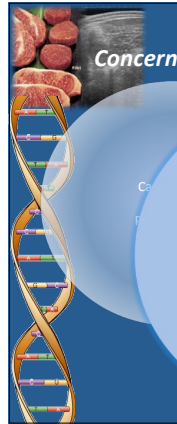


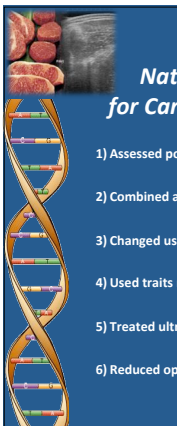
## Evolution of National Cattle Evaluation for Carcass Traits in Angus

Michael MacNeil, USDA Agricultural Research Service  
Miles City, Montana  
and  
Sally Northcutt, American Angus Association  
St. Joseph, Missouri



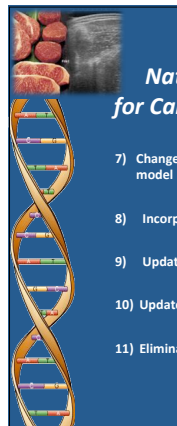
## Concerns voiced by Angus breeders

Carcass Evaluation



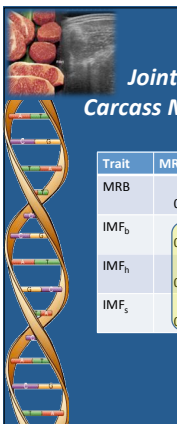
## National Cattle Evaluation for Carcass Traits of Angus Cattle

- 1) Assessed potential data integrity and structure issues
- 2) Combined analysis of data collected using ultrasound and at harvest
- 3) Changed use of data collected from steers using ultrasound
- 4) Used traits recorded via ultrasound as indicators of carcass merit
- 5) Treated ultrasound data from bulls, helpers, and steers as separate traits
- 6) Reduced opportunity for selection to bias the evaluation



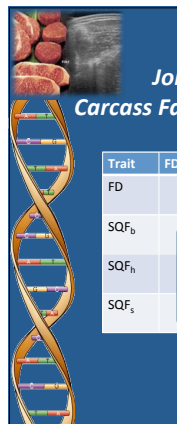
## National Cattle Evaluation for Carcass Traits of Angus Cattle

- 7) Changed analysis of carcass traits from sire model to animal model
- 8) Incorporated deeper pedigree
- 9) Updated estimates of genetic parameters
- 10) Updated calculation of accuracy values
- 11) Eliminated use of Interim EPD with weekly NCE



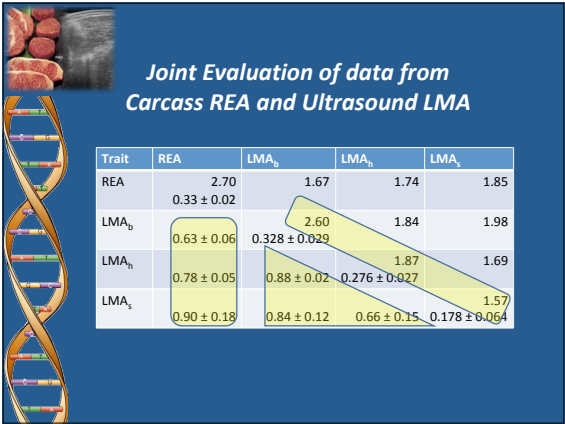
## Joint Evaluation of data from Carcass Marbling and Ultrasound IMF

Trait	MRB	IMF <sub>b</sub>	IMF <sub>h</sub>	IMF <sub>s</sub>
MRB	0.3456 0.45 ± 0.03	0.1620	0.1676	0.2482
IMF <sub>b</sub>	0.66 ± 0.05	0.1764 0.38 ± 0.03	0.2059	0.1911
IMF <sub>h</sub>	0.52 ± 0.06	0.89 ± 0.02	0.3040 0.40 ± 0.03	0.2640
IMF <sub>s</sub>	0.84 ± 0.12	0.90 ± 0.11	0.95 ± 0.08	0.2545 0.26 ± 0.09



## Joint Evaluation of data from Carcass Fat Depth and Ultrasound Sub-Q Fat

Trait	FD	SQF <sub>b</sub>	SQF <sub>h</sub>	SQF <sub>s</sub>
FD	0.0486 0.34 ± 0.02	0.01291	0.01314	0.02231
SQF <sub>b</sub>	0.53 ± 0.06	0.0120 0.39 ± 0.03	0.01043	0.01025
SQF <sub>h</sub>	0.55 ± 0.06	0.88 ± 0.02	0.0117 0.46 ± 0.04	0.00801
SQF <sub>s</sub>	0.90 ± 0.11	0.84 ± 0.12	0.66 ± 0.15	0.0125 0.26 ± 0.08



### Adding Molecular Breeding Values (MBV)

- MBV was developed using 1,710 Angus bulls born from 1955 to 2003 and genotyped with the Illumina BovineSNP50 assay
- MBV were multi-marker compound covariate prediction equations (Tukey, 1993), with covariates defined by for each marker's coded genotype and weights corresponding to allele substitution effects

### Adding Molecular Breeding Values (MBV)

Thallman (2004) envisioned incorporating MBV into NCE  
 Kachman (2008) envisioned use of MBV as correlated traits

42,493 records on the carcass traits  
 Ultrasound image data from 82,985 bulls and 66,907 heifers  
 1900 MBV from bulls, distinct from those used in development

4 generation pedigree

Variance components estimated using ASREML v3

### Adding MBV

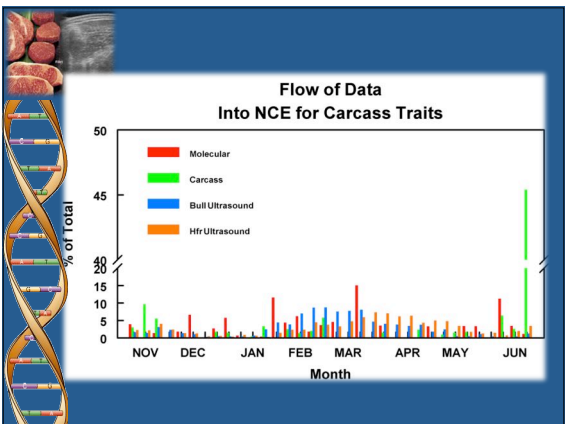
Heritability estimates for MBV → 1

Genetic correlations with targeted carcass traits were:

Carcass wt.	0.54±0.04
Longissimus Area	0.58±0.04
Sub-Q fat depth	0.50±0.04
Marbling score	0.65±0.03

Genetic correlations with indicator traits measured with ultrasound were:

	Bulls	Heifers
Scan wt	0.34±0.03	0.36±0.04
Longissimus Area	0.40±0.03	0.47±0.04
Sub-Q fat depth	0.20±0.03	0.29±0.04
Marbling	0.38±0.03	0.43±0.04



### Summary

Ultrasound and MBV are currently useful indicators of economically relevant traits in Angus cattle

To date, high accuracy EPD continue to require the collection of phenotypic data

Phenotypic data is important for the periodic re-evaluation of MBV as LD between tested SNP and targeted loci changes

Constant stream of data flowing into carcass trait evaluations and myriad of different possible incremental inputs warrants continuous evaluation