NAV GENERAL HEALTH EVALUATION

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Outline

i. Introduction

The first joint Nordic evaluation for General Health traits was introduced for routine evaluation in 2008 under the name “Other diseases”. It was during the execution of the current project that the official name of the evaluation was changed from Other Disease to General Health (GH) evaluation. The GH model released in 2008 was a multi-trait linear sire model (SM), which included disease data comparable across the three NAV-Nordic countries to provide common breeding values for metabolic diseases, early and late reproductive disorders and feet and leg problems. Nowadays, with genomic prediction models with cows in the reference population, the use of a linear animal model is a more optimal solution for the GH evaluation. Therefore, the new GH evaluation includes updates on the data, genetic parameters and in the gentic model that are collected in this document. Furthermore, previous to this project, there was no NAV evaluation for Jerseys. The national Danish evaluation for the Jersey only included metabolic disorders. The new GH evaluation includes a Jersey evaluation for all disease traits and not only metabolic disorders.

The revision of the GH evaluation was divided into two phases; the current document describes the work done in phase 1 and 2. The updated model from phase 1 was introduced during the November 2017 evaluation and the changes from phase 2 were implemented in May 2019.

Abbreviations used for countries and breeds:

DNK	Denmark, Danish
FIN	Finland, Finnish
SWE	Sweden, Swedish
HOL	Holstein
RDC	Red Dairy Cattle
JER	Jersey
FIC	Finn Cattle

ii. Trait definition

Records from 1st to 3rd lactation on early reproductive disorders (ERP), late reproductive disorders (LRP), ketosis (KET), other metabolic diseases (OMB), and feet and legs problems (FLP) are used in the genetic evaluation for GH. Indicator traits in the new GH evaluation are β-hydroxybutyrate (BHB) and acetone records from milk recording in 1st to 3rd lactation. Table 1 shows the 5 traits included in the new GH evaluation together with the group of veterinary treatments pooled into each of the 5 traits. The new trait defintions implied that the GH index changed from including 4 sub-traits to include 5 sub-traits by splitting the group of metabolic disorders into two traits: KET and OMB disorders.

Table 1. Disease groups in the genetic evaluation

Early reproductive disorders	Late reproductive disorders	*Ketosis*	Other metabolic disorders	Feet and leg problems
• Retained placenta • Hormonal reproductive disorders • Infective reproductive disorders • Other reproductive disorders	• Hormonal reproductive disorders • Infective reproductive disorders • Other reproductive disorders	• ***Ketosis***	• Milk fever • Other metabolic diseases • Other feed related disorders • Other diseases • ***β-hydroxybutyrate***[1] • ***Acetone***[1]	• Feet and leg problems

[1]New indicator traits included in the GH evaluation since November 2017

Table 2 shows the traits included in each of the past and current GH evaluations. Up until the release of the new GH evaluation in 2017 only HOL and RDC were evaluated using a NAV model. The JER evaluation considered only Metabolic Disorders, and only Danish data. Already in November 2017, the new GH evaluation all three breeds are evaluated for the same traits, and all three countries supplied JER data, however FIN and SWE in a much smaller degree than DNK (Table 2).

Table 2. Previous and current GH evaluation and included traits.

	Old GH evaluation - JER (Danish national model)	**Old – GH evaluation - RDC and HOL (NAV model)**	**Nov 2017 - NAV GH evaluation - all breeds**	**May 2019 - NAV GH evaluation - all breeds**
Traits in the GH index	-	Early Reproductive Disorders	Early Reproductive Disorders	Early Reproductive Disorders
	-	Late Reproductive Disorders	Late Reproductive Disorders	Late Reproductive Disorders
	-	Feet&Leg problems	Feet&Leg problems	Feet&Leg problems
	Metabolic Disorders	Metabolic Disorders	Ketosis	Ketosis
			Other Metabolic Disorders	Other Metabolic Disorders
Indicator traits	-	*Clinical Mastitis*	*Clinical Mastitis*	
	-		*Acetone*	*Acetone*
	-		*β-hydroxybutyrate*	*β-hydroxybutyrate*

The veterinary treatment traits included in the GH evaluation are recorded as 0 = no treatment or 1 = treatment. Multiple treatments (for a disease group) during the relevant time window are ignored, i.e. 1 = at least one treatment during the time window. BHB and acetone, are recorded in mmol/L. The definition of the traits and the abbreviations as included in the GH genetic evaluation are given in Table 3**.**

Table 3. Abbreviations and definitions of traits included in the evaluation

Abbreviation and Lactation	Definition
ERP1-ERP3	Early reproductive disorders (1) or not (0), 0 to 40 DIM
LRP1-LRP3	Late reproductive disorders (1) or not (0), 41 to 305 DIM
OMB1-OMB3	Other metabolic diseases (1) or not (0), -15 to 305 DIM
KET1-KET3	Ketosis (1) or not (0), -15 to 305 DIM
FL1-FL3	Feet and legs problems (1) or not (0), -15 to 305 DIM
BHB1-BHB3	β-hydroxybutyrate mmol/L, 10 to 60 DIM
ACE1-ACE3	Acetone, mmol/L, 10 to 60 DIM

In the old evaluation the definition of early reproductive diseases for lactation 2 and 3 was found to be -15 to 40 DIM instead of the expected from 0 to 40 DIM. This has been corrected and the new definition was implemented in November 2017 evaluation. The number of misclassified animals due to the wrong time window are in Table 4.

Table 4. Number of cows misclassified due to wrong time window.

Country	Lactation 2	Lactation 3
Denmark	8610	6174
Finland	1431	1150
Sweden	1005	755

iii. Data used for the evaluations

a. Input data

Phenotypic records in the GH evaluation come from disease treatments made, in the majority of the cases, by veterninarians, but also from AI technicians and farmers. Each country sends several input files including information on identity, birth date, breed, parental information, herd, calvings, veterinary treatments and for DNK (phase 1) and FIN (phase 2), also BHB and acetone measures (SWE also started collecting these observations in Växa's Cattle databse from January 2019 and they will be used in the GH evaluation when there is sufficient data to be used in the genetic evaluation; that is around two years of data) (Table 5). These files include all breeds: HOL, RDC, JER and FIC. The data structure of the input files differs among countries, therefore editing is at first carried out separately within each country to harmonize the codes (e.g. disease codes as well as cullings). See appendix A.

Table 5. Availability of BHB and acetone data by country and breed

	HOL	RDC	JER
Denmark	2013-	2013-	2013-
Sweden	(not included in the evaluation) Regular basis from 2019-		
Finland	Test data 2015-2017		

The input data was revised in phase 1 to improve the harmonization of the data used in the GH evaluation across all three Nordic countries. That included a revision of the culling codes, data used in FLP (DNK), herds with incomplete reporting of veterinary treatments (SWE) and the addition of BHB and acetone from Denmark and Finland (Table 6).

Table 6. Changes in data used in the General Health evaluation

Country	Changes Phase 1	Changes in Phase 2
Denmark	Claw trimmer data removed BHB and acetone data included	
Finland	Finnish Jersey data included	BHB and acetone data included
Sweden	Herds with incomplete reporting of veterinary treatments removed Swedish Jersey data included	

The data used for GH evaluation starts in years 1981, 1988 and 1990, for Sweden, Finland and Denmark, respectively; these years refer to the birth year of the females. Cows up to third lactation are included for each breed. No restriction is set that a female's records should start from heifer records since this would, e.g., penalize herds recently joined to performance recording. However the data must come from active disease-recording herds. Active herds are defined as herds in which a certain percentage of cows are treated when looking at all treatment records (more detailed information on active herds in section below: Swedish data on incomplete recording).

a. Data editing

Culling codes

The culling codes have not been changed between the old and new GH evaluation. However they were revised as there are different use of culling reason per country. Denmark doesn't include any culling code in the GH data, whereas Finland includes the culling code for mastitis and Sweden includes culling codes for all of the 5 GH traits. The fact that Swedish data includes culling reasons also for feet and legs provides an extra source of information taking into account that studies on validation of national disease databases revealed incomplete recording especially for locomotor traits. The graph below (Figure 1) shows the distribution of cullings in Sweden for 4 GH traits (before MB was split into KET and OMB) over 300 DIM. For most of the traits cullings are equally reported across time (300 DIM). However, culling codes for LPR disorders are increasing at the end of the lactation. The guarantee that culling code and culling date are linked is through the EU regulation on animal movements where a cow that is culled need to be reported between 3-5 days after the event.

For Sweden culling reasons are considered for all 4 GH traits in Figure 1 plus CM1, Finland only for CM1, and none for Denmark.

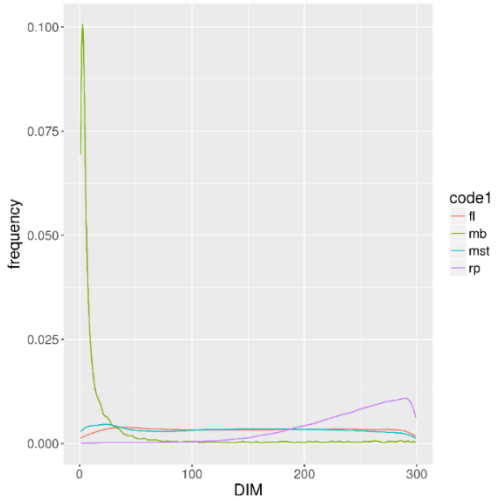
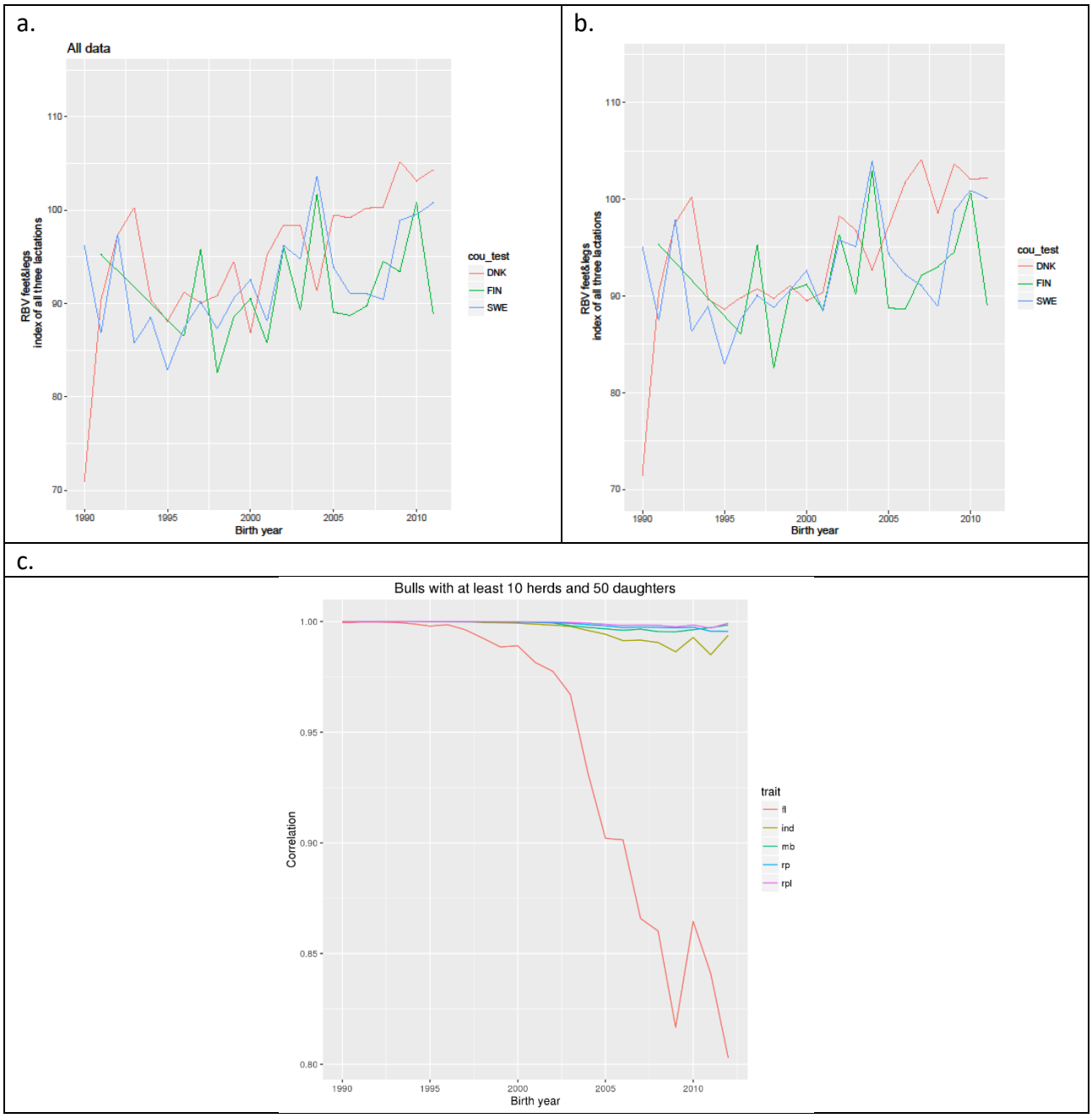


Figure 1. Culling frequencies from Swedish cows from 4 Genereal Health traits (fl = Feet&Legs, mb = metabolic disorders, mst = mastitis and rp = reproductive disorders).

Danish data on Feet and Leg problems

Data on FLP from Denmark used to, incorrectly, include claw trimmer data. This data, also included in the Claw Health evaluation, represented about 12% of all the Danish FLP records and was removed in the phase 1 of the GH evaluation (November 2017). The data overlap between the GH and the claw health evaluations was first identified by Lars-Peters in a study (interal communication) where he found a high frequency of foot root cases and laminitis records in the FLP data used in the GH evaluation. The frequency for these treatments saw a significant increase around 2007. It is presumed that this increase relates to the “health agreement scheme” implemented in Denmark in 2005 where farmers can initiate the treatment themselves.

Figure 2. Genetic trends for the Feet and Legs index including all data (a) compared to excluding claw trimmer data from Denmark (b) split by country and birth year of the cow. Correlations (b) between estimated breeding values for GH index traits (ind: GH index, fl: feet and legs (in red), mb: metabolic disorders, rp: early reproductive disorders and rpl: late reproductive disorders) from two models differing in in- or excluding claw trimmer data from Denmark.



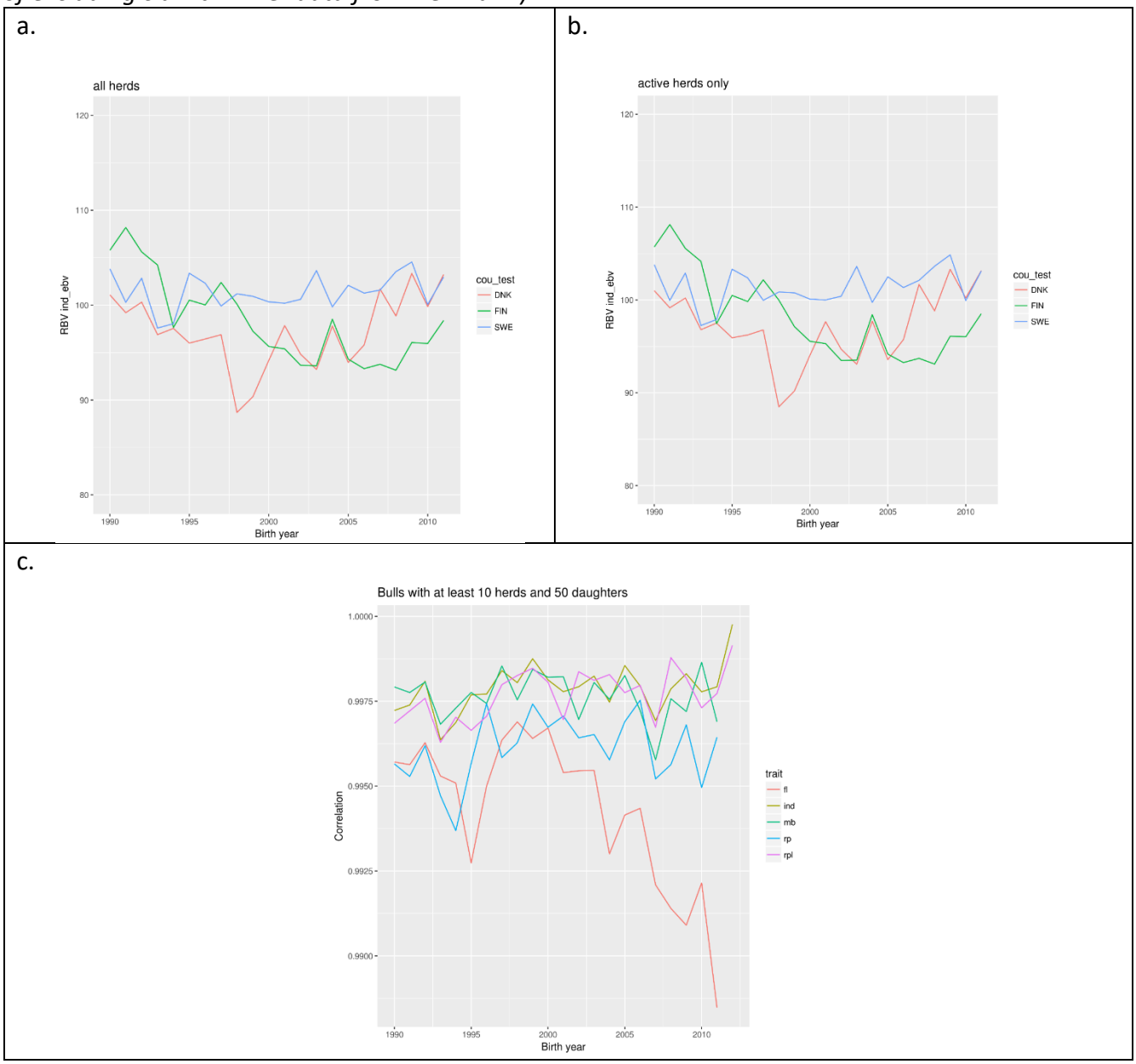
Swedish data on incomplete recording

About 10% of lactations with incomplete reporting of veterinary treatments from Sweden were removed. Denmark and Finland had already similar national editings on incomplete reporting of veterniry treatment in place (Table 6). The study on incomplete recoring in the Swedish herds

revealed that if we were to apply the same restrictions on the Swedish data as it is done in Denmark, nearly 70-75% of the data would be classified as inactive herds and therefore excluded from the analysis. Therefore instead of using only clinical mastitis to classify the herds as in Denmark or Finland, in Sweden we decided to use a pool of disease treatments; all those traits that are included in the GH evaluation: ERP, LRP, KET, OMB and F&L.

The specific editing criteria applied in the Swedish data includes two filters. The first one, at least one treatment over a 9-month period, had the biggest impact and removed about 10% of lactations with no informative data, the second one, removed those herds for which the probability of the number of treatments given the number of calving's and an average rate of 0.15 was larger than 0.05. The phenotypic trends (here: frequency of treatments) after the editing of the data increased about 10% in frequency of the whole time period, when this test was done on the February 2017 evaluation.

Figure 3. Genetic trends for the General health index including all herds (a) compared to including only active herds (b) split by country and birth year of the cow. Correlations (b) between estimated breeding values for GH index traits (ind: GH index, fl: feet and legs (in red), mb: metabolic disorders, rp: early reproductive disorders and rpl: late reproductive disorders) from two models which differ from including all herds to including active herds only. (*Obs! for the feet and legs index, correlations between breeding values from the two models also include the effect of excluding claw trimmer data from Denmark.)*



BHB and Acetone

Measures of BHB and acetone are obtained from milk samples collected on a regular basis through the milk recording scheme. Mid-infrared spectrometry technology (MilkoScan FT+, Foss Electric A/S, Hillerød, Denmark) is used on the milk to predict BHB and acetone levels. Phenotypic records on

BHB and acetone from cows with DIM from 10 to 60 are included in the evaluation. About 50% of the cows have repeated observations. Further editing measures on BHB and acetone includes cows from 1 to 3 lactations, BHB and acetone < 10, cell count < 10,000. For Danish BHB and acetone there are also measures of fat and protein percentages where only values between 1 to 12 and 1 to 6 for fat and protein, respectively are kept in the data.

The BHB and acetone data showed to be non-normal distributed and a study was carried out to test an adequate transformation to a normal distribution (taken into account that there are negative values). Four different scenarios of data transformations were investigated (x as-is, standardized x (adjusted for country adjusted according to country, calving year and breed), Ln(x+1) and cube root of x). Results from all four transformations were investigated by looking at the correlations of ketosis and OMB with BHB and acetone between daughter group means in lactations 1 to 3 (with a minimum of 250 daughters per sire). Three of the four different scenarios gave very similar results, yet the higest correlations were found when BHB and acetone data where used without using any transformation function (Table 7). Therefore, BHB and acetone data on the GH evaluation is used without applying any transformation to a normal distribution.

Table 7. Correlations between daughter groups means (lactation 1) for Holstein bulls with more than 250 daughters

	Ketosis		**Other metabolic disorders**	
	BHB	Acetone	BHB	Acetone
x (as-is)	0.26	0.43	0.18	0.25
Standardized x*	0.25	0.40	0.19	0.25
Ln(x+1)	0.25	0.39	0.17	0.23
$\sqrt[3]{x}$	0.09	0.27	0.11	0.23

* adjusted for country adjusted according to country, calving year and breed

The use of BHB and acetone in the GH evalution is as indicator traits. The highest genetic correlations between BHB and acetone with GH traits is found with ketosis (Jamrozik et al., 2016) and also OMB. To optimialy use this high genetic correlations, the group of Metabolic Disorders (from the old GH evaluation) was slippt into two traits: KET and OMB. For further details see the note on the use of BHB and acetone in the NAV GH evaluation available in Appendix B. A pilot study about BHB and acetone and the correlation with traits in the GH evaluation was done in Denmark by Ane Closter et. al. This work can be read on Appendix C.

Definition of herd-year classes

Herd-year classes are created from the file NCGE1. However this file differ across countries on the on the country code information. For DNK and SWE the country code is DNK and SWE, resp., reflecting in which country the cow has made the record and this code can be different from the country code in the individual's ID_nor; for FIN there is a wide range of country codes. The country code from the NCGE1 file is used in the creation of country-herd-year classes and any mistakes will directly affect the estimation of such effect. An example of such a problem was found when 322 Finnish individuals were wrongly classified due to the field "animcoun" (positions 4-6) in the NCGE1 file from Finland.

After data editing and the creation of fixed effects, breed specific data sets are generated to run breed-specific genetic evaluations for HOL, RDC (including FIC) and JER. For JER, Finnish and Swedish Jersey animals are included in the Danish population by changing the country code for Swedish and Finnish animals to the one from Denmark, creating in this way calving month year fixed effects as if all the animals were coming from the same population. Since Finnish and Swedish Jersey population is so small in this this we increase the size of the contemporary groups. Another exception is for the Finnish animals where both breeds HOL and RDC breeds are included in each of the HOL and RDC evaluations also with the aim of increasing the size of the contemporary groups. Besides input data from countries, NAV pedigree file is used.

iv. Genetic evaluation

Model effects have been revised in both phase 1 and phase 2. In phase 1, the model changed from a sire model to an animal model and the random effect of herd *period (5 years) was changed to a fixed effect of herd * year. In phase 2, heterogenous variance (HV) adjustment for veterinary treatment trais was upgraded and for the first time implemented in BHB and acetone traits. Further, CM1 was deleted from the GH evaluation as a correlated trait. Heterosis and breed proprotions were removed from the HOL evaluation and genetic groups was introduced for all three breeds.

Change from a sire to an animal model

The change from a sire to an animal mode implied that since February 2018, all genotyped cows with EBV for health traits could be included in the reference for genomic predictions for all breeds.

Heterogeneous variance adjustment

Disease frequencies vary across countries. See Appendix D for further information on disease frequencies before correcting for heterogenous variance. Phenotypes of all traits are pre-adjusted for heterogeneous variance due to country, year of calving and breed (all Finnish breeds are in both the Holstein and the RDC evaluation, additionaly, FIC is pooled together with RDC, to avoid small contemporary groups).

For the veterinary treatment traits, differences in disease frequencies and heritabilities are taken into account by scaling the observations with varying factors and weights over time so that adjusted observations have the same genetic variance on the observed scale (and different heritability on the observed scale). See Appendix E for a detailed description on the theory behind the heterogenous variance adjusted that is implemented for the veterninary treatment traits in the new GH evaluation.

To handle differences in phenotypic standard deviation of BHB and acetone records between Finland and Denmark and across years of sampling, the variation in phenotypic records were adjusted according to country, calving year and breed. The impact of HV adjustment for acetone and BHB has a marginal effect on the EBVs for bulls and cows.

Omission of clinical mastitis

Clinical Mastitis from lactation 1 (CM1) used as a correlated trait for the GH evaluation has been omitted from May 2019 for all breeds. The genetic correlations between CM1 and the general health traits have been re-estimated and were found to be positive but lower than assumed so far.

In the JER evaluation, removing CM1 had a larger effect than expected, especially on LRP in lactation 3. The effect of removing CM1 was also evaluated by looking at the changes in reliability estimates from a model with CM1 compared a model without CM1. Difference in reliabilities between these two models were marginal. The unexpected large impact of CM1 on LRP in JER evaluation just confirmed the poor accuracy of the genetic correlation between CM1 and LRP3 (rG=-0.31) in this population. Therefore based on the results from HOL and RDC the CM1 was also removed in the JER evaluation.

Heterosis

Unexpected heterosis effects (postivie regression coefficient for crossbred animals) where found when the hetersosis effect was investigated in the HOL, JER and RDC evaluations. Results also show to be inconsistent across lactations for the same traits. Consequebntly, the heterosis effect is excluded from the HOL GH evalution (neither JER nor RDC included heterosis effect in the old GH evaluation)

Genetic groups

One of the main changes in phase 2 of the GH evaluation is the inclusion of genetic groups for all breeds and the omission of breed proportions from the HOL evaluation. The detaild definition of the genetic groups for HOL, RDC and JER is shown in Appendix F.

Genetic models

Separate evaluations are carried out for HOL, RDC and JER. Despite separate evaluations for different breeds, for Finland all breeds are entered in the breed-specific data sets to increase the size of the contemporary groups. All traits are analyzed under linear models instead of threshold models, even if all veterinary treatment are binary traits following binomial distributions. However, applying threshold models for large data sets analyzed under multi-trait multi-lactation models is complex.

A multi-trait multi-lactation animal model is used in the prediction of estimated breeding values (EBVs) for GH traits. A total of 21 traits (7 traits x 3 lactations) are analysed using DMU 5.3 (Madsen and Jensen, 2010). The following multi-lactation animal models are fitted for each breed:

Statistical model for veterinary treatments

$$Y_{ijkl} = CHY_i + CCA_j + CYM_k + A_l + e_{ijkl} \quad (\mathbf{1}\boldsymbol{a})$$

Statistical model for BHB and acetone

$$Y_{ijklmn} = CHY_i + CCA_j + CYM_k + A_l + PE_m + b_2 \cdot LS1_n + b_3 \cdot LS2_o + e_{ijklmno} \quad (\mathbf{1}\boldsymbol{b})$$

Where, $\boldsymbol{Y_{ijkl}}$ and $\boldsymbol{Y_{ijklm}}$ are the individual observation for veterinary treatments and metabolic biomarkers, respectively, $\boldsymbol{CHY_i}$ is the country*herd * year, $\boldsymbol{CCA_j}$ is the country*calving age, $\boldsymbol{CYM_k}$ is the country*year-month of calving, $\boldsymbol{A_l}$ is the animal genetic random effect. Only for metabolic biomarkers we included $\boldsymbol{PE_m}$ which is the cow permanent environmental effect and $b_2 \cdot LS1_{ijklm}$ and $b_3 \cdot LS2_{ijklm}$ are (fixed) regression for lactation stage modelled as a second order Legendre polynomial and $\boldsymbol{e_{ijkl}}$ is the residual random effect. Genetic groups are model as random effects with a factor equal to 0.333. For computational reasons, residual correlations between lactations were set to zero and residual correlations between the veterinary treatments and metabolic biomarkers are set to zero except for KET and OMB.

Genetic parameters

In phase 1, the inclusion of BHB and acetone and the re-grouping of metabolic disorders (into KET and OMB) meant that additional genetic parameters were needed. In phase 2 the upgrade of the HV adjustment required the re-estimation of genetic parameters for the veterinary treatment traits as well as the update of genetic correlations that were not updated in phase 1 (the ones not directly involve in the inclusion of BHB and acetone data, i.e ERP, LRP and FLP). Variance components, genetic and residual correlations between these four traits and all other traits in the evaluation were estimated using a series of bivariate analyses with sire models.

For the estimation of genetic parameters, a reduced dataset of the whole dataset was used which included data on cows born 2000 onwards. For HOL and JER we used DNK data and for RDC we used SWE data. All cows were required to have a first lactation record. Offspring from high reliability bulls were included (50 offspring in 50 herds for HOL, 25 offspring in 25 herds for RDC and JER). Cows were also required to be in "large" herds (≥ 25 cows with record per herd-year for HOL and JER, ≥ 10 cows with records per herd-year for RDC).

The selection of data for the estimation of BHB and acetone data had a large impact on the results. At first comparisons of correlations with different daughter group means showd a significant increase increase in correlations when sires with larger number of daughters were used in the calculation (Table 8). Correlations also indicated that BHB seems to be an easier trait to measure compared to Acetone (more volatile), with consistently higher correlation for BHB compared to acetone across the different minimum daughter group size (columns in the table 8). Correlations also increased with the number of lactations (table 8). In table 9, genetic correlations without and with an edit on daughter group size also showed large differences comparable to the ones reported by Ane Closter in her study (Appendix C.). Furthermore, larger genetic correlations than previously reported were found when the selection of sires was on: AI bulls (≥50 daughters in ≥10 herds), having daughters in large herds, and having 1st lactation observations (AI/LH/1st in table below).

Table 8. Comparisons of correlations for BHB and acetone observations in Holstein with different daughter group means (in columns, 0, 10, 20 and 100)

	BHB				Acetone			
	0	**10**	**20**	**100**	**0**	**10**	**20**	**100**
Lact1,2	0.22	0.42	0.46	0.44	0.11	0.31	0.32	0.26
Lact1,3	0.03	0.18	0.28	0.25	-0.00	0.13	0.21	0.24
Lact2,3	0.13	0.34	0.41	0.66	0.04	0.24	0.26	0.47

Table 9. Genetic correlations for BHB and acetone for Holstein without and with an edit on daughter group size (columns 0 and 20) and between 1,2 and 3 lactations.

	BHB		Acetone	
	0	**20**	**0**	**20**
Lact1,2	0.45	0.67	0.30	0.43
Lact1,3	0.10	0.36	0.35	0.39
Lact2,3	0.66	0.74	0.66	0.70

Table 10. Genetic correlations of BHB, acetone and ketose between 1, 2 and 3 lactations when there is no selection on daughter group size (coloumn 0), with selection on daughter group size (coloum 20), when cows are required to start with first lactation (1st lact) and when the selection of sires was on: AI bulls (≥50 daughters in ≥10 herds), having daughters in large herds, and having 1st lactation observations (AI/LH/1st).

	BHB				Acetone			
	0	20	1st lact	AI/LH/1st	0	20	1st lact	AI/LH/1st
Lact1,2	0.45	0.67	0.60	0.82	0.30	0.43	0.41	0.74
Lact1,3	0.10	0.36	0.25	0.76	0.35	0.39	0.32	0.60
Lact2,3	0.66	0.74	0.85	0.97	0.66	0.70	0.81	0.93

A two-trait multi-lactation sire model was used for variance component estimation using the DMUAI software (Madsen and Jensen, 2010). Genetic parameters for BHB and acetone where estimated for HOL and JER. For RDC there were too few records to estimate breed specific parameters and the ones from HOL were used. Only those traits affected in the inclusion of BHB and acetone (i.e. KET and OMB) were re-estimated in phase 1 using the same model as describe above with a random sire effect instead of an animal random effect. In phase 2 and using the same reduced datasets, all genetic and residual variances for all three breeds were re-estimated and the genetic correlations of those traits not re-estimated in phase 1 where updated in phase two.

The genetic parameters estimated in phase 1 (BHB, acetone and the genetic correlations with the GH traits) together with the new genetic parameters estimated in phase 2 were combined in the May 2019 evaluation. A bending procedure was needed to obtain positive-definite variance-covariance matrixes; the procedure by Jorjani et al. (2013) was used for this purpose. For computational reasons, residual correlations between lactations were set to zero. The applied genetic parameters are in Tables 11, 12 and 13

Table 11. Genetic correlations (above), residual correlations (under) and heritability's on the diagonal in 1st, 2nd and 3rd lactation, Holstein

Trait	ERP1	LRP1	MB1	KET1	FL1	ERP2	LRP2	OMB2	KET2	FL2	ERP3	LRP3	OMB3	KET3	FL3	BHB1	ACE1	BHB2	ACE2	BHB3	ACE3
ERP1	**0.034**	0.37	0.40	0.31	0.15	0.72	0.32	0.29	0.33	0.08	0.64	0.18	0.30	0.20	0.16	0.05	0.03	-0.03	-0.01	-0.02	0.05
LRP1	0.02	**0.004**	0.27	0.22	0.14	0.34	0.93	0.17	0.04	0.11	0.33	0.90	0.19	0.09	0.19	0.02	0.05	-0.01	-0.06	0.01	-0.03
MB1	0.04	0.01	**0.006**	0.74	0.37	0.24	0.13	0.79	0.60	0.32	0.16	0.15	0.48	0.53	0.35	0.47	0.65	0.22	0.37	0.22	0.33
KET1	0.05	0.01	0.08	**0.010**	0.18	0.24	0.07	0.67	0.70	0.12	0.16	0.03	0.52	0.67	0.09	0.64	0.75	0.39	0.44	0.46	0.52
FL1	0.01	0.00	0.01	0.01	**0.013**	0.10	0.09	0.32	0.17	0.96	0.01	0.02	0.20	0.10	0.91	0.02	0.04	-0.01	-0.03	-0.01	0.01
ERP2	0.00	0.00	0.00	0.00	0.00	**0.030**	0.30	0.26	0.26	0.03	0.98	0.27	0.23	0.20	0.09	0.00	-0.01	-0.01	-0.02	0.00	-0.01
LRP2	0.00	0.00	0.00	0.00	0.00	0.04	**0.005**	0.13	0.06	0.11	0.35	0.94	0.15	0.10	0.22	-0.02	-0.03	0.01	0.01	0.00	0.01
MB2	0.00	0.00	0.00	0.00	0.00	0.06	0.01	**0.008**	0.60	0.32	0.25	0.11	0.83	0.61	0.39	0.47	0.54	0.32	0.50	0.37	0.51
KET2	0.00	0.00	0.00	0.00	0.00	0.05	0.01	0.08	**0.010**	0.20	0.24	0.01	0.44	0.97	0.17	0.45	0.48	0.55	0.72	0.60	0.77
FL2	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.02	0.02	**0.011**	-0.04	0.00	0.16	0.15	0.97	-0.01	-0.01	0.01	0.01	0.01	0.02
ERP3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.034**	0.34	0.22	0.19	0.04	0.00	-0.02	0.01	0.04	0.00	0.01
LRP3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	**0.005**	0.12	0.08	0.09	-0.01	0.00	0.00	0.03	0.00	0.01
OMB3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.07	0.01	**0.020**	0.49	0.22	0.40	0.33	0.38	0.45	0.50	0.58
KET3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.01	0.09	**0.015**	0.12	0.39	0.42	0.55	0.71	0.63	0.79
FL3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.02	0.02	**0.012**	0.00	0.00	0.00	0.01	-0.03	-0.02
BHB1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.15**	0.88	0.81	0.69	0.75	0.52
ACE1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.49	**0.053**	0.62	0.69	0.60	0.56
BHB2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.115**	0.88	0.96	0.75
ACE2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.49	**0.032**	0.88	0.91
BHB3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.077**	0.85
ACE3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.50	**0.030**

Table 12. Genetic correlations (above), residual correlations (under) and heritability's on the diagonal in 1st, 2nd and 3rd lactation, RDC

Trait	ERP1	LRP1	MB1	KET1	FL1	ERP2	LRP2	OMB2	KET2	FL2	ERP3	LRP3	OMB3	KET3	FL3	BHB1	ACE1	BHB2	ACE2	BHB3	ACE3
ERP1	**0.007**	0.20	0.29	0.28	0.01	0.74	0.05	0.28	0.14	0.14	0.78	0.22	0.27	0.26	0.07	0.04	0.04	-0.04	-0.06	0.02	0.01
LRP1	0.01	**0.008**	0.18	-0.08	0.17	0.36	0.83	0.03	0.07	0.11	0.28	0.75	0.12	0.22	0.09	-0.01	-0.06	0.00	0.03	0.04	0.03
MB1	0.01	0.00	**0.003**	0.63	0.43	0.09	-0.02	0.81	0.60	0.05	0.23	-0.16	0.52	0.62	0.18	0.46	0.62	0.22	0.38	0.24	0.35
KET1	0.01	0.00	0.05	**0.010**	-0.05	0.03	-0.21	0.43	0.81	-0.09	0.09	-0.17	0.29	0.71	-0.16	0.63	0.73	0.40	0.46	0.45	0.52
FL1	0.01	-0.01	0.02	0.00	**0.005**	0.14	0.09	0.21	0.05	0.80	0.12	0.02	-0.01	0.05	0.84	0.02	0.11	-0.02	0.01	-0.06	-0.04
ERP2	0.00	0.00	0.00	0.00	0.00	**0.008**	0.28	0.13	-0.09	0.20	0.96	0.37	0.11	0.10	0.09	-0.01	0.00	0.00	-0.04	0.01	-0.03
LRP2	0.00	0.00	0.00	0.00	0.00	0.03	**0.006**	-0.08	-0.14	0.07	0.23	0.92	-0.06	-0.02	0.10	0.01	0.00	-0.01	0.01	-0.03	-0.05
MB2	0.00	0.00	0.00	0.00	0.00	0.02	0.00	**0.008**	0.46	-0.03	0.27	-0.17	0.87	0.51	0.15	0.47	0.54	0.32	0.49	0.36	0.50
KET2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.06	**0.009**	-0.03	0.00	-0.08	0.37	0.95	-0.01	0.46	0.52	0.53	0.70	0.60	0.77
FL2	0.00	0.00	0.00	0.00	0.00	0.01	-0.01	0.01	0.00	**0.010**	0.09	0.21	-0.06	-0.10	0.93	0.01	-0.02	0.01	-0.03	0.00	-0.01
ERP3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.013**	0.29	0.16	0.21	0.07	-0.01	0.04	0.01	0.02	0.00	0.01
LRP3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	**0.007**	-0.07	0.01	0.15	-0.03	-0.07	0.02	0.05	0.03	0.04
OMB3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	-0.01	**0.025**	0.45	0.06	0.40	0.33	0.37	0.46	0.49	0.57
KET3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.06	**0.013**	-0.04	0.39	0.43	0.55	0.69	0.62	0.76
FL3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.02	0.00	0.00	**0.009**	-0.02	-0.03	0.02	0.02	0.00	0.01
BHB1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.149**	0.88	0.80	0.68	0.75	0.51
ACE1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.49	**0.053**	0.61	0.68	0.59	0.55
BHB2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.115**	0.88	0.96	0.75
ACE2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.49	**0.032**	0.88	0.91
BHB3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.077**	0.85
ACE3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.50	**0.030**

Table 13. Genetic correlations (above), residual correlations (under) and heritability's on the diagonal in 1st, 2nd and 3rd lactation, Jersey

Trait	ERP1	LRP1	MB1	KET1	FL1	ERP2	LRP2	OMB2	KET2	FL2	ERP3	LRP3	OMB3	KET3	FL3	BHB1	ACE1	BHB2	ACE2	BHB3	ACE3
ERP1	**0.009**	0.32	0.47	0.39	0.28	0.83	0.53	0.45	0.29	0.24	0.76	0.38	0.26	0.38	0.14	0.04	0.05	-0.01	0.00	0.00	0.01
LRP1	0.02	**0.004**	-0.05	0.10	0.04	0.33	0.81	0.17	0.26	0.23	0.35	0.81	0.05	0.48	0.01	0.00	-0.04	0.03	-0.05	-0.02	-0.01
MB1	0.02	0.00	**0.004**	0.55	0.22	0.43	0.37	0.63	0.36	0.23	0.18	0.18	0.51	0.38	0.10	0.33	0.40	0.29	0.32	0.27	0.27
KET1	0.03	0.00	0.02	**0.013**	0.34	0.10	0.40	0.47	0.45	0.19	0.13	0.16	0.07	0.49	0.12	0.60	0.72	0.29	0.37	0.26	0.33
FL1	0.00	0.00	0.01	0.01	**0.013**	0.16	0.11	0.01	0.31	0.81	0.40	-0.10	-0.04	0.39	0.85	0.08	0.04	0.05	-0.04	0.02	0.06
ERP2	0.00	0.00	0.00	0.00	0.00	**0.010**	0.47	0.38	0.37	0.18	0.88	0.45	0.27	0.27	0.23	-0.06	-0.05	-0.01	0.01	0.00	-0.01
LRP2	0.00	0.00	0.00	0.00	0.00	0.06	**0.003**	0.53	0.47	0.44	0.34	0.75	0.20	0.46	0.07	0.07	0.13	-0.02	0.06	0.01	0.04
MB2	0.00	0.00	0.00	0.00	0.00	0.04	0.01	**0.005**	0.40	0.14	0.29	0.27	0.82	0.42	0.10	0.31	0.47	0.18	0.37	0.26	0.24
KET2	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.02	**0.005**	0.32	0.32	0.58	0.17	0.70	0.26	0.23	0.26	0.15	0.10	0.24	0.31
FL2	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.02	0.00	**0.008**	0.26	0.09	-0.02	0.21	0.76	-0.07	-0.07	-0.04	-0.03	-0.02	-0.03
ERP3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.014**	0.29	0.19	0.34	0.48	0.00	0.00	0.00	-0.01	-0.01	-0.01
LRP3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	**0.002**	0.15	0.53	-0.10	0.01	-0.01	0.02	-0.04	0.02	0.04
OMB3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.01	**0.010**	0.39	0.08	0.21	0.26	0.28	0.30	0.33	0.23
KET3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.01	0.02	**0.005**	0.13	0.41	0.32	0.38	0.09	0.34	0.35
FL3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.01	0.00	0.01	0.01	**0.006**	-0.01	0.02	-0.01	0.05	0.01	-0.01
BHB1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.052**	0.91	0.79	0.46	0.60	0.22
ACE1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.53	**0.017**	0.71	0.71	0.53	0.33
BHB2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.053**	0.64	0.87	0.52
ACE2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.49	**0.013**	0.50	0.56
BHB3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.042**	0.73
ACE3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.48	**0.010**

Heritabilities on the observed scale for the GH traits are low, the majority are around 1-2% and agree with other published studies (Koeck et al., 2012; Jamrozik et al., 2016). Heritabilities for BHB and acetone were higher compared to veterinary treatments, around 15% and 6%, respectively. BHB and acetone are objectively measured and therefore heritabilities can be more accurately estimated.

Genetic correlations among veterinary treatments traits ranged from low to moderate (Tables 11, 12 and 13). Across breeds, genetic correlations among veterninary treatments vary across lactations but between KET and OMB they remain moderately high across lactations. For some traits, genetic correlations ranged widely between breeds. For instance, genetic correlations between LRP and KET in lactation 1 ranged from -0.08 for RDC to 0.22 for HOL. There were some genetic correlations very close to zero, meaning that for some health traits there is little gain from correlated information.

The two new indicator traits for metabolic disorders, BHB and acetone, showed both highest correlations to KET (Table 11-13). Moderate genetic correlations were found between the metabolic biomarkers and OMB. These favourable genetic correlations support the use of BHB and acetone as predictors for metabolic disorders in the GH evaluation. These results also corroborate other studies suggesting the use of these traits as indicator traits for metabolic disorders (Pryce et al., 2016).

v. Pedigree

Pedigree information used in the GH evaluations was constructed separately for each breed group (HOL, JER, RDC) from the full NAV pedigree file comprising approximately 45 million animals from Denmark, Finland and Sweden. First, animals that were not linked to the general health data files were pruned out. Genetic groups were created for those animlas with unknown parents in the genetic evaluation for all breeds (Tables 14, 15 and 16).

vi. Software and solving of the mixed model equations

DMU 5.3 sofware was used both for the breeding value predictions. Convergence criteria is set to 5000 1.0E-7 for JER, 5000 1.0E-7 for HOL and 8000 1.0E-9 for RDC. Running time is set to 48 hours with 1 and 8 cores for JER and RDC, respectively and 100 hours with 8 cores for HOL. MiX99 software was used to obtain approximated reliabilities (MiX99 Development Team, 2017).

vii. GH index

As a consequence of the introduction of BHB and acetone in phase 1 the GH index changed from four to five sub-index traits: ERP, LRP, KET, OMB and FLP. The new GH evaluation allows farmers, to select for KET and OMB disorders in addition to the already existing traits. Official breeding values are available for all five traits, but also BHB and acetone are publically available.

The revision of the Nordic Total Merit Index (NTM) in 2018 considered a new set of biological and economic assumptions, leading to a change in lactation and economics weights of all traits in the breeding goal including the GH index. Updated lactation weights for the sub-index traits change from 0.5, 0.3 and 0.2 to 0.3, 0.25 and 0.45 for lactation 1, lactation 2 and lactation 3 respectively. In May 2019 evaluation, lactation and economic weigths were updated

Economic weights

To combine all five sub-index into the GH index, EBVs on the original scale for ERP, LRP, OMB, KET and FLP are needed. Therefore, animal solutions are transformed. Detailed calculations of how EBVs are transformed back to its original scale are explained in a sepreate note (see Appendix G). The new economic values used to calculate the GH index changed as shown in table 14.

Table 14. Old and new economic values to calculate General Health index

Old GH evaluation February 2018	
All breeds	GH = 2.00*ERP + 1.05*LRP + 1.88*(2*OMB + KET)/3 + 1.75*FLP
New GH evaluation May 2019	
HOL	GH = 2.04*ERP + 1.78*LRP + 3.12* OMB + 1.45* KET + 1.57*FLP
RDC	GH = 2.04*ERP + 1.73*LRP + 3.12* OMB + 1.49* KET + 1.58*FLP
JER	GH = 2.04*ERP + 1.63*LRP + 3.05* OMB + 1.56* KET + 1.75*FLP

The general health index is published for sires and cows.

Standarization of breeding values

The standardization of the relative breeding values for ERP, LRP, KET, OMB and FLP (BHB and acetone) is described in the NAV documentation of routine genetic evaluations (Nordic Cattle Genetic Evaluation, 2017). The Standard deviations used in standardization of animal solutions in the old GH evaluation deviated largely from the ones use in the new evaluation. For BHB and acetone traits the standardization of relative breeding values followed the same guidelines as for the other traits but instead of selecting bulls born between 1997-1998 we selected bulls born between 2010-2011 since routine recording of metabolic traits started from 2012 bulls that has daughters with BHB and acetone meaures were used to build the bull genetic base

viii. Correlation between GH index and underlying traits

The expected progress of each trait, expressed as a percentage of maximum progress for that trait, when the index for general health is selected for is shown in Table 15. Maximum progress is obtained if selection is based solely on the trait in question.

Table 15. EBV correlations between GH index and the five sub-index traits for sires born after 2009 (and with a reliability of the GH index over 0.35) from old (February 2019) and the new (May 2019) GH evaluation, respectively

Breed	HOL		RDC		JER	
Evaluation	Old	New	Old	New	Old	New
ERP[a]	0.84	0.77	0.81	0.73	0.87	0.71
LRP[b]	0.64	0.51	0.52	0.56	0.44	0.47
OMB[c]	0.71	0.83	0.71	0.81	0.68	0.88
KET[d]	0.58	0.65	0.42	0.53	0.66	0.76
FLP[e]	0.59	0.56	0.26	0.30	0.63	0.63

[a]Early Reproductive Disorders (ERP), [b]Late Reproductive Disorders (LRP), [c]Other Metabolic Disorders (OMB), [d]Ketosis (KET), [e]Feet&Legs (FLP).

ix. Reliabilities

Approximate EBV reliabilities were computed by the method of Jamrozik et al. (2000), implemented in the Apax99 software (MiX99 Development Team, 2017). Two other approximation methods in Apax99 Misztall and Wiggans (1988) and Tier and Meyer method (2004) gave inconsistent results. More information on the study about reliability estimation can be found in the Appendix H.

For bulls and cows, overall reliabilities across parities are calculated, for the eight traits in Table 15, by using weights 0.3, 0.25 and 0.45 for the first, second, and third parity, respectively.

The benefit of including BHB and acetone in the GH evaluation was evaluated by looking at the increase in cow's EBV reliability. As expected, the largest increase in reliability for the veterinary treatments was for KET in all three breeds followed by OMB (Table 16).

Table 16. Approximate reliabilities for seven sub-traits and the GH index, for cows with observations but without own progeny, separate for cows with or without BHB and Acetone (Ace) observations. (N = number of cows in that group)

Breed	BHB&Ace observations	ERP[a]	LRP[b]	OMB[c]	KET[d]	FLP[e]	GH[f]	BHB[g]	ACE[h]	N
HOL	Yes	0.31	0.27	0.34	0.35	0.28	0.32	0.43	0.40	576,124
	No	0.29	0.26	0.28	0.27	0.26	0.29	0.25	0.26	1,972,074
RDC	Yes	0.29	0.27	0.32	0.34	0.26	0.30	0.40	0.37	98,774
	No	0.28	0.27	0.28	0.30	0.26	0.29	0.27	0.28	1,462,266
JER	Yes	0.27	0.25	0.28	0.30	0.27	0.29	0.35	0.32	89,326
	No	0.26	0.24	0.25	0.25	0.25	0.26	0.21	0.22	190,240

[a]Early Reproductive Disorders (ERP), [b]Late Reproductive Disorders (LRP), [c]Other Metabolic Disorders (OMB), [d]Ketosis (KET), [e]Feet&Legs (FLP), General Health index, [g]β-hydroxybutyrate (BHB) and [h]Acetone (ACE).

x. Genetic trends

The genetic improvement for general disease resistance of dairy breeds in Nordic countries are shown on the patterns of genetic trends shown on the Figures 2, 3 and 4 below.

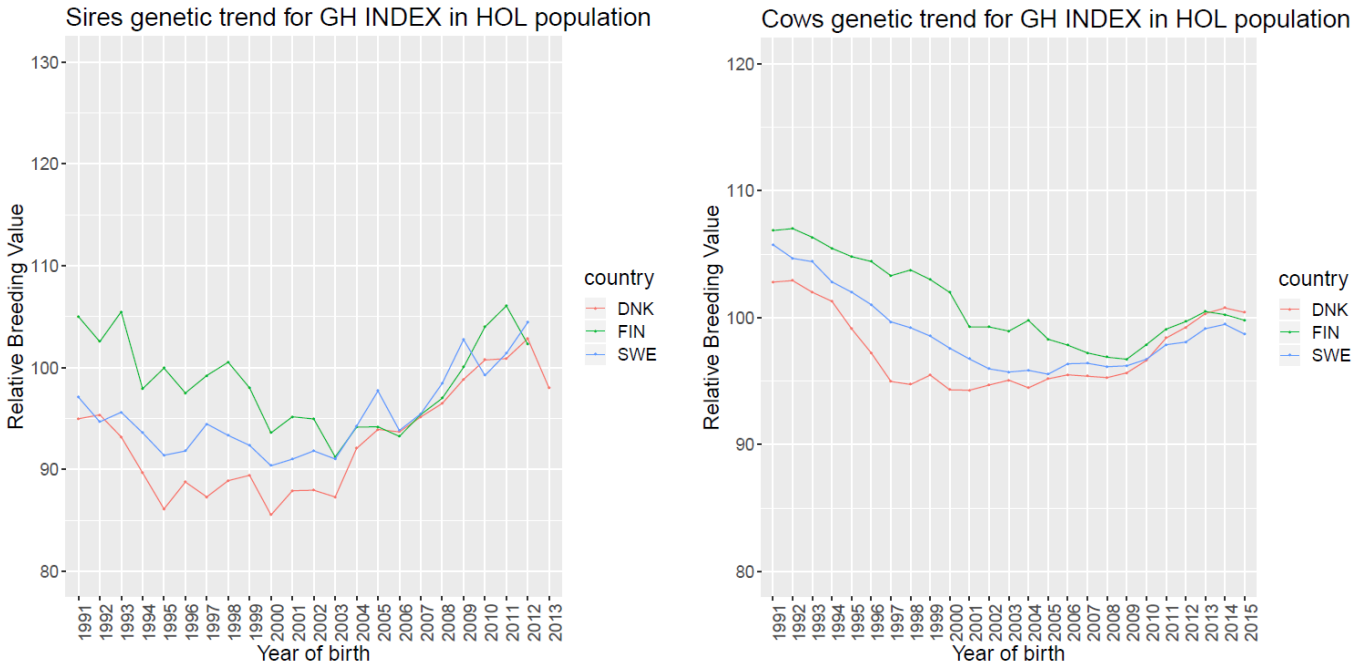


Figure 2. Genetic trends for Holstein AI sires with at least 50 daughters in 10 herds

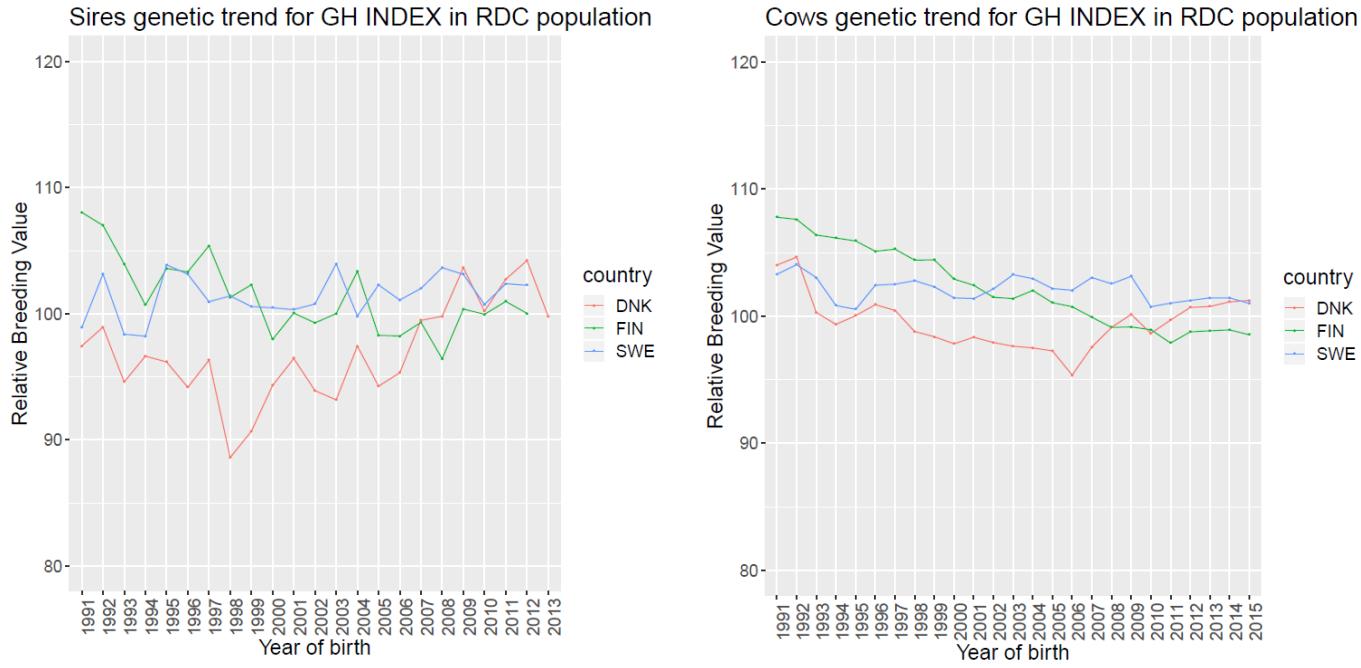


Figure 3. Genetic tends for RDC AI sires with at least 50 daughters in 10 herds

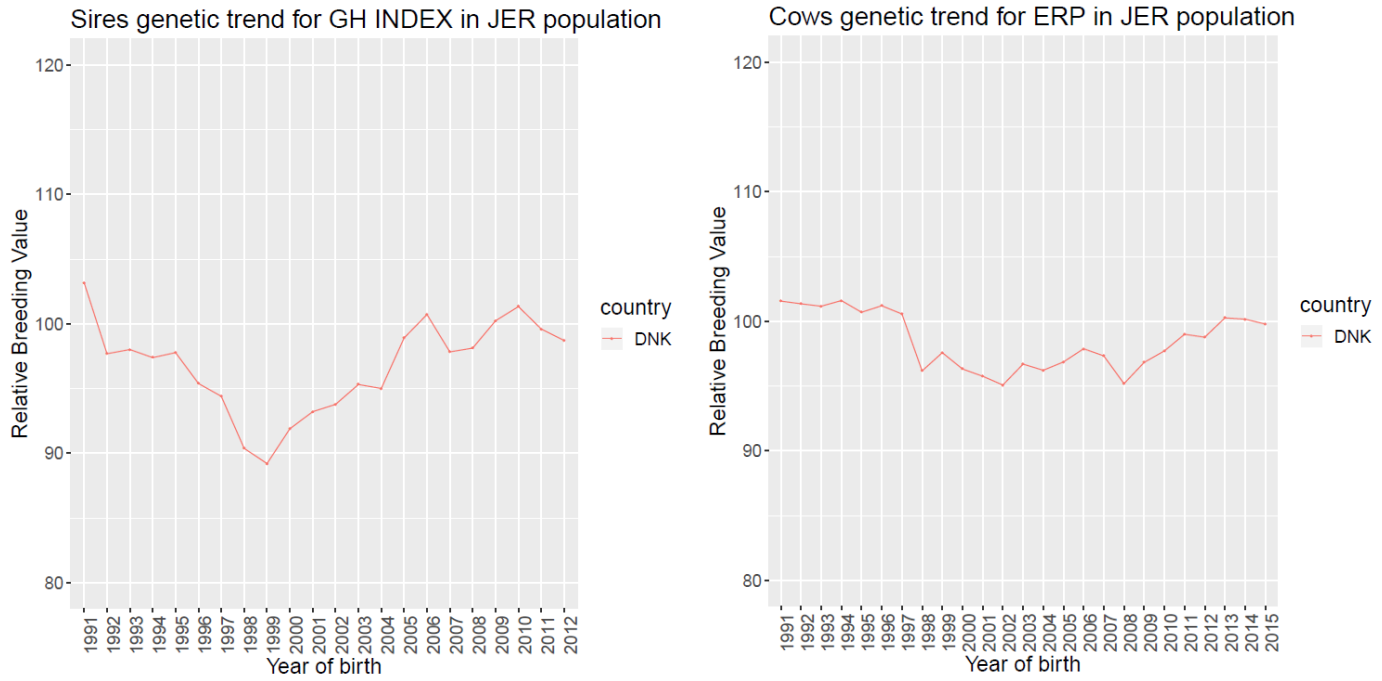


Figure 4. Genetic trends for Jersey AI sires with at least 50 daughters in 10 herds

xi. Streamlining

Cleaning up of unused programs, variables and routines.

xii. Future improvements

Swedish BHB and acetone data will be included once there is sufficient data. It is estimated that a requirement of at least two years of data is needed to be included in the current GH evaluation

xiii. References

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