

# Revision of random regression test-day model has improved genomic prediction for Nordic Red dairy cattle

T. Pitkänen, M. Koivula, J. Pösö, W.F. Fikse, U.S. Nielsen, G. P. Aamand, M.H. Lidauer





# Joint Nordic test-day model was taken into use in 2006

- The Nordic countries have established cross-country genetic evaluations for yield traits for the Nordic dairy cattle populations in 2006.
- The random regression test-day model (TD-model) was an outcome of intensive research cooperation.
- The model for the Red Dairy Cattle (RDC) breed is most complex due to a heterogeneous population structure across the three countries.



# Some model descriptions

- 9 test-day traits (milk, protein and fat) x 3 lactations
- Fixed effects nested within countries
  - calving age x breed proportion
  - year-month, days carried calf, days dry,
  - lactation curves, herd-year, herd-test-day, herd-curve
- Heterosis & recombination loss
  - by fixed and random effects
- Adjustment for heterogeneous variance (HV correction)
  - simultaneously to account for breed differences
  - across-country standardization (same genetic variance in all countries)
- Breeding values
  - 15 cow-specific coefficients define all 9 breeding value curves





# Issues in RDC yield evaluation

- The reliability of genomic estimated breeding values (GEBV) for RDC was lower than expected when compared to Holstein and Jersey breeds.
- Reasons
  - Changes in herd and population structures.
  - The existing TD-model may no longer be optimal for genomic prediction equations.
- Revision of the current TD-model for the RDC evaluation is crucial in enhancing the reliability of GEBV for selection candidate animals.

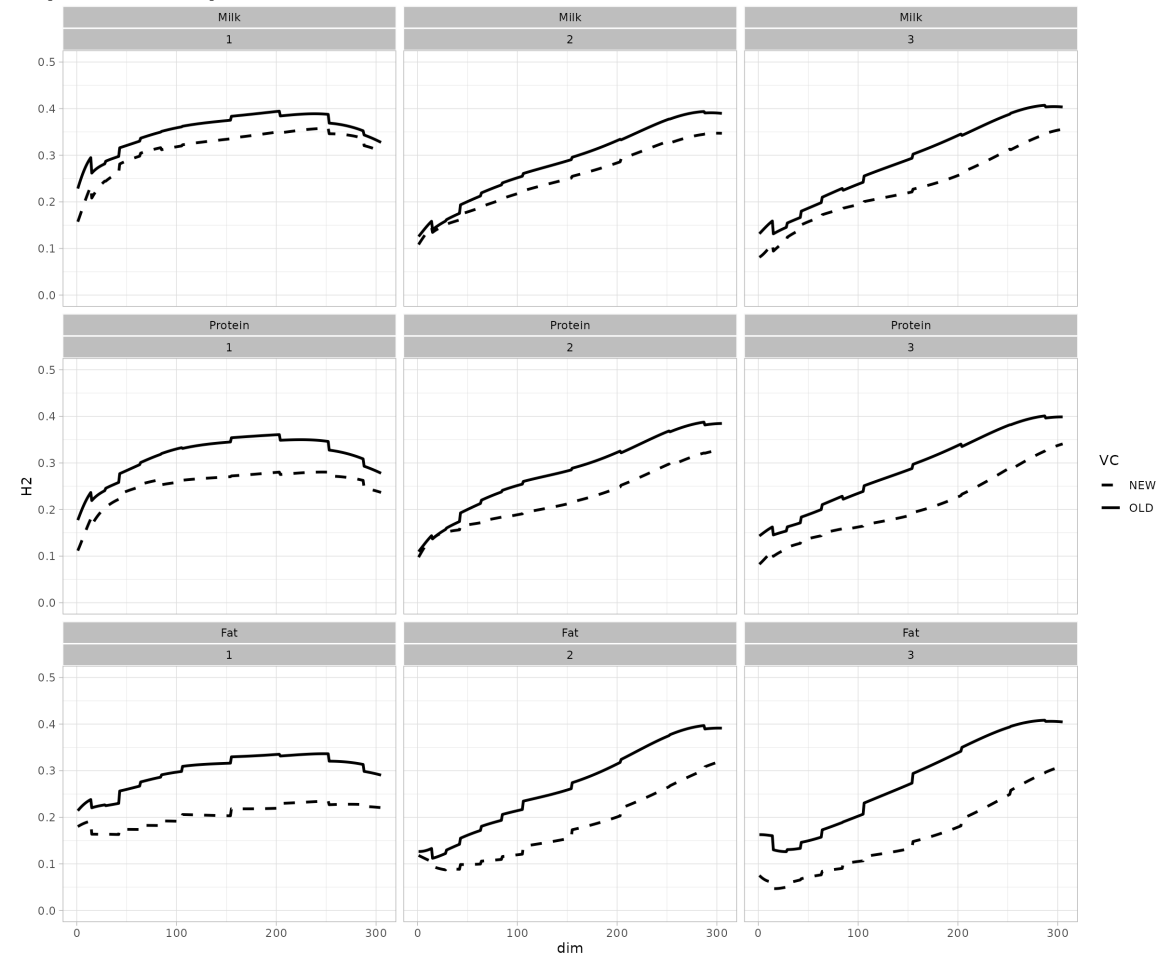


# Revising variance components

In old NAV RDC model the  $h^2$  were too high, especially for later parities.

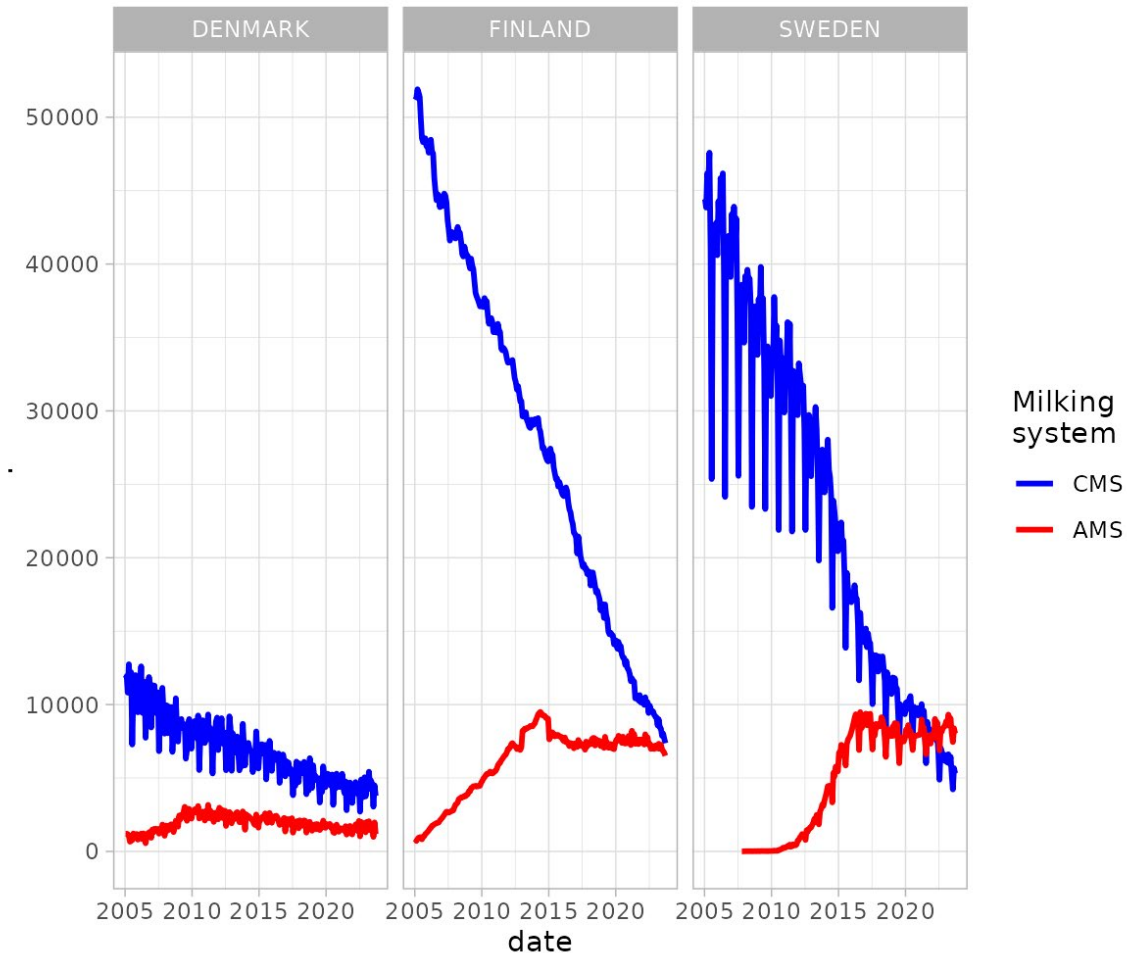
- Particularly VC for permanent environment and genetic components in the later lactations
- The situation was more critical than earlier since the weight of later lactations was set higher.
- Need to make update to variance components.
- Updated variance components are based on Finnish data – old on Swedish data
- Finnish VC give lower heritabilities, especially for protein and fat and later lactations > fits better the data

Heritabilities in old (solid line) versus updated (dashed line) model based on Finnish data



# Number of test-day observations for first lactation milk yields by country and milking system

- Rapid decrease in conventional milking system (CMS) observations.
- Slightly decreasing trend in automatic milking system in DNK, no clear trend in FIN & SWE
- Sweden and Denmark lactations 1-3 and Finland 1-10 included in the data



# Updating model and data for AMS observations

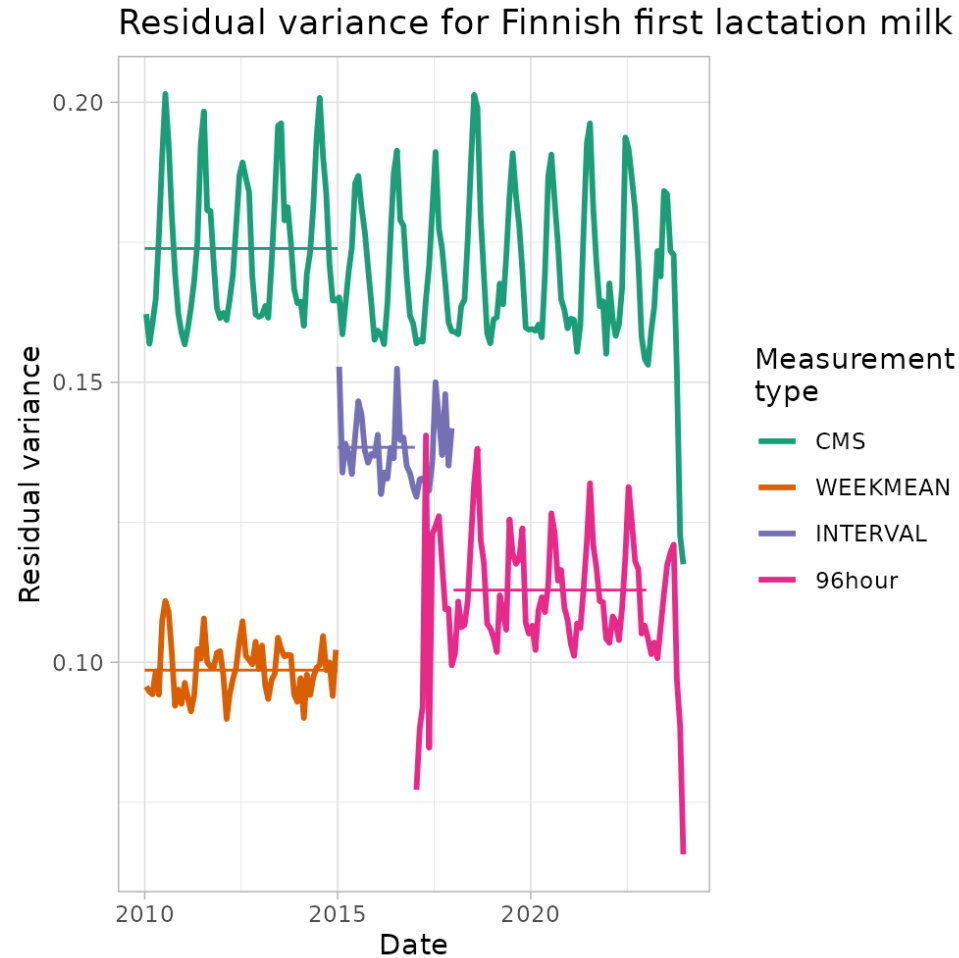
Model assumed the **same residual variance** for all **AMS observations**.

- In Finland **measurement protocol** has **changed twice** during the years.
- Heterogeneous variance (HV) correction didn't work properly.

Updates made

- **Separate residual variance** for the different **AMS methods**.
- Include correct **measurement protocol** information for AMS observations **in data**.
- Update HV correction to handle different AMS recording protocols.

# Residual variances for different milking protocols



- For **conventional milking**, the test-day yield is sum of morning and evening milkings.
- For AMS, several protocols for defining test-day yields used in Finland:
  - Average of one weeks milkings
  - Sum of 2 successive milkings scaled to 24h yield
  - Average of 4 day milkings



# Holstein observations in the Finnish RDC evaluation

- In the past, Finnish herd sizes were small. As a result, test-day records for Holstein cows were included in the model to increase contemporary group sizes
- This is not as relevant as before =>
  - Holstein observations were removed
  - Need to revise model effects that include breed interaction

# Bull validation results using Legarra-Reverter Regression § - Four years data cut

§ Regression of GEBV<sub>full</sub> or GEBV<sub>red</sub>

	Model	Bias	b <sub>1</sub>	R <sup>2</sup>
MILK	GEBV <sub>old</sub>	-473.88 (±363.7)	0.85	0.66
	GEBV <sub>new</sub>	-291.34 (±354.9)	0.92	0.70
PROTEIN	GEBV <sub>old</sub>	-17.78 (±12.3)	0.75	0.60
	GEBV <sub>new</sub>	-12.41 (±11.9)	0.84	0.63
FAT	GEBV <sub>old</sub>	-22.91 (±15.6)	0.84	0.63
	GEBV <sub>new</sub>	-18.61 (±19.6)	0.91	0.65

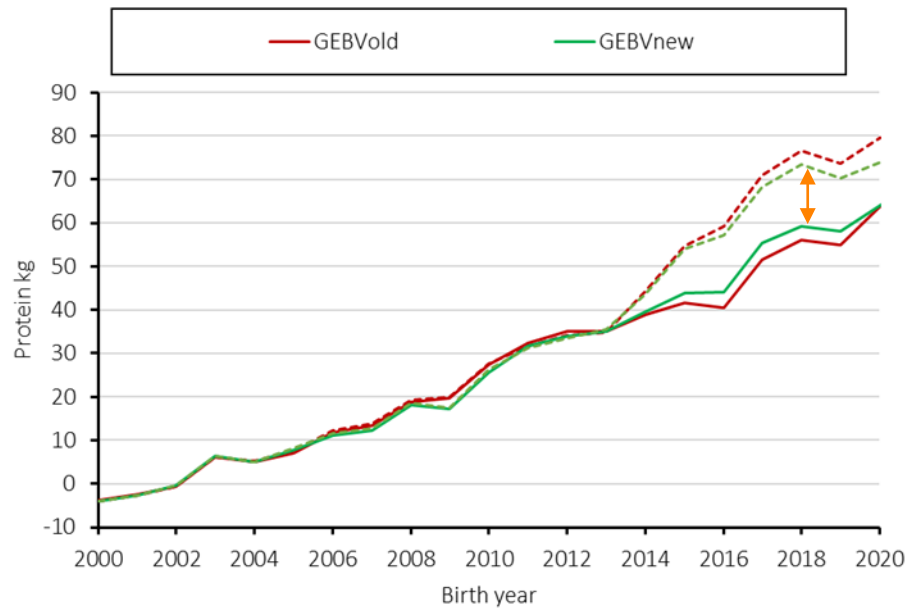
Validation bulls have daughters > 20 in full data and no daughters in reduced data, n = 222

- bias=mean(Full\_GEBV – reduced\_GEBV)
- GEBV<sub>old</sub> : Old NAV evaluation model
- GEBV<sub>new</sub>: New updated model with
  - Modelling of AMS data updated
  - New variance components
  - Records of Holstein contemporary cows removed from Finnish data

With the updated model the validation results improve: bias decrease and R<sup>2</sup> increase

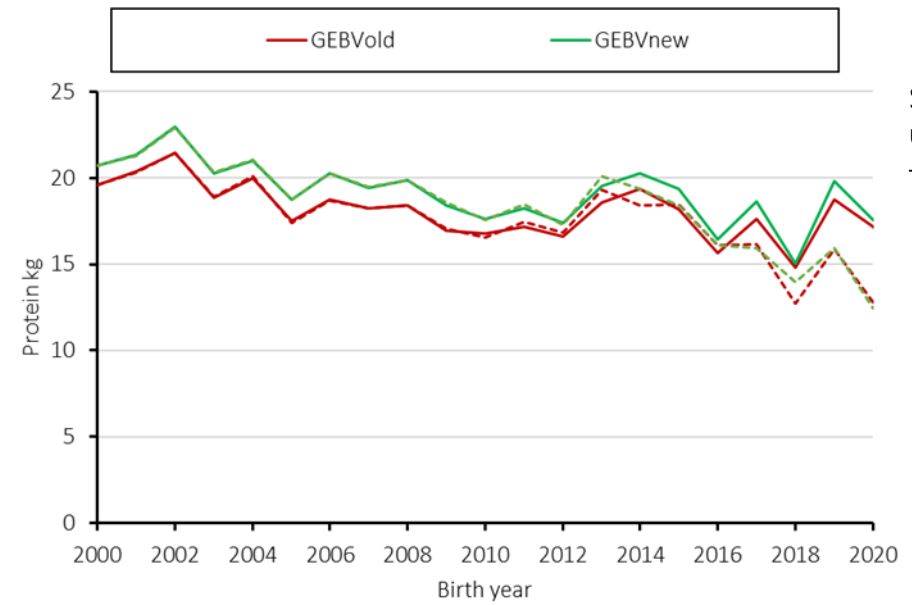
# Protein trend for selected DFS bulls

## Genetic trend



Bias decrease with updated model

## SD Genetic trend



SD increase with updated model – like expected

Solid lines from Full data run  
Dashed lines from reduced data run



# Conclusions

## **Changes in the model improved validation results:**

- New variance components
- Updated AMS residual variances for Finnish records
- Holstein observations removed (Finnish data)

## **Ongoing changes and improvements:**

- Remove old test-day records made prior 2005.
- Improve definition of calving age, heterosis and recombination effects.
- Replace UPGs with metafounders.



# Acknowledgements

Phenotypic and Genomic data  
NAV Nordic Cattle Genetic Evaluation,

Support:  
NAV, Viking Genetics



# Thank you!



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