Update of Nordic General Health prediction model.

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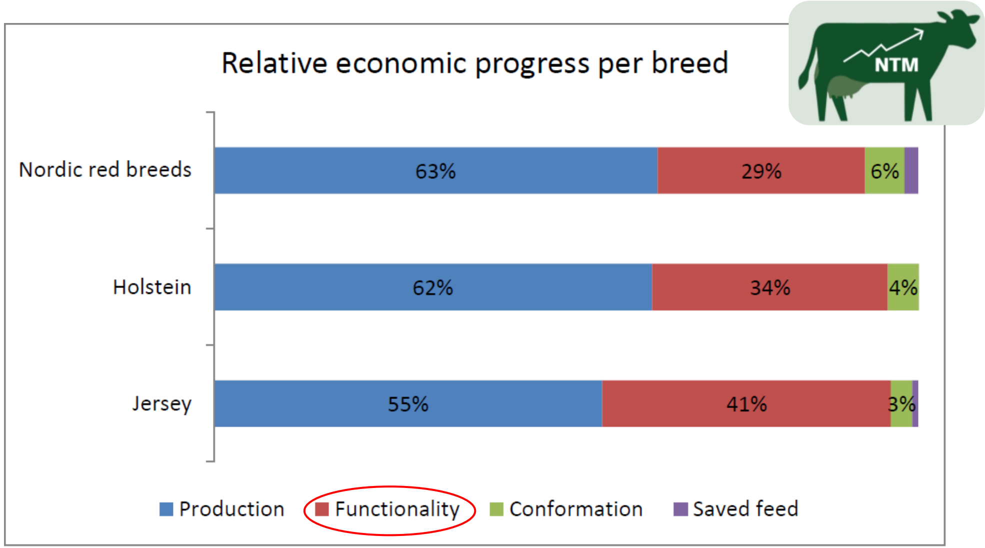
Nordic Functional traits



- Fertility
- Calving
- Longevity
- Milkability
- Temperament
- Udder health
- Claw health
- General health (model)
  - Feet and legs
  - Reproductive disorders
    - Early
    - Late
  - Metabolic disorders
    - Ketoses
    - Other Metabolic
  - Subclinical ketoses

Nordic General Health (GH) model

General Health

- Seven traits x three parity (21 trait) Animal and Single-step model for HOL, RDC, and JER
- Model was developed in 2019 (…link)
- GH Index = FL + ERP + LRP + KET + OMB
- Subclinical ketoses is NOT included in GH Index and used as correlated trait

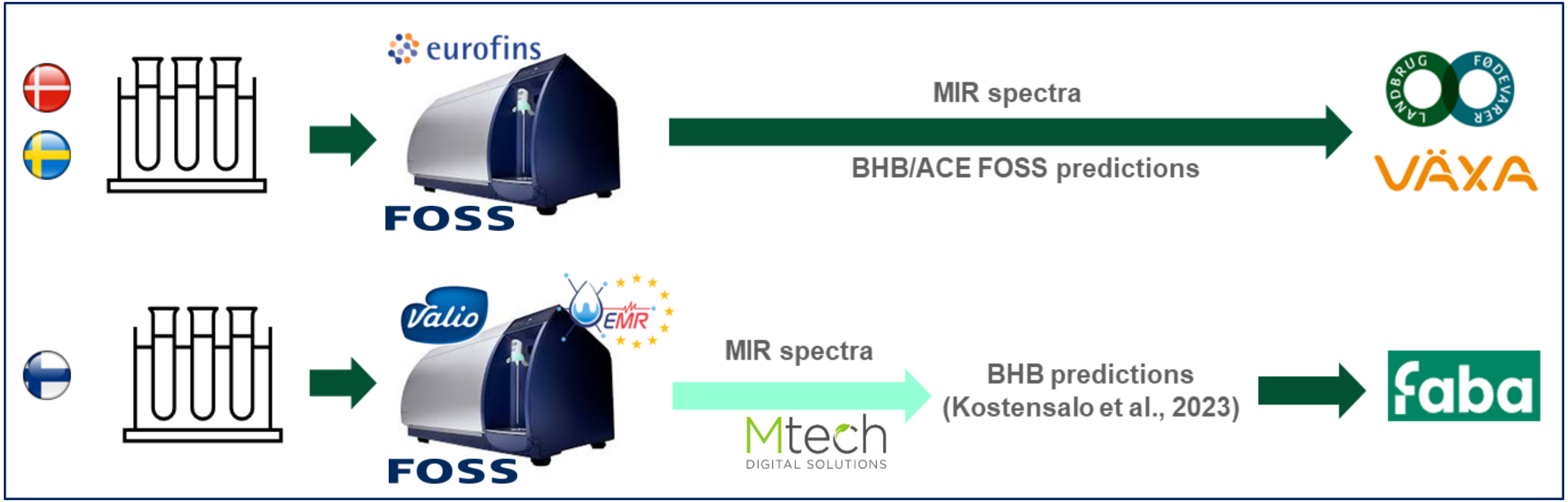
Subclinical ketoses

- Quantitative trait
- Beta-hydroxybutyrate (BHB) and Acetone (ACE) MIR measurements from milk sample
- Up to 60 days in lactation
- Include updatable DNK data, non-updatable FIN data, and no SWE data
- Variance components (VC) in RDC and JER were derived from HOL

Why to update?

- Data became available for SWE but no pipeline exist
- More data accumulated for RDC – VC can be [re]estimated
- More data accumulated for JER – VC can be [re]estimated
- Harmonize breed selection rules for FIN data
- Data became available for FIN, but…
    - No ACE records
    - BHB predicted from MIR spectra using different model

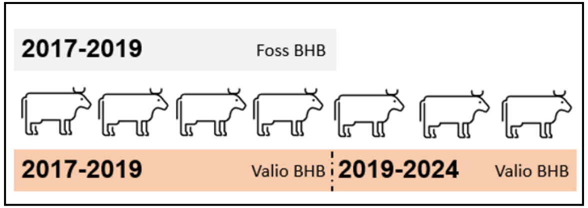
DFS BHB and ACE pipeline (June 2025)



- BHB and ACE in DNK and SWE is predicted using FOSS equation
- BHB and NEFA in FIN is predicted using Kostensalo et al. (2023) for Valio herds only
- DNK/SWE BHB phenotype is a BHB in milk, FIN BHB is a BHB in blood
- FIN analyser use EMR EEIG standardization service

BHB prediction in Finland (FOSS vs Valio)

- Valio was ordering FOSS BHB and storing raw MIR in 2017-2019

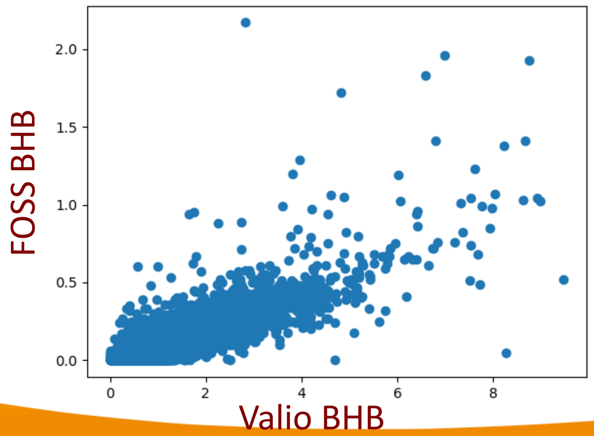


2017-2019 Foss BHB

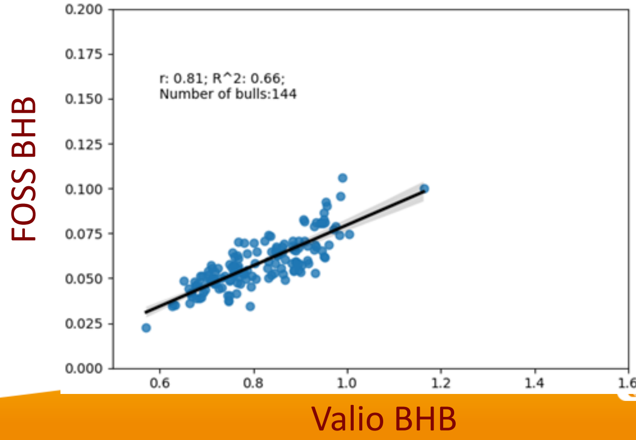
2017-2019 Valio BHB **2019-2024** Valio BHB

- Correlations between phenotypes are ~0.8
- Scale is different

HOL cows (BHB phenotype parity 1)

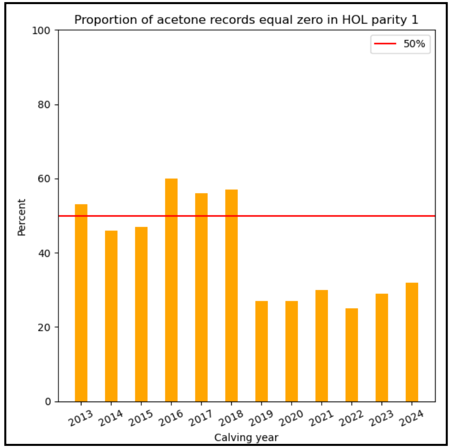


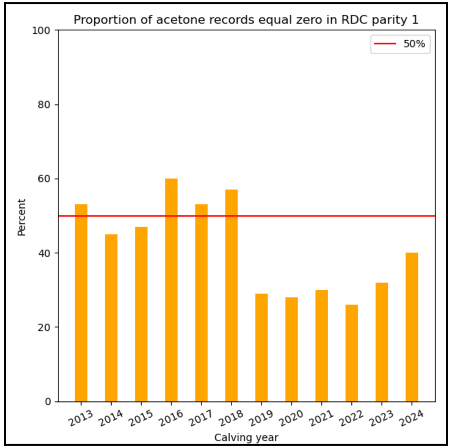
HOL sires with >50d (mean BHB pheno parity 1)



Skewed ACE distribution in DNK

- One of data quality check was ‘Local Abnormality Approach’
- Acetone records collected in DNK in period 2013-2019 show overrepresentation of rounded zero [0] value
- Over 50% of records were equal to [0]





- Records collected before CY 2019 were removed for VC and BV estimation.

Variance component estimation (VCE)

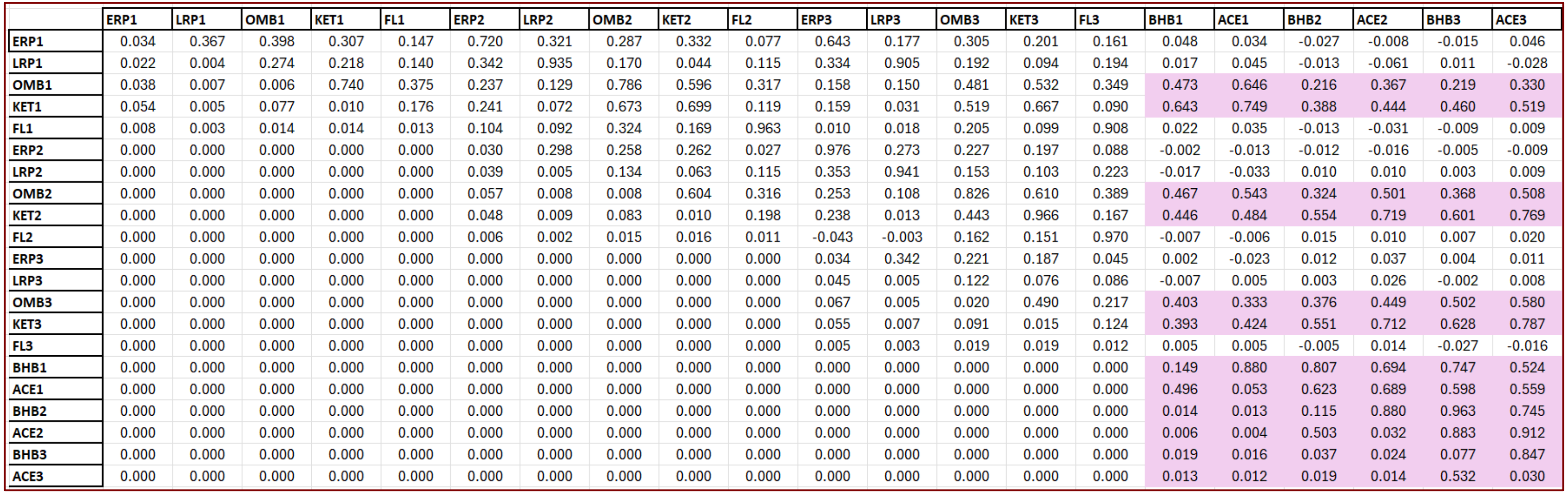
- VCE was performed using Sire Model (AI-REML, BY >2000, sires with > 50 [25] dt x hrd)
- BHB and ACE VCE was performed for each country in RDC/HOL and DNK in JER
- Genetic correlations for BHB and ACE between DFS in HOL / RDC

	BHB Parity 1		ACE Parity 1	
Country	HOL	RDC	HOL	RDC
FIN x SWE	0.86	0.88	xxx	xxx
FIN x DNK	0.84	0.79	xxx	xxx
SWE x DNK	0.95	0.97	0.95	0.97

- Estimates from DNK data were decided to be used for HOL and JER
- Estimates from SWE data were decided to be used for RDC
- BHB x ACE x KET x OMB VCE was performed for decided [breed x country] tuples

Variance component update

- Variance - Covariance matrix of GH has 21 trait
- HOL correlation table (upper – genetic; lower – pe + e; diagonal – h2)



	ERP1	LRP1	OMB1	KET1	FL1	ERP2	LRP2	OMB2	KET2	FL2	ERP3	LRP3	OMB3	KET3	FL3	BHB1	ACE1	BHB2	ACE2	BHB3	ACE3
ERP1	0.034	0.367	0.398	0.307	0.147	0.720	0.321	0.287	0.332	0.077	0.643	0.177	0.305	0.201	0.161	0.048	0.034	-0.027	-0.008	-0.015	0.046
LRP1	0.022	0.004	0.274	0.218	0.140	0.342	0.935	0.170	0.044	0.115	0.334	0.905	0.192	0.094	0.194	0.017	0.045	-0.013	-0.061	0.011	-0.028
OMB1	0.038	0.007	0.006	0.740	0.375	0.237	0.129	0.786	0.596	0.317	0.158	0.150	0.481	0.532	0.349	0.473	0.646	0.216	0.367	0.219	0.330
KET1	0.054	0.005	0.077	0.010	0.176	0.241	0.072	0.673	0.699	0.119	0.159	0.031	0.519	0.667	0.090	0.643	0.749	0.388	0.444	0.460	0.519
FL1	0.008	0.003	0.014	0.014	0.013	0.104	0.092	0.324	0.169	0.963	0.010	0.018	0.205	0.099	0.908	0.022	0.035	-0.013	-0.031	-0.009	0.009
ERP2	0.000	0.000	0.000	0.000	0.000	0.030	0.298	0.258	0.262	0.027	0.976	0.273	0.227	0.197	0.088	-0.002	-0.013	-0.012	-0.016	-0.005	-0.009
LRP2	0.000	0.000	0.000	0.000	0.000	0.039	0.005	0.134	0.063	0.115	0.353	0.941	0.153	0.103	0.223	-0.017	-0.033	0.010	0.010	0.003	0.009
OMB2	0.000	0.000	0.000	0.000	0.000	0.057	0.008	0.008	0.604	0.316	0.253	0.108	0.826	0.610	0.389	0.467	0.543	0.324	0.501	0.368	0.508
KET2	0.000	0.000	0.000	0.000	0.000	0.048	0.009	0.083	0.010	0.198	0.238	0.013	0.443	0.966	0.167	0.446	0.484	0.554	0.719	0.601	0.769
FL2	0.000	0.000	0.000	0.000	0.000	0.006	0.002	0.015	0.016	0.011	-0.043	-0.003	0.162	0.151	0.970	-0.007	-0.006	0.015	0.010	0.007	0.020
ERP3	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.034	0.342	0.221	0.187	0.045	0.002	-0.023	0.012	0.037	0.004	0.011
LRP3	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.045	0.005	0.122	0.076	0.086	-0.007	0.005	0.003	0.026	-0.002	0.008
OMB3	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.067	0.005	0.020	0.490	0.217	0.403	0.333	0.376	0.449	0.502	0.580
KET3	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.055	0.007	0.091	0.015	0.124	0.393	0.424	0.551	0.712	0.628	0.787
FL3	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.003	0.019	0.019	0.012	0.005	0.005	-0.005	0.014	-0.027	-0.016
BHB1	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.149	0.880	0.807	0.694	0.747	0.524
ACE1	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.496	0.053	0.623	0.689	0.598	0.559
BHB2	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.014	0.013	0.115	0.880	0.963	0.745
ACE2	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.006	0.004	0.503	0.032	0.883	0.912
BHB3	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.019	0.016	0.037	0.024	0.077	0.847
ACE3	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.013	0.012	0.019	0.014	0.532	0.030

- Marked parts were updated

Variance component update (continue)

- Variance - Covariance matrix of GH has 21 trait
- Genetic:
  - New: *(co)variance* of BHB and ACE
  - New: *Cov* of BHB (ACE) and OMB (KET)
  - Old: Rest parts of *Var-Cov*
- Permanent environment:
  - New: *(co)variance* of BHB and ACE
  - Rest traits have no PE effect
- Residual:
  - New: *(co)variance* of BHB and ACE
  - Old: *(co)variance* of rest
- *Cov* of BHB/ACE and OMB/KET in second and third parity were projected from the first
- Matrix bending was performed using Jorjani et al. (2003)

Summary of updates

VC file change:

- HOL >> limited change in h^2 and correlation of BHB x ACE x KET x OMB
- RDC >> slight increase in h^2 (~0.04), changes in cor of BHB x ACE x KET x OMB up to 0.2
- JER >> slight increase in h^2 (~0.03), changes in cor of BHB x ACE x KET x OMB up to 0.4

Data selection:

- ACE and BHB data from DNK Calving Year 2019 – onwards
- FIN RDC include RDC + FIC; FIN HOL only HOL + RED HOL

Adjustment of BHB and ACE:

- BHB and ACE phenotype in each country x parity strata multiplied by strata specific K

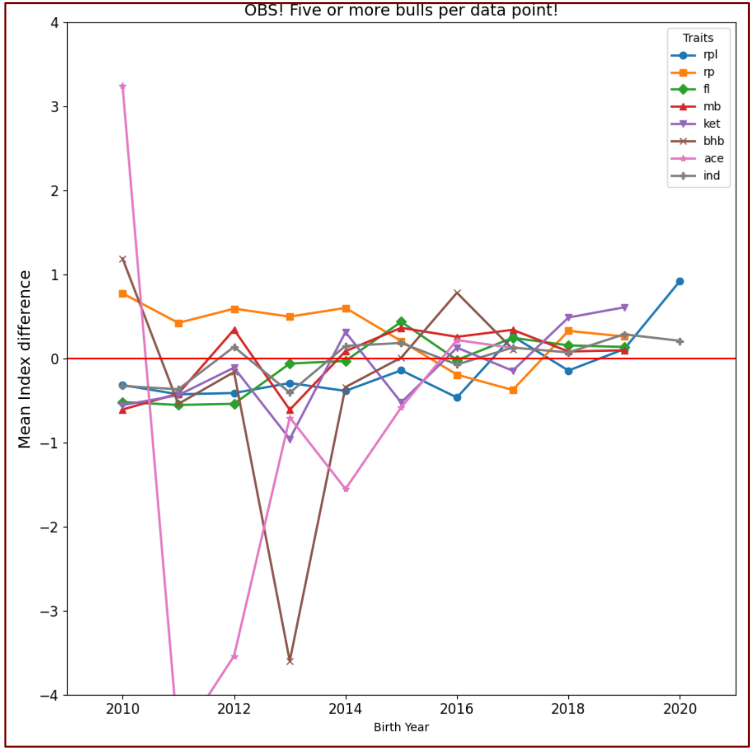
$$K = \sqrt{(4 * \boldsymbol{Var\_sire\_des\_cntr\_par})/(4 * \boldsymbol{Var\_sire\_cntr\_par})},$$

where $\boldsymbol{Var\_sire\_des\_cntr\_par}$ – sire variance in desired strata

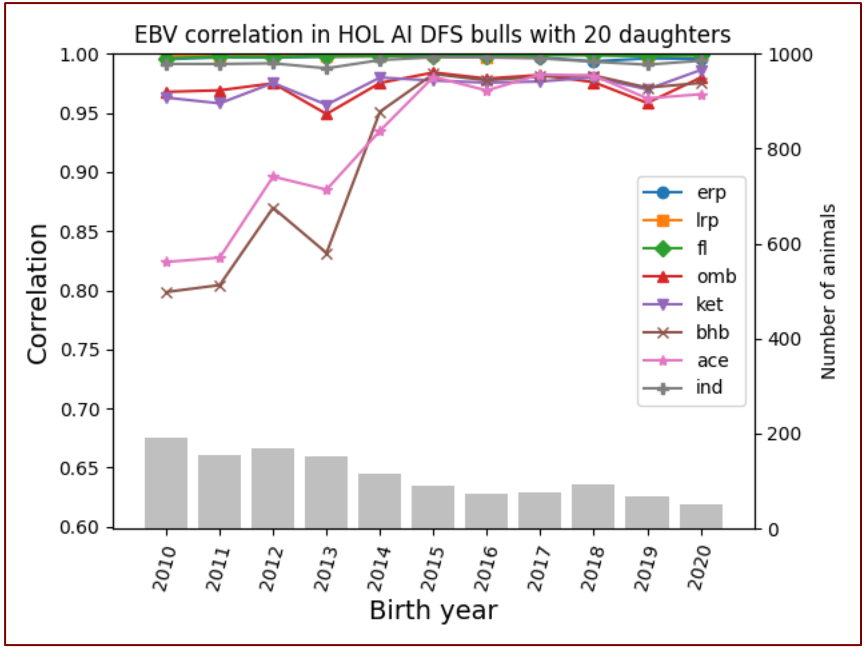
$\boldsymbol{Var\_sire\_cntr\_par}$ – sire variance in strata

Results – effect of changes on EBV (HOL)

Reranking in AI bulls with >=20 daughters

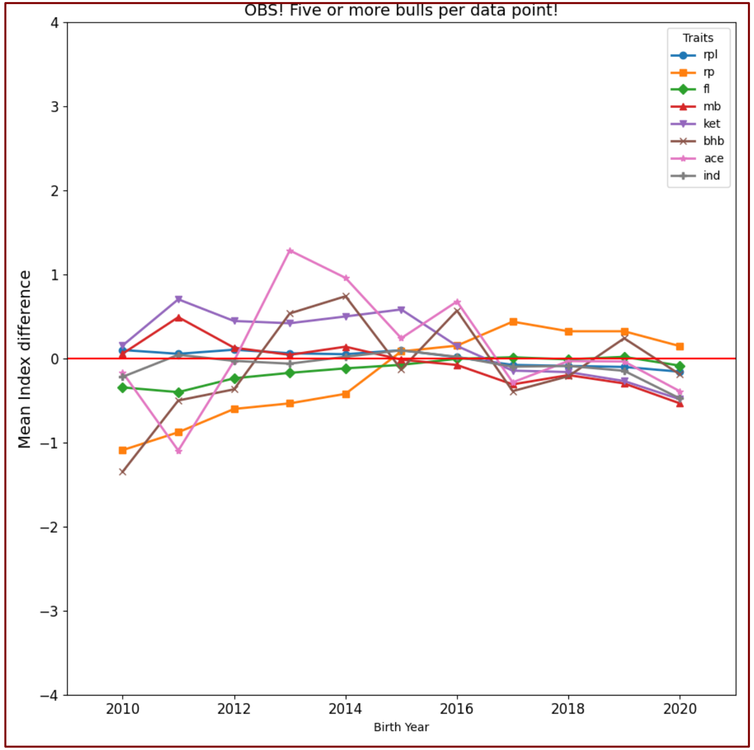


Correlation between official and new model



Results – effect of changes on EBV (RDC)

Reranking in AI bulls with >=20 daughters



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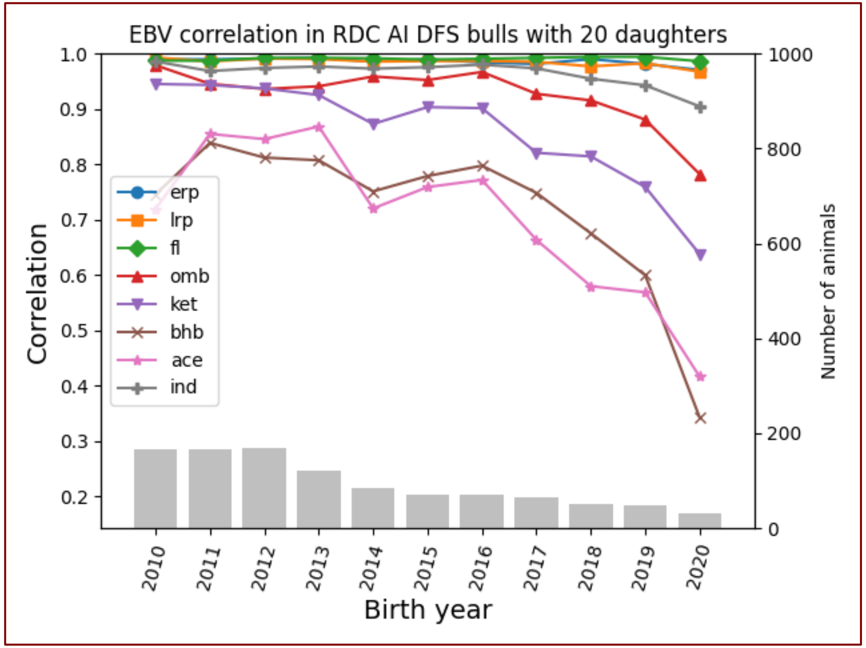
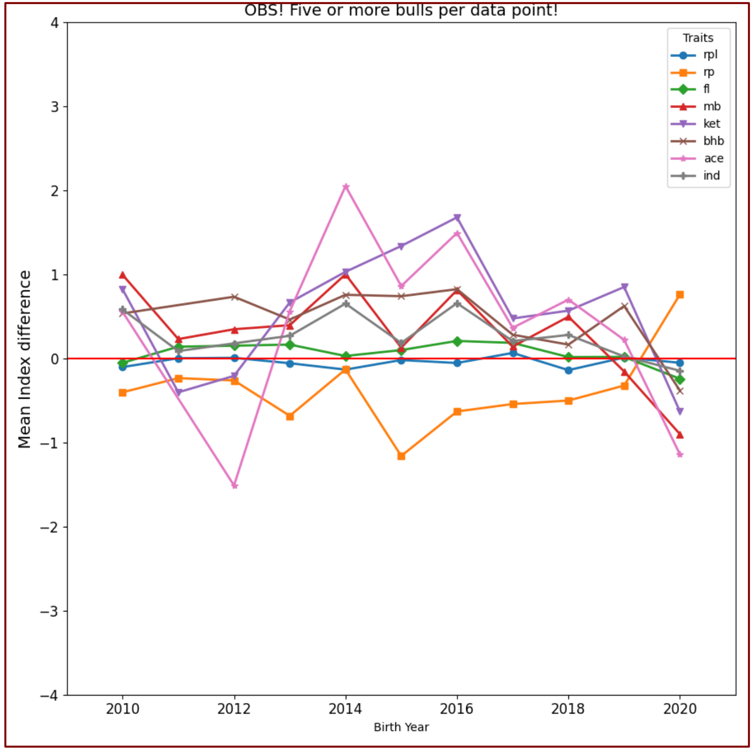


Results – effect of changes on EBV (JER)

Reranking in AI bulls with >=20 daughters



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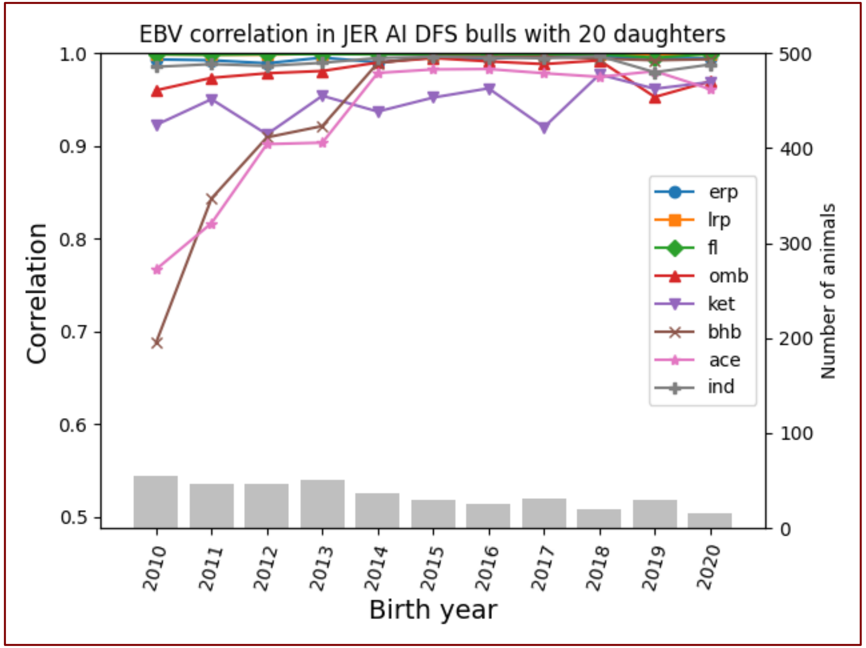

Conclusions

- Newly estimated VC in RDC and JER better align with the data
- Reranking will be observed in all breeds but especially RDC and JER
- RDC bulls will be less affected by HOL bulls due to exclusion of FIN HOL data
- New model will be implemented in November 2025
- New model and August 2025 data will be sent out for Interbull metabolic disease MACE tests from DFS

Thank you for your attention!

Questions:

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NAV Nordisk Avlsværdi Vurdering
Nordic Cattle Genetic Evaluation

faba VÄXA SVERIGE LANDBRUG FØDEVARER SEGES