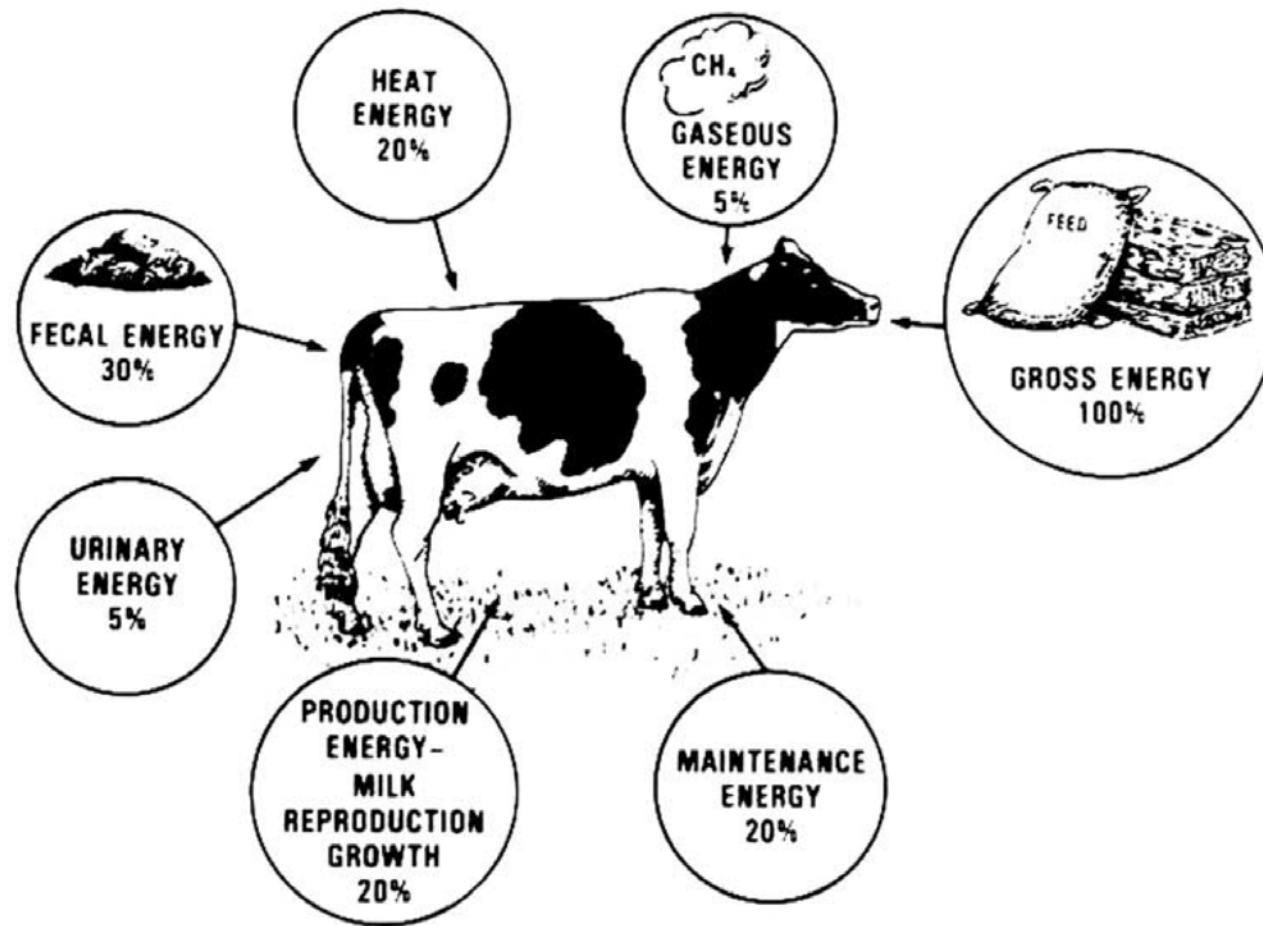


Genetic dissection of dairy cow feed efficiency



Bocquier and González-García (2010) *Animal*, 4:7, pp 1258–1273



Francisco Peñagaricano

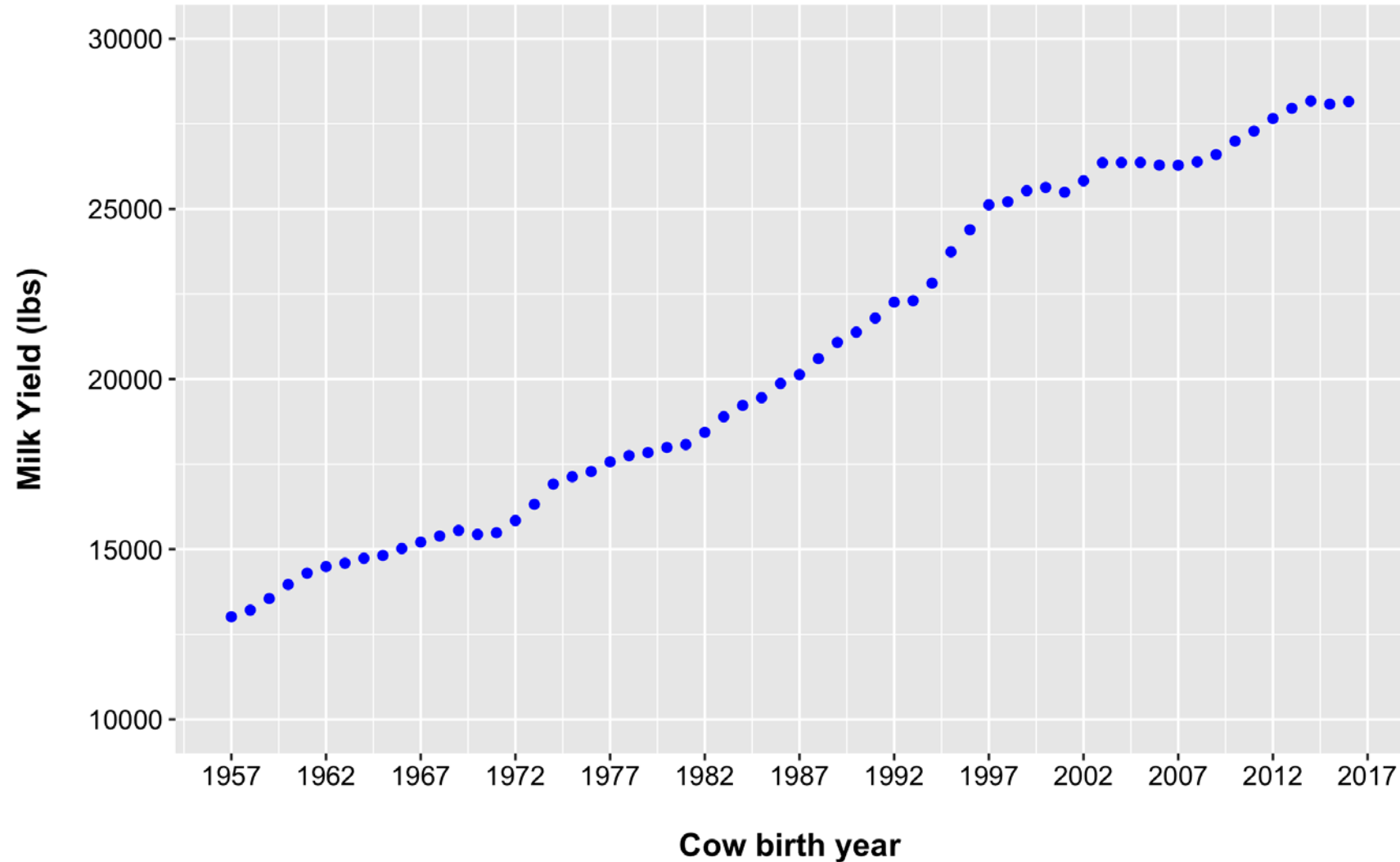
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FLORIDA

What is the importance of feed efficiency?

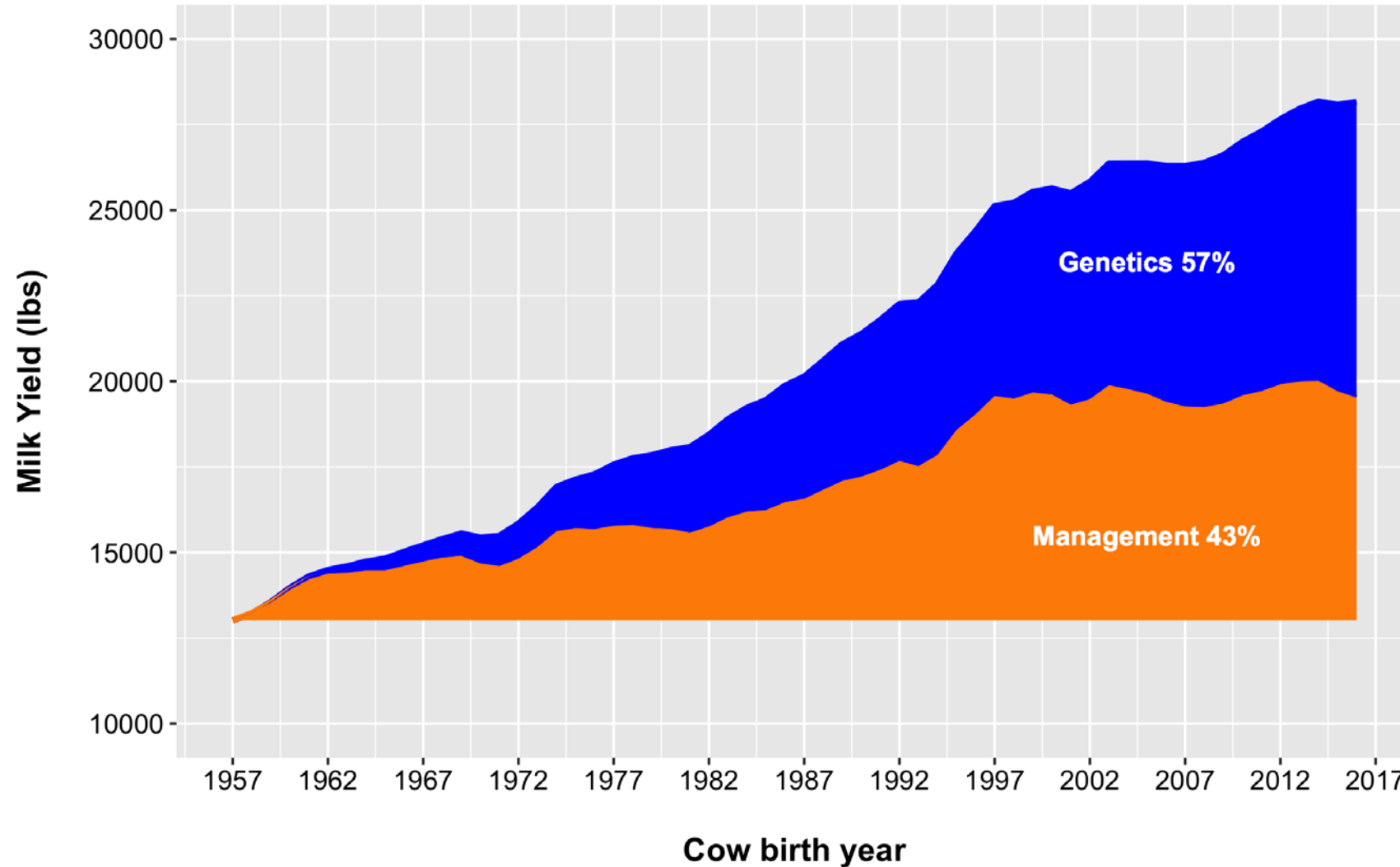
- **feed** represents **more than 50%** of the **total production costs**
- **benefits of improving feed efficiency:**
 - **increase farm profitability**
 - **reduce the environmental impact of dairy farming**
(less land needed, reduced greenhouse gas emissions)



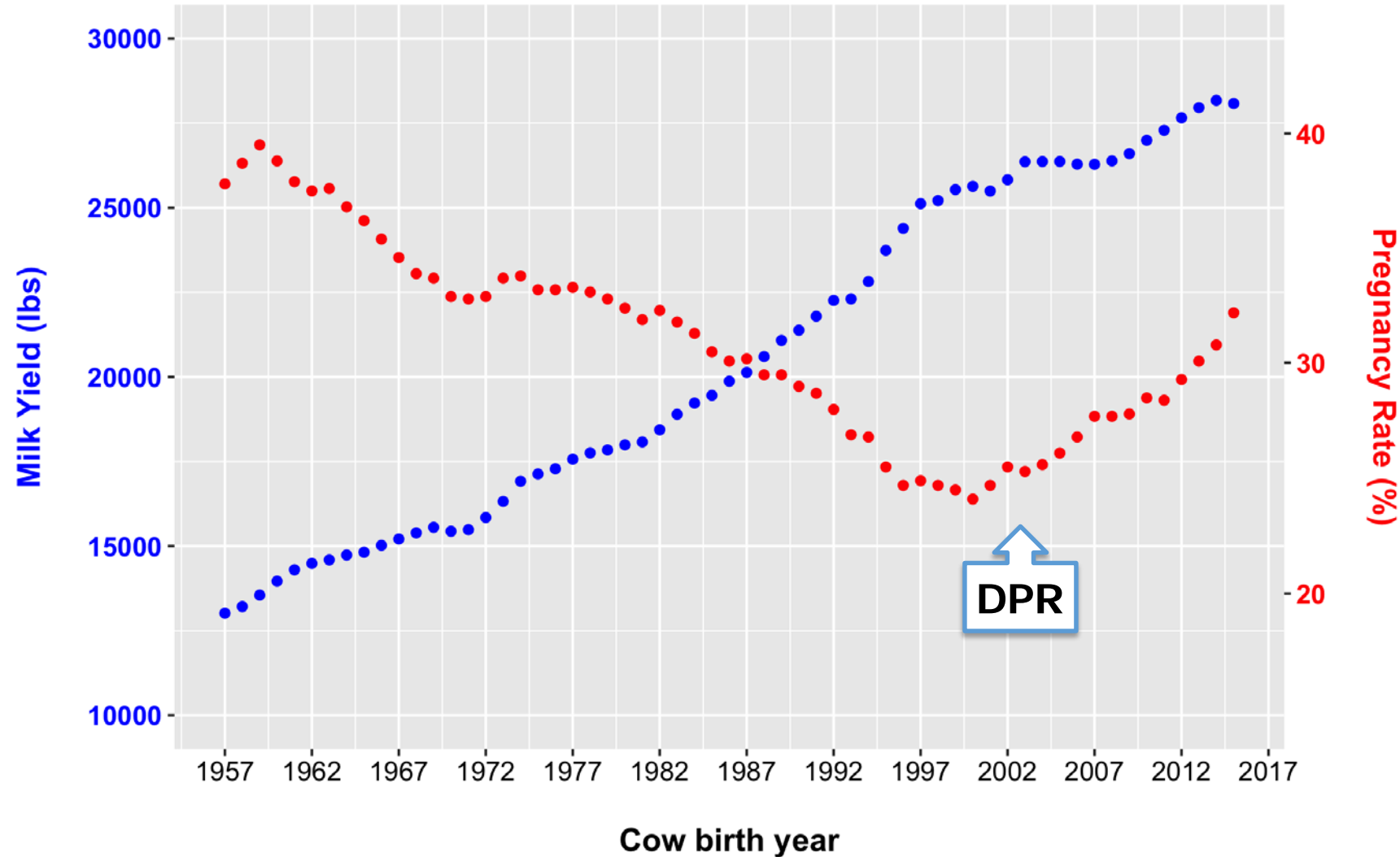
What is the importance of genetic selection?



What is the importance of genetic selection?



What is the importance of having genetic tools?



Genetic variation of feed efficiency

Table 2. Estimated variance components and heritability for feed efficiency and its component traits

Trait ¹	Genetic variance	Residual variance	Heritability
MILKE	2.69 ± 0.25	9.50 ± 0.24	0.22 ± 0.02
MBW	26.42 ± 1.64	31.98 ± 1.03	0.45 ± 0.02
DMI	1.08 ± 0.10	3.52 ± 0.09	0.23 ± 0.02
RFI	0.40 ± 0.05	2.09 ± 0.05	0.16 ± 0.02
DMI MILKE,MBW	0.38 ± 0.05	2.09 ± 0.05	0.15 ± 0.02

¹MILKE = milk energy (Mcal); MBW = metabolic BW ($\text{kg}^{0.75}$); DMI = dry matter intake (kg); RFI = residual feed intake (kg); DMI|MILKE,MBW = DMI conditional on milk energy and metabolic BW (kg/Mcal , $\text{kg}^{0.75}$).

Lu et al. (2018) JDS 101(4): 3140-3154



Grant 2011-68004-30340

Heritability (h^2) estimates

PTA trait	PTA trait													
	Milk	Fat	Protein	PL	SCS	BWC	Udder	Feet/legs	DPR	CA\$	HCR	CCR	LIV	HTH\$
Milk	0.20 ¹	0.43	0.83	0.10	0.02	-0.12	-0.10	-0.02	-0.23	0.19	-0.03	-0.16	0.03	0.03
Fat	0.69	0.20	0.59	0.15	-0.09	-0.05	-0.07	0.01	-0.15	0.13	0.03	-0.10	0.06	0.08
Protein	0.90	0.75	0.20	0.13	0.04	-0.09	-0.14	-0.01	-0.18	0.22	-0.07	-0.15	0.05	0.04
PL	0.15	0.17	0.16	0.08	-0.45	-0.10	0.18	0.14	0.64	0.40	0.32	0.62	0.70	0.56
SCS	-0.10	-0.10	-0.10	-0.40	0.12	-0.10	-0.23	-0.15	-0.27	-0.14	-0.12	-0.25	-0.25	-0.44
BWC	0.06	0.05	0.05	-0.20	-0.11	0.40	0.27	0.38	-0.052	-0.07	-0.01	-0.01	-0.14	-0.26
Udder	-0.02	-0.05	-0.06	0.15	-0.30	0.45	0.27	0.45	0.09	0.10	0.03	0.04	0.08	-0.01
Feet/legs	-0.14	-0.11	-0.18	0.08	-0.02	0.35	0.40	0.15	0.03	-0.01	-0.01	-0.04	0.06	0.02
DPR	-0.10	-0.10	-0.10	0.20	-0.05	0.00	0.00	0.00	0.04	0.41	0.87	0.35	0.43	0.42
CA\$	0.02	0.02	0.02	0.20	-0.03	-0.10	0.00	-0.02	0.09	0.07	0.16	0.34	0.36	0.33
HCR	-0.05	-0.05	-0.05	0.10	-0.04	-0.02	-0.05	-0.05	0.10	0.16	0.01	0.54	0.22	0.18
CCR	-0.10	-0.10	-0.10	0.40	-0.20	-0.10	0.03	-0.04	0.70	0.20	0.45	0.02	0.43	0.36
LIV	0.11	0.13	0.12	0.70	-0.40	-0.20	0.10	0.05	0.40	0.35	0.20	0.15	0.01	0.55
HTH\$	0.02	0.04	0.02	0.28	-0.22	-0.13	0.00	0.01	0.21	0.17	0.09	0.18	0.28	0.01

¹Holstein heritabilities in **orange** on diagonal; heritabilities for other breeds are the same except for BWC (**0.35**), udder (**0.20**), and Jersey and Brown Swiss yield traits (**0.23**).

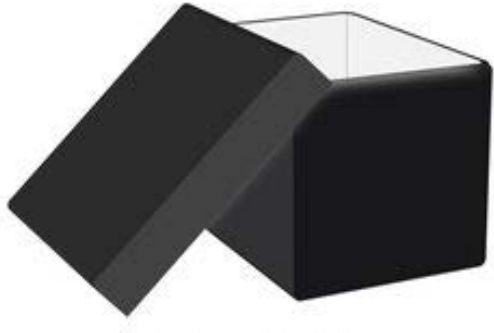
Why some cows are more efficient than others?

(some cows need less feed than others of similar body weight and milk production)



- they digest feed better
- they spend less energy on unproductive activities
- they have a more efficient metabolism

Feed efficiency: deciphering the genetic basis



open the black box:

identify genetic variants, candidate genes and biological pathways

Why we want to decipher the genetic basis?

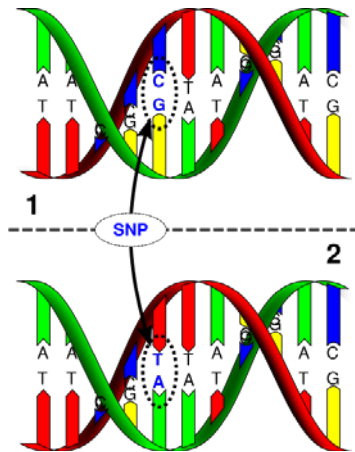
- ❑ to better understand the biology of this complex phenotype
- ❑ to generate information that can lead to the development of new nutritional therapies
- ❑ to develop novel genomic strategies for improving feed efficiency via selective breeding

How do we decipher the genetic basis?

phenotypic variation

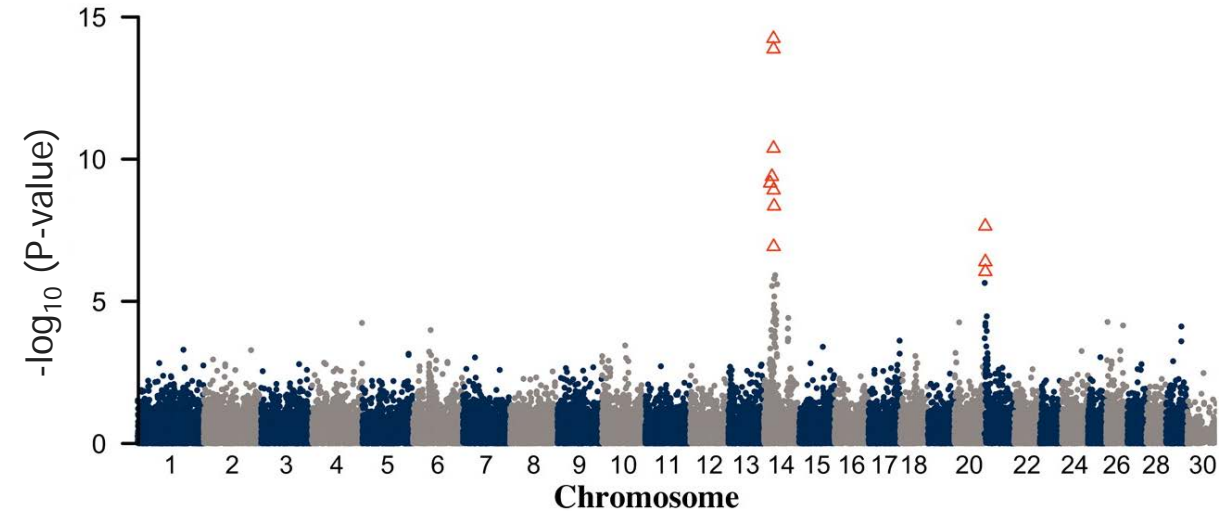


+



genome-wide SNP information

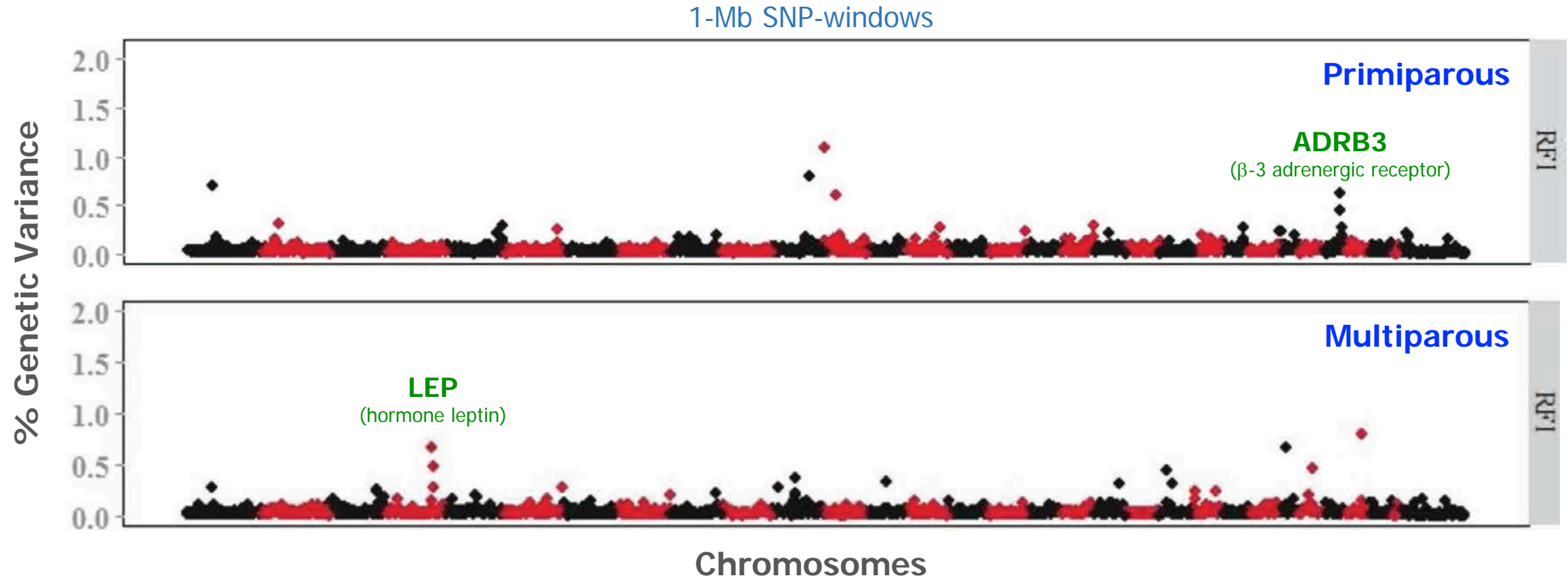
identify regions/SNPs associated with the trait under study



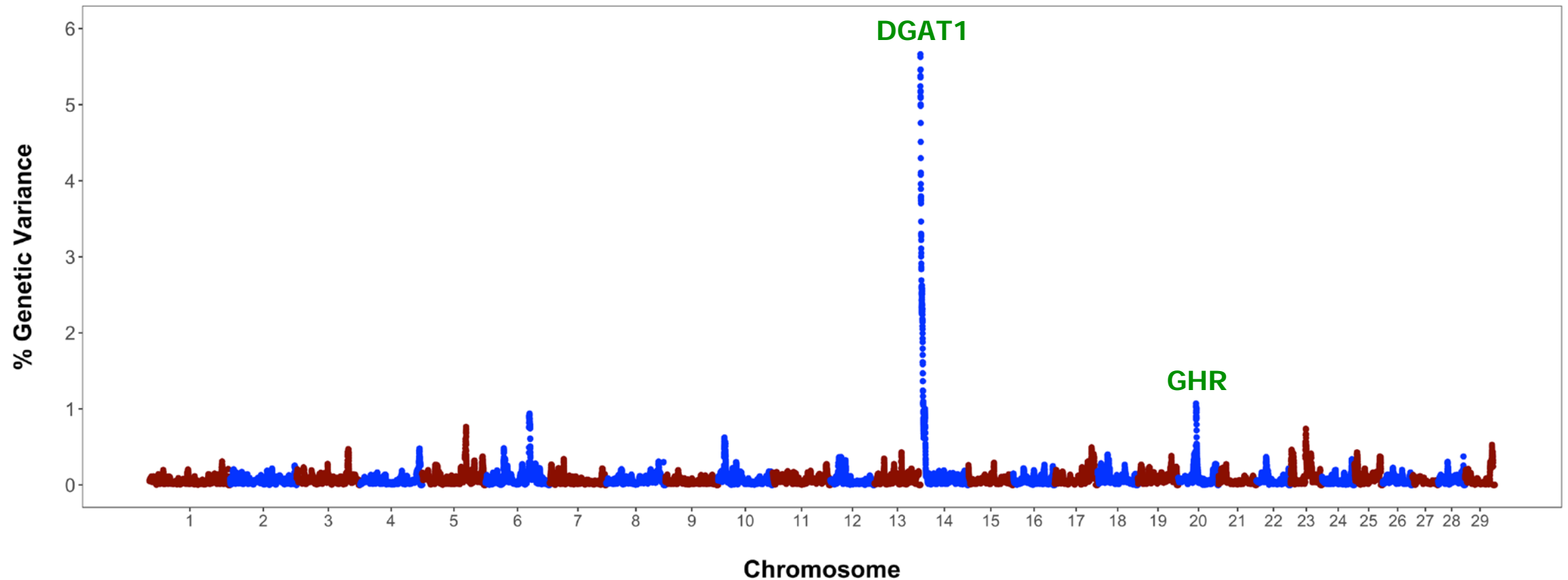
genome-wide association study
whole-genome scan

Residual Feed Intake: genomic scan (I)

- 5k Holstein cows (US + Canada + UK + the Netherlands) / 57k SNPs



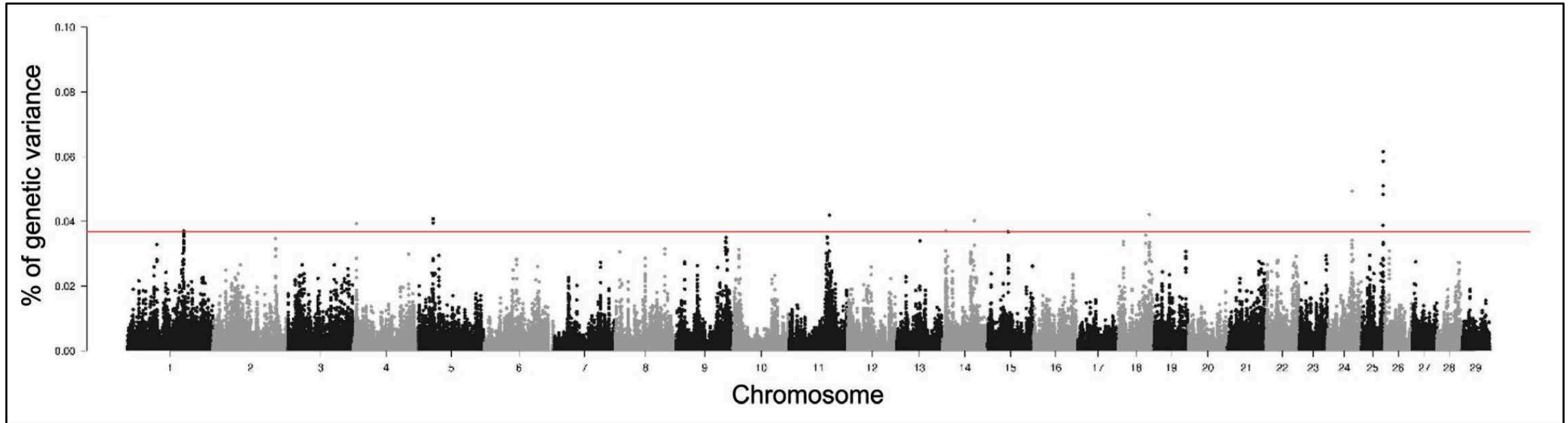
Milk production: genomic scan



Residual Feed Intake: genomic scan (II)

- 4k Holstein cows (9 US research herds) / 278k SNPs

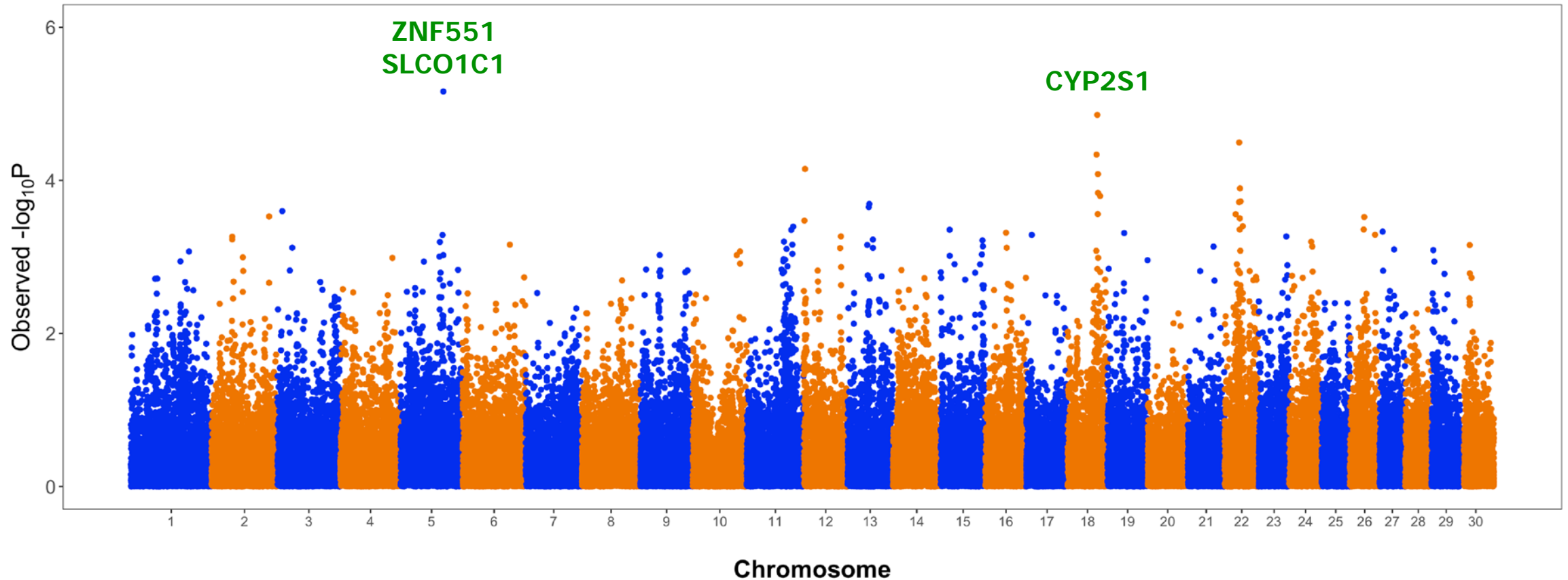
5 SNP-windows



Residual Feed Intake: genomic scan (III)

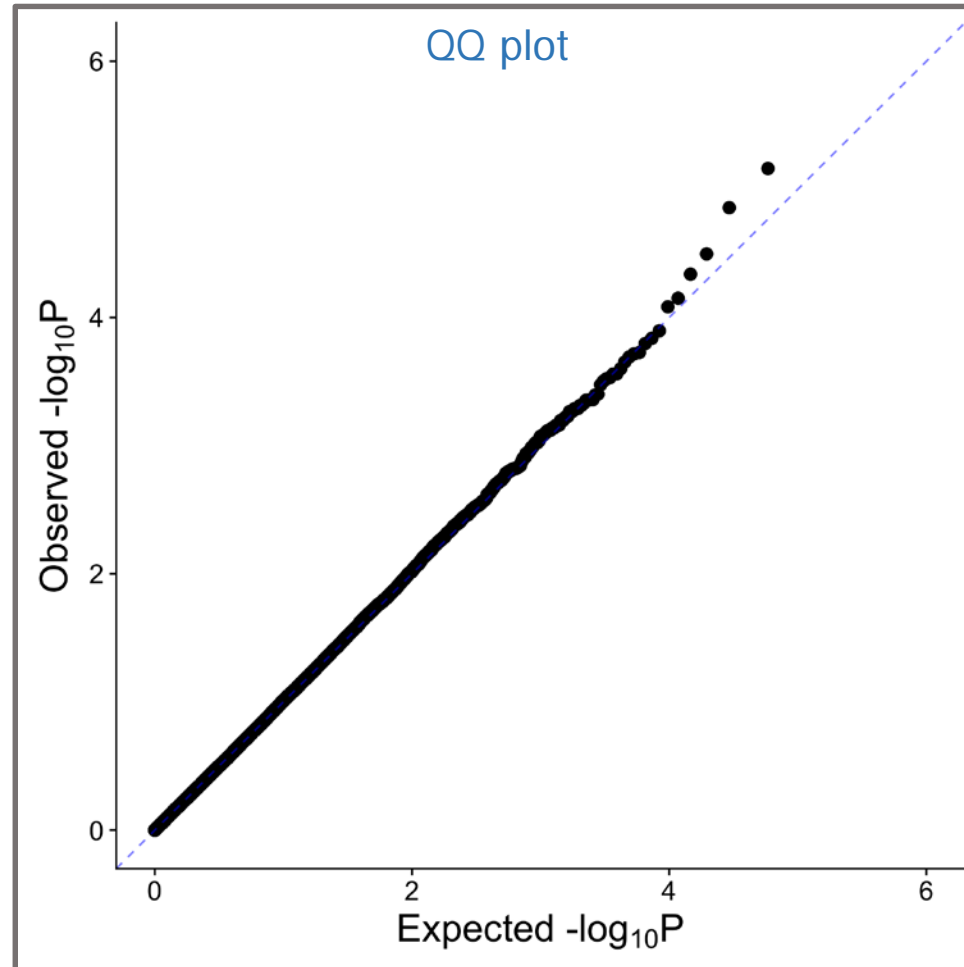
- 4k Holstein cows (9 US research herds) / 58k SNPs

Single marker regression



Residual Feed Intake: genomic scan (III)

- 4k Holstein cows (9 US research herds) / 58k SNPs



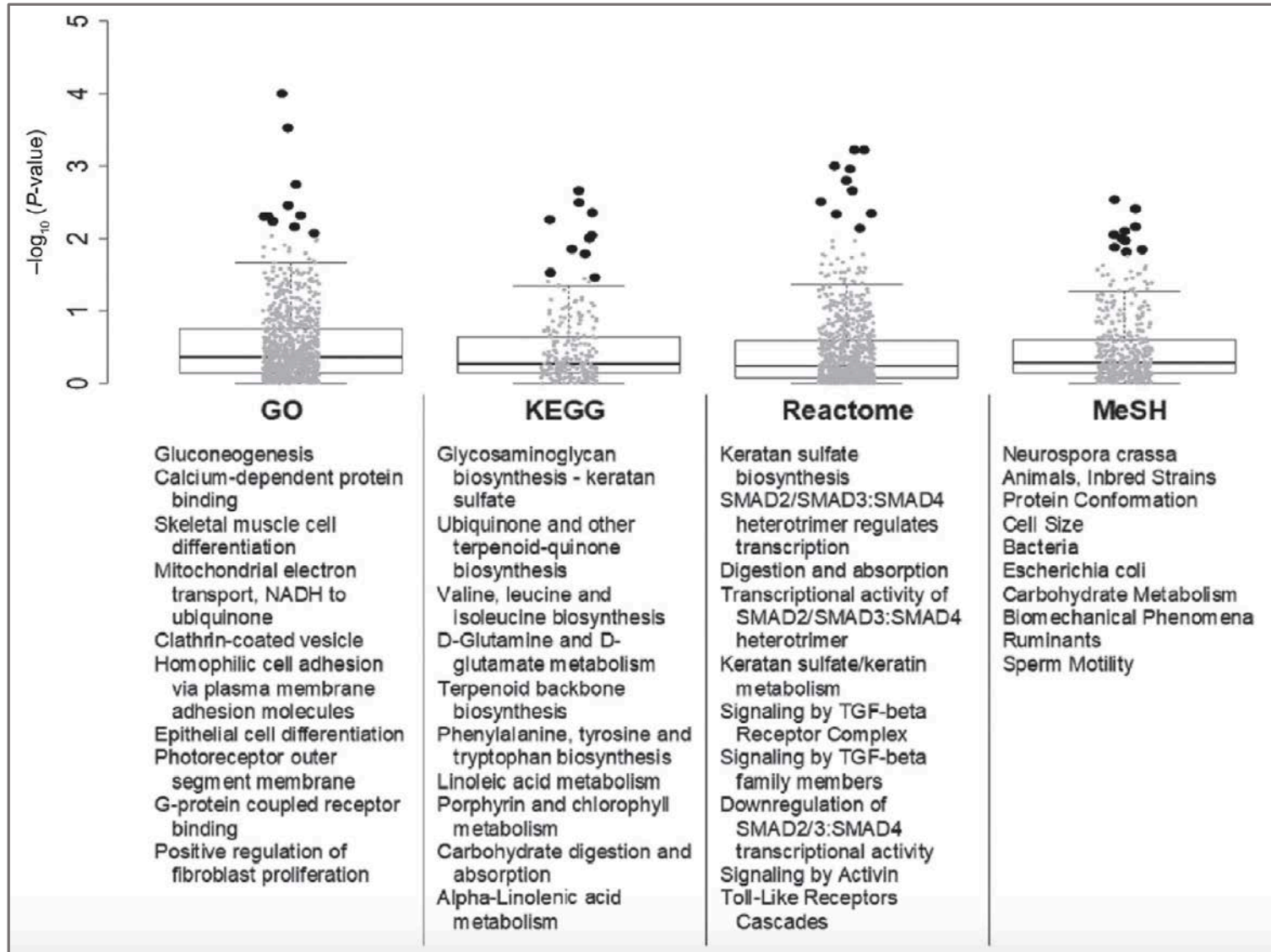
Whole Genome Association Analysis

- **genome-wide association studies** are **valuable tools**
- they focus on **genetic markers** with the **strongest evidence of association**
- these significant markers explain a **small component** of the **genetic variance**

Pathway Analysis

- test the **association** of a **set of functionally related genes**
- **multiple contributing factors** are considered simultaneously
- opportunity to identify mechanisms and pathways underlying complex phenotypes

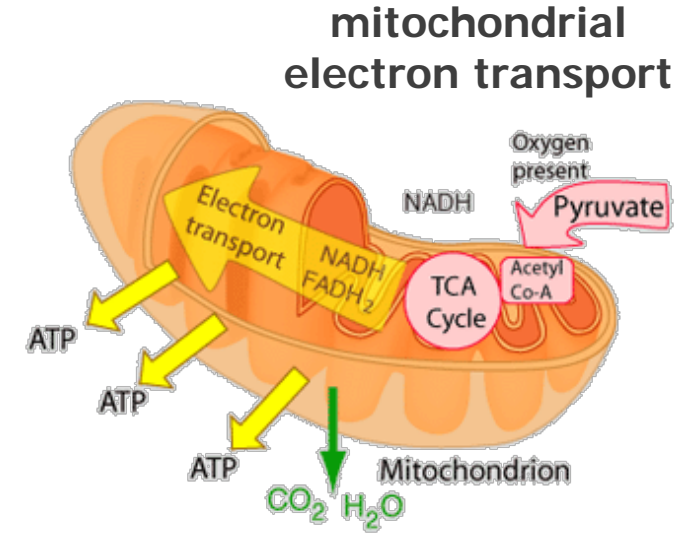
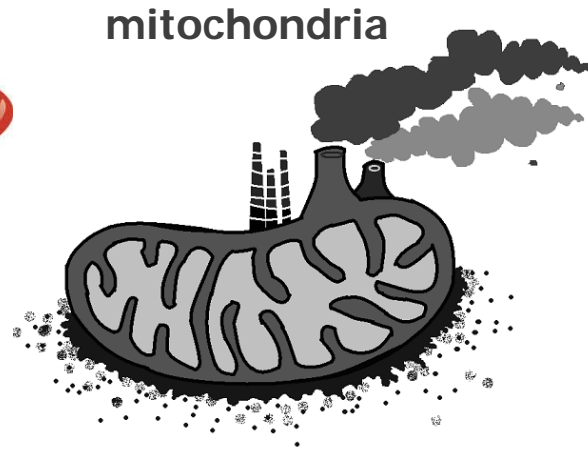
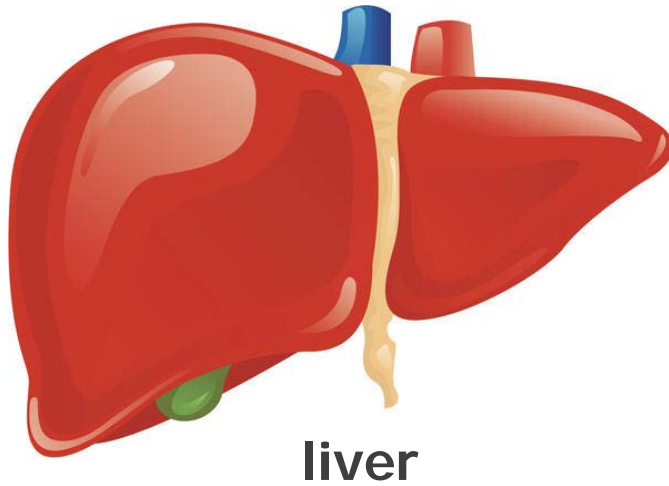
Residual Feed Intake: pathway analysis



Relevant pathways:

- Biosynthesis of amino acids
- Metabolism of proteins
- Digestion of carbohydrates
- Skeletal muscle development
- Immunity
- Rumen bacteria activity
- Mitochondrial electron transport

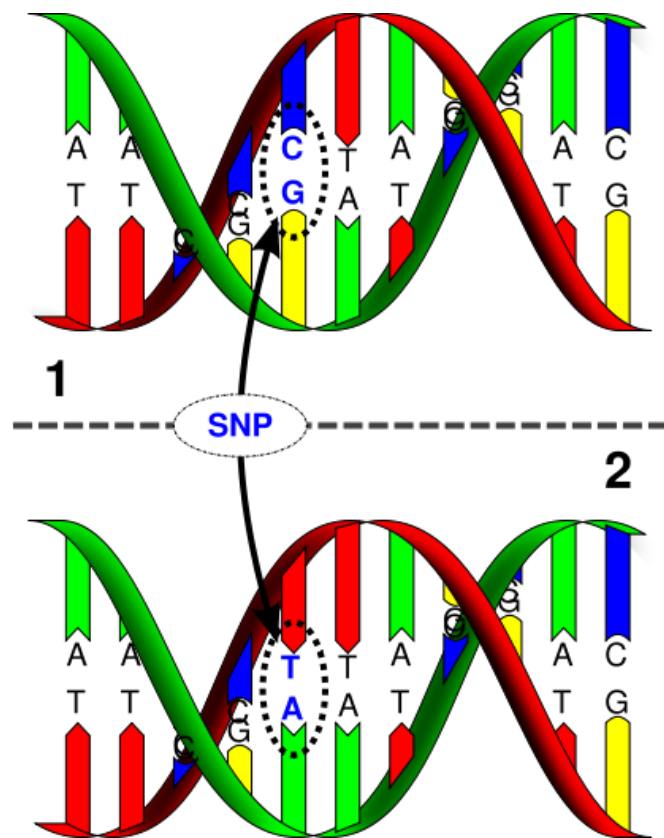
Mitochondrial function



Beef cattle: low RFI vs high RFI

- greater mitochondrial density
- greater mitochondrial function
- greater antioxidant capacity
- lower oxidative stress

Genomic selection: the latest revolution



the use of genetic markers across the genome to predict breeding values

allows to select animals at an early age



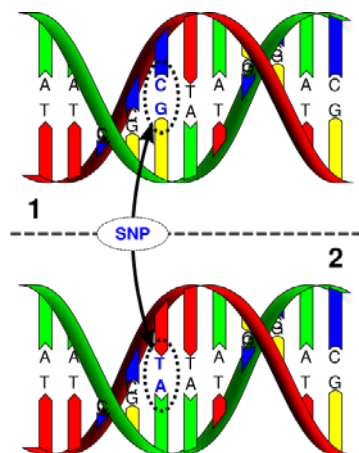
JOIN THE REVOLUTION

Genomics and feed efficiency



feed intake, body weight, milk energy output

+



genome-wide SNP information



Genomic prediction

predict genomic PTAs for the **entire population**,
including young selection candidates

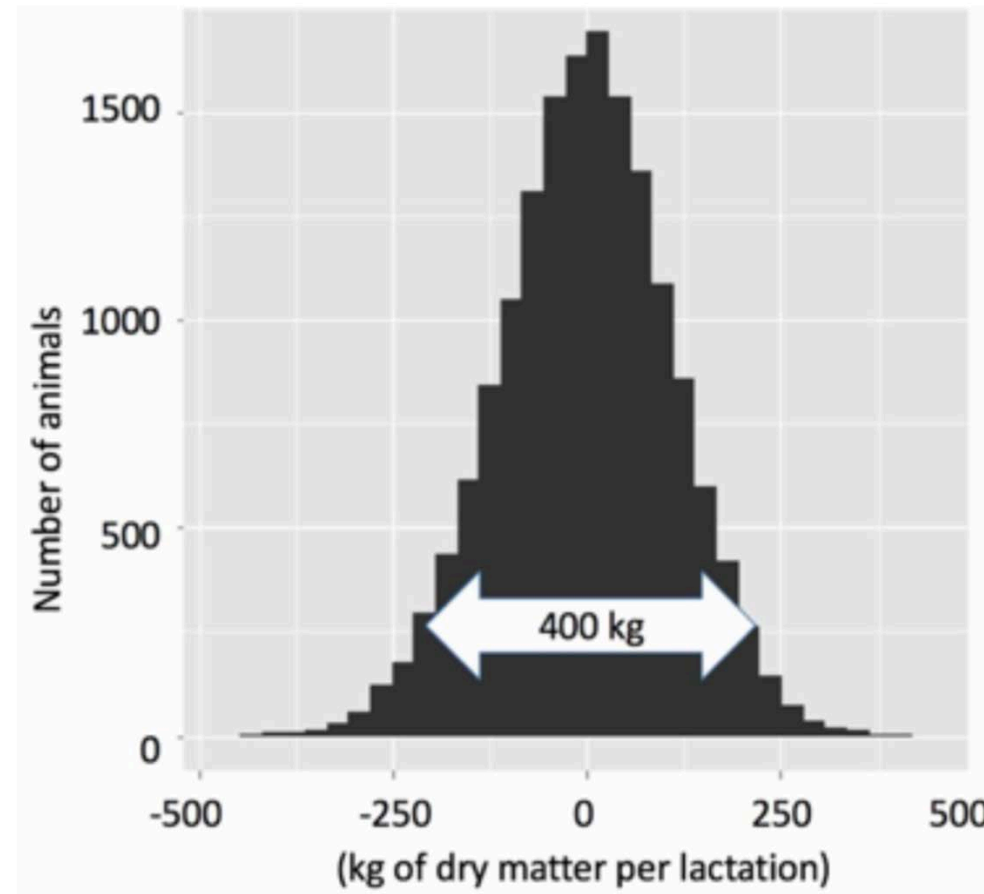
Genomic prediction

Table 4. Estimated prediction accuracies for residual feed intake (RFI), DMI, net energy in milk (MilkE), and metabolic body weight (MBW)¹

Trait	NLD						SAC				NAM				
	Across		Within	Interaction		Across		Within	Interaction		Across		Within	Interaction	
	With	With		With	With	With	With		With	With					
	SAC	NAM		SAC	NAM	NLD	NAM		NLD	NAM	NLD	SAC		NLD	SAC
RFI (kg/d)	0.27	0.24	0.29	0.26	0.29	0.17	0.12	0.14	0.11	0.13	0.15	0.15	0.18	0.14	0.15
DMI (kg/d)	0.35	0.31	0.32	0.31	0.32	0.52	0.52	0.51	0.52	0.54	0.23	0.23	0.23	0.24	0.23
MilkE (Mcal/d)	0.20	0.22	0.18	0.17	0.21	0.61	0.63	0.62	0.63	0.60	0.18	0.20	0.19	0.19	0.19
MBW (kg ^{0.75})	0.31	0.33	0.29	0.30	0.37	0.41	0.43	0.39	0.44	0.44	0.38	0.37	0.40	0.44	0.41

¹Accuracies were measured as the correlation between genomic predicted breeding values and adjusted phenotypes. Environments included North America (NAM), the Netherlands (NLD), and Scotland (SAC). Models were across-environment, within-environment, and interaction model. The average SD of correlations across 10 training-testing partitions were about 0.06, 0.08, and 0.03 for NLD, SAC, and NAM, respectively.

Distribution of GEBV for RFI



GEBVs calculated for 16k bulls using a **reference population** of 3.5k cows

Take home messages

- feed efficiency is an economically relevant trait
- residual feed intake is a heritable trait ($h^2 \approx 15\%$)
- genetic selection can effectively improve dairy feed efficiency
- residual feed intake is highly polygenic, many genes with small effects
- some relevant biological mechanisms:
metabolism of proteins and sugars, rumen bacteria activity, mitochondrial function
- genomic predictive correlations around 20%
- future: more feed intake records, more reliable genomic predictions

Thanks for your attention!



FFAR

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