Quality Checks of Danish Warmblood Breeding

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Introduction

Successful breeding is complex and depends on numerous critical aspects that determine the degree of success. To ensure successful breeding it is important to perform regular quality control of key aspects of the breeding program. Breeding programs for sport horses aim to improve several traits simultaneously, while avoiding inbreeding and being cost-effective. However, Danish Warmblood (DW) does not have a total-merit breeding goal specifying exact weights on different traits, which complicates focused selection. A recent study of inbreeding in DW found that rates of inbreeding seemed acceptable (<0.2%), but that pedigree completeness could be improved (Jensen, 2008). This study will therefore focus on the selection of stallions for the DW program and not on inbreeding. Specifically the following key aspects will be addressed: 1) validate the genetic evaluation system, 2) determine the realized selection emphasis of average breeder, and 3) compare realized and simulated genetic progress.

Material and methods

Data. Official breeding values, based on BLUP animal models, from 2003 and 2008 (BV\textsubscript{03} and BV\textsubscript{08}) were provided by the Danish Agricultural Advisory Centre (DAAC). The BV and associated reliabilities (REL\textsubscript{03} and REL\textsubscript{08}) were available for 311-414 licensed DW stallions (depending on year and trait) for the traits dressage, jumping and conformation. The stallions were born from 1962 through 2001. Dressage and jumping were aggregate indexes, each based on four different individual traits, whereas conformation was based on a single score. Both REL\textsubscript{03} and REL\textsubscript{08} ranged between 36 and 96 percent for dressage and jumping whereas it ranged between 53 and 98 percent for conformation.

Approximation of genetic variance (\(\sigma^2_a\)). Knowledge of \(\sigma^2_a\) is essential for several checks, but they were not available. Instead the following approximation was used: \(\sigma^2_a = \sigma^2_{BV}/\text{REL}_{\text{avg}}\), where \(\sigma^2_{BV}\) is the variance of all BV\textsubscript{08} and \(\text{REL}_{\text{avg}}\) is the average REL\textsubscript{08}.

Standardization of breeding values. BV\textsubscript{03} and BV\textsubscript{08} were expressed on a different genetic base and scale. As standardization factors applied in 2003 were not available, the following forced standardization of BV\textsubscript{03} was applied: BV\textsubscript{03}' = \(\mu_{BV08} + (BV\textsubscript{03} - \mu_{BV03})\sigma_{BV08}/\sigma_{BV03}\), where \(\mu_{BV03}\) and \(\sigma_{BV03}\) are the average and standard deviation of BV\textsubscript{03}, respectively, for stallions with (REL\textsubscript{08}-REL\textsubscript{03}) < 0.01.

Verification of genetic evaluations. All stallions with both BV\textsubscript{03} and BV\textsubscript{08} were considered except 5-9 stallions with REL\textsubscript{08}~REL\textsubscript{03}. Such stallions that lose information should receive special attention. The variance of the absolute difference between two sets of BV, where one

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set (i.e. BV\textsubscript{03}) is based on a subset of the information used for the other set (i.e. BV\textsubscript{08}), is:

\[ \sigma^2_{\Delta BV} = \text{var}(|BV_{08}-BV'_{03}|) = \text{PEV}_{03} - \text{PEV}_{08}, \]

where \( \text{PEV} \) is the prediction error variance (Klei et al., 2002). Often REL are available instead of PEV, but \( \text{PEV} = (1-\text{REL})\sigma^2_a \), where \( \sigma^2_a \) is the additive genetic variance assumed in both of the two consecutive genetic evaluations. The relative change in BV, given by \( |BV_{08}-BV'_{03}| / (\text{REL}_{08}\cdot\text{REL}_{03})\sigma^2_a \), is therefore expected to follow a standard normal distribution, N(0,1), and can be used to evaluate the consistency of BV over time for individual horses or groups of horses (e.g. by birth year, sex, origin). To allow checks for stallions with REL\textsubscript{08}=REL\textsubscript{03}, (REL\textsubscript{08}\cdot REL\textsubscript{03}) was set to 0.01 in those cases.

**Realized selection emphasis.** Only stallions with BV\textsubscript{03} based on at least 9 offspring were considered. The correlation between BV\textsubscript{03} and the increase in number of offspring from 2003 to 2008 was used as a measure of the realized selection emphasis on different traits. The correlation was calculated per birth year (or pairwise birth year when <10 stallions in one year). Subsequently, a pooled correlation, \( r_{BV,\Delta N} \), was calculated as the weighted average (by no. stallions per birth year -1) of the within year correlations to adjust for uneven opportunity for having extra offspring depending on age. Finally, a search for the highest \( r_{BV,\Delta N} \) was performed by varying the relative weights (b-values) in fictive total-merit selection indexes. In this search, all 1000 combinations of the 3 traits involving integer b-values of 0, 1, 2,.., 9 were investigated. This was considered a sufficient range because the best combination (highest \( r_{BV,\Delta N} \)) involved intermediate b-values.

**Realized and simulated genetic trends.** BV\textsubscript{08} for all stallions were used for calculating realized genetic trends. The realized genetic trend for each trait considered in the DW program was calculated in two ways, namely, as the regression of

1) individual BVs (un-weighted)
2) individual BVs weighted by number of offspring

on birth year of the stallions. Stallions were, however, required to have at least 9 offspring for the un-weighted analysis, but not the weighted. The un-weighted trend reflects the ability of the DW association in pre-selecting stallions for approval whereas the weighted trend reflects the genetic trend in the whole population (few years ahead of time).

Potential genetic improvement for the 3 investigated traits assuming perfect truncation selection, but similar breeding structure and selection intensities as the current DW breeding program was simulated using SelAction (Rutten and Bijma, 2001). This potential genetic improvement was compared with the realized genetic trends. Heritabilities of 0.23, 0.23 and 0.50 for dressage, jumping and conformation were available from DAAC and assumed in the simulation. Genetic correlations were approximated by Nielsen and Pless (2007). Phenotypic correlations were not available and were assumed equal to genetic correlations. Assumed correlations were 0.7 between dressage and jumping, 0.5 between dressage and conformation as well as 0.4 between jumping and conformation. Common environmental effects were assumed 0.05 for all traits. Realized economic values (v) corresponding to the b-values yielding the highest \( r_{BV,\Delta N} \) were calculated using selection index theory. Other key assumptions about the simulated breeding program were: 1) closed population with 15.000 stallions and 15.000 mares being born per generation; 2) 300 stallions and 15.000 mares were selected per generation; 3) perfect truncation selection according to the index weights; 4) information about parents, own performance, first half-sib information and first progeny information were available at 0, 3, 5 and 7 years of age.
Results and discussion

The comparisons of BV over time and of realized and simulated genetic trends depend on the true $\sigma^2_a$ being available. Here we used a rough approximation of $\sigma^2_a$ that doesn’t account for selection and this may have influenced the results.

BV seemed generally to be as consistent between 2003 and 2008 as could be expected, at least for conformation and dressage (Table 1). BV of older stallions (born <1984) were less stable than for younger stallions relative to their expectations, but older stallions were not expected to change much (low $\sigma_{\Delta BV}$). BVs for jumping were least consistent relative to expectations. There also tended to be more extreme changes ($\Delta BV>3\sigma_{BV}$) for dressage and especially jumping than for conformation and for younger stallions born after 1989 relative to expectations. This may be explained by changes in pedigrees used in BLUP between 2003 and 2008 for the involved stallions. Pedigree changes would not disturb consistency of BV for conformation and for older stallions to the same extent because of higher heritability and more progeny, respectively. The largest relative change in BV was equal to 4.55 for jumping.

The validation of the genetic evaluation system used here does not guarantee that the system is perfectly ok as BV may be consistently wrong over time. Also, changes may be explained by improvements. However, it is reassuring when changes follow expectations derived from genetic theory. If they don’t, explanations must be found. Other checks such as comparisons with simulated BV and checking patterns of mendelian sampling terms could be performed.

Table 1: Distributions of relative changes in breeding values from 2003 to 2008 for different traits and groups of stallions

<table>
<thead>
<tr>
<th>Group of stallions</th>
<th>n</th>
<th>0 – 1 $\sigma_{\Delta BV}$</th>
<th>1 – 2 $\sigma_{\Delta BV}$</th>
<th>2 – 3 $\sigma_{\Delta BV}$</th>
<th>&gt;3 $\sigma_{\Delta BV}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Dressage, all</td>
<td>310</td>
<td>72.6</td>
<td>22.3</td>
<td>4.8</td>
<td>0.3</td>
</tr>
<tr>
<td>foreign</td>
<td>145</td>
<td>76.6</td>
<td>19.3</td>
<td>3.4</td>
<td>0.7</td>
</tr>
<tr>
<td>born before 1984</td>
<td>133</td>
<td>66.9</td>
<td>24.1</td>
<td>9.0</td>
<td>0.0</td>
</tr>
<tr>
<td>born 1984 - 1989</td>
<td>96</td>
<td>75.0</td>
<td>22.9</td>
<td>2.1</td>
<td>0.0</td>
</tr>
<tr>
<td>born after 1989</td>
<td>81</td>
<td>79.0</td>
<td>18.5</td>
<td>1.2</td>
<td>1.2</td>
</tr>
<tr>
<td>Jumping, all</td>
<td>333</td>
<td>65.2</td>
<td>24.6</td>
<td>7.8</td>
<td>2.4</td>
</tr>
<tr>
<td>Conformation, all</td>
<td>335</td>
<td>89.3</td>
<td>9.6</td>
<td>1.2</td>
<td>0.0</td>
</tr>
<tr>
<td>Expected</td>
<td>∞</td>
<td>68.3</td>
<td>27.1</td>
<td>4.3</td>
<td>0.3</td>
</tr>
</tbody>
</table>

$BV_{08} - BV_{03}$ were grouped relative to $\sigma_{\Delta BV} = (REL_{08} - REL_{03})\sigma_a^2$ for each stallion

The search for the highest $r_{BV,AN}$ yielded a realized selection emphasis of b-values equal to 2, 1 and 2 for dressage, jumping and conformation, respectively. This corresponds to economic values of 10.7, 4.8 and 0.2 for the 3 traits and an $r_{BV,AN}$ of 0.50. The low $r_{BV,AN}$ indicates that breeders have different selection emphasis or that their selection decisions were based on other factors than the 3 sets of $BV$s. The $r_{BV,AN}$ only reflects the breeders preference and not the pre-selection of stallions by the DW association. The low $r_{BV,AN}$ was not surprising considering that the official DW breeding goal does not dictate exact index weights.

Realized genetic trends in Table 2 were scaled relative to the approximate $\sigma_a$ which were estimated to be 21.2, 20.9 and 17.6 for dressage, jumping and conformation, respectively. Realized genetic trends were highest for conformation and dressage which confirms the lower selection emphasis on jumping, especially in recent years and among private breeders.
Table 2: Realized genetic trends\(a\) (± SE) per year and per 0.01σ\(a\) (either weighted by no. progeny or un-weighted) for stallions of all ages and those born after 1984

<table>
<thead>
<tr>
<th>Trait</th>
<th>Weighted</th>
<th>Un-weighted</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>All ages born after 1984</td>
<td>All ages born after 1984</td>
</tr>
<tr>
<td>Dressage</td>
<td>5.5 ± 0.5</td>
<td>9.9 ± 1.2</td>
</tr>
<tr>
<td>Jumping</td>
<td>2.9 ± 0.6</td>
<td>-2.0 ± 1.7</td>
</tr>
<tr>
<td>Conformation</td>
<td>8.1 ± 0.3</td>
<td>5.6 ± 0.7</td>
</tr>
</tbody>
</table>

\(a\)Regression coefficients \((b)\) from regression of birth year on breeding value in 2008; model: \(BV/σ_a = a + b(\text{year})\).

Simulated genetic trends were 6.7, 5.8 and 4.8 per year and per 0.01σ\(a\) for dressage, jumping and conformation, respectively. Thus, realized trends were higher than expected for conformation and tended to be similar to the simulated potential for dressage, whereas the realized trends for jumping were less than could potentially have been achieved. This may be because pre-selection was largely based on conformation, which was not reflected in \(r_{BV,N}\) and the corresponding economic values assumed in the simulation. Also, there were several disagreements between the simulation and real breeding program. The simulation ignored importation of genetic material to the DW population and didn’t allow uneven number of offspring for selected stallions. A relaxation of each assumption would give higher simulated genetic trends, at least provided that domestic and foreign stallions can be objectively compared (e.g. via INTERSTALLION). Furthermore, no selection among mares was assumed. A weak selection among mares (67\% selected) yielded simulated genetic trends of 8.2, 7.1 and 5.9 per `year \times 0.01σ\(a\)` for dressage, jumping and conformation, respectively.

BV should be checked at each genetic evaluation and it is easy to implement the procedures used here on a routine basis. The genetic trends do not need to be compared with simulations so frequently; a yearly check of trends and updates of simulations in connection with larger changes in the breeding program should be sufficient. Such larger changes could concern the breeding goal, selection index, implementation of new technologies.

Conclusion

This paper emphasizes the need for regular quality control of horse breeding programs and suggests specific methods for checking key aspects of the program, exemplified by DW. Current genetic evaluations seem ok for the 3 traits, although a few specific inconsistencies in BV and REL may need further examination. Advising breeders about selection and mating decisions should be a main focus in improving the DW breeding program. Introduction of total-merit indexes will likely ease selection decisions for all decision makers and could help to close the gap between realized and simulated genetic progress, especially for jumping.

References