Selection Enhanced Estimates of Marker Effects on Means and Variances of Beef Tenderness

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Outline

- Background
- CAPN1 and CAST Effects on Means
  - Interaction
  - Mode of inheritance
    - Additive
    - Dominance
- CAST Effects on Residual Variance
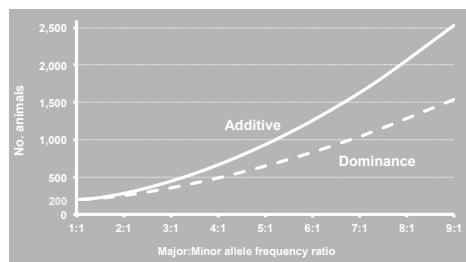
Background

- Minor allele frequencies effect estimation of genetic marker effects
  - Several early studies removed rare homozygotes from analysis
- Multiple markers had been associated with the same trait (beef tenderness)
  - Interactions between markers?
- Markers with amino acid changes assumed to have biological basis
  - Effects assumed be more consistent across populations

Background

- Initial genetic markers generally carcass oriented
- Industry application requires knowledge of effects on non-target traits
  - Weights / performance
  - Heifer fertility
  - Cow longevity
- Interest in mode of inheritance
  - Additive
  - Dominance

Number of animals needed to produce equal additive and dominance estimation variances at different major:minor allele frequency ratios

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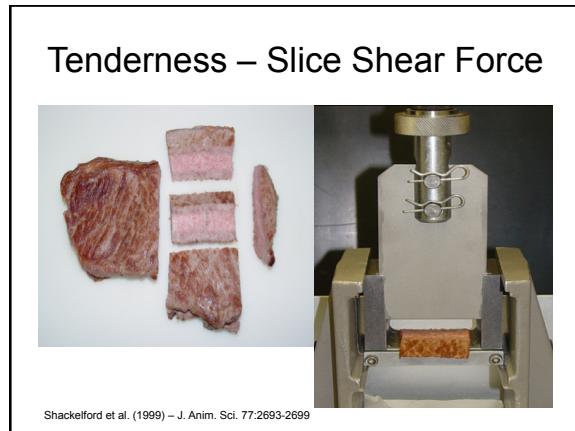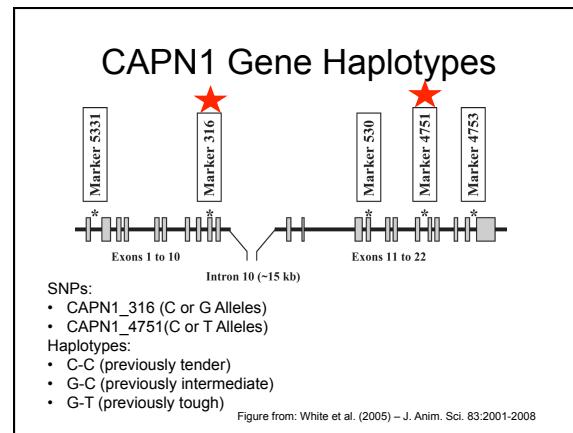
Marker Assisted Selection - Population Resources

- Four populations (Initiated ~2005):
  - MARC I
 - MARC II
  - MARC III
  - Angus

MAS SNP Markers

Marker	Anticipated Effect	Traits
CAPN1_316	Exonic – Amino Acid change	Tenderness
CAPN1_4751	Intronic (haplotypes w/ 316 most consistent results)	Tenderness
CAST	Near gene	Tenderness
GDF8	Exonic – Amino Acid change	% Retail Product / Protein Accretion
TG	Near gene	Marbling
DGAT1	Exonic – Amino Acid change	Milk Composition / Marbling
CSN1S1	Near gene	Fat / Milk Composition
GHR	Exonic – Amino Acid change	BW / % Retail Product

Base Marker Ratios

Markers	Populations			
	MARC I	MARC II	Angus	MARC III
CAPN1 (316-4751 CC:GT:CG)	2:2:5	1:2:2	2:1:1	2:4:3
CAST (T:C)	32:1	5:1	13:1	13:1
DGAT1 (A:K)	3:1	12:1	5:1	4:1
Myostatin (GDF8 F94L, F:L)	4:1	1:0	1:0	1:0
TG (C:T)	3:1	3:1	2:1	5:1
CSN1S1 (C:G)	19:1	3:1	1:0	8:1
GHR (A:T)	8:1	1:0	5:1	34:1

Selection / Evaluation Plan
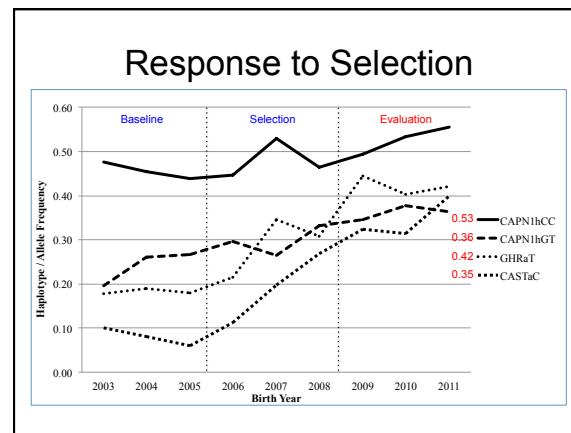
Population	Birth year								
	2004	2005	2006	2007	2008	2009	2010	2011	2012
MARC I	Sel	Sel	Sel	Eval	Eval	Eval			
MARC II	Base	Base	Sel	Sel	Eval	Eval	Eval		
Angus	Base	Base	Sel	Sel	Sel	Eval	Eval	Eval	
MARC III	Base	Base	Sel	Sel	Sel	Sel	Eval	Eval	Eval

CAPN1 Gene Haplotypes

SNPs:
- CAPN1_316 (C or G Alleles)
- CAPN1_4751(C or T Alleles)

Haplotypes:
- C-C (previously tender)
- G-C (previously intermediate)
- G-T (previously tough)

Figure from: White et al. (2005) – J. Anim. Sci. 83:2001-2008

Tenderness – Slice Shear Force

Shackelford et al. (1999) – J. Anim. Sci. 77:2693-2699

Angus Steers

μ-Calpain, calpastatin, and growth hormone receptor genetic effects on preweaning performance, carcass quality traits, and residual variance of tenderness in Angus cattle selected to increase minor haplotype and allele frequencies

Tait et al.
JAS (2014) 92:456-466

Response to Selection

Angus Steer Traits
(n = 199)

Trait	Mean	SD
Final BW, lb	1250.6	95.1
Dressing percent, %	61.6	1.7
Hot carcass weight, lb	771.3	67.0
Adjusted fat thickness, in	0.61	0.17
Marbling score[1]	5.67	0.85
LM area, sq. in	11.31	0.95
Vision yield grade	3.77	0.65
Slice shear force, kg	11.94	2.39
VISNIR predicted shear force, kg	13.03	1.65

[1] 4.00 = Slight00; 5.00 = Small00; 6.00 = Modest00

Statistical Analysis

- MTDFREML
  - Animal model
  - 7,433 animals in pedigree
  - Effects:
    - Year
    - Age of dam (2,3,4,5+)
    - Animal age, d
    - Marker Genotype (CAPN1, CAST, GHR)
   - Animal, additive genetic effect ($0.20 \leq h^2 \leq 0.70$)
    - Error
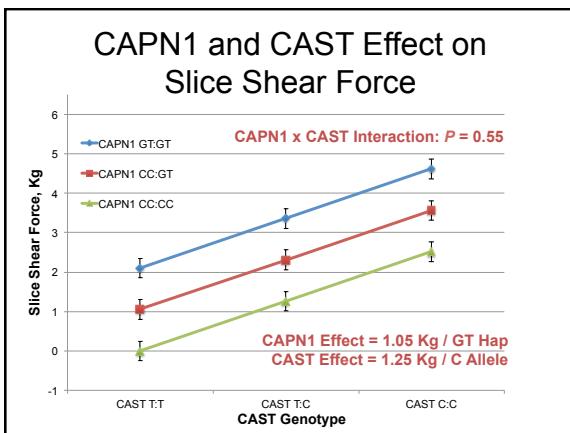
Significance of Markers
(*P*-Values)

Trait	CAPN1	CAST	h^2
Final BW, kg	0.33	0.48	0.24
Dressing percent, %	0.43	0.24	0.35
Hot carcass weight, kg	0.57	0.31	0.22
Adjusted fat thickness, mm	0.59	0.06	0.26
Marbling score[1]	0.31	0.91	0.26
LM area, sq. cm	0.69	0.16	0.70[2]
Vision yield grade	0.77	**0.02**	0.37
Slice shear force, kg	**<0.001**	**<0.001**	0.32
VISNIR predicted shear force, kg	0.53	0.16	0.20[2]

[1] 4.00 = Slight00; 5.00 = Small00; 6.00 = Modest00
[2] Constrained to $0.20 \leq h^2 \leq 0.70$
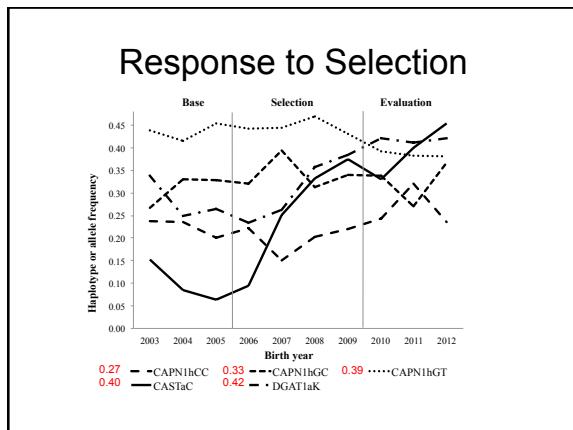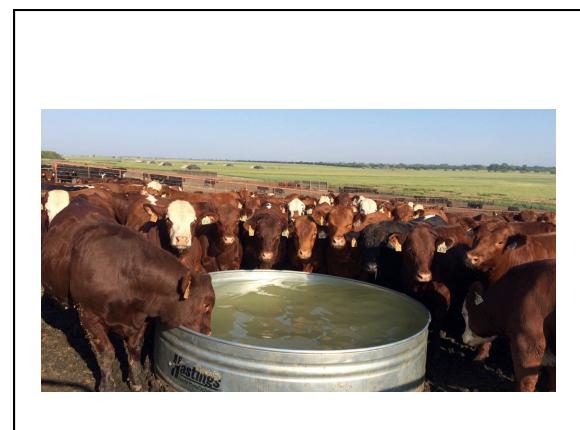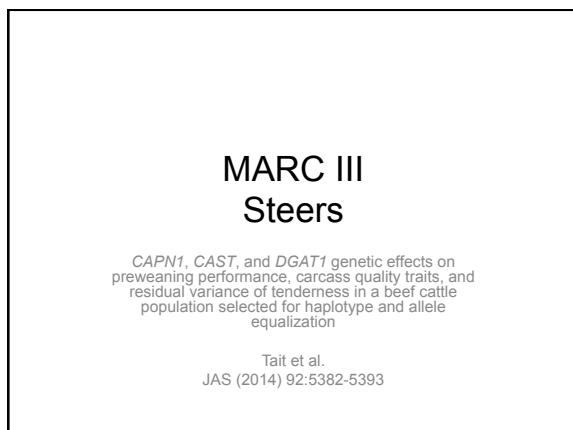
Is There Dominance?

Trait	CAPN1 Additive	CAPN1 Dominance	CAST Additive	CAST Dominance
Slice Shear Force, *P*-values	**< 0.01**	0.19	**< 0.001**	0.43

## CAPN1 and CAST Effect on Slice Shear Force

Angus Steer Conclusions

- CAPN1 and CAST effect SSF
  - Both are additive
  - No interaction

MARC III Steers

CAPN1, CAST, and *DGAT1* genetic effects on preweaning performance, carcass quality traits, and residual variance of tenderness in a beef cattle population selected for haplotype and allele equalization

Tait et al.
JAS (2014) 92:5382-5393

Response to Selection

MARC III Steer Traits
(n = 254)

Trait	Mean	SD
Final BW, lb	1259.6	107.7
Dressing percent, %	62.3	2.1
Hot carcass weight, lb	785.7	75.6
Adjusted fat thickness, in	0.53	0.17
Marbling score[1]	5.38	0.70
LM area, sq. in	12.65	1.14
Vision yield grade	3.18	0.68
Slice shear force, kg	14.95	4.59
VISNIR predicted shear force, kg	14.42	1.81

[1] 4.00 = Slight[00]; 5.00 = Small[00]; 6.00 = Modest[00]

Statistical Analysis
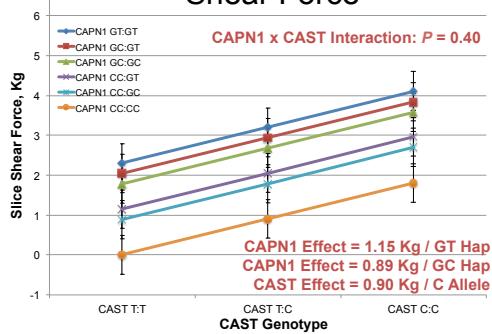
- MTDFREML
  - Animal model
  - 1,505 animals in pedigree
  - Effects:
    - Year
    - Age of dam (2,3,4,5+)
    - Animal age, d
    - Marker Genotype (CAPN1, CAST, DGAT1)
    - Animal, additive genetic effect ($0.20 \leq h^2 \leq 0.70$)
    - Error

Significance of Markers
(*P*-Values)

Trait	CAPN1	CAST	h²
Final BW, kg	0.44	0.63	0.20^2
Dressing percent, %	0.52	0.79	0.51
Hot carcass weight, kg	0.71	0.52	0.20^2
Adjusted fat thickness, mm	0.65	0.14	0.38
Marbling score[1]	0.73	0.12	0.52
LM area, sq. cm	0.35	0.31	0.28
Vision yield grade	0.46	0.20	0.55
Slice shear force, kg	0.12	< 0.01	0.22
VISNIR predicted shear force, kg	0.85	0.01	0.20^2

[1] 4.00 = Slight[00]; 5.00 = Small[00]; 6.00 = Modest[00]
[2] Constrained to $0.20 \leq h^2 \leq 0.70$

CAPN1 and CAST Effect on Slice Shear Force


MARC III Steer Conclusions
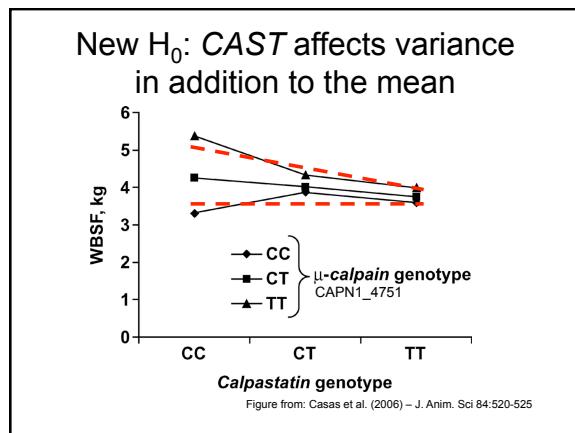
- Tendencies Similar to Angus
  - CAPN1 Extreme Haplotype Differences
  - CAPN1 GC Haplotype intermediate to CC and GT Haplotypes
- CAPN1 and CAST effect SSF
  - Both are additive
  - No interaction

New Effect of CAST on Beef Tenderness Variation

Reported within
Angus and MARC III Steer papers

Selection for Tenderness Markers

- *CAST* genotype and *CAPN1* haplotype

- Original Experimental Hypotheses:
  - Mode of inheritance
  - Effect size
  - Interaction

New H$_0$: *CAST* affects variance in addition to the mean

Figure from: Casas et al. (2006) – J. Anim. Sci 84:520-525

Testing Effects on Variance

- Tested both CAPN1 and CAST

- Specialized analysis method:
  - Genotype specific residual variance vs.
  - Standard single residual variance

Trait Means

Trait	Angus	MARC III
Harvested steers, n	199	254
14 day Slice Shear Force, kg	11.94 (SD = 2.39)	14.95 (SD = 4.59)
h^2	0.32 ± 0.22	0.22 ± 0.16
CAST, T allele freq.	0.683	0.650
CAST, C allele freq.	0.317	0.350
CAPN1, CC haplotype freq.	0.623	0.268
CAPN1, GC haplotype freq.	Not selected	0.331
CAPN1, GT haplotype freq.	0.377	0.401
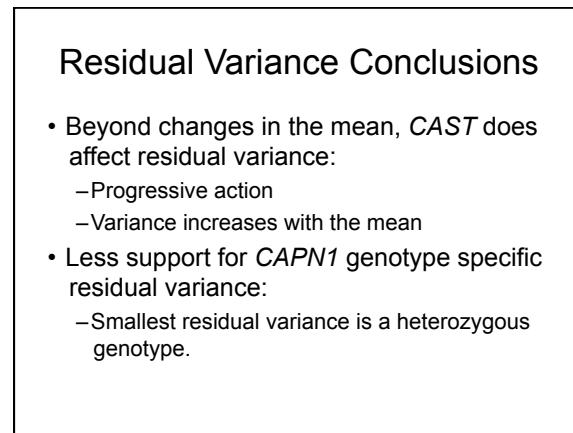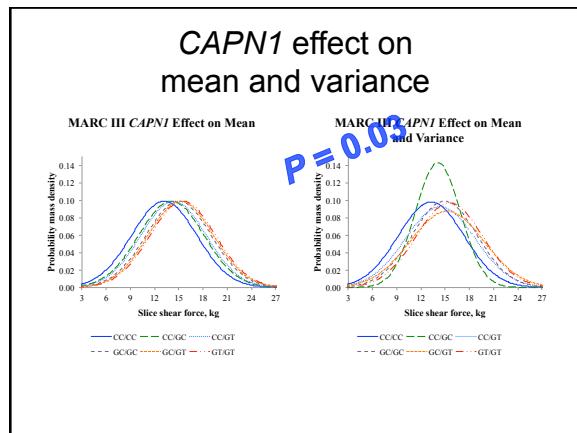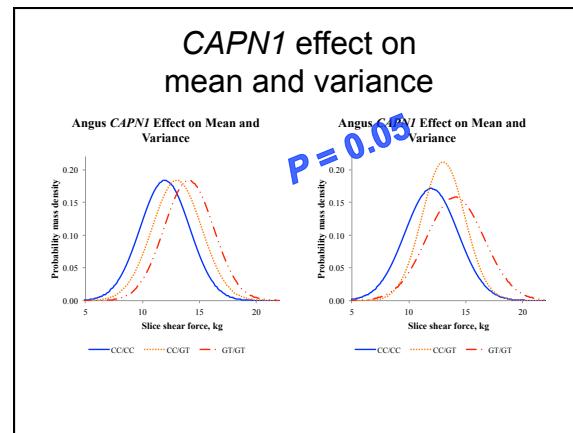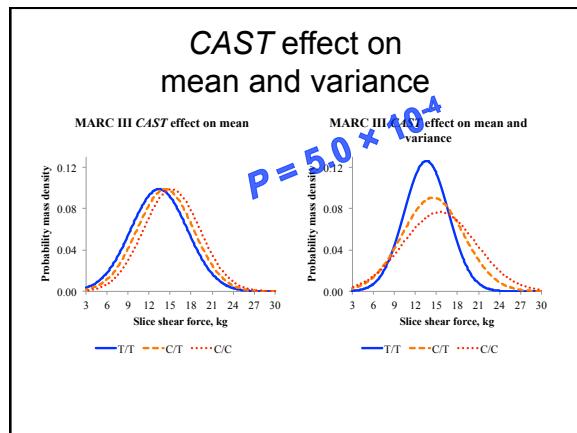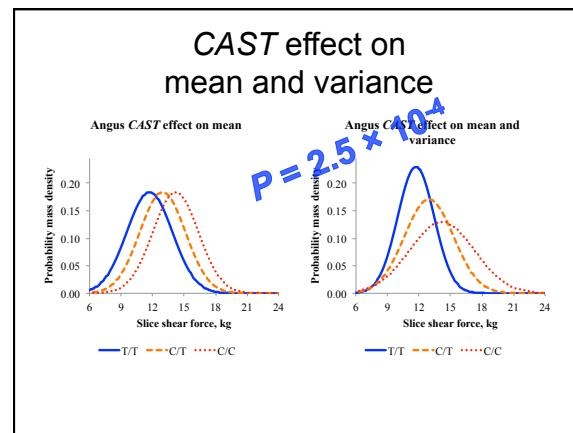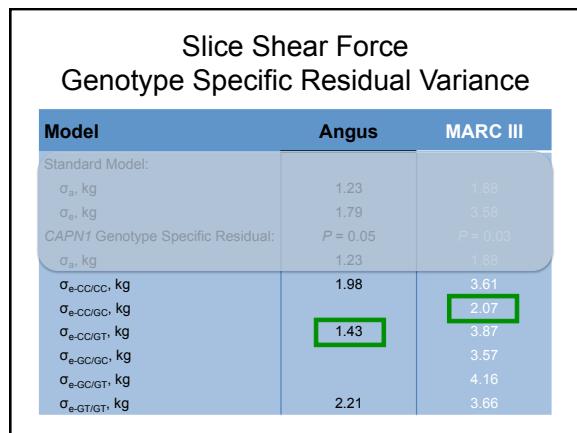
Evaluation Steer Genotypes, %

| *CAST* Genotypes						
	ANGUS			MARC III		
CAPN1 Diplotypes	TT	CT	CC	TT	CT	CC
CC:CC	13.6	20.6	4.5	2.4	5.1	0.4
CC:GC	-	-	-	8.3	9.1	2.4
CC:GT	25.6	16.1	5.5	6.7	10.6	0.8
GC:GC	-	-	-	3.9	5.9	1.2
GC:GT	-	-	-	11.8	10.2	2.4
GT:GT	8.5	4.5	1.0	6.7	9.5	2.8

## Statistical Analysis – Genotype Specific Residual Variance

- SAS
  - PROC INBREED calculate relationships
    - Full 5 gen pedigree again
  - Extract relationships amongst animals with phenotypes
    - Multiply relationships by σ_a^2 and provide via GDATA option to MIXED analysis
  - PROC MIXED analysis:
    - Single residual variance (standard model)
    - Genotype specific residual variance (REPEATED = Genotype option)
  - Likelihood Ratio Test (Genotype specific residual variance)

Slice Shear Force Genotype Specific Residual Variance

Model	Angus	MARC III
Standard:		
σ_a, kg	1.23	1.88
σ_e, kg	1.79	3.58
CAST Genotype Specific Residual:	$P = 2.5 \times 10^{-4}$	$P = 5.0 \times 10^{-4}$
σ_a, kg	1.23	1.88
$\sigma_{e\text{-}T/T}$, kg	1.22	2.54
$\sigma_{e\text{-}C/T}$, kg	1.99	3.98
$\sigma_{e\text{-}C/C}$, kg	2.82	4.86

Slice Shear Force
Genotype Specific Residual Variance

Model	Angus	MARC III
Standard Model:		
σ_a, kg	1.23	1.88
σ_e, kg	1.79	3.58
CAPN1 Genotype Specific Residual:	$P = 0.05$	$P = 0.03$
σ_a, kg	1.23	1.88
$\sigma_{e\text{-CC/CC}}$, kg	1.98	3.61
$\sigma_{e\text{-CC/GC}}$, kg		2.07
$\sigma_{e\text{-CC/GT}}$, kg	1.43	3.87
$\sigma_{e\text{-GC/GC}}$, kg		3.57
$\sigma_{e\text{-GC/GT}}$, kg		4.16
$\sigma_{e\text{-GT/GT}}$, kg	2.21	3.66

CAST effect on mean and variance

$P = 2.5 \times 10^{-4}$

CAST effect on mean and variance

$P = 5.0 \times 10^{-4}$

CAPN1 effect on mean and variance

$P = 0.03$

CAPN1 effect on mean and variance

$P = 0.03$

Residual Variance Conclusions

- Beyond changes in the mean, *CAST* does affect residual variance:
  - Progressive action
  - Variance increases with the mean
- Less support for *CAPN1* genotype specific residual variance:
  - Smallest residual variance is a heterozygous genotype.

Overall Conclusions

- MAS populations provide a unique resource to investigate new effects of tenderness markers
  - Control of variance beyond changes in mean

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Cattle Operations
Cow-calf Management
Feedlot Management

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