

Single-step genomic prediction models for metabolic body weight in Nordic Holstein, Red dairy cattle, and Jersey

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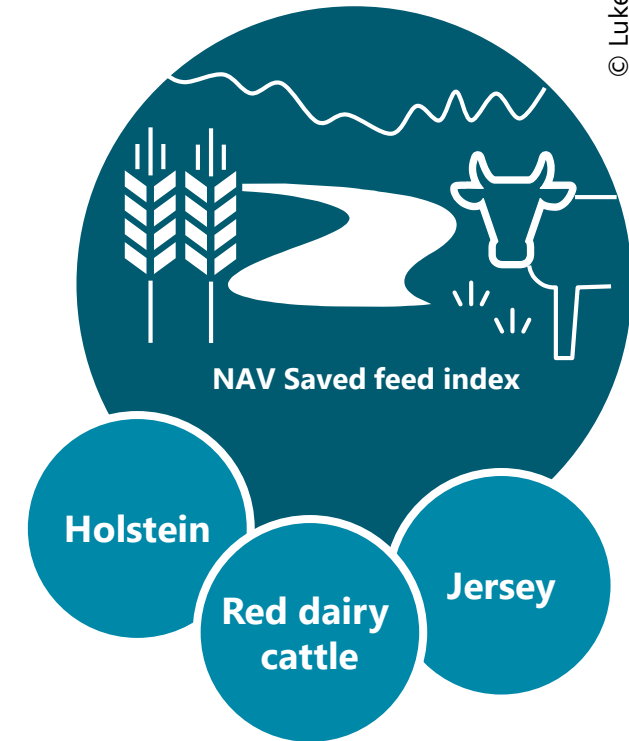
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Introduction

$$\text{NAV Saved Feed Index} = v_1 \times \text{GEBV}_{\text{Maintenance}} + v_2 \times \text{GEBV}_{\text{Metabolic}}$$



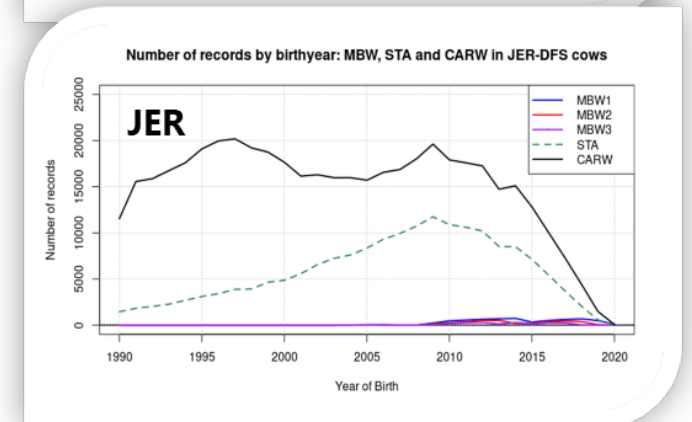
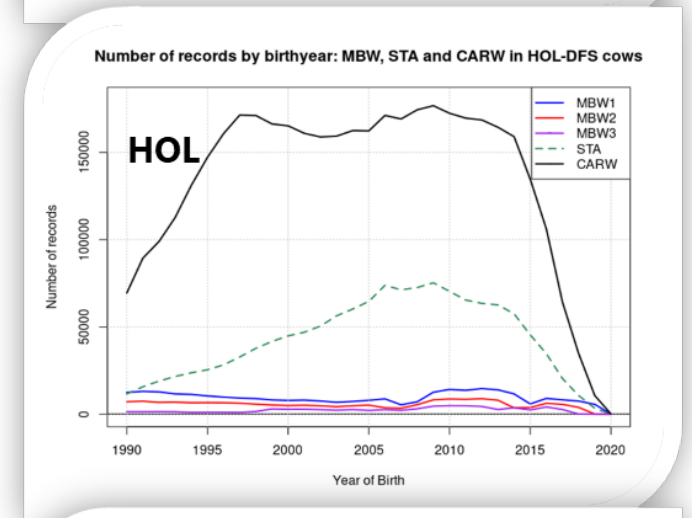
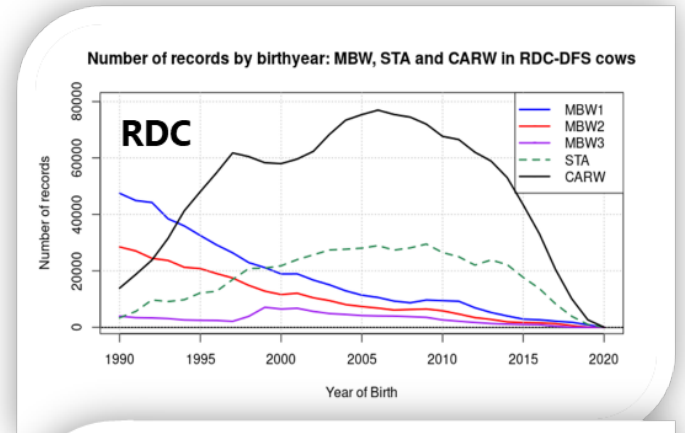
- Own evaluation for each breed
- Current multiple-trait model for metabolic body weight (MBW):
 - **metabolic body weight** in the first, second, and third parity
 - MBW1, MBW2, MBW3 as target traits
 - **conformation traits** as correlated indicator traits

- stature
- chest width
- body depth



Incorporation of carcass weight into metabolic body weight model

- Challenge: body weight recordings are decreasing, and there is no MBW data available from Sweden
- A lot of slaughter information is available across the Nordic countries and for all breeds
→ increases the amount of phenotypic information available
- Carcass weight (CARW) and MBW are highly correlated ranging from 0.77 to 0.85
- CARW has high heritability: 0.56 for HOL & RDC, and 0.37 for JER



AIM

- 1) Incorporating carcass weight data into metabolic body weight evaluation**
- 2) Upgrade the current multiple-step genomic prediction to a single-step genomic prediction**

Materials and methods

Cows with observations

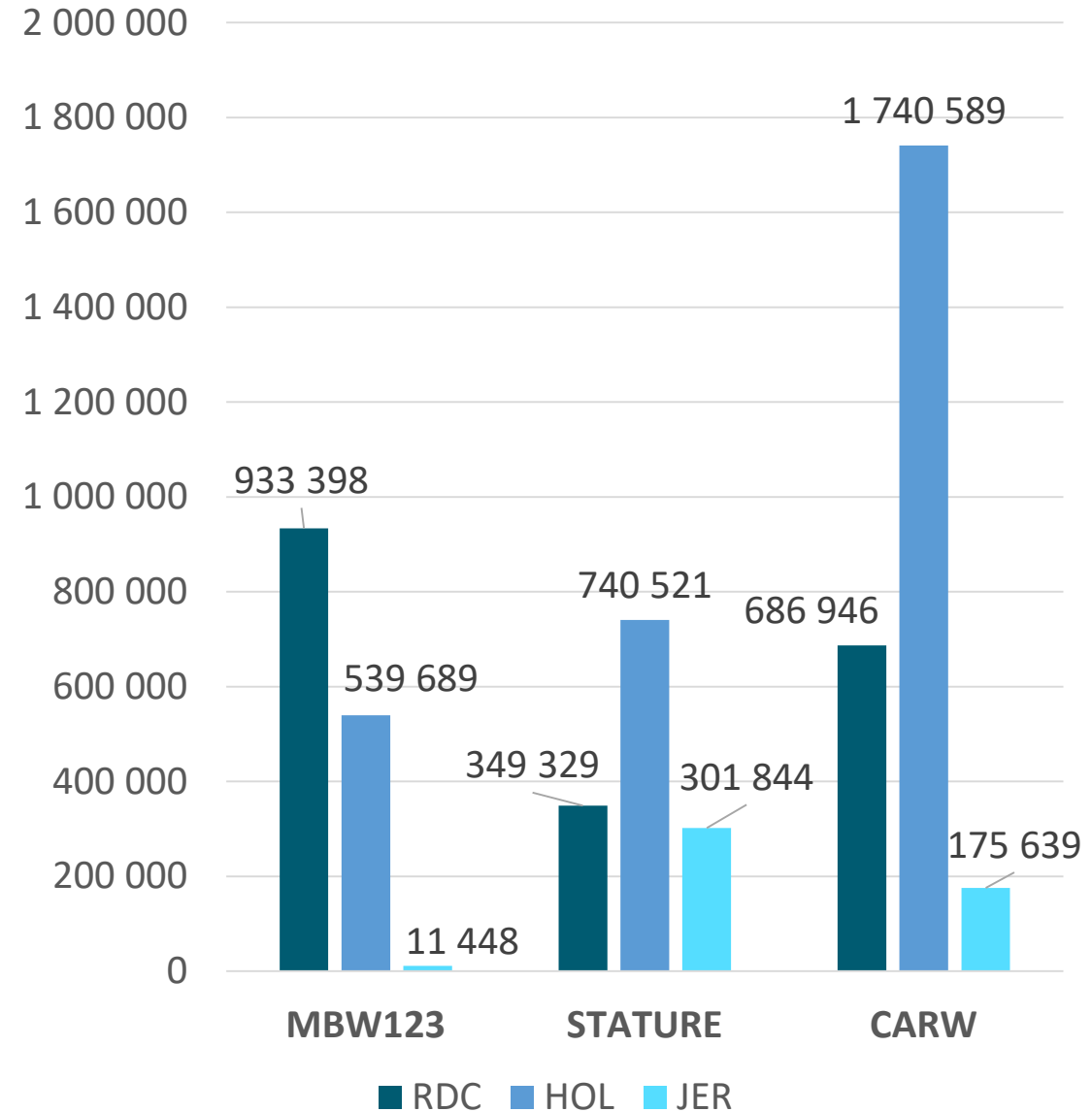
BW measurements from	> 1,5 million cows
Conformation measurement	> 1,4 million cows
Carcass weight	> 2,6 million cows

Animals with genotype information (2009 onwards)

RDC	84,232
HOL	117,845
JER	39,650



Number of records per trait and breed



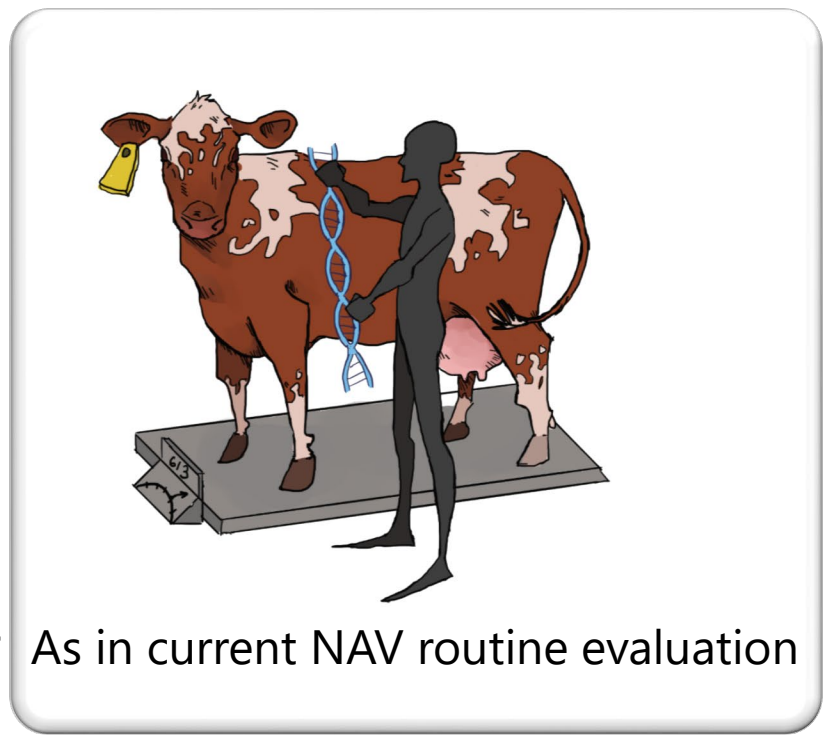
New Model

- Multiple trait model
- 5 traits
- Statistical model:

$$\text{MBW}_{1,2,3} = \text{lt } \phi(d) + \text{cage} + \text{ym} + \text{h5y} \quad + \text{hy} + \text{a} + \text{e}$$

$$\text{Stature} = \text{cage} + \text{cm} + \text{lstg} + \text{h5y} \quad + \text{hy} + \text{a} + \text{e}$$

$$\text{CARW} = \text{sageP5y} + \text{catsP5y} + \text{sym} + \text{shy} \quad + \text{a} + \text{e}$$



Fixed effects for carcass weight:

sageP5y = **slaughter age x parity x 5-year-period** (periods based on birth years)

catsP5y = **calving to slaughter x parity x 5-year-period** (periods based on birth years)

sym = **slaughter year x month**

shy = **herd of slaughter x parity x birth year**

Single-step model setup

- ssGTBLUP with allele frequency $AF=0.5$
- Genetic groups and (partial) QP transformation
- Genetic groups: 182 (RDC), 202 (HOL) and 70 (JER)
- Residual polygenic proportion $w=0.30$
- Pedigree inbreeding accounted in \mathbf{A}^{-1} and \mathbf{A}_{22}
- Solved using ssGTaBLUP in MiX99



Model validation

- Forward prediction cross-validation
- The cross-validation reliability (r^2_{cv}) was calculated as: $r^2_{cv} = \text{corr}(\text{DRP}, \text{BV}_C)^2 / r^2_{\text{DRP}}$
- Regression of full data breeding values on reduced data breeding values (Legarra & Reverter 2018)
- Reduced data: observations from most recent four years were excluded
- Criteria for validation candidates:
 - genotyped
 - bulls > 19 daughters in full data and no daughters in reduced data
 - cows ≥ 1 record in full data and no records in reduced data

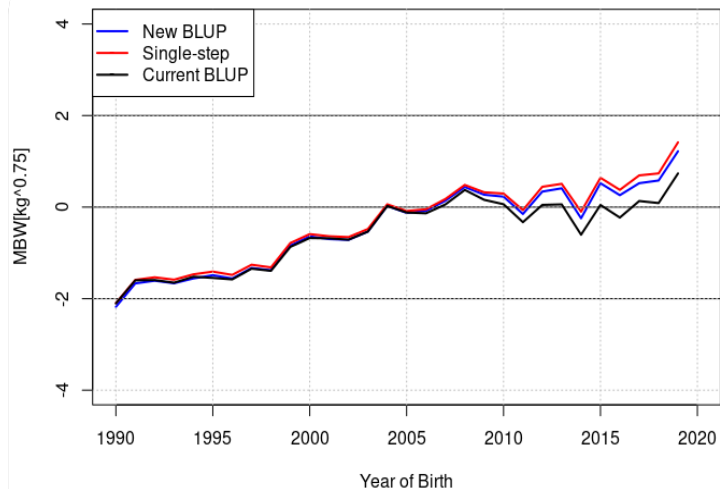
	RDC	HOL	JER
Validation; candidate cows	43,503	75,707	18,237
Validation; candidate bulls	290	470	150

Main results

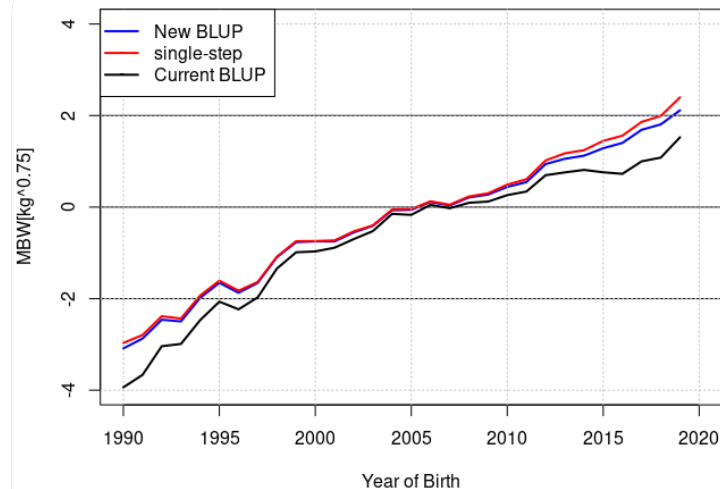
Change in genetic trends of metabolic body weight

- Genetic trend of MBW is increasing in each breed
- The new single-step model gives a slightly higher trend compared to new BLUP-model and corrects the current trend

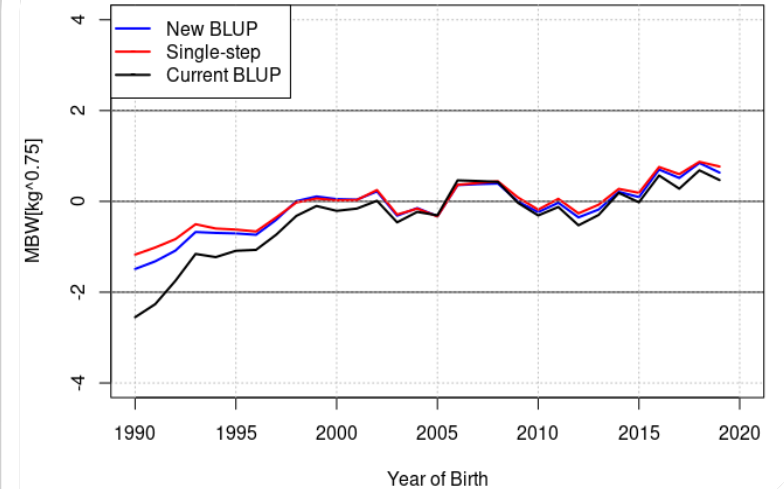
MBW1 Genetic trend of RDC cows



MBW Genetic trend of Holstein cows



MBW Genetic trend of JERSEY cows



Correlations between breeding values

BLUP breeding values: current and new model

- RDC and HOL 0.92-0.95
- JER 0.89

New model: BLUP and genomic breed values

- New BLUP and single-step models gave almost the same breeding values in genotyped bulls (0.98)
- Correlation was lower in cows (0.84-0.88)



Validation results of single-step model

- The **correlations** between candidates' BV_c and their future DRPs ranged from 0.34 to 0.48 in cows from 0.61 to 0.76 in bulls
- Correlations were the highest for both bulls and cows when BV_c were estimated with single-step

Validation results of single-step model		Cross-validation			Legarra-Reverter	
		$r_{(DRP, BV_c)}$	b_1	r^2_{cv}	b_1	R^2
RDC	Cows	0.48	1.32	0.73	1.08	0.80
	Bulls	0.76	0.92	0.61	1.06	0.71
Holstein	Cows	0.36	1.08	0.39	1.00	0.70
	Bulls	0.74	0.85	0.60	0.98	0.67
Jersey	Cows	0.34	1.39	0.51	1.03	0.59
	Bulls	0.61	0.88	0.40	1.08	0.59



Validation results of BLUP model

- In **RDC**, the b_1 estimates were larger than 1.0 indicating that BVc underpredicted the future breeding values
- In **Holstein and Jersey**, the b_1 estimates were lower than 1.0 indicating that BVc overpredict the future breeding values
- **b_1 estimates** were in better agreement between cross-validation and Legarra-Reverter for the BLUP model (DRPs were based on BLUP model)

Validation results of BLUP model		Cross-validation			Legarra-Reverter	
		$r_{(DRP, BVc)}$	b_1	r^2_{cv}	b_1	R^2
RDC	Cows	0.25	1.04	0.19	1.04	0.43
	Bulls	0.63	1.03	0.43	1.03	0.39
Holstein	Cows	0.19	0.87	0.11	0.92	0.33
	Bulls	0.60	0.88	0.40	0.88	0.36
Jersey	Cows	0.14	0.97	0.09	0.94	0.28
	Bulls	0.46	0.91	0.23	0.98	0.21



Validation results of single-step model

- Single-step gave higher **cross-validation reliability** than BLUP-model both in cows and bulls in all breeds. It ranged from:
 0.40 to 0.73 in cows – a big benefit for cows
 0.40 to 0.61 in bulls
- R²**: Single-step approach had much better predictive ability of the model (0.59-0.80) than BLUP approach (0.21-0.43)

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Conclusions

- In A⁺⁺Cow project we developed models that include carcass weight data as correlated information for predicting genomic breeding values for MBW
- CARW data significantly increased the amount of phenotypic information used for the genomic evaluation in all Nordic breeds
- This along with the single-step genomic prediction development contributes positively to the reliability and unbiasedness of predictions of Maintenance efficiency
- Animals will get more accurate breeding values than before



Acknowledgements

Phenotypic and Genomic data

NAV Nordic Cattle Genetic Evaluation



Thank you!



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