Genetic solutions to improve resource efficiency in dairy cattle

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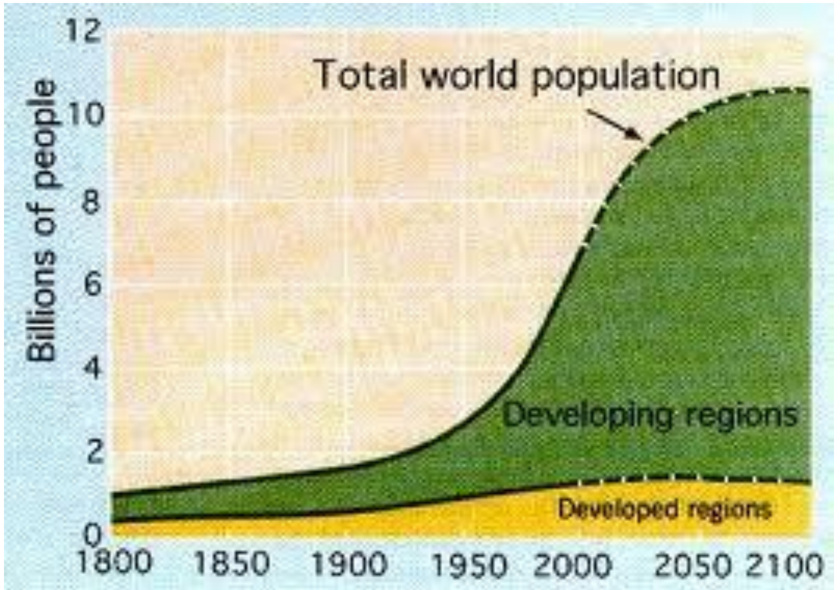
Importance of improving efficiency

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



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Importance of improving efficiency

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- Feed is major variable cost in animal production
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Resource efficiency:

- Efficient use of available resources, like land, water, labour, feed, etc.
    - Feed efficiency
    - Methane emissions

Outline presentation

A) Overview of research we have performed so far on:

1. Genetic parameters for environmental phenotypes

2. Additional value of combining data worldwide

B) Future outlook

1. What are genetic parameters for environmental phenotypes?

e.g., residual feed intake and predicted methane production

1. Genetics of environmental phenotypes

- Residual feed intake (RFI in MJ/d)
  - Energy intake – energy requirements for milk, fat, protein, lactose, and maintenance (as function of metabolic body weight)

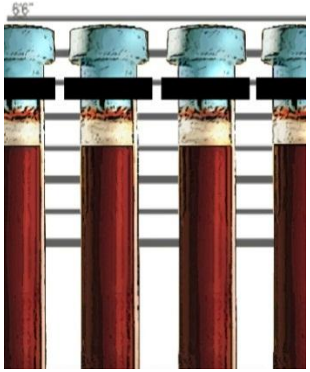
- Predicted methane emission (PME in gram/day):

  = feed intake (in kg DM/d)
  x energy content of kg DM (= 18.4 (MJ/kg DM))
  / energy generated by methane (= 0.05565 (MJ/g))
  x percentage methane of gross energy (= 0.06)
  x scaling factor [1 + (2.38 – level of intake (multiples of maintenance level)) x 0.04]

Collected data

- Experimental farm: 613 cows (1990-1997)
  - Feed intake + ration (daily)
  - Body weight (weekly)
  - Milk production & milk contents (weekly)

- Blood samples: 599 cows
  - Illumina 50k Chip



Heritabilities & Genetic correlations

	PME	RFI	FPCM
PME	**0.35**		
RFI	0.32	**0.40**	
FPCM	0.31	*	**0.38**

Accuracies of predicting RFI and PME

	RFI	PME
Pedigree	0.37	0.21
Pedigree + SNP	0.52	0.37

Verbyla et al., JDS 2010
De Haas et al., JDS 2011

1. Conclusions – environmental phenotypes

- Genetic correlation PME with feed efficiency is positive: Cows with low RFI (i.e. high feed eff.) have low PME
- The use of SNP information showed an increase in the accuracy to predict BV for environmental phenotypes
- In future, selection for environmental phenotypes could be performed using genomic selection

2. What is additional value of combining data from both ends of the world?

Available data

Country	Heifer type	No. anim.	No. SNPs	Rec. period
Australia	Growing	843	624,930	For 60-70d starting at age of 200d
Netherlands	Lactating	599	37,069	First 100d in lactation
UK	Lactating	359	37,069	First 100d in lactation

40 bulls genotyped in both Australia and Europe

Aim of this study

Estimate the accuracy of genomic breeding values (GEBV's) across countries for dry matter intake, when analysed as one trait, or a separate trait per country (multitrait)

Accuracy of genomic selection

	Uni within		
AU	0.38 *(0.03)*		
EU	0.31 *(0.05)*		
UK	0.30 *(0.04)*		
NL	0.33 *(0.09)*		

De Haas et al., JDS 2012

Accuracy of genomic selection

	Uni within	Uni multi	
AU	0.38 *(0.03)*	0.34 *(0.05)*	
EU	0.31 *(0.05)*	**0.32** *(0.05)*	
UK	0.30 *(0.04)*	**0.33** *(0.06)*	
NL	0.33 *(0.09)*	0.31 *(0.09)*	

De Haas et al., JDS 2012

Accuracy of genomic selection

		Uni multi	**Tri: AU-UK-NL**
AU		0.34 *(0.05)*	**0.39** *(0.04)*
EU		0.32 *(0.05)*	**0.33** *(0.05)*
UK		0.33 *(0.06)*	**0.33** *(0.03)*
NL		0.31 *(0.09)*	**0.33** *(0.09)*

De Haas et al., JDS 2012

2. Conclusions – international collaboration

- Accuracy of GEBVs for DMI can be increased by:
  - combining datasets across countries, and
  - using a multitrait approach

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

Future outlook

global Dry Matter Initiative: gDMI

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.)

Variance components

Country	N	Mean	SDg	Heritability
Cows				
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		
Heifers				
Australia	843	8.3	0.77	0.20 (0.11)
New Zealand	941	7.6	0.66	0.34 (0.12)

Overall summary

- Improving efficiency is important in dairy production
- Selection for feed efficiency (and methane) impossible a few years ago, with genomics a realistic prospect

- A challenge is to increase the accuracy of genomic prediction
  - Combine data internationally, and use multi-trait genomic prediction models

Thank you for your attention

Questions??

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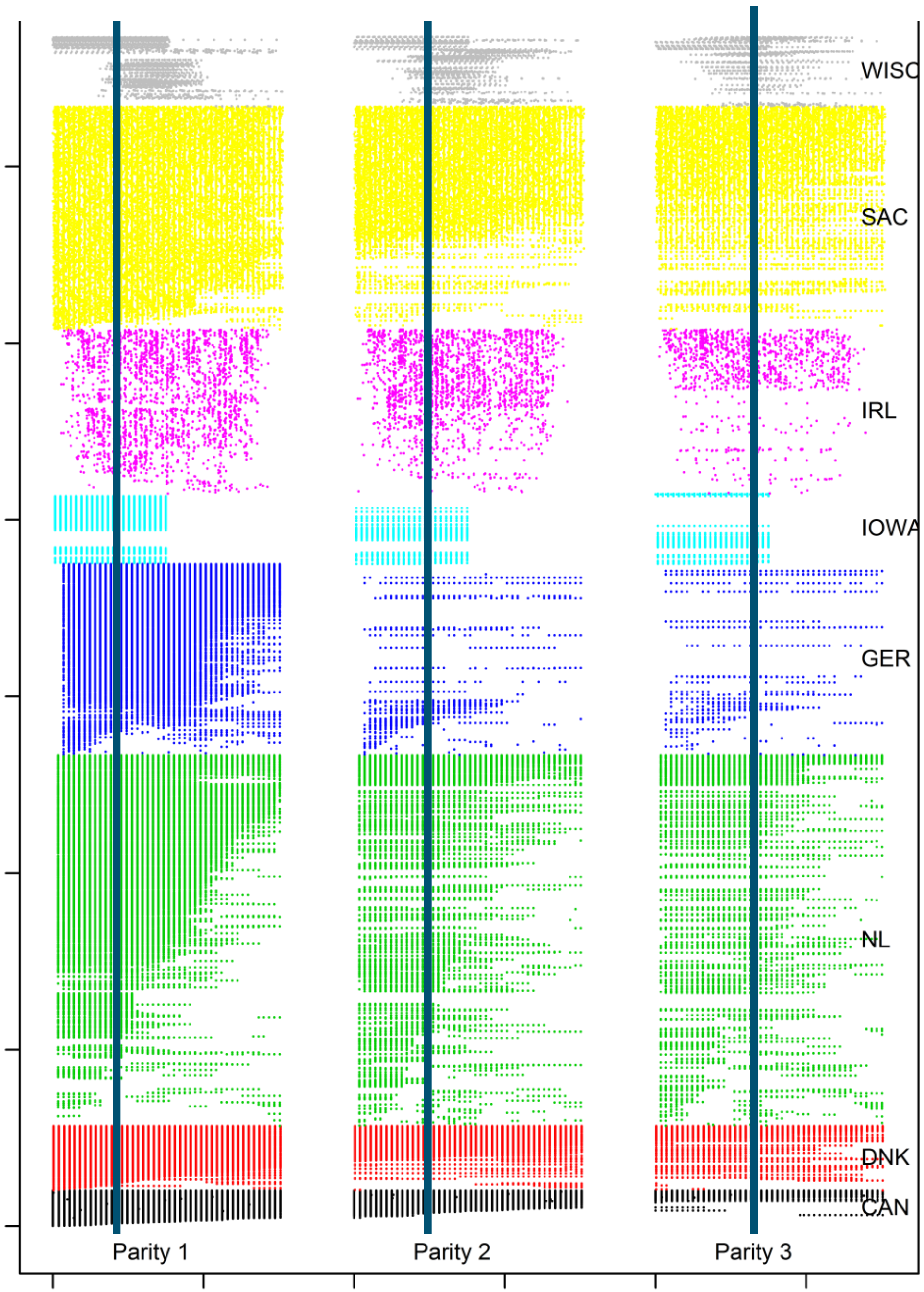
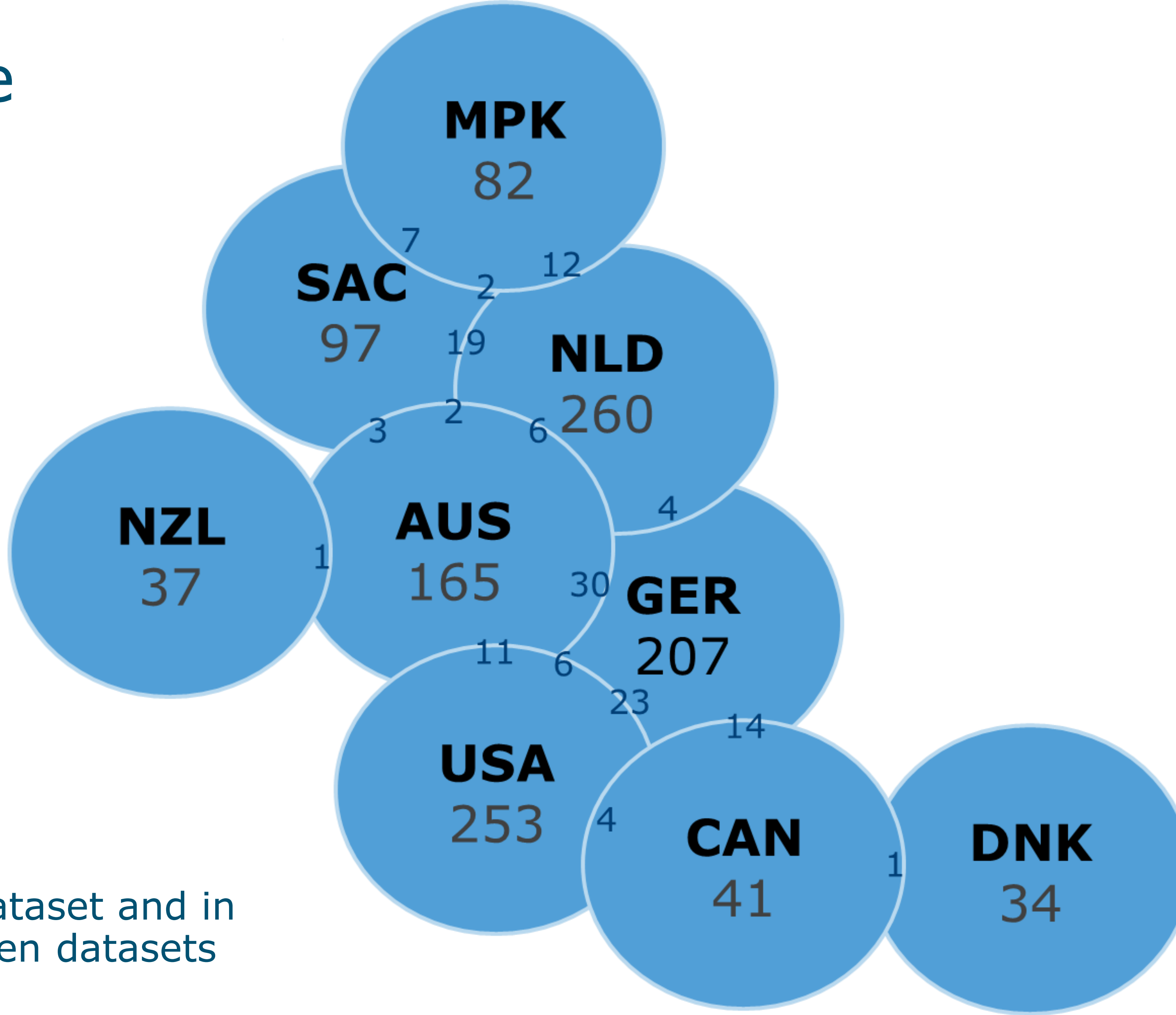
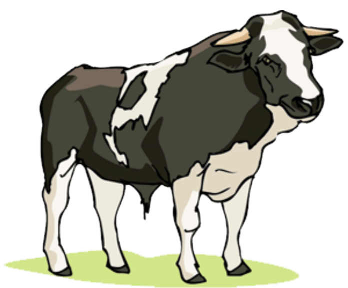
Our data



Pedigree





Sires in each dataset and in common between datasets

First 3 principal components of the GRM