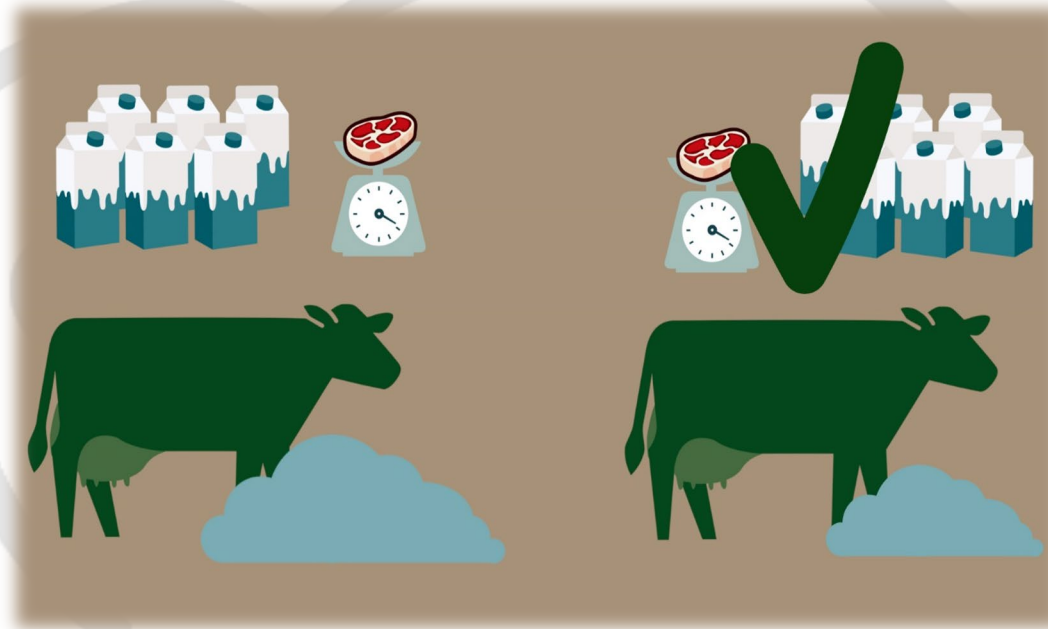


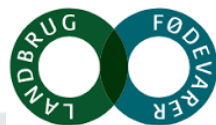
Genetic evaluation for Saved feed

– Genomic prediction of residual feed intake in the Nordic breeds using data from research herds and 3D cameras in commercial herds



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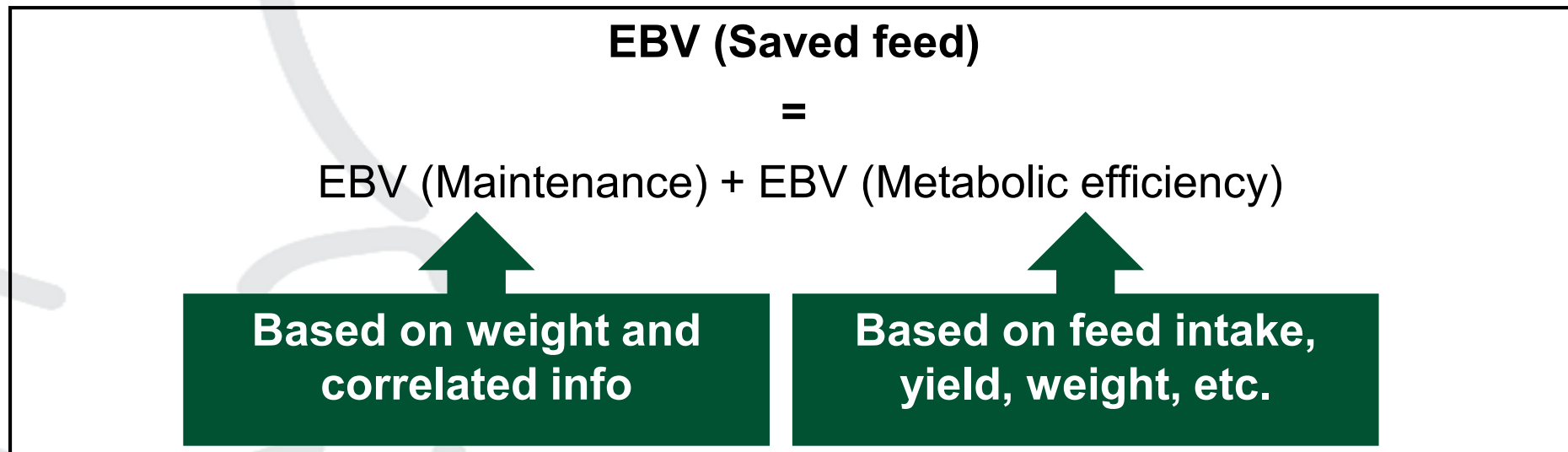
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Nordic Cattle Genetic Evaluation

The overall aim of Saved feed

Saved feed for all Nordic breeds

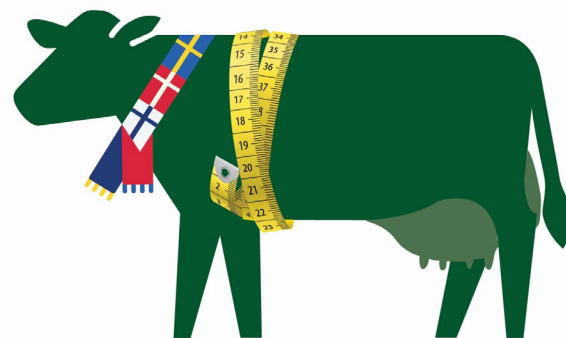
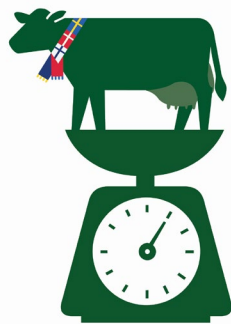
- Maintenance (Aug '19) – (covered by Lidauer et al., 2019)
- Saved feed in NTM (Aug '20)
- Metabolic efficiency (Nov '20) – Residual feed intake



Weight data (maintenance)

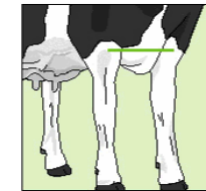
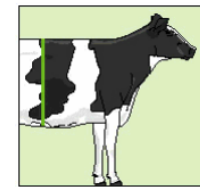
Core trait

- Weight from scales
- Tape measurements
- Weight predicted from pictures (CFIT)



Indicator traits

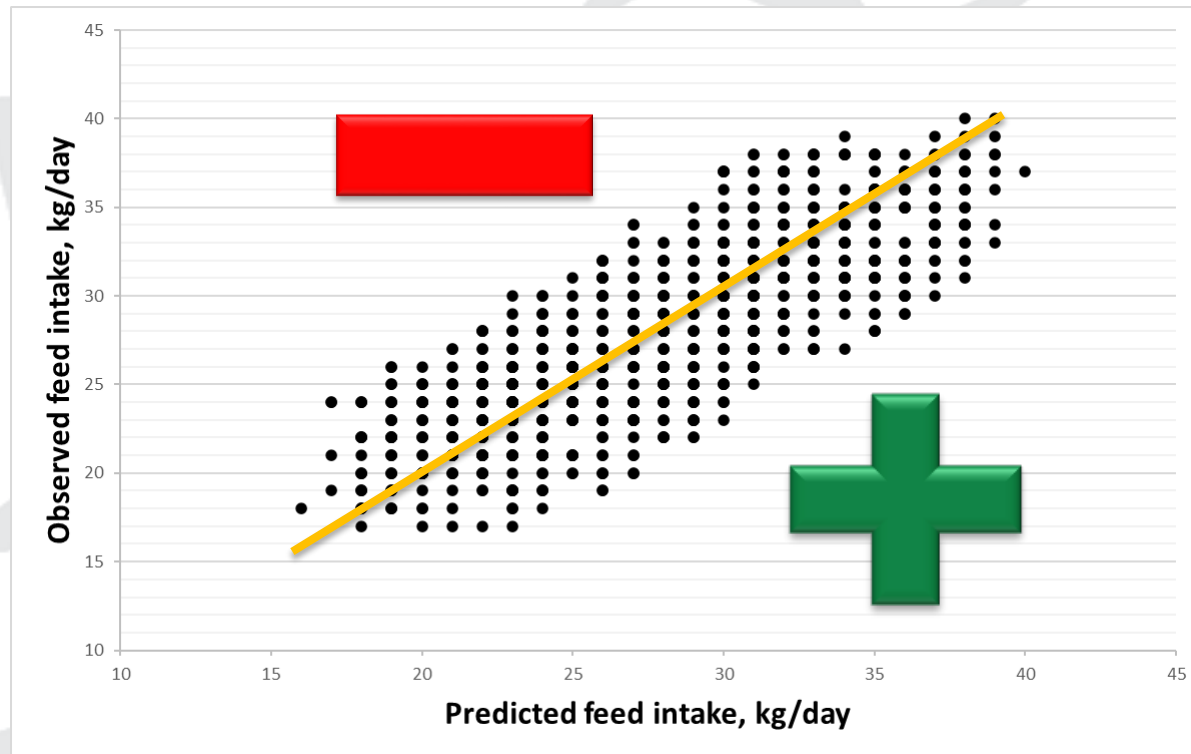
- Slaughter weight
- Stature
- Chest width
- Body depth



Metabolic efficiency – what is that?

Metabolic efficiency = observed feed intake – predicted feed intake

- Predicted feed intake is based on yield, maintenance, mobilization, etc.



Feed intake data (metabolic eff.)

Core trait

- Complete lactations with feed intake data
- Prefer more than one lactation


Most reliable information include early lactation



Indicator traits

- Feed intake from parts of the lactation (eg. day 60-120)
- Feed intake only in 1st lactation
- Heifer feed intake

Less reliable – genetic correlation < 1.00 lactation



Feed intake data (metabolic eff.)

- We have access to feed intake data from
 1. 3D camera system from VikingGenetics (CFIT)
 - We gratefully acknowledge VikingGenetics
 - *See ICAR2021 - 10.5 Lassen et al - Identification of cows and individual feed intake records using a 3D camera system in commercial farms*
 2. EDGP research farm data
 - We gratefully acknowledge the EDGP project
 3. Luke research farm data
 - We gratefully acknowledge Luke



Feed intake data (metabolic eff.)

- **Nordic HOL (Foulum+CFIT)** | Repeated records from 1st to 6th parity
- **HOL abroad (AUS, CAN, USA)** | Repeated records from 1st to 6th parity
- **Nordic RDC (Luke+CFIT)** | Repeated records from 1st to 6th parity
- **Nordic JER (CFIT)** | Repeated records from 1st to 6th parity

Number of cows	Research farms	Private farms April 21	Private farms Dec 2021
Holstein	2,600	430	3,000
<i>RDC</i>	725	270	2,000
Jersey	0	1,500	2,000

Descriptive statistics for phenotypes

- All statistics presented as kg per day
- Levels are as expected compared to knowledge from practice and research herds
- Differences on production is caused by distribution of lactations – RDC have majority of data from 1st parity

	Nordic HOL		Nordic RDC		Nordic JER	
	Mean	SD	Mean	SD	Mean	SD
DMI	21.8	3.6	20.2	3.6	17.4	2.6
ECM	34.0	8.2	29.7	5.4	34.8	6.7
MBW	128.4	11.3	119.2	8.8	101.3	6.5

Pedigree and T-matrix construction

- **Pedigrees traced for 5 generations in JER/RDC and 3 generations for HOL**
 - Holstein was traced fewer generations since EDGP only deliver 3 generations
 - Genetic groups added – birth year, breed and country
 - All candidates were added to get GEBVs
- **Pedigree and genomic information has been incorporated by setting up a ssGTaBLUP model (Strandén and Mäntysaari, 2017)**
 - 10% weight on residual polygenic effect
 - QP transformation used
 - Inbreeding coefficients used – calculated with RelaX2 (Strandén and Vouri, 2006)

Metabolic efficiency model – 1st step

- **DMI =**
 - **Linear regression on calving age and calving age²**
 - Nested within parity (parity = 1, 2, ..., 6)
 - **Lactation period**
 - Nested within parity (parity = 1, 2, ..., 6)
 - **Herd x Year x Season**
 - **Year x Season x lactation period**
 - **Regression on ECM, MBW and Δ BW**
 - ECM and Δ BW is nested with in lactation period and 1st or later parities
 - MBW is nested within 1st or later parities
 - **Residual** used for further analysis

Genetic model – 2nd step

- **Heterogenous variance correction for**
 - Parity
 - Lactation period
 - Year x season
- **Fixed effects of HYS and YS_{lactp} from LS-model is back transferred to phenotype**
 - Ensure that additive effects not are lost
- **Genetic model = $HYS + YS_{lactp} + PE + A + e$**
 - Single trait model for JER and RDC
 - Multi country model for HOL
 - Solver used is ssGTaBLUP in MiX99 (MiX99 Development Team, 2019)

Genetic parameters

Assumptions

- **Heritability: 15% for all 3 breeds**
- **Same trait across parities and within lactation**
- **It is a rough assumption but a consequence of few data**

Extra reliability in addition to pedigree information

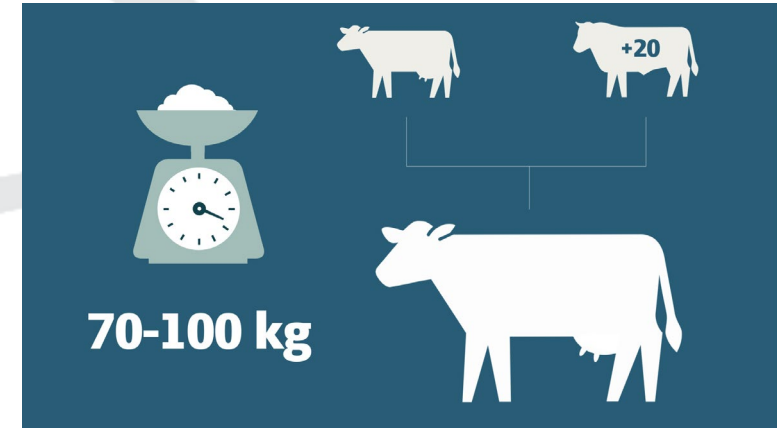
- Tested for production traits from research data
 - Finnish RDC data 310 cows, Lidauer, M. (2019)
 - EDGP HOL data 1,650 cows, Stephansen, R.B. & Nielsen, U.S. (2019)

	RDC	HOL
Extra reliability	1-3%	3-7%

- Expected increase in reliability for metabolic eff. about the same size as for production traits
- More females in the reference population will increase genomic reliability

The Saved feed index

- The effect of 1 index unit is the same for maintenance and metabolic efficiency
 - RDC = 9.8 kg DMI per annual cow
 - HOL = 8.2 kg DMI per annual cow
 - JER = 6.7 kg DMI per annual cow
- The correlation between the index for maintenance and metabolic efficiency is 0
- Currently, the maintenance breeding values influence the Saved feed index most



Summary

- **Both component traits of Saved feed are available**
 - Jersey, Red Dairy Cattle & Holstein
- **Reliable GEBVs depends on large scale feed intake recording in production herds**
- **Data from CFIT is used in the genetic evaluation**
 - Feed intake data of good quality, whole lactations and data from production herds
- **Selection for the Saved feed index will lead to:**
 - More profitable and climate friendly cattle