GENETIC PARAMETERS FOR COW-SPECIFIC DIGESTIBILITY

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INTRODUCTION

Improvement of feed efficiency is
beneficial for the farmers and the environment

Measuring of cow-specific digestibility has been challenging

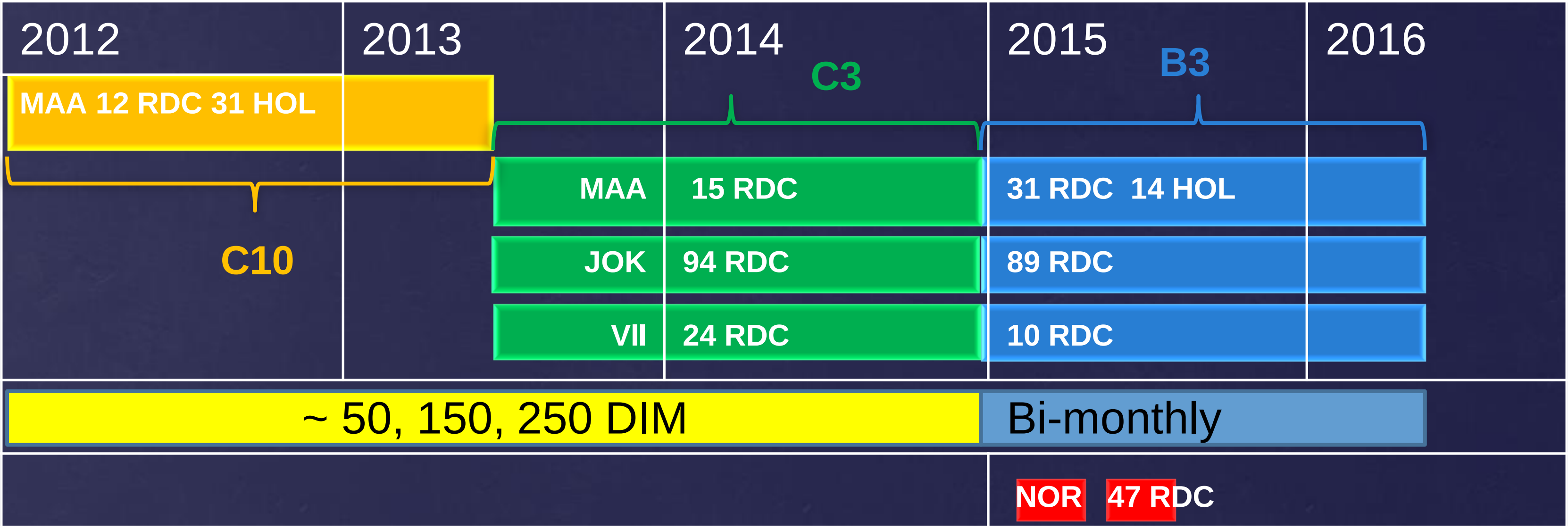
- Total faecal collection
- Markers
- NIRS (near-infrared spectroscopy)
  - → iNDF (indigestible neutral detergent fibre) content in faeces can be predicted with good accuracy

MAIN AIM

To estimate genetic parameters for digestibility predictions based on NIRS

DATA

The total data set (T) included 931 observations from 328 cows



2012
2013
2014
2015
2016

MAA 12 RDC 31 HOL

C10

C3

MAA 15 RDC
JOK 94 RDC
VII 24 RDC

B3

31 RDC 14 HOL
89 RDC
10 RDC

~ 50, 150, 250 DIM

Bi-monthly

NOR 47 RDC

C10 = composite sample of 10 faecal samples (5 consecutive morning and evening samples)
C3 = composite sample of 3 faecal samples (3 consecutive mornings) collected 50, 150 and 250 DIM
B3 = composite sample of 3 faecal samples collected bi-monthly
NOR = composite sample of 3 faecal samples collected in Norway in Feb and Mar 2015

Data set B, collected bi-monthly in Finland, included 441 feacal samples from 144 cows and in addition to B3 samples:

- B1 = day one sample
- B2 = composite sample from day one and two

TRAITS

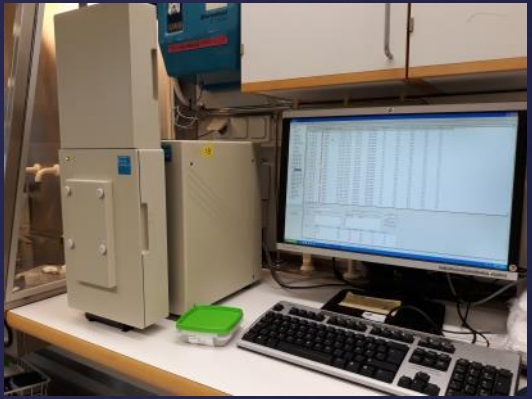
$\mathbf{iNDF_{faeces}}$ (g/kg)

= directly predicted by NIRS

$\mathbf{DMD_{iNDF}}$ (g/kg)

$$= \left(\frac{\mathrm{iNDF}_{\mathrm{faeces}} - \mathrm{iNDF}_{\mathrm{feed}}}{\mathrm{iNDF}_{\mathrm{faeces}}}\right) \times 1000$$

- $\mathrm{iNDF}_{\mathrm{feed}}$ predicted by NIRS



Statistics of NIRS calibration models

	n	SECV	R^2_{cv}
$\mathrm{iNDF}_{\mathrm{faeces}}$	476	16.6	0.86
$\mathrm{iNDF}_{\mathrm{feed}}$	448	14.9	0.87

SECV = standard error of cross-validation (g/kg); R^2_{cv} = the coefficient of determination

STATISTICAL ANALYSES

MODEL FOR TOTAL DATA SET (T):

$y_{ijklmn} = breed_i + parity_j + lactation\ stage_k + feeding\ level_l + HYM_m + iNDF_{feedn} + g_n + pe_n + e_{ijklmn},$ where

4 different residual variances for different sampling protocols (C10, C3, B3 and NOR)

MODEL FOR DATA SET B:

$y_{ijkmn} = breed_i + parity_j + lactation\ stage_k + HYM_m + iNDF_{feedn} + g_n + pe_n + e_{ijkmn},$ where

y = $iNDF_{faeces}$ or DMD_{iNDF} (g/kg) predicted by NIRS
breed = fixed effect of breed (RDC or HOL)
parity = fixed effect of parity (primiparous or multiparous)
lactation stage = fixed effect of lactation stage (<100, 100-199, >199 DIM)
feeding level =fixed effect of different feeding levels in C10 and Norway data
HYM = fixed effect of contemporary groups consuming the same feed (herd-year-month)
$iNDF_{feed}$ = regression coefficient of iNDF content in feed

RESULTS

Genetic parameter estimates using the total data (data set T, 328 cows)

	σ^2_{pe} (se)	σ^2_g (se)	σ^2_e (se)	h^2
DMD_{iNDF}	2.96 (45.5)	110.66 (50.3)		
C3			687.32 (78.0)	0.14
B3			281.44 (25.0)	0.28
NOR			609.24 (116.2)	0.15
C10			102.55 (22.3)	0.51
$iNDF_{faeces}$	1.08 (14.7)	38.67 (16.2)		
C3			239.90 (25.8)	0.14
B3			74.65 (6.9)	0.34
NOR			255.88 (50.0)	0.13
C10			40.76 (8.1)	0.48

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Estimates for genetic parameters and repeatabilities using bi-monthly data (data set B, 144 cows)

	σ^2_{pe} (se)	**σ^2_{g} (se)**	**σ^2_{e} (se)**	**h^2**	**r**
DMD_{iNDF}					
B1*	87.62 (101.4)	18.34 (101.4)	534.05 (44.5)	0.03	0.17
B2*	88.30 (71.9)	20.06 (70.5)	334.97 (27.9)	0.05	0.24
B3	69.71 (94.8)	73.30 (100.7)	268.95 (22.4)	0.18	0.34
$iNDF_{faeces}$					
B1*	19.38 (31.0)	14.28 (32.6)	146.02 (12.2)	0.08	0.19
B2*	22.94 (24.2)	14.38 (25.5	91.70 (7.7)	0.11	0.28
B3	13.63 (30.0)	33.92 (32.9)	72.33 (6.0)	0.28	0.39

r = repeatability estimate
* Poor convergence in the genetic analysis

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CONCLUSIONS

- **Genetic variation in digestibility exists**
  - Heritability estimates ranged from 0.13 to 0.51 depending on the sampling protocol

- Sampling protocol needs to be carefully planned

→ **iNDF$_{\textbf{faeces}}$ can be used as an indicator trait**

- New practical methods still needed for faecal sampling and processing

THANK YOU!

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