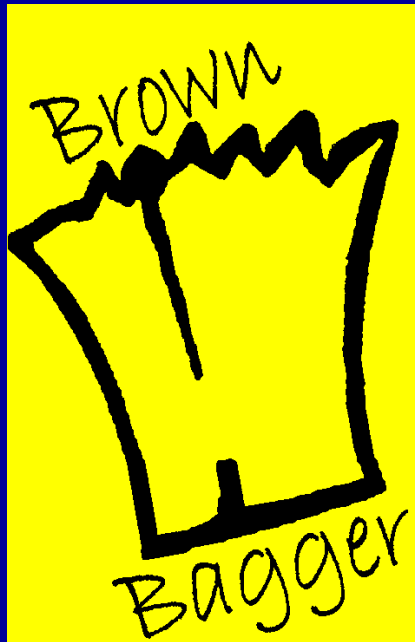




Session 4 – Part 1

Status update on genomically enhanced genetic evaluation by breeds



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Past Status=Confusion

	CE	BW	WW	YW	MCE	MM	MWW
Adj.		90	700	1320			
Ratio		101	107				
EPD	9	-1.0	25	49	3	11	23
Acc	.29	.37	.30	.27	.18	.19	.23

	YG	Marb	BF	REA
Adj.		4.65%	.23	12.5
Ratio		106	100	95
EPD	.21	.44	.05	-.39
Acc	.32	.31	.33	.34

REA	TEND	MARB
7	6	8

Merger of All Information

◆ American Simmental Association

➤ Tenderness

◆ American Angus Association

➤ “Correlated Trait Approach”—Kachman (2008)

➤ Made widely known by MacNeil (2010)

Adoption of Genomic Predictions

- ◆ **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 Molecular Breeding Values (MBV; Result of DNA Test)**
 - **% GV = squared genetic correlation**

Tremendous First Step

- ◆ **Simplification**
- ◆ **Conceptually appealing**
- ◆ **Fit current NCE**
- ◆ **Information benefits more than just the genotyped animal**
- ◆ **Multiple companies increases complexity**
- ◆ **Assumes MBV predicts all animals equally as well**

Other Breeds Made An Investment

- ◆ Existing projects helped as a starting platform
 - 2,000 Bull Project
 - University of Missouri
 - Weight Trait Project

Paradigm SHIFT

- ◆ **Other breeds sought help from the NBCEC (Garrick) in training**
- ◆ **Process now largely moved back to companies/breed associations**

Current Methods

- ◆ **All different themes on the Two-Step Approach**
- ◆ **Why?**
 - **Method of inclusion dependent on NCE provider (and software)**
 - **Initially, genotypes were unavailable**
 - **Fear of computational (and storage) demands**

Current Status

Breed	No. Anim	LD Impute	Provider	Method
Angus	160,000	Y	GS, Z	CORR
Red Angus	13,700	Y	GS, Z	BLEND
Hereford	15,780	Y	GS	BLEND-Ext.
Simmental	10,800	Y	GS	BLEND
Limousin	5,660	Y	GS	BLEND
Gelbvieh	3,880	Y	GS	BLEND
Charolais	2,136	N	GS	CORR
Santa Gertrudis	3,160	N	GS	SS-GBLUP
Brangus	3,909	Y	GS, Z	SS-GBLUP



Correlated Trait

- ◆ Similar to what has been done before, but now we include MBV

$$\begin{array}{rcll} Y_{MBV} & X_1\beta_1 & Z_1u_1 & e_1 \\ Y_{IMF} & = X_2\beta_2 & + Z_2u_2 & + e_2 \\ Y_{MARB} & X_3\beta_3 & Z_3u_3 & e_3 \end{array}$$

MacNeil et al., 2010

Variable Accuracy

- ◆ **American Simmental Association attempted this**
- ◆ **Logical philosophy**
- ◆ **Relationship differences between target animals and training animals**

“Blending”

- ◆ **Post evaluation indexing of EPD and MBV**
- ◆ **Benefits only genotyped animals**
- ◆ **Simplicity**
- ◆ **Fits within framework of NCE**
- ◆ **Must “blend” correctly...**

Blending

- ◆ Assumes base is set zero
- ◆ If not, need to adjust both EBV and MBV for differences in base

$$EBV_1 = \frac{1-R_i^2}{1-r_g^2 R_i^2} MBV_i + \frac{1-r_g^2}{1-r_g^2 R_i^2} EBV_i$$

Threshold Traits Are Different

Trait	N	NBCEC Prediction Observed Scale Genetic Correlation	NBCEC Prediction Underlying Scale Genetic Correlation
Calving Ease Maternal	170	0.458	0.679 (0.058)
Calving Ease Direct	176	0.479	0.588 (0.067)
Heifer Pregnancy	64	0.616	0.610 (0.124)
Stayability	104	0.801	0.787 (0.118)

Kachman and Spangler, 2013



Future Status

Breed	No. Anim	LD Impute	Provider	Method
Angus	160,000	Y	GS, Z	SS
Red Angus	13,700	Y	GS, Z	SS
Hereford	15,780	Y	GS	SS
Simmental	10,800	Y	GS	SS
Limousin	5,660	Y	GS	SS
Gelbvieh	3,880	Y	GS	SS
Charolais	2,136	N	GS	SS
Santa Gertrudis	3,160	N	GS	SS
Brangus	3,909	Y	GS, Z	SS

Single Step (s)

◆ **Two fundamental camps**

➤ UGA, ssGBLUP—Misztal

➤ Theta Solutions/ISU, ss“Hybrid”—
Fernando, Garrick, Golden

◆ **One difference is in the weighting of individual markers**

Lourenco et al., 2015 JAS

Fernando et al., 2014, GSE



Unaccounted for bias

- ◆ **Training sets represent a selected subset**
 - Problem erodes overtime with more genotyped animals and dynamic training
 - **When $N > p$**
 - Problems likely most notable for traits that are hallmarks of the breed

Moving forward

- ◆ **We have made tremendous progress**
- ◆ **More work to do**
- ◆ **Evolutions in:**
 - **Methodology**
 - **NCE platforms**
 - **Cannot continue to make genomics “fit”**
 - **Opportunity to rebuild instead of patch**
 - **Continuous NCE**



Understanding

◆ Collection of phenotypes

- Retraining efforts
- Increase in accuracy above what genomics can do

Moving Forward-novel traits

- ◆ **Training will occur on phenotypes (not deregressed EBV)**
- ◆ **Expense of data collection could reasonably lead to highly selected training sets**
- ◆ **Inference becomes challenging**
- ◆ **Bias could become a real issue**
- ◆ **Multiple trait models could help**

Summary

- ◆ **Phenotypes are still critical to collect**
- ◆ **Methods for lower cost genotyping are evolving**
- ◆ **Breeds must build training populations to capitalize**
- ◆ **Genomic information has the potential to increase accuracy**
 - **Proportional to %GV**
 - **Impacts inversely related to prior EPD accuracy**