

# Genetics of feed efficiency in dairy cattle

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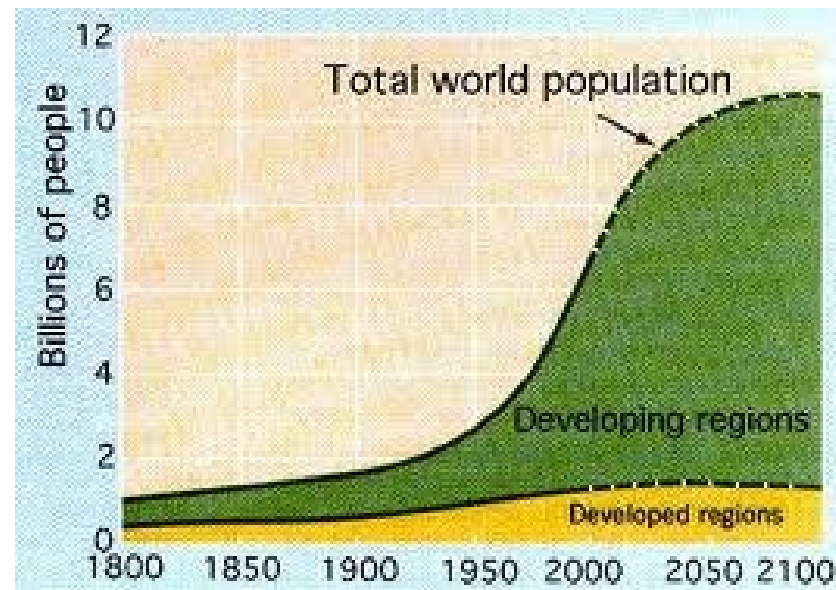


LIVESTOCK RESEARCH  
WAGENINGEN UR

Animal Breeding &  
Genomics Centre

# Importance of improving feed efficiency

- Feed a growing population
- Feed is major variable cost in animal production
- Environmental issues (manure & greenhouse gas)

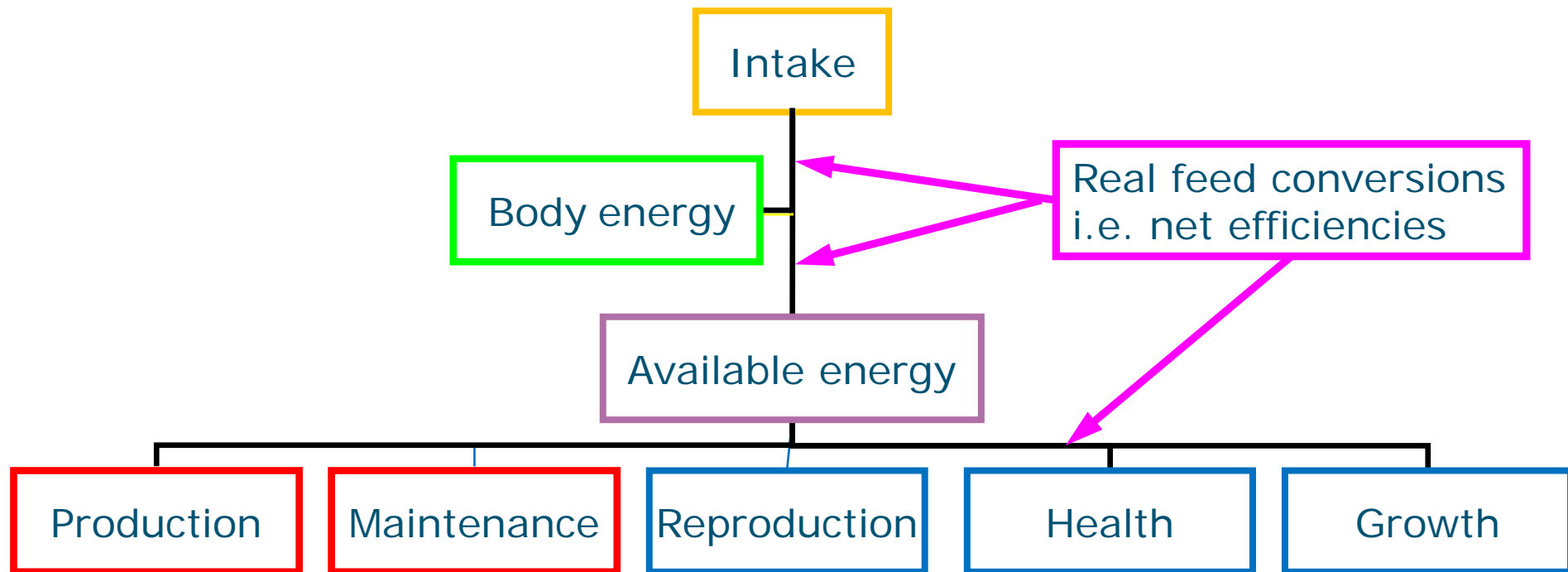


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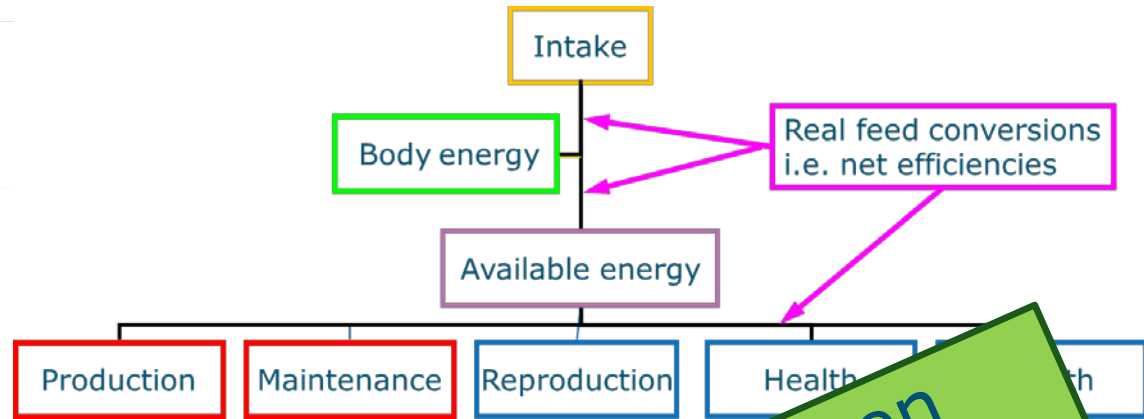
# Role of genetics

- Making use of natural variation between animals
  - Cost-effective
  - Permanent and cumulative changes in performance
  
- Information on feed efficiency is needed on many animals!

# Feed utilisation complex (simplified)



# Feed efficiency

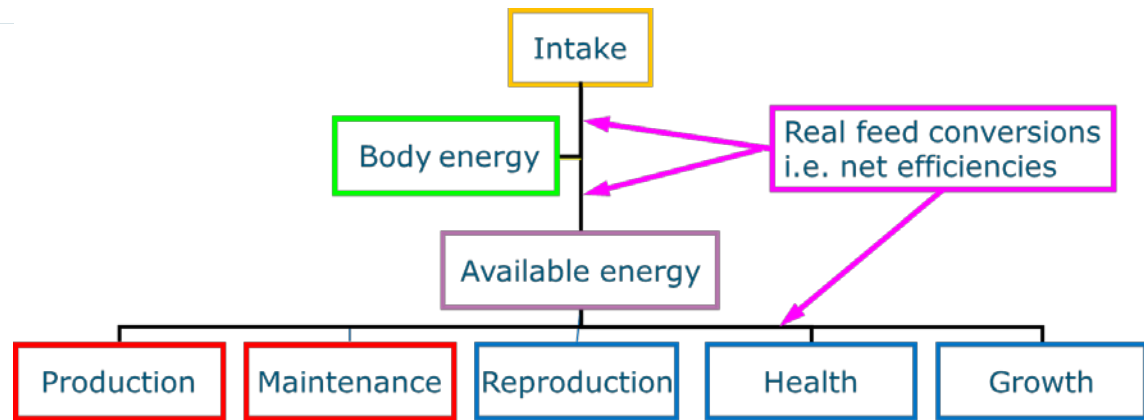


## Net efficiency

Efficiency of converting feed into production, maintenance, health and growth

Residual feed intake: difference between actual feed intake and predicted feed intake

# Feed efficiency

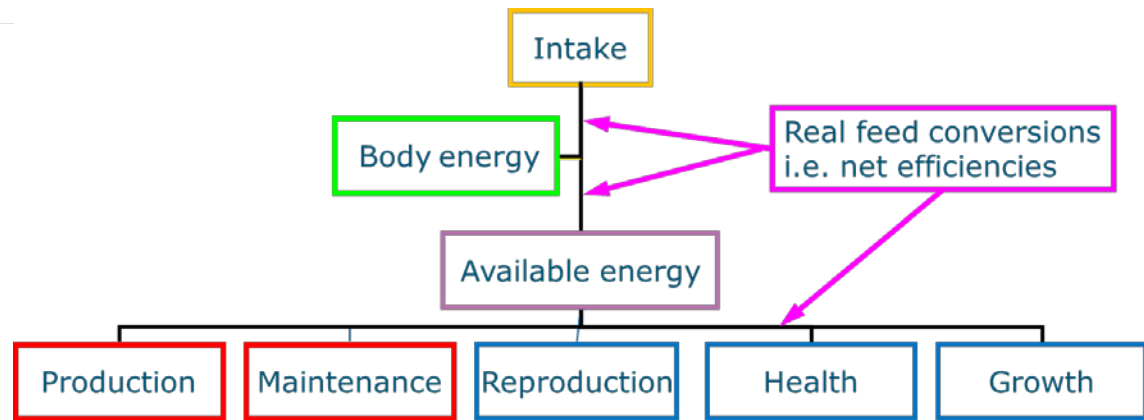


Energy balance:

Intake – milk – maintenance



# Feed efficiency

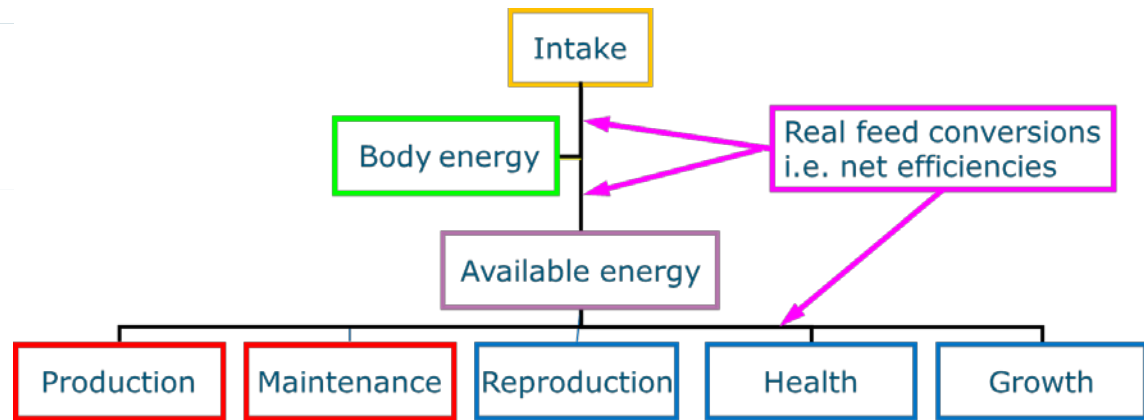


Gross efficiency:

Milk / Intake



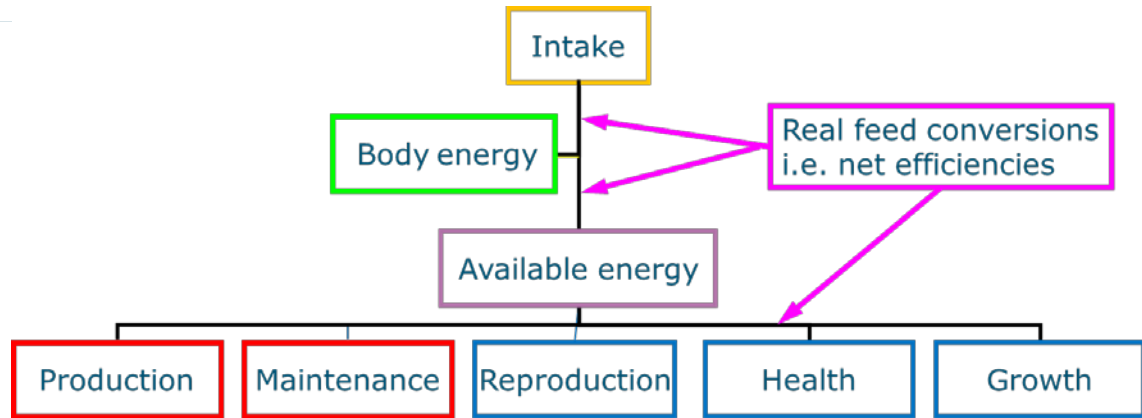
# Feed efficiency



	Net efficiency	Energy balance	Gross efficiency
Dry matter intake	✓	✓	✓
Body condition score	✓		
Milk, fat, protein	✓	✓	✓
Live weight	✓	✓	
Live weight change	✓		
Reproduction, health etc.	✓		



# Feed efficiency



Dry matter intake	Expensive
Body condition score	Difficult
Milk, fat, protein	Easy
Live weight	Not often measured – predicted using type
Live weight change	Difficult
Reproduction, health etc.	Very difficult

Energy balance:

$\text{Intake} - \text{milk} - \text{maintenance}$

Gross efficiency:

$\text{Milk} / \text{Intake}$

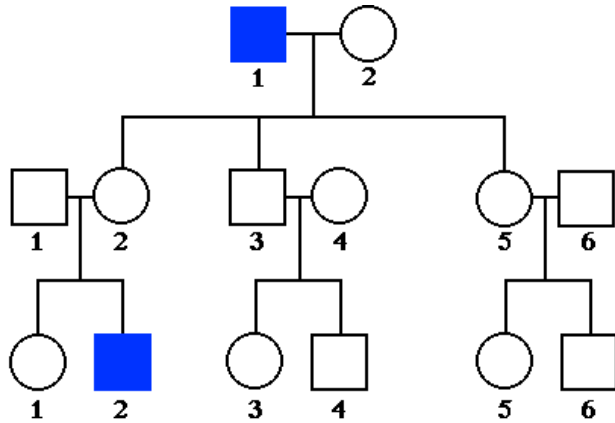
# Outline

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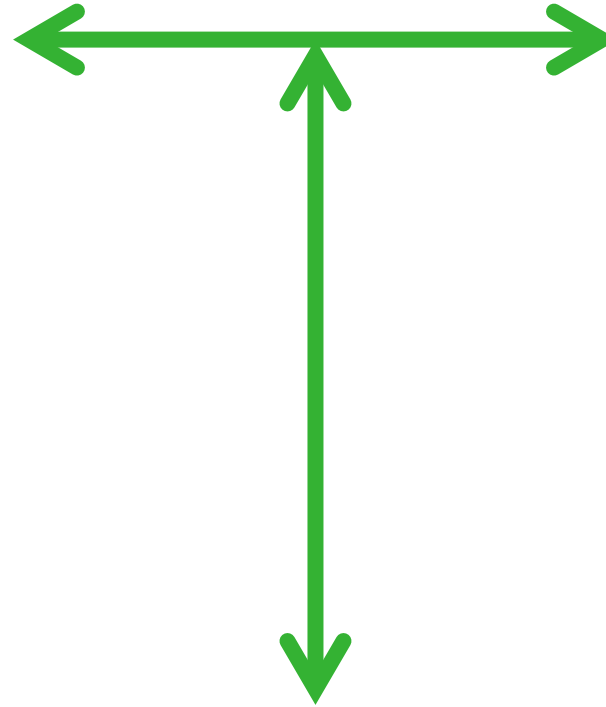
- Can we get traditional breeding value for feed efficiency?
- Is genomics the missing link?
  - Individual genes
  - Genome wide selection
- Conclusions & Future outlook

# Traditional breeding

Pedigree



Phenotypes



Estimated breeding value (BLUP)

# Available data

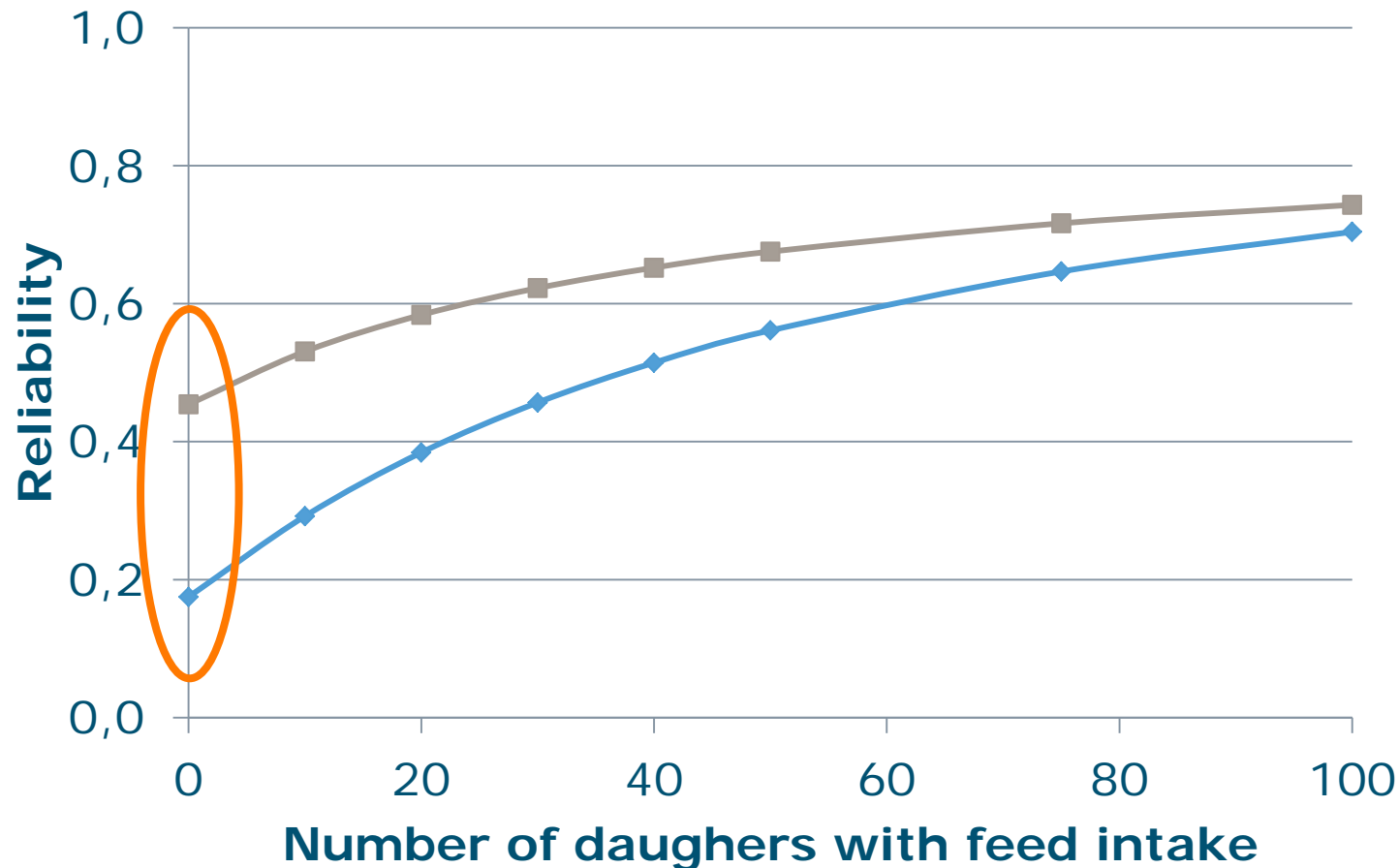
- Data nutritional experiments on Dutch research herds
  - Nearly 3000 lactations with
    - Daily feed intake
    - Ration and chemical composition
    - Milk production
    - Live weight



# Can milk yield and metabolic live weight predict breeding value for feed efficiency?



# 100 daughters with milk and live weight



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# Feed efficiency from predictor traits

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Can milk yield and live weight be used to predict a breeding value for feed efficiency?

■ **YES!!**

BUT:

■ Information on feed intake is still needed!

# Recording feed intake

- Expensive equipment
- Labour intensive measurements
- Not on practical farms, only in research herds
  - small impact
  - not always representative for national population



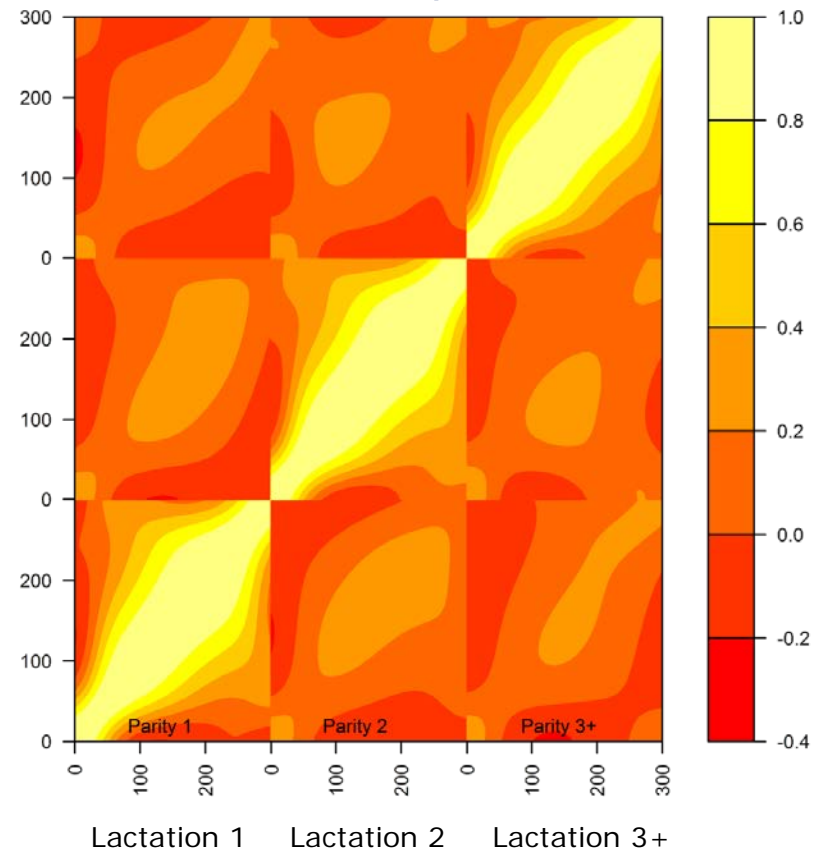


# Recording feed intake

- More variable than milk yield and less correlated within and across lactations

→ measure feed intake at different stages and lactations

**Correlations between feed intake at different days in milk in lactation 1, 2 and 3+**



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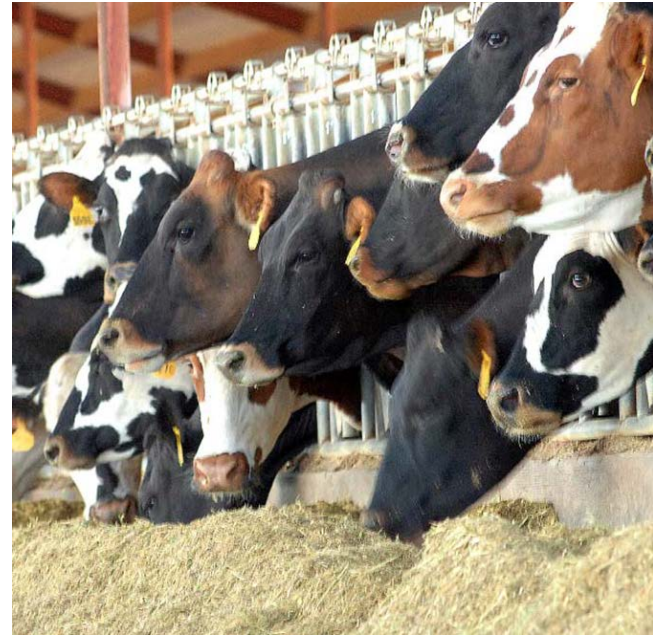
# How to get info on DMI on national scale?

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1. Use correlated traits to determine feed intake
2. Use genomics for feed intake
  - Individual genes
  - Genome wide selection

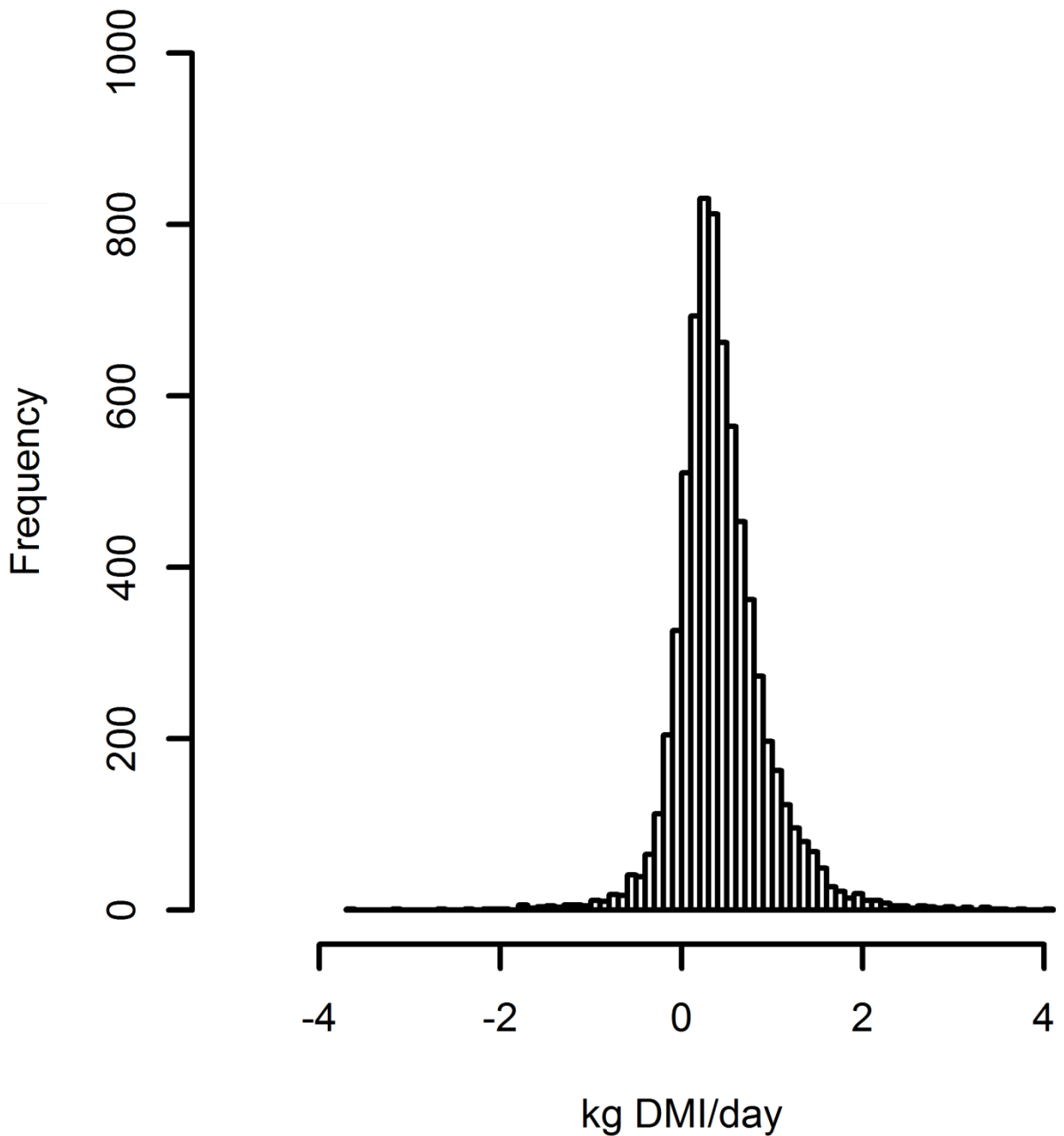
# Correlated traits to predict feed intake

- Milk yield
  - Fat yield
  - Protein yield
  - Stature
  - Chest width
- Production of cow
- Size of cow



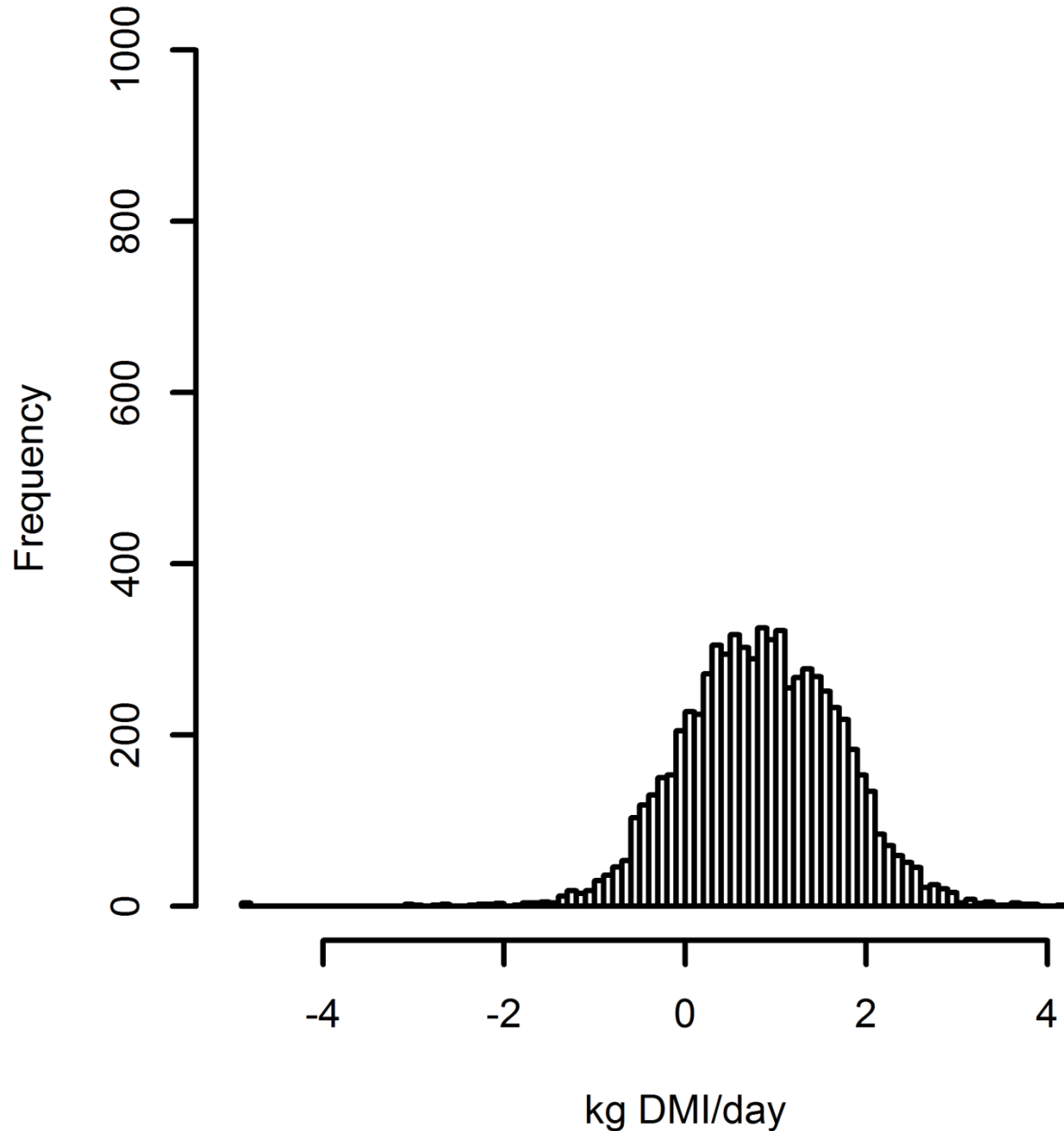
# DMI research herd cows

Breeding value for feed intake

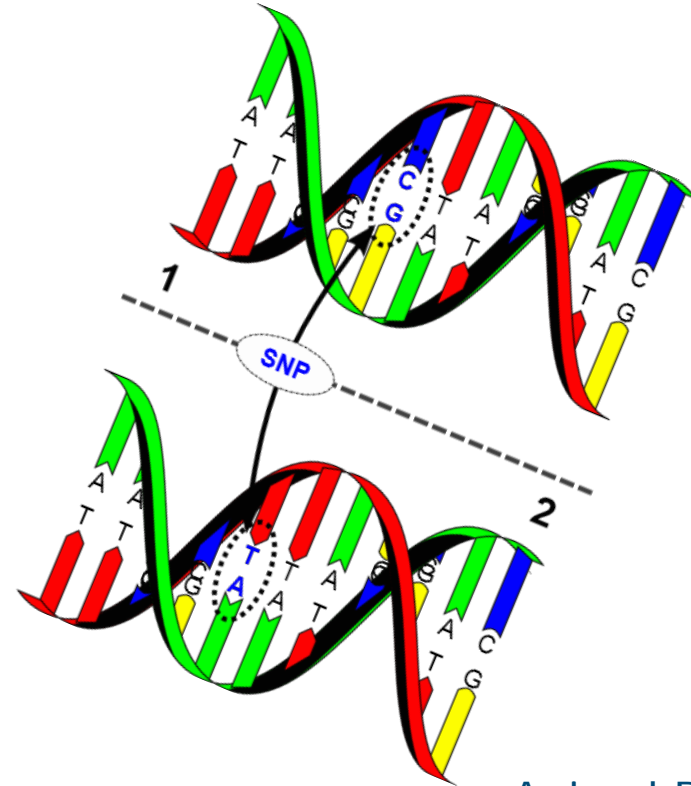


# Breeding value for feed intake

## DMI + Predictors



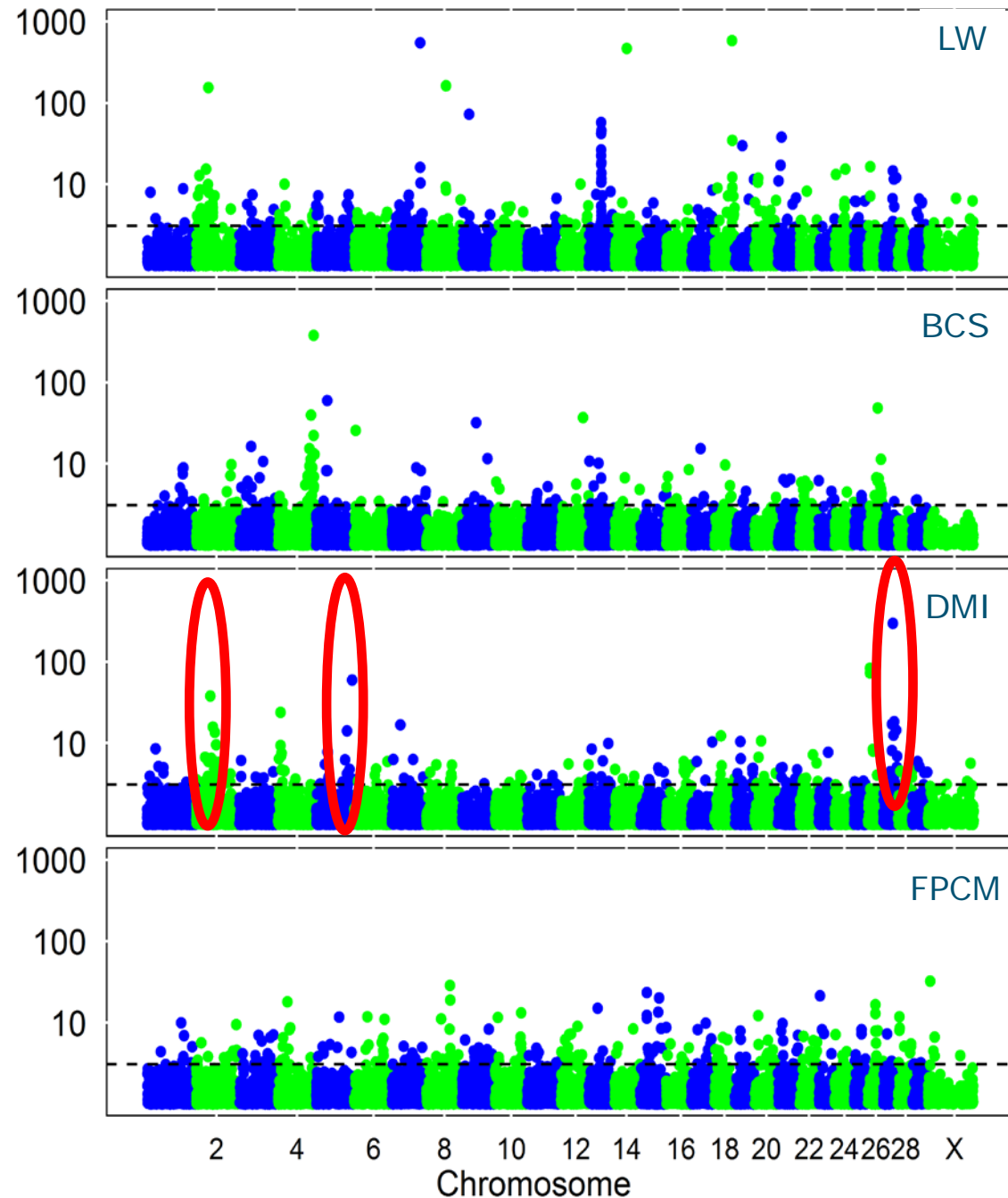
# Is genomics the missing link?



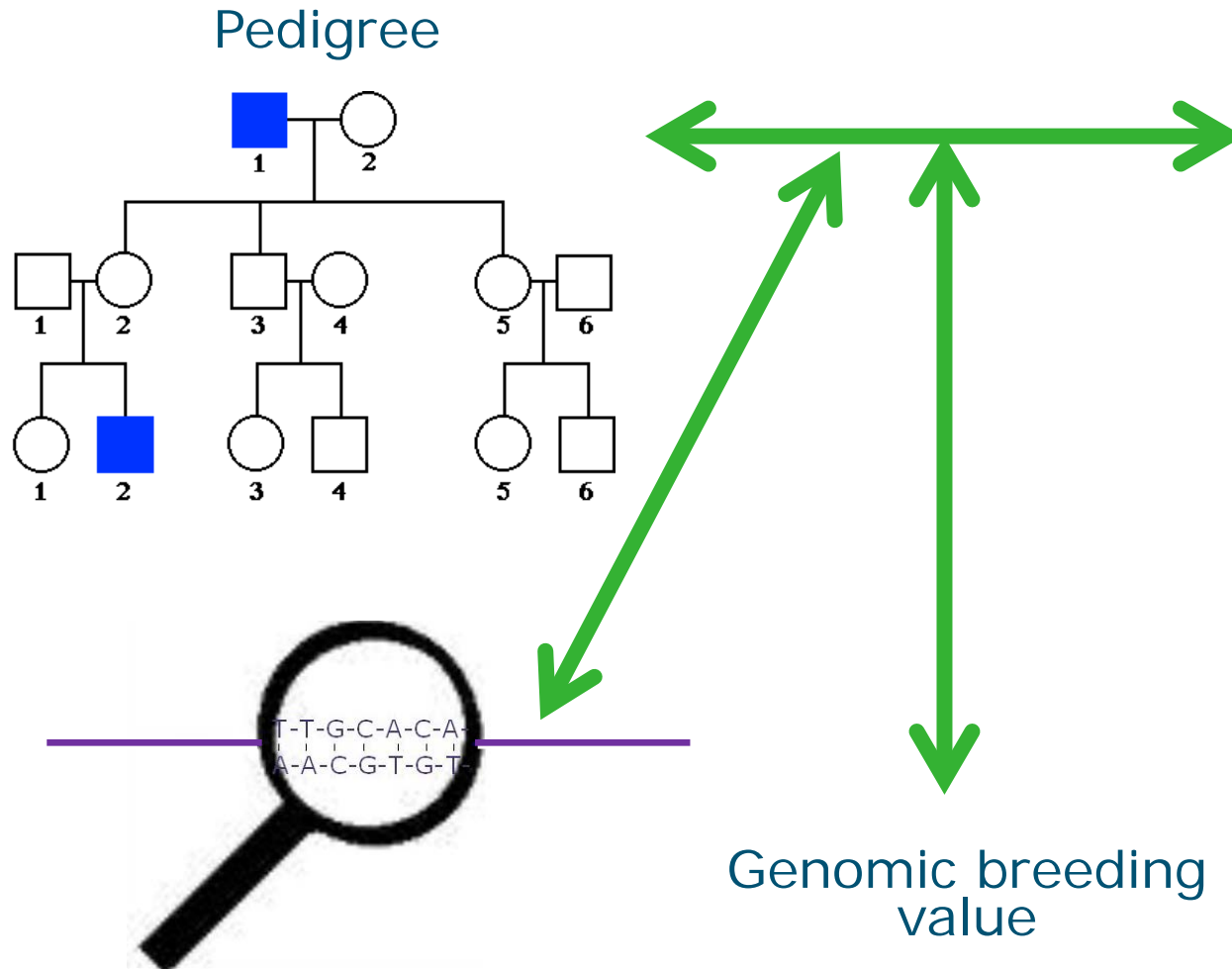
# Individual genes

- Three SNP for DMI in genes:
  - Tryptophan
  - Insulin genes
  - Epidermal growth factors

Veerkamp et al, 2012 (Animal)



# Genomic selection



## Phenotypes





# Genomic selection

**Reference population:**  
Pedigree, phenotypes, markers

**Estimate marker breeding values**  
(calibrate markers)

**National population:**  
Accurate breeding values for young  
bulls and for animals with no records



# Genomic selection – national data

Data in NL was initially 600 cows with feed intake:

- Reliability = 0.11 for feed intake

(De Haas et al., 2011 & 2012 (JDS))

In the age of the genotype:

Phenotype is king!



collaboration

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# Genomic selection – shared data

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

# Reliability of genomic selection

De Haas et al, 2012 (JDS)

	Within	
Australia	14%	
United Kingdom	9%	
The Netherlands	11%	

# Reliability of genomic selection

De Haas et al, 2012 (JDS)

	Within	Shared
Australia	14%	15%
United Kingdom	9%	11%
The Netherlands	11%	12%

Reliabilities can be increased by:

- combining datasets across countries, and
- using a multi-trait approach

Reliabilities for your country only increase if you contribute direct national data to the analyses

# global Dry Matter Initiative: gDMI

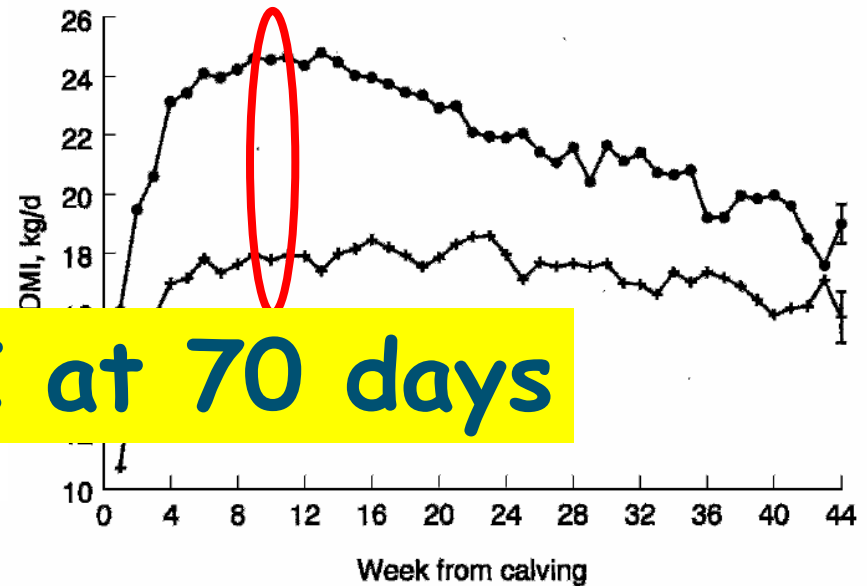
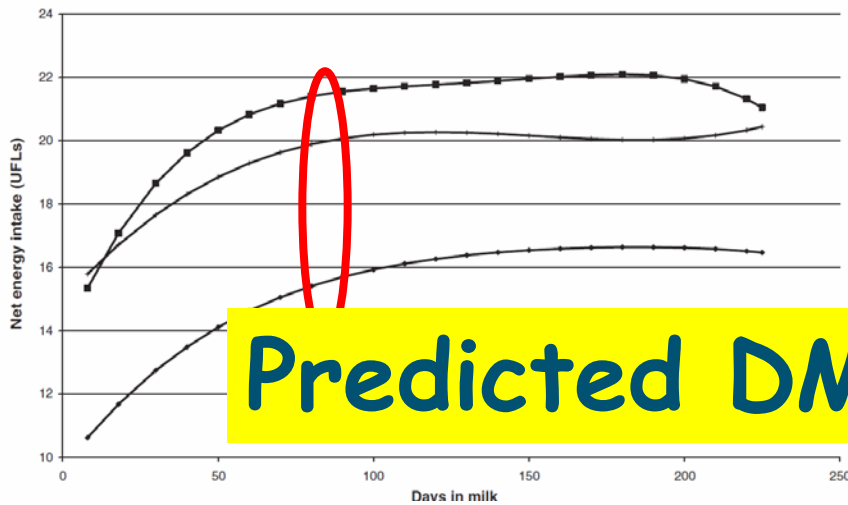
- 10 countries, 15 parties
- ~9,000 genotyped animals
- 591,621 SNPs HD-imputed

- Key research questions:

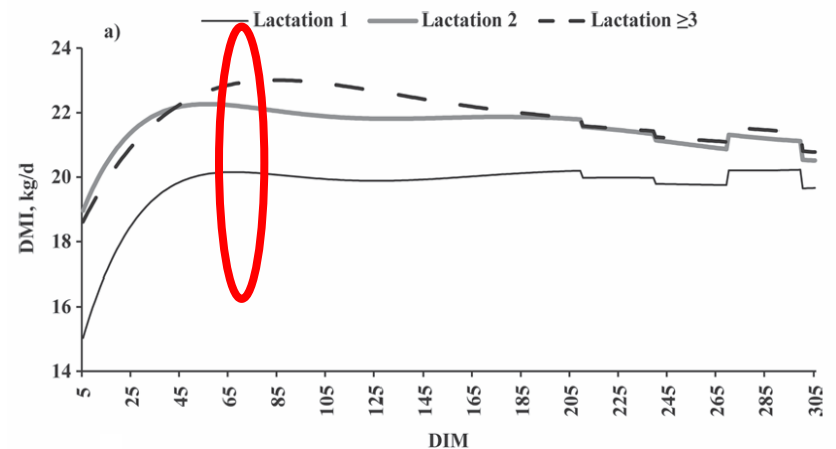
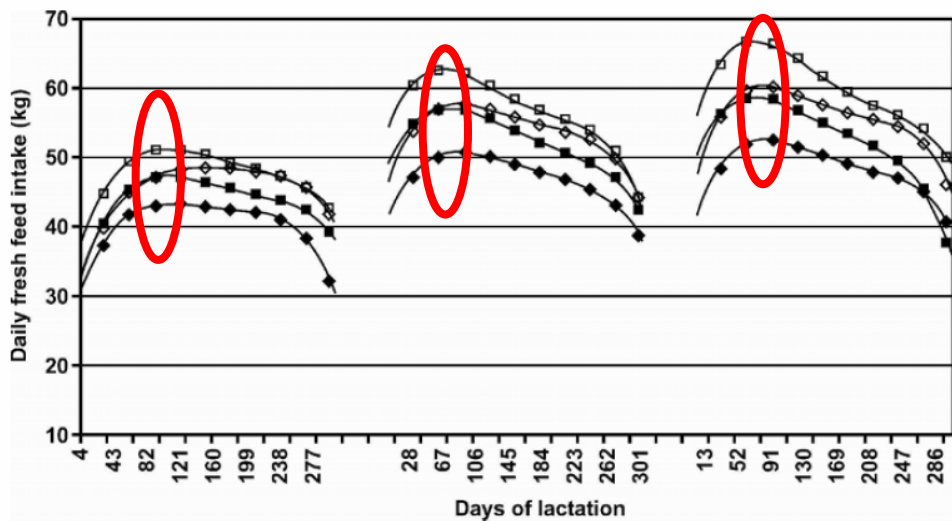
- How to combine, homogenise and standardise phenotypes? (Berry et al., 2013 submitted)
- Genomic similarity between population? (Pryce et al., 2013 submitted)
- Can we predict DGV for DMI for different partners? (De Haas et al., 2013 in prep.)



# Combine, homogenise and standardise

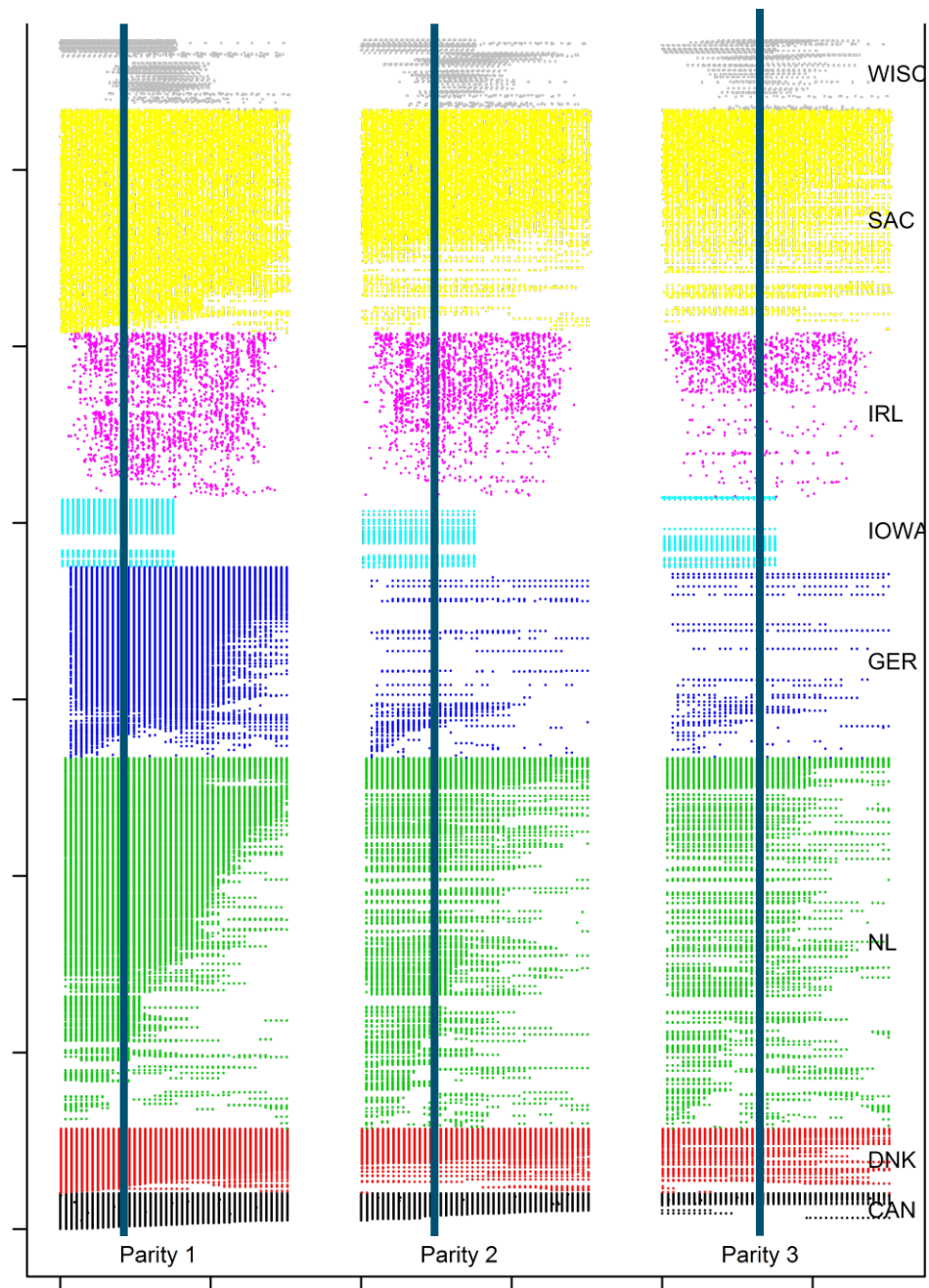


**Predicted DMI at 70 days**



*Berry et al. (2006) ; Coffey et al. (2004)  
Frignens et al. (1998); Vallimont et al (2010)*

# Our data

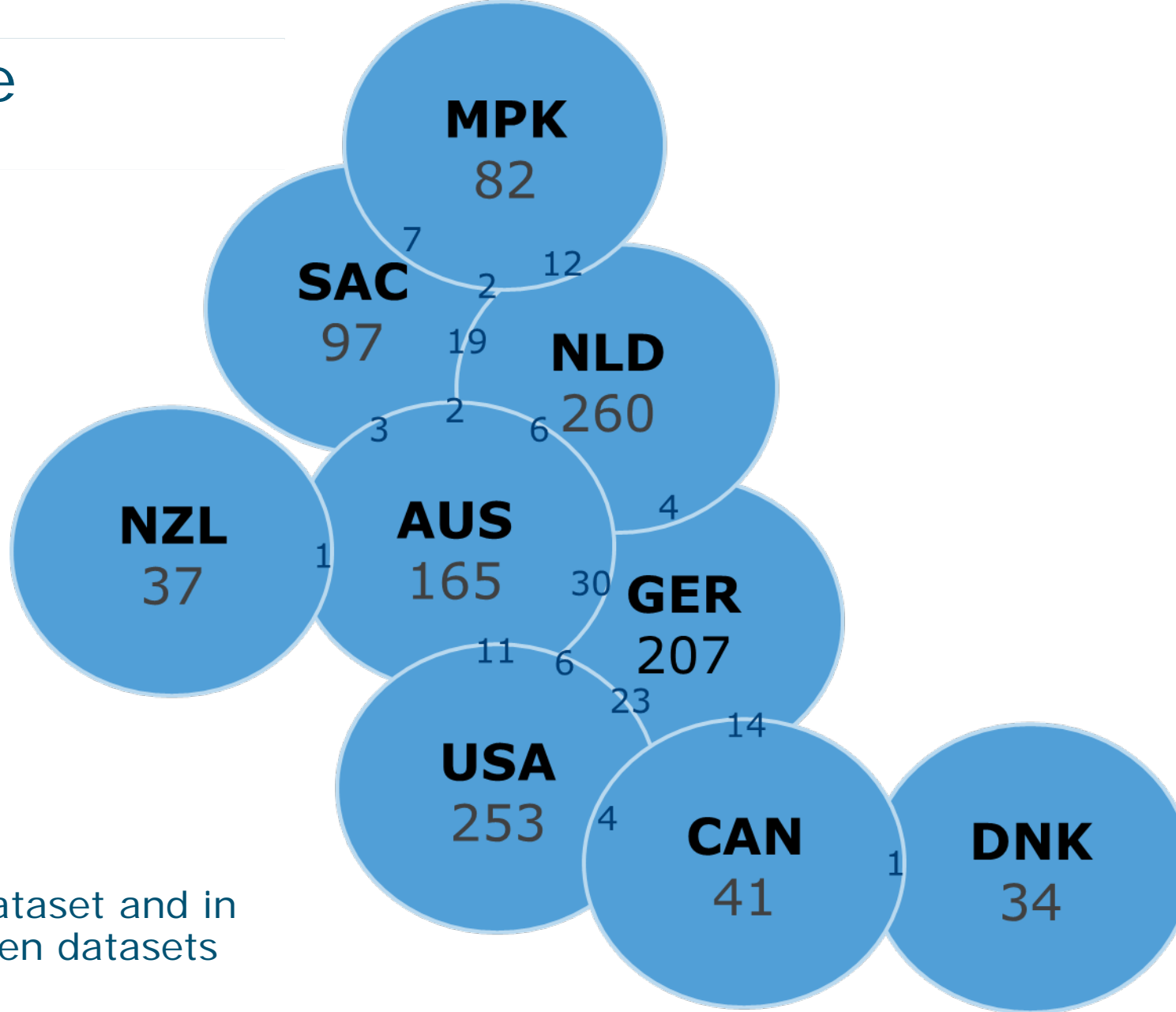




# Variance components

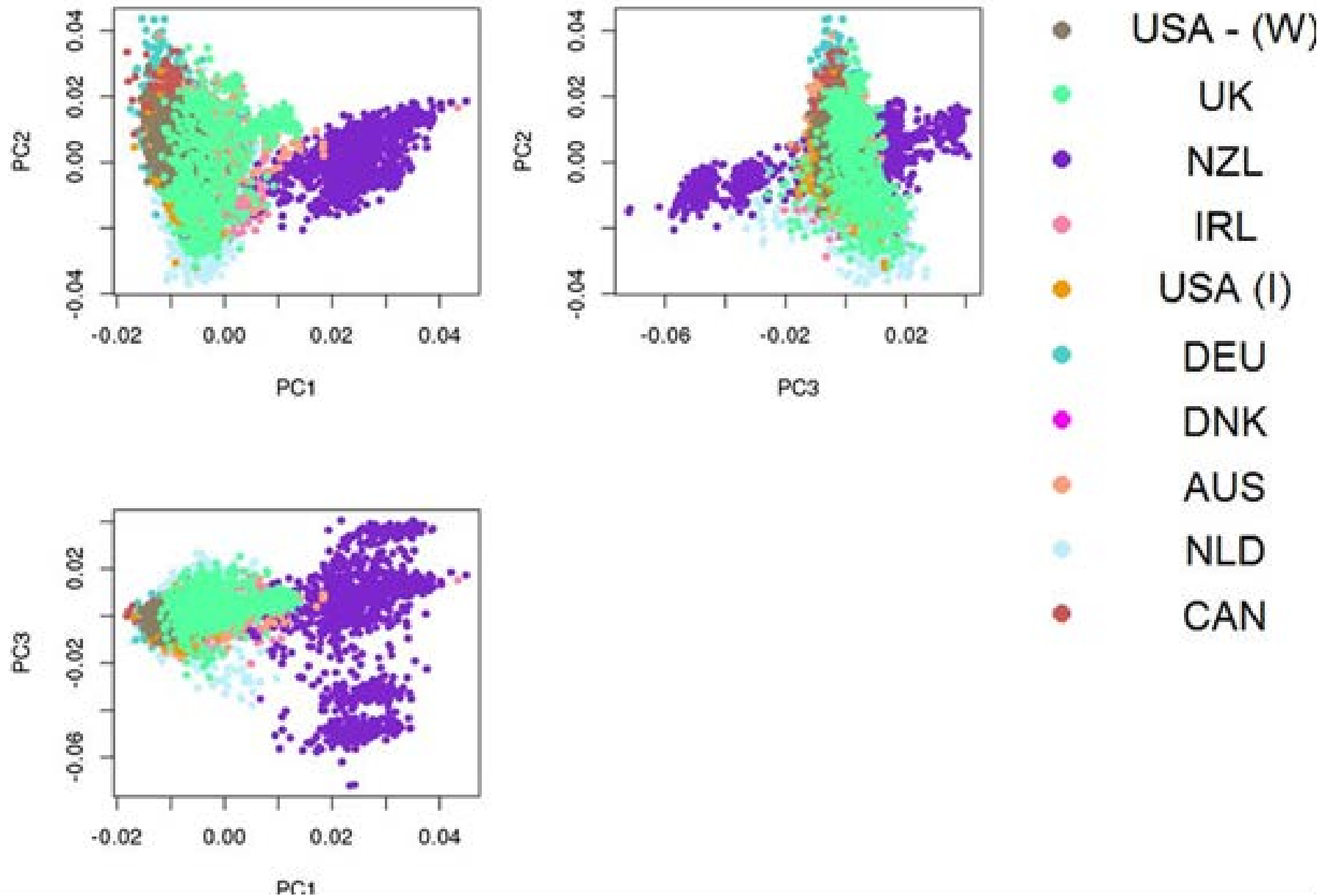
Country	N	Mean	SDg	Heritability
<b>Cows</b>				
All	10,008	19.7	1.13	0.34 (0.03)
Canada	411	22.2	1.01	0.19 (0.14)
Denmark	668	22.1	1.48	0.52 (0.12)
Germany	1,141	20.2	0.64	0.08 (0.06)
Iowa	398	23.5	1.48	0.41 (0.14)
Ireland	1,677	16.7	0.88	0.41 (0.10)
Netherlands	2,956	21.4	1.15	0.39 (0.05)
UK	2,840	17.4	1.07	0.31 (0.06)
Wisconsin	447	24.9	0.90	0.24 (0.16)
Australia	103	15.6		
<b>Heifers</b>				
Australia	843	8.3	0.77	0.20 (0.11)
New Zealand	941	7.6	0.66	0.34 (0.12)

# Pedigree



Sires in each dataset and in common between datasets

# First 3 principal components of the GRM



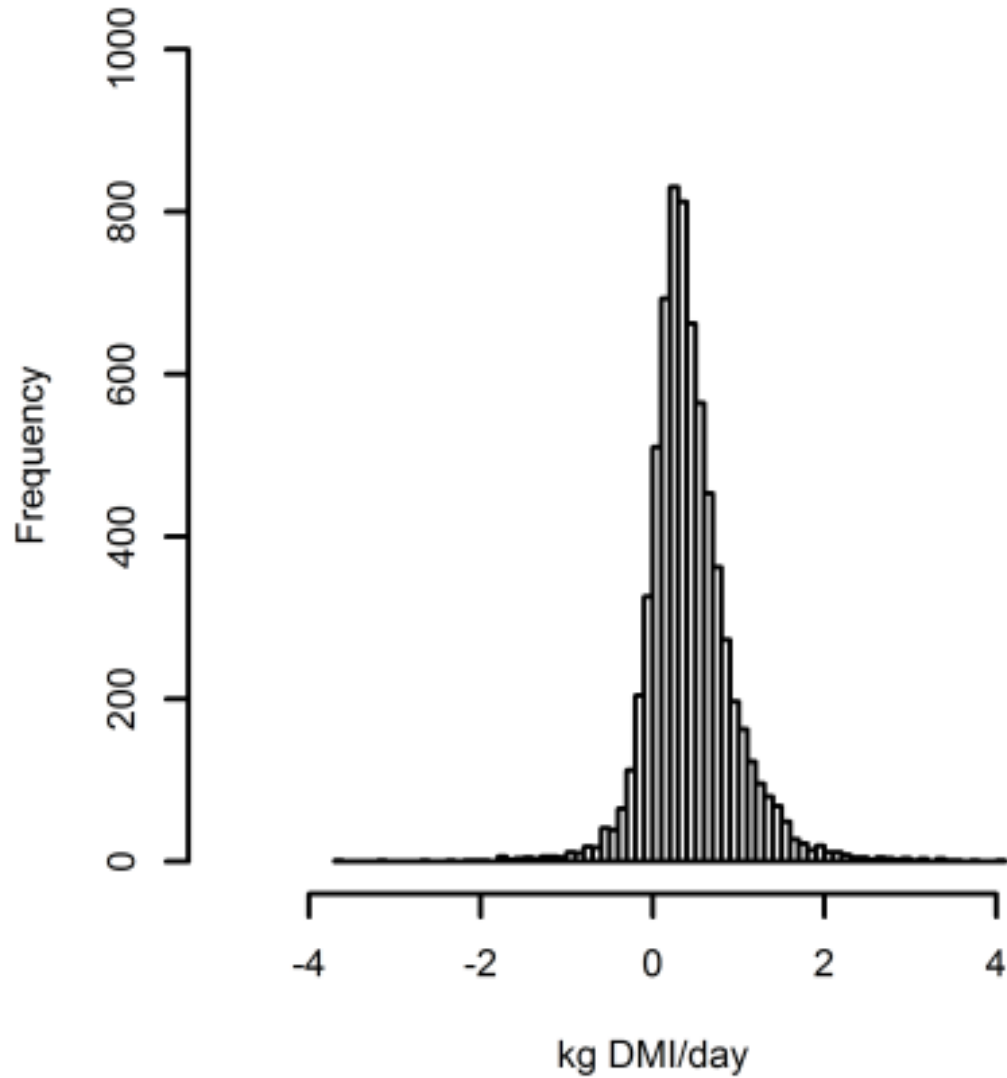


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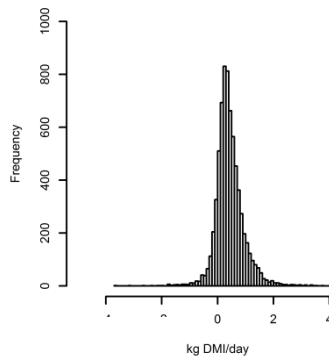
# Future outlook

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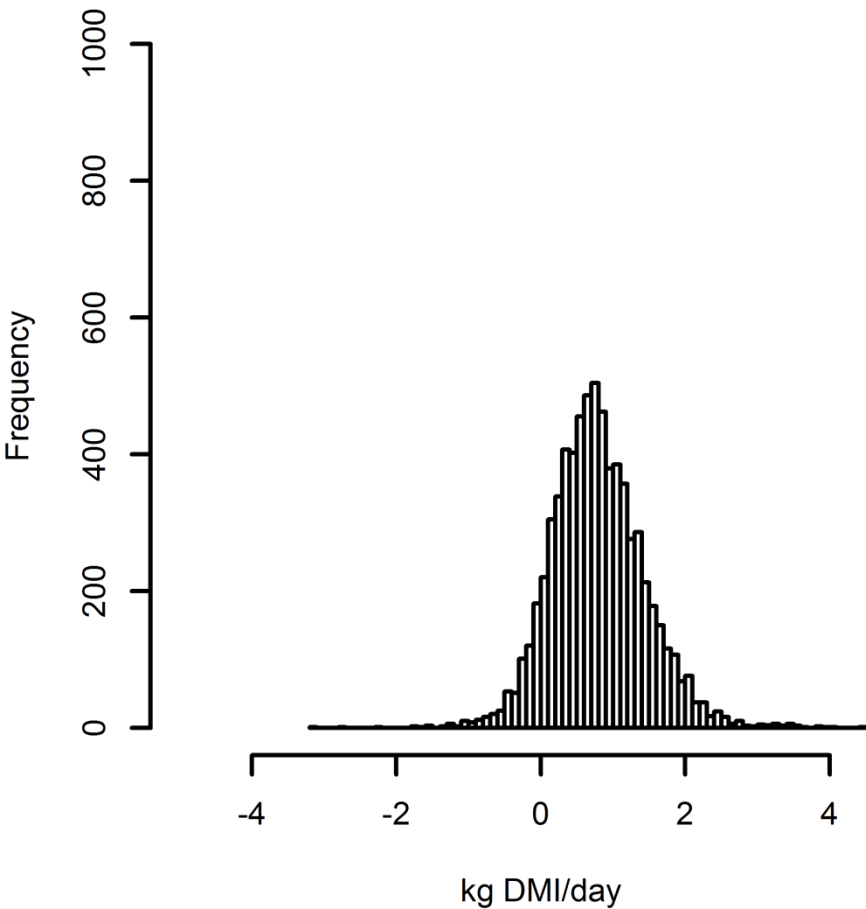
## DMI research herd cows



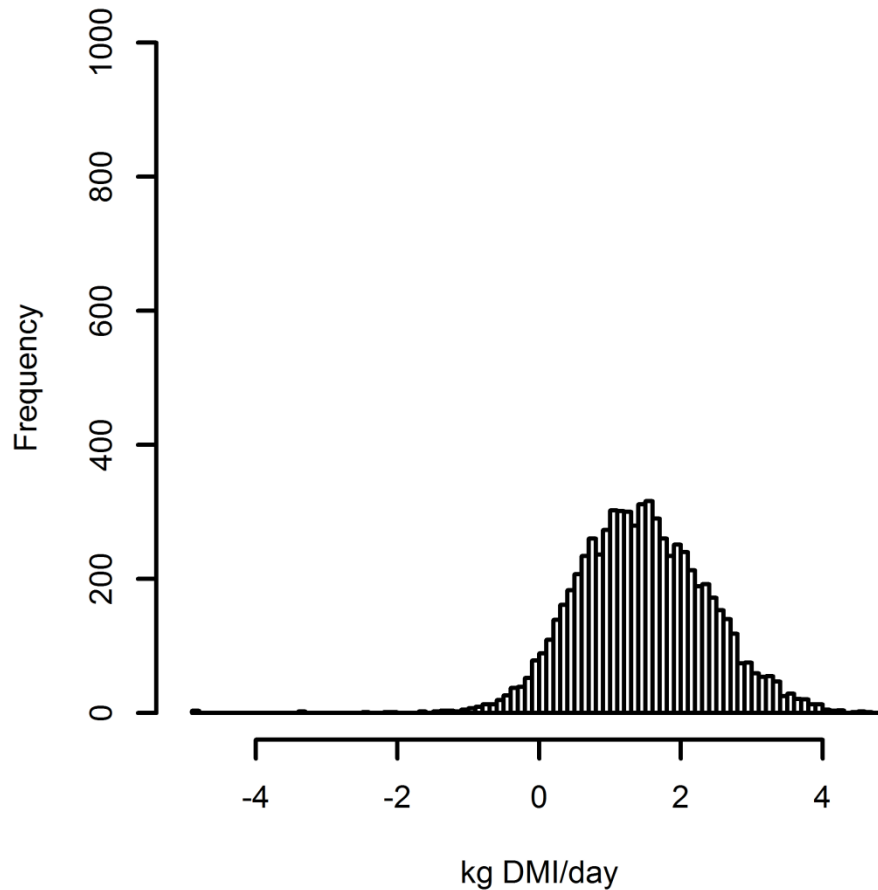
DMI research herd cows



DMI research herd cows + genomics



DMI + Predictors + genomics



# Conclusions

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- Feed efficiency is important in dairy production
- Selection for feed efficiency impossible a few years ago, with genomics a realistic prospect
  - Yield and type make a good first step
  - Genomics should identify 'net efficient cows'
- A challenge is to increase the accuracy of genomic prediction
  - Combine data internationally, and use multi-trait genomic prediction models

# Acknowledgements



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## Global Dry Matter Initiative (gDMI)



Animal Breeding & Genomics Centre



*Thank you for your attention*



Questions??



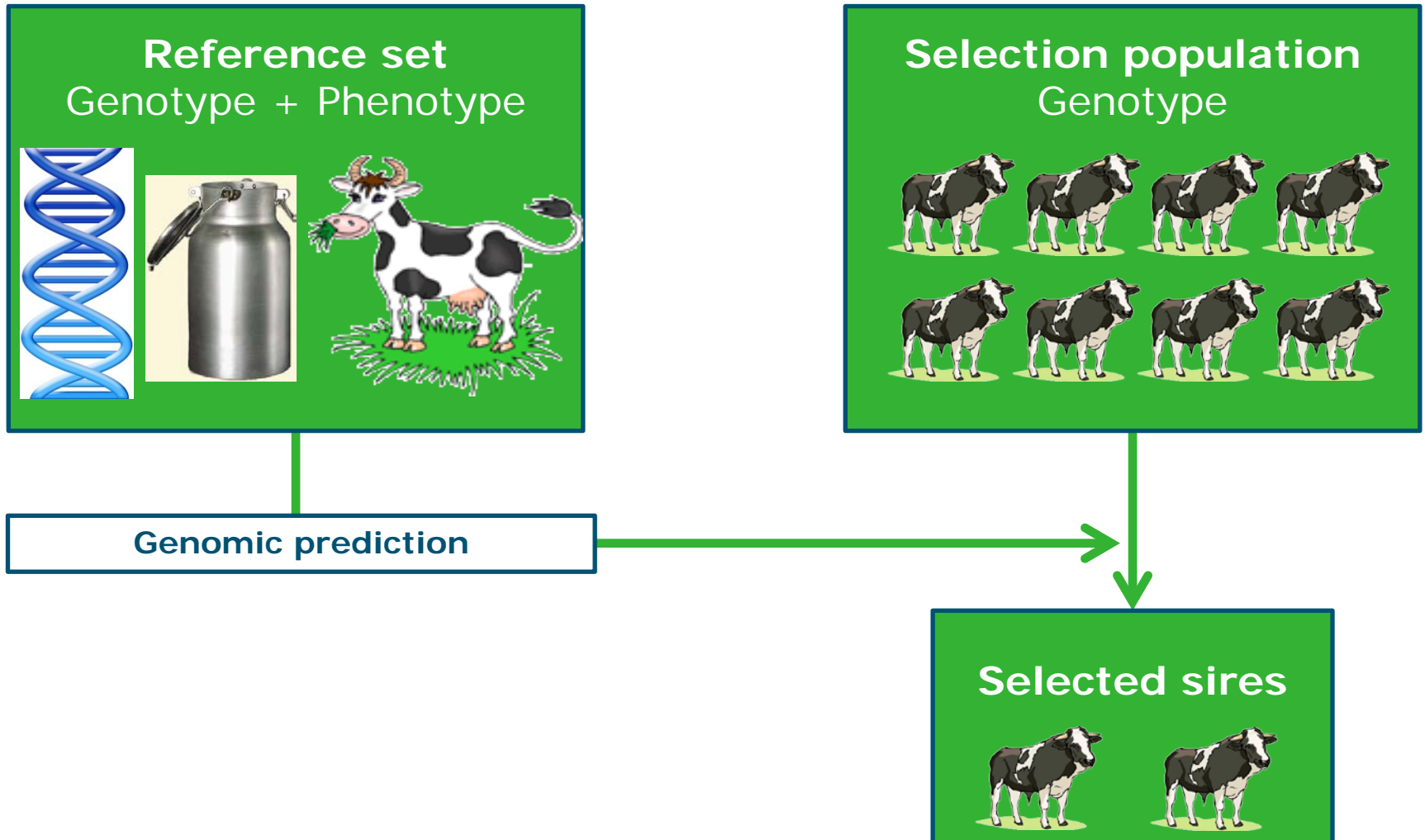
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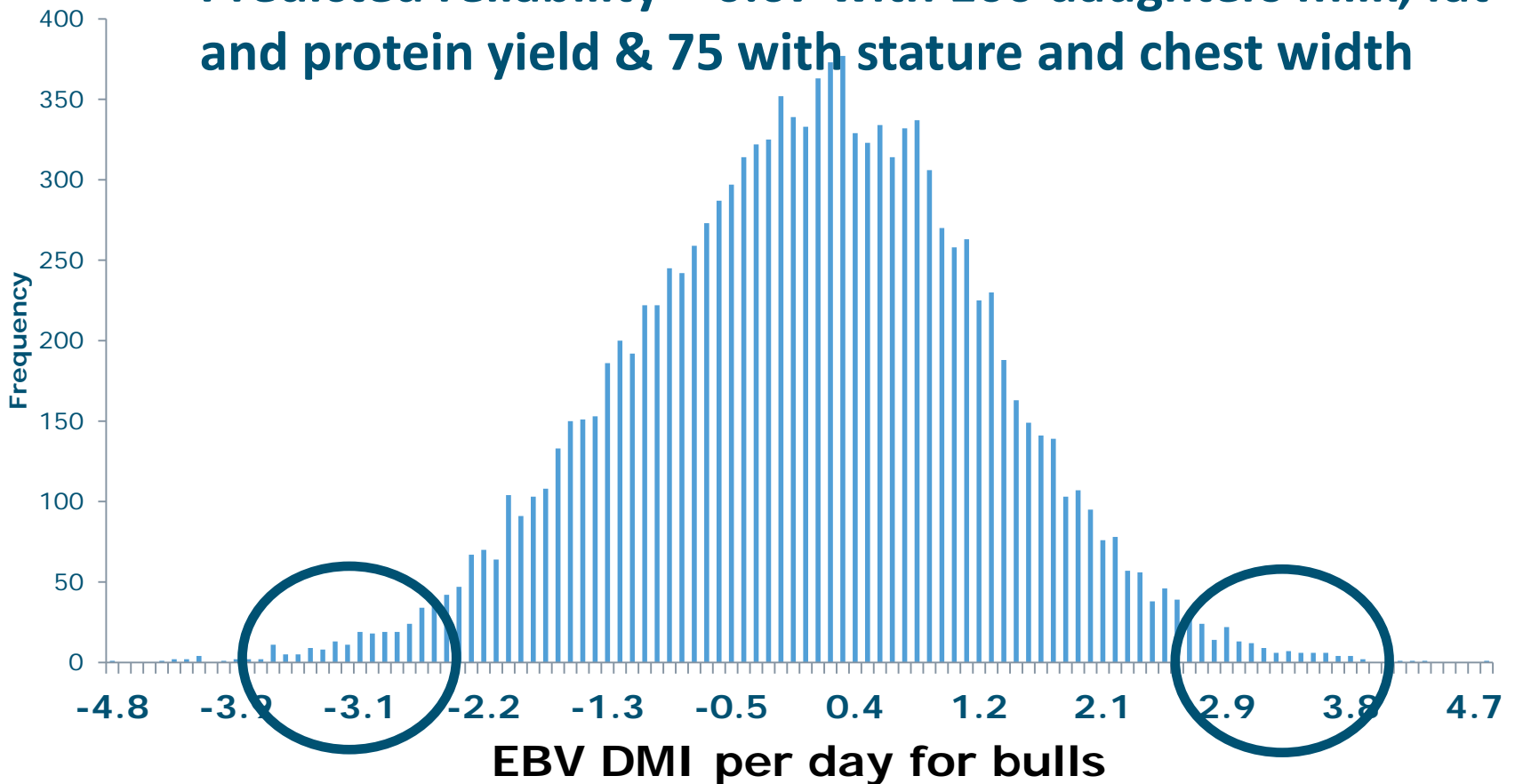


# Genomic selection

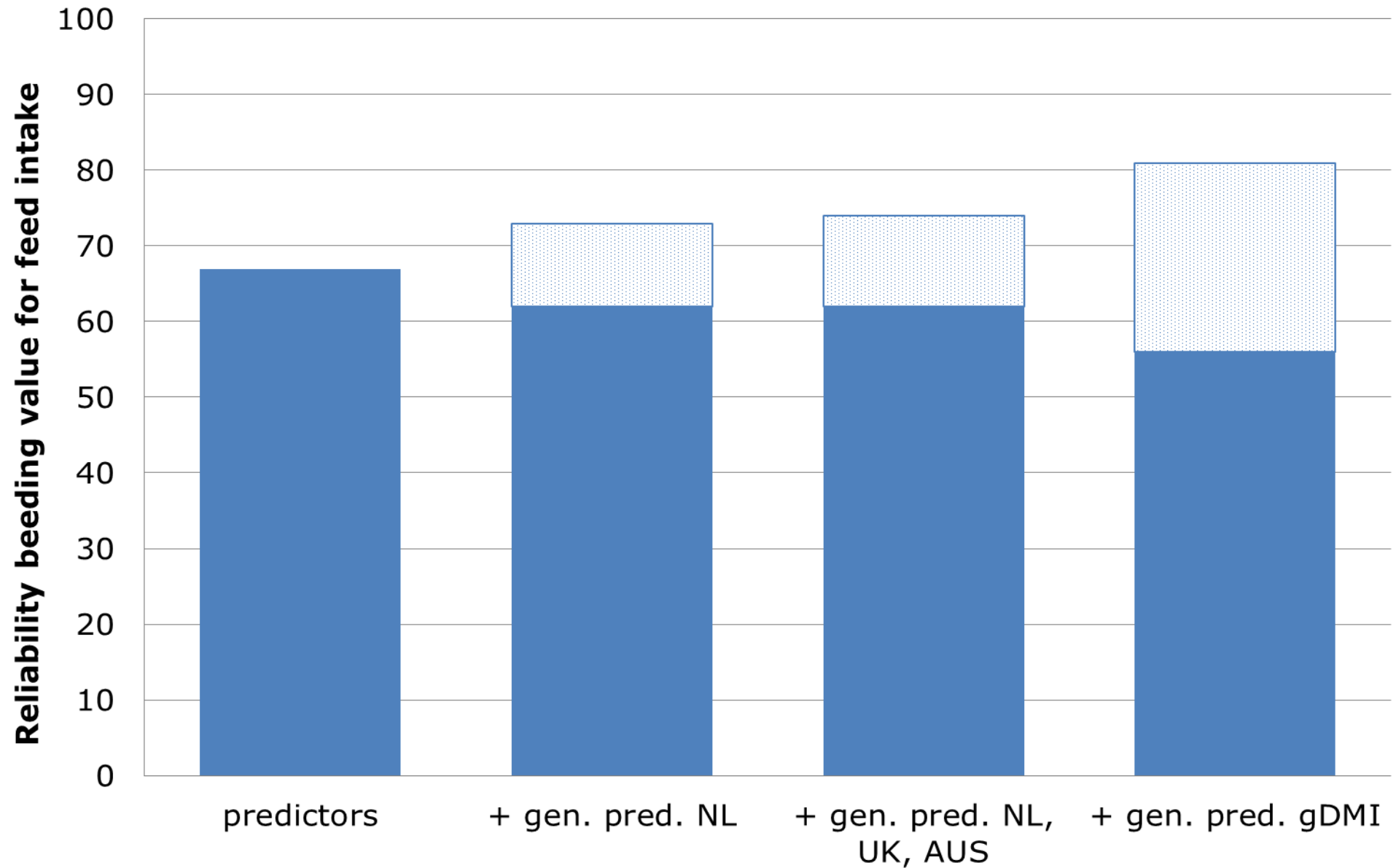


# Breeding value for feed intake

**Predicted reliability = 0.67 with 100 daughters milk, fat and protein yield & 75 with stature and chest width**



# Combining phenotypes and genomics



# Genotypes

## Imputation strategy

