

Multi-breed beef genomics

Research update April 2015

Donagh Berry

Teagasc, Moorepark

Herdbooks, April 2015

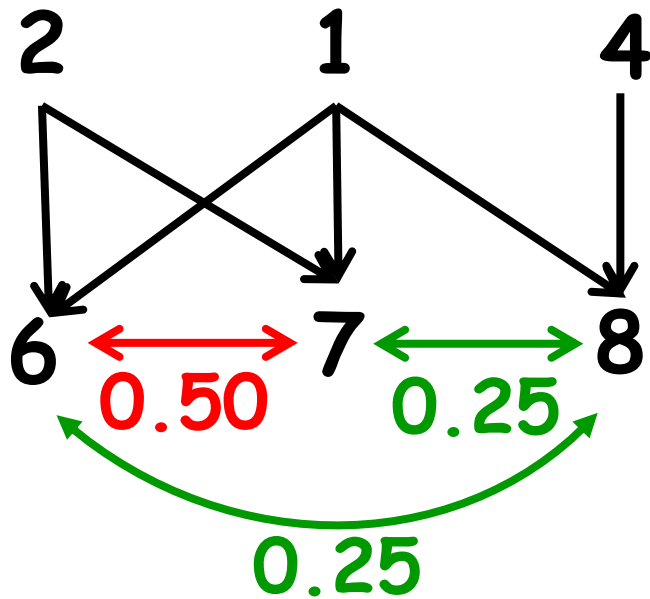
Genomic selection

- Uses DNA information to supplement pedigree information to identify the genetically elite animals
- DNA is the same throughout life and in each cell of the body
- Even if you know the genetic merit of parents with 100%, max reliability of progeny is 50%
 - Which half of the genes did you inherit from each parent?

International perspective

- Implemented in dairy in Ireland in 2009
 - Up to 54% more accurate
 - 60% of semen sold last year
- Within-breed genomic predictions in US and Canada
 - Run by Dorian Garrick
 - Black Angus, Red Angus, Limousin ...
- Within-breed genomic predictions in France
 - CH, LM, BA official in Autumn

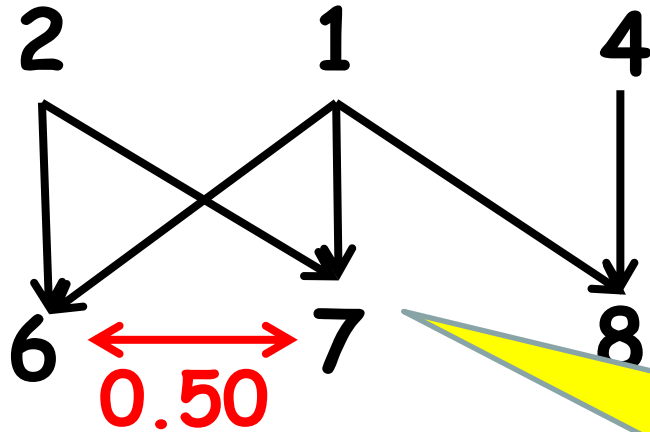
Approach



	6	7	8
6	1.00	0.50	0.25
7	0.50	1.00	0.25
8	0.25	0.25	1.00

Approach

+20 kg +10 kg

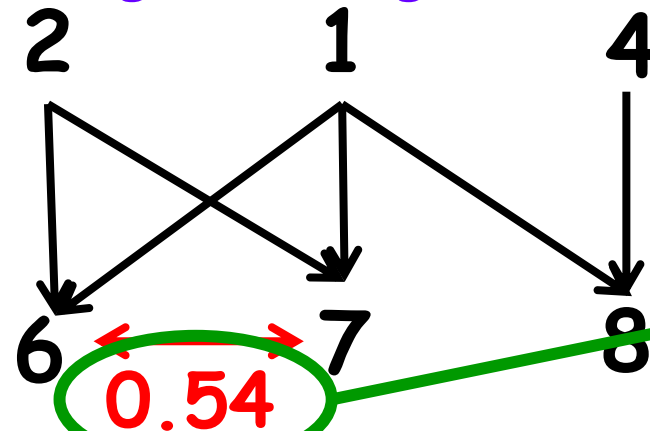


	6	7	8
6	1.00	0.50	0.25
7	0.50	1.00	0.25
8	0.25	0.25	1.00

Geometric relationships

+15 kg +15 kg

+20 kg +10 kg



	6	7	8
6	1.00	0.54	0.22
7	0.54	1.00	0.28
8	0.22	0.28	1.00

+14 kg +16 kg

Imputation

- Use 40,000 DNA markers
 - Costs €79
- Lower cost of ~14,000 DNA markers
 - Predict (Impute) the remaining 26,000
- Genotyping v mobile phones
 - More power but the same price
 - ~14,000 DNA markers → 40,000 DNA markers for the same price
- Beagle → Fimpute software
 - Faster and more accurate - cost

Imputation - test

Breed	N	Mean	Min	Max
AA	2897	0.98	0.59	1.00
AU	61	0.76	0.75	0.79
BA	133	0.78	0.74	0.90
BB	457	0.98	0.86	1.00
CH	9335	0.98	0.59	1.00
FR	1188	0.96	0.54	0.99
HE	2285	0.98	0.56	1.00
HO	6128	0.97	0.56	1.00
IM	46	0.87	0.80	0.91
JE	32	0.98	0.95	0.99
LM	8903	0.98	0.72	1.00
PI	23	0.75	0.72	0.81
PT	172	0.75	0.71	0.97
SA	135	0.79	0.75	0.99
SH	98	0.86	0.82	0.95
SI	1507	0.98	0.81	1.00

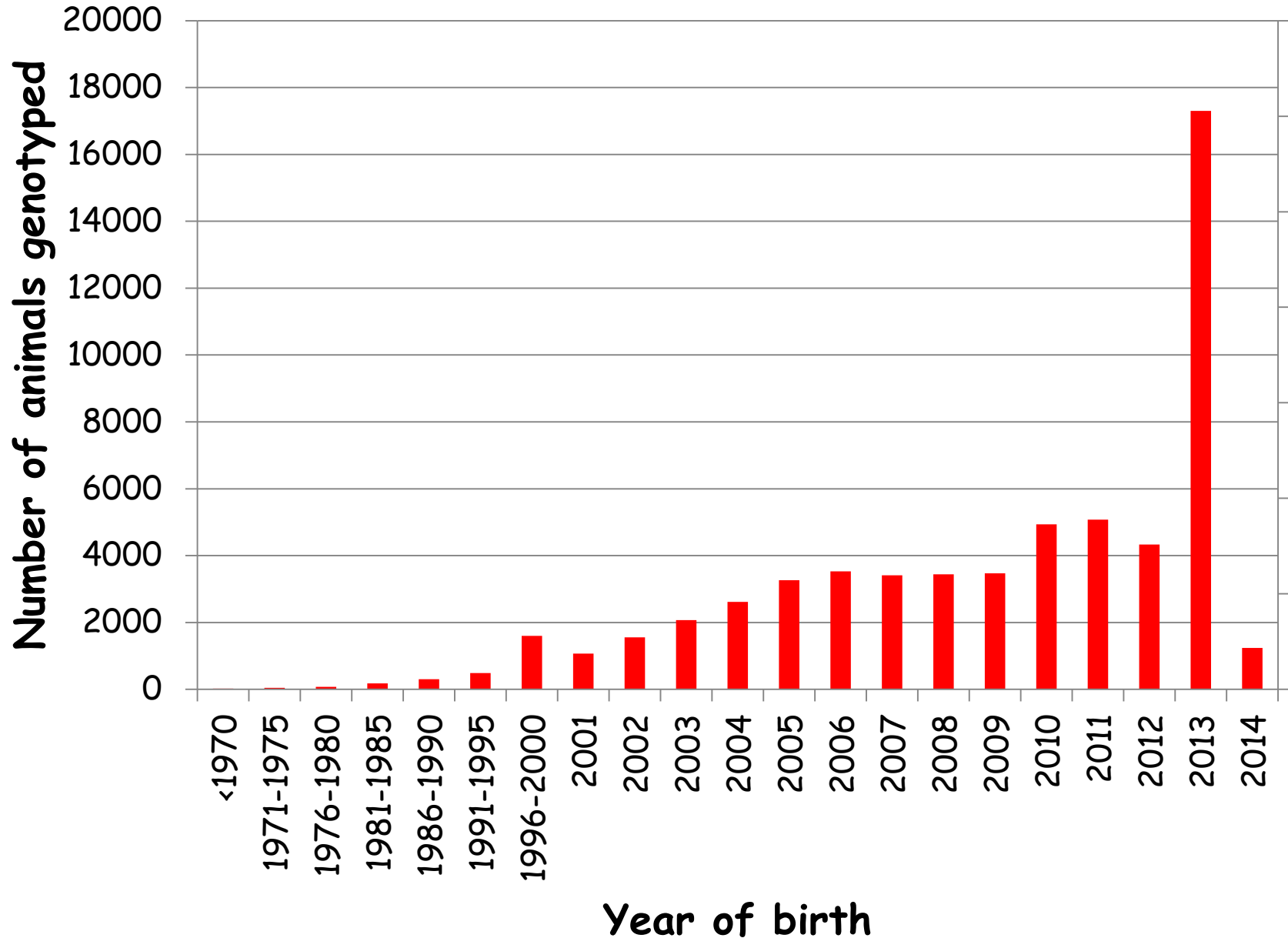
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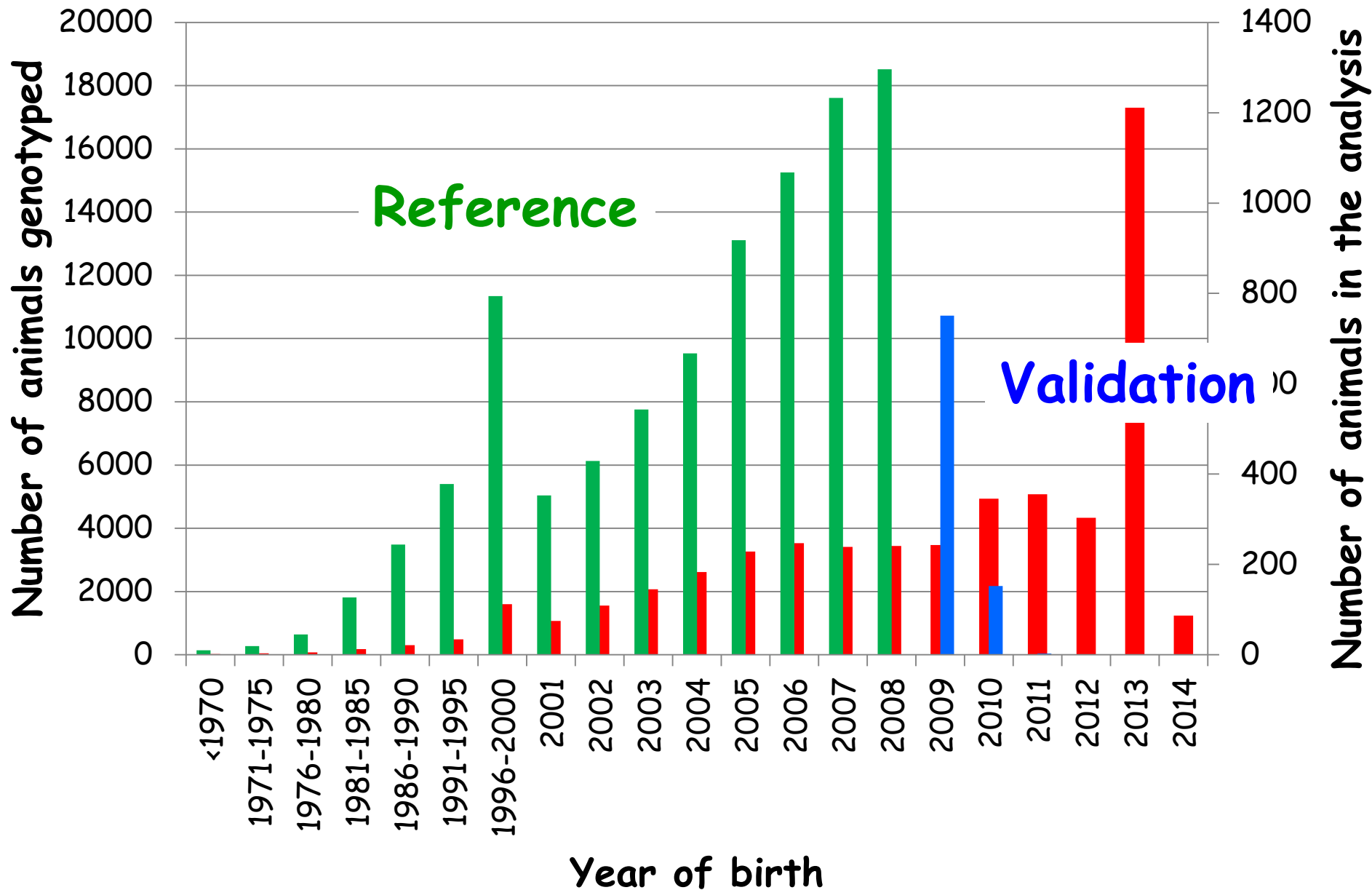
**Genotyping
the minority
breeds in
the coming
weeks**

Genomic predictions

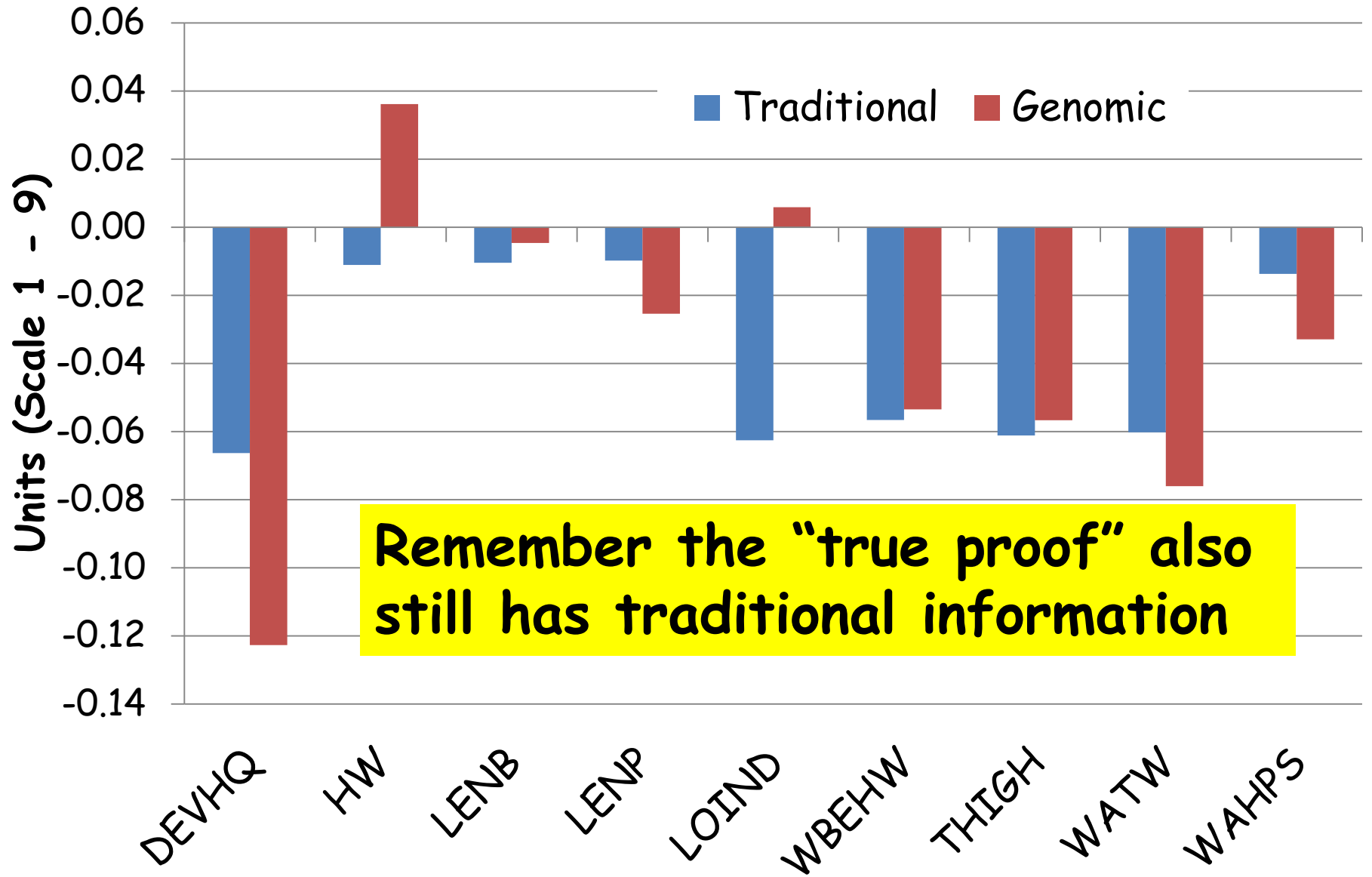
Genotyped animals



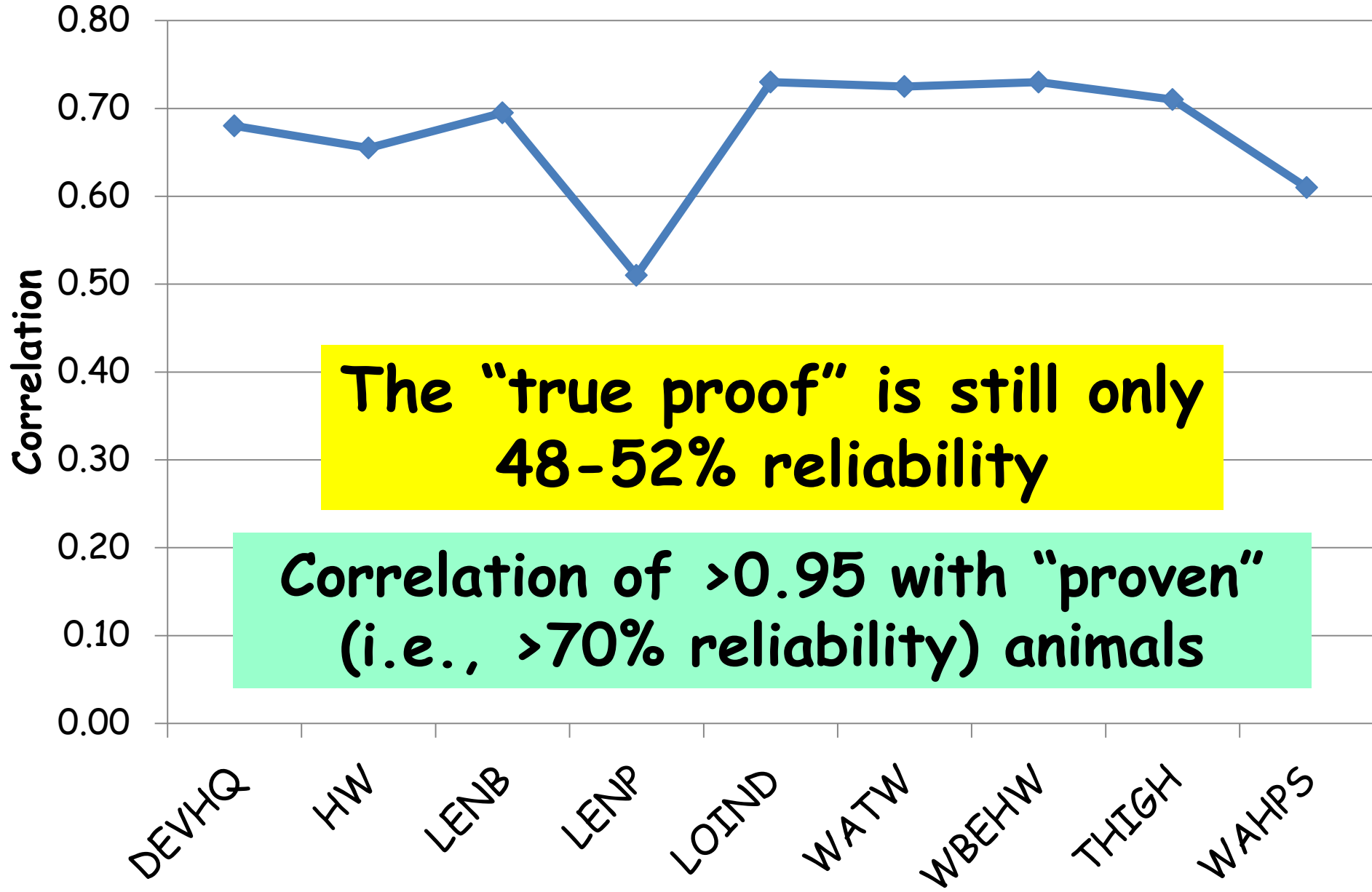
Genotyped animals



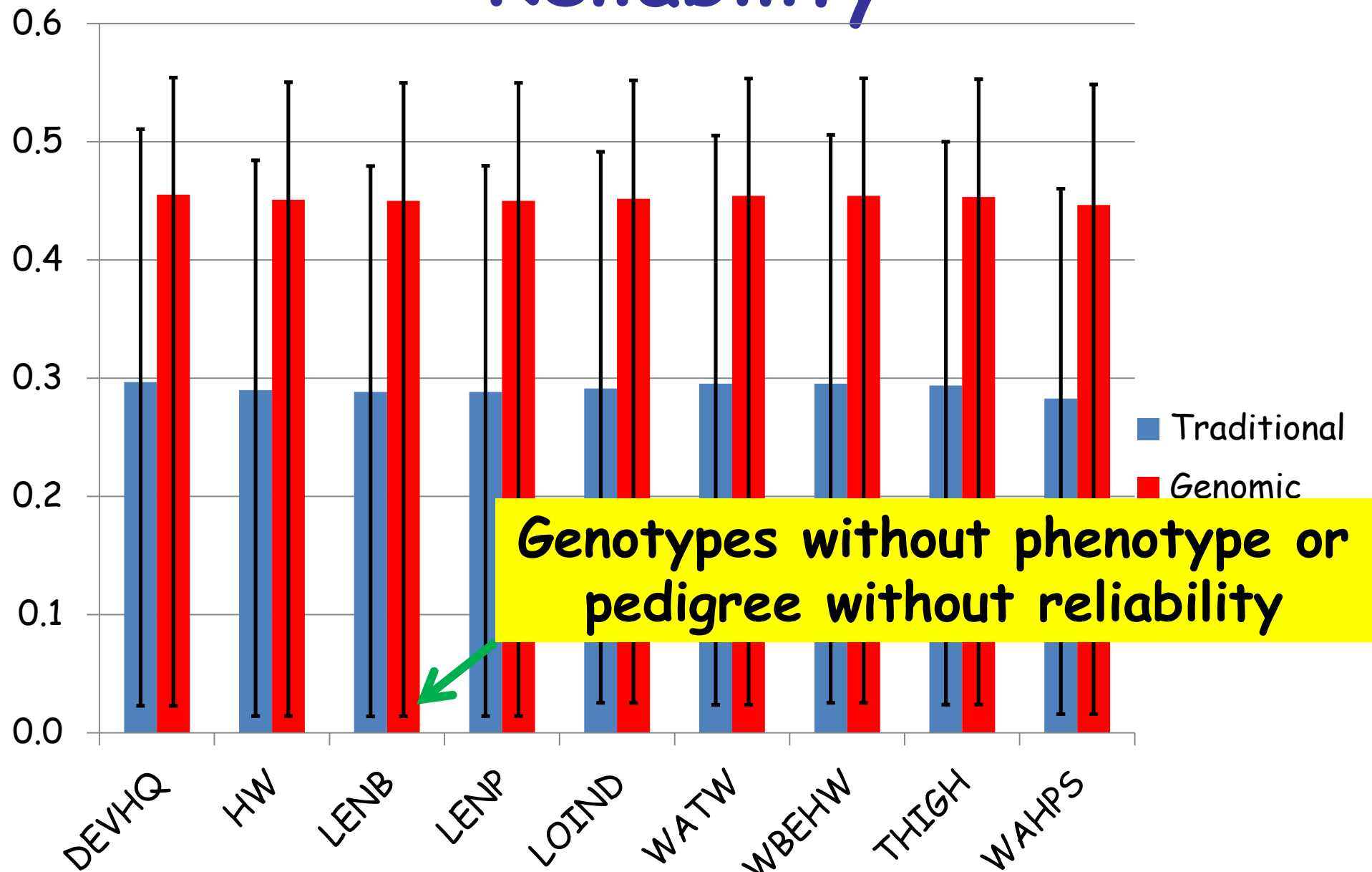
Mean Bias



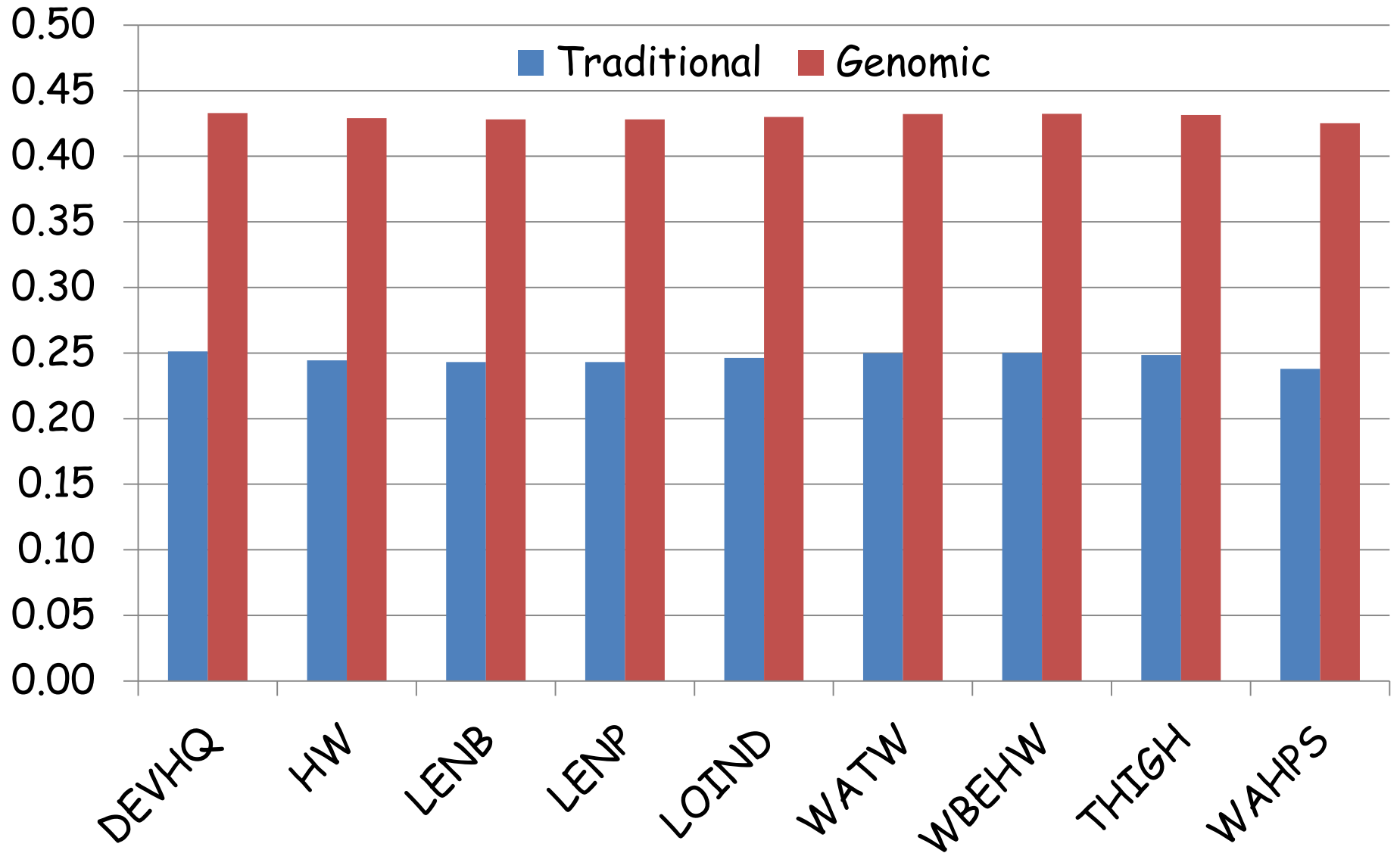
Correlation



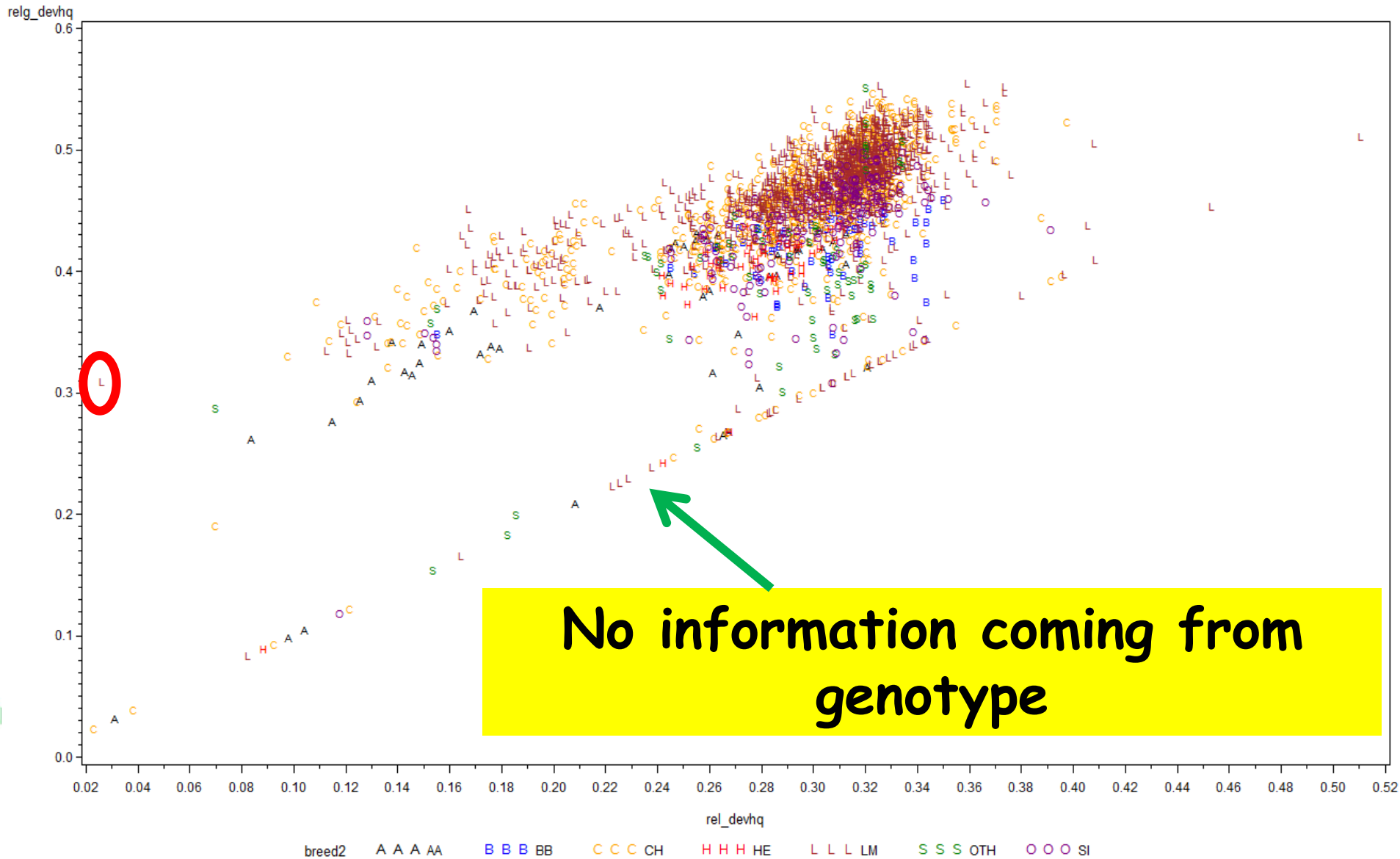
Reliability



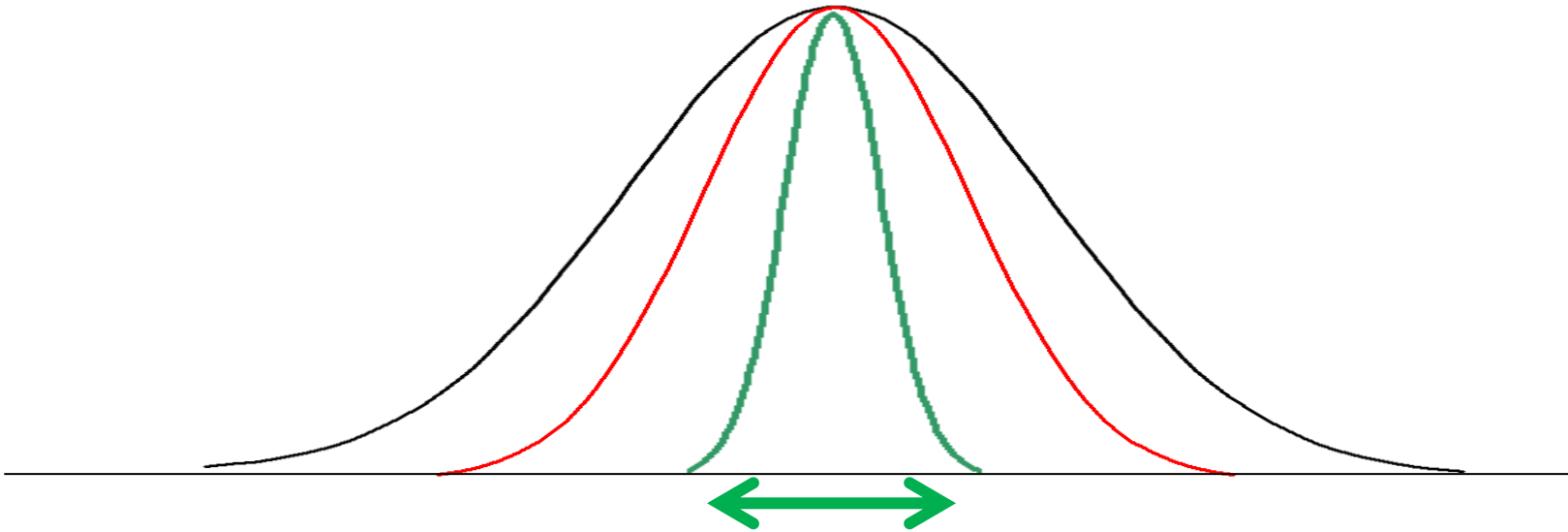
Reliability - 2013 calves (no records)



Reliability



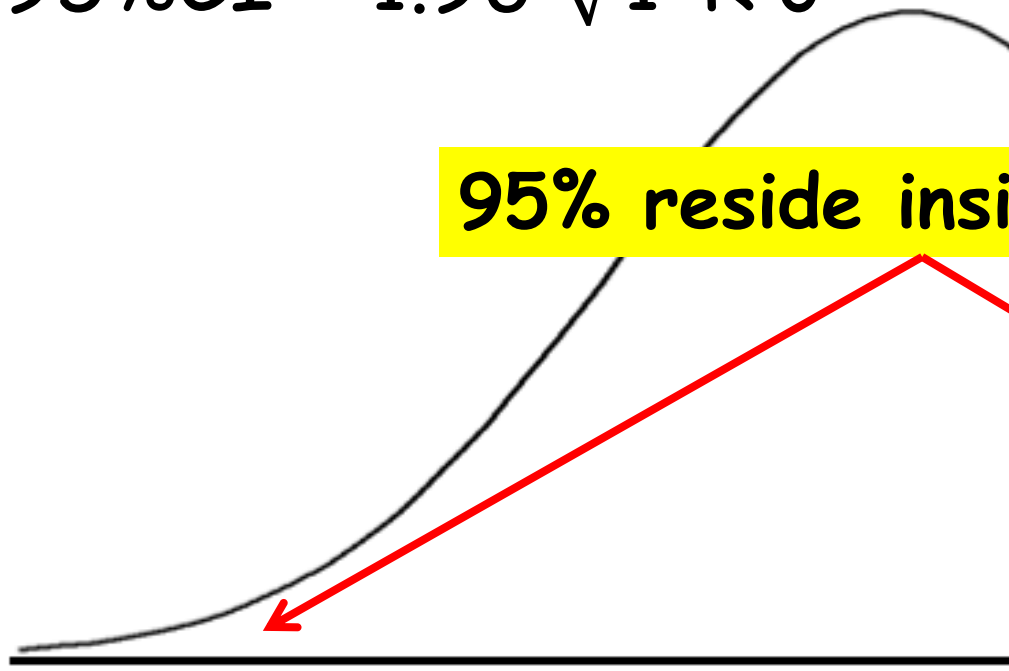
Reliability



Proof likely to move less with time

Reliability

$$95\%CI = 1.96 \sqrt{1-R} \cdot \sigma$$



Trait	Proportion >95% CI
DEVHQ	1.03
HW	2.40
LENB	2.05
LENP	7.68
LOIND	2.70
WBEHW	0.19
THIGH	3.12
WATW	0.49
WAHPS	3.99

Bull movements with records (HqDev)

		Traditional			Sum
		Down	Stay	Up	
Genomic	Down	0.22	0.54	0.24	1.00
	Stay	0.19	0.48	0.34	1.00
	Up	0.14	0.49	0.37	1.00

Of the animals that genomic predictions said would improve relative to parental average, 14% got worse, 49% stayed the "same" and 37% went up

Almost 3 times more likely to increase than decrease

Bull movements with records (Loin Dev.)

		Traditional			Sum
		Down	Stay	Up	
Genomic	Down	0.26	0.46	0.29	1.00
	Stay	0.17	0.48	0.35	1.00
	Up	0.15	0.46	0.39	1.00

Almost 3 times more likely to increase
than decrease

Bull movements with records (length of Back)

		Traditional			Sum
		Down	Stay	Up	
Genomic	Down	0.29	0.42	0.29	1.00
	Stay	0.25	0.49	0.26	1.00
	Up	0.19	0.46	0.34	1.00

Almost 2 times more likely to increase
than decrease

Conclusions

- Little or no bias in genetic evaluations
 - No over-prediction of genetic merit of young animals
- Good lift in reliability
 - 29% → 45%
 - 0.5% increase for proven animals
- Good (early) indicator of animals likely to increase in genetic merit with time

Acknowledgements

- Research Stimulus Fund - MultiGS
- Breed societies, AI stations and farmers
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