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## Optimizing Traditional and Marker Assisted Evaluation

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## National Cattle Evaluation

- Genetic evaluation is conducted (inter)nationally on breed-specific basis
  - EPD are generally not comparable across breeds
  - For any breed, NCE systems contain both common and novel traits
- Methods for EPD prediction are mature
  - National cattle evaluation (NCE) systems have been in place for more than 2 decades
  - We have validated the correspondence between expected and realized progeny differences
  - Genetic trend shows pervasive industry and producer uptake of EPD technology
  - New traits for NCE follow the framework for economic relevance
- EPD are the "sum" of small, additive genetic effects
  - To some extent, EPD are a genetic "black box"

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## Properties of NCE Traits

Desirable property	Good examples	Poor examples
Direct effect on revenue or cost	Feed intake, carcass yield	Birth weight, scrotal
Easily and cheaply measured	Weight	Feed intake, carcass merit
Stable genetic parameters	Weight rate	Fertility
High data density	Growth rate	Feed intake, carcass merit
Few genetic antagonisms	(few)	(most)
Measured early in life	Pre-yearling traits	Longevity, mature size
EPD are user friendly	Weight	Calving ease, stayability
High genetic variance	Growth rate	Carcass yield
Several indicators	Carcass merit, fertility	Longevity

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## Genetic Evaluation/NCE in the "-omics" Era

- There is tremendous interest in identifying *major genes* which explain EPD
  - Models are still developing, but most partition EPD into marker and polygenic effects
  - The "information package" should rely on industry familiarity with EPD/accuracy
- Marker assisted evaluation has large potential benefits for NCE accuracy
  - Young sires
  - Traits that are difficult and costly to measure
- Focus on the *optimal combination of marker and phenotypic data*
  - Recognize the importance of phenotypic data, and incorporate marker information
  - Methods to better allow for utilization of high-density SNP marker chips
  - Desirable approaches for animals with only phenotypic or only marker data

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## "Traditional" NCE

$$y = Xb + Zu + e \implies \begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + \Lambda^{-1}\lambda \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{u} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$

## Marker Assisted NCE (MA-BLUP?)

$$y = Xb + \{Zu + Wg\} + e \implies \begin{bmatrix} X'X & X'Z & X'W \\ Z'X & Z'Z + \Lambda^{-1}\lambda & Z'W \\ W'X & W'Z & W'W + M^{-1}\mu \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{u} \\ \hat{g} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \\ W'y \end{bmatrix}$$

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## Data Density, Polygenic Heritability, and Accuracy

### Deciding for Marker Assisted Evaluation

**Phenomic** cost/value decisions underlying marker assisted evaluation (MAE)

- **MAE will be beneficial for ERT where:**
  - Phenotypic data collection is costly and time-consuming, or is likely to never exist
  - Few or no indicator traits have been/ can be identified
  - Genetic variance attributable to "marker set" is at least *moderate*
  - Cost of genotyping is justifiable
- **Some candidates have been identified**
  - Feed intake and efficiency
  - Fertility
  - Disease resistance
  - Palatability and meat composition



### Feed Intake as an Example

- **Feed intake is clearly a cost-side ERT**
  - Feed and supplementation account for >65% of non-fixed production costs
- **Intake and efficiency have complex intercorrelations with other ERT**
  - Growth rate, mature size, and body composition are all directly related to intake
  - Must be considered within the context of multiple trait selection
- **Traditional evaluation of feed utilization has progressed slowly**
  - Data collection cost exceeds \$150 per head
  - Very low data density at the population or breed level
  - Expression of intake/efficiency (e.g., RFI) forces few indicators
  - Polygenic architecture is well known and stable, but NCE are still prototypical

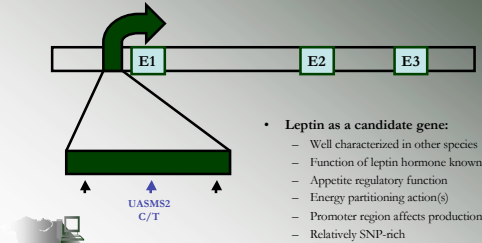


### Feed Intake as an ERT

Desirable property	Intake:	Comments:
Direct effect on revenue or cost	Yes	Major production cost
Easily and cheaply measured	No	~\$150 per head
Stable genetic parameters	Yes	$h^2 = 0.40$ in most studies
High data density	No	Infrastructure is sparse
Few genetic antagonisms	Can be forced	Independent of anything as RFI
Measured early in life	Relatively	Near yearling ages is common
EPD are user friendly	Sort of...	Remember negative is better
High genetic variance	Yes	$\pm 3$ lb DM per day is genetic
Several indicators	Yes, but...	Consider antagonisms



### Leptin: Intake/Efficiency Candidate Gene



- **Leptin as a candidate gene:**
  - Well characterized in other species
  - Function of leptin hormone known
  - Appetite regulatory function
  - Energy partitioning action(s)
  - Promoter region affects production
  - Relatively SNP-rich



### UASMS2 in Angus and Charolais

1. Genotype and allele frequencies by breed

Breed	n	CC	CT	TT	f(C)	f(T)	HWE
Angus	451	234	182	35	0.721	0.279	Yes
Charolais	413	319	90	4	0.881	0.119	Yes

2. DM intake and RFI means by genotype and breed

Breed	DM Intake			RFI		
	CC	CT	TT	CC	CT	TT
Angus	7.15	7.20	7.50	-0.015	-0.006	0.094
Charolais	7.74 a	7.58 b	6.49 a	0.052 a	-0.142 b	-0.983 c



### UASMS2 Marker Breeding Value (Charolais)

Breed	DM Intake			RFI		
	CC	CT	TT	CC	CT	TT
Scaled Mean	0.625	0.465	-0.625	0.518	0.324	-0.518
MBV	0.065	-0.207	-0.478	0.065	-0.207	-0.478

- Total additive genetic variance =  $V(p)h^2 = (0.56)(0.40) = 0.224$
- Additive genetic variance attributable to UASMS2 =  $2pq\alpha = 0.0154$
- UASMS2 accounts for <5% of the genetic variance in intake =  $d$

Not enough alone!



### Multiple Markers on SNP Panels

- Commercial SNP panels are now available for intake, RFI and other traits
  - Built from multiple validated SNP markers as a set
  - Marker breeding value (MBV) computed based on genotypes/haplotypes
  - Growing evidence that panels will be population (breed) specific to some degree
- High density SNP genotyping platforms are now in use
  - 10K SNP
  - 50K SNP
  - 300K SNP
- There are still issues with deriving MBV from high density "chips"
  - Information overload?
  - How much will be informative?



### Genomic Breeding Value (GBV)

- Genomic breeding value (GBV) combines EPD and MBV
  - $GBV = I = b_1m + b_2u$  where  $m = MBV$  and  $u = \text{polygenic BV}$
- Optimal combination depends on:
  - Polygenic breeding value (EPD) accuracy ( $r^2$ )
  - Genetic variance attributable to the marker set ( $d$ )
- Gain in evaluation accuracy due to adding marker information:
  - Increases with increasing  $d$
  - Decreases with increasing polygenic accuracy
  - Could be significant for animals with no phenotypic data:  $GBV \approx m$
  - Will be essentially zero for old animals (founders?) with no marker data



### MAE: Implementation and Adoption

- Increasing the contribution of markers to evaluation accuracy
  - Low polygenic accuracy ( $r < 50\%$ )
  - High predictive power of the marker set ( $d > 10\%$ )
- Industry adoption will largely depend on genotyping cost
  - For beef producers, threshold genotyping costs will likely be less than \$100
- Marker validation and calibration must be an ongoing exercise
  - Marker effects are likely to change under selection
- Information packaging is important
  - Independent selection for MBV (marker "score") and EPD can be antagonistic



### GBV Information Packaging

Sire XYZ  
Bull ABC ————  
Dam ABC

Which is correct ?

CED	BWT	WWT	YWT	MLK	TMAT	SCR	LMY	MARB
-3.5	+6.8	+35.2	+96.5	-4.5	+13.1	+0.9	0.0	-1.3
76	82	77	80	63		76	72	72
2	5	85	95	35		55	50	18

PRO<sup>®</sup> Marbling : +5



### GBV Information Packaging, 2

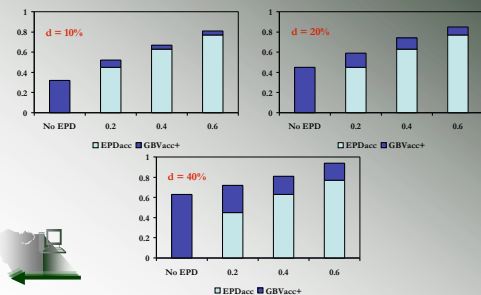
Sire KLM  
Bull DEF ————  
Dam DEF

CED	BWT	WWT	YWT	MLK	TMAT	SCR	LMY	MARB
+7.5	-0.2	+35.2	+76.5	+1.5	+19.1	+2.5	+0.6	+1.3
76	82	77	80	63		76	72	72
82	85	85	75	50		85	40	92

PRO<sup>®</sup> Marbling : 0



### Increasing Accuracy with MAE



### Some Final Thoughts

- **Marker assisted evaluation of ERT in beef cattle needs continued development**
  - Marker sets must be (re)validated
  - Marker panels will likely be specific (breeds, traits, etc.)
- **Evaluation using markers will impact some traits more than others**
  - Don't bother with growth
  - Time- and cost-intensive phenotypes have larger potential benefits with MAE
  - Traits for which no phenotypes will be available are good candidates for MAE
- **Cost versus benefit decisions must be made**
  - Investment in phenotyping
  - Cost of genotyping



Thanks.

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