

Selection for feed intake in dairy cattle using genomic selection.

Roel Veerkamp, Mario Calus and Yvette de Haas
RobustMilk & gDMI



Animal Breeding & Genomics Centre

Introduction

- Importance of feed efficiency
 - Global food, forest or fuel discussions
 - Environmental issues (manure & greenhouse gas)
 - Feed important variable cost at farm level

→ Selection impossible in progeny testing scheme.

"Can we beat this dilemma in the era of genomics"

(work in progress)



Animal Breeding & Genomics Centre

Outline

- Predict EBV feed efficiency from correlated traits
- Genomics
 - Individual genes
 - Genome wide selection
- Future perspective
 - Progeny tested bull
 - Genomically tested bull



Animal Breeding & Genomics Centre

Predict EBV from correlated traits

Predict EBV from correlated traits



Animal Breeding & Genomics Centre

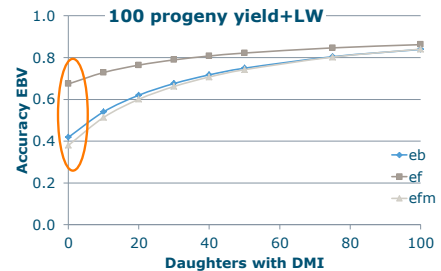
Predictor traits

- Data Dutch research herds
 - nearly 2000 lactations with feed intake, ration, chemical composition, liveweight ...
- Can $LW^{0.75}$ and FPCM predict EBV for feed efficiency?



Animal Breeding & Genomics Centre

Predicting EBV for feed efficiency (35-70 DIM)



$$EB = NE_{intake} - (NE_{maintenance} + NE_{milk})$$

$$EFF = NE_{milk} / NE_{intake}$$

$$EFM = NE_{milk} / (NE_{intake} - NE_{maintenance})$$

Predicting EBV for feed intake

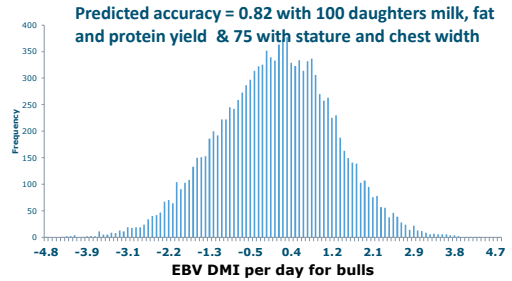
	Energy Intake (35-70 DIM+ 120 - 155 DIM)
Milk 305	0.61
Fat 305	0.54
Protein 305	0.67
Stature	0.76
Body depth	0.21
Chest with	0.60
Rump with	0.10
BCS	0.06

Probably too high ?
 r_g between liveweight
and intake was: 0.52



Animal Breeding & Genomics Centre

EBV DMI based on yield and type



Animal Breeding & Genomics Centre

Genomics: Individual genes

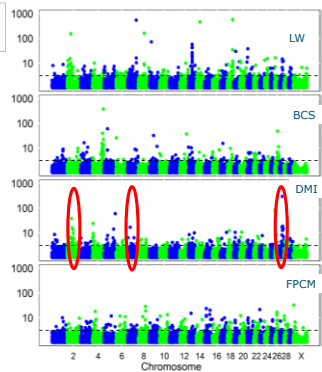
Genomics: Individual genes



Animal Breeding & Genomics Centre

Individual genes

- 500 unique genes in vicinity of SNP; 27 both BCS & DMI
- Biology: 32 genes smell, taste & pheromone
- Three SNP for DMI in genes:
 - Tryptophan
 - Insulin genes
 - Epidermal growth factors



Veerkamp et al, in press



Animal Breeding & Genomics Centre

Genomics: Genome wide selection

Genomics: Genome wide selection

Genome wide selection

- Data in own country was initially 600 cows with feed efficiency.
- Accuracy of GWS in the order of 0.36 for feed efficiency (e.g. Verbyla et al)
- Phenotype is king → collaboration



Animal Breeding & Genomics Centre



Animal Breeding & Genomics Centre

Genome wide selection: shared data

- Australia (DPI)
 - 843 calves with genotypes (624,930 SNPs)
- RobustMilk (SAC & WLR)
 - 599 Dutch cows with genotypes (37,069 SNPs)
 - 359 Scottish cows with genotypes (37,069 SNPs)
- Common
 - 40 bulls genotyped in both datasets



Animal Breeding & Genomics Centre

Genetic parameters (with Genomic RM)

	AU	UK	NL
AU	0.41 (0.09)		
UK	0.74 (0.34)	0.38 (0.12)	
NL	0.36 (0.22)	0.50 (0.28)	0.59 (0.10)

- Need a multitrait GBLUP model



De Haas et al, submitted

Animal Breeding & Genomics Centre

Accuracy of genomic selection

	Within	Shared
AU	0.38 (0.03)	0.39 (0.04)
UK	0.30 (0.04)	0.33 (0.03)
NL	0.33 (0.10)	0.34 (0.09)

- Need a multitrait GBLUP model; otherwise might lose accuracy
 - Variable results in NL depending on validation set



De Haas et al, submitted

Animal Breeding & Genomics Centre

Global dry matter initiative: gDMI



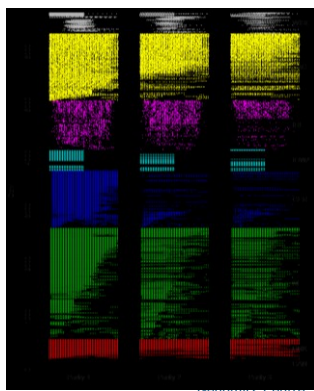
- Combine DMI phenotypes
- Common pedigree
- Combine genotypes
- Key research questions:
 - Genomic similarity between population?
 - How to combine, homogenise and standardise phenotypes?
 - Can we predict DGV for DMI for different partners?



Animal Breeding & Genomics Centre

DMI phenotypes

- #cows: 7000
- #lactations: 11700
- #calves: 1800 (Donagh Berry)



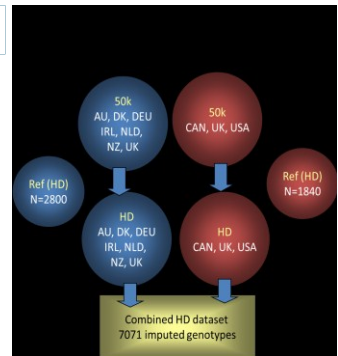
Genomics Centre

Genotypes

#genotyped: 6347

Impute all 50k genotypes to HD with 777K

Jennie Pryce (DPI Melbourne) & Jarmila Johnston & Filippo (CDN)



Animal Breeding & Genomics Centre

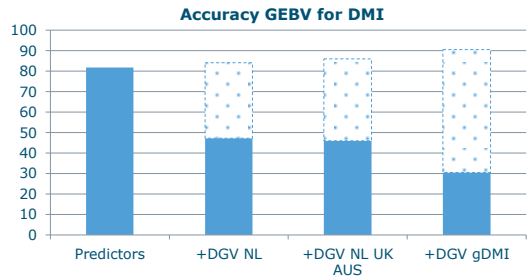
Future perspective: combination

Future perspective: combination



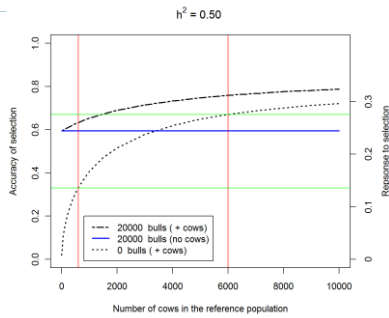
Animal Breeding & Genomics Centre

Prospective for a progeny tested bull



Animal Breeding & Genomics Centre

Prospective for genomically tested bull



Calus et al, in press

Animal Breeding & Genomics Centre

Conclusions

- Selection for feed efficiency impossible a few years ago, with genomics a realistic prospect for future
 - Yield and type to make the first step
 - Genomics should identify 'net efficient cows'
- Breeding goals is more complicated
 - Energy balance; liveweight; economics fat:protein
- Phenotyping is still king; collaboration is leading



Animal Breeding & Genomics Centre

Acknowledgements



The Dutch Dairy Board



The RobustMilk project is financially supported by the European Commission under the Seventh Research Framework Programme, Grant Agreement KBBE-211708. This publication represents the views of the authors, not the European Commission, and the Commission is not liable for any use that may be made of the information.



Mike Coffey Eileen Wall
Jennie Pryce Ben Hayes



Animal Breeding & Genomics Centre