Genetic Evaluation for Maintenance – Towards Genomic Breeding Values for Saved Feed in Nordic Dairy Cattle

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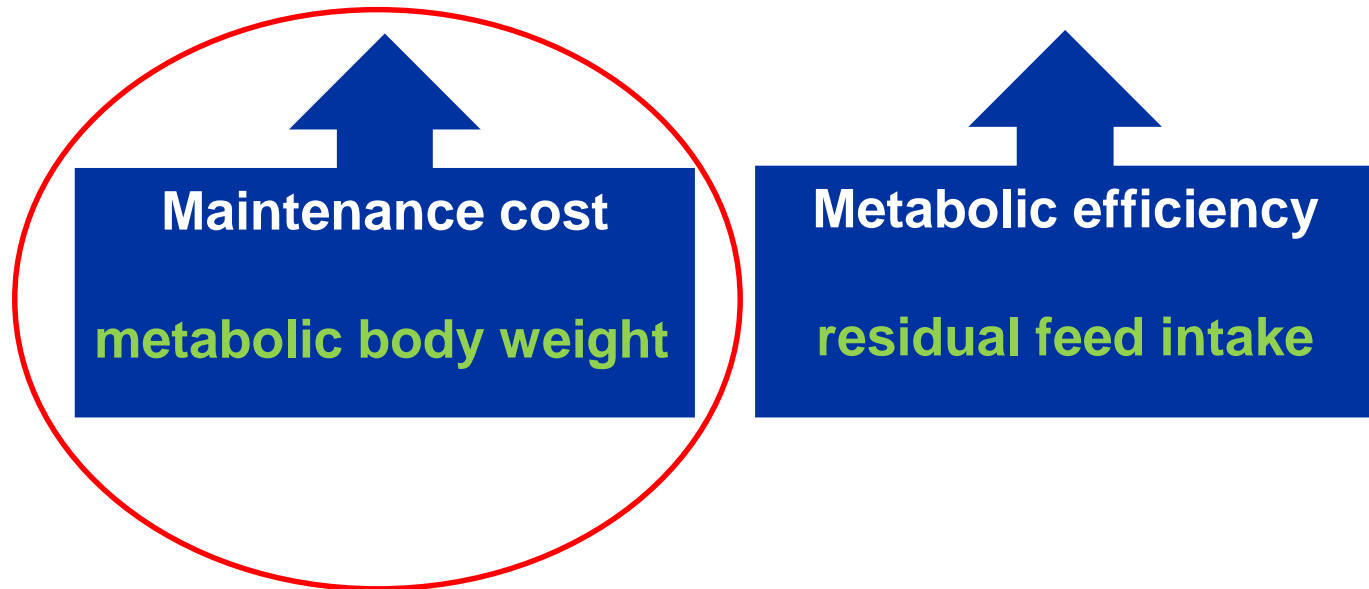
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AIM

- Genomic breeding values for Saved Feed

- For all dairy breeds in the NAV countries (Denmark, Finland, Sweden)

Saved Feed Index

Two components:

Saved Feed = $v_1 \times \textbf{GEBV}_\textbf{Maintenance}$ **+** $v_2 \times \textbf{GEBV}_\textbf{Metabolic}$

Maintenance cost

metabolic body weight

Metabolic efficiency

residual feed intake

Included in the launching phase
of the Saved Feed Index

Why maintenance

- ~1/3 of feed intake is needed for cows' maintenance

- → for a cow of 600 kg: ~ 6 kg dry matter intake / day

- Relationship between maintenance and metabolic body weight (MBW)

  energy requirement for maintenance = 0.515 [MJ ME / kg$^{0.75}$] x MBW
  where MBW [kg$^{0.75}$] = (body weight)$^{0.75}$

- 2 genetic SD improvement in MBW
  → Saved Feed ~ 220 kg dry matter / cow / year (~ 3% feed)

Available data

Cows with observations

- BW measurements by tape (heart girth)   >800 000 cows
- BW measurements by scale   >90 000 cows
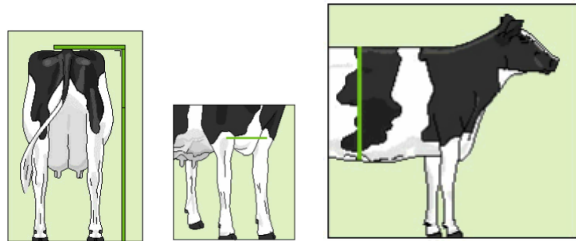- Conformation measurements   >2 900 000 cows

Observations by trait and breed

Trait	Holstein	Nordic Red	Jersey
MBW 1	269 746	521 289	4 113
MBW 2	157 556	323 195	2 157
MBW 3	67 701	106 134	1 215
Stature	1 829 079	841 718	256 962
Chest width	1 823 373	798 341	261 614
Body depth	1 823 374	798 351	261 613

Available data

Phenotypic means of metabolic body weight by lactation and breed

Trait	Holstein	Nordic Red	Jersey
MBW 1	112.9 (545kg BW)	107.8 (513kg BW)	86.2 (380kg BW)
MBW 2	122.4 (608kg BW)	115.2 (560kg BW)	96.8 (444kg BW)
MBW 3	127.2 (629kg BW)	119.2 (587kg BW)	101.1 (471kg BW)

Model design

- Multiple-trait model

- Metabolic body weight (MBW)
  - 1st , 2nd and 3rd lactation considered as different traits
  - Lactation averages of MBW are modelled
  - Weights for MBW observations
    - single tape measurements have lower measurement errors than single scale measurements
    - cows can have over 400 scale measurements per lactation

- Correlated traits
  - Stature
  - Chest width
  - Body depth

ICAR THE GLOBAL STANDARD FOR LIVESTOCK DATA

- For each breed an own evaluation

Variance components for Holstein & Nordic Red
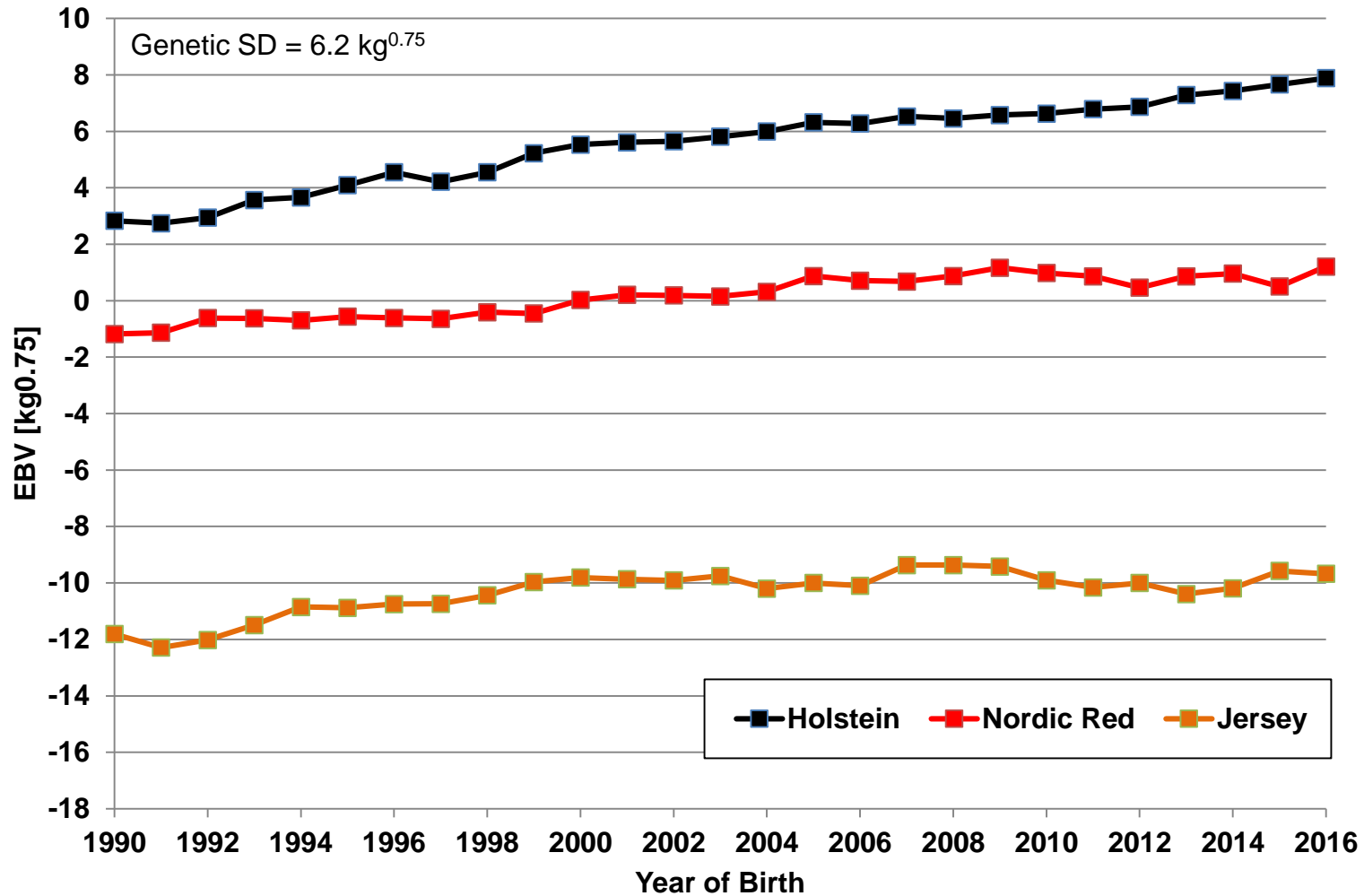
Heritabilities (on diagonal) and genetic correlations

	MBW1	MBW2	MBW3	Stature	Chest width	Body depth
MBW 1	**0.46**	0.98	0.96	0.65	0.58	0.51
MBW 2		**0.51**	0.99	0.68	0.55	0.49
MBW 3			**0.56**	0.68	0.53	0.48
Stature				**0.60**	0.17	0.21
Chest width					**0.18**	0.55
Body depth						**0.26**

Model effects for metabolic body weight traits

- Fixed effects
  - MBW curve (c_1 x DIM + c_2 x DIM^2+c_3 x $e^{-0.1DIM}$) nested within breed, country and time periods
  - linear regression on calving age nested within breed
  - year x season
  - herd x 5-year time periods

- Random effects
  - herd x year
  - additive genetic
  - Residual

- Accuracy of MBW observations is accounted for by weights

Genetic trends in cows for combined EBV $(0.30ebv_{MBW1}+0.25ebv_{MBW2}+0.45ebv_{MBW3})$

Genetic SD = 6.2 kg$^{0.75}$

Legend: Holstein, Nordic Red, Jersey

X-axis: Year of Birth (1990–2016)
Y-axis: EBV [kg$^{0.75}$]

Correlation of MBW index with other index traits

- MBW index $= 100 - \dfrac{(0.30 \times ebv_{MBW1} + 0.25 \times ebv_{MBW2} + 0.45 \times ebv_{MBW3}) - ebv_{base}}{0.1 \times SD(ebv_{base})}$

- AI bulls born 2005 to 2010

- r^2 for EBV_{MBW} >0.8

Traits	Holstein (N=729)	Nordic Red (N=568)
Frame	-0.78	-0.72
Beef production	-0.12	-0.29
Milk production	-0.01	0.05
Mastitis	0.06	0.06
Female fertility	0.06	0.03
Claw health	0.14	0.18
Calving traits	0.10	0.35
Longevity	0.18	0.20
Nordic Total Merit (NTM)	0.04	0.11

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Genomic prediction

- SNPBLUP

  $y = 1\mu + Wa + Zg + e$

  where

  y … de-regressed proofs for combined EBV $(0.30ebv_{MBW1}+0.25ebv_{MBW2}+0.45ebv_{MBW3})$

  a … random polygenic effects (proportion: 10%)

  g … random SNP marker effects

- Reference population
  - All bulls with EBV reliability >0.5
  - All cows with observations

	Holstein	Nordic Red	Jersey
Bulls	7 268	5 487	1 556
Cows	39 630	38 737	18 799
Total	**46 898**	**44 224**	**20 355**

Validation of genomic prediction

- Forward prediction
  - DGV from SNPBLUP prediction, where data from most recent four years of bulls (+progenies) were excluded

  - $DRP = b_0 + b_1 * DGV + e$

    where

      - DRP … de-regressed proofs for candidates
      - DGV … genomic breeding values from reduced data

  - $R^2_{validation} = \frac{corr(DRP,DGV)^2}{r^2_{DRP}}$

Validation statistics

	N	b_1	$R^2_{validation}$
Holstein	584	0.87	0.59
Nordic Red	519	0.95	0.74
Jersey	188	0.91	0.65

Next steps

- Saved Feed Index introduction in August 2019

- Aim to include Saved Feed Index into Nordic Total Merit in 2020

- Upgrading Saved Feed Index (metabolic efficiency) in 2020

Thank you!