Selection for feed intake in dairy cattle using genomic selection.

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RobustMilk & gDMI

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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)

Outline

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

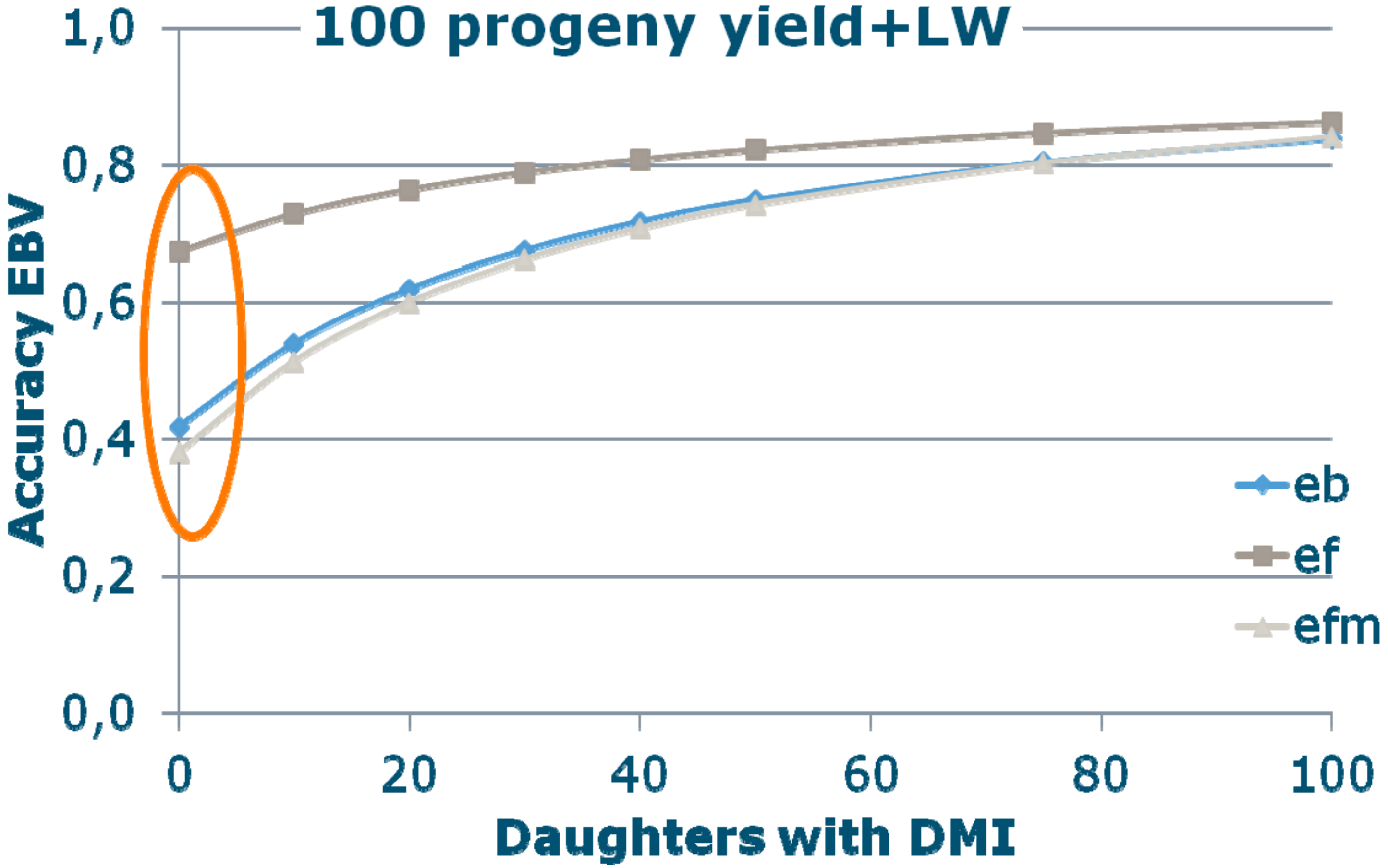
Predict EBV from correlated traits

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?

Predicting EBV for feed efficiency (35-70 DIM)



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

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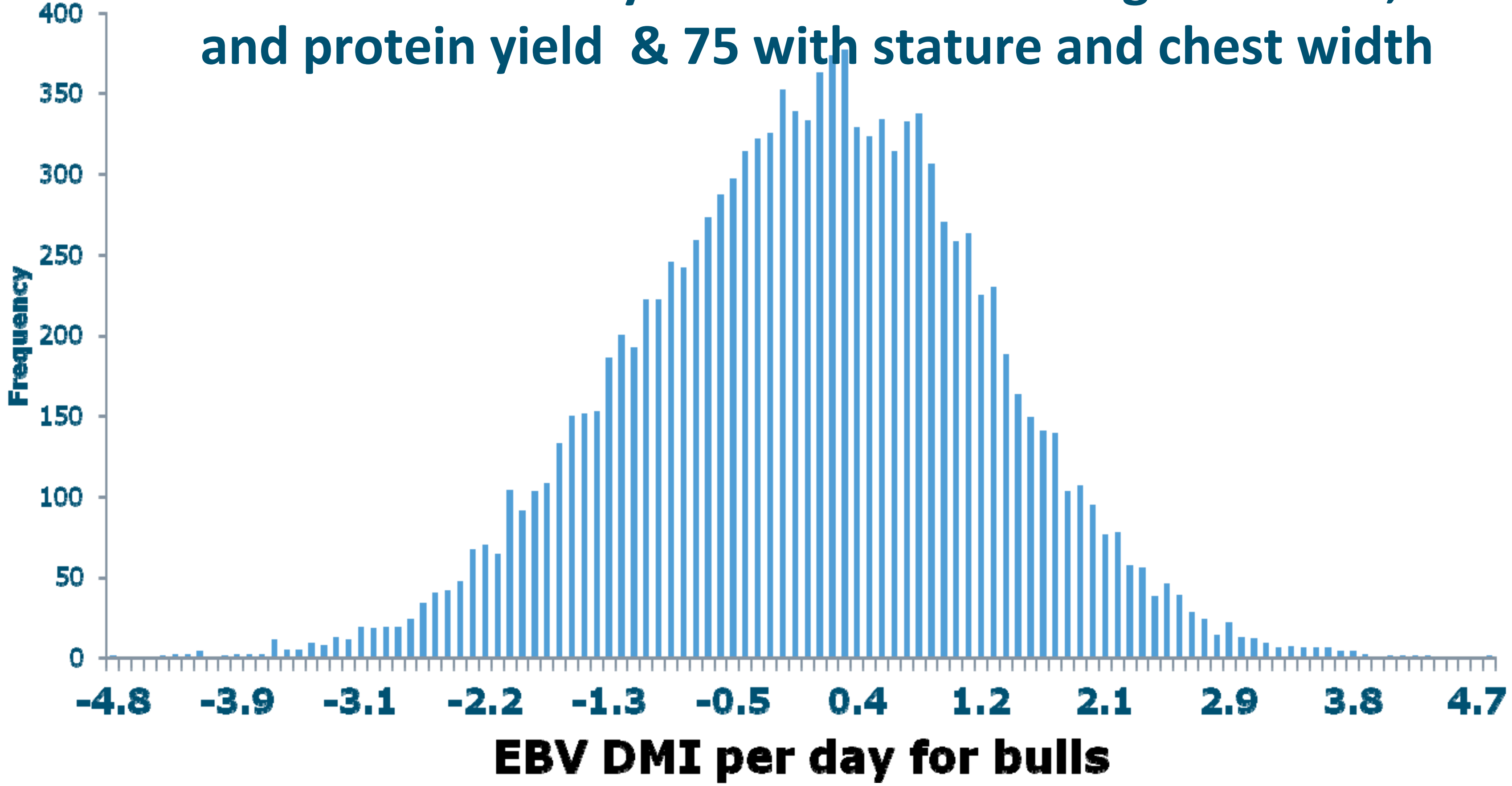
Predicting EBV for feed intake

	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

EBV DMI based on yield and type

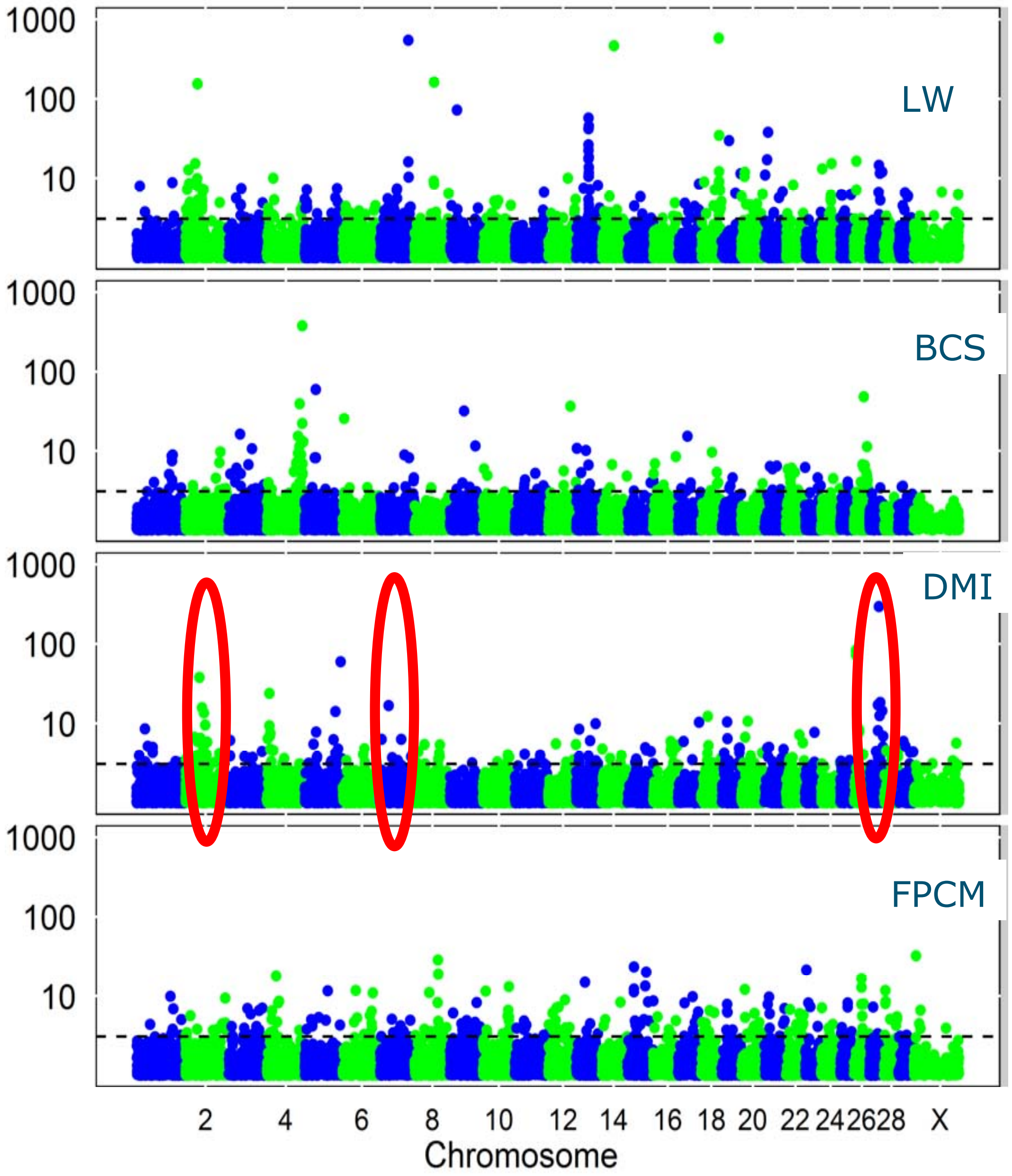
Predicted accuracy = 0.82 with 100 daughters milk, fat and protein yield & 75 with stature and chest width



Genomics: Individual genes

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

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

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

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

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 loose accuracy
- Variable results in NL depending on validation set

De Haas et al, submitted

Global dry matter initiative: **g**DMI

- 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?

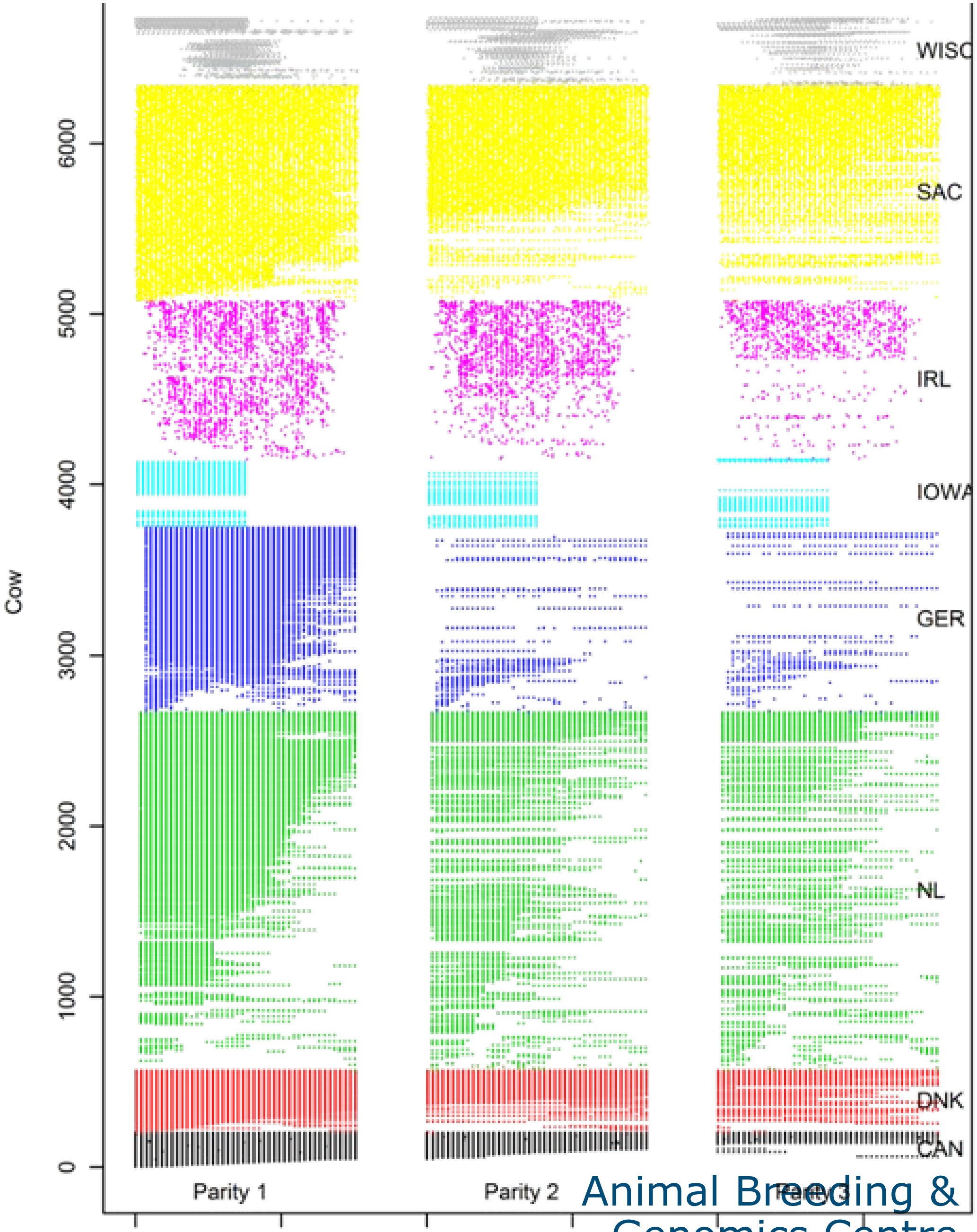
DMI phenotypes

#cows: 7000

#lactations: 11700

#calves: 1800

(Donagh Berry)



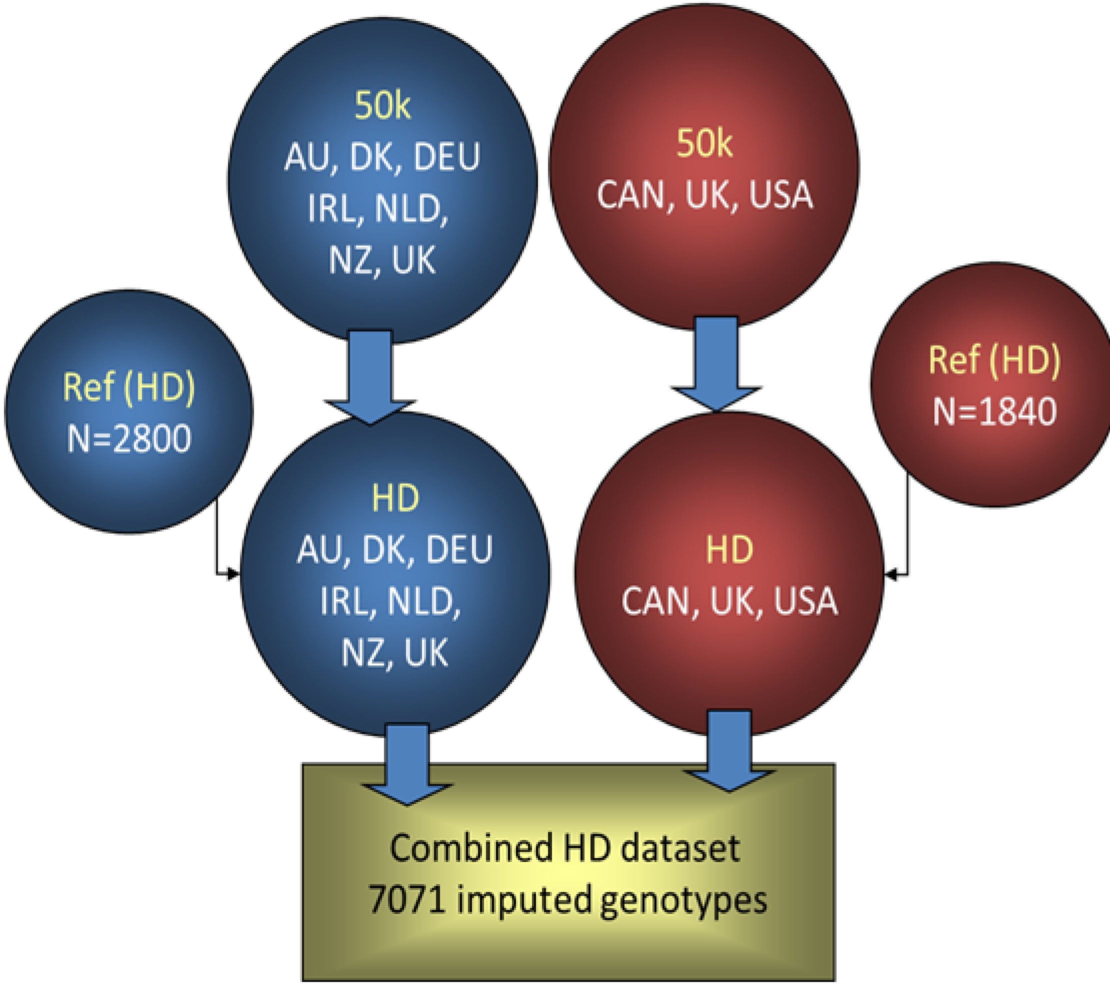
Genotypes

#genotyped: 6347

Impute al 50k genotypes to HD with 777K

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

Imputation strategy



50k
AU, DK, DEU
IRL, NLD,
NZ, UK

50k
CAN, UK, USA

Ref (HD)
N=2800

Ref (HD)
N=1840

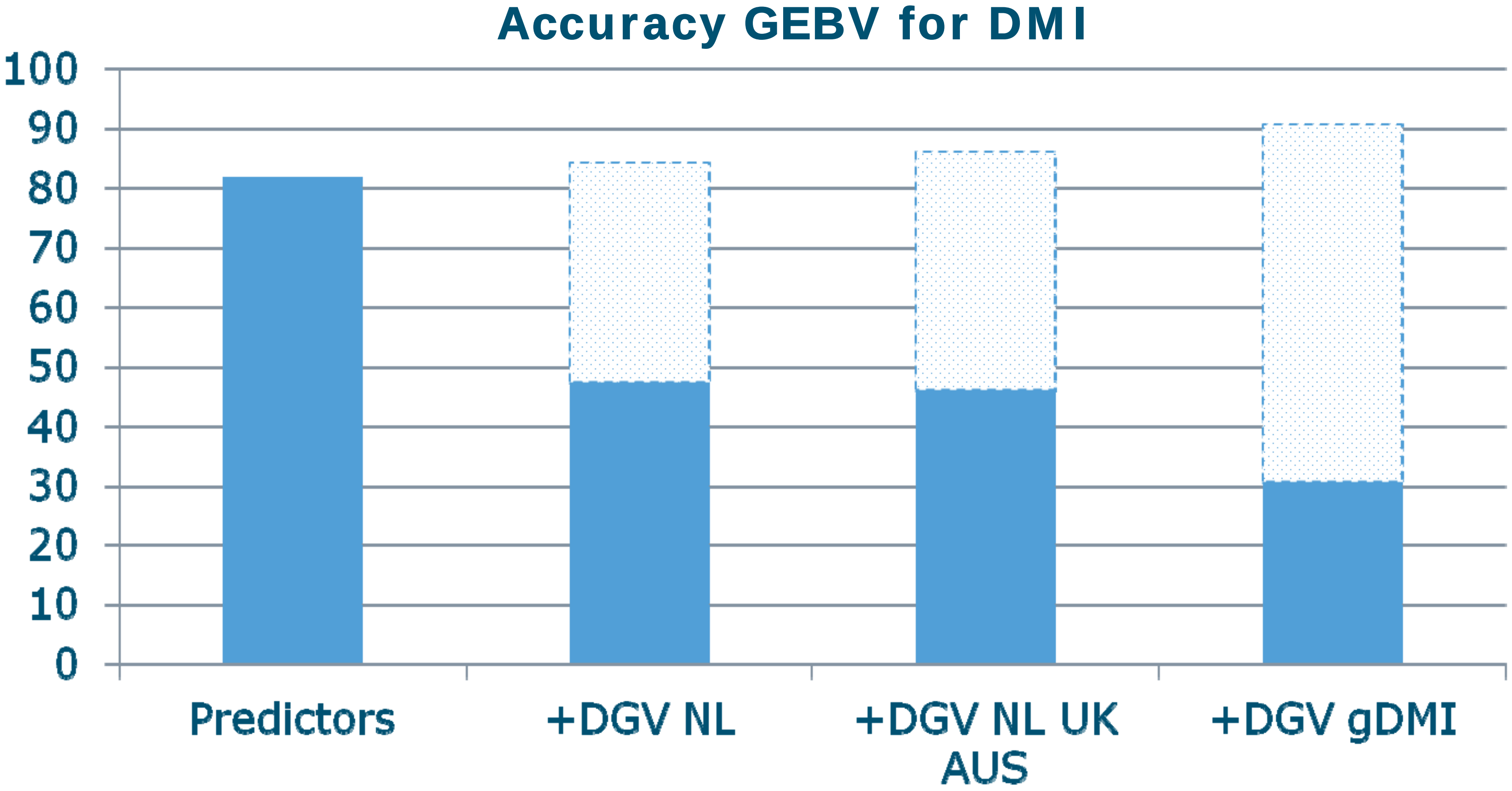
HD
AU, DK, DEU
IRL, NLD,
NZ, UK

HD
CAN, UK, USA

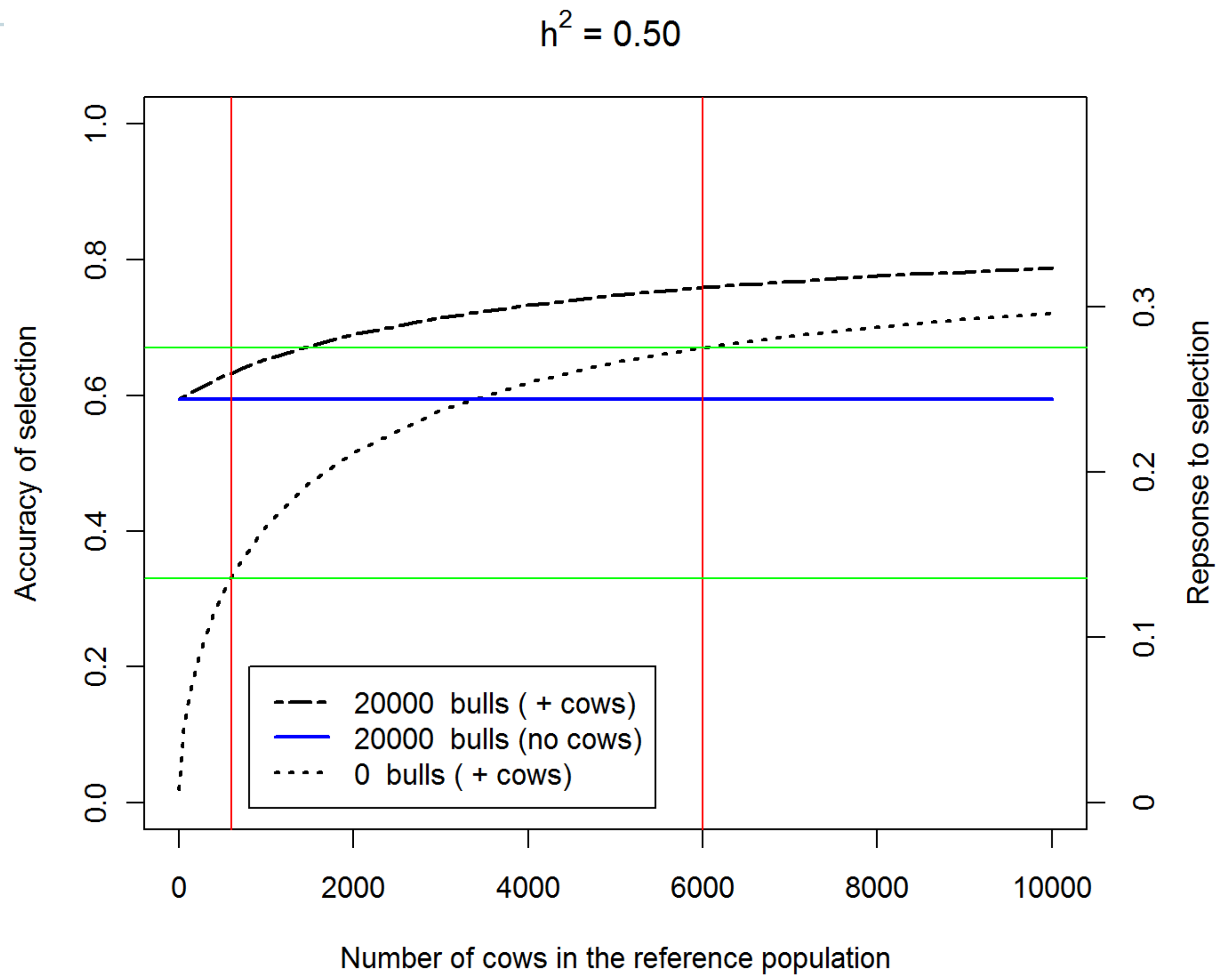
Combined HD dataset
7071 imputed genotypes

Future perspective: combination

Prospective for a progeny tested bull



Prospective for genomically tested bull



Calus et al, in press

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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

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Feed utilisation complex