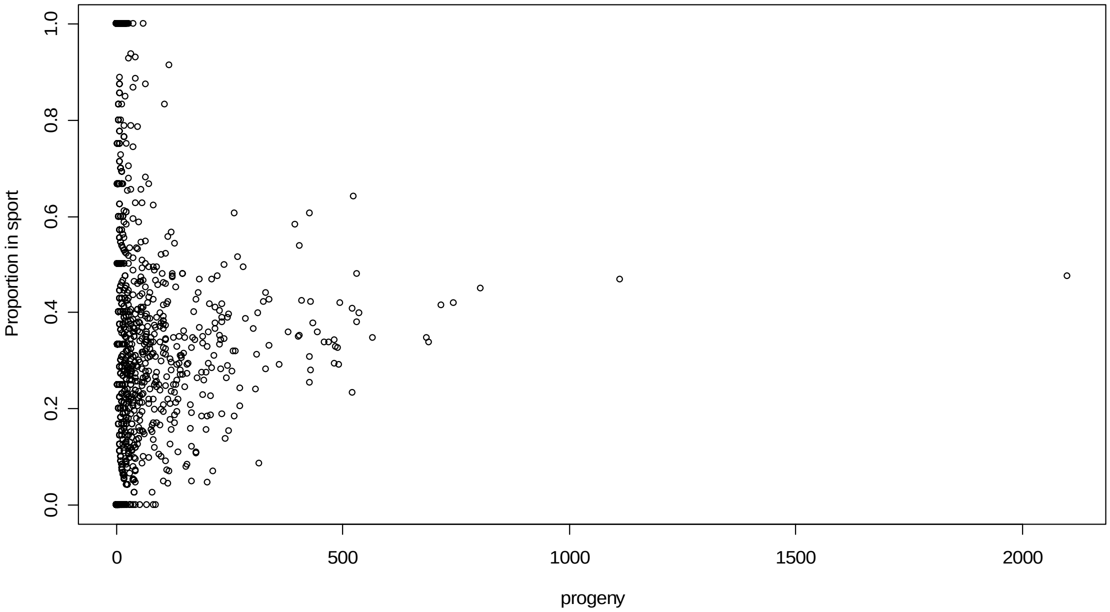

Figure 1 **The proportion of progeny with jumping performance plotted against the total number of progeny per sire in Belgian Warmblood horses. Jumping performance data from 1992-2006.**

Descriptive statistics of the chains are presented in table 2. The choice of the prior distributions did not have a determining effect on the posterior distributions and information coming from the data seemed to dominate (illustrated with figure 1 genetic correlation between JR and ST).

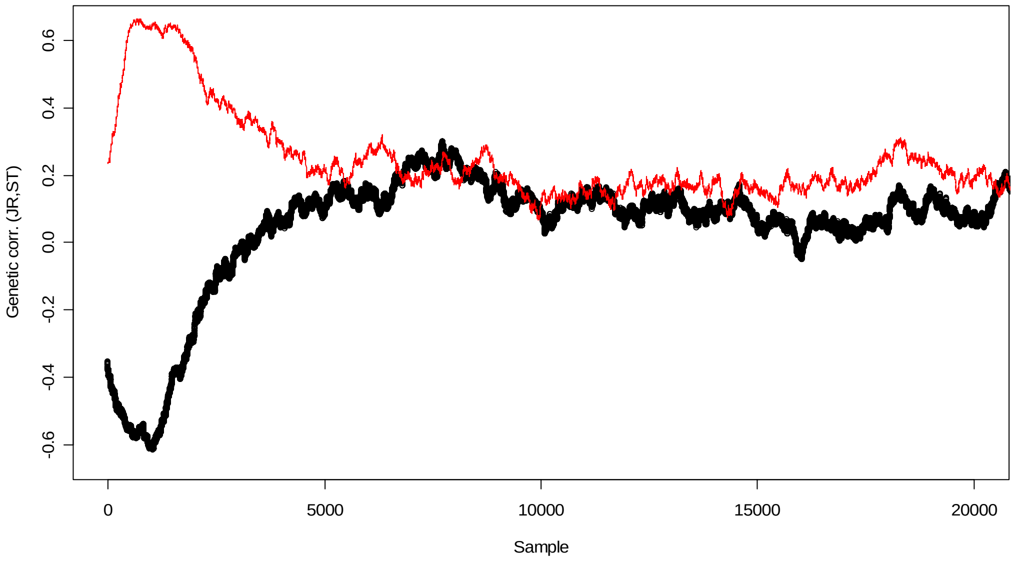

Figure 2 **Comparison of 2 chains generated with the Gibbs sampler for the genetic correlation between JR and ST**

Posterior means of the heritability coefficients for JN and JR were approximately 0.08 and 0.10 in both chains. Heritability estimates for ST were high (0.71) indicating a large genetic component in the sport-status of the horse.

The posterior means of the genetic correlation between JN and JR were 0.67 and 0.71, 0.13 and 0.15 between JR and ST and 0.42 and 0.45 between JN and ST. All 95% HPR's did largely overlap indicating that chains did not differ significantly.

Table 2: **Posterior mean, standard deviation and highest posterior region for heritabilities and genetic correlations in a 3-trait animal model on jumping performance (JR, JN) and sport status (ST). 2 chains (A,B) with different prior distributions**

PARAMETER	CHAIN/START VALUE	POSTERIOR MEAN	 STDEV	 HPR95	 HPR95
$h^2_{(JR)}$	A,0.10	0.094	0.008	0.078	0.110
	B,0.20	0.105	0.010	0.086	0.127
$h^2_{(JN)}$	A,0.10	0.075	0.007	0.062	0.087
	B,0.20	0.086	0.011	0.067	0.108
$h^2_{(ST)}$	A,0.05	0.708	0.041	0.687	0.736
	B,0.29	0.710	0.027	0.689	0.734
$r_{g(JR,JN)}$	A,0.50	0.707	0.051	0.608	0.804
	B,-0.50	0.668	0.090	0.575	0.775
$r_{g(JR,ST)}$	A,0.24	0.147	0.082	0.024	0.266
	B,-0.35	0.129	0.091	0.034	0.242
$r_{g(JN,ST)}$	A,0.24	0.446	0.051	0.345	0.535
	B,-0.35	0.415	0.103	0.332	0.524

JN = jumping performance in national level competitions, JR = jumping performance in recreational competitions, ST = status (horse with or without performance in show jumping)

Discussion and conclusions

Status in jumpers

About 62% of the registered horses in the Belgian population were considered as non performers. This proportion is high compared to percentages cited for trotters (40% in Sweden (Arnason, 1995), 35% Standardbred and 45% of Finnish trotters in Finland (Saastamoinen, 1999 cited by Bugislaus et al. 2005), 41% in French trotters (Langlois and Vrijenhoek, 2004) and 35% of German trotters (Bugislaus et al., 2005). However there could be additional reasons why warmblood horses have no jumping records. Apart from injuries, lack of talent, character, etc., warmblood horses could be used in other disciplines (dressage, eventing, as a private riding horse etc.). Horses competing in other disciplines could not be identified and were treated as not-performing in jumping. Horses competing in jumping outside Belgium or competing in lower level competitions were also not recorded in the performance data and thus regarded as not competing.

Extra information about the sports career and the status of a horse (still alive at 4 years?) would improve data quality. In this study, classification of horses for ST depended on the completeness and the matching of data and some misclassifications cannot be excluded.

Heritability

The posterior distributions obtained for the heritability of JN and JR had mean values very close to REML-estimates obtained previously on the Belgian data. The heritability coefficients varied between 8 and 10%, indicating that genetic variation of performance in competition data is difficult to assess and/or has low magnitude. However, our results are well in the range of values cited in the literature (Tavernier et al., 2000).

Compared to JN and JR, heritability of sport status was very high (HPR95 0.69 to 0.74). In trotters, heritabilities of 0.25 (0.40 on the underlying scale, Arnason, 1999), 0.30 (as a linear trait, Bugislaus et al., 2005) and 0.28 to 0.43 (Langlois and Vrijenhoek, 2004) were estimated. The high heritability in the 3-trait model was confirmed in univariate and bivariate models (results not shown). To our knowledge, there have been no estimates published for “status” in jumping horses so comparisons cannot be made. One explanation for the high heritability of ST might be the presence of dressage horses in the data. In the last decades, specialized lines have developed for dressage and for jumping and candidate stallions are judged for one of these breeding objectives. Consequently, more genetic variance may develop for performing in jumping.

In future research, we will try to identify horses that perform in other disciplines and subsequently leave them out from the analysis. Also, sire models will be tested to confirm the results obtained in animal models.

Genetic correlations

The genetic correlation between JN and JR had HPR95’s (0.61, 0.80) and (0.58, 0.78) which covers the value used in routine evaluations. The intervals indicate that the performance traits are probably more closely related than in the past, due to accumulation of data and/or more resemblance between jumping competitions (skill levels becoming more uniform ?).

The genetic correlation between ST and JR was low (HPR95 0.024 to 0.266) and between ST and JN moderately high (0.33 to 0.54). This indicates that a positive association exists between performance and status but that the association is relevant only for performance at national level.

The virtual absence of a genetic correlation between JR and ST means that performances in recreational competitions do not interact with status.

Although ST is highly heritable, it is useless as a direct selection trait. Its main role would be to correct ebv's for eventual bias due to preselection of horses by owners or breeders.

Table 3: Correlations between breeding values estimated in the current genetic evaluation model and a model extended with "status". Number of individuals that is replaced in the 15% or 5% highest ranked animals based on current ebv

	Correlation current ebv, ebv in 3 trait model	Top 15%	Top 5%
All horses (n=75970*)	0.91	2645	804
Stallions (n=926*)	0.95	16	9

**Numbers of horses and stallions correspond to the numbers in the genetic evaluation 2006.*

Breeding values

Correlation coefficients between ebv's obtained in the current genetic model and in an extended model were 0.90 and 0.95 for all horses and for stallions respectively. When considering the highest 5 or 15% of stallions, respectively 20% and 14% of the group is replaced. Effects are noted for young stallions that have high ebv's, due to good own performances and favourable pedigree information but with little or no competing progeny.

Rerankings of stallions occur and the effects of including ST on stallion indexes in subsequent years of computation will now be investigated.

Acknowledgements

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