

Genetic Markers

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What is a Genetic Marker ?

A DNA sequence variation that has been associated with a given trait in one or more populations







Companies that are offering DNA tests for marker-assisted selection for beef cattle traits



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Tests for quantitative traits – currently 3-100 SNPs

Meat Tenderness Quality Grade (Marbling) Beef Cattle Feed Efficiency Meat Yield Disease Resistance Dairy Form Milk and Milk Component Yield

	GeneSTAR	Population	Unfavorable Frequency	Favorable Frequency
	M1 (TG5)	Charolais X Angus	0.78	0.22
UNIVERSITY		Hereford	0.90	0.10
CALIFORNIA		STARS (Brahman)	0.97	0.03
		Angus	0.81	0.19
		Shorthorn	0.82	0.18
		⁶ Mixed Breed	0.78	0.22
		Angus	0.70	0.31
		<mark>Wagyu</mark>	<mark>0.37</mark>	<mark>0.63</mark>
		⁷ Other Breeds	0.77	0.23
		Red Angus	0.63	0.37
		Holstein	0.75	0.25
		Charolais	0.76	0.24
		Sanga	1.00	0.00

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Marker-assisted selection (MAS)

The process of using the results of DNAmarker testing to predict the **genetic** merit of the animal being tested and assist in the selection of individuals to become parents in the next generation. The word "assisted" implies that the selection is also influenced by other sources of information, such as animal's observed performance and EPD.



Which would you rather have???

 A bull that is 'homozygous' for a positive genetic variant with a trait EPD of +3, or

 A bull carrying no copies of that genetic variant with a trait EPD of +3







Both are important!!

- The 'homozygous' bull is a source of favorable form of the genetic variant. Can eventually be used to create homozygous calves
- The other bull contributes other favorable genes, which will improve the other genes affecting the trait.
- Breeding the marker-associated form of the gene into the bull that has no copies should improve the trait by combining all of the good forms of the genes together in one animal

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Validation

Prior to moving genetic markers from discovery populations to commercialization, it is important to validate their purported effects on the trait of interest in different breeds and environments, and assess them for correlated responses in associated traits





http://www.nbcec.org/nbcec/

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Background

Sample Populations

Marker Assisted Selection

Glossary

The purpose of the NBCEC commercial DNA test validation is to independently verify associations between genetic tests and traits as claimed by the commercial genotyping company using phenotypes and DNA from reference cattle populations

The validation process is a partnership of the owners of DNA and phenotypes (e.g., breed associations) and genomics companies, facilitated by the NBCEC

A. L. Van Eenennaam, J. Li, R. M. Thallman, R. L. Quaas, M. E. Dikeman, C. A. Gill, D. E. Franke, M. G. Thomas. 2007. Validation of commercial DNA tests for quantitative beef quality traits. Journal of Animal Science. 85:891-900.

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Many unvalidated MAS tests are available and more are coming

Bovigen/Pfizer – feed efficiency

- "GeneSTAR[®] Feed Efficiency consists of four markers which together identify as much as a 15% difference in daily feed consumption with no effect on other traits like Average Daily Gain, Carcass Weight, Quality Grade or Yield Grade" according to company website
- Igenity Docility, Maternal Traits, Feed Efficiency
- MMI Average daily gain (not available yet)



The Bovine Genome Sequence



The sequencing of the bovine genome allowed for a collaboration between MARC, BARC, UMC and UA to develop a set of 50,000 SNPs that are located throughout the entire genome

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"MAS is about to go nuclear"

58,000 SNP bovine CHIP array is now available (Illumina 58k bovine panel) This single enormous test panel which costs ~ \$500 per animal will immediately characterize the entire genome and estimate the value of every chromosome fragment contributing variation in a population with phenotypic observations



12 samples can be run on 50,000 SNPs for approximately \$200/sample!





Whole genome-assisted selection (WGS)

The use of these dense markers across the entire genome enables an estimation of the genetic merit of every chromosome fragment contributing variation in a population with phenotypic observations Can simultaneously test 50,000 markers Can be used to predict merit for all traits for which phenotyped populations exist



WGS effectively estimates an EPD for every chromosome fragment in the genome

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CBCIA/CCA to host BIF 2009! Mark your calendars!

http://www.calcattlemen.org/bif2009

2009 Beef Improvement Federation Annual Research Symposium and Annual Meeting





Sacramento, California April 30 – May 3, 2009









CALIFORNIA CATTLEMEN.

CCA

Wednesday April 29th Thursday April 30th

Friday May 1st Saturday May 2nd Sunday May 3rd Early Registration Registration and Evening Reception

Eastern Tour "Foothill Bovines, Equines and Fine Wines" Convention, Family/Spouse Tour, Evening Dinner Convention and Evening on your Own in Sacramento Western Tour "Ocean Wines and Bovines"

BEEF RUSH '09

CALIFORNIA





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