Update on global collaborative research in the area of genetics of feed efficiency

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What is missing to breed on feed efficiency?

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

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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

Long term relationships

global Dry Matter Initiative: **g**DMI

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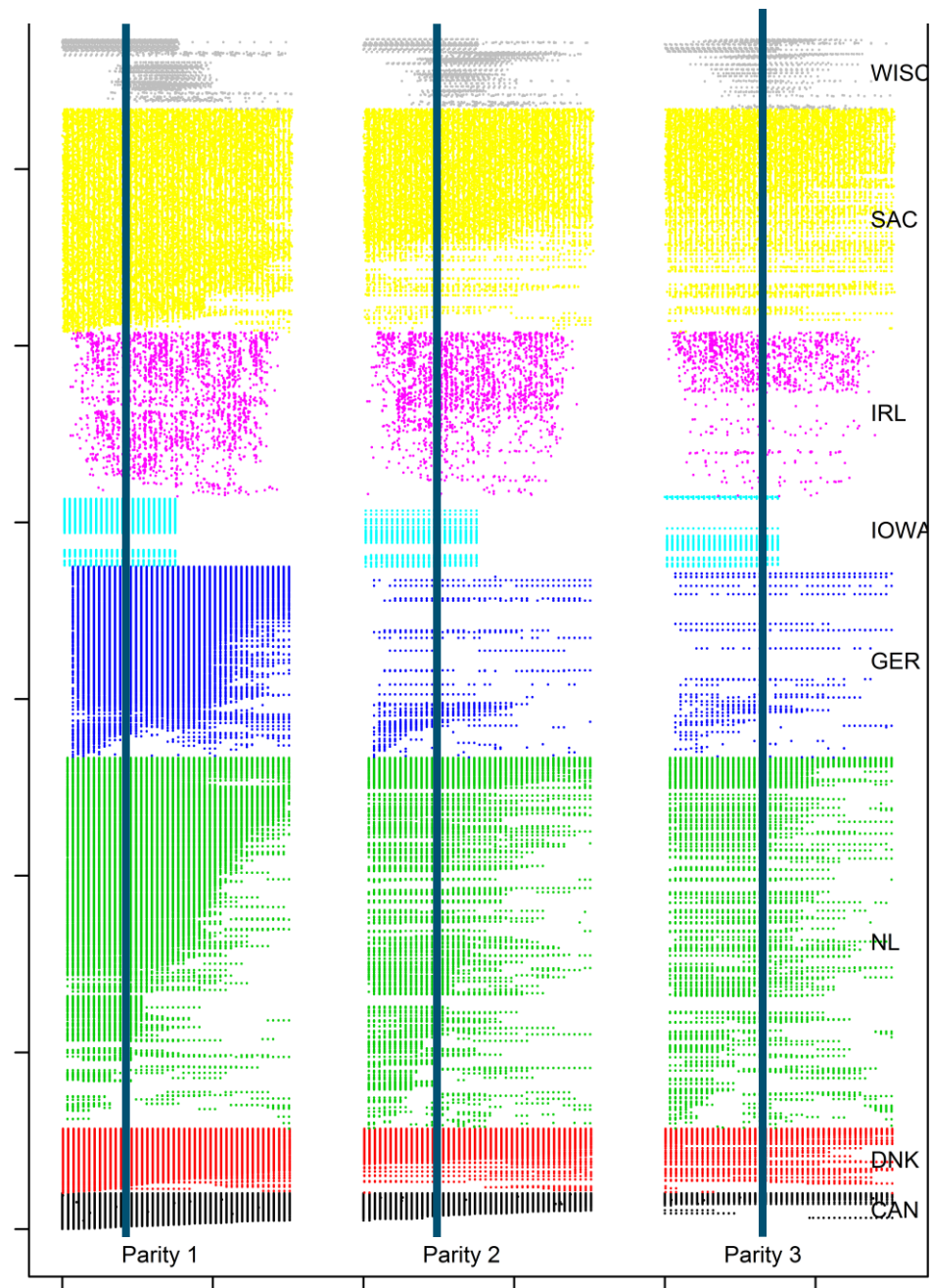- ~12,000 parities
- 591,621 SNPs HD-imputed

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global Dry Matter Initiative: **g**DMI

- Key research questions (part I):

    - How to combine, homogenise and standardise phenotypes? (Berry et al., 2013 submitted)

    - Genomic similarity between population? (Pryce et al., 2013 submitted)

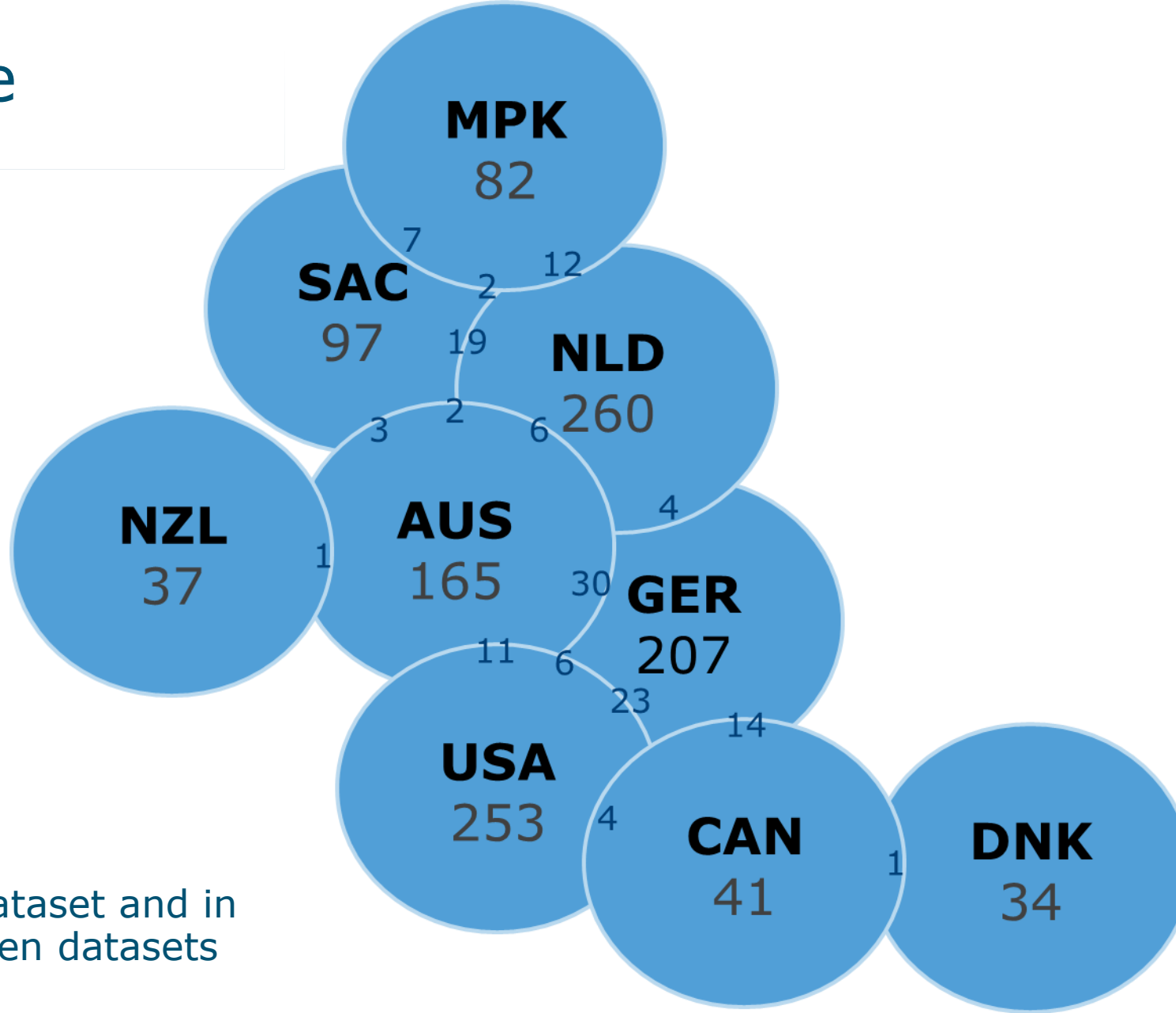   - Can we predict DGV for DMI for different partners? (De Haas et al., 2013 in prep.)

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Our data

Variance components

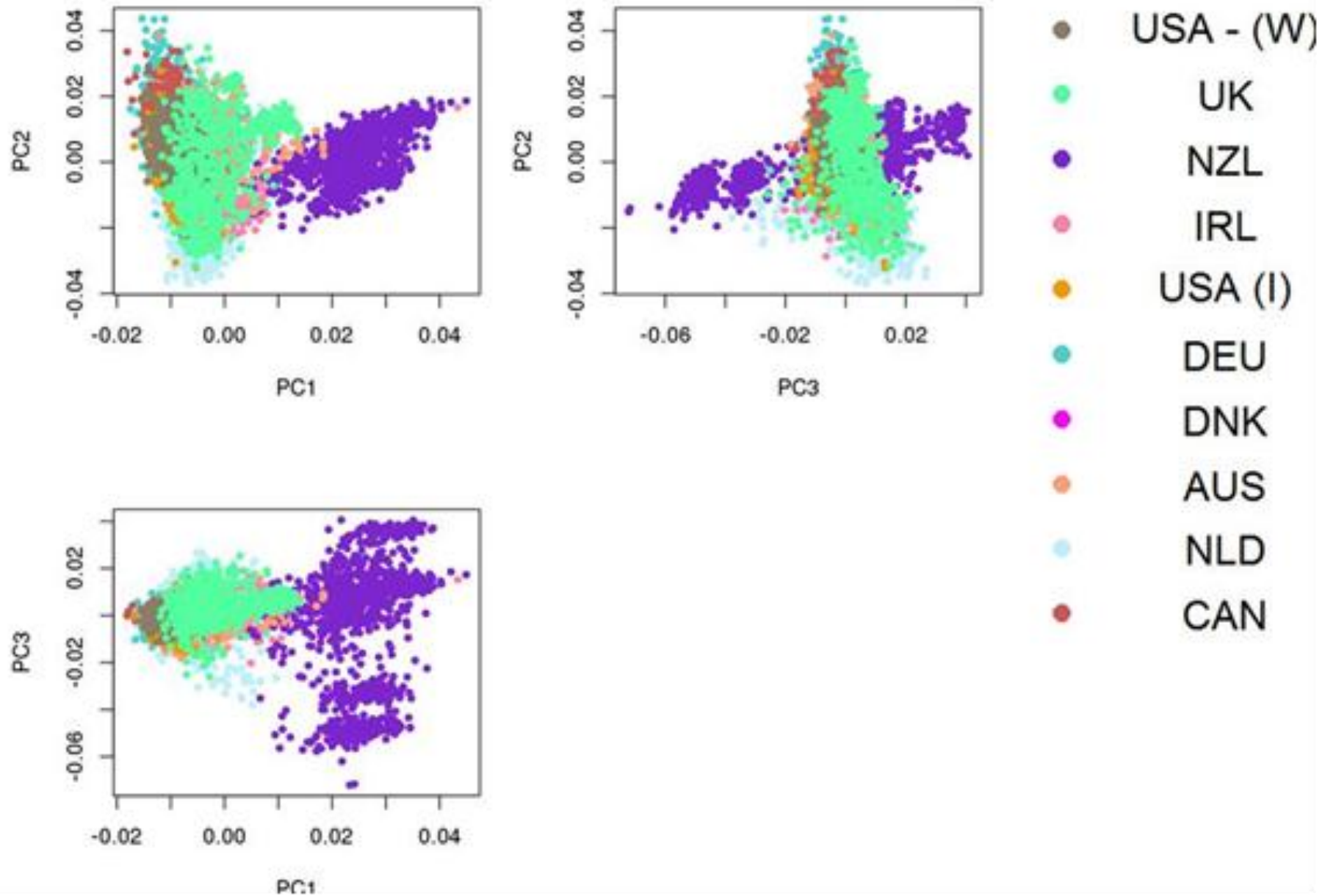| Country	N	Mean	SDg	Heritability
Cows				
All	10,008	19.7	1.13	0.34 (0.03)
Canada	411	22.2	1.01	0.19 (0.14)
Denmark	668	22.1	1.48	0.52 (0.12)
Germany	1,141	20.2	0.64	0.08 (0.06)
Iowa	398	23.5	1.48	0.41 (0.14)
Ireland	1,677	16.7	0.88	0.41 (0.10)
Netherlands	2,956	21.4	1.15	0.39 (0.05)
UK	2,840	17.4	1.07	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)

Pedigree

Sires in each dataset and in common between datasets

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Links between countries (based on SNPs)

Genomic predictions

- 9 groups of lactation cows
- 2 groups of growing heifers

Impossible to run a 11-trait analysis!

Clustering of animals:

- 5 groups: North America, Grazing, EU high-input, EU low-input, Growing heifers (paper Donagh)

- PC-analyses based on phenotypes (possibly (1) combination of repeated records into 1 phenotype, and/or (2) weighted according to accuracy)
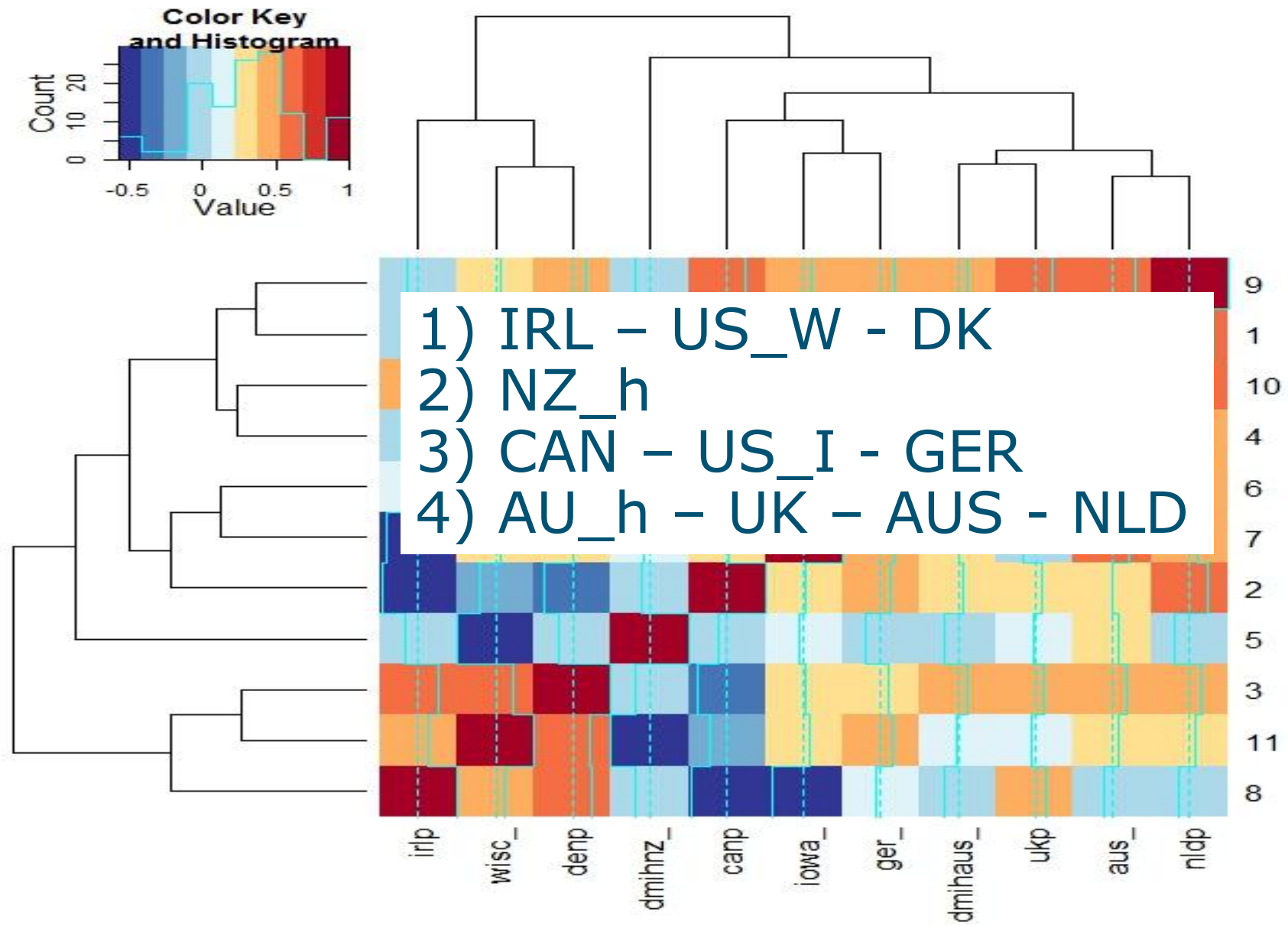
- Dendrogram based on genetic correlations

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Genetic correlations between countries

	AUS	CAN	DK	AU_h	NZ_h	GER	US_I	IRL	NLD	UK	US_W
AUS	1.00	0.22	0.50	0.35	0.34	0.17	0.55	0.03	0.67	0.47	0.34
CAN	0.22	1.00	-0.36	0.32	0.04	0.40	0.24	-0.51	0.57	0.33	-0.11
DK	0.50	-0.36	1.00	0.40	-0.09	0.36	0.24	0.61	0.46	0.39	0.58
AU_h	0.35	0.32	0.40	1.00	-0.07	0.17	0.25	-0.08	0.40	0.52	0.18
NZ_h	0.34	0.04	-0.09	-0.07	1.00	-0.08	0.11	-0.07	-0.09	0.18	-0.57
GER	0.17	0.40	0.36	0.17	-0.08	1.00	0.49	0.13	0.49	0.23	0.45
US_I	0.55	0.24	0.24	0.25	0.11	0.49	1.00	-0.42	0.38	-0.03	0.32
IRL	0.03	-0.51	0.61	-0.08	-0.07	0.13	-0.42	1.00	0.00	0.42	0.42
NLD	0.67	0.57	0.46	0.40	-0.09	0.49	0.38	0.00	1.00	0.58	0.33
UK	0.47	0.33	0.39	0.52	0.18	0.23	-0.03	0.42	0.58	1.00	0.13
US_W	0.34	-0.11	0.58	0.18	-0.57	0.45	0.32	0.42	0.33	0.13	1.00

Genetic correlations between countries

	AUS	CAN	DK	AU_h	NZ_h	GER	US_I	IRL	NLD	UK	US_W
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Dendrogram

1) IRL – US_W - DK
2) NZ_h
3) CAN – US_I - GER
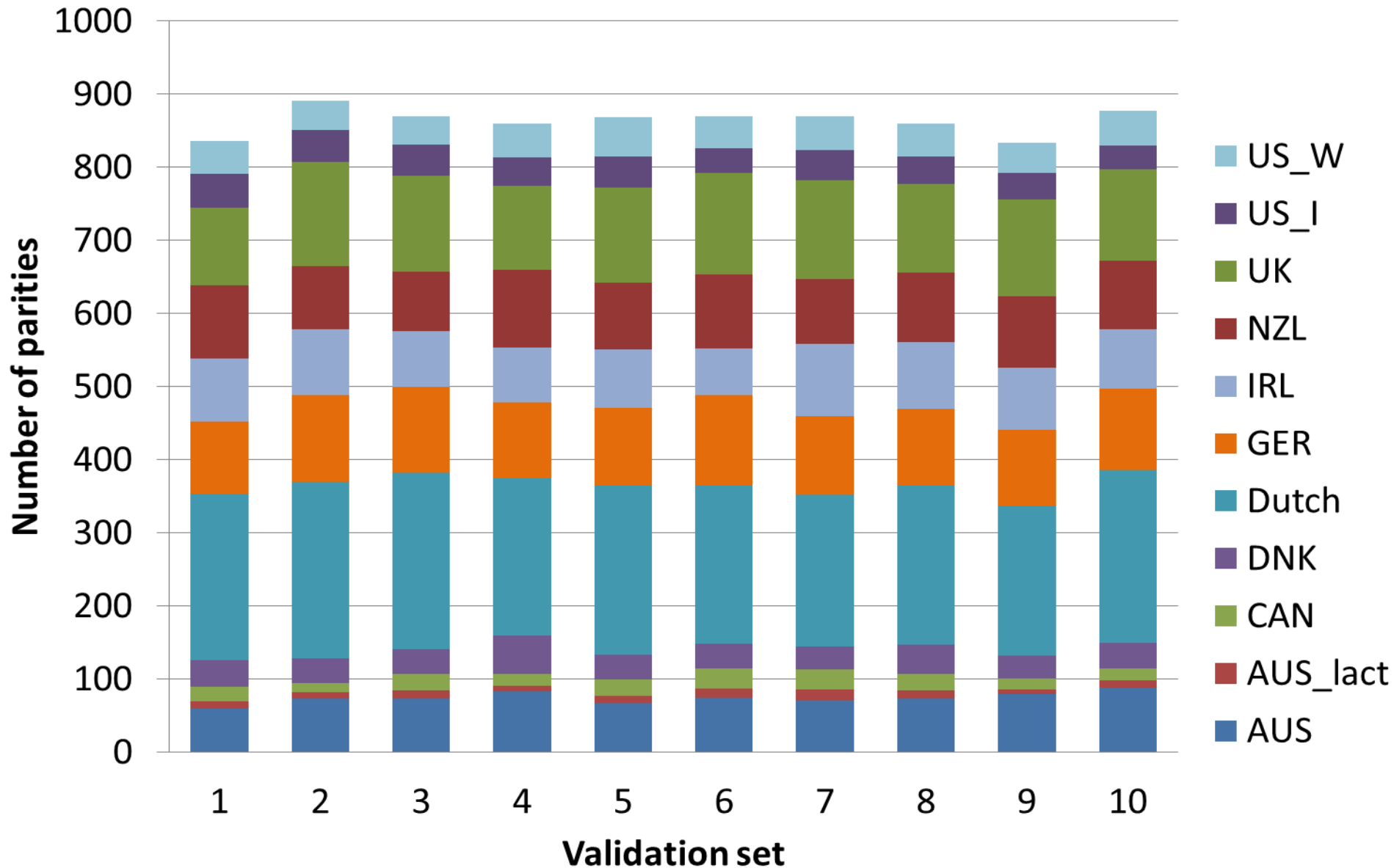4) AU_h – UK – AUS - NLD

Validation strategy 1

- Validation sets based on progeny groups of sires in the different countries/sources.

  - *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.

    → **But we think this is real life!**

Validation sets

Validation strategy 2

- Validation sets based on country/population.

  - *What is added value of contributing data? Can countries benefit as well when no data is contributed?*

  - <u>Risk</u> that achieved accuracy is highly related with size of validation set (i.e., 3000 Dutch parities *vs.* 400 parities in Iowa).

    → **But isn't this real life as well?!**

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Overall summary

- Improving efficiency is important in dairy production

- Selection for feed efficiency 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

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Questions for discussion

- Best way of clustering phenotypes?

- Best validation strategies?

- How to continue with **g**DMI part II?
    - Add other phenotypes (what phenotypes?)
    - Add more data (dairy? beef? lactating? growing?)
    - Set up validation population (what countries?)
    - What does the industry want to get out of gDMI? What do scientists want to get out of gDMI?

Thank you for your attention

Questions??

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