



Joint Nordic Beef x Dairy Genetic Evaluation of Gestation length

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1 Background

Gestation length plays a crucial role in effective calving pattern management on dairy farms. This importance is amplified for dairy farmers participating in beef on dairy programs, as gestation length varies across different beef breeds (Norman et al. 2009). This insight underscores the potential for managing this trait through careful selection of the beef bull used for breeding with the cow.

The process of selecting the appropriate beef bull becomes much smoother when having access to a system that allows comparing bulls from different breeds, based on data collected from their offspring when used on dairy cows. Hence the request expressed by the industry to include gestation length to the list of traits evaluated by NAV for beef bulls used in dairy herds.

Table 1 below lists abbreviations for beef breeds used in this document along with their full names.

Table 1: Abbreviations used for beef sire breeds' names

| Abbreviation | Full Name |
|--------------|--------------------|
| AAN | Angus |
| BAQ | Blonde d'Aquitaine |
| BBL | Belgian Blue |
| BSH | British Shorthorn |
| CHA | Charolais |
| DXT | Dexter |
| GLW | Galloway |
| HER | Hereford |
| HLA | Highland |
| INR | INRA 95 |
| LIM | Limousin |
| MGR | Murray Grey |
| PIE | Piedmontese |
| SAL | Salers |
| SIM | Simmental |
| WAG | Wagyu |

2 Trait definition

Gestation length is defined as the time interval, measured in days, from the moment of conception to the subsequent occurrence of parturition. Phenotypes are calculated based on insemination records and registered calving dates.

Distinct traits are evaluated separately for heifers and cows. Based on the outcomes, decisions will be deliberated concerning the continuation of treating these traits distinctly or combining

them into a single trait.

3 Input data

This analysis utilized Beef on Dairy data from the November 2022 NAV routine evaluation. In the case of Finland, gestation length data were already incorporated within the routine calving files. For Denmark and Sweden, new national calving files were generated, including information on gestation length, using the same national data extractions employed for the November 2022 NAV dairy evaluation.

In Denmark, gestation lengths below 260 or above 300 days are discarded. Sweden includes gestation lengths ranging from 260 to 310 days, while Finland initially considers gestation lengths within the range of 260 to 350 days. However, in the current NAV routine calving evaluation, Finnish data with gestation lengths exceeding 310 days are excluded, effectively limiting the upper limit for Finland to 310 days when considering only gestations that resulted in a registered calving.

4 Data edits

The gestation length input data is processed in conjunction with the BxD calving traits data, and both datasets undergo identical editing procedures as those applied to calving data. The comprehensive details of this editing process can be found in Fikse et al. (2020). This approach has the specific purpose of excluding gestations that did not lead to a registered calving event, ensuring a more pertinent and precise foundation for the evaluation of gestation length.

In addition to the previously mentioned edits, a systematic method was elaborated to identify and eliminate outliers within the data. Detailed insights into this method are provided in the Outliers Detection section below.

5 Data description

5.1 Counts

After edits, the total number of calves was about 1160030 distributed per country and sire breed as in Table 2 below. More than 99.8% of the data originates from the eight predominant sire breeds, namely BBL, BAQ, LIM, AAN, SIM, CHA, HER, and INR, while the remaining 0.2% represents data from a few smaller breeds with only a handful of calves across all three countries. In the subsequent sections of this report, our focus will be exclusively on presenting statistics and results for these main sire breeds.

Table 2: Total number of observations per country and sire breed

| Sire breed | DNK | FIN | SWE |
|-------------------|------------|------------|------------|
| BBL | 342215 | 0 | 0 |
| BAQ | 12886 | 221768 | 4127 |
| LIM | 24851 | 119725 | 29953 |
| AAN | 24777 | 77992 | 31853 |
| SIM | 20451 | 29802 | 48228 |
| CHA | 36634 | 27760 | 41410 |
| HER | 2620 | 13311 | 36130 |
| INR | 11300 | 0 | 0 |
| PIE | 799 | 20 | 0 |
| WAG | 320 | 0 | 0 |
| HLA | 69 | 151 | 277 |
| MGR | 249 | 0 | 0 |
| BSH | 196 | 0 | 0 |
| SAL | 57 | 0 | 0 |
| GLW | 40 | 15 | 28 |
| DXT | 13 | 3 | 0 |

Only 6.47% of the observations were from first parity dams (Table 3). Only a very few calves are born from Jersey cows in both Finland and Sweden (Table 4).

Table 3: Number of observations in heifers versus cows

| Sire breed | Cows | Heifers |
|-------------------|-------------|----------------|
| BBL | 339952 | 2263 |
| BAQ | 228815 | 9966 |
| LIM | 164194 | 10335 |
| CHA | 104417 | 1387 |
| AAN | 97594 | 37028 |
| SIM | 93610 | 4871 |
| HER | 43302 | 8759 |
| INR | 11201 | 99 |
| PIE | 791 | 28 |
| HLA | 392 | 105 |
| WAG | 258 | 62 |
| MGR | 213 | 36 |
| BSH | 171 | 25 |
| GLW | 56 | 27 |
| SAL | 42 | 15 |
| DXT | 11 | 5 |

Table 4: Number of observations per country and dam breed

| Dam breed | DNK | FIN | SWE |
|------------------|------------|------------|------------|
| HOL | 361974 | 183625 | 93955 |
| RDC | 34984 | 305230 | 96969 |
| JER | 81319 | 1692 | 1082 |

5.2 Gestation length data

5.2.1 Distribution

The analysis of gestation length distribution, as presented in Figure 1, reveals consistent patterns across different countries, despite divergent overall averages. Finland has the highest average gestation length, followed by Sweden and Denmark, as detailed in Table 5. These variations in averages are directly attributed to the diverse array of beef breeds employed in each country. Examining the statistics within each sire breed (Table 6) shows a remarkably uniform distribution pattern across all countries.

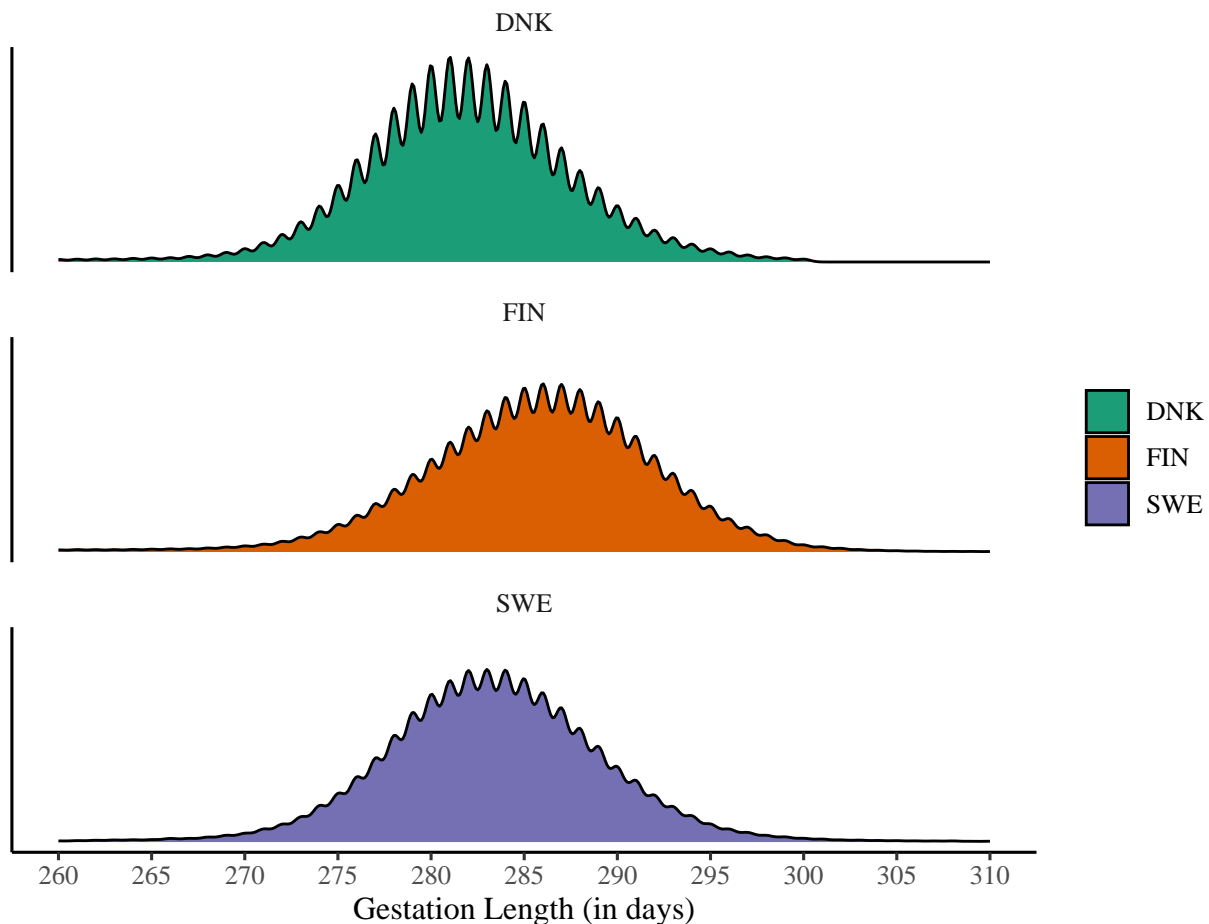


Figure 1: Distribution of gestation length data within country

All data combined, gestation length was about two days shorter on average for heifers (282 days) compared to cows (284 days) and about one day on average shorter for females (283 days) compared to males (284 days). Phenotypic means of gestation lengths vary by sire breed, with Angus and BBL breeds having the shortest gestation periods, while Limousine and BAQ breeds have the longest, as outlined in Figure 2.

Table 5: Average of gestation length (in days) per country

| country | mean | sd | min | max |
|---------|-------|-----|-----|-----|
| DNK | 281.9 | 5.6 | 260 | 300 |
| FIN | 285.7 | 6.2 | 260 | 310 |
| SWE | 283.4 | 5.9 | 260 | 310 |

Table 6: Mean, SD and Median of gestation length (in days) per country and sire breed

| Sire breed | Mean | | | SD | | | Median | | |
|------------|-------|-------|-------|-----|-----|-----|--------|-----|-----|
| | DNK | FIN | SWE | DNK | FIN | SWE | DNK | FIN | SWE |
| AAN | 280.4 | 280.6 | 280.5 | 5 | 5.2 | 5.4 | 280 | 281 | 280 |
| BAQ | 287.2 | 287.4 | 287.4 | 5.3 | 5.6 | 5.6 | 287 | 288 | 288 |
| BBL | 281.0 | | | 5.1 | | | 281 | | |
| CHA | 283.6 | 283.3 | 283.6 | 5.4 | 5.6 | 5.7 | 284 | 283 | 284 |
| HER | 282.4 | 281.2 | 281.7 | 5.2 | 5.3 | 5.3 | 282 | 281 | 282 |
| INR | 285.2 | | | 6.2 | | | 285 | | |
| LIM | 287.0 | 287.3 | 286.1 | 5.7 | 5.8 | 5.8 | 287 | 287 | 286 |
| SIM | 284.6 | 284.7 | 284.3 | 5.7 | 5.4 | 5.6 | 285 | 285 | 284 |

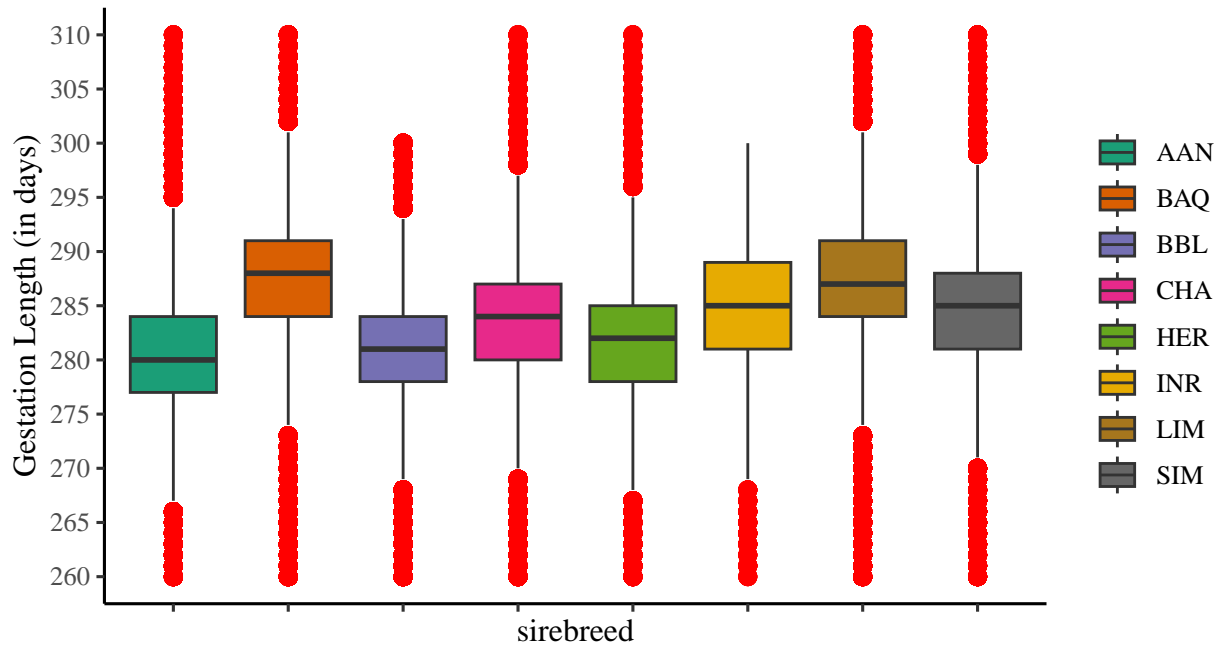


Figure 2: IQR plot per Sire breed

5.2.2 Phenotypic trend and variance

As expected and in the absence of a genetic selection based on gestation length, a flat trend is observed for all the main sire breeds (Figure 3).

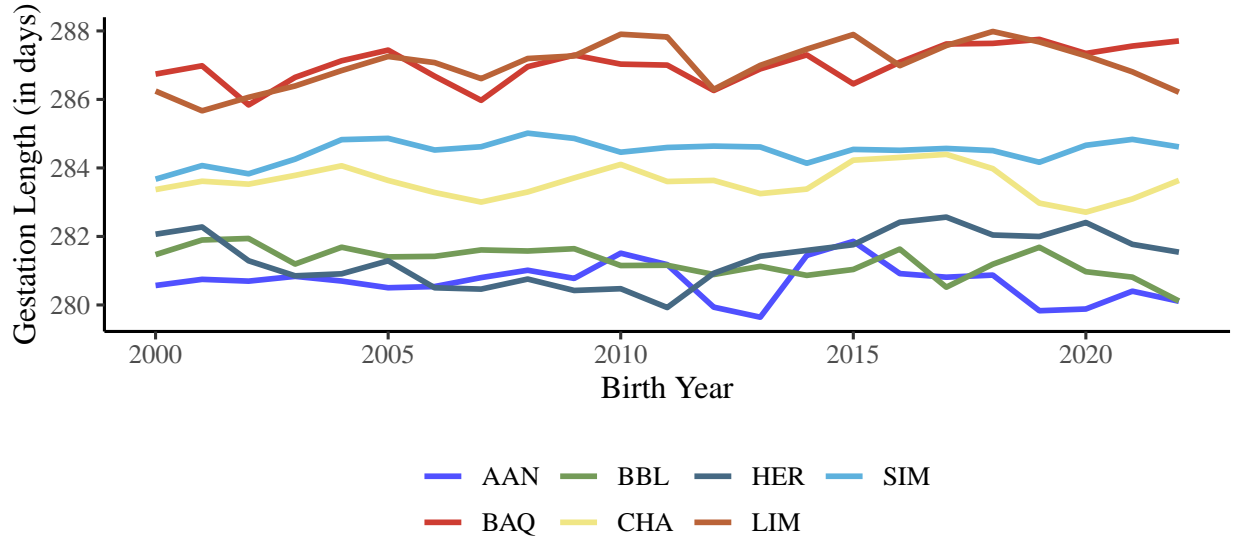


Figure 3: Average of gestation length per sire breed

Over the past two decades, a review of the data reveals that the average gestation length has followed a similar trajectory across different sexes, as shown in Figure 4. When data from all breeds and countries are combined, a consistent divergence in phenotypic variance was seen (Figure 5). This divergence is most likely an artifact caused by a shift towards using single breeds over the years, alongside varying breed preferences across countries.

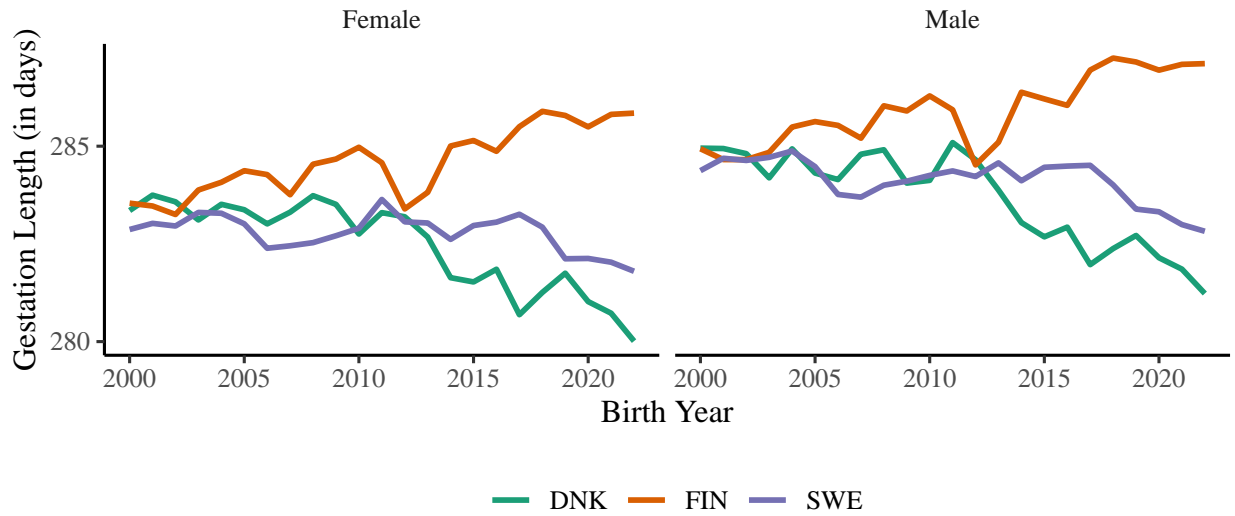


Figure 4: Average of gestation length per birth year, country and sex

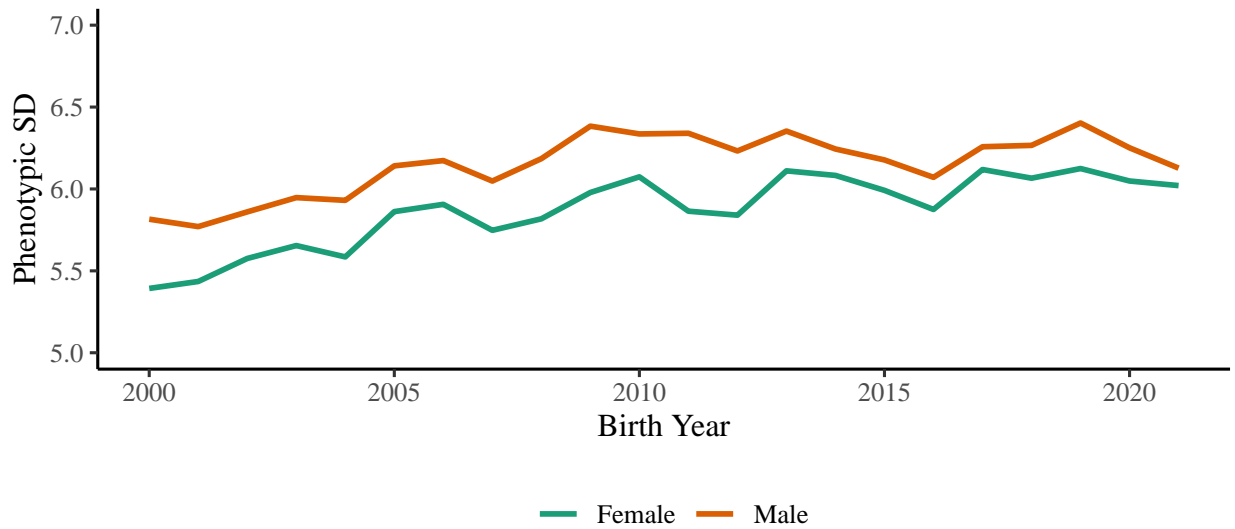


Figure 5: SD of gestation length (in days) per birth year and sex all breeds and countries combined

If we look at the data within sire breed, we also notice a systematic difference in the phenotypic SD in heifers versus cows (Table 7).

Table 7: SD of gestation length (in days) per sirebreed in heifers versus cows

| Parity | AAN | | BAQ | | BBL | | CHA | | HER | | INR | | LIM | | SIM | |
|---------|-------|-----|--------|-----|--------|-----|--------|-----|-------|-----|-------|-----|--------|-----|-------|-----|
| | N | SD | N | SD | N | SD | N | SD | N | SD | N | SD | N | SD | N | SD |
| Cows | 97594 | 5.2 | 228815 | 5.6 | 339952 | 5.1 | 104417 | 5.6 | 43302 | 5.3 | 11201 | 6.2 | 164194 | 5.8 | 93610 | 5.6 |
| Heifers | 37028 | 5.3 | 9966 | 5.7 | 2263 | 5.4 | 1387 | 6.0 | 8759 | 5.3 | 99 | 5.9 | 10335 | 5.9 | 4871 | 5.8 |

5.2.3 Outliers detection

Two outliers' detection methods were applied within sire breeds and compared to each other: The IQR method and the MAD method (used in the purebred beef NAV routine evaluation for body weight).

The IQR Method (Interquartile Range) is a statistical measure used to assess the spread or dispersion of a dataset. It is the range between the first quartile (25th percentile) and the third quartile (75th percentile) of the data. The IQR method for outlier detection defines data points as outliers if they fall below the first quartile minus 1.5 times the IQR or above the third quartile plus 1.5 times the IQR (Figure 6). This method is based on the assumption that the majority of the data should lie within the central range.

The MAD Method (Median Absolute Deviation) is a robust measure of the variability of a dataset. It is the median of the absolute deviations of each data point from the overall median of the dataset (Figure 7). The MAD method for outlier detection involves calculating the MAD for the entire dataset and then identifying data points as outliers if their absolute deviation from the median exceeds a certain threshold, often a multiple of the MAD (in this case 3.5 times the MAD).

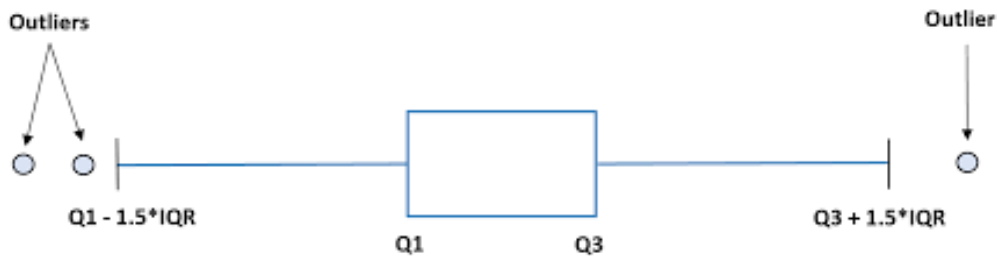


Figure 6: The IQR method

When compared, more outliers were captured by the IQR method (Table 8) and the upper and lower limits seemed more meaningful compare to those obtained with the MAD method (Table 9).

The working group agreed on using the IQR method to detect outliers within sire breeds. The final number of outliers per country and the impact of excluding outliers on the summary statistics of gestation length data are shown in tables 10 and 11 respectively.

Table 8: Number of gestation length outliers (in days) per method and sire breed

| Sirebreed | IQR method | | MAD method | |
|-----------|------------|---------------|------------|---------------|
| | N_outliers | Percentage(%) | N_outliers | Percentage(%) |
| AAN | 2372 | 1.79 | 1709 | 1.29 |
| BAQ | 5524 | 2.37 | 4256 | 1.81 |
| BBL | 8186 | 2.45 | 3617 | 1.07 |
| CHA | 2243 | 2.17 | 1588 | 1.52 |
| HER | 1031 | 2.02 | 770 | 1.50 |
| INR | 121 | 1.08 | 62 | 0.55 |
| LIM | 4211 | 2.47 | 1282 | 0.74 |
| SIM | 2193 | 2.28 | 1567 | 1.62 |

Table 9: Upper and lower gestation length limits (in days) per method and sire breed

| Sire breed | IQR method | | | MAD method | |
|------------|-------------|-------------|--------|-------------|-------------|
| | Lower limit | Upper limit | Median | Lower limit | Upper limit |
| AAN | 266 | 294 | 280 | 264 | 296 |
| BAQ | 274 | 302 | 288 | 272 | 304 |
| BBL | 269 | 293 | 281 | 265 | 297 |
| CHA | 270 | 298 | 284 | 268 | 300 |
| HER | 268 | 296 | 282 | 266 | 298 |
| INR | 269 | 301 | 285 | 264 | 306 |
| LIM | 274 | 302 | 287 | 266 | 308 |
| SIM | 270 | 298 | 285 | 269 | 301 |

Table 10: Number of gestation length outliers (in days) within country

| Country | Number of outliers | Percentage(%) |
|---------|--------------------|---------------|
| DNK | 10549 | 2.26 |
| FIN | 11042 | 2.30 |
| SWE | 4332 | 2.31 |

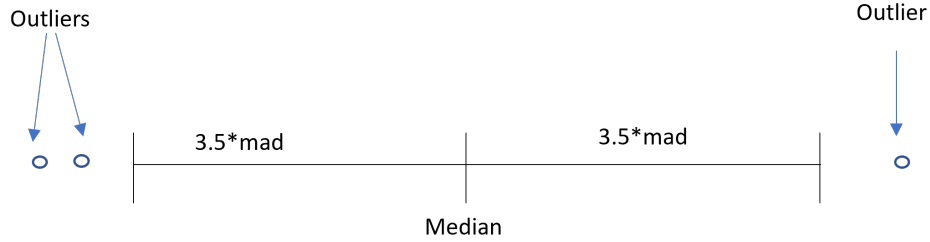


Figure 7: The MAD method

Table 11: Gestation length (in days) before and after discarding outliers

| Sire breed | Including outliers | | | | Excluding outliers | | | |
|------------|--------------------|----|-----|-----|--------------------|----|-----|-----|
| | Mean | SD | Min | Max | Mean | SD | Min | Max |
| AAN | 280 | 5 | 260 | 310 | 281 | 5 | 267 | 294 |
| BAQ | 287 | 6 | 260 | 310 | 288 | 5 | 274 | 301 |
| BBL | 281 | 5 | 260 | 300 | 281 | 4 | 269 | 293 |
| CHA | 284 | 6 | 260 | 310 | 284 | 5 | 270 | 297 |
| HER | 282 | 5 | 260 | 310 | 282 | 5 | 268 | 295 |
| INR | 285 | 6 | 260 | 300 | 285 | 6 | 269 | 300 |
| LIM | 287 | 6 | 260 | 310 | 287 | 5 | 274 | 301 |
| SIM | 284 | 6 | 260 | 310 | 285 | 5 | 271 | 298 |

6 Genetic evaluation

As previously indicated, the evaluation of gestation length begins with separate assessments for cows and heifers. Existing literature highlights strong genetic correlations between the breeding values of heifers and cows, which has led to their joint evaluation becoming a common practice in many countries' routine assessments. The choice to combine these evaluations or keep them separate in routine assessments was determined by the findings of the initial evaluation, particularly the results concerning genetic correlations and variances.

Given the sparse representation of the Jersey dam breed in both Finland and Sweden (Table 4), the decision was made to exclude the Jersey data from those two countries from the evaluation.

6.1 Heterogeneous variance adjustments

A simple correction for phenotypic variance was applied with respect to sex, addressing a noticeable systematic difference observed in the phenotypic standard deviation for both traits (Table 12).

6.2 The model

The group discussed several factors reported in the literature but currently omitted from the calving model, including the conception month, the dam’s permanent effect, and the cow’s lactation length and milk yield.

The conception month is typically incorporated into models where birth month is absent to avoid confounding; however, as our model already includes birth month, adding conception month is unnecessary. Similarly, approximately 72.5% of the dams produce only one calf, complicating the estimation of the dam’s permanent environment. Integrating milk yield and lactation length would be also operationally challenging and lacks robust biological justification. Consequently, the group resolved to maintain the existing model used in calving evaluations (Fikse et al. 2020).

6.3 Genetic parameters estimation

The genetic parameters were estimated using DMUAI (Madsen and Jensen 2013) with a multiple-trait model including data from all countries. To assess the robustness of these findings, we conducted separate estimations using exclusively Danish data, followed by Holstein-specific data.

The estimated parameters fall within the ranges reported in literature (Eaglen et al. (2013); Hansen et al. (2004); Haile-Mariam and Pryce (2019); Amer et al. (2016); Norman et al. (2009)) with high heritabilities and a very high genetic correlation between gestation length in heifers and cows (Table 13). Results were consistent across the different datasets indicating a good stability of the findings (Table 13). The lower genetic correlation between gestation length in heifers and cows in the Danish dataset (0.84 as opposed to 0.99) is attributable to the limited number of heifer records available in Denmark.

While genetic variances for heifers and cows were found to be similar, they were not identical (Table 13). Therefore, the decision was made to continue estimating breeding values by treating these as distinct traits. Parameters estimated using all countries’ data were used for the genetic evaluation.

Table 12: Phenotypic SD of gestation length (in days) per sex before and after implementing variance adjustment

| Sex | Heifers | | Cows | |
|--------|-----------|----------|-----------|----------|
| | SD_Before | SD_After | SD_Before | SD_After |
| Female | 5.44 | 5.58 | 5.52 | 5.64 |
| Male | 5.65 | 5.58 | 5.68 | 5.64 |

Table 13: Heritability and correlation

| | h2 Gestation length heifers | h2 Gestation length cows | Genetic correlation |
|---------------|--------------------------------|-----------------------------|---------------------|
| All countries | 0.56 ± 0.03 | 0.57 ± 0.02 | 0.99 ± 0.00 |
| Only HOL | 0.54 ± 0.03 | 0.59 ± 0.03 | 0.99 ± 0.01 |
| Only DNK | 0.57 ± 0.07 | 0.57 ± 0.03 | 0.84 ± 0.05 |

Table 14: Genetic variance

| | Gestation length heifers | Gestation length cows |
|---------------|--------------------------|-----------------------|
| All countries | 3.01 ± 0.18 | 3.2 ± 0.16 |
| Only HOL | 2.93 ± 0.21 | 3.28 ± 0.17 |
| Only DNK | 3.1 ± 0.46 | 3 ± 0.20 |

Table 15: Phenotypic variance

| | Gestation length heifers | Gestation length cows |
|---------------|--------------------------|-----------------------|
| All countries | 21.62 ± 0.21 | 22.36 ± 0.16 |
| Only HOL | 21.63 ± 0.26 | 22.34 ± 0.17 |
| Only DNK | 21.89 ± 0.53 | 21.14 ± 0.20 |

6.4 Breeding values

A genetic evaluation including data from all countries and breeds was performed. Sires' breeding values were calculated as the sum of the fixed breed effect and the random sire effect. In total 1032 sires were evaluated (Table 16).

Figures 8 and 9 feature boxplots summarizing the breeding values for each sire breed during periods 1 and 2, respectively. Each plot's central box represents the interquartile range (IQR) of the data, with the median breeding value indicated by the horizontal line within. The whiskers extend to the minimum and maximum values that are within 1.5 times the IQR. Points outside this range are classified as outliers, indicating sires with notably distinct breeding values from the general population.

These illustrations provide a comprehensive view of the distribution of breeding values across different sire breeds, spotlighting the genetic diversity among breeds as well as the variation within each breed. The data emphasize the critical role of multi-breed evaluations, suggesting that selecting sires based on breed alone may not be sufficient. Instead, it's crucial for breeders to examine the specific characteristics of individual bulls when making breeding decisions.

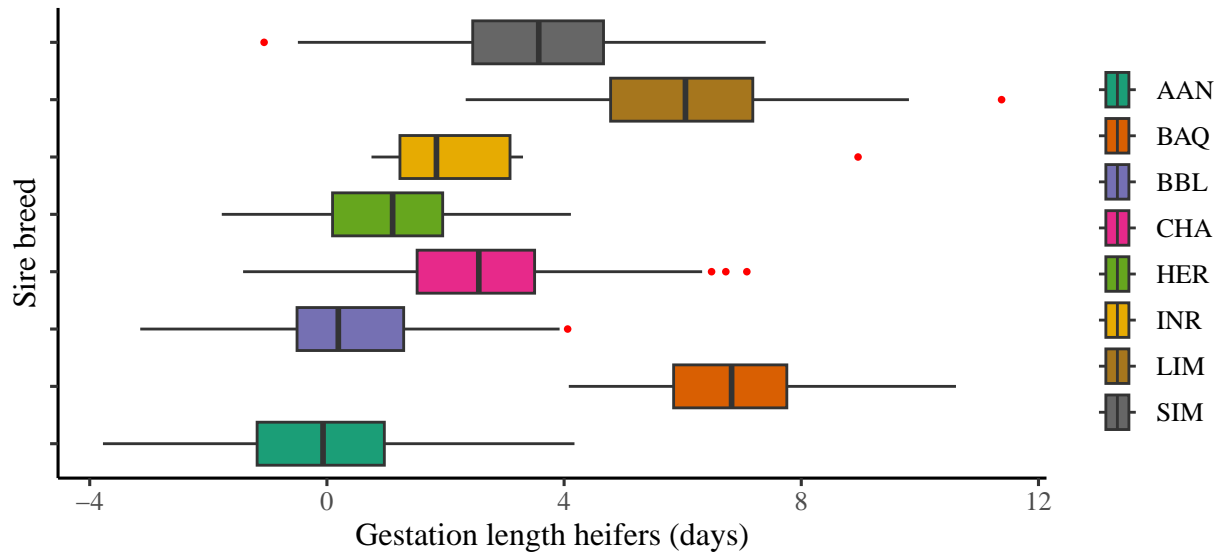


Figure 8: Boxplot of gestation length breeding values for heifers per sire breed

Table 16: Number of sires per sire breed (Only main breeds are shown)

| Sire breed | N |
|------------|-----|
| SIM | 292 |
| BBL | 160 |
| LIM | 139 |
| CHA | 130 |
| AAN | 116 |
| HER | 82 |
| BAQ | 76 |
| INR | 10 |

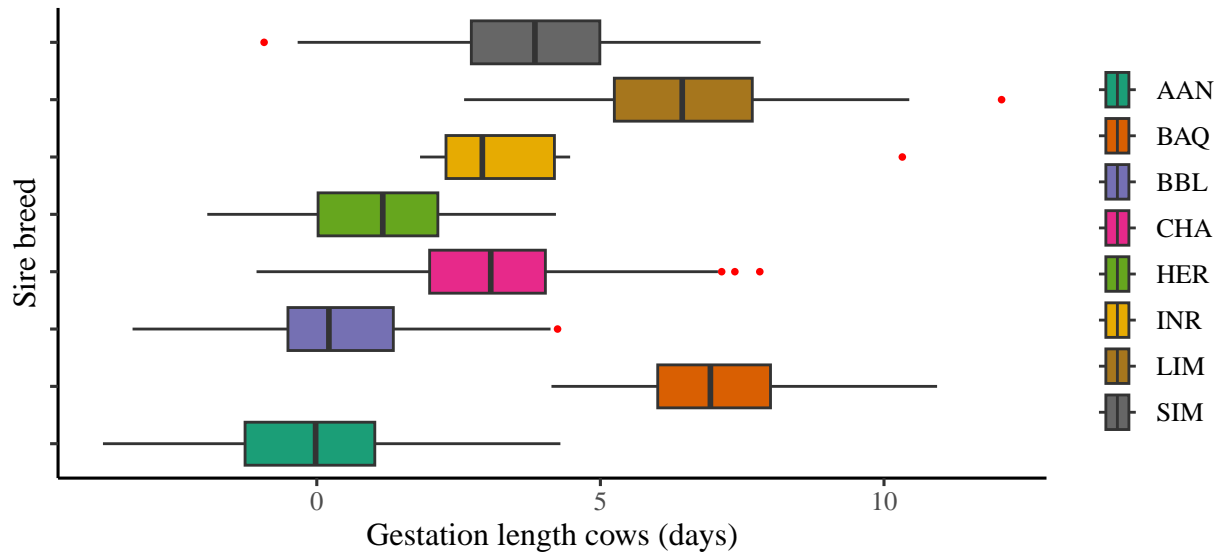


Figure 9: Boxplot of gestation length breeding values for cows per sire breed

When evaluating the genetic level evolution per birth year, the results demonstrate a flat trend for all sire breeds for both traits (Figures 10 and 11). These results are expected in the absence of a current selection program on gestation length.

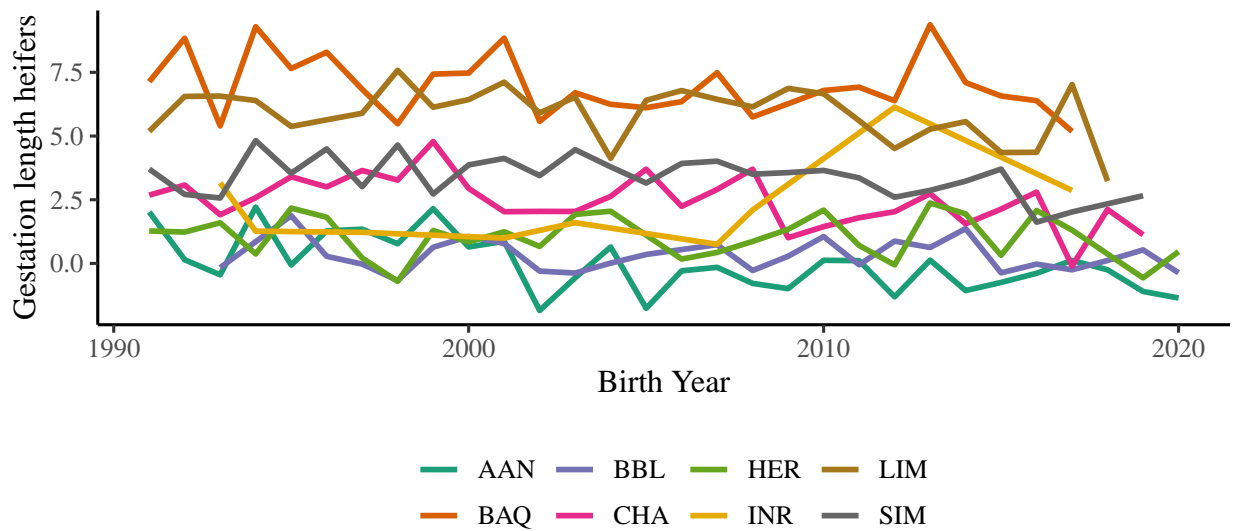


Figure 10: Genetic Trend per sire breed for heifers

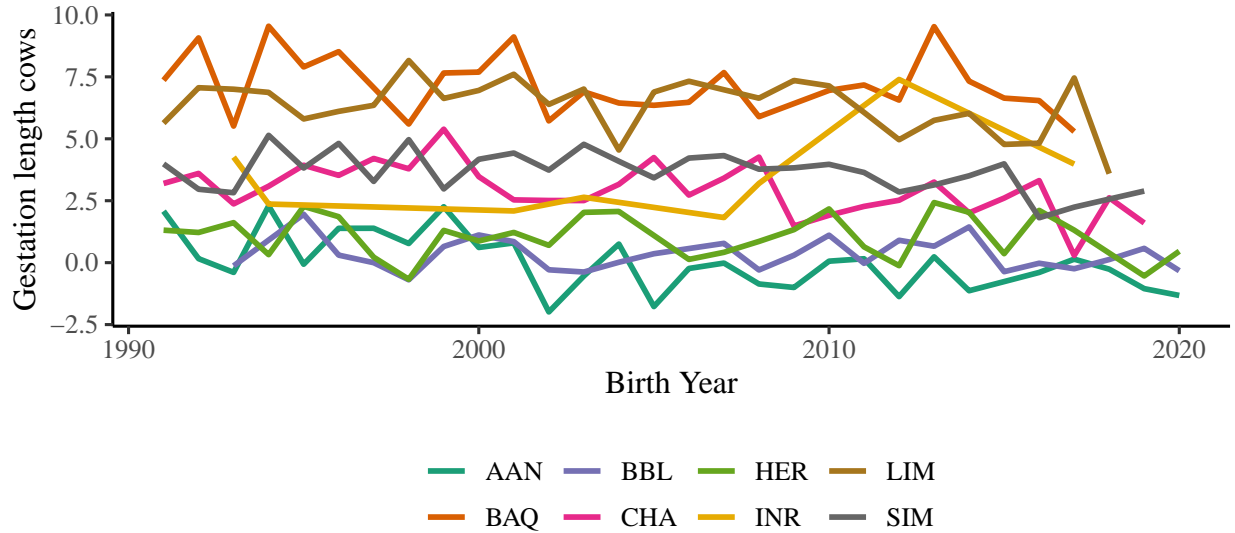


Figure 11: Genetic Trend per sire breed for cows

6.5 Reliability

As for the other NAV BxD traits (Fikse et al. 2020), exact reliabilities were calculated as $REL = 1 - \frac{SEP^2}{\sigma_s^2}$ where SEP is the standard error of prediction (calculated by DMU4) and σ_s^2 is the sire variance.

Reliabilities were very high for both heifers and cows (Figure 12). Reliabilities within sire breed are shown in figures 13 and 14 below. The lower reliabilities observed for the INRA breed is due to the very few sires which affects the estimation of the breed fixed effect (Fikse et al. 2020).

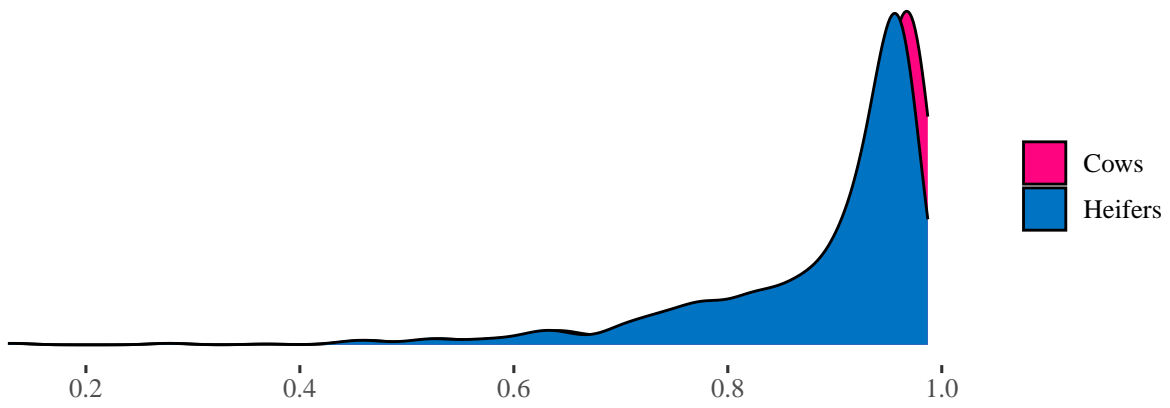


Figure 12: Reliability of breeding values

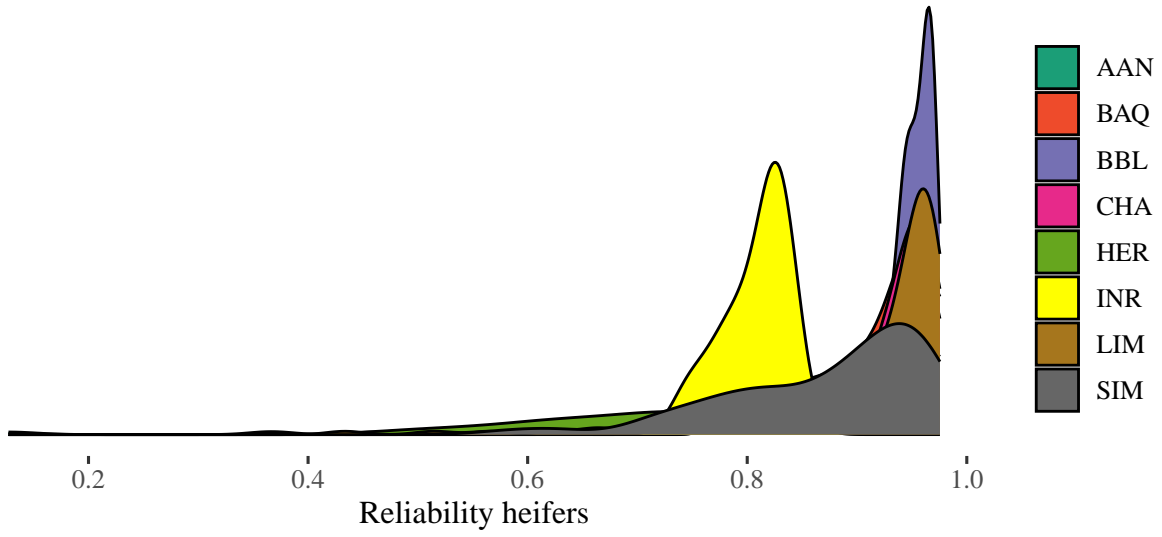


Figure 13: Reliability per sire breed, heifers

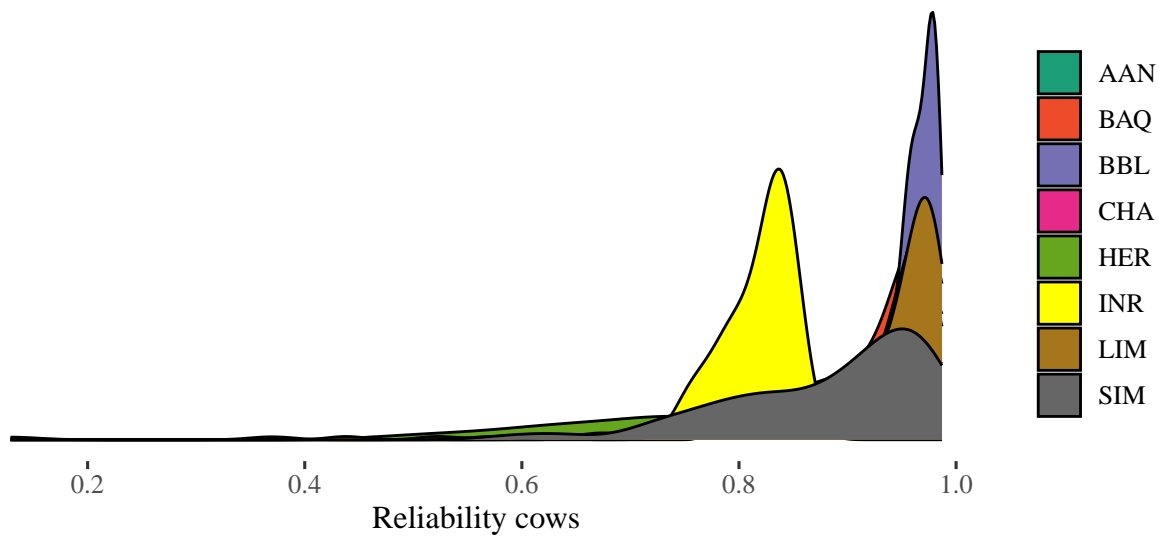


Figure 14: Reliability per sire breed, cows

7 Validation of the breeding values

7.1 Validation plan

To evaluate the accuracy of the genetic model, a comprehensive validation plan was implemented, consisting of the following steps:

1- Correlation with Phenotypic Means:

The first step involved comparing the estimated sires' breeding values (EBV) with their corresponding phenotypic means. This comparison served as a preliminary assessment of how well the genetic model's predictions aligned with the actual observed values.

The sires were classified in three different categories: <50, 50-300 or >300 offspring. Correlations were calculated between the phenotypic mean of the sires' offspring, and the estimated EBV.

2- Cross-Validation studies

Multiple cross-validation studies were conducted using various reduced datasets to test the robustness of the genetic model. Each cross-validation study involved the following procedure:

a. Creation of Reduced Datasets:

Eight different reduced datasets were generated to cover various scenarios:

a. Creation of Reduced Datasets:

Eight different reduced datasets were generated to cover various scenarios:

- One country at a time compared to all countries
- One dam breed at a time compared to all dam breeds
- Males/females at a time compared to all data : The model was evaluated separately for males and females, allowing for an assessment of any gender-specific variations.
- Truncated data (YYYY-N) to All Birth Years: The model's performance was tested using data from specific birth years (truncated data) and then compared against its performance when trained on data from all birth years. N was set to 1 after examining the evolution of the number of observations over the last 4 years. By limiting N to 1, we avoided losing significant amounts of data in the reduced set, which could have otherwise compromised the validity of the validation study.

b. Regression Analysis:

For each validation set, regression analyses of the full datasets EBVs on the reduced datasets EBVs, were performed. The bias (intercept) and the spread (slope) were calculated within sire breed in each case.

c. Correlations:

For each validation set, correlations between the full datasets EBVs and the reduced datasets EBVs were calculated for each sire breed and compared to the expected correlations calculated as in (Reverter et al. 1994).

7.2 Results

Detailed results of the validation are thoroughly presented in the annex at the end of this document. Generally, the outcomes are positive, demonstrating correlations that align well with expected values, with only a few exceptions.

One particular point of interest is the performance of BBL bulls when mated with RDC cows compared to Holstein cows, as illustrated in Figures 19 and 20. This variation can largely be attributed to the significant loss of information that occurs when the Holstein dam breed is excluded from the analysis. It should be highlighted that BBL bulls are predominantly used with Holstein cows in Denmark.

Another exception is the behavior of BAQ bulls in Sweden, which markedly deviates from the patterns observed in other countries (Table 24). Often, the Swedish sire breeding values were calculated based on a very limited number of offspring, whereas the same sires had a more substantial progeny count in Finland (Table 17). The different performance of BAQ bulls in Sweden can be then explained by the insufficient data available in Sweden compared to when all countries are included.

Table 17: Number of offspring of the BAQ bulls in Sweden compared to Finland

| Sire ID | Heifers | | Cows | |
|------------|---------|------|------|-------|
| | SWE | FIN | SWE | FIN |
| 1000577913 | 1 | 6 | 0 | 0 |
| 1019225191 | 2 | 1718 | 18 | 21511 |
| 1212201870 | 0 | 0 | 22 | 1555 |
| 1300089685 | 73 | 63 | 1722 | 3949 |
| 1300396019 | 1 | 32 | 52 | 2219 |
| 1300675581 | 0 | 0 | 77 | 11 |
| 1300675664 | 0 | 0 | 7 | 119 |
| 1300863125 | 4 | 64 | 205 | 4859 |
| 1301169185 | 0 | 0 | 1 | 8368 |
| 1301169186 | 3 | 781 | 1 | 16830 |
| 1301169187 | 0 | 0 | 1 | 8022 |

| | | | | |
|------------|----|-----|-----|-------|
| 1301308284 | 0 | 0 | 15 | 440 |
| 1301466955 | 3 | 730 | 117 | 18764 |
| 1301515145 | 0 | 0 | 3 | 1085 |
| 1301612645 | 11 | 880 | 163 | 17443 |

8 Publication of breeding values

Gestation Length breeding values are expressed in days and as a deviation from a standard dairy gestation length average fixed at 280 days. This makes it easier to interpret by the farmers since the primary use of the gestation length breeding values is to help management of the calving patterns.

The genetic base is defined as 2-5 years old crossbreds born after beef breeds which can be used in all 3 countries.

Many studies such as Hansen et al. (2004) and Eaglen et al. (2013) did not support selection for shorter neither longer duration but rather opt for intermediate values which were found by many studies to be optimal for other traits like productive life and calving ease (Norman et al. 2009). Consequently, there is no plan to incorporate gestation length into the NBDI.

Due to the very high genetic correlation between heifers and cows breeding values, a decision has been made to exclusively publish gestation length for cows.

Breeding values for gestation length, cow are published if the beef bull has got official breeding values for calving traits and the reliability for gestation length is higher than 50%.

Figure 15 below, shows the distribution of the relative breeding values for gestation length cow. Averages per sire breed are shown in Table 18.

Table 18: Average RBV per sire breed

| Sire breed | N | Average |
|------------|-----|---------|
| AAN | 124 | 1.27 |
| BAQ | 77 | 8.53 |
| BBL | 162 | 1.79 |
| CHA | 131 | 4.50 |
| HER | 82 | 2.53 |
| LIM | 140 | 7.89 |
| SIM | 292 | 5.27 |

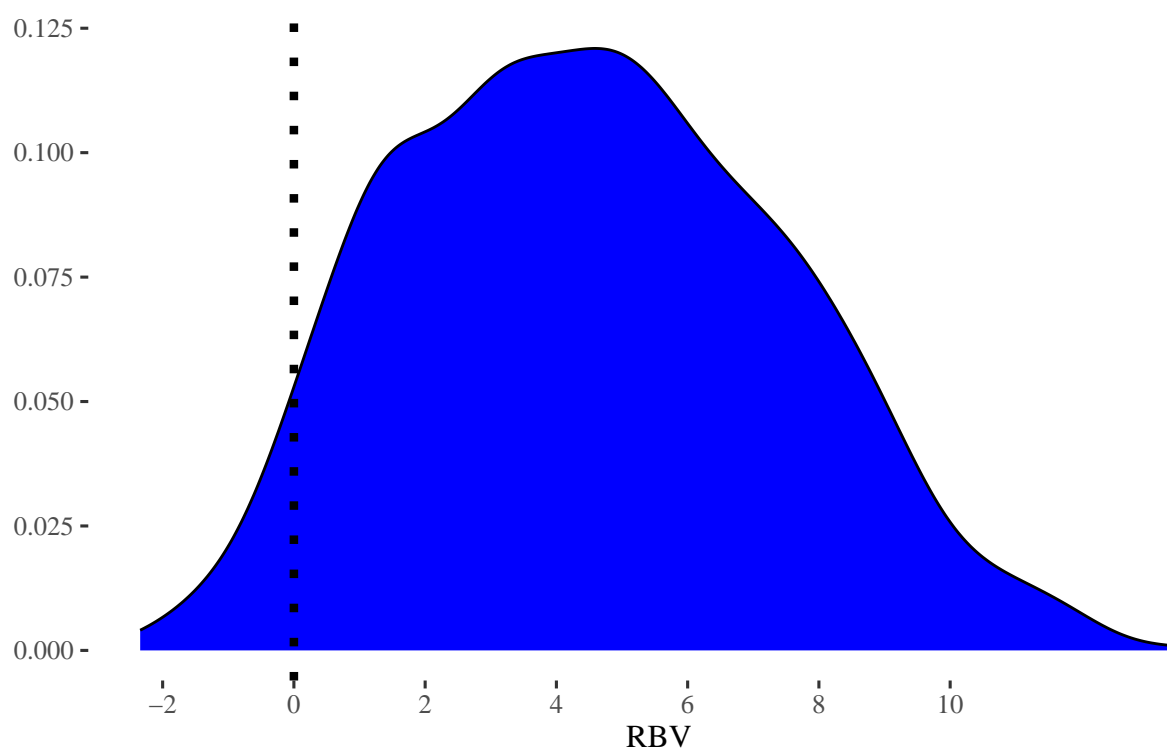


Figure 15: Distribution of the relative breeding values for gestation length cows

9 References

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Appendix: Validation results

9.1 Correlations with sire phenotypic means

Table 19: Correlations with sire phenotypic means

| Number of offspring | Heifers | | | | | | Cows | | | | | |
|---------------------|---------|-------|-------------|------|-------|------|------|------|-------------|------|-------|------|
| | >50 | | [50 to 300] | | > 300 | | >50 | | [50 to 300] | | > 300 | |
| | N | cor | N | cor | N | cor | N | cor | N | cor | N | cor |
| Sirebreed | | | | | | | | | | | | |
| AAN | 43 | 0.54 | 28 | 0.95 | 40 | 0.97 | 41 | 0.88 | 21 | 0.87 | 54 | 0.96 |
| BAQ | 48 | 0.63 | 13 | 0.94 | 11 | 0.97 | 27 | 0.93 | 8 | 0.97 | 41 | 0.96 |
| BBL | 117 | 0.44 | 4 | 0.88 | 0 | | 46 | 0.94 | 4 | 0.99 | 110 | 0.95 |
| CHA | 102 | 0.37 | 6 | 0.95 | 0 | | 39 | 0.93 | 21 | 0.91 | 70 | 0.98 |
| GLW | 4 | 0.34 | 0 | | 0 | | 0 | | 4 | 0.62 | 0 | |
| HER | 42 | 0.31 | 27 | 0.96 | 10 | 0.99 | 20 | 0.93 | 25 | 0.87 | 37 | 0.97 |
| HLA | 8 | 0.47 | 0 | | 0 | | 0 | | 5 | 0.97 | 0 | |
| INR | 10 | 0.80 | 0 | | 0 | | 4 | 0.98 | 0 | | 6 | 1 |
| LIM | 72 | 0.72 | 52 | 0.93 | 7 | 0.99 | 45 | 0.96 | 20 | 0.93 | 74 | 0.96 |
| PIE | 7 | -0.08 | 0 | | 0 | | 0 | | 4 | 0.95 | 0 | |
| SIM | 236 | 0.41 | 25 | 0.96 | 0 | | 136 | 0.94 | 89 | 0.92 | 67 | 0.97 |

A. One country at a time vs. all countries

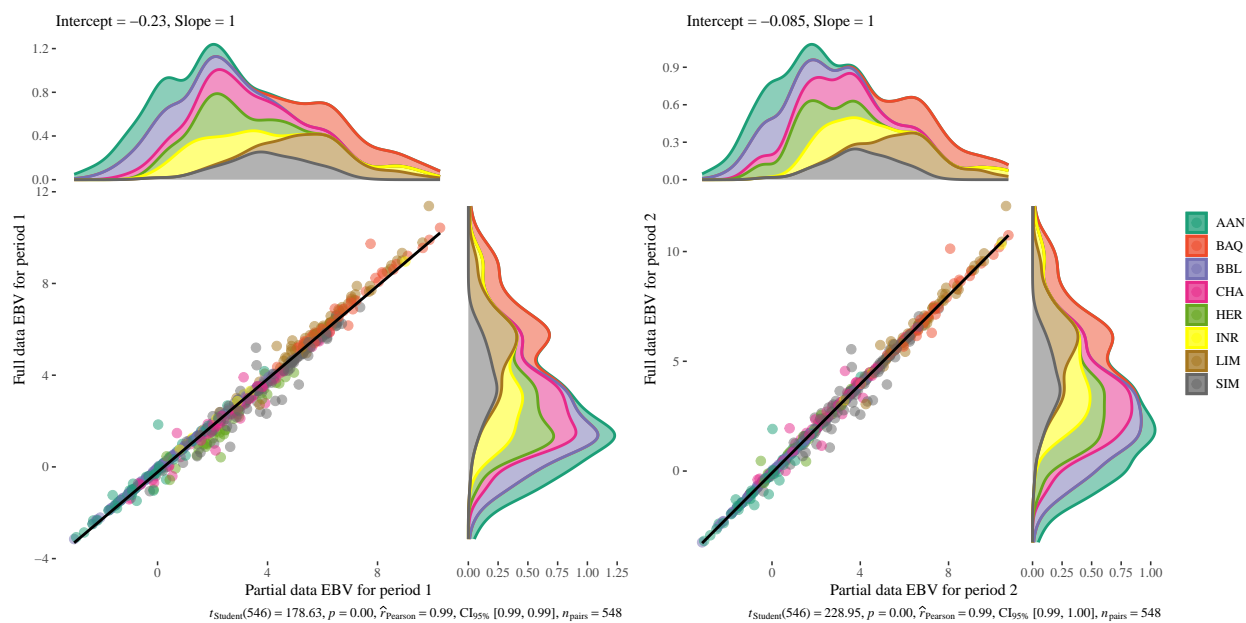


Figure 16: DNK: Regression results when all breeds are included

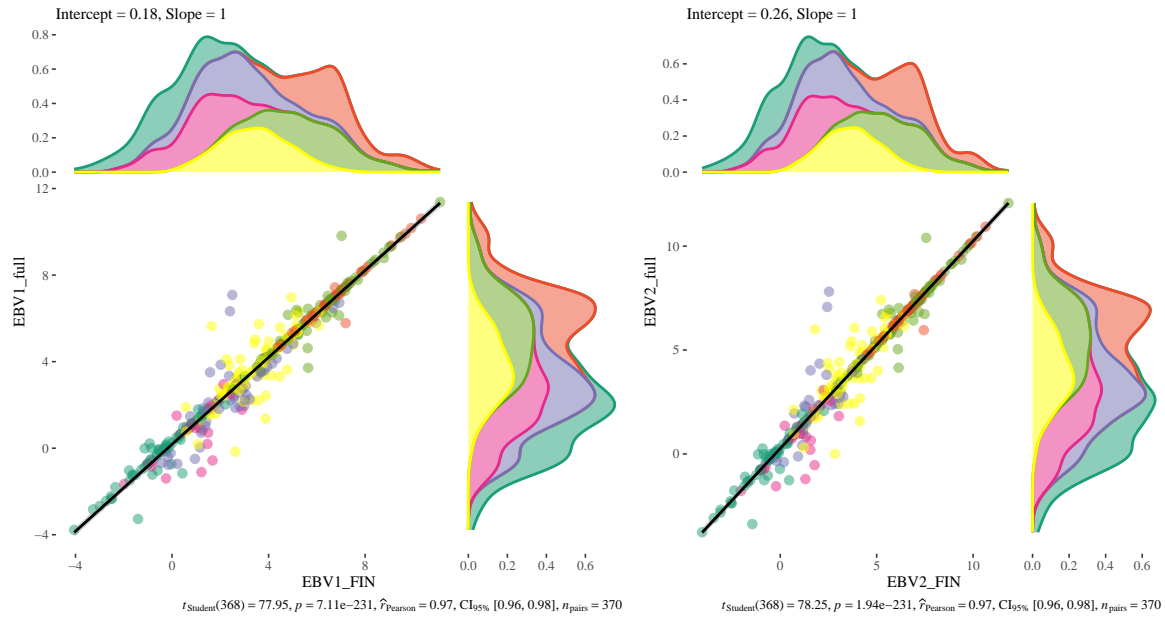


Figure 17: FIN: Regression results when all breeds are included

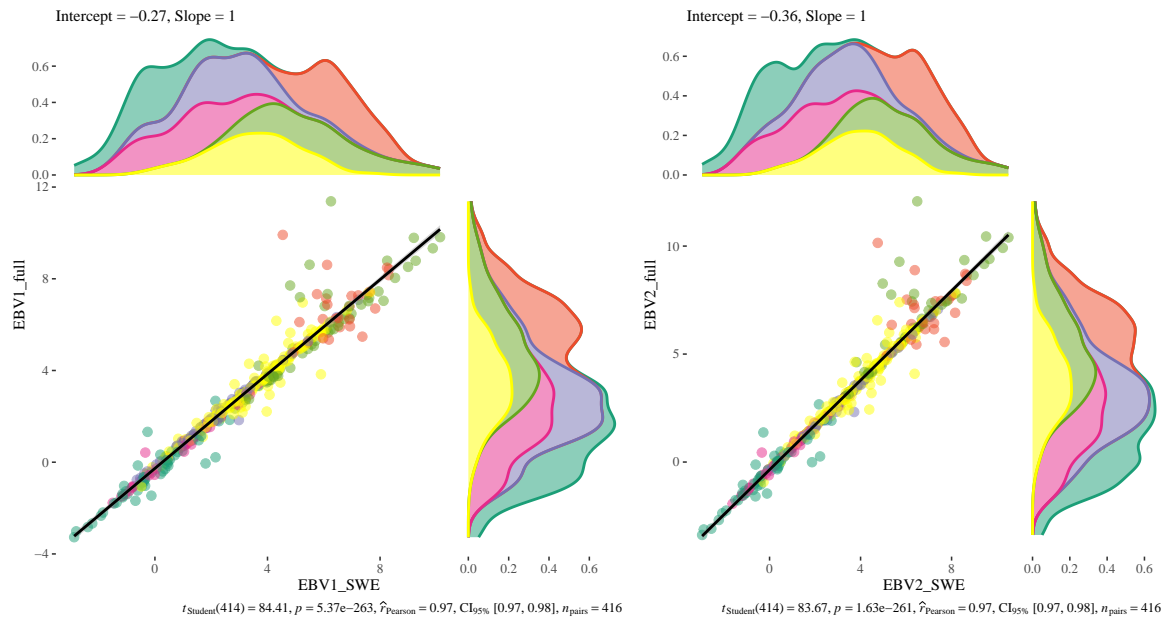


Figure 18: SWE: Regression results when all breeds are included

Table 20: DNK: Cross-validation results per sire breed. All sires

| Sire breed | N | Period 1 | | | | Period 2 | | | |
|------------|-----|---------------|---------------|------|----------|---------------|---------------|------|----------|
| | | bias | slope | corr | Exp_corr | bias | slope | corr | Exp_corr |
| AAN | 58 | -0.10 ± 00.04 | 01.02 ± 00.03 | 0.97 | 0.92 | -0.10 ± 00.04 | 01.01 ± 00.03 | 0.98 | 0.92 |
| BAQ | 35 | -0.16 ± 00.33 | 01.04 ± 00.05 | 0.97 | 0.91 | -0.28 ± 00.35 | 01.04 ± 00.05 | 0.97 | 0.91 |
| BBL | 160 | -0.11 ± 00.00 | 01.00 ± 00.00 | 1.00 | 1.00 | -0.08 ± 00.00 | 01.00 ± 00.00 | 1.00 | 1.00 |
| CHA | 61 | -0.30 ± 00.07 | 00.99 ± 00.02 | 0.98 | 0.90 | 00.05 ± 00.08 | 00.98 ± 00.02 | 0.98 | 0.90 |
| HER | 29 | -0.75 ± 00.12 | 00.98 ± 00.04 | 0.97 | 0.96 | 00.02 ± 00.09 | 00.98 ± 00.04 | 0.97 | 0.96 |
| HLA | 3 | 03.84 ± 01.33 | 01.30 ± 00.74 | 0.87 | 0.78 | -0.58 ± 01.76 | 01.28 ± 00.71 | 0.87 | 0.78 |
| INR | 10 | -0.04 ± 00.02 | 01.00 ± 00.00 | 1.00 | 1.00 | -0.05 ± 00.02 | 01.00 ± 00.00 | 1.00 | 1.00 |
| LIM | 62 | -0.24 ± 00.15 | 01.06 ± 00.02 | 0.98 | 0.96 | -0.39 ± 00.17 | 01.06 ± 00.02 | 0.98 | 0.96 |
| MGR | 3 | -0.38 ± 00.00 | 01.00 ± 00.00 | 1.00 | 1.00 | -0.09 ± 00.00 | 01.01 ± 00.00 | 1.00 | 1.00 |
| PIE | 7 | 00.25 ± 00.07 | 01.00 ± 00.01 | 1.00 | 1.00 | -0.07 ± 00.07 | 01.00 ± 00.01 | 1.00 | 1.00 |
| SIM | 133 | -0.41 ± 00.09 | 01.01 ± 00.02 | 0.97 | 0.93 | -0.16 ± 00.09 | 01.01 ± 00.02 | 0.97 | 0.93 |
| WAG | 3 | -0.10 ± 00.01 | 01.01 ± 00.00 | 1.00 | 1.00 | -0.13 ± 00.01 | 01.01 ± 00.00 | 1.00 | 1.00 |

Table 21: DNK: Cross-validation results per sire breed. Sires with Reliability over 0.5

| Sire breed | N | Period 1 | | | | Period 2 | | | |
|------------|-----|---------------|---------------|------|----------|---------------|---------------|------|----------|
| | | bias | slope | corr | Exp_corr | bias | slope | corr | Exp_corr |
| AAN | 55 | -0.10 ± 00.05 | 01.02 ± 00.03 | 0.97 | 0.97 | -0.10 ± 00.05 | 01.01 ± 00.03 | 0.98 | 0.98 |
| BAQ | 33 | -0.08 ± 00.19 | 01.02 ± 00.03 | 0.99 | 0.97 | -0.19 ± 00.18 | 01.02 ± 00.02 | 0.99 | 0.97 |
| BBL | 160 | -0.11 ± 00.00 | 01.00 ± 00.00 | 1.00 | 1.00 | -0.08 ± 00.00 | 01.00 ± 00.00 | 1.00 | 1.00 |
| CHA | 61 | -0.30 ± 00.07 | 00.99 ± 00.02 | 0.98 | 0.97 | 00.05 ± 00.08 | 00.98 ± 00.02 | 0.98 | 0.97 |
| HER | 26 | -0.83 ± 00.05 | 01.02 ± 00.02 | 1.00 | 0.97 | -0.04 ± 00.04 | 01.02 ± 00.02 | 1.00 | 0.97 |
| INR | 10 | -0.04 ± 00.02 | 01.00 ± 00.00 | 1.00 | 1.00 | -0.05 ± 00.02 | 01.00 ± 00.00 | 1.00 | 1.00 |
| LIM | 62 | -0.24 ± 00.15 | 01.06 ± 00.02 | 0.98 | 0.98 | -0.39 ± 00.17 | 01.06 ± 00.02 | 0.98 | 0.98 |
| PIE | 7 | 00.25 ± 00.07 | 01.00 ± 00.01 | 1.00 | 1.00 | -0.07 ± 00.07 | 01.00 ± 00.01 | 1.00 | 1.00 |
| SIM | 128 | -0.44 ± 00.07 | 01.02 ± 00.02 | 0.98 | 0.97 | -0.18 ± 00.07 | 01.02 ± 00.02 | 0.98 | 0.97 |
| WAG | 3 | -0.10 ± 00.01 | 01.01 ± 00.00 | 1.00 | 1.00 | -0.13 ± 00.01 | 01.01 ± 00.00 | 1.00 | 1.00 |

Table 22: FIN: Cross-validation results per sire breed. All sires

| Sire breed | N | Period 1 | | | | Period 2 | | | |
|------------|----|---------------|---------------|------|----------|---------------|---------------|------|----------|
| | | bias | slope | corr | Exp_corr | bias | slope | corr | Exp_corr |
| AAN | 69 | 00.23 ± 00.05 | 00.98 ± 00.04 | 0.96 | 0.94 | 00.23 ± 00.06 | 00.98 ± 00.04 | 0.96 | 0.94 |
| BAQ | 45 | 00.32 ± 00.18 | 00.99 ± 00.03 | 0.98 | 0.94 | 00.32 ± 00.19 | 00.99 ± 00.03 | 0.98 | 0.94 |
| CHA | 46 | 00.09 ± 00.31 | 00.97 ± 00.10 | 0.83 | 0.80 | 00.56 ± 00.32 | 00.97 ± 00.10 | 0.82 | 0.80 |
| HER | 34 | 00.05 ± 00.17 | 00.93 ± 00.11 | 0.84 | 0.81 | -0.01 ± 00.18 | 00.93 ± 00.10 | 0.84 | 0.82 |
| HLA | 6 | 02.31 ± 00.18 | 00.81 ± 00.10 | 0.97 | 0.92 | 00.30 ± 00.24 | 00.81 ± 00.10 | 0.97 | 0.92 |
| LIM | 84 | 00.27 ± 00.20 | 01.00 ± 00.03 | 0.96 | 0.89 | 00.25 ± 00.21 | 01.00 ± 00.03 | 0.96 | 0.89 |
| SIM | 92 | 00.43 ± 00.24 | 00.95 ± 00.06 | 0.84 | 0.78 | 00.50 ± 00.26 | 00.95 ± 00.06 | 0.84 | 0.78 |

Table 23: FIN: Cross-validation results per sire breed. Sires with Reliability over 0.5

| Sire breed | N | Period 1 | | | | Period 2 | | | |
|------------|----|---------------|---------------|------|----------|---------------|---------------|------|----------|
| | | bias | slope | corr | Exp_corr | bias | slope | corr | Exp_corr |
| AAN | 60 | 00.32 ± 00.03 | 00.98 ± 00.02 | 0.99 | 0.98 | 00.32 ± 00.03 | 00.98 ± 00.02 | 0.99 | 0.98 |
| BAQ | 45 | 00.32 ± 00.18 | 00.99 ± 00.03 | 0.98 | 0.99 | 00.32 ± 00.19 | 00.99 ± 00.03 | 0.98 | 0.99 |
| CHA | 31 | -0.35 ± 00.11 | 01.03 ± 00.03 | 0.99 | 0.96 | 00.11 ± 00.12 | 01.03 ± 00.03 | 0.98 | 0.96 |
| HER | 23 | 00.18 ± 00.08 | 01.06 ± 00.05 | 0.98 | 0.96 | 00.13 ± 00.09 | 01.05 ± 00.05 | 0.98 | 0.96 |
| HLA | 5 | 02.35 ± 00.31 | 00.85 ± 00.27 | 0.88 | 0.91 | 00.25 ± 00.74 | 00.82 ± 00.27 | 0.87 | 0.91 |
| LIM | 75 | 00.31 ± 00.12 | 00.99 ± 00.02 | 0.99 | 0.97 | 00.29 ± 00.13 | 00.99 ± 00.02 | 0.99 | 0.97 |
| SIM | 65 | 00.43 ± 00.18 | 00.96 ± 00.05 | 0.93 | 0.95 | 00.49 ± 00.20 | 00.96 ± 00.05 | 0.93 | 0.95 |

Table 24: SWE: Cross-validation results per sire breed. All sires

| Sire breed | N | Period 1 | | | | Period 2 | | | |
|------------|-----|---------------|---------------|------|----------|---------------|---------------|------|----------|
| | | bias | slope | corr | Exp_corr | bias | slope | corr | Exp_corr |
| AAN | 53 | -0.43 ± 00.07 | 00.93 ± 00.05 | 0.93 | 0.94 | -0.41 ± 00.07 | 00.93 ± 00.05 | 0.94 | 0.94 |
| BAQ | 28 | 04.03 ± 01.45 | 00.41 ± 00.22 | 0.34 | 0.80 | 04.12 ± 01.50 | 00.41 ± 00.22 | 0.34 | 0.80 |
| CHA | 69 | -0.15 ± 00.03 | 01.00 ± 00.01 | 1.00 | 0.98 | -0.35 ± 00.04 | 01.00 ± 00.01 | 1.00 | 0.98 |
| HER | 43 | -0.27 ± 00.04 | 00.98 ± 00.02 | 0.99 | 0.99 | -0.30 ± 00.04 | 00.98 ± 00.02 | 0.99 | 0.99 |
| HLA | 6 | -1.39 ± 00.80 | 00.97 ± 00.22 | 0.91 | 0.78 | -0.12 ± 00.74 | 00.96 ± 00.22 | 0.91 | 0.78 |
| LIM | 51 | 00.04 ± 00.54 | 00.98 ± 00.09 | 0.85 | 0.86 | 00.30 ± 00.56 | 00.98 ± 00.09 | 0.85 | 0.86 |
| SIM | 172 | -0.20 ± 00.07 | 01.01 ± 00.02 | 0.98 | 0.93 | -0.31 ± 00.07 | 01.01 ± 00.02 | 0.97 | 0.93 |

Table 25: SWE: Cross-validation results per sire breed. Sires with Reliability over 0.5

| Sire breed | N | Period 1 | | | | Period 2 | | | |
|------------|-----|---------------|---------------|------|----------|---------------|---------------|------|----------|
| | | bias | slope | corr | Exp_corr | bias | slope | corr | Exp_corr |
| AAN | 50 | -0.49 ± 00.05 | 00.90 ± 00.04 | 0.96 | 0.97 | -0.47 ± 00.05 | 00.91 ± 00.04 | 0.96 | 0.97 |
| BAQ | 18 | 00.33 ± 01.02 | 00.91 ± 00.15 | 0.84 | 0.94 | 00.32 ± 01.08 | 00.90 ± 00.15 | 0.83 | 0.94 |
| CHA | 68 | -0.14 ± 00.03 | 01.00 ± 00.01 | 1.00 | 0.99 | -0.35 ± 00.04 | 01.00 ± 00.01 | 1.00 | 0.99 |
| HER | 41 | -0.32 ± 00.02 | 01.00 ± 00.01 | 1.00 | 0.99 | -0.35 ± 00.02 | 01.00 ± 00.01 | 1.00 | 0.99 |
| HLA | 4 | -1.21 ± 00.53 | 00.98 ± 00.14 | 0.98 | 0.92 | 00.06 ± 00.51 | 00.97 ± 00.14 | 0.98 | 0.92 |
| LIM | 41 | -0.40 ± 00.31 | 01.01 ± 00.05 | 0.96 | 0.97 | -0.16 ± 00.33 | 01.01 ± 00.05 | 0.95 | 0.97 |
| SIM | 163 | -0.20 ± 00.04 | 01.01 ± 00.01 | 0.99 | 0.98 | -0.31 ± 00.04 | 01.00 ± 00.01 | 0.99 | 0.98 |

B. One dam breed at a time *vs.* all dam breeds

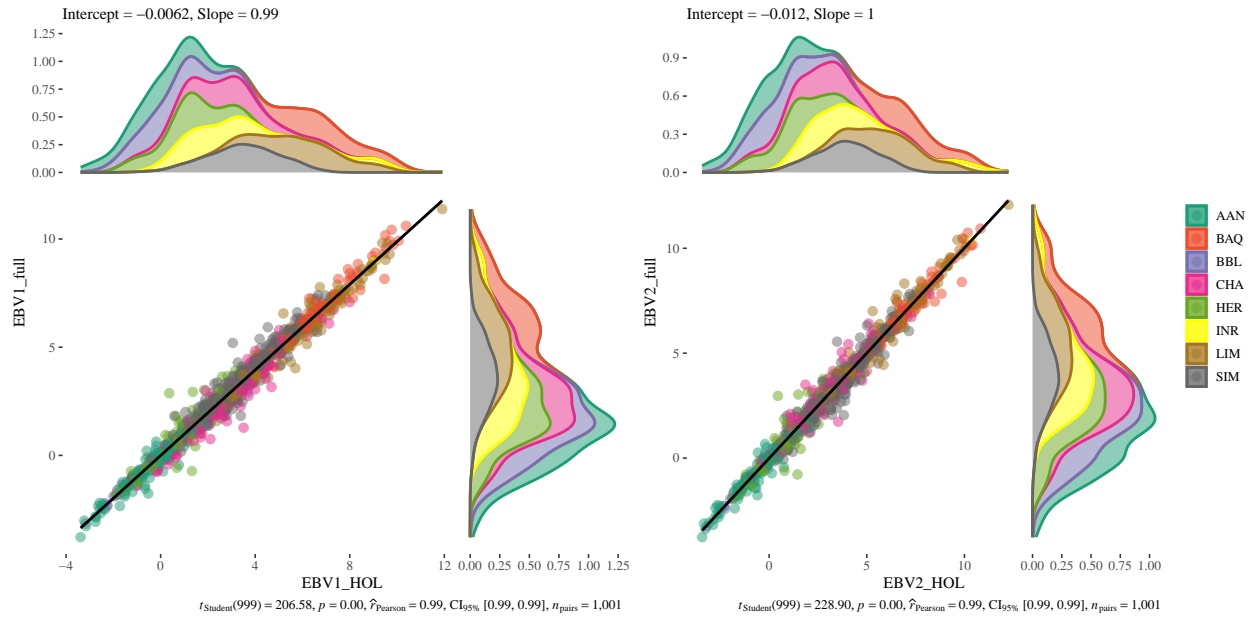


Figure 19: HOL: regression results when all sire breeds are included

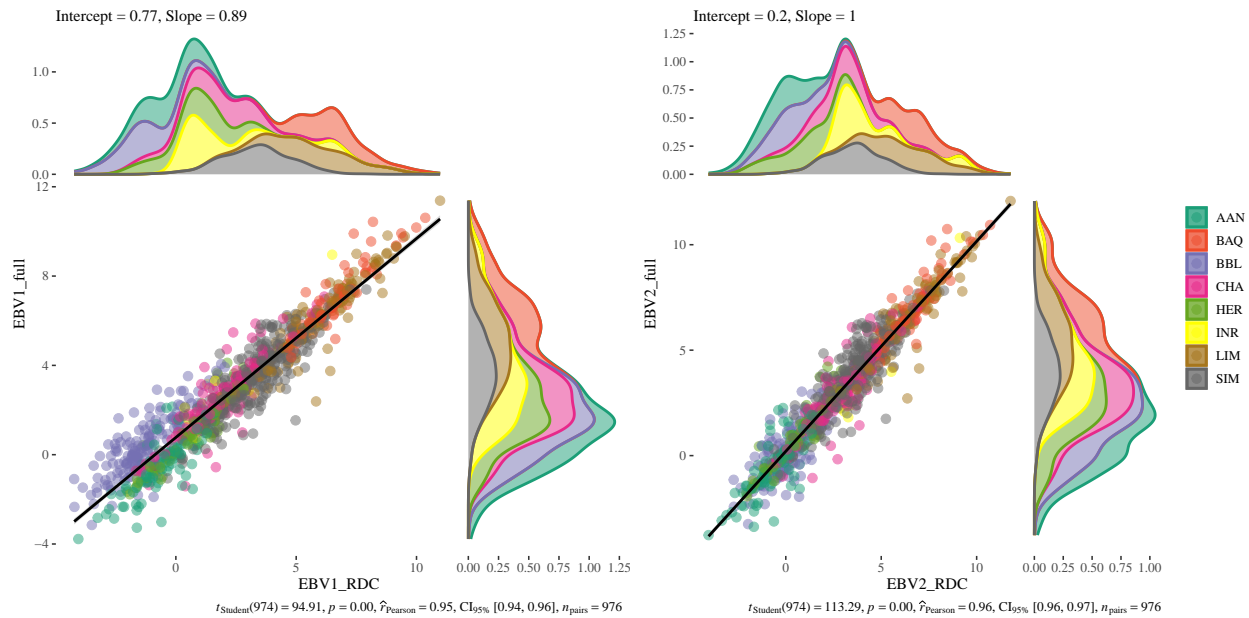


Figure 20: RDC: regression results when all breeds are included

Table 26: Holstein: Cross-validation results per sire breed. All sires

| Sire breed | N | Period 1 | | | | Period 2 | | | |
|------------|-----|---------------|---------------|------|----------|---------------|---------------|------|----------|
| | | bias | slope | corr | Exp_corr | bias | slope | corr | Exp_corr |
| AAN | 114 | -0.08 ± 00.03 | 00.98 ± 00.02 | 0.97 | 0.97 | -0.07 ± 00.03 | 00.97 ± 00.02 | 0.98 | 0.97 |
| BAQ | 76 | 00.15 ± 00.19 | 00.99 ± 00.03 | 0.97 | 0.98 | 00.09 ± 00.20 | 00.98 ± 00.03 | 0.97 | 0.98 |
| BBL | 160 | 00.05 ± 00.01 | 00.98 ± 00.01 | 1.00 | 1.00 | -0.01 ± 00.01 | 00.98 ± 00.01 | 1.00 | 1.00 |
| CHA | 129 | -0.33 ± 00.08 | 00.98 ± 00.02 | 0.97 | 0.97 | 00.17 ± 00.08 | 00.98 ± 00.02 | 0.97 | 0.97 |
| HER | 82 | 00.09 ± 00.08 | 01.02 ± 00.05 | 0.92 | 0.95 | -0.01 ± 00.09 | 01.03 ± 00.05 | 0.92 | 0.95 |
| HLA | 8 | -0.20 ± 00.90 | 00.81 ± 00.37 | 0.67 | 0.87 | 00.10 ± 01.20 | 00.81 ± 00.37 | 0.67 | 0.87 |
| INR | 10 | -0.11 ± 00.06 | 01.00 ± 00.02 | 1.00 | 0.99 | -0.05 ± 00.08 | 01.00 ± 00.02 | 1.00 | 0.99 |
| LIM | 139 | -0.25 ± 00.12 | 01.00 ± 00.02 | 0.98 | 0.97 | 00.04 ± 00.13 | 01.00 ± 00.02 | 0.98 | 0.97 |
| PIE | 7 | 03.21 ± 00.51 | 01.07 ± 00.11 | 0.97 | 0.97 | -0.08 ± 00.76 | 01.07 ± 00.11 | 0.97 | 0.98 |
| SIM | 291 | 00.06 ± 00.06 | 01.02 ± 00.02 | 0.97 | 0.97 | -0.11 ± 00.06 | 01.02 ± 00.02 | 0.97 | 0.97 |
| WAG | 3 | 02.13 ± 00.36 | 00.83 ± 00.06 | 1.00 | 0.94 | 00.85 ± 00.43 | 00.81 ± 00.06 | 1.00 | 0.94 |

Table 27: Holstein: Cross-validation results per sire breed. Sires with Reliability over 0.5

| Sire breed | N | Period 1 | | | | Period 2 | | | |
|------------|-----|---------------|---------------|------|----------|---------------|---------------|------|----------|
| | | bias | slope | corr | Exp_corr | bias | slope | corr | Exp_corr |
| AAN | 109 | -0.09 ± 00.03 | 00.98 ± 00.02 | 0.98 | 0.98 | -0.08 ± 00.03 | 00.98 ± 00.02 | 0.98 | 0.98 |
| BAQ | 75 | 00.12 ± 00.19 | 00.99 ± 00.03 | 0.97 | 0.98 | 00.05 ± 00.19 | 00.98 ± 00.03 | 0.98 | 0.98 |
| BBL | 160 | 00.05 ± 00.01 | 00.98 ± 00.01 | 1.00 | 1.00 | -0.01 ± 00.01 | 00.98 ± 00.01 | 1.00 | 1.00 |
| CHA | 121 | -0.35 ± 00.07 | 00.99 ± 00.02 | 0.98 | 0.98 | 00.16 ± 00.07 | 00.99 ± 00.02 | 0.98 | 0.98 |
| HER | 73 | 00.11 ± 00.06 | 01.02 ± 00.04 | 0.95 | 0.96 | 00.01 ± 00.07 | 01.03 ± 00.04 | 0.95 | 0.96 |
| HLA | 5 | -0.28 ± 00.51 | 00.94 ± 00.18 | 0.95 | 0.89 | -0.09 ± 00.64 | 00.94 ± 00.18 | 0.95 | 0.89 |
| INR | 10 | -0.11 ± 00.06 | 01.00 ± 00.02 | 1.00 | 0.99 | -0.05 ± 00.08 | 01.00 ± 00.02 | 1.00 | 0.99 |
| LIM | 131 | -0.24 ± 00.12 | 01.00 ± 00.02 | 0.98 | 0.98 | 00.05 ± 00.12 | 01.00 ± 00.02 | 0.98 | 0.98 |
| PIE | 7 | 03.21 ± 00.51 | 01.07 ± 00.11 | 0.97 | 0.97 | -0.08 ± 00.76 | 01.07 ± 00.11 | 0.97 | 0.98 |
| SIM | 281 | 00.05 ± 00.05 | 01.01 ± 00.01 | 0.97 | 0.98 | -0.11 ± 00.06 | 01.02 ± 00.01 | 0.97 | 0.98 |

Table 28: RDC: Cross-validation results per sire breed. All sires

| Sire breed | N | Period 1 | | | | Period 2 | | | |
|------------|-----|---------------|---------------|------|----------|---------------|---------------|------|----------|
| | | bias | slope | corr | Exp_corr | bias | slope | corr | Exp_corr |
| AAN | 111 | 00.15 ± 00.07 | 00.97 ± 00.05 | 0.86 | 0.90 | 00.14 ± 00.08 | 00.97 ± 00.06 | 0.86 | 0.90 |
| BAQ | 74 | 00.03 ± 00.34 | 01.05 ± 00.05 | 0.93 | 0.92 | -0.01 ± 00.35 | 01.05 ± 00.05 | 0.92 | 0.92 |
| BBL | 151 | 01.62 ± 00.09 | 00.92 ± 00.05 | 0.82 | 0.84 | 00.18 ± 00.07 | 00.92 ± 00.05 | 0.82 | 0.84 |
| CHA | 127 | 00.64 ± 00.11 | 01.00 ± 00.04 | 0.90 | 0.92 | 00.08 ± 00.14 | 01.00 ± 00.04 | 0.90 | 0.92 |
| HER | 79 | 00.27 ± 00.07 | 01.01 ± 00.04 | 0.94 | 0.91 | 00.26 ± 00.07 | 01.01 ± 00.04 | 0.94 | 0.91 |
| HLA | 8 | 00.36 ± 00.35 | 01.01 ± 00.20 | 0.90 | 0.92 | -0.13 ± 00.60 | 01.01 ± 00.21 | 0.90 | 0.92 |
| INR | 10 | 00.68 ± 00.37 | 01.20 ± 00.15 | 0.94 | 0.81 | -1.15 ± 00.68 | 01.20 ± 00.15 | 0.94 | 0.81 |
| LIM | 138 | 00.21 ± 00.20 | 00.99 ± 00.03 | 0.93 | 0.94 | 00.16 ± 00.22 | 00.99 ± 00.03 | 0.93 | 0.94 |
| SIM | 286 | 00.36 ± 00.12 | 00.96 ± 00.03 | 0.87 | 0.88 | 00.44 ± 00.13 | 00.96 ± 00.03 | 0.87 | 0.88 |

Table 29: RDC: Cross-validation results per sire breed. Sires with Reliability over 0.5

| Sire breed | N | Period 1 | | | | Period 2 | | | |
|------------|-----|---------------|---------------|------|----------|---------------|---------------|------|----------|
| | | bias | slope | corr | Exp_corr | bias | slope | corr | Exp_corr |
| AAN | 85 | 00.13 ± 00.04 | 00.99 ± 00.03 | 0.97 | 0.96 | 00.13 ± 00.04 | 01.00 ± 00.03 | 0.97 | 0.96 |
| BAQ | 62 | 00.16 ± 00.21 | 01.02 ± 00.03 | 0.97 | 0.97 | 00.13 ± 00.22 | 01.02 ± 00.03 | 0.97 | 0.97 |
| BBL | 105 | 01.73 ± 00.08 | 00.98 ± 00.04 | 0.92 | 0.93 | 00.20 ± 00.06 | 00.98 ± 00.04 | 0.92 | 0.93 |
| CHA | 110 | 00.61 ± 00.09 | 01.01 ± 00.04 | 0.94 | 0.94 | 00.04 ± 00.12 | 01.01 ± 00.04 | 0.94 | 0.94 |
| HER | 58 | 00.20 ± 00.04 | 00.98 ± 00.03 | 0.98 | 0.97 | 00.19 ± 00.04 | 00.98 ± 00.03 | 0.98 | 0.97 |
| HLA | 6 | 00.24 ± 00.57 | 01.04 ± 00.30 | 0.87 | 0.94 | -0.29 ± 00.99 | 01.04 ± 00.30 | 0.87 | 0.94 |
| INR | 7 | 00.73 ± 00.34 | 01.27 ± 00.13 | 0.97 | 0.88 | -1.27 ± 00.59 | 01.27 ± 00.13 | 0.97 | 0.88 |
| LIM | 126 | 00.32 ± 00.15 | 00.98 ± 00.03 | 0.96 | 0.96 | 00.28 ± 00.17 | 00.98 ± 00.03 | 0.96 | 0.96 |
| SIM | 228 | 00.31 ± 00.11 | 00.97 ± 00.03 | 0.91 | 0.92 | 00.39 ± 00.11 | 00.97 ± 00.03 | 0.91 | 0.92 |

C. One gender at a time *vs* all

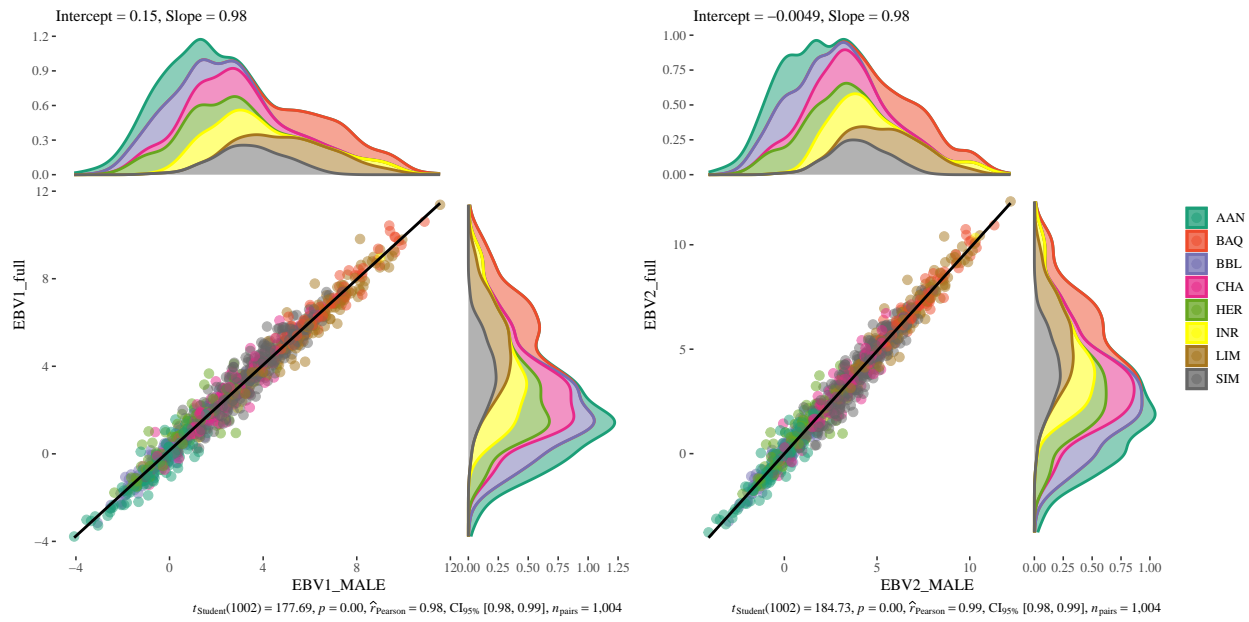


Figure 21: Males: Regression results when all breeds are included

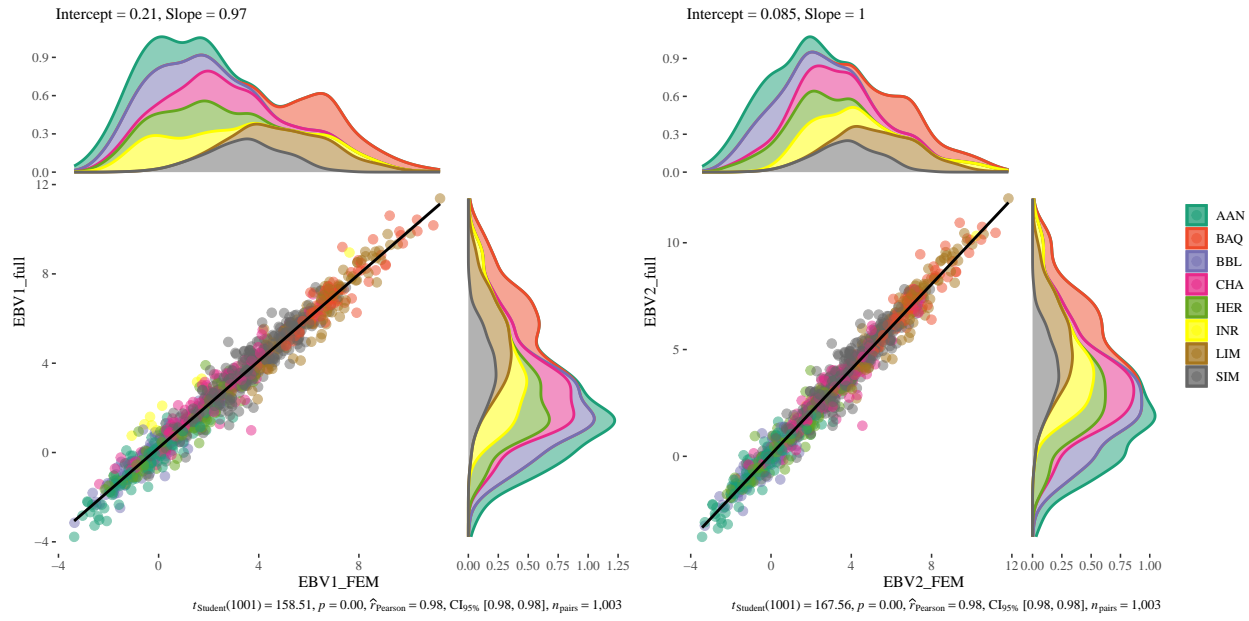


Figure 22: Females: Regression results when all breeds are included

Table 30: Males: Cross-validation results per sire breed. All sires

| Sire breed | N | Period 1 | | | | Period 2 | | | |
|------------|-----|---------------|---------------|------|----------|---------------|---------------|------|----------|
| | | bias | slope | corr | Exp_corr | bias | slope | corr | Exp_corr |
| AAN | 116 | -0.00 ± 00.04 | 00.99 ± 00.03 | 0.95 | 0.97 | -0.01 ± 00.05 | 01.00 ± 00.03 | 0.95 | 0.97 |
| BAQ | 76 | 00.25 ± 00.21 | 00.97 ± 00.03 | 0.97 | 0.98 | 00.14 ± 00.22 | 00.97 ± 00.03 | 0.97 | 0.98 |
| BBL | 160 | 00.15 ± 00.03 | 01.01 ± 00.02 | 0.97 | 0.99 | -0.01 ± 00.03 | 01.01 ± 00.02 | 0.97 | 0.99 |
| CHA | 130 | 00.17 ± 00.07 | 01.00 ± 00.03 | 0.96 | 0.97 | -0.00 ± 00.09 | 01.00 ± 00.03 | 0.96 | 0.97 |
| HER | 82 | 00.42 ± 00.08 | 00.92 ± 00.05 | 0.91 | 0.96 | 00.23 ± 00.08 | 00.93 ± 00.05 | 0.91 | 0.96 |
| HLA | 8 | -0.60 ± 00.19 | 00.89 ± 00.07 | 0.98 | 0.90 | 00.12 ± 00.22 | 00.89 ± 00.07 | 0.98 | 0.90 |
| INR | 10 | -0.31 ± 00.19 | 01.02 ± 00.05 | 0.99 | 0.98 | -0.25 ± 00.23 | 01.02 ± 00.05 | 0.99 | 0.98 |
| LIM | 139 | -0.03 ± 00.15 | 00.98 ± 00.02 | 0.96 | 0.98 | 00.02 ± 00.16 | 00.98 ± 00.02 | 0.96 | 0.98 |
| MGR | 3 | 01.62 ± 00.08 | 00.79 ± 00.09 | 0.99 | 0.93 | -0.05 ± 00.25 | 00.80 ± 00.09 | 0.99 | 0.93 |
| PIE | 7 | 00.59 ± 01.44 | 01.19 ± 00.24 | 0.91 | 0.93 | -1.52 ± 01.69 | 01.20 ± 00.24 | 0.92 | 0.93 |
| SIM | 291 | 00.06 ± 00.08 | 01.02 ± 00.02 | 0.95 | 0.96 | -0.23 ± 00.09 | 01.02 ± 00.02 | 0.95 | 0.96 |
| WAG | 3 | -3.27 ± 01.44 | 01.97 ± 00.28 | 0.99 | 0.95 | -5.42 ± 01.64 | 01.90 ± 00.26 | 0.99 | 0.95 |

Table 31: Males: Cross-validation results per sire breed. Sires with Reliability over 0.5

| Sire breed | N | Period 1 | | | | Period 2 | | | |
|------------|-----|---------------|---------------|------|----------|---------------|---------------|------|----------|
| | | bias | slope | corr | Exp_corr | bias | slope | corr | Exp_corr |
| AAN | 111 | -0.02 ± 00.04 | 00.99 ± 00.03 | 0.96 | 0.98 | -0.02 ± 00.04 | 01.00 ± 00.03 | 0.96 | 0.98 |
| BAQ | 74 | 00.25 ± 00.21 | 00.97 ± 00.03 | 0.97 | 0.98 | 00.13 ± 00.22 | 00.97 ± 00.03 | 0.97 | 0.98 |
| BBL | 159 | 00.15 ± 00.03 | 01.01 ± 00.02 | 0.97 | 0.99 | -0.01 ± 00.03 | 01.01 ± 00.02 | 0.97 | 0.99 |
| CHA | 125 | 00.16 ± 00.07 | 01.00 ± 00.03 | 0.96 | 0.98 | -0.01 ± 00.09 | 01.00 ± 00.03 | 0.96 | 0.98 |
| HER | 71 | 00.38 ± 00.07 | 00.98 ± 00.04 | 0.94 | 0.97 | 00.18 ± 00.07 | 00.99 ± 00.04 | 0.94 | 0.97 |
| HLA | 6 | -0.32 ± 00.23 | 00.82 ± 00.07 | 0.98 | 0.93 | 00.44 ± 00.26 | 00.82 ± 00.07 | 0.98 | 0.93 |
| INR | 10 | -0.31 ± 00.19 | 01.02 ± 00.05 | 0.99 | 0.98 | -0.25 ± 00.23 | 01.02 ± 00.05 | 0.99 | 0.98 |
| LIM | 135 | -0.01 ± 00.14 | 00.98 ± 00.02 | 0.97 | 0.98 | 00.04 ± 00.15 | 00.98 ± 00.02 | 0.97 | 0.98 |
| PIE | 4 | 01.87 ± 01.74 | 01.01 ± 00.30 | 0.92 | 0.95 | -0.08 ± 02.07 | 01.02 ± 00.30 | 0.92 | 0.95 |
| SIM | 283 | 00.05 ± 00.08 | 01.02 ± 00.02 | 0.95 | 0.96 | -0.24 ± 00.09 | 01.02 ± 00.02 | 0.95 | 0.96 |

Table 32: Females: Cross-validation results per sire breed. All sires

| Sire breed | N | Period 1 | | | | Period 2 | | | |
|------------|-----|---------------|---------------|------|----------|---------------|---------------|------|----------|
| | | bias | slope | corr | Exp_corr | bias | slope | corr | Exp_corr |
| AAN | 116 | 00.01 ± 00.04 | 00.93 ± 00.03 | 0.95 | 0.96 | 00.01 ± 00.05 | 00.93 ± 00.03 | 0.95 | 0.96 |
| BAQ | 76 | 00.27 ± 00.28 | 00.96 ± 00.04 | 0.94 | 0.97 | 00.40 ± 00.28 | 00.96 ± 00.04 | 0.94 | 0.97 |
| BBL | 160 | 00.22 ± 00.03 | 00.94 ± 00.02 | 0.96 | 0.98 | 00.06 ± 00.03 | 00.94 ± 00.02 | 0.96 | 0.98 |
| CHA | 130 | 00.45 ± 00.08 | 00.93 ± 00.03 | 0.95 | 0.97 | 00.20 ± 00.09 | 00.93 ± 00.03 | 0.95 | 0.97 |
| HER | 82 | 00.14 ± 00.08 | 00.90 ± 00.04 | 0.92 | 0.95 | 00.09 ± 00.08 | 00.90 ± 00.04 | 0.93 | 0.95 |
| HLA | 8 | -0.73 ± 00.88 | 00.95 ± 00.33 | 0.76 | 0.91 | 00.09 ± 00.93 | 00.95 ± 00.33 | 0.76 | 0.91 |
| INR | 10 | 01.62 ± 00.12 | 00.94 ± 00.05 | 0.99 | 0.98 | 00.50 ± 00.19 | 00.94 ± 00.05 | 0.99 | 0.98 |
| LIM | 137 | -0.12 ± 00.16 | 01.02 ± 00.03 | 0.96 | 0.97 | -0.05 ± 00.17 | 01.02 ± 00.03 | 0.96 | 0.97 |
| MGR | 3 | -1.04 ± 01.37 | 01.38 ± 00.72 | 0.89 | 0.92 | -0.02 ± 01.21 | 01.37 ± 00.72 | 0.88 | 0.92 |
| PIE | 7 | 05.08 ± 00.58 | 00.91 ± 00.17 | 0.92 | 0.92 | 01.40 ± 01.09 | 00.91 ± 00.17 | 0.92 | 0.92 |
| SIM | 292 | 00.24 ± 00.08 | 00.97 ± 00.02 | 0.94 | 0.95 | 00.26 ± 00.09 | 00.97 ± 00.02 | 0.94 | 0.95 |
| WAG | 3 | 02.53 ± 00.13 | 00.82 ± 00.02 | 1.00 | 0.90 | 01.39 ± 00.15 | 00.82 ± 00.02 | 1.00 | 0.90 |

Table 33: Females: Cross-validation results per sire breed. Sires with Reliability over 0.5

| Sire breed | N | Period 1 | | | | Period 2 | | | |
|------------|-----|---------------|---------------|------|----------|---------------|---------------|------|----------|
| | | bias | slope | corr | Exp_corr | bias | slope | corr | Exp_corr |
| AAN | 108 | -0.01 ± 00.04 | 00.93 ± 00.03 | 0.95 | 0.97 | -0.00 ± 00.05 | 00.92 ± 00.03 | 0.95 | 0.97 |
| BAQ | 75 | 00.25 ± 00.28 | 00.97 ± 00.04 | 0.94 | 0.97 | 00.39 ± 00.28 | 00.96 ± 00.04 | 0.94 | 0.97 |
| BBL | 159 | 00.23 ± 00.03 | 00.94 ± 00.02 | 0.96 | 0.98 | 00.07 ± 00.03 | 00.95 ± 00.02 | 0.96 | 0.98 |
| CHA | 122 | 00.43 ± 00.07 | 00.94 ± 00.03 | 0.96 | 0.97 | 00.18 ± 00.09 | 00.94 ± 00.03 | 0.96 | 0.97 |
| HER | 73 | 00.11 ± 00.07 | 00.91 ± 00.04 | 0.95 | 0.96 | 00.06 ± 00.07 | 00.91 ± 00.04 | 0.95 | 0.96 |
| HLA | 7 | -0.16 ± 00.78 | 00.81 ± 00.28 | 0.79 | 0.92 | 00.71 ± 00.82 | 00.81 ± 00.28 | 0.79 | 0.92 |
| INR | 10 | 01.62 ± 00.12 | 00.94 ± 00.05 | 0.99 | 0.98 | 00.50 ± 00.19 | 00.94 ± 00.05 | 0.99 | 0.98 |
| LIM | 131 | -0.01 ± 00.16 | 01.00 ± 00.02 | 0.96 | 0.98 | 00.07 ± 00.16 | 01.01 ± 00.02 | 0.96 | 0.98 |
| PIE | 5 | 05.11 ± 01.09 | 00.90 ± 00.30 | 0.87 | 0.93 | 01.45 ± 02.00 | 00.90 ± 00.30 | 0.87 | 0.93 |
| SIM | 281 | 00.22 ± 00.08 | 00.97 ± 00.02 | 0.94 | 0.95 | 00.24 ± 00.08 | 00.97 ± 00.02 | 0.94 | 0.95 |

D. Truncated data *vs.* all

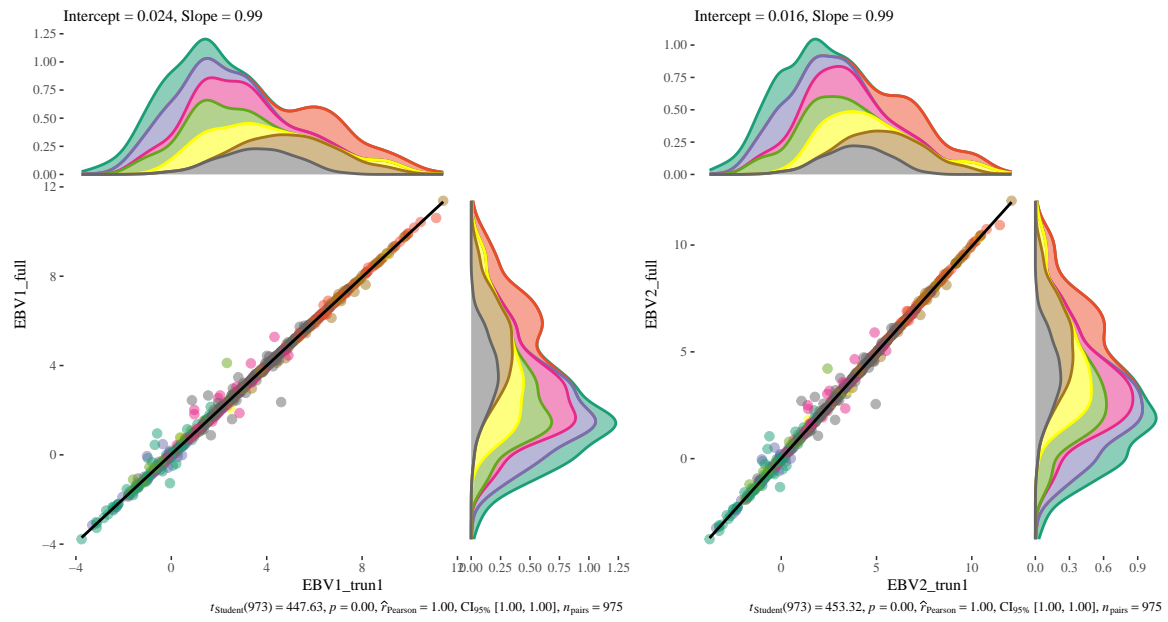


Figure 23: Truncated data: Regression results when all breeds are included

Table 34: Truncated data: Cross-validation results per sire breed. All sires

| Sire breed | N | Period 1 | | | | Period 2 | | | |
|------------|-----|---------------|---------------|------|----------|---------------|---------------|------|----------|
| | | bias | slope | corr | Exp_corr | bias | slope | corr | Exp_corr |
| AAN | 106 | 00.03 ± 00.03 | 00.99 ± 00.02 | 0.98 | 0.98 | 00.03 ± 00.03 | 00.99 ± 00.02 | 0.98 | 0.98 |
| BAQ | 73 | 00.10 ± 00.05 | 00.98 ± 00.01 | 1.00 | 1.00 | 00.09 ± 00.05 | 00.98 ± 00.01 | 1.00 | 1.00 |
| BBL | 153 | -0.01 ± 00.01 | 00.98 ± 00.01 | 1.00 | 1.00 | -0.02 ± 00.01 | 00.98 ± 00.01 | 1.00 | 1.00 |
| CHA | 128 | 00.04 ± 00.03 | 00.99 ± 00.01 | 0.99 | 0.99 | 00.07 ± 00.04 | 00.99 ± 00.01 | 0.99 | 0.99 |
| GLW | 4 | 00.19 ± 00.10 | 00.85 ± 00.07 | 0.99 | 0.99 | 00.10 ± 00.06 | 00.84 ± 00.07 | 0.99 | 0.99 |
| HER | 81 | 00.06 ± 00.03 | 01.00 ± 00.02 | 0.99 | 1.00 | 00.04 ± 00.03 | 00.99 ± 00.02 | 0.99 | 1.00 |
| HLA | 8 | 00.07 ± 00.08 | 00.95 ± 00.03 | 1.00 | 1.00 | 00.09 ± 00.11 | 00.95 ± 00.03 | 1.00 | 1.00 |
| INR | 9 | -0.02 ± 00.09 | 00.98 ± 00.02 | 1.00 | 0.99 | 00.03 ± 00.11 | 00.98 ± 00.03 | 1.00 | 0.99 |
| LIM | 133 | -0.06 ± 00.03 | 01.00 ± 00.01 | 1.00 | 1.00 | -0.05 ± 00.03 | 01.00 ± 00.00 | 1.00 | 1.00 |
| PIE | 7 | -0.69 ± 00.38 | 01.03 ± 00.05 | 0.99 | 0.99 | -0.38 ± 00.34 | 01.03 ± 00.05 | 0.99 | 0.99 |
| SIM | 292 | 00.05 ± 00.03 | 00.99 ± 00.01 | 0.99 | 0.99 | 00.03 ± 00.03 | 00.99 ± 00.01 | 0.99 | 0.99 |
| WAG | 3 | 02.76 ± 04.32 | 00.65 ± 00.66 | 0.70 | 0.86 | 02.65 ± 03.91 | 00.64 ± 00.66 | 0.69 | 0.86 |

Table 35: Truncated data: Cross-validation results per sire breed. Sires with Reliability over 0.5

| Sire breed | N | Period 1 | | | | Period 2 | | | |
|------------|-----|---------------|---------------|------|----------|---------------|---------------|------|----------|
| | | bias | slope | corr | Exp_corr | bias | slope | corr | Exp_corr |
| AAN | 100 | 00.04 ± 00.02 | 01.00 ± 00.01 | 0.99 | 0.99 | 00.04 ± 00.02 | 00.99 ± 00.01 | 0.99 | 0.99 |
| BAQ | 73 | 00.10 ± 00.05 | 00.98 ± 00.01 | 1.00 | 1.00 | 00.09 ± 00.05 | 00.98 ± 00.01 | 1.00 | 1.00 |
| BBL | 152 | -0.01 ± 00.01 | 00.98 ± 00.01 | 1.00 | 1.00 | -0.02 ± 00.01 | 00.98 ± 00.01 | 1.00 | 1.00 |
| CHA | 127 | 00.04 ± 00.03 | 00.99 ± 00.01 | 0.99 | 0.99 | 00.07 ± 00.04 | 00.99 ± 00.01 | 0.99 | 0.99 |
| HER | 79 | 00.06 ± 00.01 | 00.98 ± 00.01 | 1.00 | 1.00 | 00.03 ± 00.01 | 00.98 ± 00.01 | 1.00 | 1.00 |
| HLA | 8 | 00.07 ± 00.08 | 00.95 ± 00.03 | 1.00 | 1.00 | 00.09 ± 00.11 | 00.95 ± 00.03 | 1.00 | 1.00 |
| INR | 9 | -0.02 ± 00.09 | 00.98 ± 00.02 | 1.00 | 0.99 | 00.03 ± 00.11 | 00.98 ± 00.03 | 1.00 | 0.99 |
| LIM | 132 | -0.05 ± 00.03 | 01.00 ± 00.01 | 1.00 | 1.00 | -0.05 ± 00.03 | 01.00 ± 00.00 | 1.00 | 1.00 |
| PIE | 7 | -0.69 ± 00.38 | 01.03 ± 00.05 | 0.99 | 0.99 | -0.38 ± 00.34 | 01.03 ± 00.05 | 0.99 | 0.99 |
| SIM | 290 | 00.05 ± 00.02 | 00.99 ± 00.01 | 1.00 | 1.00 | 00.02 ± 00.02 | 00.99 ± 00.01 | 0.99 | 1.00 |