

EVALUATION OF GENOMIC PREDICTIONS: THE WEIGHT TRAIT PROJECT

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Adoption of Genomic Predictions

- AAA, with others quickly following
- Efficacy of this technology is not binary
- The adoption of this must be centered on the gain in EPD accuracy
 - ▣ This is related to the proportion of genetic variation explained by a MBV
 - ▣ This is equal to the squared genetic correlation

Questions Remain

- What are reasonable expectations for 50K based genomic predictions?
- What proportion of genetic variance can we explain if a breed specific MBV is used in another breed?
- Can we pool breeds together in training and predict in purebred populations?
- What impact does the relationship between training and validation have on the accuracy of 50K predictions?



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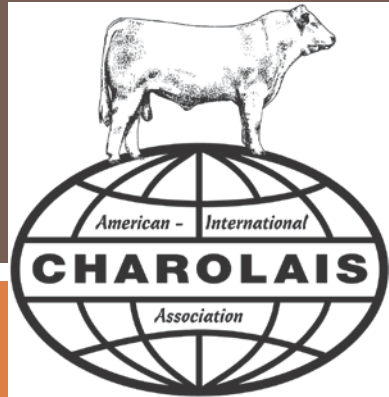
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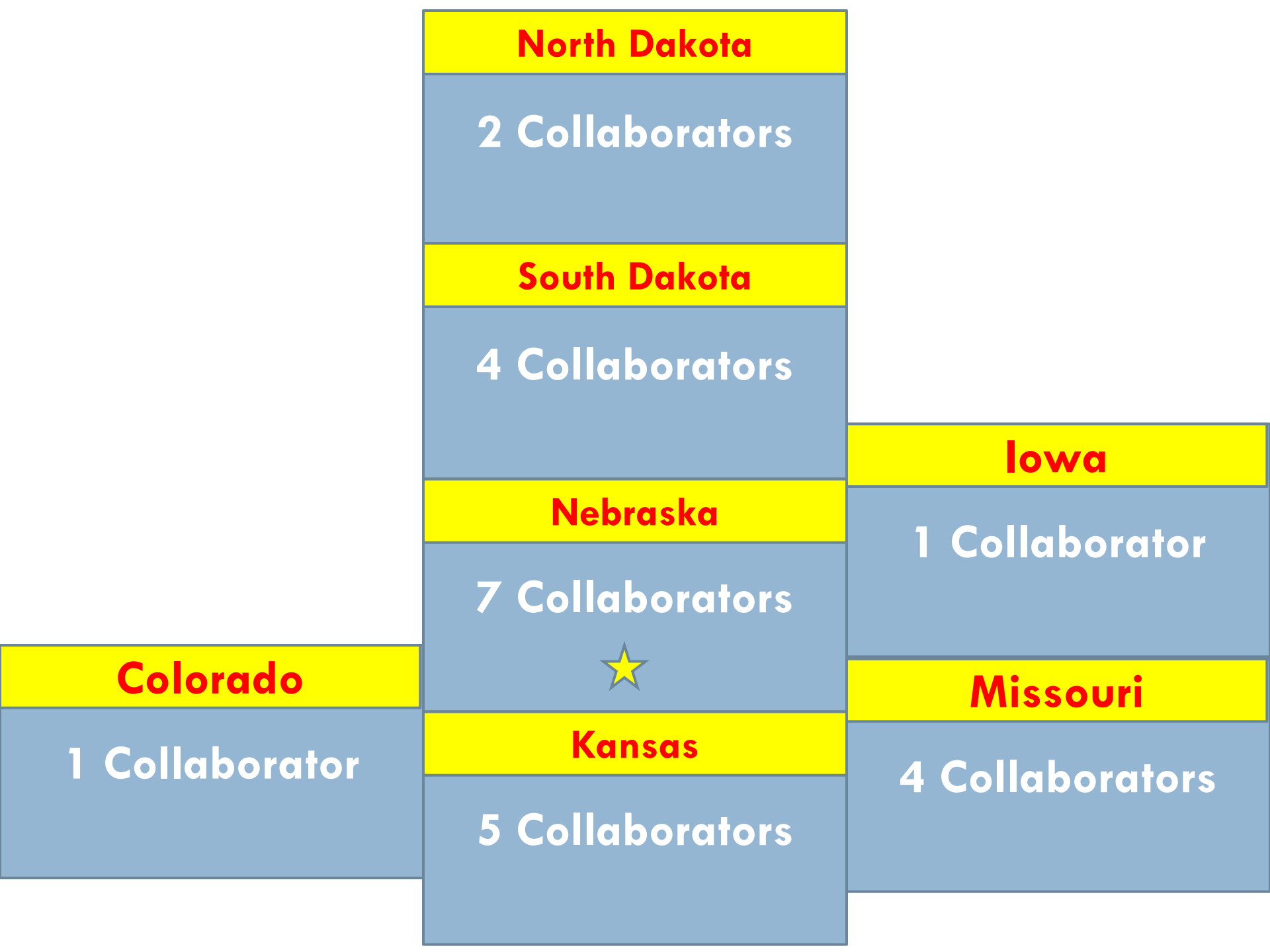
NDSU



Building Better Beef...
Red Angus



ANGUS
 THE BUSINESS BREED



North Dakota

2 Collaborators

South Dakota

4 Collaborators

Nebraska

7 Collaborators



Kansas

5 Collaborators

Colorado

1 Collaborator

Iowa

1 Collaborator

Missouri

4 Collaborators

Process



$$MBV = \sum_{i=1}^s x_i \hat{\beta}_i$$

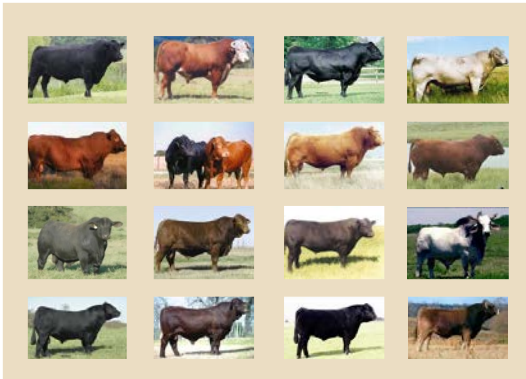
Weight Trait Project Population

Producer owned herd bulls
genotyped with the 50K (~300)

This population is continuing to
grow!



Types of Discovery Populations



- Purebreds of a Single Breed
- Purebreds of Multiple Breeds
- Crossbreds

Purebred

- AN, HH, and LM
- Utilized all available genotypes in ISU database
- Genomic predictions were trained using deregressed EBV

Pooled Composite

- Combined AN, AR, HH, LM, and SM
- All available genotypes from these breeds in ISU database
- Genomic predictions were trained using deregressed EBV with effect of breed in the model

2,000 Bull Project: Number of Sires Sampled



• Angus 402



• Hereford 317



• Simmental 253



• Red Angus 173



• Gelbvieh 136



• Limousin 131



• Charolais 125



• Shorthorn 86



• Brangus 68



• Beefmaster 64



• Maine-Anjou 59



• Brahman 53



• Chiangus 47



• Santa Gertrudis 43



• Salers 42



• Braunvieh 27

Total =2026
1834 Used In Training

Germ Plasm Evaluation

- Cycle VII at MARC
- Composite cattle
 - 16 breeds
 - AN, AR, and HH = 57%
 - 8 breeds < 1%
- Genomic predictions trained using adjusted phenotypes and effect of breed in the model

Training and Validation Populations

	T	T	T	T	E	E	E	E
	2KBULL	GPE (%)	PED	GS	2KBULL	GPE	PED	GS
AN	373	27.8	2,739	3,604	760	891	962	97
AR	143	6.6	89	178	50	95	139	50
CH	103	6.6	0	0	31	56	81	31
GV	113	7.1	0	0	23	70	129	23
HH	463	23.2	1,038	1,184	104	169	185	39
LM	104	7.2	1,696	2,275	500	548	599	20
SM	231	8.2	276	430	38	117	182	28

Analysis

- MBV fitted as a correlated trait
 - Per Kachman (2008)
 - Same process as AAA
 - Focused on WW (direct) and YW

Training and Evaluation Sets

- Training
 - 2K Bull
 - GPE
 - 5 Breed Pooled
 - Breed Specific
- Evaluation
 - 7 breeds, pedigrees from WTP
 - PED=All animals in WTP pedigrees excluded from training
 - GS=Only WTP sires excluded from training

Heritability for WW and TW

Breed	WW h ²	YW h ²
Angus	0.26 (.03)	0.27 (0.04)
Hereford	0.21 (0.05)	0.34 (.10)
Red Angus	0.34 (0.04)	0,28 (0.05)
Charolais	0.13 (0.03)	0.29 (0.04)
Gelbvieh	0.19 (0.03)	0.18 (0.04)
Limousin	0.38 (0.04)	0.50 (0.06)
Simmental	0.30 (0.04)	0.20 (0.05)

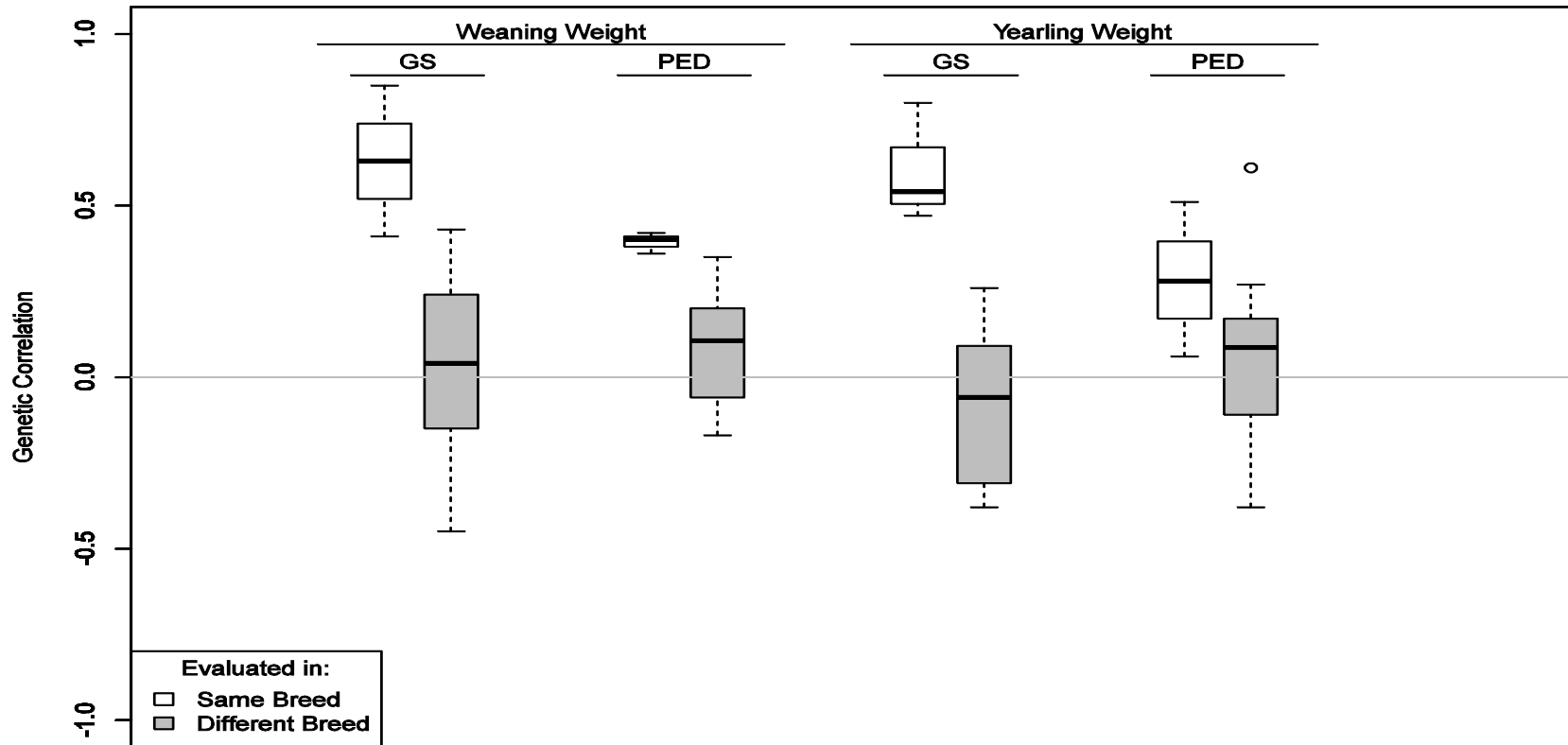
Within Breed-PED

	AAA_WW	AHA_WW	NALF_WW	AAA_YW	AHA_YW	NALF_YW
AN	0.24±0.14	0.16±0.14	-0.09±0.15	0.40±0.14	0.28±0.14	-0.29±0.15
AR	0.04±0.28	-0.05±0.30	-0.49±0.21	-0.04±0.29	-0.24±0.31	-0.29±0.29
CH	-0.28±0.25	-0.29±0.23	0.30±0.25	-0.14±0.22	-0.37±0.23	0.54±0.23
GV	0.19±0.30	0.33±0.27	-0.20±0.26	0.44±0.27	0.00±0.31	0.31±0.29
HH	0.66±0.27	0.47±0.31	0.24±0.33	0.04±0.44	-0.74±0.31	0.14±0.44
LM	-0.09±0.32	0.38±0.29	0.31±0.29	-0.42±0.27	0.28±0.30	0.14±0.29
SM	-0.21±0.28	0.42±0.27	-0.18±0.29	-0.07±0.32	0.09±0.35	0.00±0.36

Within Breed Trained-GS

	AAA_WW	AHA_WW	NALF_WW	AAA_YW	AHA_YW	NALF_YW
AN	0.41±0.13	0.14±0.14	-0.15±0.14	0.54±0.13	0.26±0.14	-0.20±0.15
AR	0.28±0.27	0.00±0.30	-0.45±0.22	-0.36±0.28	-0.17±0.32	-0.31±0.27
CH	-0.11±0.28	-0.24±0.25	0.11±0.29	-0.10±0.28	-0.35±0.23	0.22±0.27
GV	0.43±0.21	0.39±0.24	-0.23±0.25	0.09±0.32	0.05±0.31	0.00±0.30
HH	0.35±0.35	0.85±0.20	0.24±0.30	-0.37±0.36	0.47±0.40	0.26±0.41
LM	-0.15±0.33	0.18±0.37	0.63±0.19	-0.38±0.26	0.20±0.32	0.80±0.17
SM	-0.25±0.29	0.08±0.30	-0.10±0.31	0.00±0.32	-0.02±0.35	-0.12±0.34

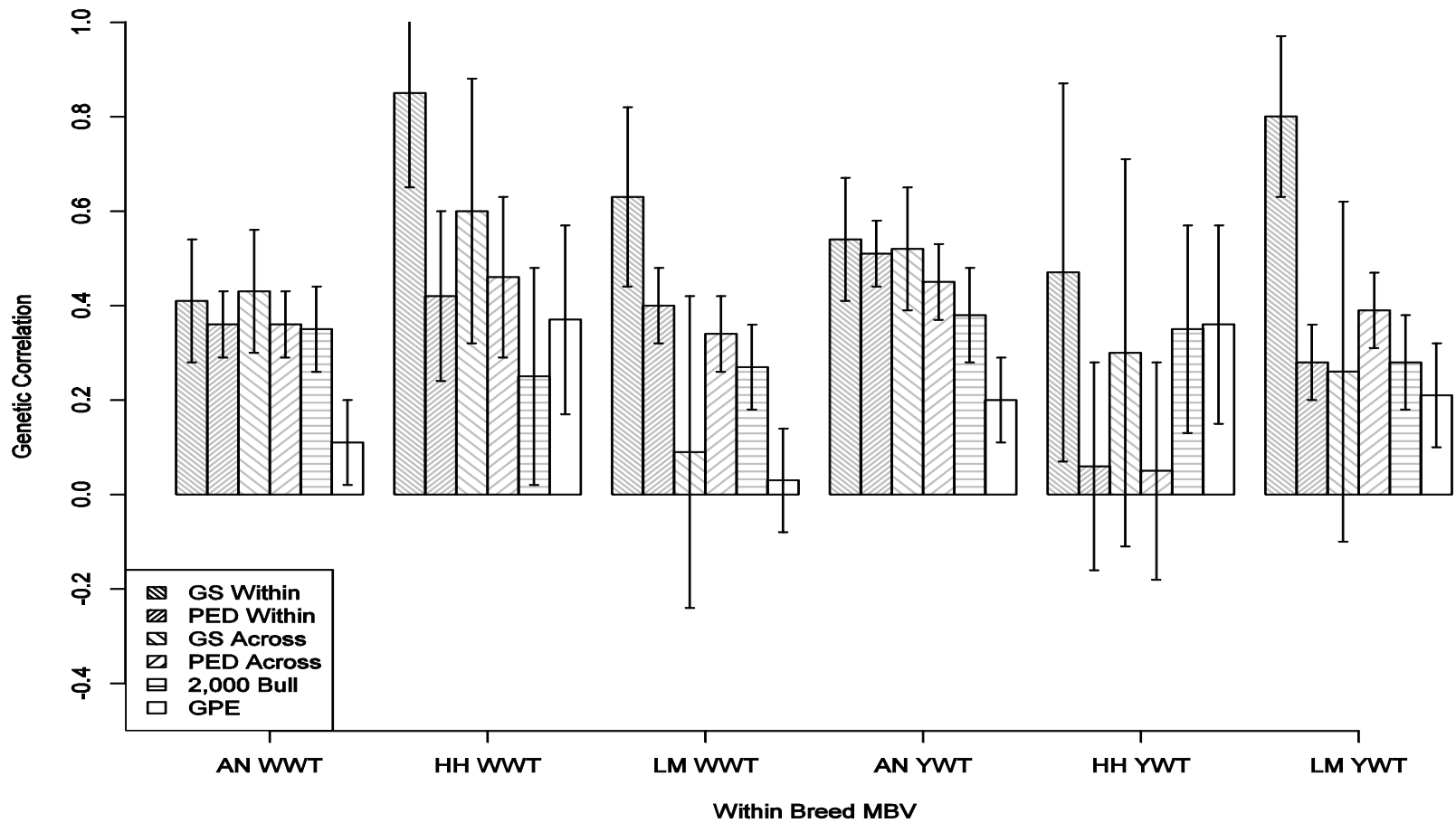
Within Breed



Across Breed Trained

	2KBUL L	GPE	PED	GS	2KBUL L	GPE	PED	GS
AN	0.35±0.09	0.11±0.09	0.36±0.07	0.43±0.13	0.38±0.10	0.20±0.09	0.45±0.08	0.52±0.13
AR	-0.14±0.26	0.23±0.20	0.33±0.14	0.55±0.21	-0.40±0.26	0.17±0.20	-0.03±0.17	-0.12±0.28
CH	0.24±0.20	-0.32±0.19	0.06±0.19	-0.13±0.24	0.00±0.27	0.01±0.20	-0.02±0.18	-0.18±0.24
GV	0.56±0.20	0.09±0.20	0.47±0.12	0.52±0.20	0.59±0.26	0.14±0.24	0.21±0.16	-0.07±0.31
HH	0.25±0.23	0.37±0.20	0.46±0.17	0.60±0.28	0.35±0.22	0.36±0.21	0.05±0.23	0.30±0.41
LM	0.27±0.09	0.03±0.11	0.34±0.08	0.09±0.33	0.28±0.10	0.21±0.11	0.39±0.08	0.26±0.36
SM	0.32±0.21	0.35±0.15	0.11±0.14	0.15±0.28	0.69±0.23	0.43±0.21	0.09±0.17	0.49±0.29

All Sets



Conclusions

- Within-breed 50K genomic predictions work
- Relationship to training is important
- These are not robust across breeds
 - ▣ Works best in the breed it was trained
- Across-breed trained predictions can add accuracy
 - ▣ Target breed should be included in training

Team

- Garry Bennett
- Larry Kuehn
- John Pollak
- Warren Snelling
- Mark Thallman

- Kathy Hanford
- Steve Kachman