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Implications of epigenetic influences for cattle breeding systems and genetic evaluation

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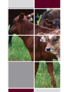
Beef Improvement Federation
44th Research Symposium and Annual Meeting

Improving Life through Science and Technology.

Research Partners



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What is "epigenetics?"

- Conrad H. Waddington (1905–1975) observed altered wing vein patterns in Drosophila pupae after they were treated with heat; the altered phenotype persisted in the population suggesting that exposure to an environmental factor during a critical developmental period could produce a changed phenotype that lasted a lifetime, and, was manifested in subsequent generations.

What is "epigenetics?"

- There are mechanisms that make cells, tissues and organs different in expression and function although the identical nature of the DNA in every cell in the body.
- These mechanisms are "inherited" through mitosis as new cells are formed.
- Non-coding RNAs, DNA methylation and histone modifications influence gene expression

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What is "epigenetics?"

- Early on the term epigenetics was used to describe the developmental events of an organism, but now represents genetic phenomena that do not follow a traditional (Mendelian) expression pattern.
- Heritable changes in gene expression (phenotype) that occur without alterations in DNA sequence.

What is "epigenetics?"

- The term imprinting has been used to describe gene loci where there is a different expression pattern of alleles inherited from the male parent vs. from the female parent.

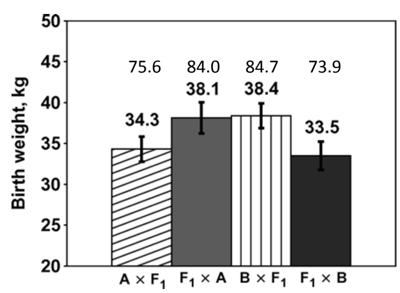
Some unusual aspects associated with *Bos indicus*-*Bos taurus* crosses

Average birth weights at the TAMU McGregor Station (1992-1997) produced through natural service

		Birth Weight (lb)		
Sire breed	Dam breed	bulls	heifers	average
Hereford	Hereford	80	76	78
Brahman	Brahman	74	71	72.5
Hereford	Brahman	75	73	74
Brahman	Hereford	101	87	94

Data reported by Sanders

Reciprocal differences in Angus-*Bos indicus* ET calves



Amen et al. (2007) J. Anim. Sci. 85:365-372.

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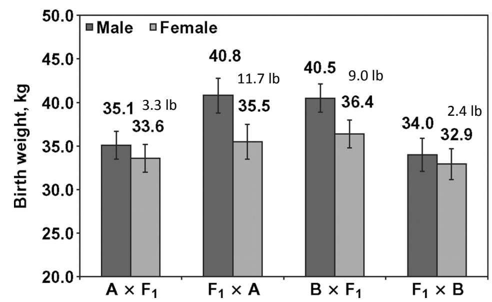

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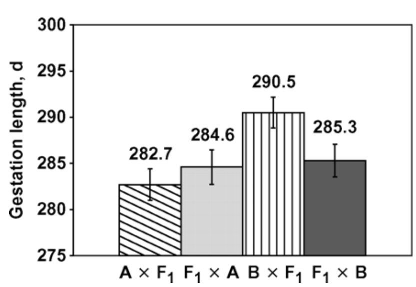

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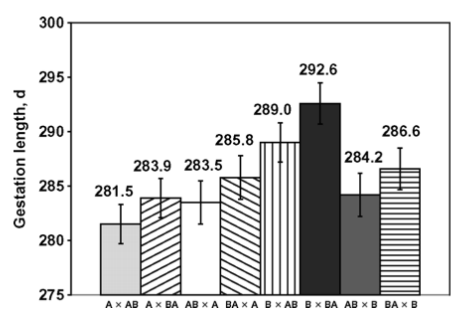

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Inconsistent Reports of Heterosis Retention

- Rendel (1980) reported very low (60.7%) calving rates in F_2 Brahman(B)-British (Hereford-Shorthorn) (referred to as BX) *versus* F_1 BX cows (81.2%), and later (MacKinnon et al., 1989) estimates of F_1, F_2, and F_n (F_3 and greater) BX cows were 16.4%, 5.2%, and 1.6%, respectively.

Inconsistent Reports of Heterosis Retention

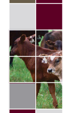
- Sanders et al. have found heterosis retention lower than expectations in F_2 Brahman-Angus females, and higher than expectations in F_2 Brahman-Hereford females.
- The level of heterosis may be related to the reciprocal type of the F_1 parents.
- F_1 BX females produced at the Belmont Research Station were also Brahman-sired (J.E. Frisch, personal communication).

Performance of reciprocal cross F_2 cows through 5 years of age at McGregor.

F_2 cow type	Calf crop born	Calf survival	BWT (lb)	WWT (lb)	Cow wt. (lb)
HB x HB	0.87	0.97	84.4	490	1085
BH x BH	0.74	0.81	92.3	487	1174
HB x BH	0.88	0.96	83.0	471	1049
BH x HB	0.83	0.79	90.3	494	1140

Wright, 2006 M.S. thesis, Texas A&M University

McGregor Genomics Project



Based on Nelore-Angus crosses

Cycle I	Cycle II	Cycle III
F_2 cattle embryo transfer and natural service cattle born – All F_1 parents Nelore-sired (NA).	Reciprocal F_2 cattle (all 4 types: NANA, NAAN, ANAN, ANNA) produced by natural service.	F_3 cattle produced through natural service breeding F_2 sons of two bulls to F_2 daughters of other two bulls and vice versa.
2003-2007	2009-2012	2009-2012

By 2013, should have over 700 cows in production.

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A report by Post and Reich (1980) from the Belmont station in Queensland, Australia reported potential differences in age of puberty for reciprocal F_2 Africander cross-Brahman cross matings (AXBX); females from Africander-British (AB)-sired bulls had earlier puberty onset than cows from Brahman-British (BA)-sired bulls.

Genotype	n	Age puberty (d)	Weight (kg)
ABAB	11	494	264
ABBA	8	508	279
BAAB	8	576	283
BABA	11	536	284

Simple means for birth weight (lb) among reciprocal Brahman-Hereford F_2 crosses

	F_1 Sire			
	BH		HB	
F_1 Dam	F	M	F	M
BH	70.3	80.9	69.5	79.8
HB	74.7	73.2	77.6	71.7
M - F diff.	10.6		10.4	
	-1.5		-6.0	

Boenig, 2011 M.S. thesis, Texas A&M University

Simple means for preweaning gain (lb) among reciprocal Brahman-Hereford F_2 crosses

	Sire			
	BH		HB	
Dam	F	M	F	M
BH	384.6	415.0	364.5	424.0
HB	396.0	415.2	397.1	394.0
M - F diff.	30.4		59.5	
	19.2		-3.1	

Boenig, 2011 M.S. thesis, Texas A&M University

There have been some reports where *Bos indicus* crossbred cattle have had less desirable temperament scores than purebred contemporary averages (negative heterosis).

Bonsma, J. 1975a. Judging cattle for functional efficiency. Beef Cattle Sci. Handb. 12:23-36 (cited by Grandin and Deesing, 2005).

Bonsma, J. 1975b. Crossbreeding for increased cattle production. Beef Cattle Sci. Handb. 12:37-49 (cited by Grandin and Deesing, 2005).

Grandin, T. and M. J. Deesing. 2005. Genetics and behavior during handling, restraint, and herding. Available at: http://www.grandin.com/references/cattle.during.handling.html. Accessed on March 15, 2005.

Riley, D. G., C. C. Chase, Jr., S. W. Coleman, R. D. Randel, and T. A. Olson. 2004. Assessment of temperament at weaning in calves produced from diallele matings of Angus, Brahman, and Romosinuano. J. Anim. Sci. 82(Suppl 1.):6(Abstr.).

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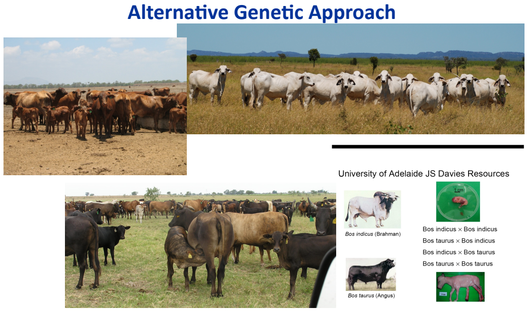
Precision Beef Cattle Production Through an Alternative Genetic Approach



- Fitzsimmons et al. (2008) reported divergence in fetal size as well as uterine and placental size in reciprocal Angus-Brahman F_1 calves, at day 153 of gestation, which follows the same pattern in birth weight differences that has been observed among these types of crosses.
- Burns et al. (2010) recently reported that placental characteristics seem to explain variation in birth weight more than early fetal size measurements in Droughtmaster calves (50% Brahman, 50% Shorthorn).

QTL Mapping Considerations

- Early QTL analyses in Cycle I McGregor cattle have shown multiple "parent-of-origin" effects for a variety of traits (size, temperament).
- Simply looking for "parent-of-origin" effects of gene markers can give false results:
  - Assumptions are that foundation populations are fixed for alternate alleles.

Considerations for Genetic Evaluation

- Engellandt and Tier (2002) evaluated estimation of variance components of carcass composition in 2,744 German Gelbvieh bulls due to "imprinting."
- Modeled sire as a random uncorrelated effect.
- 14 to 16% influence of paternally expressed genes for internal fat and meat yield.

J. Anim. Breed. Genet. 119:154-165.

Considerations for Genetic Evaluation

- Neugebauer et al. (2010) evaluated parent-of-origin effects on carcass traits in 65,233 German Simmental bulls.
- Incorporated two additive genetic effects per animal (paternal and maternal pattern).
- Estimated breeding values on animal as a sire and as a dam, and assumed the difference in 2 EBV was due to imprinting.

J. Anim. Sci. 88:523-532.

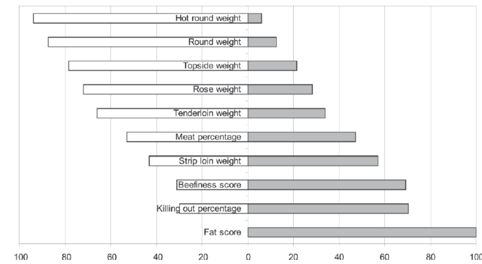


Figure 2. Parental contributions to imprinting variance of significant traits (expressed in percentage of the total imprinting variance): maternal contributions on the left, paternal contributions on the right.

Of 25 traits, 10 showed significant "imprinting" effects with influence of 8% to 25% of additive genetic variance.

Neugebauer et al. (2010) J. Anim. Sci. 88:523-532.

Consider a single gene locus model with 2 alleles

(traditional, Mendelian model with <u>no dominance</u>)

Genetic value:	-a	d	+a
Genotype:	A_2A_2	A_1A_2	A_1A_1
Performance:	0 units	+20	+40

All of the genetic differences in performance are due to differences in breeding value.

Progeny that inherit A_1 allele from a parent will have a different level of performance, and a different breeding value than the progeny that inherit an A_2 allele.

Consider a single gene locus model with 2 alleles

(traditional, Mendelian model with <u>complete dominance</u>)

Genetic value:	-a	d +a
Genotype:	A_2A_2	A_1A_1 A_1A_2
Performance:	0 units	+40

Some of the genetic differences in performance are due to differences in breeding value, and some are due to dominance (allele combinations).

Still though,
Progeny that inherit A_1 allele from a parent will have a different level of performance, and a different breeding value than the progeny that inherit an A_2 allele, but the performance of the one with the A_2 allele depends upon what the other allele is.

Assumptions: (1) two alleles (A_1 and A_2), (2) A_1 is completely dominant to A_2 and (3) allele inherited from sire is fully expressed but allele from dam is not expressed at all.

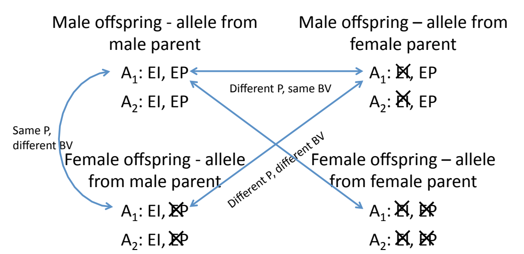
Male parent A_1A_2 ✖ Female parent A_1A_2

Potential genotypes and performance of progeny :

A_1A_1	+40
A_1A_2	+40
A_2A_1	+0
A_2A_2	+0

If the allele is expressed differently when inherited from the sire versus the dam, the relationship between individuals' phenotypes and breeding values becomes more complicated (similar phenotypes can have different breeding values, and vice versa). This has the most implications in heterozygotes (as does dominance and other gene combinations).

Breeding value implications from a paternally expressed locus



EI = expressed in individual; EP = expressed in progeny; P = phenotype; BV = breeding value.

Questions for Consideration

- How many gene loci have "substantial" epigenetic effects in *Bos indicus-Bos taurus* crosses or other cattle populations?
- Is there equal representation of paternal and maternal expression?
- Are there different biological types of traits that are more/less prone to epigenetic influence?

Questions for Consideration

- If "substantial" epigenetic influences exist, how should this affect the calculation (and interpretation) of covariances among relatives?
- Could this lead to different considerations (or calculations) of EPDs of maternal vs. paternal parents (or grandparents)?