



Joint Nordic Beef x Dairy Genetic Evaluation of YoungStock Survival

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1 Background

Improving survival in young animals can be beneficial for both farmers and consumers given the implications on both economy and animal welfare. Youngstock survival is already included in the joint breeding goal Nordic Total Merit (NTM) for dairy cattle and when this project was initiated, Denmark was running a national genetic evaluation for youngstock survival for beef x dairy (BxD) calves. Since the launch of the NAV beef × dairy evaluation in 2018 for calving and carcass traits, requests have been put forward by the industry to add youngstock survival to the list of the evaluated traits.

The goal of this project was to develop a genetic evaluation for youngstock survival for beef on dairy crossbreds. Experiences from both the NAV dairy cattle and the Danish BxD evaluations served as inspiration to achieve our goal.

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

In dairy cattle evaluation, youngstock survival (YSS) is divided on sex and rearing period to create four separate single traits. For both heifers and bulls the first period is from day two after calving to one month of age. The second period is from 2 to 15 months for heifers and from 2 to 6 months for bulls (Carlen et al. 2016). However, the former Danish routine evaluation adopted a simplified approach, considering only two traits: survival day 1-30 and

survival day 31-200. In this evaluation, there is no differentiation between sexes, as it is argued that both male and female BxD crossbreeds are intended for eventual slaughter.

As in the former Danish BxD routine evaluation, two traits were considered in this project:

- Survival day 1-30: equal to 1 if the calf is alive at day 30, otherwise, it is set to 0
- Survival day 31-200: equal to 1 if the calf is alive at day 200, otherwise, it is set to 0

The evaluation does not take into account any genetic differences between sexes. Nonetheless, to ensure the validity of this assumption, it was thoroughly tested in the validation plan.

3 Data used for the evaluation

3.1 Input data

Data from the February 2022 NAV dairy routine evaluation was used for this analysis. For both Finland and Denmark, survival files submitted for the dairy evaluation contained raw information for crossbred calves as well and thus were used. Swedish files submitted for the dairy evaluation were pre-edited and included final survival scores based on the trait definition used in dairy. Therefore, new Swedish files were created based on the same national database extraction used for the February 2022 NAV dairy evaluation.

3.2 Data edits

3.2.1 Edits common to all NAV BxD traits:

Like for the other trait groups in the NAV BxD evaluation, YSS input data are submitted to a set of common edits. These edits are described in details in the report on the development of the joint Nordic Beef \times Dairy Genetic Evaluation (Fikse et al. 2020) and can be summarized as follows:

- Only BxD offspring of AI sires are included
- Only BxD offspring of Holstein, RDC, and Jersey cows are included
- Animals with missing sire/dam/birth date are deleted
- Only calves born from 2000 and onwards
- Herds must have both beef and dairy calves within the same herd * year
- Herds must have at least 5 purebred dairy calves each year
- Delete all observations where dams have parity >10
- A minimum of 50 BxD offspring per breed is required for the breed to be included in the evaluation

3.2.2 Additional edits applied to YSS data

Besides the common edits, specific edits were applied to the YSS data. These additional filters follow, when it is applicable, the same rules as for the NAV purebred dairy evaluation of YSS.

- Records of :
 - Twins, ET, stillborn, calves born with defect, and those with unknown destiny (missing vitality records)
 - Animals that die on day 1
 - Animals younger than 30 days at the day of extraction
 - Animals, slaughtered or exported within the period
 - Animals with missing birthdate/birth herd/sex
 - Finnish animals born before 2004
 - Deviating gestation length are excluded were deleted.
- Parity >5 is set to 6
- Danish calves dead after 24 hours without an official ID and with unknown death date, are set to having lived for 4 days.
- Survival data for period 2 is set to missing for animals younger than 200 days at extraction or if survival data for period 1 is missing.
- When the information was available (Denmark), only transfer between herds was considered.

4 Data description

After edits, the total number of calves was about 873688 distributed per country as in Table 2 below.

Table 2: Total number of calves per country

country	N
DNK	346456
FIN	402091
SWE	125141

4.1 Distribution of the dataset by birth year and country

Figure 1 below shows the distribution of data by birth year, per country and sex, where we observe the significant increase in the number of beef X dairy calves over the last decade.

The slight decrease we see for birth year 2021 is simply due to the fact that, at the time of the run, we have not received yet the full data for that year.

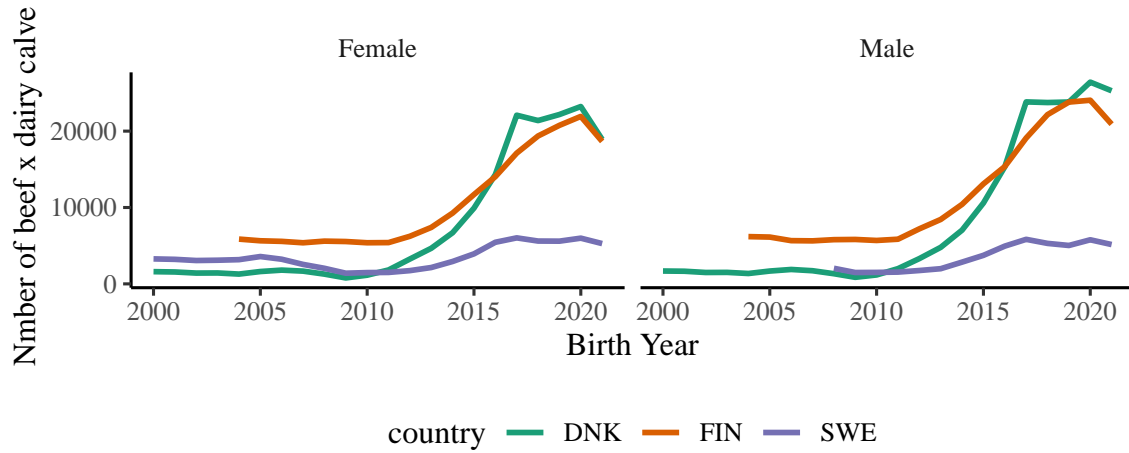


Figure 1: Distribution by country and birth year per sex

4.2 Distribution per country and sex

The dataset contained almost as much males as females for both Finland and Denmark. The higher number of female calves in the Swedish data (Figure 2) is only due to the different cut-off birth years for males and females (2008 for males and 2000 for females). This can be verified by looking at the sex distribution starting from 2008 when male calves were first submitted (Table 3)

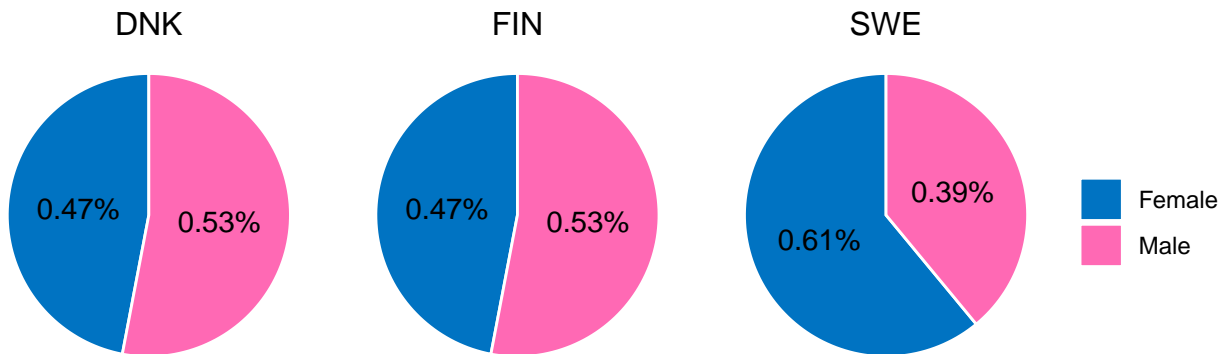


Figure 2: Distribution by country and sex

Table 3: Distribution of Swedish calves born since 2008 per sex

BY	Female	Male
2008	0.50	0.50
2009	0.48	0.52
2010	0.50	0.50
2011	0.49	0.51
2012	0.50	0.50
2013	0.52	0.48
2014	0.51	0.49
2015	0.51	0.49
2016	0.52	0.48
2017	0.51	0.49
2018	0.51	0.49
2019	0.53	0.47
2020	0.51	0.49
2021	0.51	0.49

4.3 Distribution per country and dam breed

Table 4 below presents the count of calves categorized by dam breed for each country. Jersey breed is mainly present in Denmark where Holstein is dominating the field. Over the last few years, Holstein seems to gain popularity in Finland whereas Sweden maintains a more stable figure with a continuing co-existence of RDC and Holstein over time (Figure 3).

Table 4: Distribution of calves per country and dam breed

dambreed	DNK	FIN	SWE
HOL	262335	152056	59905
RDC	28356	248622	64485
JER	55765	1413	751

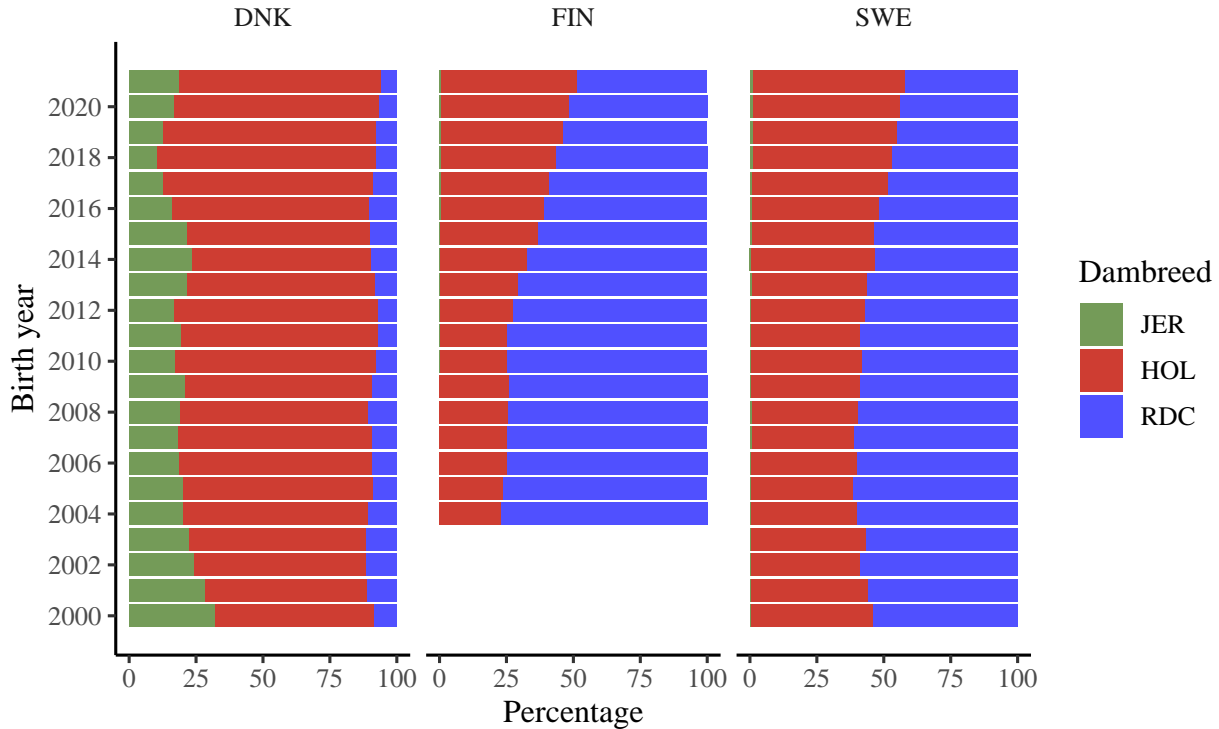


Figure 3: Distribution of dam breeds within BY per country

4.4 Distribution per country and sire breed

Table 5 displays the count of calves per sire breed for each country, while Figure 4 illustrates the evolution of these numbers over time. Over time, there has been a noticeable shift in the distribution of sire breeds, as BBL in Denmark and BAQ in Finland have progressively gained popularity.

Table 5: Distribution of calves per country and sire breed

sirebreed	DNK	FIN	SWE
BBL	245264	0	0
BAQ	10275	186724	2498
LIM	22466	95047	19218
AAN	11361	64768	19809
SIM	17906	24316	31724
CHA	26037	21285	26600
HER	1863	9794	25087
INR	10054	0	0
PIE	589	21	0
WAG	237	0	0

BSH	182	0	0
HLA	58	134	180
MGR	60	0	0
SAL	55	0	0
GLW	37	0	25
DXT	12	2	0

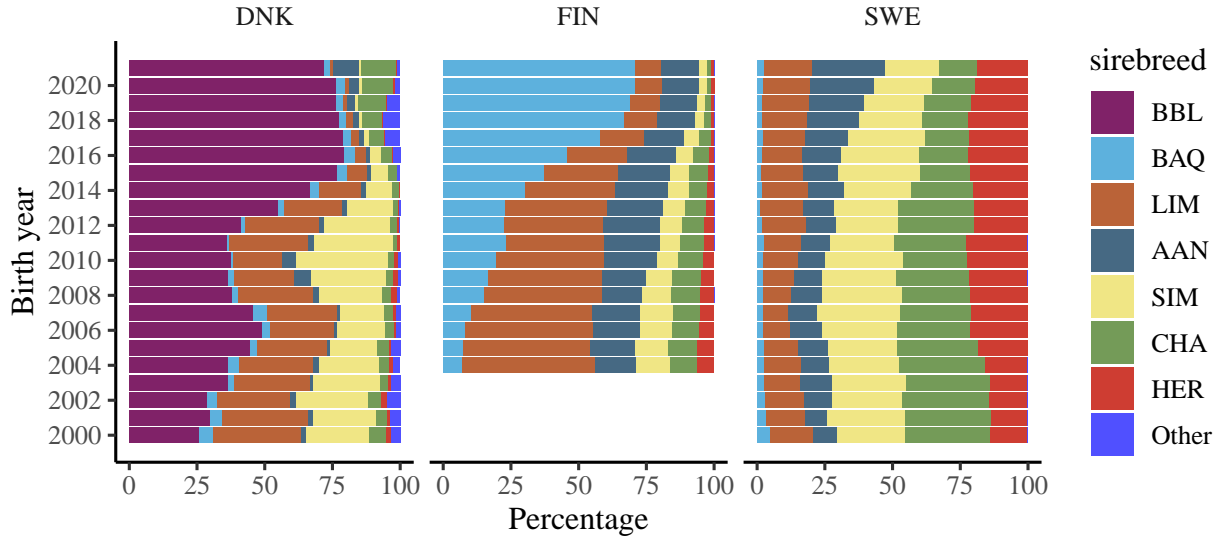


Figure 4: Distribution of sire breeds within birth year

4.5 Birth Herds

The dataset included a total of 20693 birth herds, distributed by sire breed and country as shown in Table 6. The distribution of the herd size per country shows larger herds and herd*BY classes in Denmark compared to Finland and Sweden (Figures 5 and 6).

Table 6: Number of herds per country and sire breed

sirebreed	DNK	FIN	SWE
AAN	832	6179	2448
BAQ	709	6053	644
BBL	2936	0	0
BSH	20	0	0
CHA	1069	3461	3291
DXT	8	2	0
GLW	20	0	15

HER	431	2866	3348
HLA	31	85	117
INR	431	0	0
LIM	2444	7851	2770
MGR	10	0	0
PIE	93	3	0
SAL	27	0	0
SIM	1704	4078	3715
WAG	68	0	0

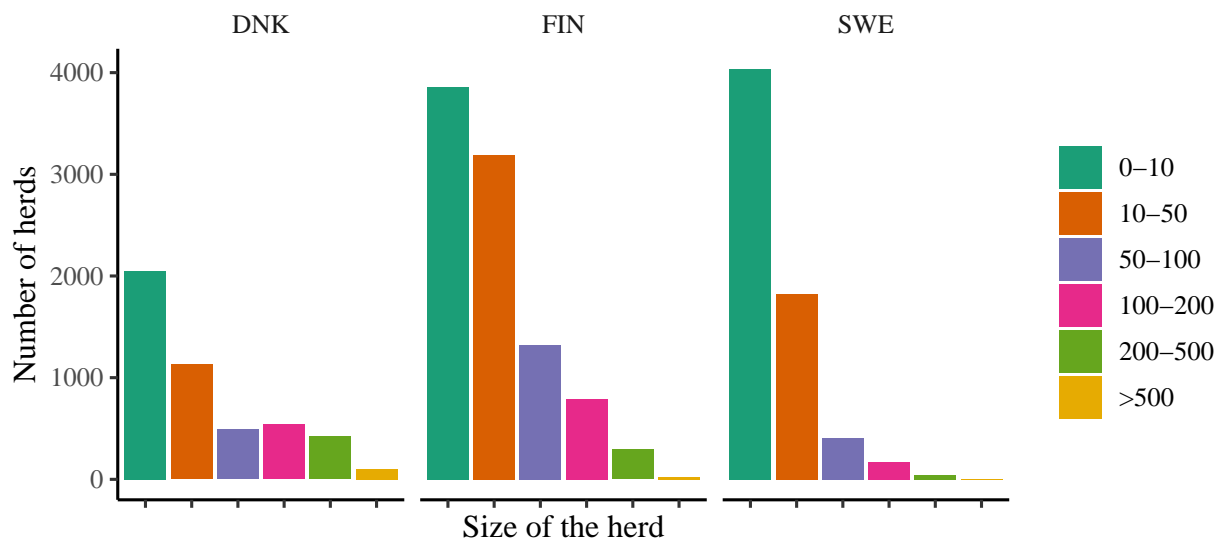


Figure 5: Distribution of herd size

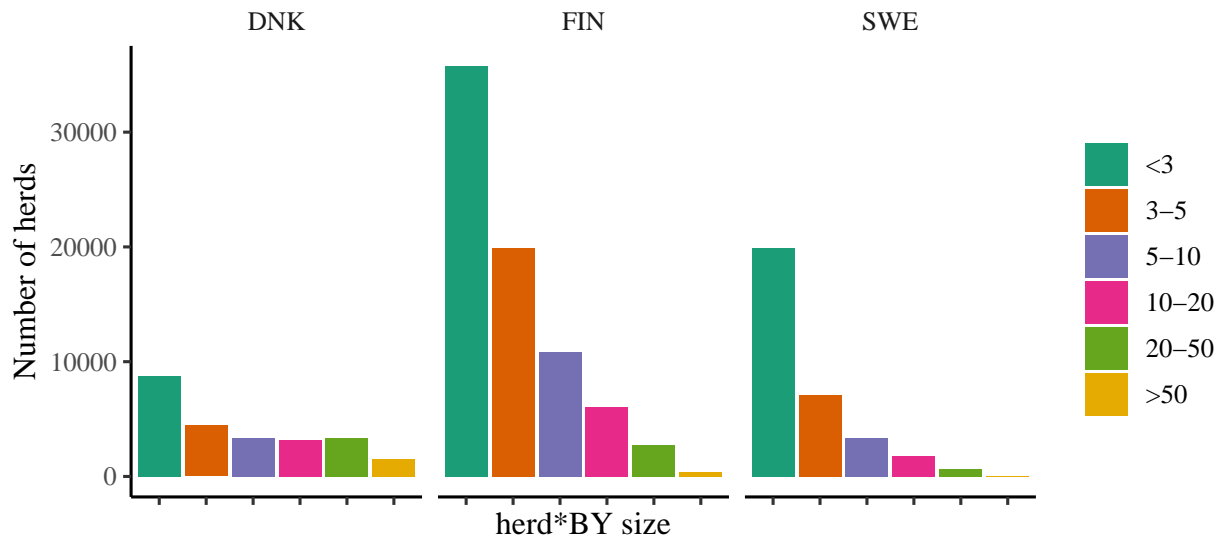


Figure 6: Distribution of the herd*BY classes size

4.6 Survival data

The raw survival data in the input files was used to calculate a phenotypic survival binary value for both period 1: 1:30 (P1) and period 2: 31-200 (P2) for each country. When considering data from all countries and breeds, females exhibited a slightly higher survival rate average for both periods (Table 7). When all data are combined, Jersey cows exhibited a lower survival rate for both periods 1 and 2 compared to other breeds (Table 8). For a comprehensive overview of average survival rates per country, sex, and dam breed for period 1 and period 2, refer to Table 9.

Table 7: Average survival rate for period 1 and period 2 per sex

Period 1		Period 2	
Female	Male	Female	Male
0.97	0.96	0.96	0.95

Table 8: Average survival rate for period 1 and period 2 per dam breed

Period 1			Period 2		
HOL	JER	RDC	HOL	JER	RDC
0.97	0.95	0.97	0.96	0.94	0.96

Table 9: Average survival rate for period 1 and period 2 per country, sex and dam breed

Country	sex	Period 1			Period 2		
		HOL	JER	RDC	HOL	JER	RDC
DNK	Female	0.96	0.95	0.97	0.96	0.95	0.95
DNK	Male	0.96	0.95	0.97	0.94	0.93	0.93
FIN	Female	0.98	0.98	0.98	0.97	0.99	0.96
FIN	Male	0.96	0.97	0.96	0.96	0.98	0.95
SWE	Female	0.98	0.99	0.98	0.97	0.96	0.97
SWE	Male	0.98	0.98	0.98	0.97	0.97	0.97

Looking at the phenotypic SD per period and dam breed (Figure 7)/sire breed (Figure 8), we see a higher variance in period 2 compared to period 1, Jersey dam breed compared to Holstein and RDC and a lower variation in AAN and HER compared to the other sire breeds.

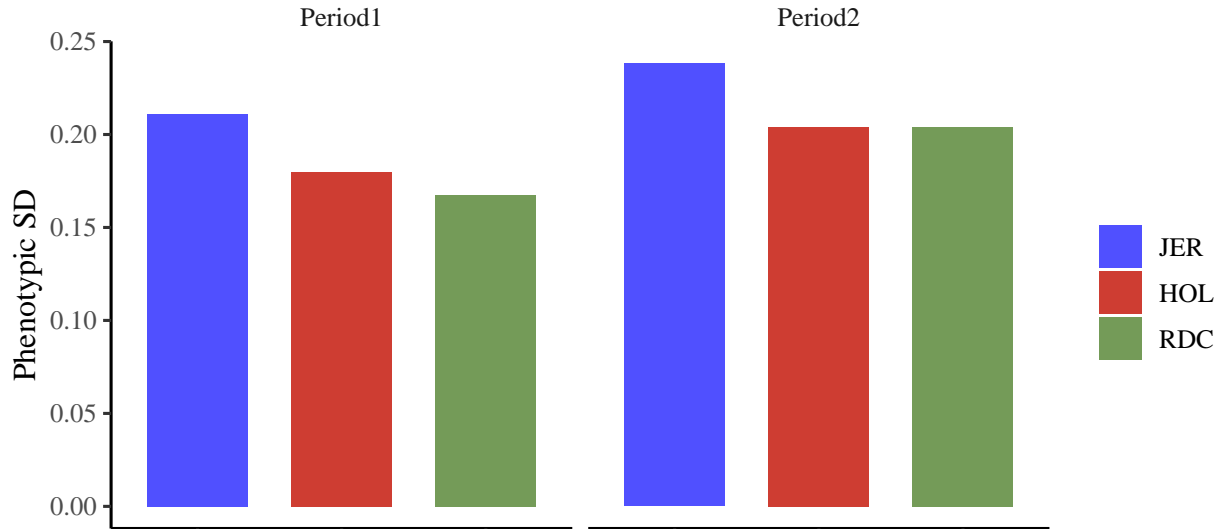


Figure 7: Phenotypic SD per dam breed and trait

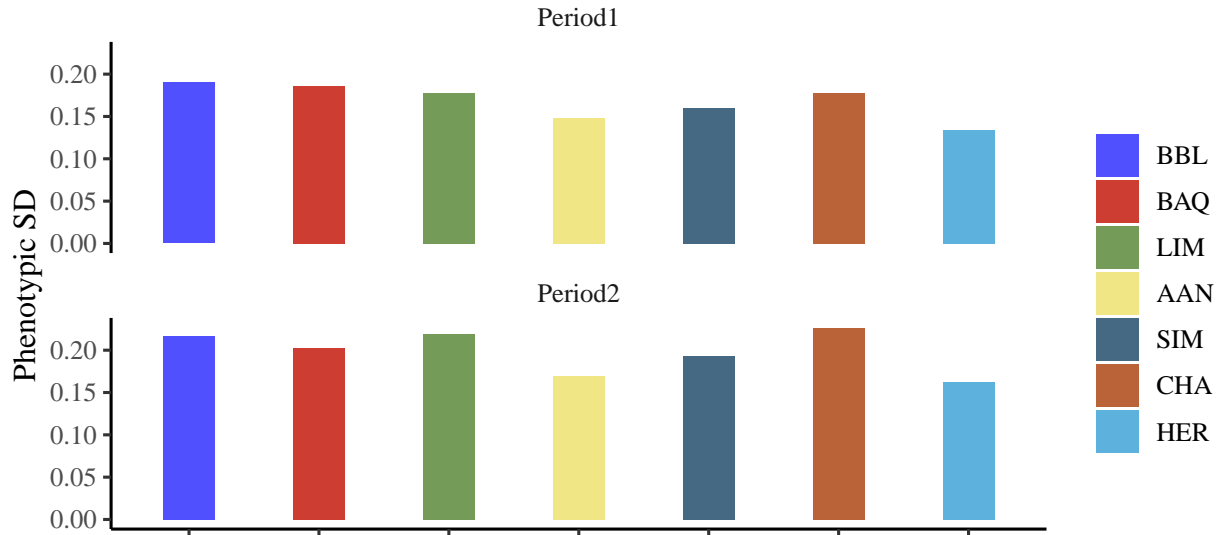


Figure 8: Phenotypic SD per sire breed and trait (only main breeds included)

4.6.1 Changes over time: within country

Figures 9 and 10 illustrate the phenotypic average of the survival rate per birth year within each country and period. Notably, there is a discernible decline in the average survival rate in Finland over the last 10 years, specifically in period 1.

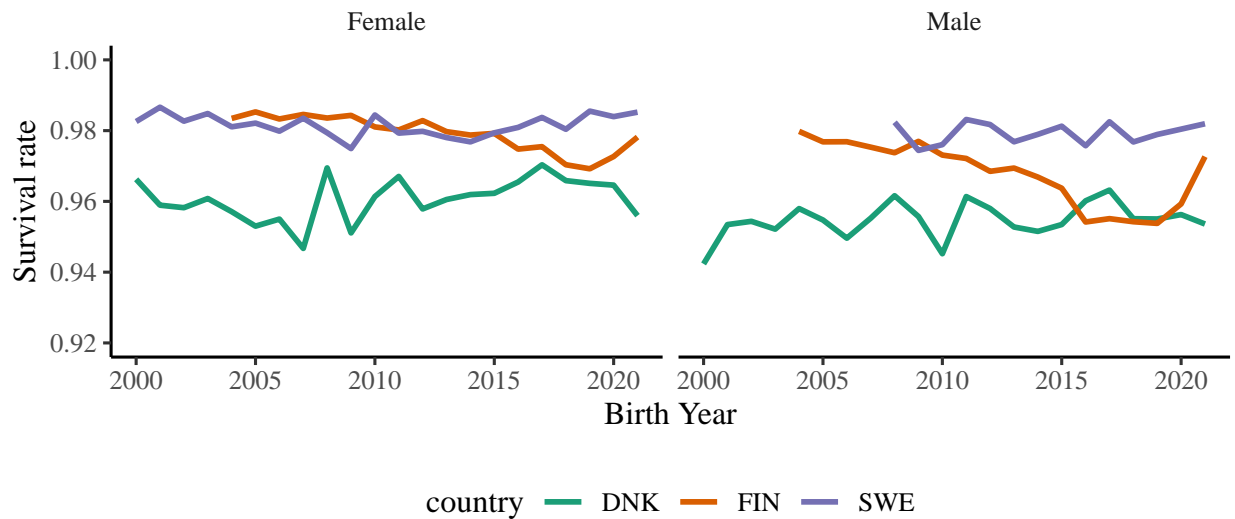


Figure 9: Calves survival rate in period 1 per country

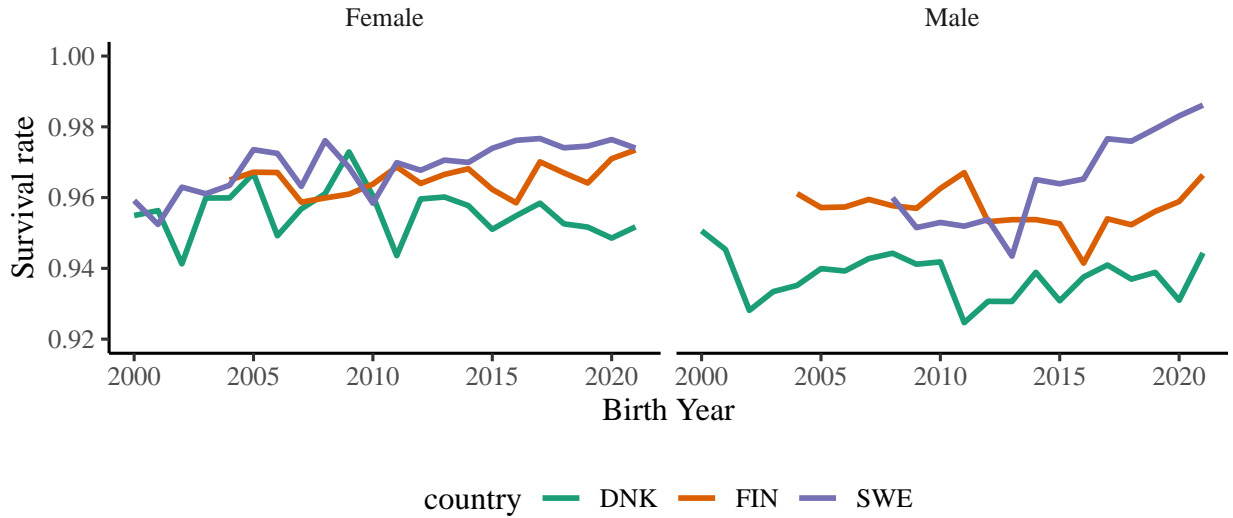


Figure 10: Calves survival rate in period 2 per country

As mentioned earlier in this document, the distribution of dam and sire breeds within birth year (Figures 3 and 4) indicate a rising trend in the popularity of BAQ sires and Holstein dams in Finland over the past decade. However and despite the apparent shift in dam and sire breed preferences, Figures 11 and 12 do not reveal any specific dam breed or sire breed responsible for the decrease in the average survival rate in Finland. The situation seems to be more complex, and other factors may be contributing to the observed changes.

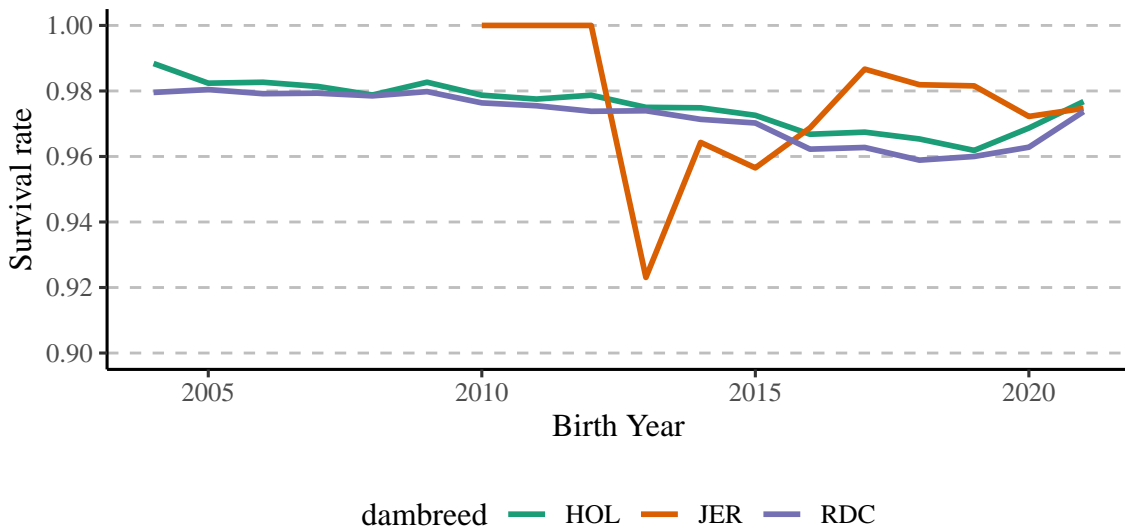


Figure 11: Survival Rate of Calves in Finland: Average by Dam Breed in period 1

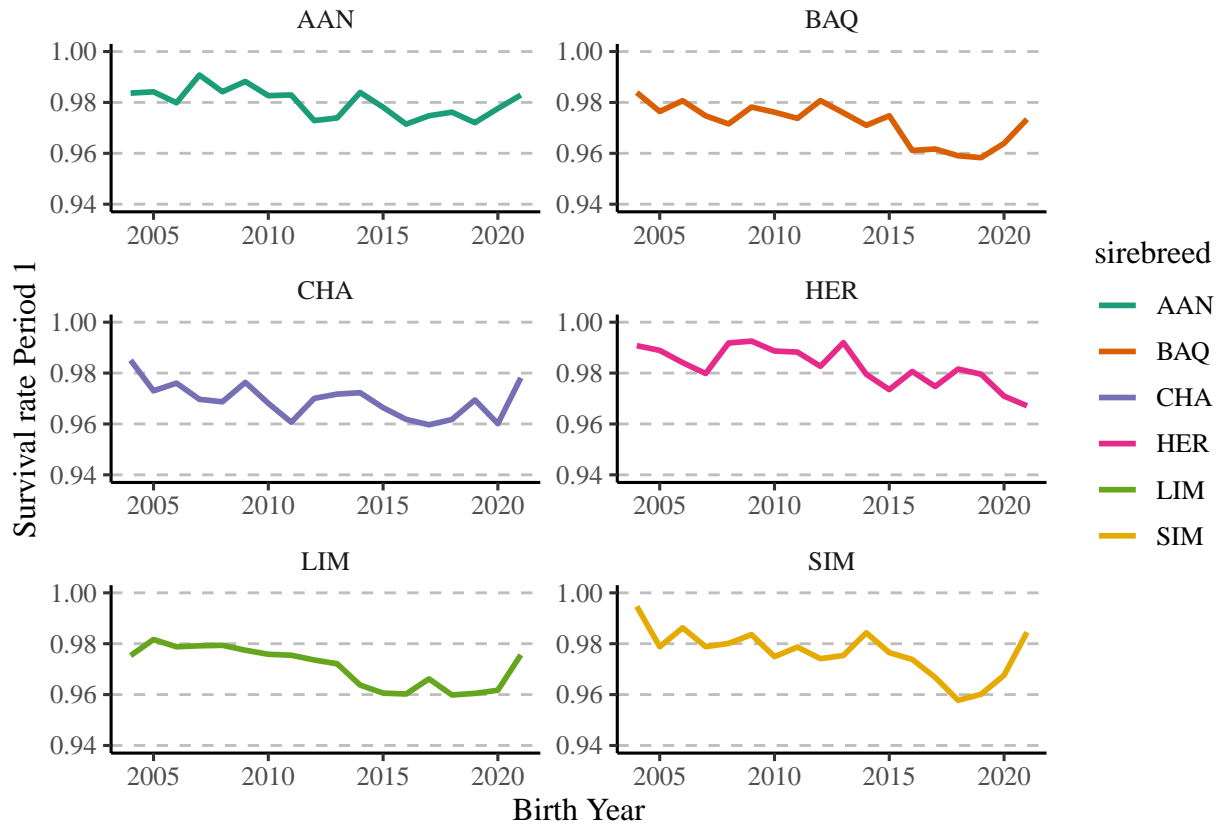


Figure 12: Calves survival rate in period 1 per sire breed in Finland

4.6.2 Changes over time: within sire breed

Figures 13 and 14 show average survival rates per sire breed for periods 1 and 2 respectively. We clearly see differences between sire breeds but no trend over time was observed for any breed. The drop in survival rate in period 2 (Figure 14) for CHA was due to a drop in Denmark (Figure 15) probably caused by the use of some bulls with poor survival.

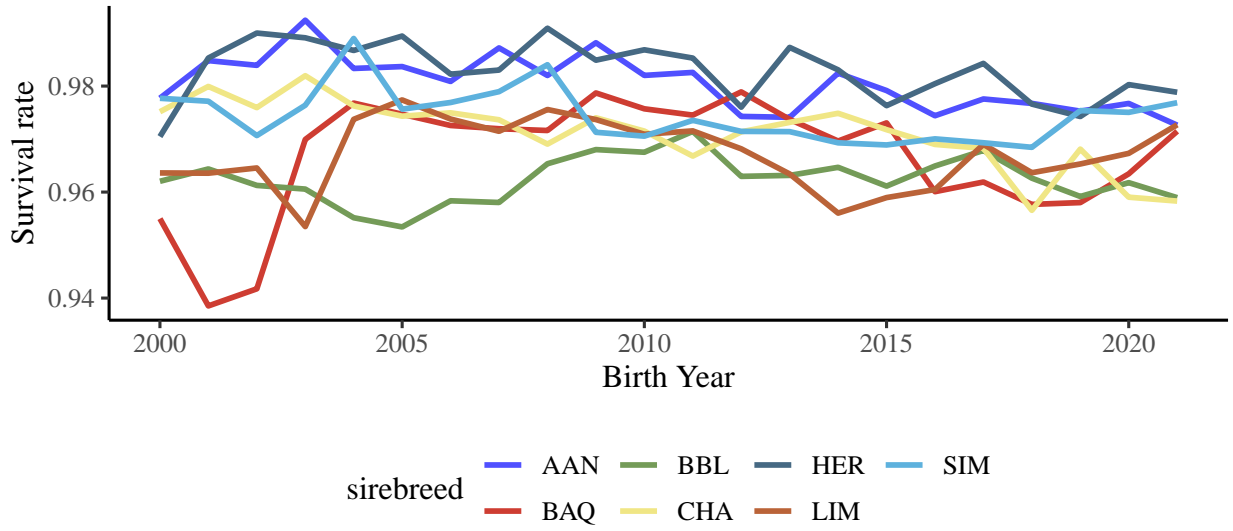


Figure 13: Calf survival rate in period 1 per sire breed

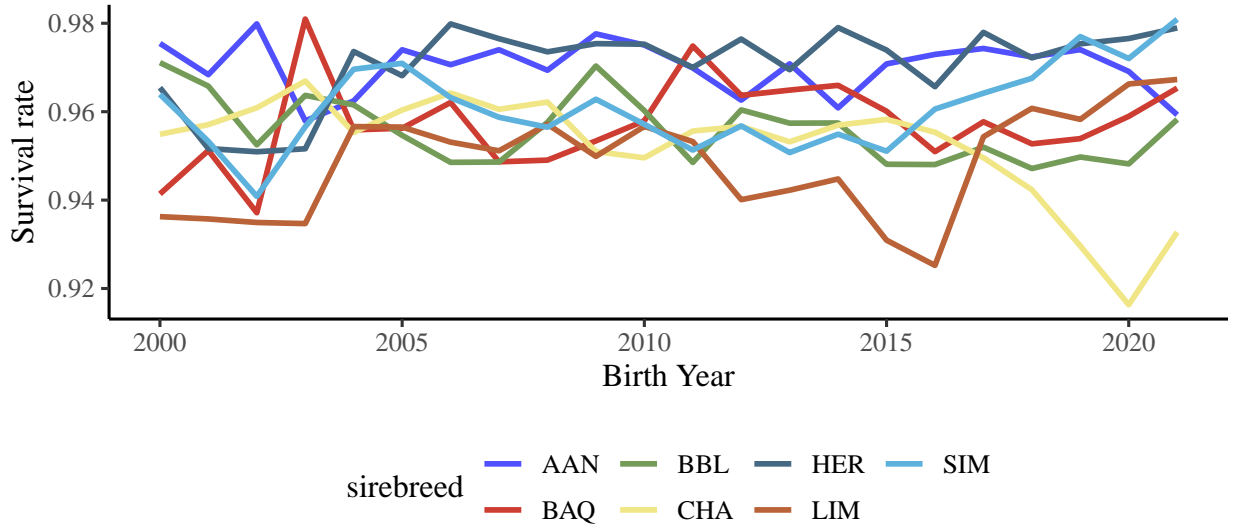


Figure 14: Calf survival rate in period 2 per sire breed

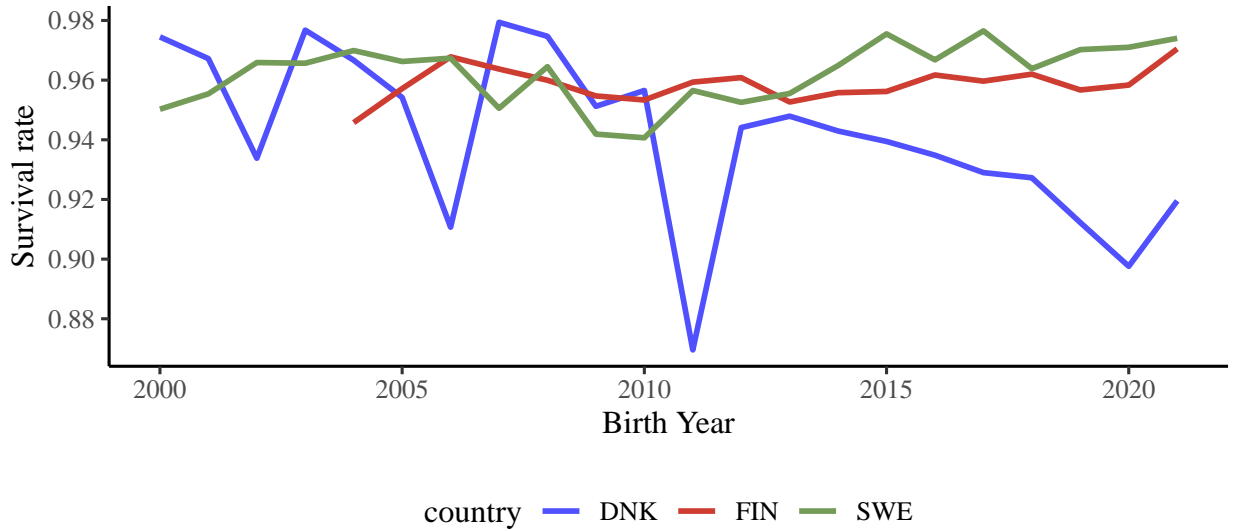


Figure 15: Calf survival rate in period 2 in Charolais

4.7 Age at death

The average age at death was consistent across countries and sex (Figure 16). On average, most of the calves died around 2 weeks during period 1 and around 3 months of age in period 2. As shown in Table 10, the average of age at death was higher for Jersey dam breed but this trend was observed only in Sweden and Finland.

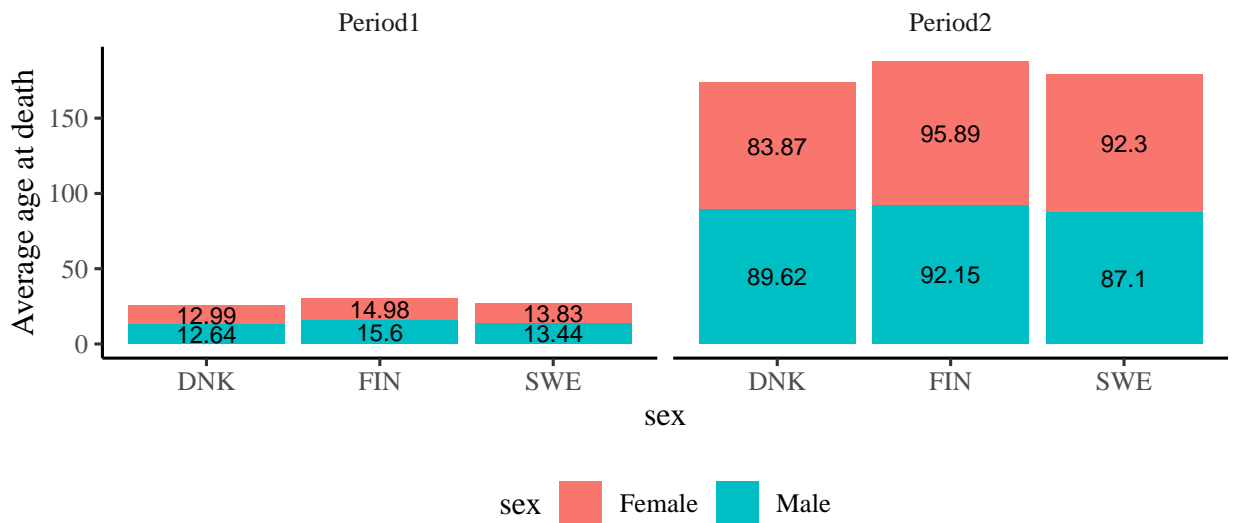


Figure 16: Average age at death

Table 10: Average age at death (in days) for period 1 and period 2 per country, sex and dambreed

Country	sex	Period 1			Period 2		
		HOL	JER	RDC	HOL	JER	RDC
DNK	Female	12.7	13.6	13.9	85.5	74.3	97.1
DNK	Male	12.5	13.2	13.1	90.5	83.0	99.2
FIN	Female	14.6	14.2	15.2	92.3	107.5	97.4
FIN	Male	15.5	14.8	15.6	89.3	125.9	93.3
SWE	Female	13.3	11.6	14.3	92.1	106.8	92.4
SWE	Male	12.9	14.7	14.0	87.2	95.5	86.9

4.8 Transfer

It is a common practice in the industry that calves destined for beef production are often transported from their birth dairy herds to specialized farms since early age. Subsequently, in some cases, they may undergo further transfers to finishing farms before being slaughtered. This process of transportation is well-known to be a recognized stressful event for young calves and can potentially impact their survival (Roadknight et al. (2021)).

In both the NAV dairy evaluation and the Danish BxD evaluation of YSS, transfer was included as a fixed effect in the model. However, there are slight variations between the two evaluations in how transfer is defined.

In the NAV routine dairy evaluation, transfer is defined as a binary variable with a value of 1 if the calf was moved to another location during the first 60 days of life, and 0 if no transfer occurred during that period. In the Danish BxD evaluation of YSS, transfer is defined similarly, but the considered period spans the entire 200 days.

To determine the most appropriate definition of transfer in the current project, transfer data was first thoroughly analyzed within each country.

4.8.1 Frequency of transfers

When looking at the first 200 days of life of the calves, the frequency of transfers within each country showed most of the calves get transferred at least once in Denmark and Finland while 84% of the calves do not get transferred at all in Sweden (Table 11). Finland stands out with approximately 27% of the calves being transferred more than once, a practice where dairy farmers sell the calves to specialized herds at 14 days of age, followed by a second transfer to “finishing” herds before slaughter.

Looking specifically at the first 60 days of their lives, transfer rates are around 64%, 73%, and 7% in Denmark, Finland, and Sweden, respectively (Table 12).

Table 11: Percentage of transfered animals per country and sex

	No_transfer	One_transfer	Atleast_twice
DNK	0.25	0.67	0.08
FIN	0.18	0.55	0.27
SWE	0.84	0.16	0.00

Table 12: Percentage of animals transferd within the first 60 days per country and sex

	Not_transfered	Transfered
DNK	0.36	0.64
FIN	0.27	0.73
SWE	0.93	0.07

4.8.2 Age at transfer.

On average, females tend to be transferred at a later age than males in all three countries, as shown in Table 13. In Finland, the average age at first transfer is higher than the expected two weeks. However, this can be attributed to a typical delay between the time when the calf is sold and when it is actually transferred to the next herd, which usually takes around two weeks of waiting time.

Moreover, the average age at transfer is higher in Sweden compared to the other countries. This suggests a potentially different approach to calf transfers in Sweden, which may contribute to the variation in transfer ages among the three countries.

Table 13: Average age (in days) at first and second transfer per country and sex

country	sex	transferage1	transferage2
DNK	Female	41.5	123.2
DNK	Male	35.5	129.5
FIN	Female	32.0	157.5
FIN	Male	26.1	164.4
SWE	Female	74.7	132.0
SWE	Male	59.3	108.6

4.8.3 Transfer and survival rate

To gain initial insights into the potential relationship between transfer and calf survival rates, the survival data of transferred and non-transferred calves were summarized per period in figures 17 and 18. The results indicate that transferred calves appear to have higher survival

rates during period 1 in all countries. However, it is important to consider that this result may be biased since only calves that survived long enough to be transferred are included in the transferred group. This introduces a potential bias, making it challenging to obtain an accurate estimate of the effect of transfer on calves during period 1. As a result, including the transfer effect in the evaluation model for period 1 could be contentious.

For period 2, the survival rates of transferred and non-transferred calves were relatively similar in both Finland and Denmark, as shown in Figure 18. In Sweden, the few calves that were transferred seemed to have higher survival rates, potentially due to being selected based on their health conditions. To address this bias in Sweden, a national edit is applied, excluding calves from farms that sell more than 10% of their calves. This is a common practice when editing Swedish youngstock survival for dairy animals.

Moreover, a separate analysis was conducted focusing on calves transferred only during the first 100 days. The results (Figure 19) show a lower survival rate for transferred calves during period 2 (except in Sweden), where the effect of transfer on calf survival aligns with expectations.

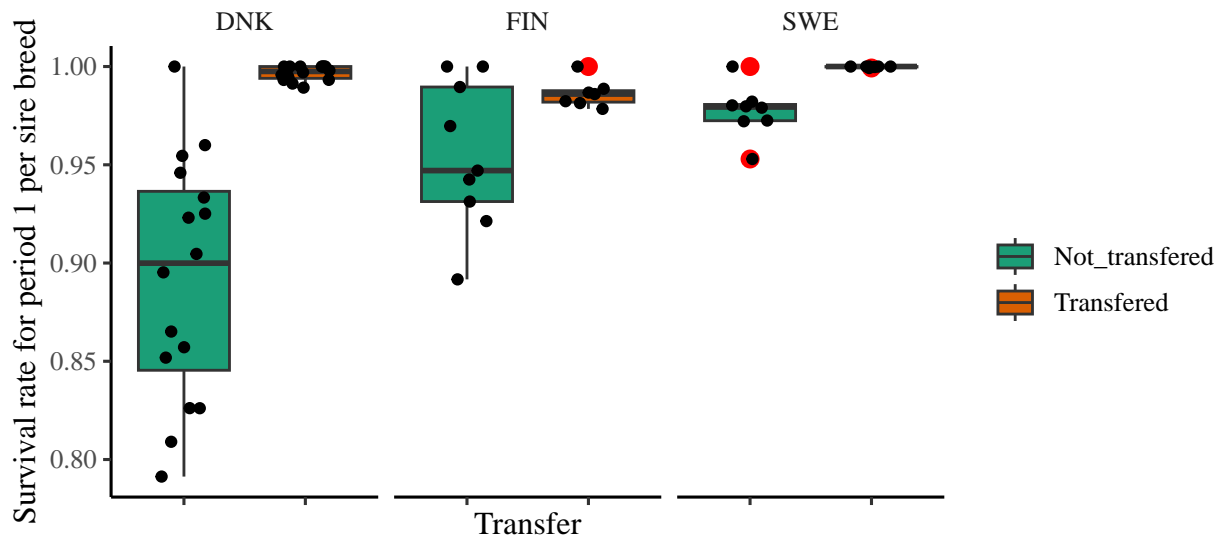


Figure 17: Relationship between survival rate for period 1 and transfer

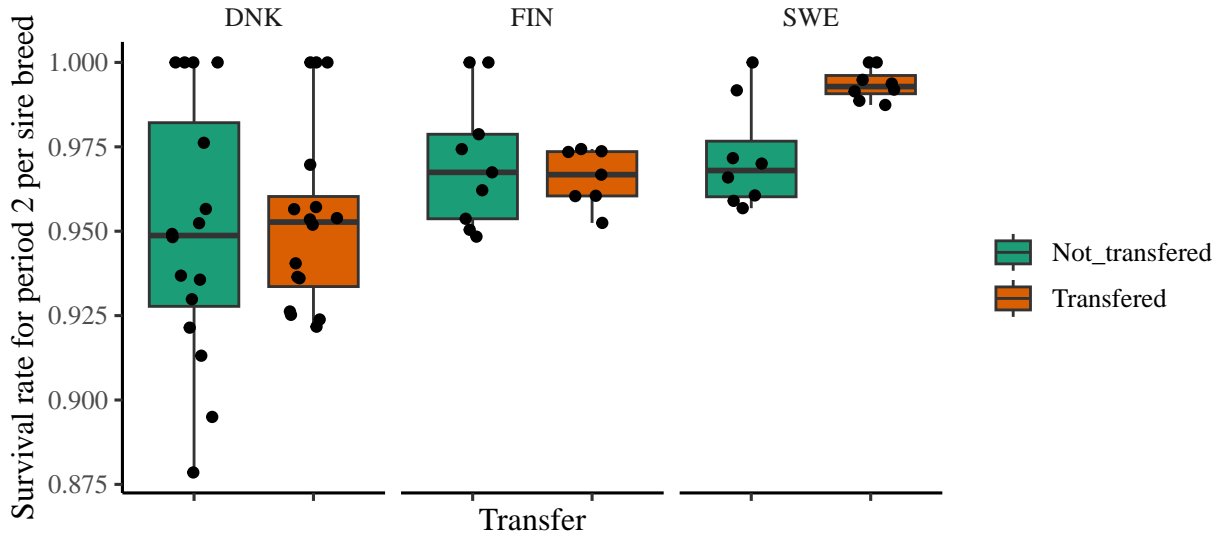


Figure 18: Relationship between survival rate for period 2 and transfer

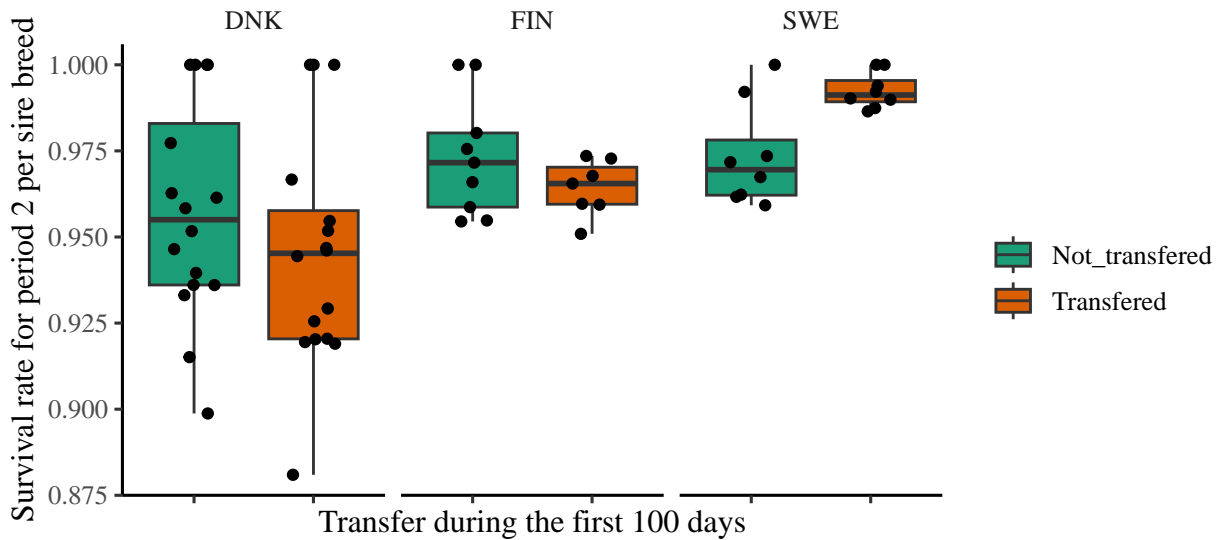


Figure 19: Relationship between survival rate for period 2 and transfer during the first 100 days

4.8.4 Time spent in the different herds

The distribution of the time spent by calves in each herd (Figure 20) shows an obvious dominance of the second herd (herd 2) as the herd with the maximum time spent in by the calf when it is transferred at least once.

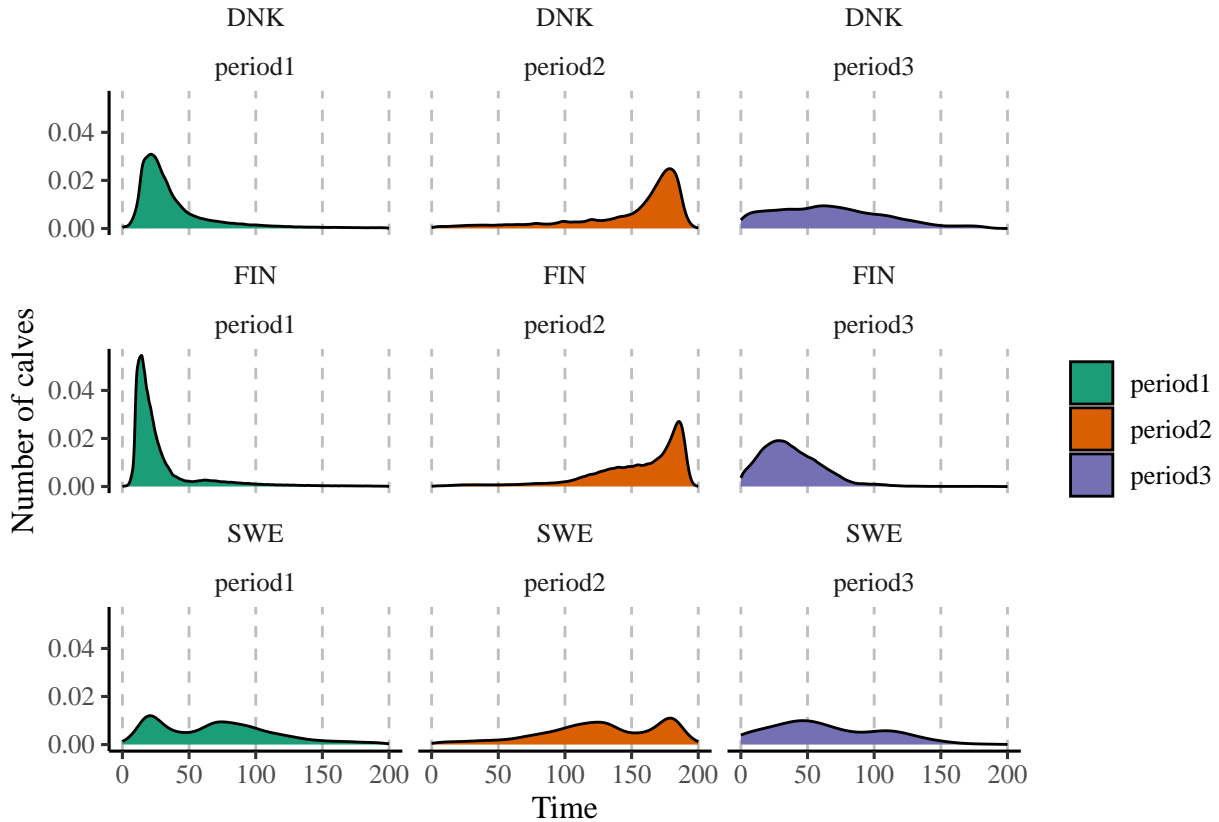


Figure 20: Distribution of the time spent in each herd for transferred animals

5 Genetic evaluation

5.1 Heterogeneous variance adjustments

Given the differences in average levels of youngstock survival between countries, years, sexes and dam breeds observed earlier combined with the binomial nature of the records, variances are expected to be heterogeneous. To address this issue, a data transformation method known as Snell score (Snell 1964) is used. Groups used for the transformation are subclasses of country - sex - year - dam breed. Years with less than 1000 records were regrouped.

However, for Jersey calves in both Sweden and Finland, even after grouping all years together, the minimum requirement of 1000 records could not be met (see Table 14). Consequently, the records of Jersey calves born in both countries were excluded from the evaluation.

The Snell transformed survival data will be referred to as snP1 for period 1 and snP2 for period 2. Figures 21 and 22 display the SD distribution in both periods, revealing an increase in variance after the Snell transformation, while the pattern across years remains unchanged.

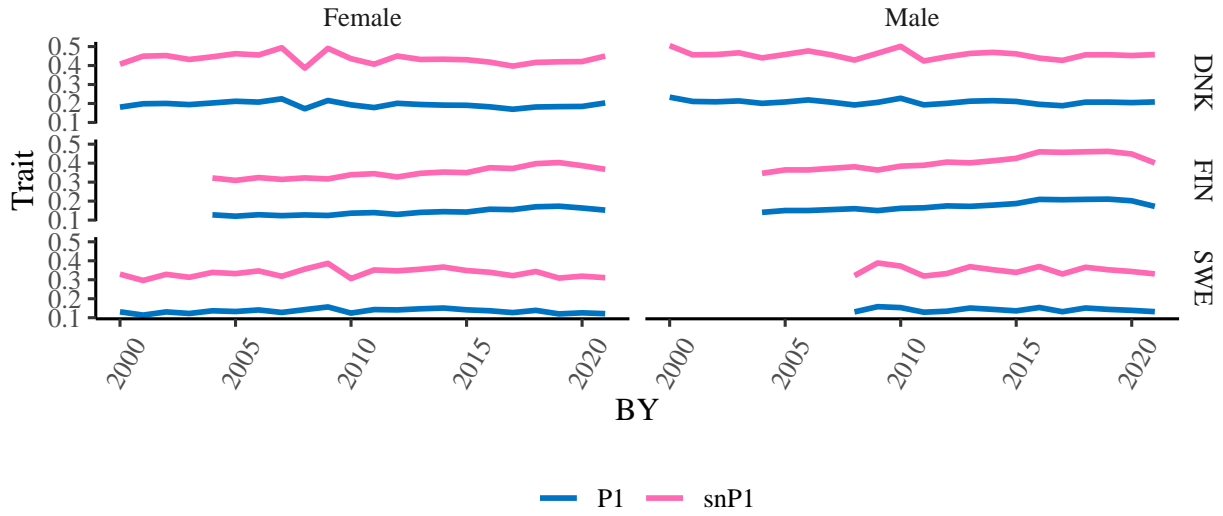


Figure 21: SD distribution of youngstock survival in period 1 before and after the Snell transformation

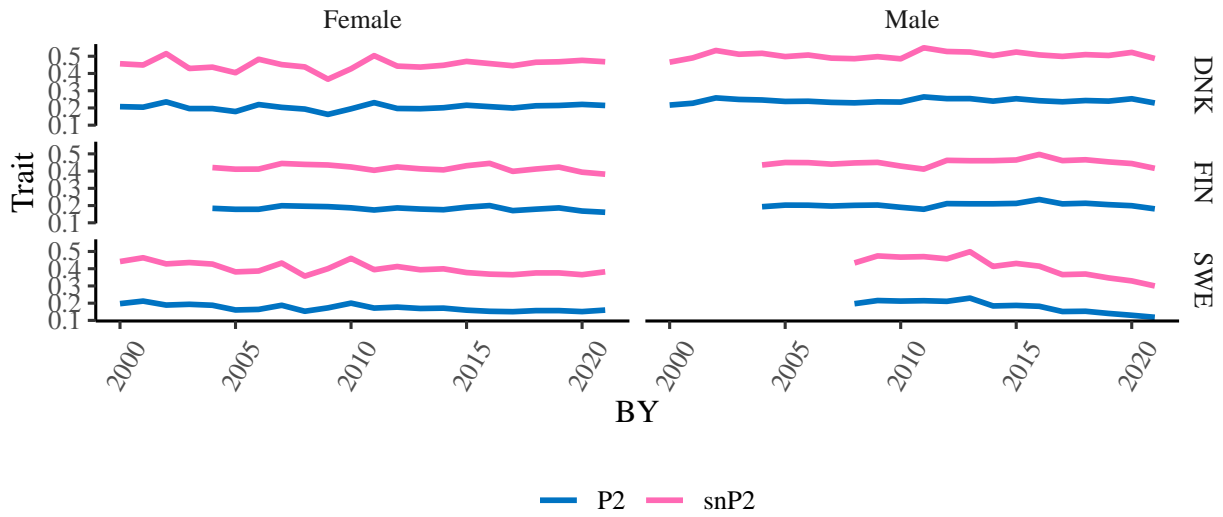


Figure 22: SD distribution of youngstock survival in period 2 before and after the Snell transformation

Table 14: Number of Jersey crosses per year in Sweden and Finland

Year	FIN		SWE	
	Females	Males	Females	Males
2000	0	0	7	0
2001	0	0	8	0
2002	0	0	5	0
2003	0	0	2	0
2004	0	0	8	0
2005	0	0	6	0
2006	0	0	12	0
2007	0	0	14	0
2008	0	0	12	14
2009	0	0	6	3
2010	1	1	6	4
2011	1	1	7	4
2012	1	3	5	5
2013	6	7	7	12
2014	14	14	14	8
2015	36	33	11	21
2016	58	70	24	34
2017	72	78	32	33
2018	95	126	54	48
2019	134	137	54	49
2020	149	139	57	65
2021	113	124	44	56

5.2 The model

As for the other BxD NAV traits, the model used for the evaluation is a multi-trait sire model, including a fixed effect of sire breed to adjust for systematic differences between beef sire breeds, a fixed effect of breed and birth year of dam to adjust for the genetic trend in the dairy breeds and not accounting for heterosis. The selection of the environmental effects draws inspiration from two main sources: the existing NAV routine model for YSS in dairy breeds and the current Danish model for evaluating YSS in BxD crossbreds.

Fixed effects included in the model are listed below.

- Country – herd – year of birth of calf
- Country – year – month of birth of calf
- Country – year – sex of calf
- Country – parity of dam
- Breed – year of birth of dam
- Breed of (beef) sire
- Country – transfer - 5 birth years (only for period 2)

5.2.1 Defining transfer and herd for period 2

As discussed earlier in this document, including a transfer effect in the model for period 1 may introduce a bias as dead calves can not be transferred. Thus, it was decided to include the transfer effect only for period 2.

For the purpose of this study, two definitions of the transfer effect and the herd for period 2 were examined:

- Definition 1: Following the Danish BxD evaluation for YSS, the transfer effect is defined as a binary variable with a value of 1 if the calf was transferred to another herd during the first 200 days and 0 if no transfer occurred during that period. The herd for period 2 is then defined as the one where the calf spent the majority of its life within the first 200 days.
- Definition 2: The transfer is defined as a binary variable equal to 1 if the calf was transferred during the first 100 days and 0 otherwise. The herd for period 2 in this case is simply the herd to which the calf is first transferred and will be referred to as “Next herd”.

Both definitions were tested and compared against each other. While Definition 1 offers the advantage of considering the most meaningful herd for period 2, accounting for cases where a calf may be transferred to multiple herds in a short span of time, it demands precise and complete transfer data, which may not always be available. On the other hand, Definition 2 is simpler to implement and requires less demanding transfer data.

Upon comparison, it was found that both definitions of the herd for period 2 resulted in the same herd for 95% , 98% and 98% of the transfer cases in Denmark, Finland, and Sweden, respectively. Given the high overlap between both definitions, definition 2 was preferred due to its simplicity.

5.2.2 Contemporary groups

Contemporary groups were constructed as Country - Birth herd - year for period 1 and Country - Next herd - year for period 2. To ensure sufficient records per class, small contemporary groups were combined based on the herd, aiming for a minimum of three records per group. If there were fewer than three beef \times dairy crossbreds over the entire time period in a herd, the records of that herd were removed. This procedure was applied separately for period 1 and period 2 records.

5.3 Test evaluation using the Danish routine BxD genetic parameters

In a first step, genetic parameters used in the former routine Danish BxD evaluation for YSS were used to run a test evaluation. The purpose from this first step was to compare both

evaluations and assess their correlation. To ensure compatibility, variances were re-scaled to fit the Snell transformation. Data from all countries and sire breeds were included.

DMU software (Madsen and Jensen 2013) was used to solve the mixed model equations. More details about the evaluation and software can be found in BxD final report as we followed exactly the same set-up and used the same modules as for the other traits (Fikse et al. 2020).

5.3.1 Phenotypic data

Before proceeding with the evaluation, a comparison of the Danish phenotypic data (which is common between both evaluations) was conducted. The objective was to identify any potential discrepancies or differences in the data between the evaluations.

5.3.1.1 Total number of records

Compared to the Danish evaluation, the final dataset in the NAV test evaluation contained 62755 more Danish records (Figure 23). The reasons for this difference can be attributed to two factors:

- 1) Exclusion of calves born from first parity dams: In the Danish evaluation, calves born from first parity dams were excluded from the phenotypic file. This edit was implemented due to the limited number of heifers used for BxD crossbreeding in Denmark and accounts for approximately 14% of the missing phenotypic records.
- 2) Filtering based on death/slaughter event registration: The Danish data only include animals that have a death or slaughter event registered. Ignoring this filter in the NAV test evaluation resulted in approximately 60 000 additional Danish records being included in the current project. The motivation behind this filter is not known but one possible reason could be to exclude animals that are kept for other purposes, such as suckler cows, which may be managed under different production conditions. However, in the current project, such cases are expected to be rare, and those females would be kept in separate herds from those considered here. Applying the Danish filter could cause a significant delay in obtaining the information from the field, as it would require waiting until animals are slaughtered. Consequently, this filter was skipped in the current project.

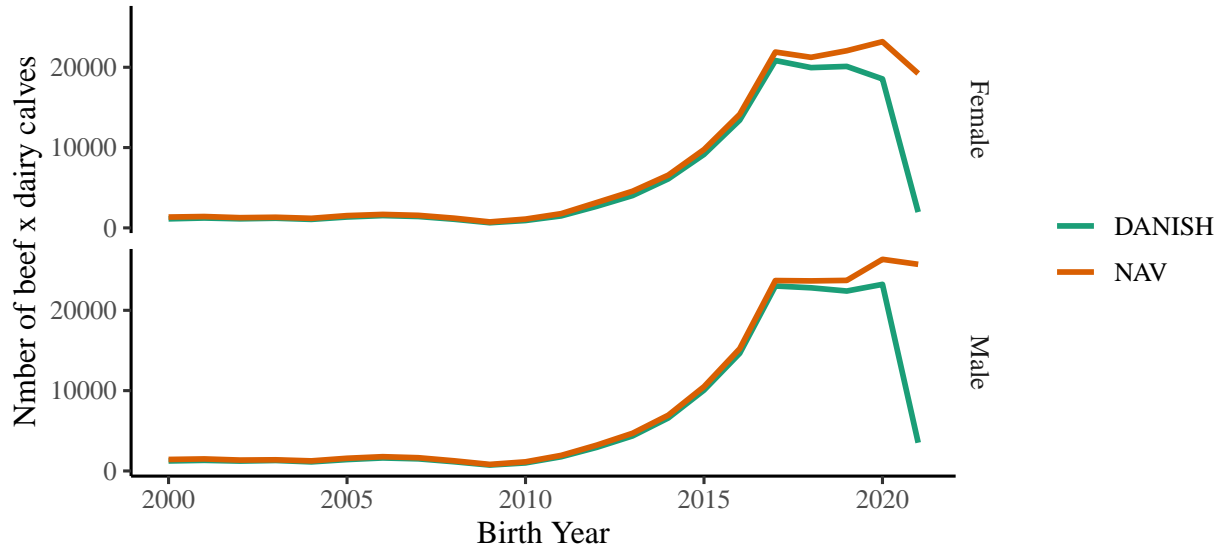


Figure 23: Distribution of the number of records per evaluation, birth year and sex

5.3.1.2 Common records

The correlation between survival variables across evaluation were found to be very high and very few calves had different survival data (Table 15). These minor variations are primarily due to differences in data processing approaches between the NAV evaluation and the Danish evaluation. In the NAV evaluation, a more rigorous data processing method was employed, which involved the exclusion of data that followed a death event, resulting in a slightly stricter filtering compared to the Danish evaluation.

Table 15: Correlations and counts of survival data.

	Period 1	Period 2
Correlation	0.995	0.999
Number of different phenotypes	119	38

5.3.2 Results

Sires' breeding values were calculated as the sum of the fixed breed effect and the random sire effect. In total 966 sires were evaluated (Table 16) with only 534 among them being common with the current routine danish BxD evaluation.

The correlations of breeding values from both evaluations were 0.78 for period 1 and 0.85 for period 2 (Figures 24 and 25). The correlations within sire breed are presented in Table 17.

Table 16: Number of sires per sire breed

sirebreed	N
SIM	284
BBL	151
LIM	130
CHA	123
AAN	96
HER	77
BAQ	73
INR	9
HLA	8
PIE	7
GLW	3
BSH	2
WAG	2
SAL	1

Both BBL and INR breeds have offspring exclusively in Denmark thus higher correlations were expected.

However, it is essential to consider the numerous differences that exist between both evaluations when interpreting the correlation values.

These differences include:

- Different model effects
- Snell transformation in NAV test *vs.* binary data in the Danish evaluation
- Different data processing (in particular data cleaning)
- Different edits on raw data
- Inclusion of data from other countries

Considering these differences, the observed correlations can be deemed acceptable.

Table 17: Correlation between the test evaluation and the Danish BxD breeding values within sire breed

sirebreed	N	Period1	Period2
AAN	42	0.36	0.52
BAQ	36	0.72	0.75
BBL	150	0.86	0.87
CHA	62	0.69	0.81
HER	24	0.76	0.42
INR	9	0.97	0.92
LIM	66	0.78	0.82
PIE	7	0.88	0.60
SIM	138	0.81	0.73

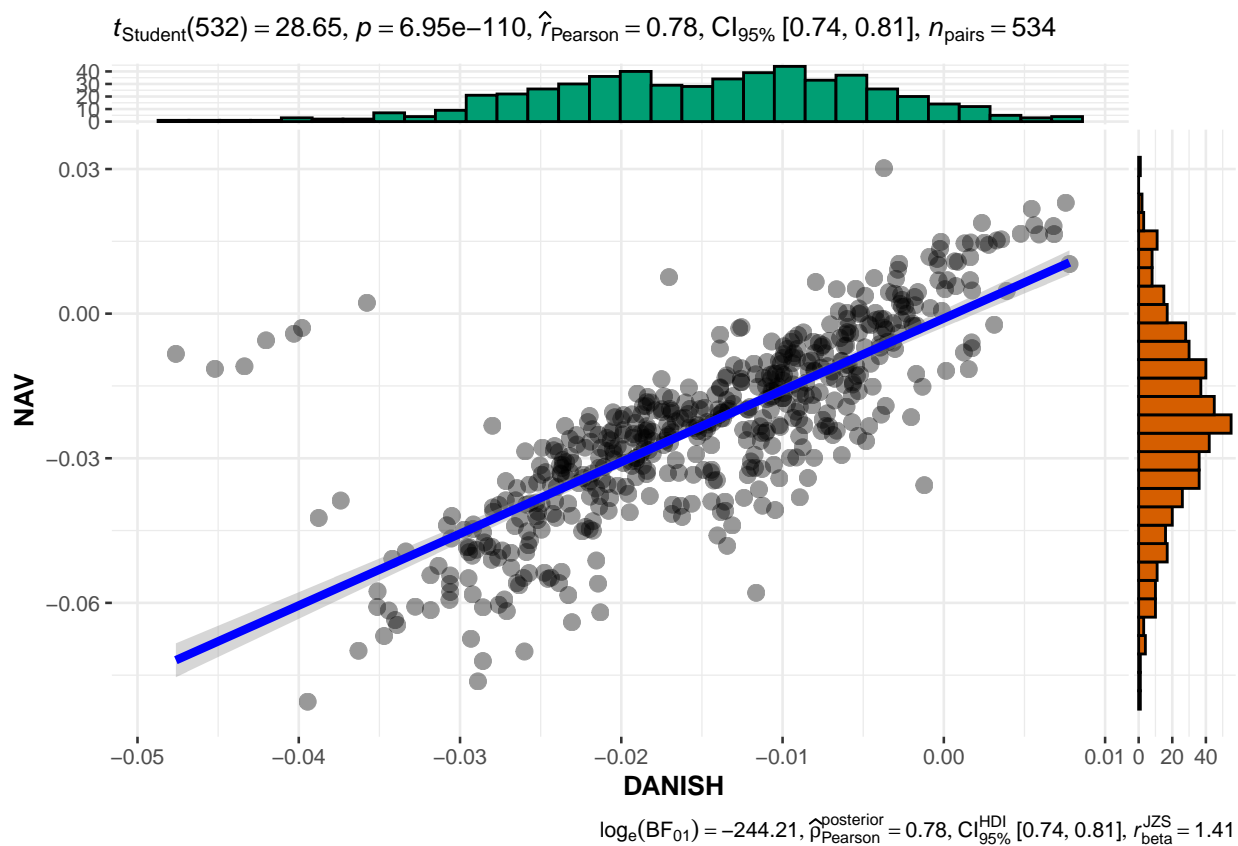


Figure 24: Correlations between the test evaluation and the Danish BxD breeding values for period 1

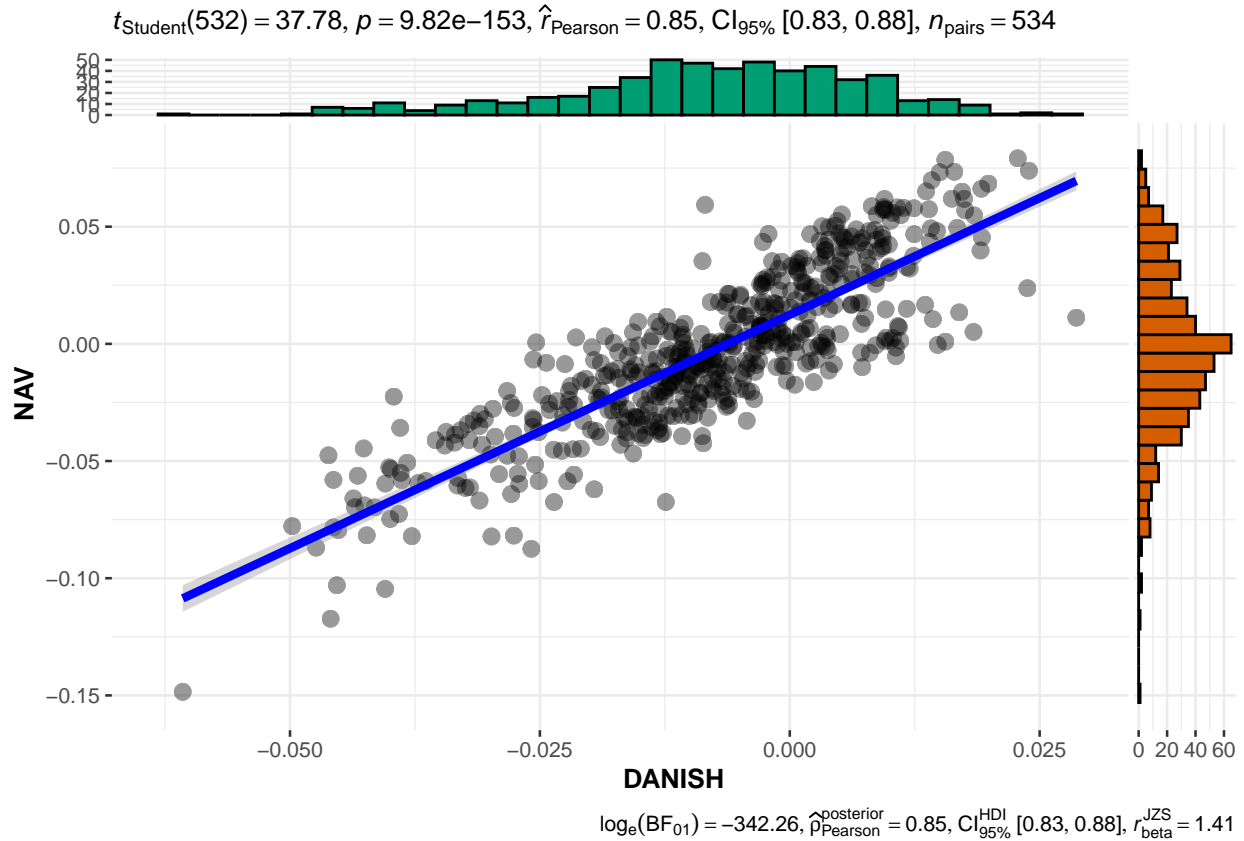


Figure 25: Correlations between the test evaluation and the Danish BxD breeding values for period 2

5.4 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 evaluate the stability of the results, the parameters were separately estimated using data from Denmark only and then solely Holstein data. Given the nature of the data (an animal can not be dead in both periods at the same time), estimating the residual covariance was not possible, and it was therefore set to zero.

The results presented in tables 18 and 19 showed variability across runs and, in general, were lower than the former official Danish BxD parameters.

Table 18: Heritability and correlation

	h2 Trait1	h2 Trait2	Genetic correlation
NAV all countries	0.005 ± 0.0007	0.014 ± 0.0020	0.321 ± 0.0830
NAV only DNK	0.009 ± 0.0018	0.021 ± 0.0031	0.052 ± 0.1200
NAV only Holstein	0.007 ± 0.0010	0.012 ± 0.0020	0.302 ± 0.1070
Danish BxD	0.012	0.022	fixed to be 0.5

Table 19: Phenotypic variance*

	Trait 1	Trait 2
NAV all countries	0.162 ± 0.0000	0.2 ± 0.0004
NAV only DNK	0.182 ± 0.0005	0.229 ± 0.0010
NAV only Holstein	0.164 ± 0.0000	0.198 ± 0.0000
Danish BxD	0.039	0.042

*Results from NAV and Danish evaluations are on different scales (Snell scores *vs.* binary scores)

Due to the observed instability in the results obtained from the different datasets, the estimated parameters could not be used directly. Consequently, after thorough discussion, the working group reached a decision to use the following parameters instead:

Table 20: Final parameters

h2 Trait1	h2 Trait2	Genetic correlation
0.01	0.015	0.3

Since the current analysis involves a sire model where the most interesting bulls being those with substantial offspring numbers, adjusting the heritability from 0.005 to 0.01 is not expected to significantly impact the sires' ranking.

5.5 Breeding values

Once the genetic parameters estimated, a new genetic evaluation including data from all countries and breeds was then performed using the final parameters shown in Table 20. As

in the previous test, the breeding values shown here were calculated as the sum of the fixed breed effect and the random sire effect.

Figures 26 and 27 present a boxplot summarizing the breeding values per sire breed for periods 1 and 2, respectively. In each graph, the central box in each group represents the interquartile range (IQR) of the data, with the horizontal line inside indicating the median breeding value. The lower and upper whiskers extend to the minimum and maximum values within 1.5 times the IQR, respectively. Data points outside this range are identified as outliers, representing sires with extreme breeding values compared to the rest of the population.

The graphs provide an insightful overview of the distribution of breeding values across different sire breeds, highlighting both the genetic variations among breeds and the variability within each breed. The results underscore the importance of multiple breed evaluation, highlighting that breed selection alone may not suffice. Instead, farmers should pay close attention to individual bulls to make their breeding decisions.

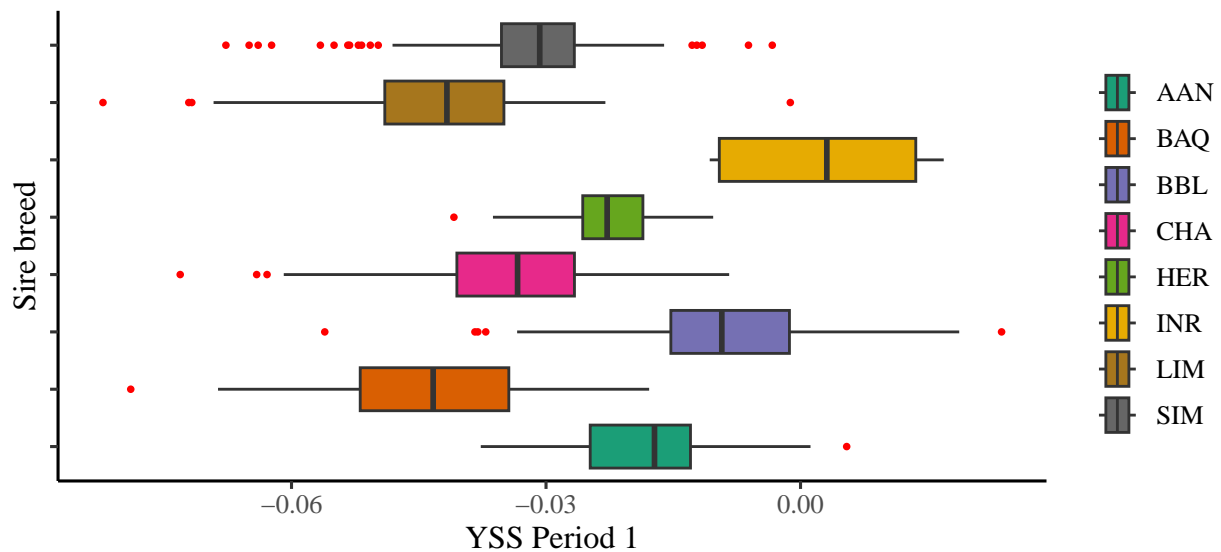


Figure 26: Boxplot of YSS breeding values for Period 1 per sire breed

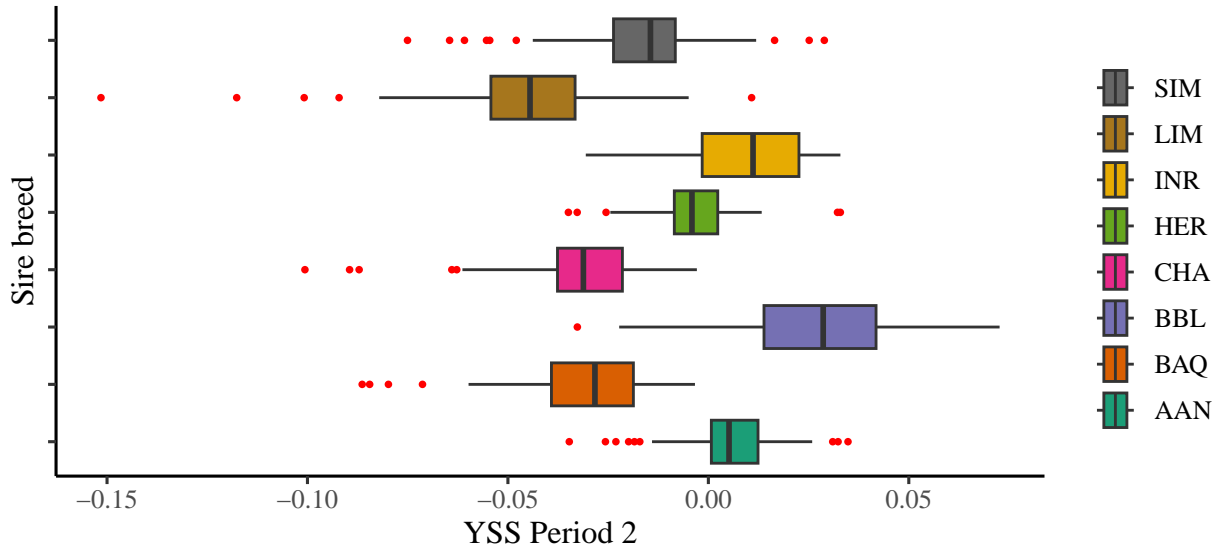


Figure 27: Boxplot of YSS breeding values for Period 1 per sire breed

When evaluating the genetic level evolution per birth year, the results demonstrate a flat trend for all sire breeds for both periods (Figures 28 and 29). These results are expected in the absence of a current selection program on YSS.

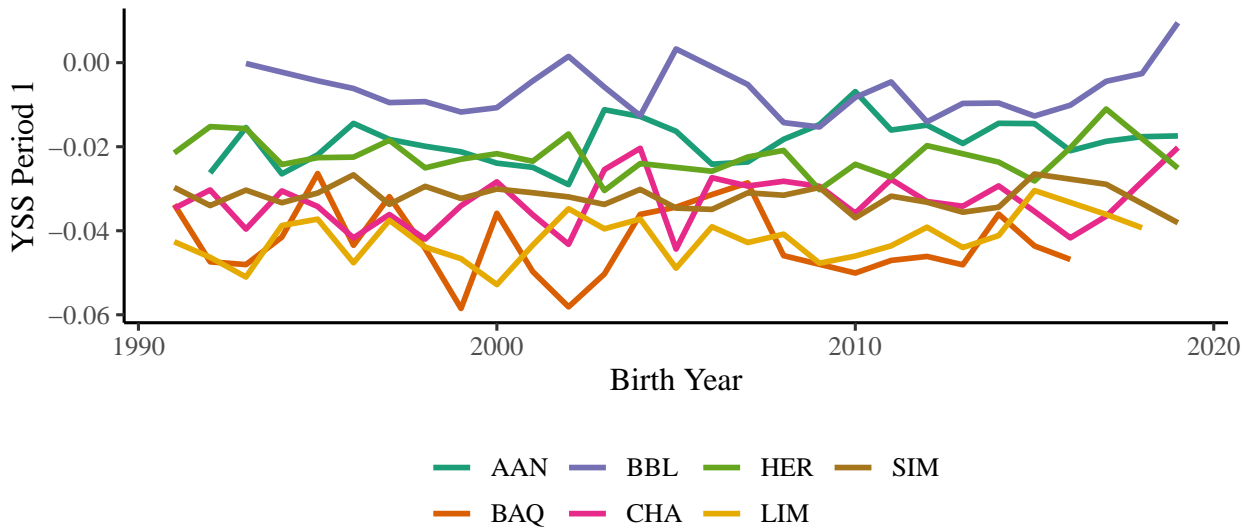


Figure 28: Genetic Trend per sire breed for Period 1

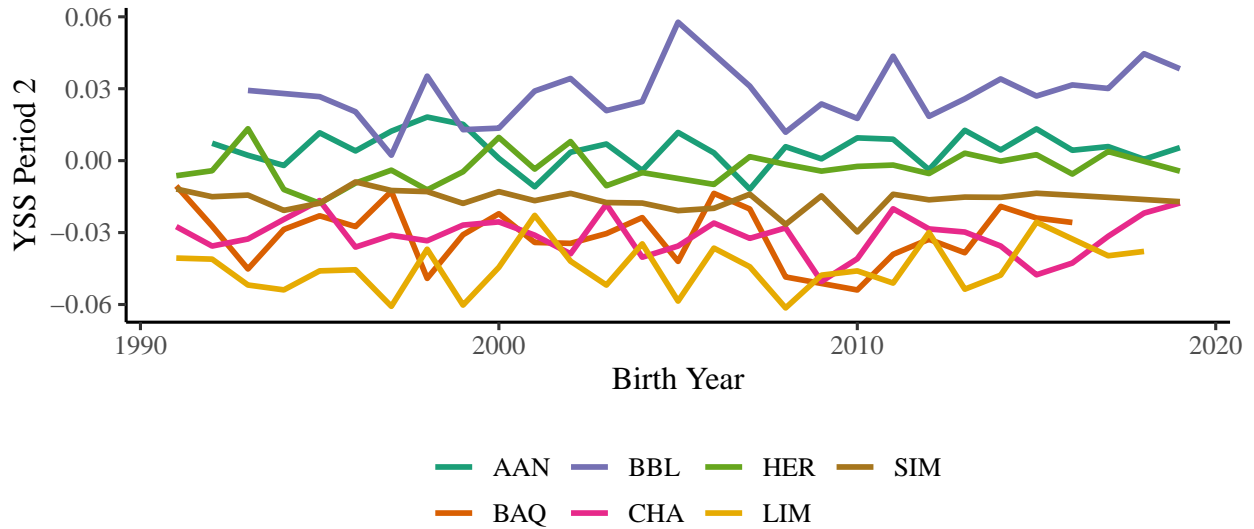


Figure 29: Genetic Trend per sire breed for Period 2

5.6 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.

Because of the low heritability of YSS, reliabilities were in general low but higher for period 2 compared to period 1 and that is because of the higher heritability associated with that trait (Figure 30). Reliabilities within sire breed (Figures 31 and 32) reveal that in general, less than 50% of the sires have a reliability higher than 50%. For the smaller breeds (PIE, HLA and GLW) none of the sires crossed this threshold.

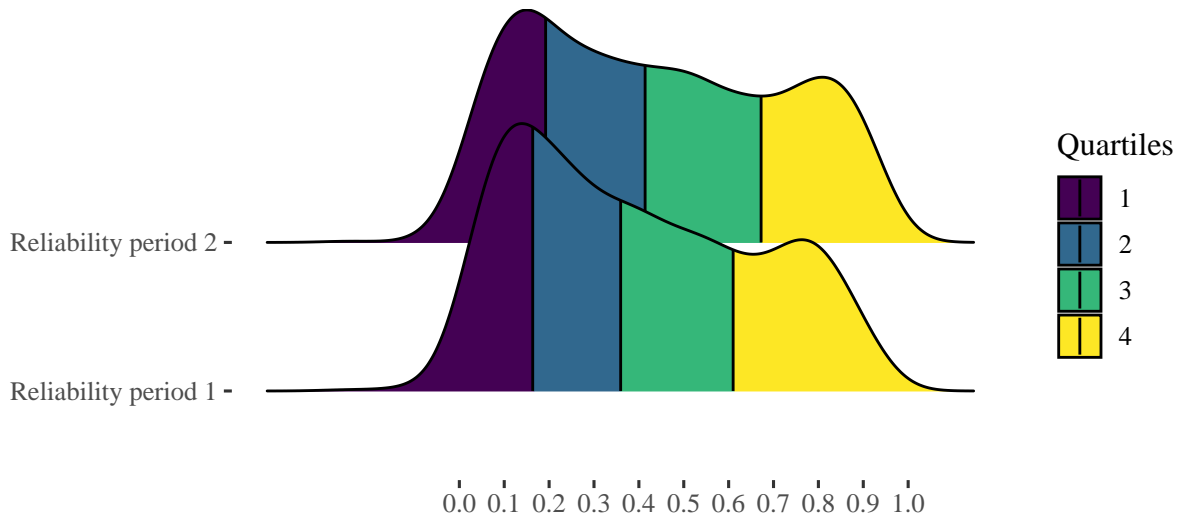


Figure 30: Reliability of breeding values for each period

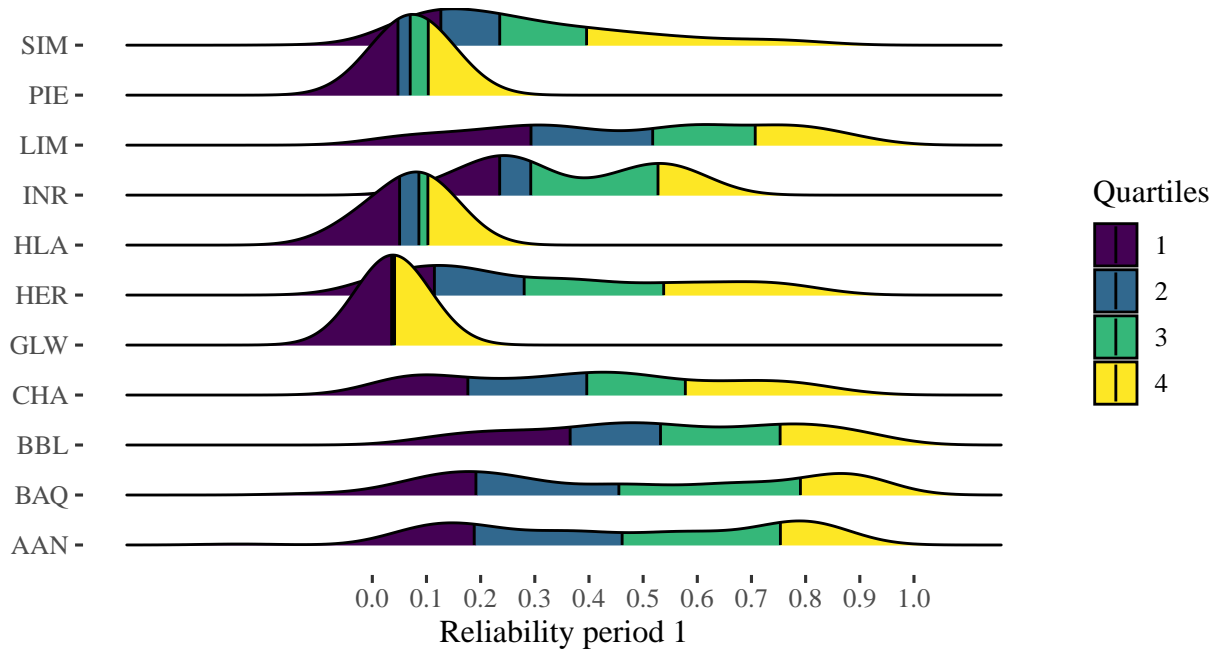


Figure 31: Reliability per sire breed, period 1

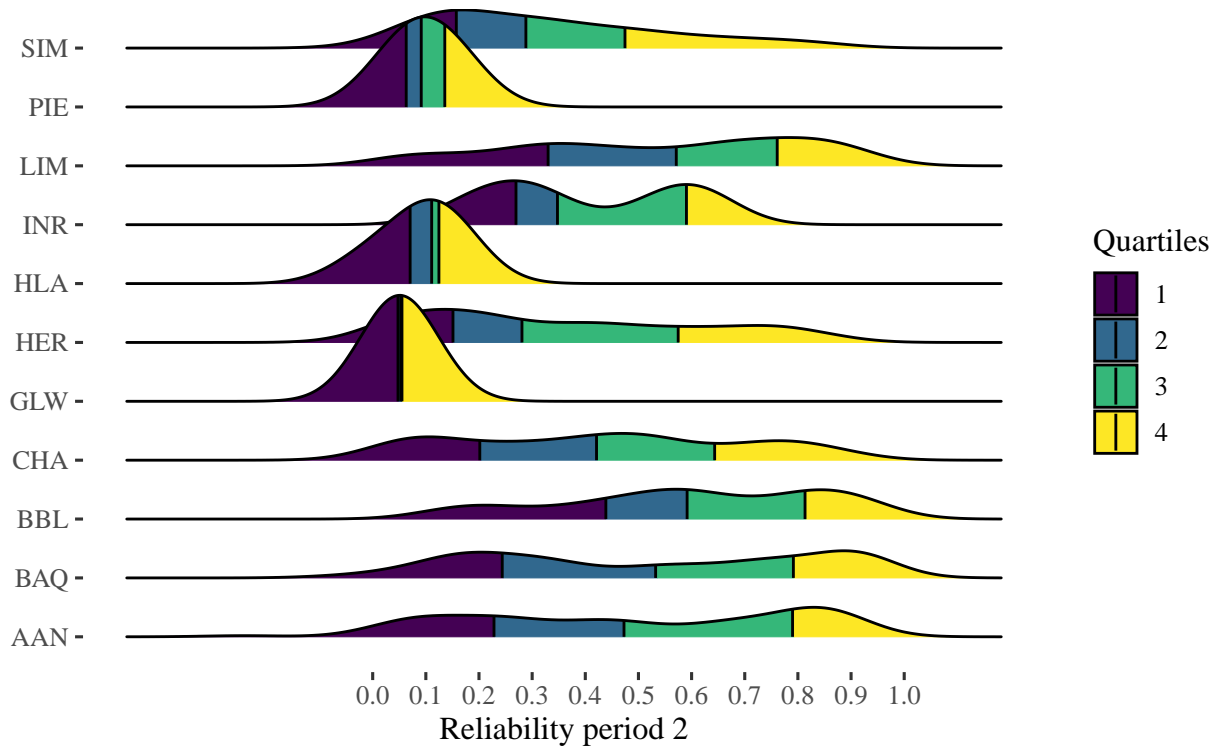


Figure 32: Reliability per sire breed, period 2

5.7 Solutions of the sire breed fixed effect

The solutions for the sire breed fixed effect, relative to SIM breed solutions are represented below (Figure 33). The graph clearly illustrates significant variations between breeds, with BBL, INR, and AAN exhibiting the highest solutions and Limousine showing the lowest.

Interestingly, despite these differences in breed solutions, certain LIM sires may still outperform some BBL sires in terms of their rankings (Figures 26 and 27). This observation emphasizes the powerful advantage of utilizing the BxD multibreed NAV evaluation, which allows for direct comparisons of sires from different breeds based on their individual breeding values. This approach shifts the focus from merely considering one breed over another to a more comprehensive evaluation of sires' genetic potential across diverse breeds.

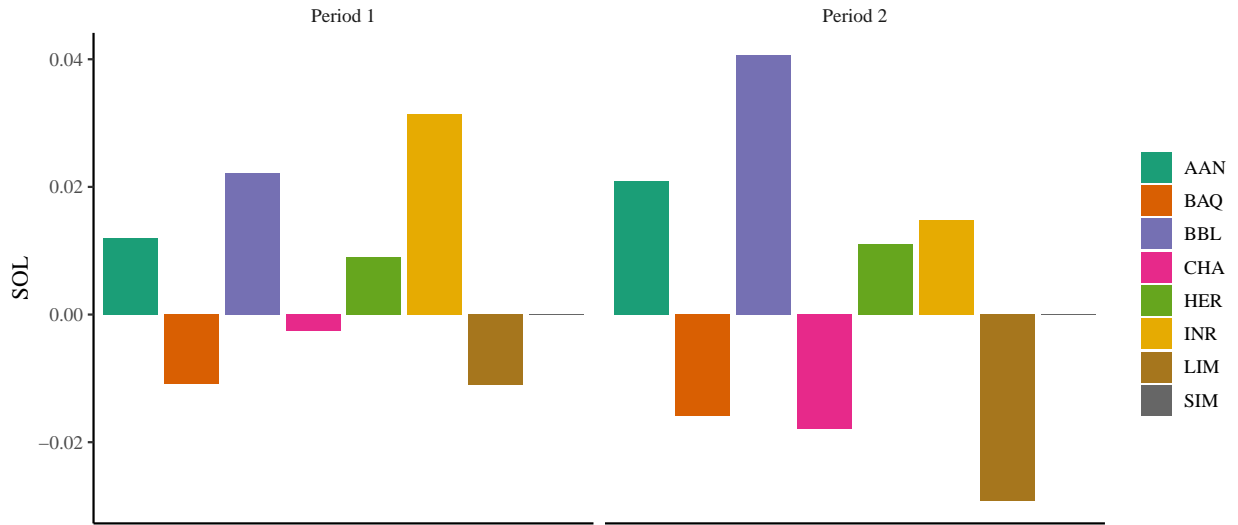


Figure 33: Solutions for sire breed fixed effect for period 1 and 2

5.8 Solutions of the breed - birth year of the dam fixed effect

The solutions for the breed – birth year of the dam fixed effect show a flat trend over the years (Figure 34) reflecting a lack of genetic progress in dairy young stock survival in the Nordic countries over the last 20 years.

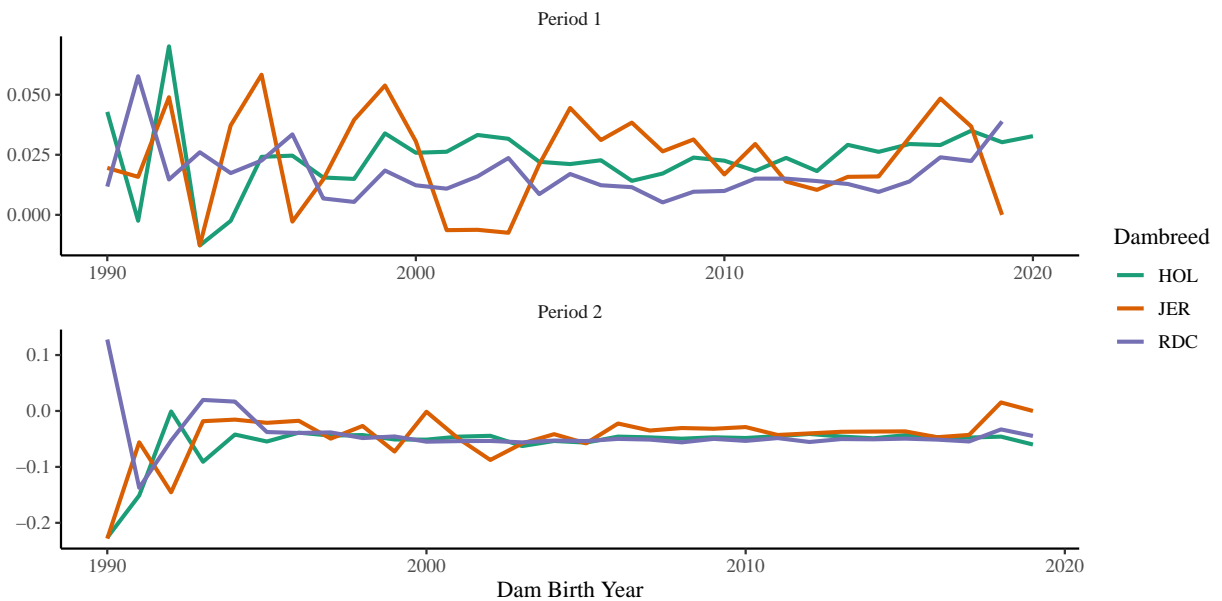


Figure 34: Solutions of the dam breed * birth year fixed effect for period 1 and 2

6 Validation of the breeding values

6.1 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.

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:

- 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).

6.2 Results

The comprehensive validation results are elaborated upon in the annex at the end of this document. With only a few exceptions to consider, the overall outcome is good, showcasing correlations that are either in close alignment with, or at times, even surpassing the expected ones.

One exception that warrants attention involves the behavior of BBL bulls when applied to RDC cows as opposed to Holstein cows (Figures 39 and 40). Nevertheless, the divergent outcomes can be easily clarified by the substantial loss of information resulting from the omission of the Holstein dam breed. It is worth noting that the predominant utilization of the BBL breed is on Holstein cows in Denmark.

Yet another exception worth noting is the distinctive behavioral pattern exhibited by BAQ bulls in Sweden, which stands in obvious contrast to the trends witnessed in the other countries. Despite considering only sires with a reliability of over 50%, the correlations remained notably low (Tables 28 and 29). However, in most of the cases, the Swedish sire means were based on a very small number of progeny while the same sires had much more offspring in Finland (Table 21). The peculiar performance of BAQ bulls in the Swedish context can be attributed to the insufficient data available for segregating sires on the Swedish scale. It is the information sourced from Finland that helps reaching that purpose.

Table 21: Number of offspring of the BAQ bulls in Sweden compared to Finland

Sire	Number of offspring	
	SWE	FIN
1	1	15777
2	1	1109
3	1119	3940
4	26	1948
5	28	3
7	212	4866
8	1	3300
9	3	15974
10	1	7965
11	12	490
12	84	19265
13	2	1391
14	149	17874
15	1	0
16	29	0

7 Relative breeding values

7.1 Standardization of breeding values

As previously indicated, the breeding values presented in the preceding sections of this report are computed by adding the sire breed fixed effect solution to the random sire effect. Subsequently, similar to the methodology employed for other BxD traits as outlined in (Fikse et al. 2020), these breeding values are then standardized to a mean of 100 and a standard deviation of 10. The genetic base animals constitutes of 2-5 year old crossbreds born after beef breeds which can be marketed in all 3 countries (This excludes essentially BBL breed from the base).

Figure 35 below, shows the distribution of the relative breeding values for both periods. Averages per sire breed are shown in Table 22.

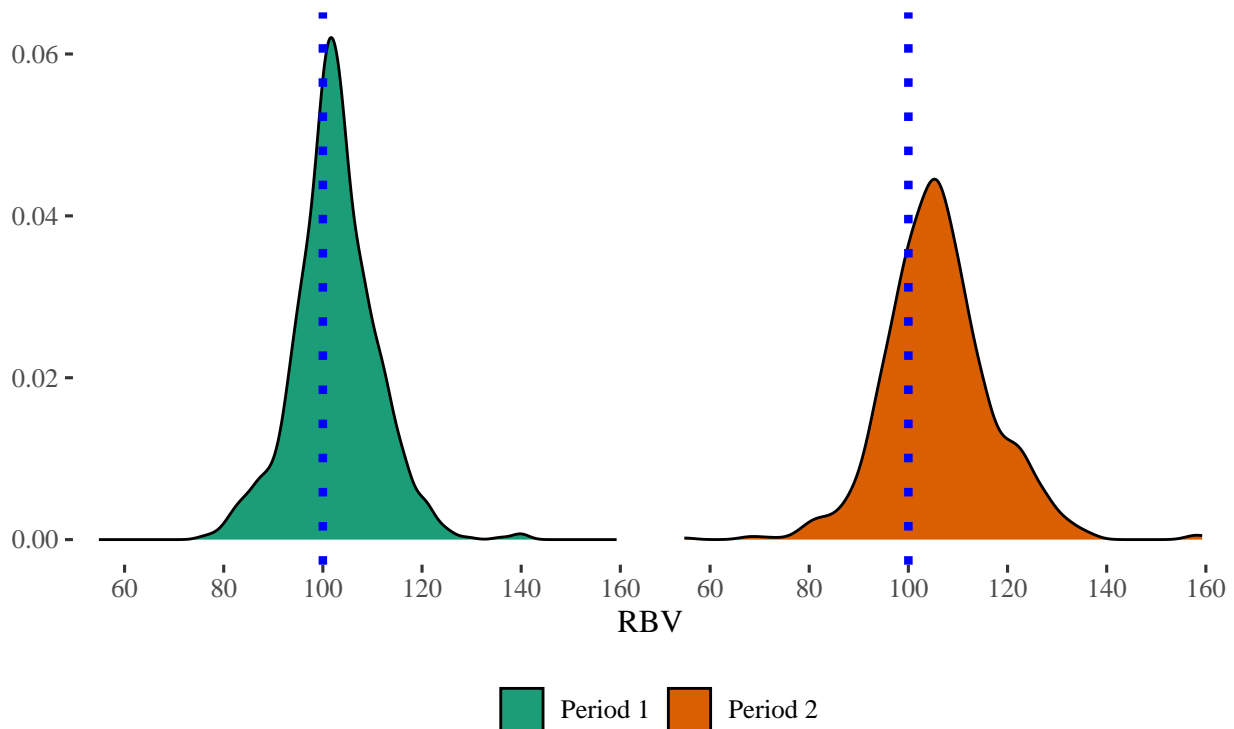


Figure 35: Distribution of the relative breeding values for both periods

7.2 Publication

Besides the EBVs for youngstock survival in the two periods (YSS1 and YSS2), it was decided to publish a third combined breeding value (YSS) for youngstock survival that is constructed given equal weight to the two single EBVs. The current weight utilized for the computation

Table 22: Average RBV per sire breed and period

Sire breed	N	Period 1	Period 2
AAN	110	107.83	112.01
BAQ	76	94.91	99.25
BBL	157	112.06	119.92
CHA	125	99.67	99.72
HER	79	105.41	109.65
LIM	133	95.21	93.68
SIM	290	100.55	104.22

of this combined index is provisional and is subject to revision upon the completion of the estimation process for economic weights associated with youngstock survival.

Breeding values for youngstock survival are made public under the following conditions:

- A bull’s EBV reliability is equal to or exceeds 50% for YSS2, or there are at least 500 offspring with YSS2 phenotypes in the bull’s progeny dataset.
- The bull possesses official EBVs for Calving and Growth traits.

7.3 Inclusion in the NBDI

Given its economic significance, youngstock survival assumes a crucial role and warrants its incorporation into the NBDI (Nordic Beef on Dairy Index). The process of estimating the economic values attributed to youngstock survival is currently ongoing, with the aim of revising the weights employed in calculating the combined index for YSS and including it in the NBDI by the year 2024.

8 References

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Appendix: Validation results

8.1 Correlations with sire phenotypic means

Table 23: Correlations between EBVs and sire phenotypic means

Sirebreed	<50 offspring			[50,300] offspring			>300 offspring		
	N	Period 1	Period 2	N	Period 1	Period 2	N	Period 1	Period 2
AAN	13	0.83	-0.3	34	0.71	0.63	49	0.79	0.44
BAQ	18	0.58	0.36	18	0.74	0.54	37	0.81	0.68
BBL	0			54	0.7	0.68	94	0.61	0.78
CHA	25	0.26	0.41	45	0.71	0.6	53	0.67	0.81
HER	24	0.58	0.45	26	0.62	0.62	27	0.63	0.82
HLA	5	-0.28	0.69	0			0		
INR	0			5	0.7	0.93	4	0.95	0.75
LIM	20	0.19	0.21	39	0.78	0.53	71	0.75	0.83
PIE	4	0.58	0.97	0			0		
SIM	102	0.5	0.53	129	0.7	0.64	53	0.73	0.56

A. One country at a time *vs.* all countries

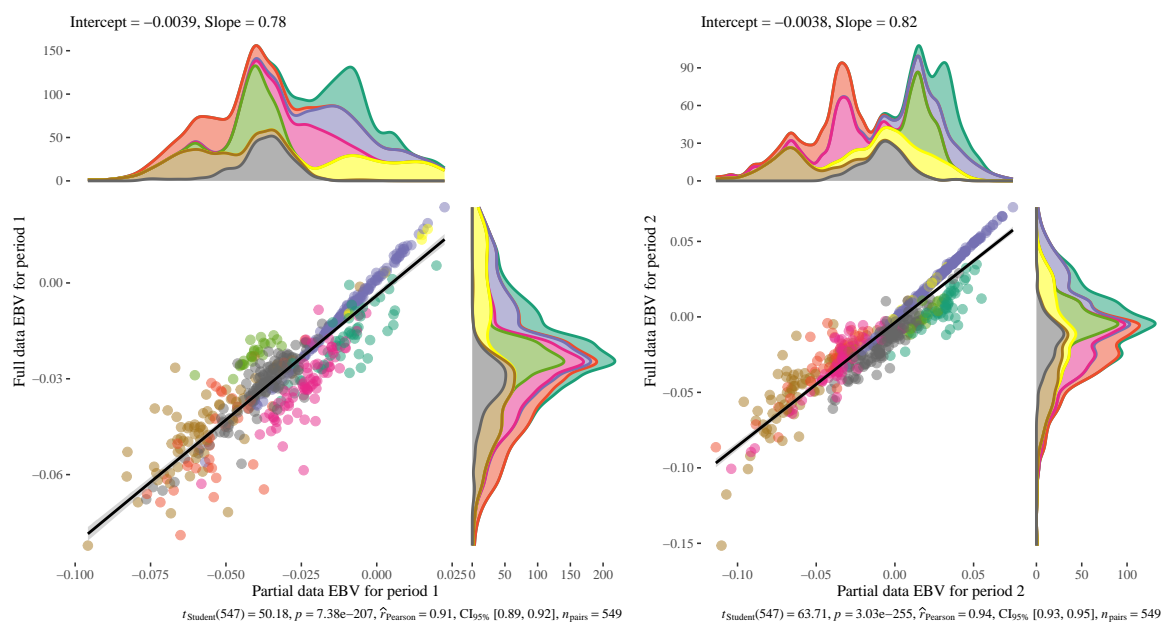


Figure 36: DNK: Regression results when all breeds are included

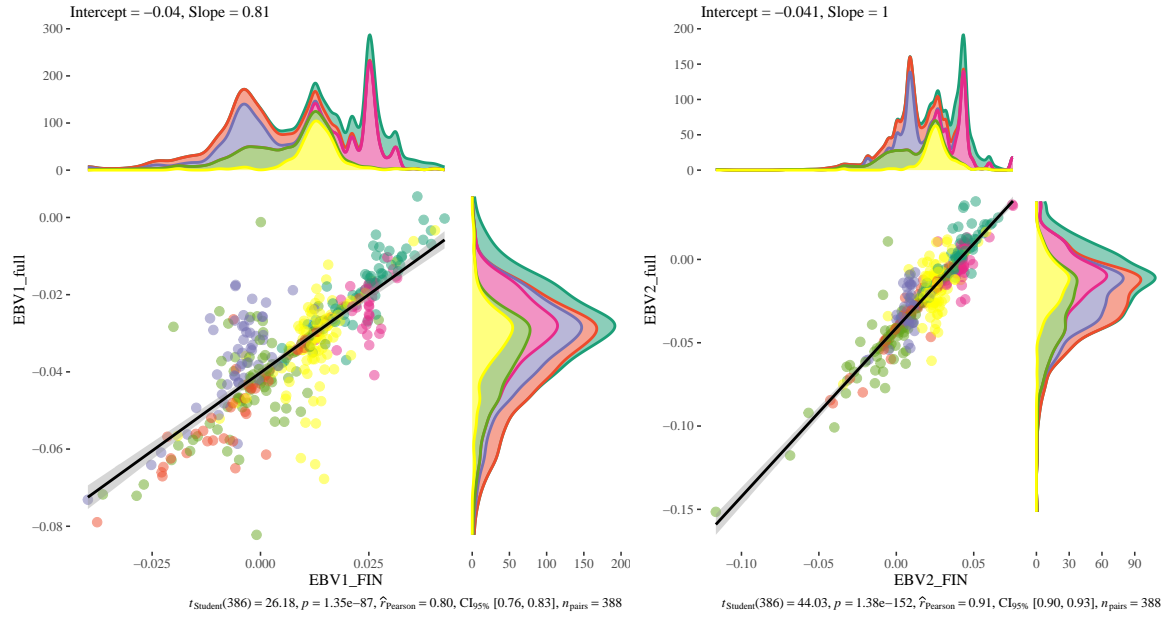


Figure 37: FIN: Regression results when all breeds are included

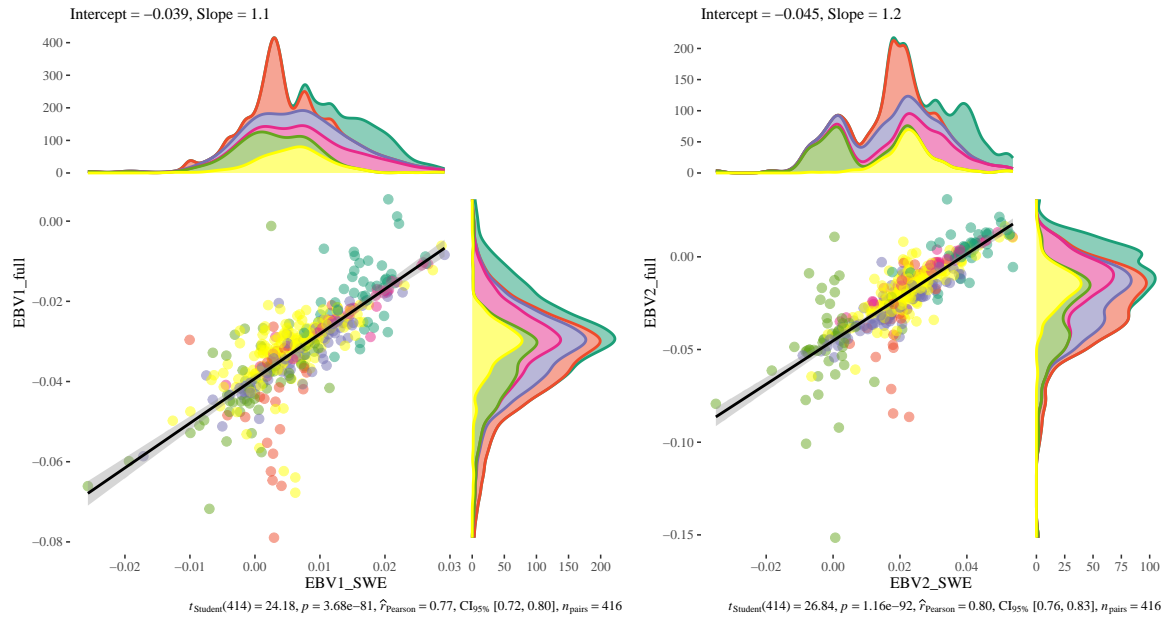


Figure 38: SWE: Regression results when all breeds are included

Table 24: 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	49	-0.01 ± 00.00	00.75 ± 00.08	0.80	0.66	-0.02 ± 00.00	00.91 ± 00.10	0.79	0.63
BAQ	37	-0.00 ± 00.01	00.84 ± 00.14	0.72	0.65	00.01 ± 00.00	00.88 ± 00.08	0.88	0.66
BBL	151	00.00 ± 00.00	01.00 ± 00.00	1.00	0.96	-0.00 ± 00.00	01.00 ± 00.00	1.00	0.94
CHA	72	-0.01 ± 00.00	01.01 ± 00.08	0.84	0.71	00.00 ± 00.00	00.99 ± 00.05	0.92	0.69
GLW	3	00.00 ± 00.00	00.88 ± 00.12	0.99	0.60	-0.08 ± 00.06	01.51 ± 00.47	0.96	0.59
HER	25	-0.00 ± 00.00	00.52 ± 00.08	0.81	0.64	-0.02 ± 00.00	00.99 ± 00.10	0.89	0.65
HLA	3	-0.13 ± 00.19	-0.33 ± 00.93	-0.33	0.46	00.02 ± 00.00	-0.20 ± 00.10	-0.90	0.45
INR	9	00.00 ± 00.00	00.98 ± 00.02	1.00	0.94	-0.00 ± 00.00	00.97 ± 00.01	1.00	0.92
LIM	66	-0.00 ± 00.00	00.73 ± 00.07	0.80	0.77	00.01 ± 00.01	01.01 ± 00.08	0.83	0.78
PIE	7	-0.00 ± 00.00	00.98 ± 00.02	1.00	0.82	00.00 ± 00.00	00.98 ± 00.04	1.00	0.80
SIM	140	00.00 ± 00.00	00.88 ± 00.03	0.91	0.77	-0.01 ± 00.00	00.95 ± 00.04	0.91	0.77

Table 25: 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	24	-0.01 ± 00.00	00.65 ± 00.13	0.74	0.60	-0.02 ± 00.01	00.85 ± 00.18	0.71	0.56
BAQ	14	-0.01 ± 00.02	00.74 ± 00.30	0.58	0.61	00.01 ± 00.01	00.87 ± 00.14	0.87	0.61
BBL	82	00.00 ± 00.00	01.00 ± 00.01	1.00	0.97	-0.00 ± 00.00	00.99 ± 00.00	1.00	0.96
CHA	29	-0.01 ± 00.00	01.00 ± 00.11	0.87	0.72	00.00 ± 00.00	00.98 ± 00.07	0.93	0.68
HER	3	-0.01 ± 00.01	00.35 ± 00.20	0.86	0.46	-0.03 ± 00.01	02.26 ± 00.73	0.95	0.44
INR	3	00.00 ± 00.00	00.91 ± 00.09	0.99	0.96	-0.00 ± 00.00	01.00 ± 00.07	1.00	0.95
LIM	35	-0.00 ± 00.01	00.72 ± 00.10	0.78	0.76	00.01 ± 00.01	01.02 ± 00.12	0.84	0.77
SIM	25	-0.00 ± 00.00	00.80 ± 00.09	0.87	0.73	-0.01 ± 00.00	00.90 ± 00.11	0.85	0.74

Table 26: 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	63	-0.04 ± 00.00	00.99 ± 00.07	0.89	0.87	-0.04 ± 00.00	00.99 ± 00.09	0.83	0.87
BAQ	50	-0.04 ± 00.00	00.98 ± 00.06	0.91	0.94	-0.04 ± 00.00	01.05 ± 00.05	0.96	0.93
CHA	50	-0.03 ± 00.00	01.09 ± 00.15	0.73	0.64	-0.04 ± 00.00	00.95 ± 00.15	0.68	0.65
HER	32	-0.04 ± 00.01	00.77 ± 00.29	0.43	0.58	-0.04 ± 00.01	00.91 ± 00.18	0.69	0.60
HLA	6	-0.09 ± 00.04	00.76 ± 01.06	0.34	0.47	00.00 ± 00.02	00.62 ± 00.64	0.44	0.53
LIM	88	-0.04 ± 00.00	00.75 ± 00.10	0.62	0.84	-0.04 ± 00.00	00.98 ± 00.05	0.89	0.82
SIM	105	-0.04 ± 00.00	00.94 ± 00.11	0.63	0.63	-0.04 ± 00.00	00.88 ± 00.10	0.65	0.63

Table 27: 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	42	-0.04 ± 00.00	00.96 ± 00.07	0.90	0.89	-0.04 ± 00.00	00.95 ± 00.10	0.84	0.89
BAQ	32	-0.04 ± 00.00	00.97 ± 00.03	0.99	0.97	-0.04 ± 00.00	01.06 ± 00.03	0.99	0.96
CHA	26	-0.03 ± 00.00	01.09 ± 00.22	0.72	0.70	-0.03 ± 00.00	00.87 ± 00.18	0.70	0.71
HER	15	-0.04 ± 00.01	00.87 ± 00.36	0.56	0.64	-0.04 ± 00.01	00.88 ± 00.23	0.73	0.66
LIM	54	-0.04 ± 00.00	00.78 ± 00.13	0.65	0.86	-0.04 ± 00.00	00.99 ± 00.06	0.92	0.85
SIM	35	-0.04 ± 00.00	00.88 ± 00.16	0.70	0.70	-0.04 ± 00.00	00.91 ± 00.13	0.78	0.71

Table 28: 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	46	-0.03 ± 00.00	00.97 ± 00.25	0.50	0.73	-0.02 ± 00.01	00.66 ± 00.18	0.48	0.68
BAQ	26	-0.05 ± 00.00	00.41 ± 00.70	0.12	0.37	-0.06 ± 00.02	01.38 ± 00.87	0.31	0.35
CHA	67	-0.04 ± 00.00	01.03 ± 00.06	0.90	0.86	-0.05 ± 00.00	00.99 ± 00.07	0.87	0.82
HER	43	-0.04 ± 00.00	00.95 ± 00.04	0.96	0.92	-0.04 ± 00.00	00.98 ± 00.03	0.98	0.88
HLA	6	-0.03 ± 00.01	01.11 ± 00.16	0.96	0.41	-0.11 ± 00.03	01.21 ± 00.29	0.90	0.36
LIM	53	-0.04 ± 00.00	01.00 ± 00.19	0.60	0.64	-0.05 ± 00.00	00.85 ± 00.38	0.30	0.59
SIM	181	-0.04 ± 00.00	00.89 ± 00.08	0.65	0.74	-0.04 ± 00.00	01.09 ± 00.06	0.79	0.70

Table 29: 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	26	-0.03 ± 00.01	00.82 ± 00.42	0.37	0.74	-0.02 ± 00.01	00.53 ± 00.26	0.39	0.70
BAQ	12	-0.04 ± 00.01	00.09 ± 01.27	0.02	0.32	-0.10 ± 00.07	03.06 ± 03.32	0.28	0.31
CHA	20	-0.04 ± 00.00	01.01 ± 00.09	0.94	0.88	-0.04 ± 00.00	00.89 ± 00.13	0.86	0.85
HER	16	-0.04 ± 00.00	00.85 ± 00.10	0.91	0.94	-0.04 ± 00.00	00.97 ± 00.04	0.99	0.91
LIM	28	-0.04 ± 00.00	01.06 ± 00.30	0.56	0.63	-0.04 ± 00.01	00.79 ± 00.64	0.24	0.58
SIM	24	-0.04 ± 00.00	01.01 ± 00.27	0.62	0.83	-0.04 ± 00.00	00.92 ± 00.15	0.79	0.80

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

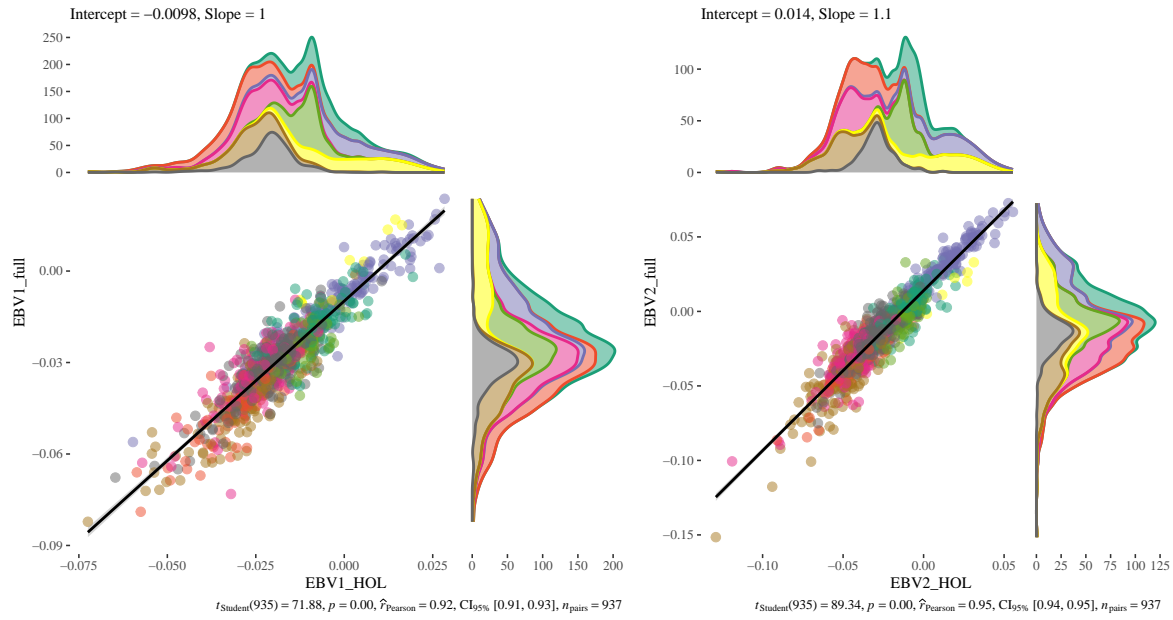


Figure 39: HOLS: regression results when all sire breeds are included

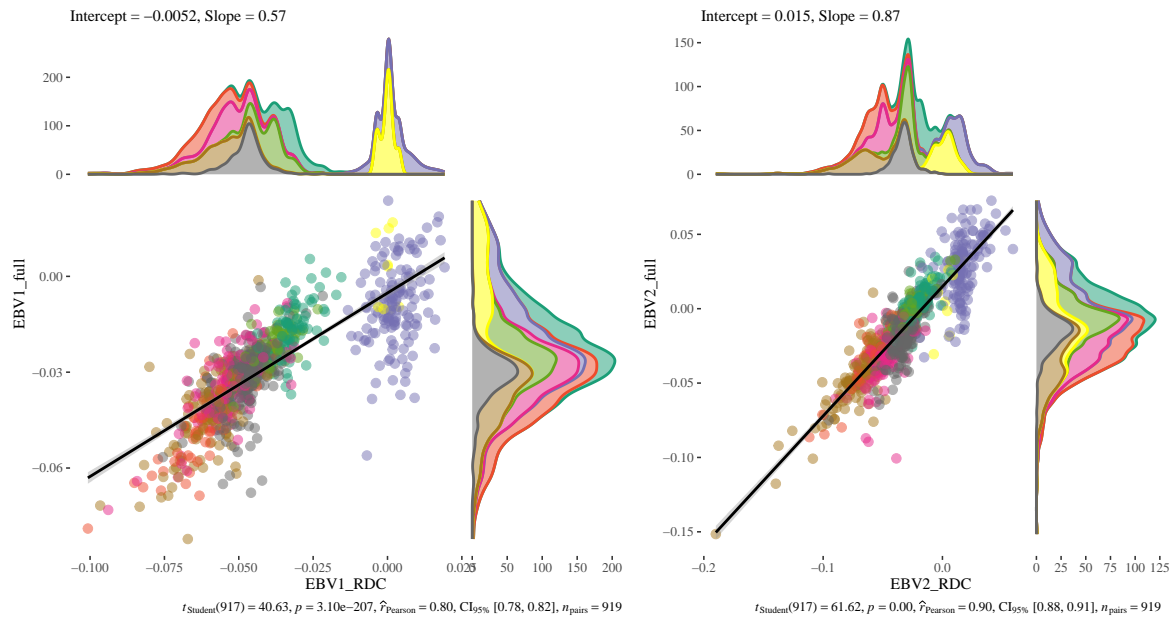


Figure 40: RDC: regression results when all breeds are included

Table 30: 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	95	-0.01 ± 00.00	00.75 ± 00.08	0.70	0.77	00.01 ± 00.00	00.84 ± 00.08	0.72	0.75
BAQ	73	-0.01 ± 00.00	01.04 ± 00.07	0.87	0.85	00.01 ± 00.00	01.10 ± 00.07	0.88	0.84
BBL	151	-0.01 ± 00.00	00.87 ± 00.02	0.94	0.92	00.02 ± 00.00	00.97 ± 00.02	0.97	0.91
CHA	122	-0.01 ± 00.00	00.98 ± 00.07	0.78	0.80	00.01 ± 00.00	00.97 ± 00.07	0.79	0.78
GLW	3	00.05 ± 00.05	01.18 ± 00.67	0.87	0.53	-0.41 ± 00.10	03.51 ± 00.63	0.98	0.51
HER	75	-0.02 ± 00.00	00.68 ± 00.13	0.53	0.67	00.01 ± 00.00	01.22 ± 00.17	0.65	0.65
HLA	8	00.02 ± 00.05	01.05 ± 00.66	0.55	NaN	-0.10 ± 00.04	02.13 ± 00.68	0.79	0.13
INR	9	00.00 ± 00.00	00.97 ± 00.09	0.97	0.88	-0.00 ± 00.00	00.97 ± 00.07	0.98	0.86
LIM	128	-0.02 ± 00.00	00.97 ± 00.05	0.86	0.78	00.02 ± 00.00	01.16 ± 00.07	0.82	0.78
PIE	7	00.02 ± 00.00	01.26 ± 00.23	0.92	0.69	-0.01 ± 00.01	00.85 ± 00.71	0.47	0.67
SIM	284	-0.01 ± 00.00	00.92 ± 00.04	0.84	0.77	00.01 ± 00.00	01.00 ± 00.04	0.85	0.76

Table 31: 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	46	-0.01 ± 00.00	00.70 ± 00.11	0.69	0.81	00.01 ± 00.00	00.80 ± 00.11	0.73	0.81
BAQ	34	-0.01 ± 00.00	00.99 ± 00.08	0.90	0.88	00.01 ± 00.00	01.14 ± 00.10	0.90	0.88
BBL	82	-0.01 ± 00.00	00.86 ± 00.04	0.94	0.94	00.02 ± 00.00	00.95 ± 00.03	0.97	0.93
CHA	41	-0.01 ± 00.00	01.01 ± 00.08	0.89	0.84	00.01 ± 00.00	01.00 ± 00.09	0.88	0.83
HER	22	-0.02 ± 00.00	00.65 ± 00.23	0.54	0.73	00.02 ± 00.01	01.44 ± 00.36	0.66	0.71
INR	3	-0.00 ± 00.00	01.16 ± 00.32	0.96	0.93	-0.00 ± 00.01	00.96 ± 00.43	0.91	0.92
LIM	67	-0.02 ± 00.00	00.95 ± 00.07	0.87	0.81	00.02 ± 00.00	01.22 ± 00.09	0.86	0.81
SIM	45	-0.01 ± 00.00	00.89 ± 00.09	0.84	0.82	00.02 ± 00.00	01.07 ± 00.09	0.88	0.81

Table 32: 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	94	00.01 ± 00.00	00.90 ± 00.10	0.69	0.78	00.02 ± 00.00	00.94 ± 00.09	0.75	0.77
BAQ	72	00.02 ± 00.00	01.07 ± 00.08	0.85	0.84	00.02 ± 00.00	00.96 ± 00.06	0.88	0.83
BBL	140	-0.01 ± 00.00	00.54 ± 00.17	0.27	0.52	00.02 ± 00.00	00.78 ± 00.12	0.48	0.54
CHA	119	00.01 ± 00.00	00.87 ± 00.08	0.73	0.67	00.01 ± 00.01	00.83 ± 00.11	0.58	0.65
GLW	3	-0.17 ± 00.02	-2.36 ± 00.33	-0.99	0.31	-0.30 ± 00.10	02.35 ± 00.54	0.97	0.27
HER	76	00.01 ± 00.00	00.81 ± 00.08	0.75	0.76	00.02 ± 00.00	00.98 ± 00.06	0.88	0.74
HLA	8	00.00 ± 00.02	01.20 ± 00.33	0.83	0.40	00.01 ± 00.00	01.04 ± 00.21	0.89	0.43
INR	9	00.00 ± 00.00	-0.35 ± 01.88	-0.07	0.44	00.00 ± 00.01	01.20 ± 00.91	0.45	0.47
LIM	130	00.01 ± 00.01	00.84 ± 00.09	0.65	0.78	00.01 ± 00.00	00.86 ± 00.05	0.85	0.77
PIE	5	00.02 ± 00.03	00.55 ± 00.71	0.41	0.23	-0.03 ± 00.00	-1.20 ± 00.61	-0.75	0.22
SIM	279	00.00 ± 00.00	00.76 ± 00.07	0.54	0.60	00.01 ± 00.00	00.92 ± 00.06	0.66	0.58

Table 33: 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	46	00.01 ± 00.00	00.87 ± 00.11	0.75	0.85	00.02 ± 00.00	00.90 ± 00.10	0.80	0.84
BAQ	34	00.02 ± 00.00	01.02 ± 00.07	0.92	0.90	00.02 ± 00.00	00.97 ± 00.07	0.92	0.90
BBL	82	-0.01 ± 00.00	00.69 ± 00.19	0.37	0.57	00.02 ± 00.00	00.75 ± 00.14	0.52	0.60
CHA	41	00.01 ± 00.01	00.88 ± 00.13	0.73	0.74	00.01 ± 00.01	00.86 ± 00.20	0.56	0.73
HER	22	00.00 ± 00.00	00.76 ± 00.09	0.88	0.86	00.02 ± 00.00	00.93 ± 00.06	0.96	0.84
INR	3	00.01 ± 00.01	-0.89 ± 02.56	-0.33	0.51	00.02 ± 00.01	00.70 ± 00.48	0.82	0.54
LIM	67	00.01 ± 00.01	00.88 ± 00.11	0.71	0.83	00.02 ± 00.00	00.92 ± 00.06	0.89	0.82
SIM	45	00.00 ± 00.01	00.74 ± 00.15	0.59	0.75	00.02 ± 00.00	00.94 ± 00.09	0.85	0.74

C. One gender at a time *vs* all

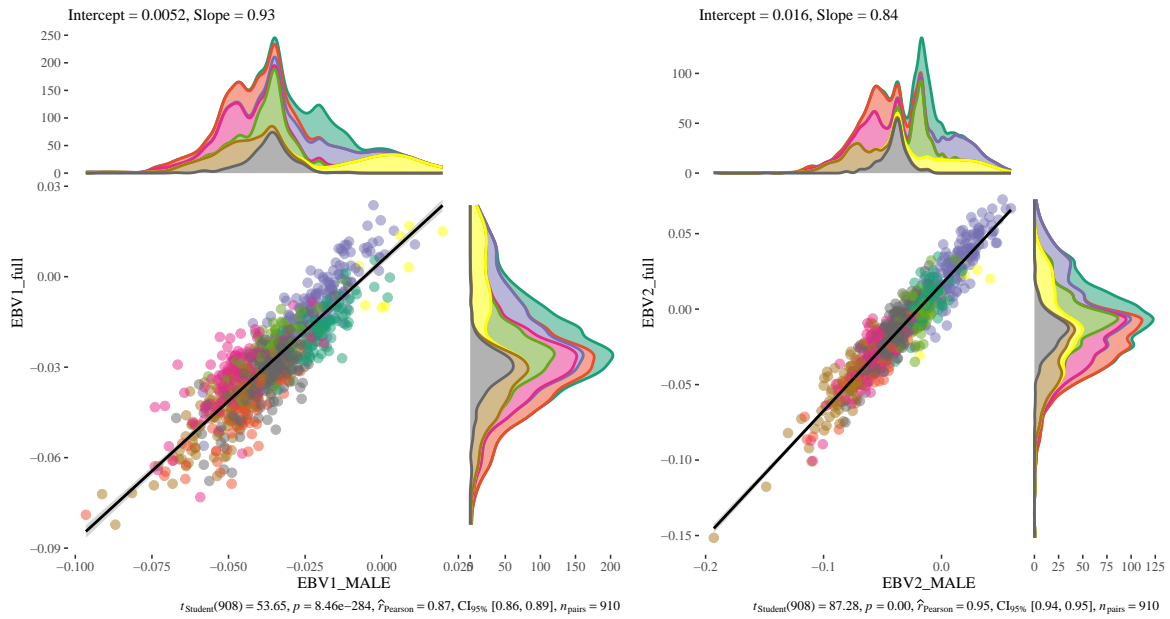


Figure 41: Males: Regression results when all breeds are included

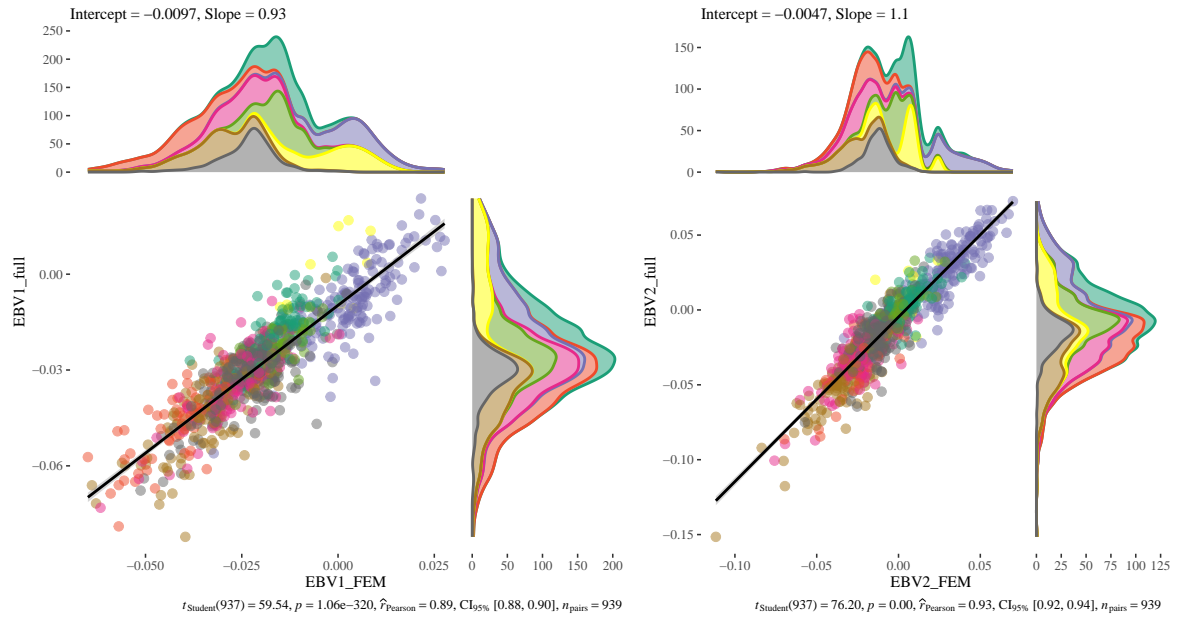


Figure 42: Females: Regression results when all breeds are included

Table 34: 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	95	00.00 ± 00.00	00.89 ± 00.06	0.82	0.80	00.02 ± 00.00	00.84 ± 00.08	0.73	0.79
BAQ	71	-0.00 ± 00.00	00.89 ± 00.06	0.85	0.85	00.01 ± 00.00	00.84 ± 00.05	0.90	0.84
BBL	151	00.01 ± 00.00	00.96 ± 00.04	0.87	0.84	00.02 ± 00.00	00.95 ± 00.04	0.87	0.83
CHA	117	00.00 ± 00.00	00.78 ± 00.07	0.72	0.74	00.02 ± 00.00	00.88 ± 00.06	0.81	0.71
GLW	3	-0.21 ± 00.12	02.14 ± 01.43	0.83	0.53	-0.03 ± 00.20	01.26 ± 01.62	0.61	0.52
HER	73	00.00 ± 00.00	00.68 ± 00.09	0.68	0.68	00.01 ± 00.00	00.81 ± 00.14	0.56	0.63
HLA	8	-0.07 ± 00.00	00.96 ± 00.57	0.56	NaN	00.05 ± 00.01	00.97 ± 00.55	0.58	NaN
INR	9	00.00 ± 00.00	00.74 ± 00.27	0.72	0.80	00.00 ± 00.00	00.79 ± 00.17	0.86	0.79
LIM	127	00.00 ± 00.00	00.88 ± 00.05	0.83	0.80	00.02 ± 00.00	00.92 ± 00.04	0.90	0.79
PIE	7	-0.02 ± 00.01	00.51 ± 00.38	0.52	0.60	00.10 ± 00.04	01.08 ± 00.32	0.83	0.58
SIM	267	00.00 ± 00.00	00.87 ± 00.05	0.73	0.68	00.02 ± 00.00	00.97 ± 00.04	0.82	0.66

Table 35: 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	46	00.00 ± 00.00	00.84 ± 00.08	0.85	0.86	00.01 ± 00.00	00.78 ± 00.10	0.76	0.85
BAQ	34	-0.00 ± 00.00	00.89 ± 00.05	0.95	0.90	00.01 ± 00.00	00.84 ± 00.06	0.94	0.89
BBL	82	00.01 ± 00.00	00.96 ± 00.05	0.91	0.88	00.02 ± 00.00	00.95 ± 00.05	0.90	0.88
CHA	41	00.00 ± 00.00	00.76 ± 00.09	0.81	0.81	00.02 ± 00.01	00.92 ± 00.08	0.87	0.79
HER	22	-0.00 ± 00.00	00.54 ± 00.12	0.71	0.78	00.01 ± 00.01	00.86 ± 00.28	0.57	0.74
INR	3	00.01 ± 00.01	00.38 ± 00.80	0.43	0.86	00.02 ± 00.01	00.21 ± 00.47	0.41	0.86
LIM	67	00.00 ± 00.00	00.89 ± 00.07	0.85	0.84	00.03 ± 00.00	00.95 ± 00.05	0.93	0.83
SIM	45	00.00 ± 00.00	00.91 ± 00.11	0.78	0.78	00.02 ± 00.00	00.96 ± 00.09	0.84	0.77

Table 36: 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	95	-0.00 ± 00.00	00.98 ± 00.09	0.73	0.80	-0.00 ± 00.00	00.84 ± 00.08	0.73	0.79
BAQ	73	-0.00 ± 00.00	01.00 ± 00.08	0.83	0.84	-0.01 ± 00.00	01.14 ± 00.09	0.83	0.83
BBL	151	-0.01 ± 00.00	00.97 ± 00.06	0.80	0.83	-0.00 ± 00.00	01.03 ± 00.06	0.83	0.82
CHA	123	-0.01 ± 00.00	00.95 ± 00.07	0.80	0.79	-0.01 ± 00.00	00.91 ± 00.07	0.75	0.79
GLW	3	00.07 ± 00.06	01.03 ± 00.62	0.86	0.60	-0.07 ± 00.10	01.55 ± 00.81	0.89	0.59
HER	76	-0.01 ± 00.00	00.78 ± 00.09	0.71	0.77	-0.00 ± 00.00	00.98 ± 00.08	0.83	0.76
HLA	8	00.02 ± 00.05	01.03 ± 00.58	0.59	0.34	-0.01 ± 00.02	00.89 ± 00.38	0.70	0.41
INR	9	00.00 ± 00.00	00.70 ± 00.44	0.51	0.77	00.00 ± 00.01	00.78 ± 00.53	0.49	0.77
LIM	128	-0.01 ± 00.00	00.96 ± 00.07	0.77	0.80	-0.01 ± 00.00	01.13 ± 00.06	0.88	0.80
PIE	7	00.04 ± 00.02	00.73 ± 00.25	0.79	0.54	-0.07 ± 00.01	01.07 ± 00.39	0.78	0.52
SIM	284	-0.01 ± 00.00	00.81 ± 00.05	0.71	0.72	-0.00 ± 00.00	01.02 ± 00.06	0.71	0.73

Table 37: 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	46	-0.00 ± 00.00	00.91 ± 00.12	0.74	0.84	-0.00 ± 00.00	00.78 ± 00.10	0.75	0.84
BAQ	34	-0.00 ± 00.00	01.01 ± 00.11	0.85	0.88	-0.00 ± 00.00	01.25 ± 00.13	0.86	0.88
BBL	82	-0.01 ± 00.00	00.97 ± 00.08	0.81	0.87	-0.00 ± 00.00	01.01 ± 00.07	0.85	0.87
CHA	41	-0.01 ± 00.00	00.95 ± 00.13	0.77	0.83	-0.01 ± 00.00	00.95 ± 00.11	0.81	0.83
HER	22	-0.01 ± 00.00	00.65 ± 00.16	0.67	0.81	-0.00 ± 00.00	01.08 ± 00.13	0.89	0.82
INR	3	00.01 ± 00.00	00.65 ± 00.52	0.78	0.84	00.02 ± 00.01	00.31 ± 00.48	0.55	0.85
LIM	67	-0.01 ± 00.00	00.97 ± 00.09	0.79	0.82	-0.01 ± 00.00	01.18 ± 00.07	0.90	0.83
SIM	45	-0.01 ± 00.00	00.90 ± 00.09	0.85	0.80	-0.00 ± 00.00	01.07 ± 00.11	0.83	0.81

D. Truncated data *vs.* all

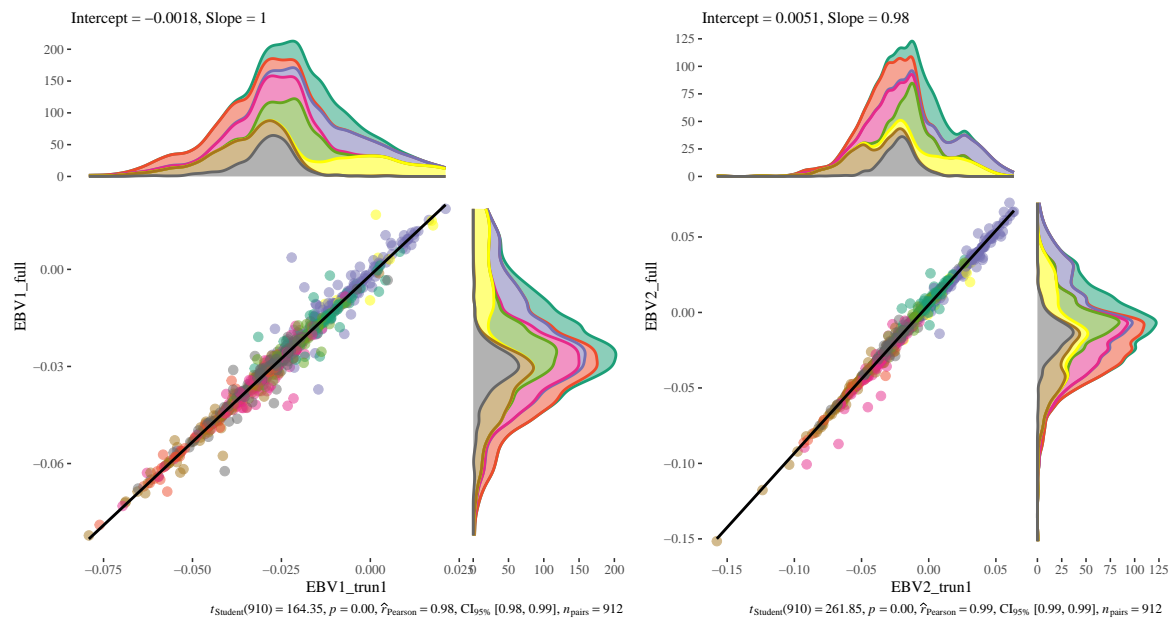


Figure 43: Truncated data: Regression results when all breeds are included

Table 38: 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	87	-0.00 ± 00.00	00.93 ± 00.04	0.94	0.90	00.01 ± 00.00	00.95 ± 00.03	0.95	0.91
BAQ	71	-0.00 ± 00.00	01.02 ± 00.02	0.99	0.93	00.00 ± 00.00	00.98 ± 00.01	0.99	0.93
BBL	145	-0.00 ± 00.00	00.97 ± 00.03	0.94	0.93	00.00 ± 00.00	01.01 ± 00.01	0.99	0.93
CHA	115	-0.00 ± 00.00	00.98 ± 00.02	0.97	0.91	00.01 ± 00.00	01.08 ± 00.03	0.96	0.90
GLW	3	00.01 ± 00.01	01.04 ± 00.28	0.97	0.81	00.01 ± 00.01	01.00 ± 00.08	1.00	0.80
HER	75	-0.00 ± 00.00	00.94 ± 00.04	0.93	0.91	00.01 ± 00.00	00.98 ± 00.02	0.99	0.89
HLA	8	-0.01 ± 00.01	01.03 ± 00.12	0.96	0.77	00.00 ± 00.00	01.04 ± 00.04	1.00	0.76
INR	9	00.00 ± 00.00	00.89 ± 00.23	0.83	0.88	00.00 ± 00.00	00.94 ± 00.08	0.98	0.88
LIM	129	-0.00 ± 00.00	01.01 ± 00.02	0.99	0.94	00.01 ± 00.00	01.00 ± 00.01	1.00	0.93
PIE	7	00.01 ± 00.00	00.66 ± 00.10	0.94	0.84	00.00 ± 00.00	00.99 ± 00.02	1.00	0.82
SIM	281	-0.00 ± 00.00	01.01 ± 00.01	0.97	0.90	00.01 ± 00.00	00.99 ± 00.01	0.99	0.88

Table 39: 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	43	-0.00 ± 00.00	00.89 ± 00.05	0.93	0.92	00.01 ± 00.00	00.90 ± 00.06	0.93	0.93
BAQ	33	-0.00 ± 00.00	01.00 ± 00.02	0.99	0.94	00.00 ± 00.00	00.98 ± 00.02	0.99	0.95
BBL	80	-0.00 ± 00.00	00.97 ± 00.04	0.94	0.95	00.00 ± 00.00	01.00 ± 00.01	0.99	0.95
CHA	40	-0.00 ± 00.00	00.97 ± 00.04	0.97	0.93	00.01 ± 00.00	01.14 ± 00.05	0.97	0.93
HER	22	-0.01 ± 00.00	00.90 ± 00.09	0.90	0.94	00.01 ± 00.00	00.96 ± 00.03	0.99	0.92
INR	3	-0.00 ± 00.00	00.93 ± 00.13	0.99	0.94	00.00 ± 00.01	00.74 ± 00.50	0.83	0.94
LIM	67	-0.00 ± 00.00	01.00 ± 00.02	0.99	0.95	00.01 ± 00.00	01.01 ± 00.01	1.00	0.94
SIM	45	-0.00 ± 00.00	00.97 ± 00.04	0.97	0.94	00.01 ± 00.00	00.99 ± 00.01	1.00	0.93