Update of genetic parameters and inclusion of Swedish and Finnish β-hydroxybutyrate and acetone measurements to the Nordic General Health evaluation model

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Abstract

The Nordic (Denmark, Finland, Sweden) General Health (GH) evaluation model was introduced in 2008 and significantly revised between 2017 and 2019. The current GH index includes reproductive disorders, feet and leg disorders, clinical ketosis, and other metabolic diseases recorded as veterinary treatments. Acetone and β-hydroxybutyrate (BHB) measurements from milk mid-infrared (MIR) spectra are used as correlated traits in mixed model equations and supplied primarily from Danish herds. Although the collection of Swedish acetone and BHB measurements began in 2018, this data has not yet been incorporated into official evaluations. Furthermore, new Finnish measurements are available only for BHB and predicted from MIR using a different equation than those used in Denmark and Sweden.

Swedish BHB and acetone, along with Finnish BHB data, were integrated into the official Nordic evaluation pipeline. Genetic correlations between Finnish and Swedish/Danish BHB were estimated at around 0.8. Genetic parameters were newly estimated for Holstein, Red Dairy Cattle (RDC), and Jersey breeds. The largest changes in heritability and genetic correlations between clinical and subclinical ketosis were observed for RDC and Jersey. Correspondingly, the largest changes in breeding values were observed for RDC and JER Nordic AI bulls. The updated model is planned to be implemented in November 2025.

Key words: BHB, Nordic Dairy Cattle Evaluation, Metabolic disorders, Variance component

Introduction

Metabolic disorders are commonly observed conditions in high-yielding dairy cattle, affecting health, productivity, and economics of a herd. Ketosis and subclinical ketosis are considered as the most prevalent metabolic disorders in dairy cows (Eduardo and Barrientos-Blanco, 2024). Joint selection for resistance to clinical ketosis in Denmark, Finland, and Sweden (DFS) began in 2008 when the first General Health (GH) model and index were developed (Johansson et al., 2008). In 2017, the GH model was enhanced by inclusion of milk biomarker traits β-hydroxybutyrate (BHB) and acetone (ACE) to perform selection against subclinical ketosis (Rius-Villarasa et al., 2018).

Biomarkers show a strong correlation with clinical ketosis and other metabolic diseases. In DFS, BHB and ACE indexes are not summands of the GH index and only used as correlated traits in the mix model equation. Phenotypes are measured using mid-infrared (MIR) milk spectra during the first 60 days of lactation. In the current workflow, biomarker data primary originates from Denmark; data from Finland is a fixed data set collected between 2016 and 2019, and there is no data from Sweden. Due to limited data for Red Dairy Cattle (RDC) and

Jersey (JER) available for variance component (VC) estimation, parameters were derived from the Holstein breed (HOL).

The aims of the current project were: 1) inclusion of Swedish BHB and ACE, and Finnish BHB data into the Nordic GH model; 2) estimation of genetic parameters for BHB and ACE in RDC and JER; 3) investigation of differences of the BHB and ACE phenotypes between countries.

Materials and Methods

Data

The Nordic GH model includes five treatment traits and two biomarker traits (Table 1). Treatment data was previously described in Rius-Villarasa et al. (2018) and include veterinary records for early and late reproductive disorders (ERP and LRP), feet and legs disorders (FL), clinical ketosis (KET), and other metabolic diseases (OMB). Biomarker data (BHB and ACE) were based on mid-infrared spectra analyzed by Foss MilkoScan (MilkoScan FT+, Foss Electric A/S, Hillerød, Denmark). For Denmark (DNK) and Sweden (SWE) BHB and ACE concentrations in milk were predicted from the spectra using the Foss prediction equation. For Finland (FIN) BHB concentrations in blood were predicted from the spectra using the approach shown in Kostensalo et al. (2023). Subset of FIN cows (n=134,232) had BHB phenotypes predicted using both the Foss and Kostensalo et al. (2023); however, BHB from the Foss predictions were not used in the estimation of genetic parameters or breeding values.

Table 1: Number of cows with records by trait and breed.

Trait*	HOL	RDC	JER
erp1	7802789	4366832	668042
lrp1	7712623	4326174	655709
fl1	7712623	4326174	655709
ket1	7712623	4326174	655709
omb1	7712623	4326174	655709
bhb1	1422300	181433	252271
ace1	1422300	181433	252271
erp2	5531607	3166152	462345
lrp2	5463053	3132902	454798
fl2	5463053	3132902	454798
ket2	5463053	3132902	454798
omb2	5463053	3132902	454798
bhb2	1121718	147311	200307
ace2	1121718	147311	200307
erp3	3488821	1992511	307564
lrp3	3435200	1966113	301615
fl3	3435200	1966113	301615
ket3	3435200	1966113	301615
omb3	3435200	1966113	301615
bhb3	789610	101109	142485
ace3	789610	101109	142485

*erp – early reproductive disorder; lrp – late reproductive disorder; fl – feet and legs disorders; ket – clinical ketosis; omb – other metabolic disease; bhb – β-hydroxybutyrate; ace – acetone.

Data for variance component estimation

For the estimation of genetic parameters subsets with highly reliable bulls were used. The subsets were defined as bulls with ≥ 50 daughters in ≥ 25 herds for HOL, and ≥ 25 daughters in ≥ 10 herds for RDC and JER. For BHB and ACE, records from DNK collected from 2019 onwards were used. Genetic parameters for KET, OMB, BHB, and ACE were calculated using breed x country specific combinations. Data from DNK were used for HOL and JER breeds, while SWE data were used for RDC (Table 2).

Table 2: Number of sires and cows by trait and breed used for 12 trait VCE.

Trait*	HOL		RDC		JER	
	sires	cows**	sires	cows**	sires	cows**
bhb1	546	493	295	69	162	109
ace1	546	493	295	69	162	109
ket1	528	414	295	65	153	89
omb1	528	414	295	65	153	89
bhb2	515	307	283	35	150	64
ace2	515	307	283	35	150	64
ket2	459	229	277	32	130	46
omb2	459	229	277	32	130	46
bhb3	447	169	238	17	126	33
ace3	447	169	238	17	126	33
ket3	383	116	230	14	110	21
omb3	383	116	230	14	110	21

*erp – early reproductive disorder; lrp – late reproductive disorder; fl – feet and legs disorders; ket – clinical ketosis; omb – other metabolic disease; bhb – β-hydroxybutyrate; ace – acetone
**Cows are in thousands (*1000)

Mixed model equation

The following mixed model equations were applied for veterinary treatments and biomarkers:

$$Y_{ijkl} = CHY_i + CCA_j + CYM_k + u_l + e_{ijkl}$$

and

$$Y_{ijklm} = CHY_i + CCA_j + CYM_k + L1_{ijklm} + L2_{ijklm} + u_l + pe_m + e_{ijklm}$$

Where, Y_{ijkl} and Y_{ijklm} were individual observations for veterinary treatments and metabolic biomarkers, respectively. Fixed effects were: CHY_i – the country-herd-year, CCA_j – the country-calving-age; CYM_k – the country-heard-month. $L1_{ijklm}$ and $L2_{ijklm}$ were regression for lactation stage modelled as a first and second order Legendre polynomial. Random effects pe_m and e_{ijkl} were permanent environment and residual effects, respectively. Random effect u_l is the animal effect in the breeding value estimation and sire effect in the variance component estimation.

Variance component estimation

Variance component estimation was performed using sire model and DMUv6. r.5.6 software (Madsen and Jensen, 2024) in two setups: 1) to estimate genetic correlations between countries and establish adjustment factors (κ) for BHB and ACE where each country-parity combination was treated as a separate trait; 2) to estimate new parameters for routine use, a 12-trait model including BHB, ACE, KET, and OMB in parities 1-3 was used. Newly estimated parameters for BHB and ACE (6x6 block) were used to replace current routine estimates. Newly estimated covariances between BHB[ACE] and OMB, and between BHB[ACE] and KET were used to update routine covariances. The matrix bending procedure (Jorjani et al., 2003) was applied to make the 21 trait (co)variance matrix positive definite.

Biomarkers data adjustment

Prior to breeding value evaluation BHB and ACE records were multiplied by country-parity specific κ calculated as:

$$\kappa = \sqrt{4\sigma^2_{s\_des}/4\sigma^2_{s\_obser}}$$

Where $\sigma^2_{s\_des}$ is sire genetic variance in desired breed-country-parity strata, and $\sigma^2_{s\_obser}$ is sire genetic variance in observed breed-country-parity strata. For HOL and JER the variance was estimated based on DNK data, and for RDC variance was estimated based on SWE data.

Because sire variance was not possible to estimate for FIN and SWE JER, variance ($\sigma^2_{s\_CNTR}$) was approximated by parity using following formula:

$$\sigma^2_{s\_CNTR} = \left(\frac{\sigma^2_{s\_DNK}}{\sigma^2_{p\_DNK}}\right) * \sigma^2_{p\_CNTR},$$

where $\sigma^2_{s\_DNK}$ is a sire variance in DNK data, $\sigma^2_{p\_DNK}$ is a phenotypic (data) variance in DNK data, and $\sigma^2_{p\_CNTR}$ is a phenotypic (data) variance in FIN or SWE.

Results & Discussion

Biomarker data difference

Inter-country genetic correlations of BHB and ACE in parity 1 for HOL and RDC are shown in Table 3. The average genetic correlation between FIN and the other countries was 0.84. A similar correlation (0.81) was obtained from regression of FIN cows phenotypes predicted using the Foss vs Kostensalo et al. (2023) approach (Figure 1).

Table 3: Inter-country genetic correlations for BHB and ACE in parity 1

Countries	HOL	RDC
	BHB	
SWE x DNK	0.95	0.97
FIN x SWE	0.86	0.88
FIN x DNK	0.84	0.79
	ACE*	
SWE x DNK	0.95	0.97

*No ACE data available for Finland

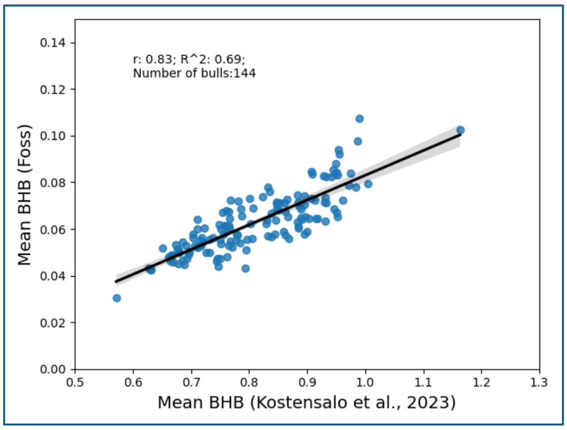

Figure 1. Scatter Plot and Linear Regression of first parity mean BHB phenotypes of daughters of HOL bulls with >50 daughters.

The correlation between milk and blood BHB concentration was expectedly high. However, FIN BHB trait is similar, but not identical to DNK and SWE. The scale difference in the phenotype was handled by data adjustment factor (κ). As BHB and ACE are not summand of the GH index it was decided to use blended-origin trait.

Genetic parameters

Newly estimated heritability, genetic and permanent environment correlations for BHB and ACE are presented in Table 4. For HOL the heritability was slightly lower for BHB (average: 0.04) and slightly higher (average: 0.01) for ACE compared to current routine estimates. Changes in correlations ranged from -0.10 to 0.14. For RDC the heritability increased for both BHB and ACE, with a range from 0.01 to 0.06. Overall heritability in RDC was estimated to be higher than in other breeds. Genetic correlation between BHB and ACE, and between parities, also increased by 0.01-0.33. For JER the heritability increased for both BHB and ACE, with an average of 0.03. Genetic and permanent environment correlations increased in the range of 0.02 to 0.37. Overall changes for HOL were concluded to be limited, but sufficient and positively accepted for RDC and JER.

Genetic correlations between biomarkers and metabolic traits are shown in Table 5. For HOL, the largest difference compared to currently used parameters were observed for the BHB x KET and ACE x OMB combinations, with decreases of 0.16 and 0.17, respectively. For JER, a slight increase (0.13) was observed for the BHB x OMB correlation. A large decrease in correlation was observed in RDC for BHB x OMB and ACE x OMB pairs - 0.15 and 0.36, respectively. Although the decrease in correlation is unfavorable, it is important to note that the RDC parameters were previously approximated from HOL, whereas they are now directly estimated.

Table 4. Heritability, genetic and permanent environment correlation in BHB and ACE parity 1-3.

			Holstein			
Traits	BHB1	ACE1	BHB2	ACE2	BHB3	ACE3
BHB1	**0.08***	0.88	0.85	0.72	0.78	0.66
ACE1	0.53	**0.05**	0.73	0.80	0.67	0.70
BHB2	0.00	0.00	**0.09**	0.89	0.95	0.86
ACE2	0.00	0.00	0.60	**0.05**	0.87	0.94
BHB3	0.00	0.00	0.00	0.00	**0.08**	0.92
ACE3	0.00	0.00	0.00	0.00	0.62	**0.04**
			Red Dairy Cattle			
Traits	BHB1	ACE1	BHB2	ACE2	BHB3	ACE3
BHB1	**0.14**	0.89	0.93	0.81	0.90	0.85
ACE1	0.68	**0.09**	0.83	0.89	0.77	0.87
BHB2	0.00	0.00	**0.14**	0.90	0.93	0.88
ACE2	0.00	0.00	0.71	**0.09**	0.80	0.91
BHB3	0.00	0.00	0.00	0.00	**0.13**	0.92
ACE3	0.00	0.00	0.00	0.00	0.72	**0.09**
			Jersey			
Traits	BHB1	ACE1	BHB2	ACE2	BHB3	ACE3
BHB1	**0.08**	0.93	0.86	0.62	0.81	0.54
ACE1	0.56	**0.05**	0.82	0.74	0.79	0.69
BHB2	0.00	0.00	**0.09**	0.84	0.94	0.73

ACE2	0.00	0.00	0.60	**0.04**	0.81	0.87
BHB3	0.00	0.00	0.00	0.00	**0.08**	0.84
ACE3	0.00	0.00	0.00	0.00	0.65	**0.04**

*Diagonal – heritability, upper triangle – genetic correlation, lower triangle – permanent environment correlation.

Table 5. Genetic correlations between biomarker (BHB and ACE) and metabolic traits (KET) in first lactation.

Breed	HOL		RDC		JER	
Traits	BHB	ACE	BHB	ACE	BHB	ACE
KET	0.56	0.59	0.63	0.63	0.64	0.67
OMB	0.47	0.48	0.31	0.26	0.46	0.47

Breeding value.

Impact of the new genetic parameters and added biomarker data on EBVs is presented through; 1) Correlation of the current and new sub-indexes (Figure 2, 4 & 6), and 2) Reranking of sub-indexes (Figure 3, 5 & 7) in Nordic AI bulls with ≥20 daughters.

Correlation was high (>0.95) and reranking was limited for HOL bulls born after 2015. The largest changes were observed for BHB, ACE, KET, and OMB traits. For this group of traits, low correlation (<0.95) and a mean reranking > 1 index unit were observed for bulls born 2010-2014, due to the absence of BHB and ACE data before 2018 (historic Danish BHB and ACE data was discarded from the data).

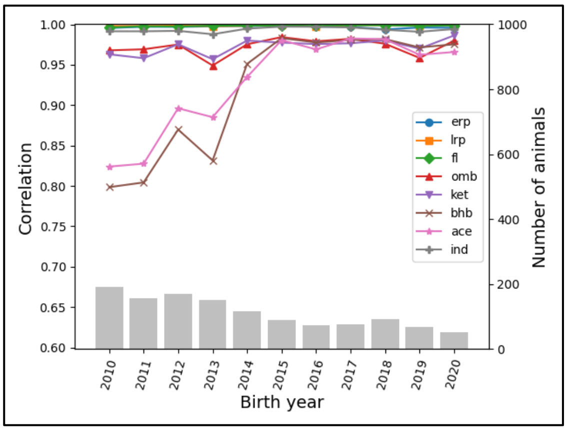

Figure 2. Correlation of current and new GH (sub)indexes in HOL AI bulls with ≥ 20 daughters.

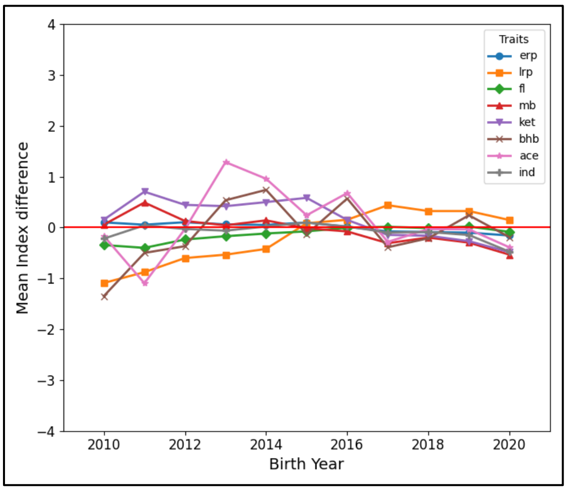

Figure 3. Mean index difference between current and new GH model in HOL AI bulls with ≥ 20 daughters.

In RDC, the correlation was below 0.90 for BHB and ACE across all year classes. For OMB and KET, the correlation declined from 2016 onwards which can be explained by a gap in SWE treatment data recording during 2023-2025 and absence of ACE records in FIN data. The main sources of RDC data were SWE and FIN. High reranking (> 1 index unit) was observed in the BHB and ACE subindexes of bulls born before 2015.

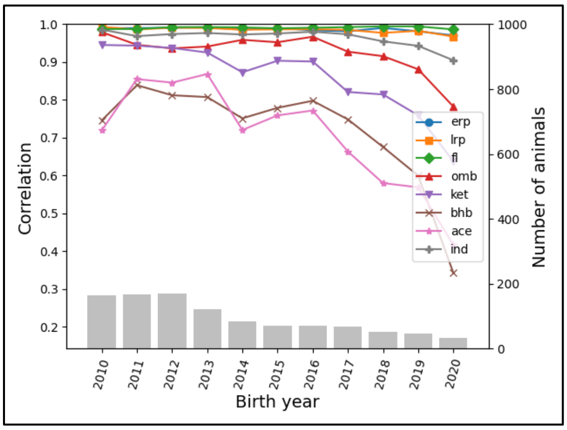

Figure 4. Correlation of current and new GH (sub)indexes in RDC AI bulls with ≥ 20 daughters.

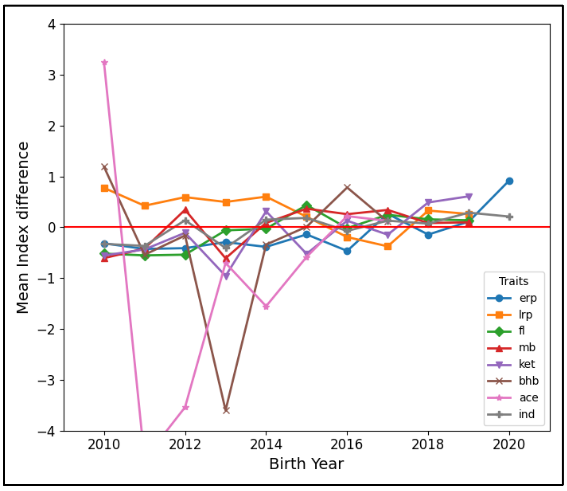

Figure 5. Mean index difference between current and new GH model in RDC AI bulls with ≥ 20 daughters.

For JER, the correlation between current and new models for BHB and ACE was below 0.9 in bulls born between 2010-2013. The correlation below 0.95 was also observed for KET. The highest reranking was seen in BHB, ACE, OMB, KET, and LRP. Presumably, the LRP trait was influenced through its correlation with OMB and KET. The maximum observed mean reranking was 2 index units.

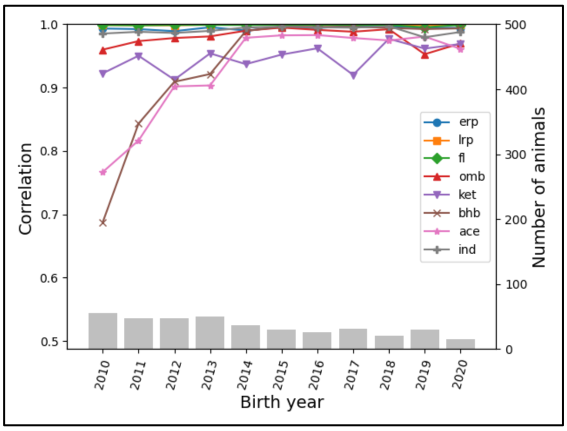

Figure 6. Correlation of current and new GH (sub)indexes in JER AI bulls with ≥ 20 daughters.

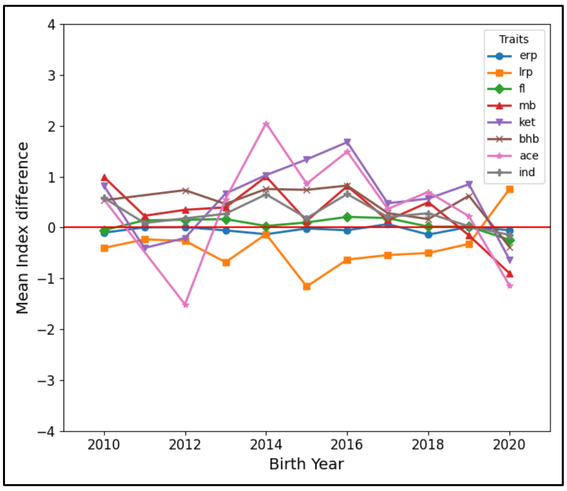

Figure 7. Mean index difference between current and new GH model in JER AI bulls with ≥ 20 daughters.

Correlation and reranking patterns were as expected. Stepwise changes to the model showed that the largest effect was caused by new genetic parameters and changes in data structure.

Conclusions

The inclusion of Swedish BHB and ACE records has expanded data set, especially for RDC breed. Genetic parameters for RDC and JER were based on direct estimation rather than approximation and better align with the data. The new parameters caused greater reranking in RDC and JER than in HOL. Aceton records for RDC will be predominantly based on SWE data, as FIN has stopped ACE recording.

The updated GH index will be available to Nordic farmers starting in November 2025. The presence of national data is expected to increase trust from Swedish farmers towards the GH index.

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