

# Genomic predictions for dry matter intake using the international reference population of **gDMI**

Yvette de Haas and **gDMI** consortium



# Breeding for feed efficiency is gaining importance!

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### Research will be key in improving dairy sector efficiency

13 May 2014 | By Olivia Midgley

MORE research must be targeted at feed efficiency in ruminants in order to 'catch up' with advancements in the pig and poultry sector.



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Tuesday 15 April 2014 06:00

## Alberta Farmer

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### New study aims to improve protein efficiency in dairy COWS

Researcher to study how to lower protein content without compromising milk production



Posted May 6, 2014 by Alma Release in Livestock, News



# What is missing to breed on feed efficiency?

- Feed intake records on daughters of sires
  - Expensive measurements
  - Labour intensive
  - Not practical for daily practice -> only research herds (small impact)



# Pilot international collaboration (AUS-NL-UK)

## Conclusion of pilot:

- Accuracy of genomic breeding values for dry matter intake can be increased by:
  - combining datasets across countries, and
  - using a multitrait approach
- Average accuracy  $r(\text{GEBV}, \text{TBV})$ : 0.35



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## Improved accuracy of genomic prediction for dry matter intake of dairy cattle from combined European and Australian data sets

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LIVESTOCK RESEARCH

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# global Dry Matter Initiative: gDMI

- 15 parties in consortium (science + industry)
- 9 countries, 10 groups
- ~10,000 phenotyped animals
- ~6,000 genotyped animals
- ~12,000 parities
- 591,621 SNPs HD-imputed

## Global Dry Matter Initiative (gDMI)



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# global Dry Matter Initiative: **g**DMI

## ■ Key research questions:

- How to combine, homogenise and standardise phenotypes? (Berry et al., 2014)
- Genomic similarity between population? (Pryce et al., 2014)
- Can we predict DGV for DMI for different partners? (De Haas et al., 2014 in prep.)

## ■ Aim of today is to present:

- Estimated accuracies of genomic breeding values (GEBV's) across countries for dry matter intake with international dataset of **g**DMI



# Our data (Berry et al., 2014)

Country	N	Mean
<b>Cows</b>		
All	10,008	19.7
Canada	411	22.2
Denmark	668	22.1
Germany	1,141	20.2
Iowa	398	23.5
Ireland	1,677	16.7
Netherlands	2,956	21.4
UK	2,840	17.4
Wisconsin	447	24.9
Australia	103	15.6
<b>Heifers</b>		
Australia	843	8.3
New Zealand	941	7.6

# Phenotype for genetic parameters

“Weighted average” phenotype per animal for DMI on day 70 in parity 2

- Predicted from estimated quadratic DMI curve for each animal by 5 parities => 120 (co)variances
  - Fixed effects: parity-DIM, HYS, experimental treatment
  - Random effects: cow-parity-DIM difference in residual variances across HYS and herd curve
- Predicted DMI with low reliabilities were discarded => ~8,500 animals remained

■ Parameters estimated with H-matrix



# Heritability for each country

	<b>DMI on 70d in par2</b>
CAN	<b>0.21</b>
DNK	<b>0.46</b>
AU_h	<b>0.32</b>
NZ_h	<b>0.24</b>
GER	<b>0.17</b>
US_I	<b>0.53</b>
IRL	<b>0.26</b>
NLD	<b>0.38</b>
UK	<b>0.26</b>
US_W	<b>0.12</b>



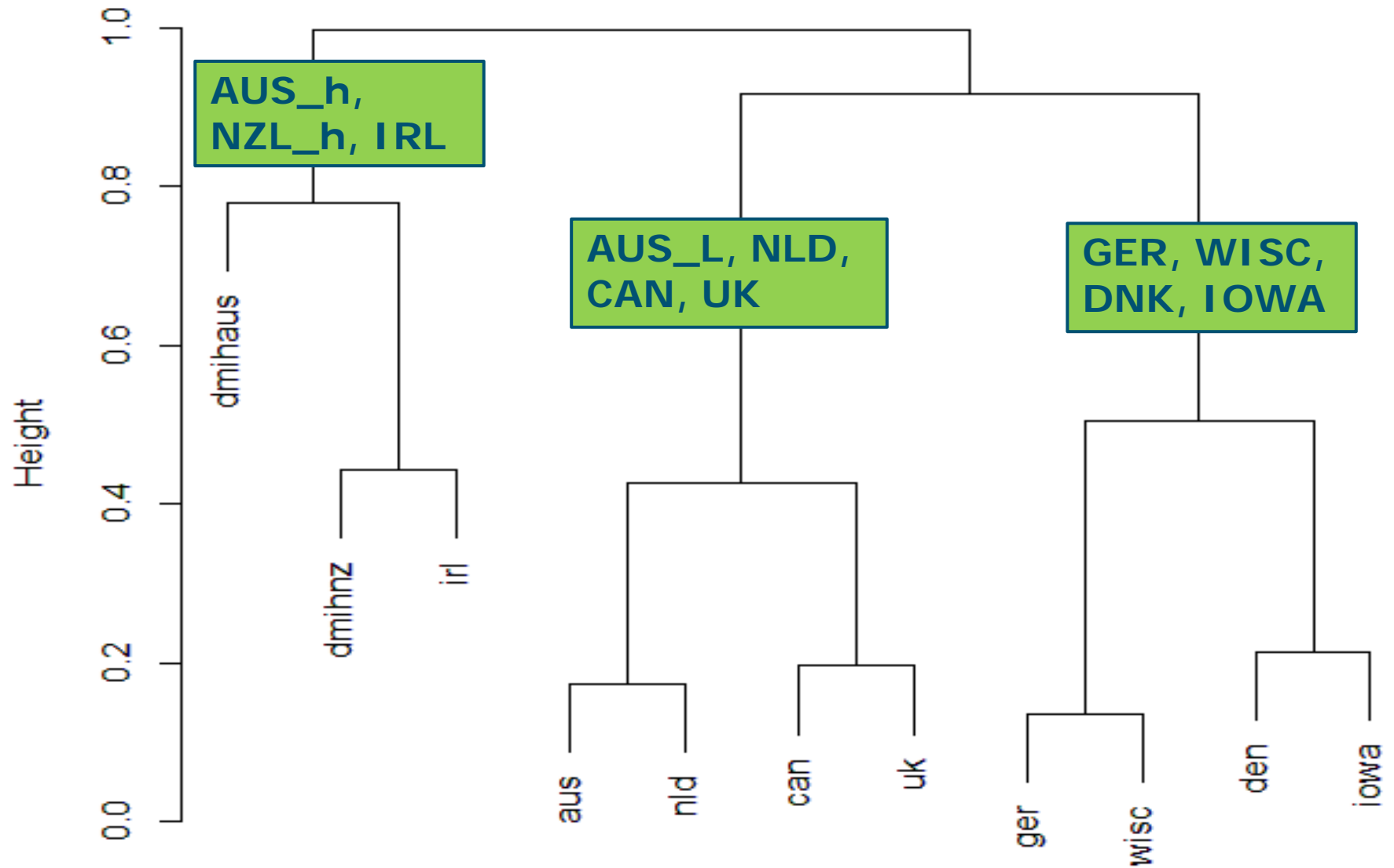
# Genetic correlations between countries

	AUS	CAN	DNK	AU_h	NZ_h	GER	US_I	IRL	NLD	UK
CAN	0.66									
DNK	0.56	0.32								
AU_h	0.27	0.30	0.05							
NZ_h	-0.26	0.09	-0.19	0.22						
GER	0.32	0.13	0.85	0.17	0.17					
US_I	0.36	0.14	0.79	-0.14	-0.06	0.68				
IRL	0.00	0.04	0.16	0.39	0.56	0.45	-0.15			
NLD	0.83	0.77	0.82	0.20	-0.14	0.62	0.63	0.02		
UK	0.57	0.80	0.37	0.61	0.40	0.46	0.08	0.50	0.68	
US_W	0.53	0.52	0.75	0.29	0.15	0.86	0.50	0.35	0.80	0.76

# Genetic correlations between countries

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UK	0.57	0.80	0.37	0.61	0.40	0.46	0.08	0.50	0.68	
US_W	0.53	0.52	0.75	0.29	0.15	0.86	0.50	0.35	0.80	0.76

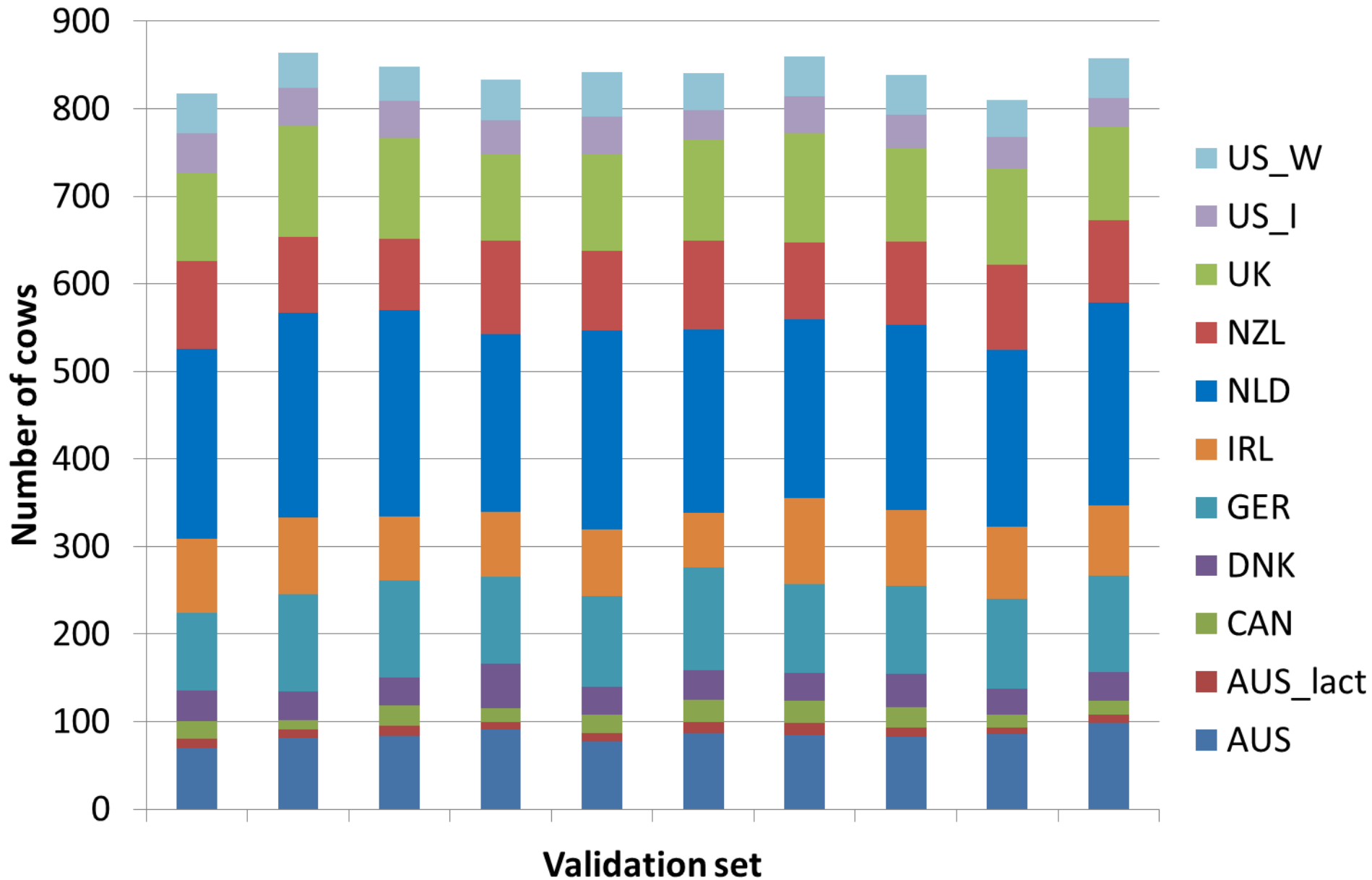
# Dendrogram



# Validation strategy

- Validation sets based on progeny groups of sires in the different countries
  - *Can we increase the accuracy of bull GEBVs by using multi-country reference populations?*
  - Risk that by having all the progeny of particular sires only within one validation population might mean lower accuracies than if the progeny were spread across the validation populations.

# Validation sets



# Accuracy of genomic selection $r(\text{GEBV}, \text{TBV})$

	CAN	DNK	AU_h	NZ_h	GER	IOWA	IRL	NLD	UK	WISC
$h^2$	0.21	0.46	0.32	0.24	0.17	0.53	0.26	0.38	0.26	0.12
Acc	0.40	0.37	0.39	0.44	0.45	0.46	0.48	0.54	0.49	0.38
SE	0.19	0.08	0.04	0.05	0.07	0.06	0.06	0.04	0.08	0.15

	Average
Accuracy	0.44
Standard error	0.08

AUS\_lact: 0.48 (0.08)



# Accuracy of genomic selection $r_{(GEBV, TBV)}$

Correlations between countries: 0.0

	CAN	DNK	AU_h	NZ_h	GER	IOWA	IRL	NLD	UK	WISC
$h^2$	0.21	0.46	0.32	0.24	0.17	0.53	0.26	0.38	0.26	0.12
Acc	0.17	0.33	0.39	0.42	0.39	0.43	0.46	0.51	0.43	0.20
SE	0.19	0.10	0.05	0.05	0.07	0.05	0.06	0.04	0.08	0.13

# Accuracy of genomic selection $r(\text{GEBV}, \text{TBV})$

Correlations between countries: 0.95

	CAN	DNK	AU_h	NZ_h	GER	IOWA	IRL	NLD	UK	WISC
$h^2$	0.21	0.46	0.32	0.24	0.17	0.53	0.26	0.38	0.26	0.12
Acc	0.33	0.36	0.30	0.38	0.43	0.43	0.44	0.51	0.48	0.35
SE	0.20	0.09	0.04	0.05	0.07	0.07	0.07	0.04	0.08	0.14

# Accuracy of genomic selection $r_{(GEBV, TBV)}$

## Overview

	CAN	DNK	AU_h	NZ_h	GER	IOWA	IRL	NLD	UK	WISC
Rg	0.40	0.37	0.39	0.44	0.45	0.46	0.48	0.54	0.49	0.38
Rg0	0.17	0.33	0.39	0.42	0.39	0.43	0.46	0.51	0.43	0.20
Rg1	0.33	0.36	0.30	0.38	0.43	0.43	0.44	0.51	0.48	0.35

	Avg Acc
Rg	0.44
Rg0	0.37
Rg1	0.40

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# Conclusions

- Average accuracy of genomic breeding values with **gDMI** dataset: 0.44
  - Average accuracy in pilot (AUS-UK-NL): 0.35

Further research questions:

- Sensitivity for chosen phenotype (70DIM; par 2)
- Sensitivity for validation strategies
- Sensitivity for half sib groups across countries
- Sensitivity for genetic correlations (bending procedure)

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And many others

## Global Dry Matter Initiative (gDMI)



*Thank you for your attention*



**Open meeting of gDMI on  
Thursday, 13.30h, room 30610**



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