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Animal breeding research in Luke

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Slides by prof. Martin Lidauer

MTK-Satakunta ja Varsinais-Suomi visiting LUKE 1.8.2023


Terhi Mehtiö

Quantitative genetics research team

Researchers

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- Nina Schulman, group manager
- Marja-Liisa Sevón-Aimonen
- Ismo Strandén, Prof.
- Matti Taskinen
- Napoleon Vargas Jurado
- Anna-Kaisa Ylitalo

- International research group: 7 different nationalities

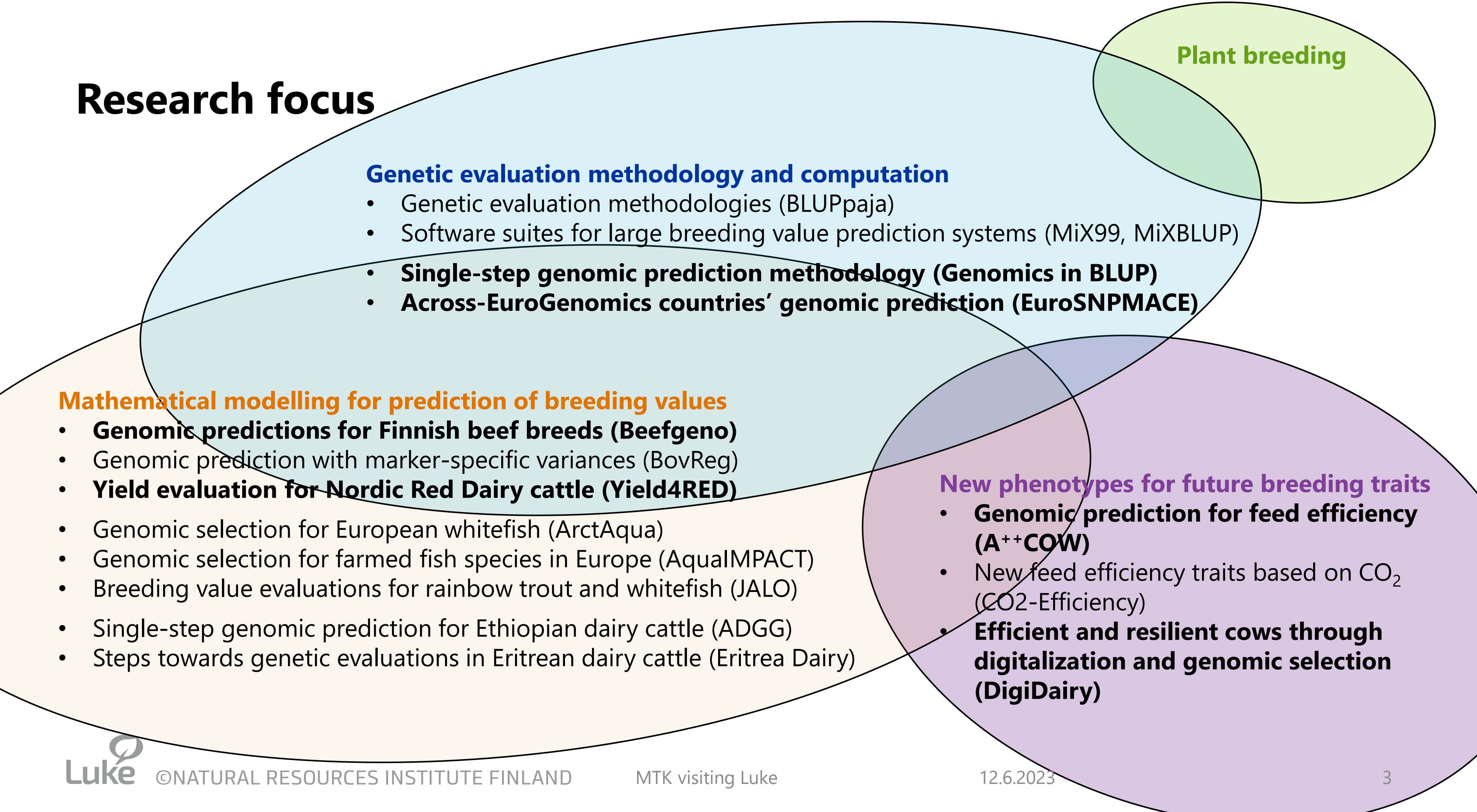
Academic background

10 animal breeding
3 mathematics
2 biology
1 statistics
1 biometrics
(16 PhD from 11 different universities)

18 research projects

16 Luke-outside funded projects
(9 projects with significant funding from the dairy industry)

Research focus



Genetic evaluation methodology and computation

- Genetic evaluation methodologies (BLUPpaja)
- Software suites for large breeding value prediction systems (MiX99, MiXBLUP)
- **Single-step genomic prediction methodology (Genomics in BLUP)**
- **Across-EuroGenomics countries' genomic prediction (EuroSNPMACE)**

Mathematical modelling for prediction of breeding values

- **Genomic predictions for Finnish beef breeds (Beefgeno)**
- Genomic prediction with marker-specific variances (BovReg)
- **Yield evaluation for Nordic Red Dairy cattle (Yield4RED)**
- Genomic selection for European whitefish (ArctAqua)
- Genomic selection for farmed fish species in Europe (AquaIMPACT)
- Breeding value evaluations for rainbow trout and whitefish (JALO)
- Single-step genomic prediction for Ethiopian dairy cattle (ADGG)
- Steps towards genetic evaluations in Eritrean dairy cattle (Eritrea Dairy)

New phenotypes for future breeding traits

- **Genomic prediction for feed efficiency (A^{++}COW)**
- New feed efficiency traits based on CO$_2$ (CO2-Efficiency)
- **Efficient and resilient cows through digitalization and genomic selection (DigiDairy)**

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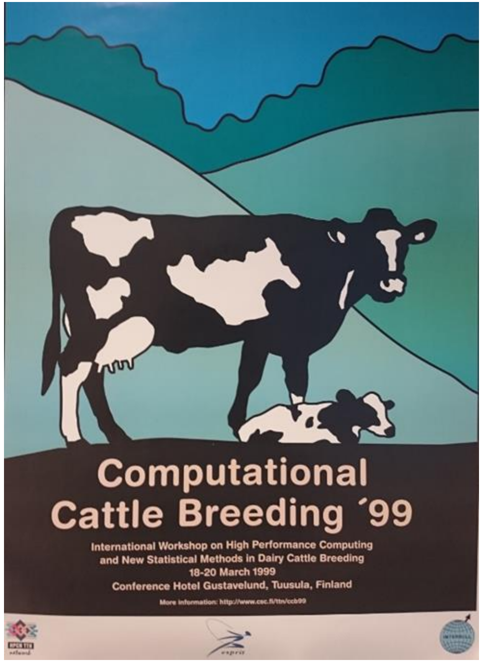
Genetic Evaluation methodology and computation

Genetic evaluations in animal breeding

- Massive amount of data
    - Phenotypic measurements from different traits
    - Pedigree information
    - Genotype information
- Large and complex models for predicting breeding values
- Need for efficient solving algorithms and software

→ strong focus on solving large linear mixed models



Solving large linear modes is one of our key research topics since 3 decades

A recent research activity

Making single-step genomic prediction feasible for very large evaluations

Single-step genomic prediction (Christensen & Lund, 2010; Aguilar et al., 2010)

- **Allows to model all source of information (data, pedigree, genotypes) at the same time**
- Most appropriate approach for genomic prediction in cattle

$$\begin{bmatrix} \mathbf{X'X} & \mathbf{X'W} \\ \mathbf{W'X} & \mathbf{W'W}+\lambda\mathbf{H}^{-1} \end{bmatrix} \begin{bmatrix} \hat{\mathbf{b}} \\ \hat{\mathbf{a}} \end{bmatrix} = \begin{bmatrix} \mathbf{X'y} \\ \mathbf{Z'y} \end{bmatrix}, \quad \text{where } \mathbf{H}^{-1} = \begin{bmatrix} \mathbf{A}^{11} & \mathbf{A}^{12} \\ \mathbf{A}^{21} & \mathbf{A}^{22} \end{bmatrix} + \begin{bmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}^{-1} - (\mathbf{A}_{22})^{-1} \end{bmatrix}$$

- How one can compute $\mathbf{G}^{-1}$ and $\mathbf{A}_{22}^{-1}$?

→ Component-wise single-step computations implemented into **MiX99 software suite** in spring 2023

Component-wise single-step genomic evaluation

Single-step GBLUP
Nordic Red Dairy Cattle test-day model

230 000 genotyped animals
4.7 million animals with records
6.3 million animals

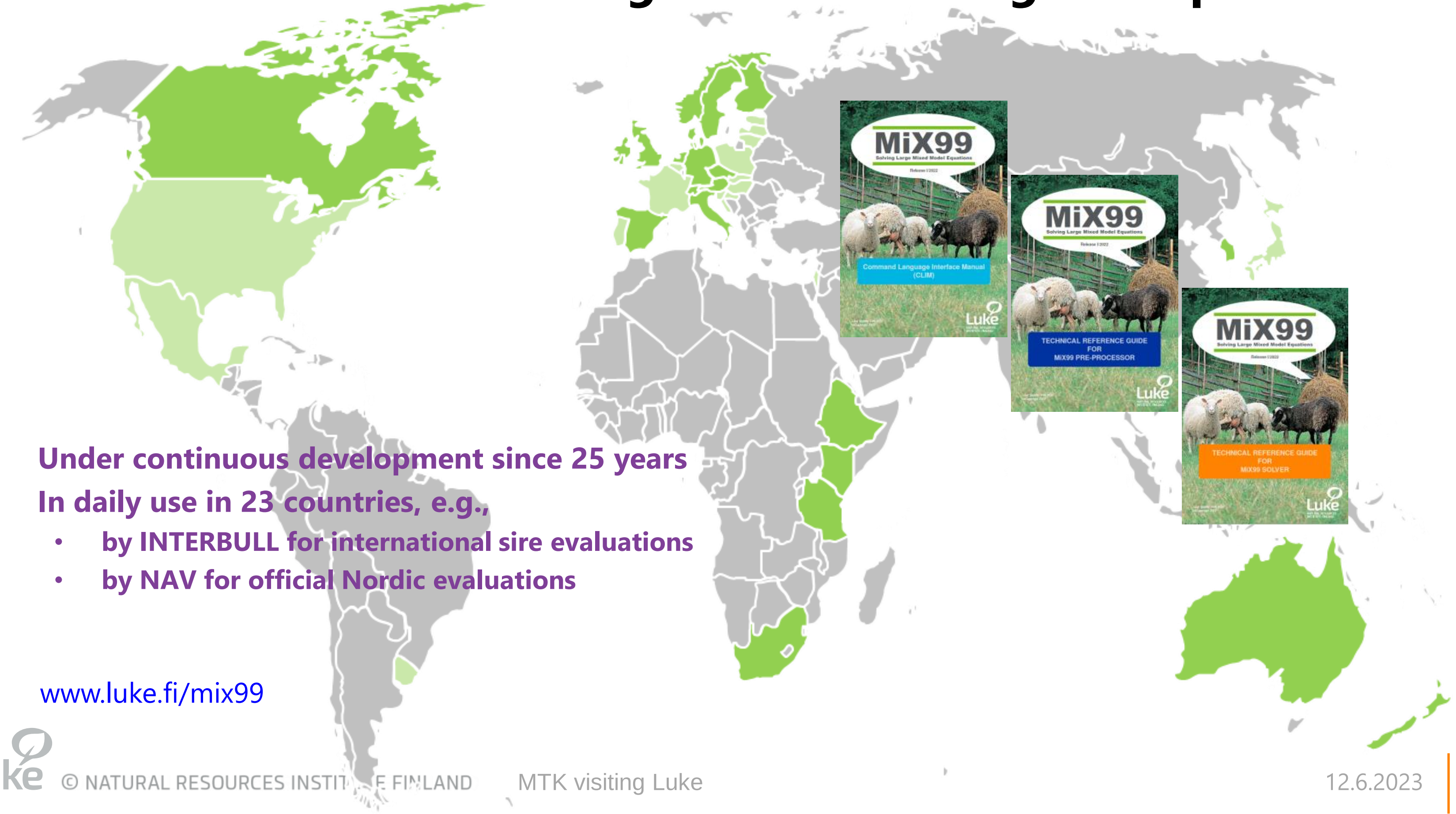
	Current	New
RAM memory use	110 GB	42 GB
Solving time	63 h	48 h

Single-step SNPBLUP
German Holstein test-day model

>1.0 million genotyped animals
25 million animals with records
38 million animals

	Current	New
RAM memory use	760 GB	57 GB

MiX99 software suite for large-scale breeding value predictions



- Under continuous development since 25 years
- In daily use in 23 countries, e.g.,
  - by INTERBULL for international sire evaluations
  - by NAV for official Nordic evaluations

www.luke.fi/mix99

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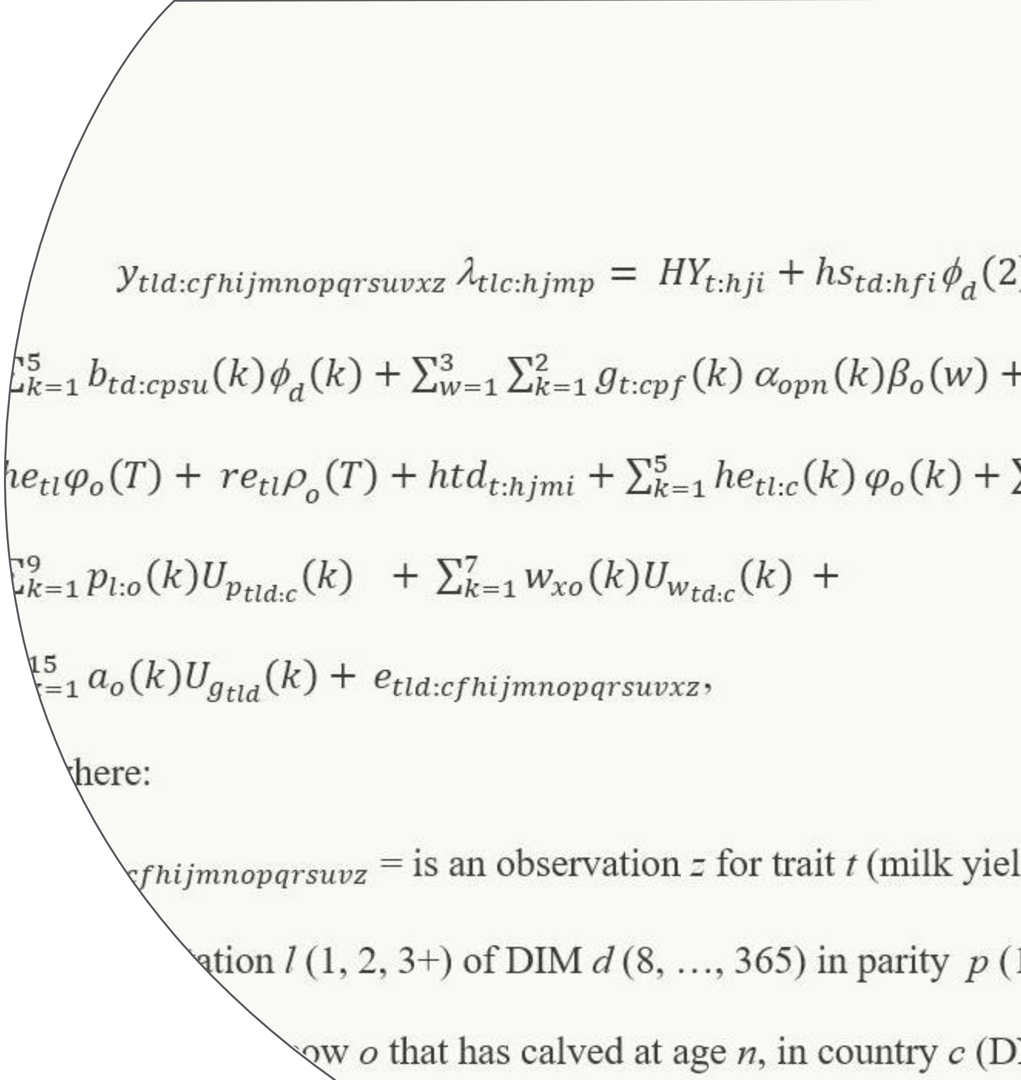
Mathematical modelling for prediction of breeding values



$y_{tld:cfhijmnopqrsuvxz}\ \lambda_{tlc:hjmp} = HY_{t:hji} + hs_{td:hfi}\phi_d(2$

$\sum_{k=1}^{5} b_{td:cpsu}(k)\phi_d(k) + \sum_{w=1}^{3}\sum_{k=1}^{2} g_{t:cpf}(k)\ \alpha_{opn}(k)\beta_o(w) +$

$he_{tl}\varphi_o(T) + re_{tl}\rho_o(T) + htd_{t:hjmi} + \sum_{k=1}^{5} he_{tl:c}(k)\ \varphi_o(k) +$

$\sum_{k=1}^{9} p_{l:o}(k)U_{p_{tld:c}}(k) + \sum_{k=1}^{7} w_{xo}(k)U_{w_{td:c}}(k) +$

$\sum^{15} a_o(k)U_{g_{tld}}(k) + e_{tld:cfhijmnopqrsuvxz},$

here:

$cfhijmnopqrsuvz$ = is an observation z for trait t (milk yiel

ation l (1, 2, 3+) of DIM d (8, …, 365) in parity p (

ow o that has calved at age n, in country c (D

Developing breeding value prediction models for animal breeding

- Close cooperation with industry from Finland and abroad

  → win-win situation

  - Industry partners: access to newest scientific developments
  - Research: access to data
  - Society: benefits from research on topical challenges

- Genetic improvement under continuous change
  - Progress in science, sensor technology, computing technologies, etc.

    → new opportunities for improving prediction models

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Breeding values estimation models for Nordic cattle

2000	Finnish random regression test-day model evaluation for yield traits
2006	Nordic random regression test-day model evaluation for yield traits
2010	Nordic **udder health** evaluation for somatic cell score and mastitis traits
2012	Updating Nordic random regression test-day model evaluations for yield traits (new variance comp.)
2014	Updating Nordic random regression **test-day model evaluations for yield traits** (modelling AMS herds)
2017	Nordic female **fertility** evaluations for conception rate and interval traits
2019	Nordic evaluation for **metabolic body weight** (part of Saved feed index)
2023	Single-step genomic prediction for Finnish **beef cattle**

Some current research activities

Upgrading current genomic prediction models for metabolic body weight

Save feed index contains two parts: maintenance cost and metabolic efficiency.

- Maintenance energy and feed requirement depend on cow's MBW

AIM

- Using slaughter weight as a correlated trait
- Upgrading current multi-step evaluations to single-step genomic predictions

New model for metabolic body weight

Traits: new versus current model

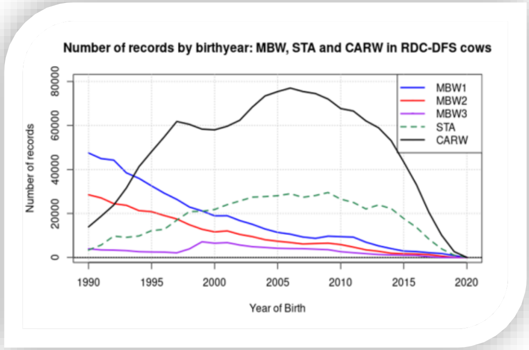
New model	Current model
Metabolic body weight 1.P	Metabolic body weight 1.P
Metabolic body weight 2.P	Metabolic body weight 2.P
Metabolic body weight 3.P	Metabolic body weight 3.P
Stature	Stature
	Body depth
	Chest width
Carcass weight	

Genetic correlation between metabolic body weight and carcass weight

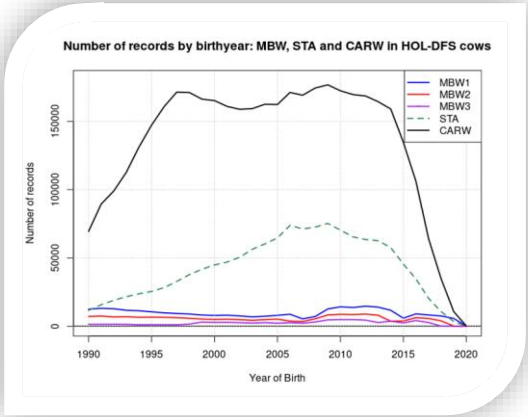
	Carcass weight
MBW 1st P.	0.78
MBW 2nd P.	0.84
MBW 3rd P.	0.86

Available data for metabolic body weight evaluation

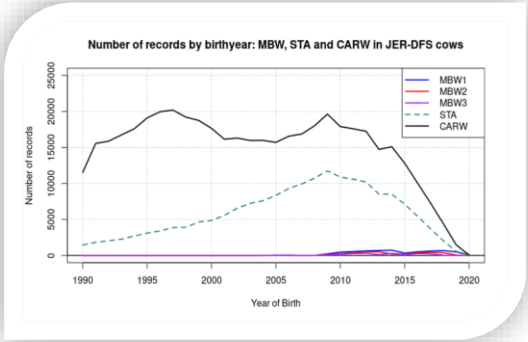
Nordic Red Dairy cattle



Holstein



Jersey



- CARW data significantly increased the amount of phenotypic information used for the genomic evaluation in all Nordic breeds
- CARW strengthen the maintenance cost evaluation in Saved feed index

New single-step GBLUP evaluation *versus* current evaluation

A^{++}Cow project was the first one in the world that used carcass weight information in the prediction model of MBW

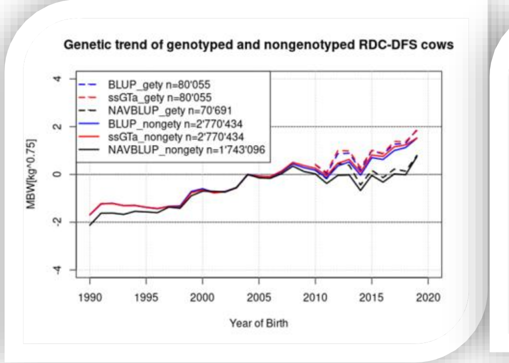
Reliability of genomic breeding values increases

Animals will get more accurate breeding values than before

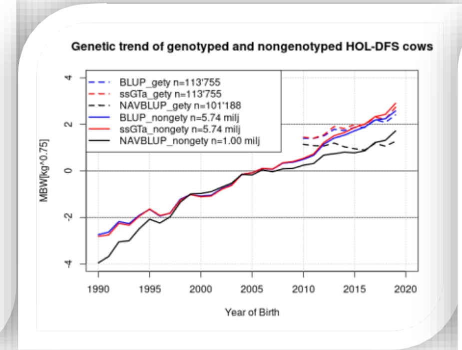
Genetic trends

- Genetic trends are more as we would expected

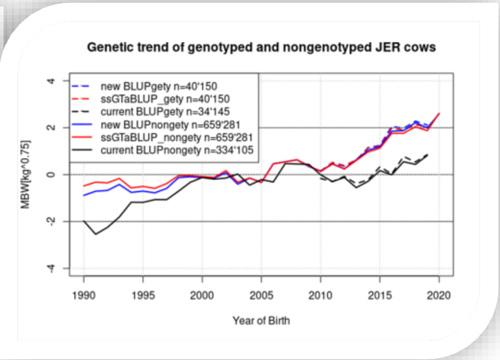
Nordic Red Dairy cattle



Holstein



Jersey



New metric for metabolic efficiency

Instead of residual feed intake we proposed:

Regression on expected feed intake (ReFI)

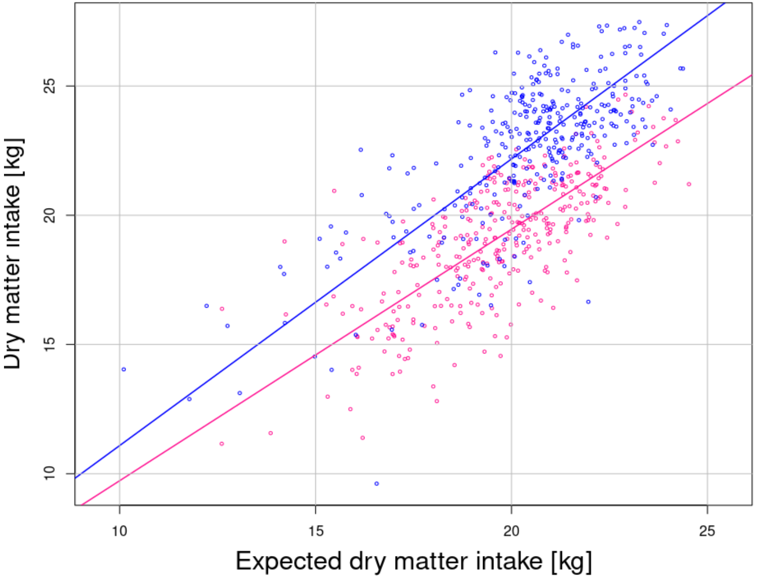
$$\mathrm{DMI}_{ijk} = \beta_i \times \mathrm{eDMI}_{jk} + \psi_k \times \mathrm{eDMI}_{jk} + \alpha_k \times \mathrm{eDMI}_{jk} + \varepsilon_{ijk}$$

- **Approach:** Expected feed intake is based on parameters from dairy cattle nutrition studies

Regression on expected feed intake versus RFI

	ReFI	RFI
Heritability	0.20	0.10
Genetic variation σ_A	4.7%	2.7%
Gen. correlation with feed intake	-0.06	0.72
Selecting 10% best, based on genomic breeding values		
Energy conversion efficiency	+12%	+4%
Milk yield (energy corrected)	+7%	-4%

based on Finnish research farm feed efficiency data (645 cows)



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New phenotypes for future breeding traits

From sensor data to valuable information for breeding

Cow health

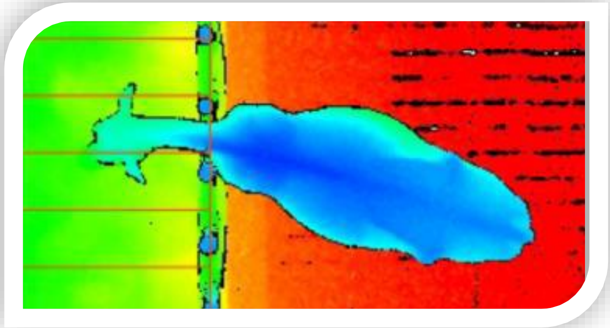
- Milk mid-infrared spectral readings (milk fatty acids, NEFA, BHB)
- Cow-activity tags (cow welfare)
- Herd Navigator (progesterone, BHB)
- 3-D images (body condition score)

Feed efficiency

- 3-D images (CFIT, body weight)
- Near-infrared reflectance spectroscopy (iNDF; digestibility)

Greenhouse gases (GHG)

- Sniffer (CH_4-, CO_2- concentration)
- GreenFeed (CH_4-, CO_2- flux)



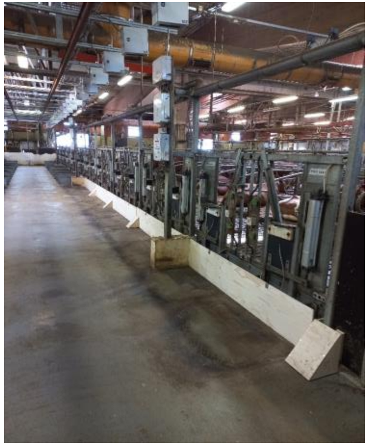
Feed intake prediction by CFIT

Trial 1: 60 cows, (eating from own place)

- Each cow was measured 21 day

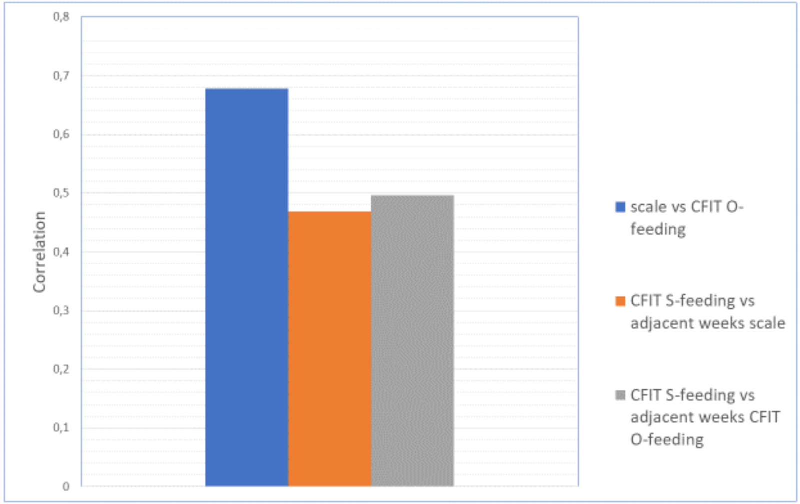
Trial 2: 40 cows, (eating from a swath)

- Each cow was eating from swath for 2 weeks
- Each cow was eating from own place for 2 weeks



Preliminary results from Trial 2

Correlations between CFIT and scale measurements



Methane exhalation measurements from Nordic Red Dairy cows

CH_4, CO_2 concentration measurements

- Continuous recording since 2010
- By photoacoustic spectroscopy ("Sniffer")
- 350 cows with weekly records

CH_4, CO_2, flux measurements

- Continuous recording since 2021
- Respiration flux ("**GreenFeed**")
- 80 cows with weekly records

https://www.c-lockinc.com/researchers/products/greenfeed-large-animals

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More resource efficient and resilient cows through digitalization and genomic selection

DigiDairy

2023-2025
Luke, University of Helsinki, Ministry of Agriculture and Forestry
Valio, Finland,
VikingGenetics, Denmark,
Faba Finland
ProAgria, Finland

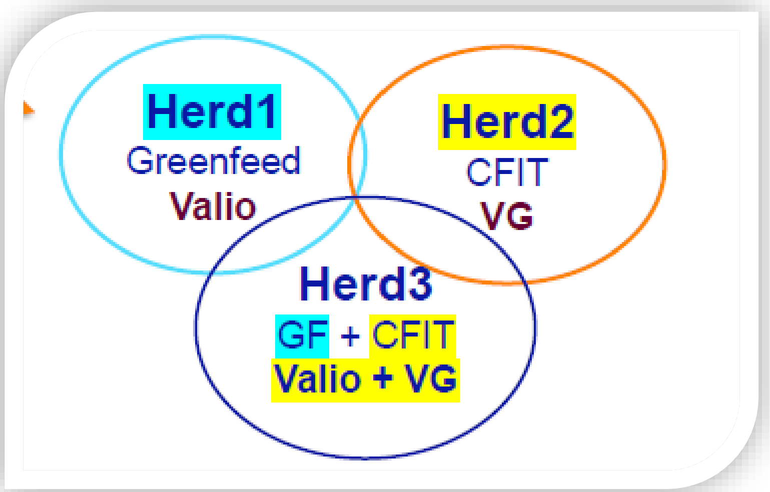
Establisment of living lab herds

Aim

- From research farms → commercial farms
- Continuous recording of metabolic efficiency and GHG emission in living lab reference farms

Requirements

- Participation in milk recording
- 40-60 Nordic Red dairy heifers per year
- All cows genotyped
- Milking robots
- Activity sensors



The DigiDairy project

MAIN AIM: *To develop **novel phenotypes** and tools to boost the improvement of dairy cows' **resource efficiency, resilience and welfare** by **animal breeding** and **herd management**. The development work will be done by utilizing **new technologies** implemented in research farms and **Living Lab** herds.*

WP1. THE LIVING LAB HERDS

1.1. Establishment of the Living Labs

- 3 pilot Living Lab herds furnished with GreenFeed and CFIT systems

WP2. RESOURCE-EFFICIENT COWS

2.1. Recording of feed efficiency and methane emission phenotypes

- Comprehensive data set of feed efficiency and GHG emission metrics collected from research herds and Living Labs

2.2. Genomic prediction models for feed efficiency

- Genetic parameters for $ReCO_2$ available
- Comparison of different models for ReFI, $ReCO_2$, RFI and RCO_2

2.3. Genomic prediction models for methane emissions

- Genetic parameters for CH_4 output traits
- Genetic correlations between CH_4 output traits and production traits

WP3. RESILIENT AND WELLBEING COWS

3.1. Energy status indicator tool

- A tool of based on NEFA and BHB predictions available for herd managament for farmers

3.2. Genetic analyses of resilience indicators based on daily milk yield and feeding time records

- Novel resilience phenotypes developed
- Genetic parameters for the resilience traits
- Genetic correlations between resilience, fertility and energy status

3.3. Development of data-based welfare indicators

- WQ assessments of the Living Lab herds
- XGBoost model developed and validated to predict the welfare

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Thank you