ECONOMICS OF USING DNA MARKERS FOR BULL SELECTION IN THE SEEDSTOCK INDUSTRY

Alison Van Eenennaam, Ph.D.

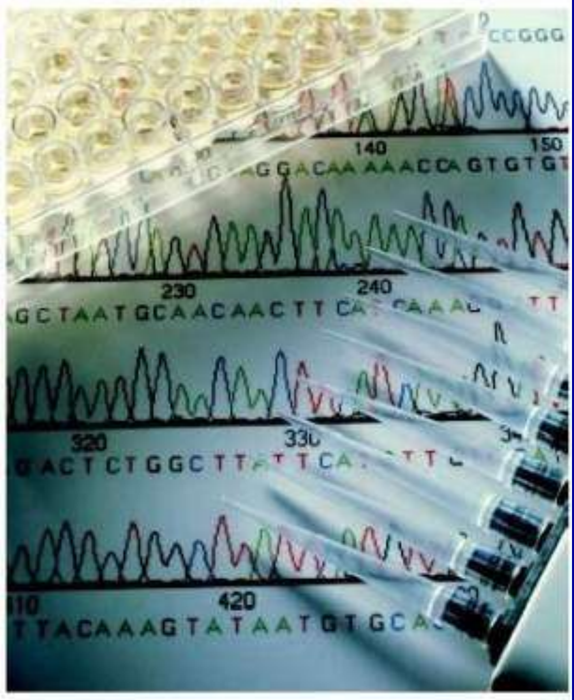
Cooperative Extension Specialist

Animal Biotechnology and Genomics

University of California, Davis

alvaneenennaam@ucdavis.edu

(530) 752-7942



animalscience.ucdavis.edu/animalbiotech

In the beginning

There are various companies offering DNA tests for marker-assisted selection in beef cattle

GeneSTAR
SureTRAK
SireTRACE
GeneSTAR
Pfizer
Pfizer Animal Genetics

igenity

GENETICVISIONS

ImmGen.

BIOGENETIC SERVICES, INC.

genmark

GENESEEK
Molecular Solutions for Breeding and Genetics

ANGUSURE

PRESCRIBE GENOMICS

MMI GENOMICS, INC.
BREED TRU
DNA VERIFIED

METAMORPHIX, INC.

PRESCRIBE GENOMICS

Prescribe Genomics Co.

Prescribe Genomics Wagyu Tests

Order Form

Cattle DNA Collection Guide

Pfizer Animal Genetics can offer Prescribe Genomic tests. Pfizer Animal Genetics will send DNA from Wagyu samples to the Prescribe Genomics laboratory in Japan for testing. Prescribe Genomics offers two DNA tests: GH Exon 5 and SCD.

GH Exon 5

This test represents a method for evaluating Wagyu cattle for the characteristics of growth rate and marbling using genetic polymorphism of the growth hormone Exon 5. Wagyu variants of this gene are A, B & C, therefore there are six genotypes: AA, AB, AC, BB, BC & CC. Prescribe Genomics suggests the preferred genotypes for producing bulls for F1 production are BB, BC and CC.

SCD

This test is designed to assist in the selection of cattle that show a genotype that produces a superior fat composition. Stearic acid, which corresponds to the amino acid Valine (V), makes deposited fat harder. Oleic acid, which corresponds to the amino acid Alanine (A), makes deposited fat softer, which Prescribed Genomics states is more palatable to the Japanese market. There are three possible genotypes for SCD, these are AA, VA and VV. AA is the preferred type.

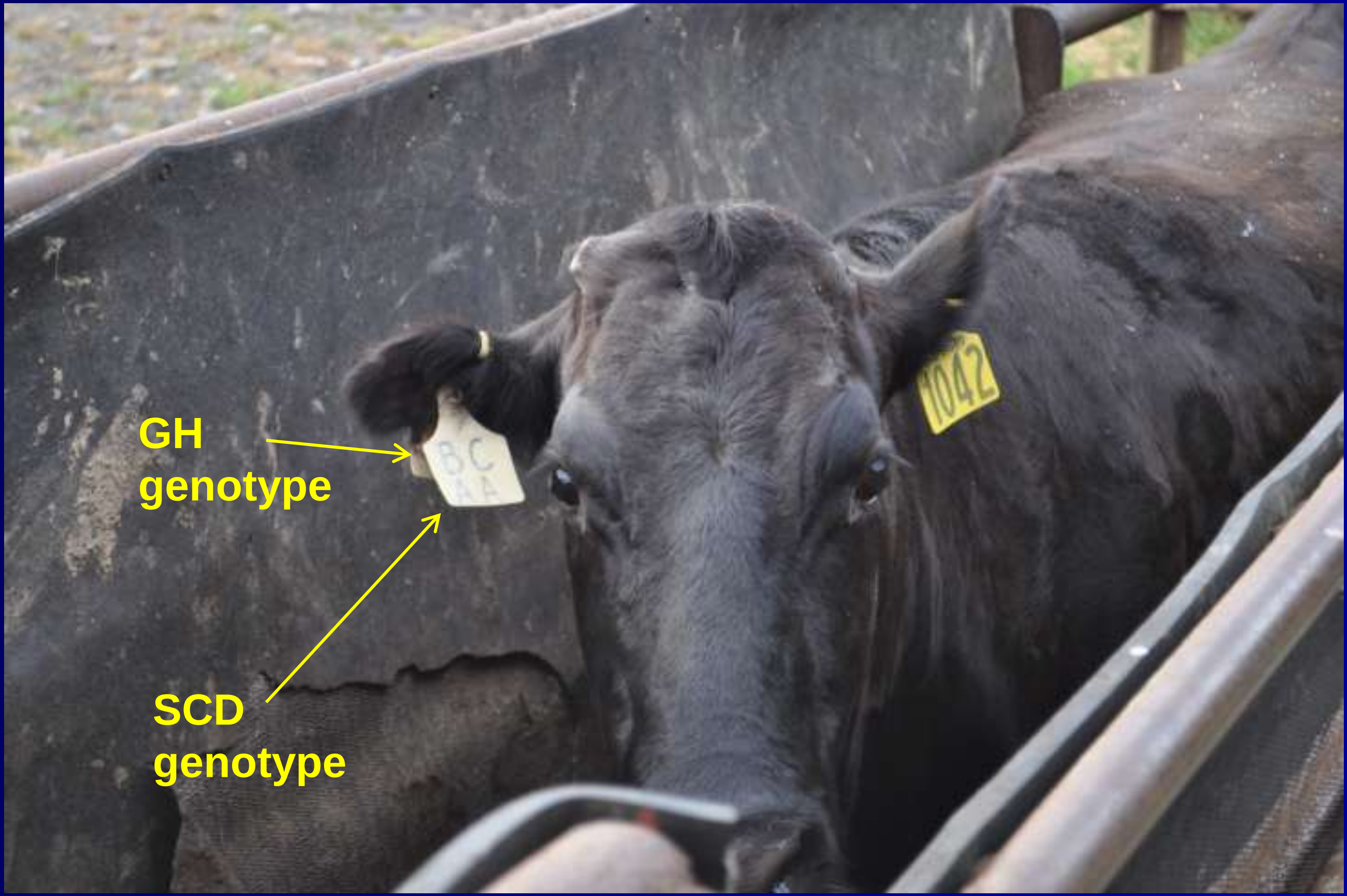
Pricing from:

GH Exon 5 only	$91+GST
SCD only	$82+GST
GH Exon 5 & SCD	$155+GST

~AU$170 per test

All prices are excluding GST

Markers are being used by producers to make selection/breeding decisions!



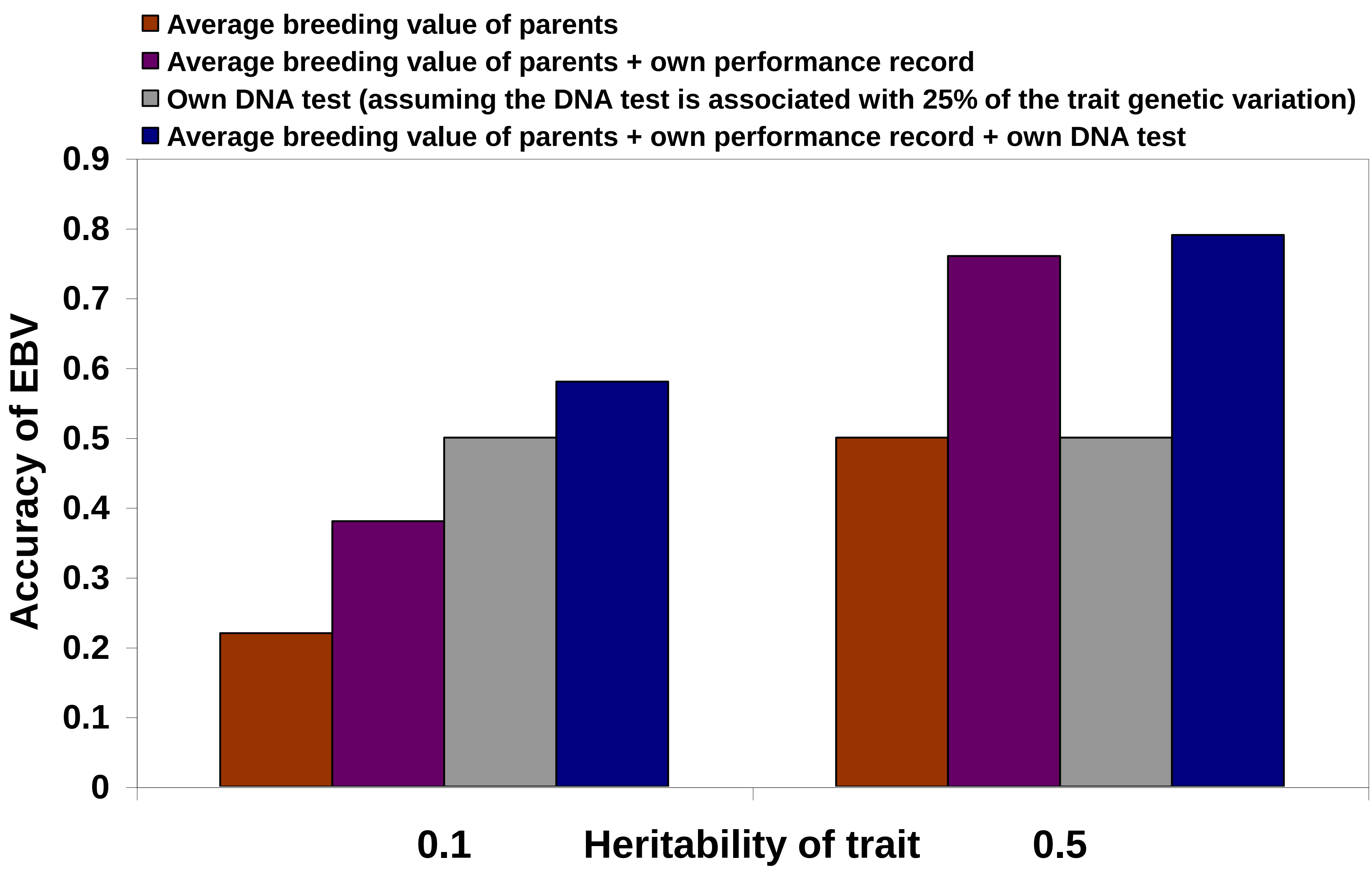
What is the value of a DNA test ?

DNA tests can increase the accuracy of genetic merit estimates:

$$\Delta G = (i_m\ r_m + i_f\ r_f) / (L_m + L_f)$$

Effect of markers on r will depend on how much testing improves the accuracy of EBVs over the use of traditional phenotypes of individual and relatives

Consider a DNA test associated with 25% of the additive genetic variation



Australian beef DNA results - Beef CRC - Beef Genetic Technologies - Windows Internet Explorer

http://www.beefcrc.com.au/Aus-Beef-DNA-results

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Australian beef DNA results - Beef CRC - Beef Genetic...

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Beef Genetic Technologies

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Success Stories

Beef CRC project aimed at improving beef industry profitability gains national recognition

MORE

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Home > DNA markers > Australian beef DNA results

Australian beef DNA results

As part of its role in delivering DNA markers to the Australian beef industry, Beef CRC has agreed to independently test new panels of DNA markers as they are commercialised by companies such as Pfizer Animal Genetics, Igenity /Merial and Metamorphix Inc.

Results of all independent testing of commercially-available DNA markers undertaken by Beef CRC will be presented on this site, outlining the size and direction of effect and the amount of genetic variation that is accounted for by each panel of markers for the different traits (e.g. marbling, feed efficiency, tenderness etc).

Additional information is provided to help beef businesses interpret the results for themselves to determine the value to their own businesses from an investment in the particular panel of DNA markers.

Those decisions very much depend on the individual business' attitude to risk and can only be made effectively by the individual business.

It is possible that the panel of markers has also been independently evaluated in North American herds by the US National Beef Cattle Evaluation Consortium, so for further information on the size and direction of effect of the markers in those populations, please visit http://www.ansci.cornell.edu/nbcec/

Pfizer GeneStar results

Pfizer interpretation

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Proportion of genetic variance (r_g^2) explained by DNA-tests that have been independently assessed by AGBU in Australia. The test was not predictive ($p < 0.05$) of the target trait in cells that are not shaded.

Population	IMF%	MSA Marble Score	SF (kg)	NFI (kg)
1. *Bos taurus*	0.3%	1.7%	2.9%	6.2%
2. *Bos indicus*	0.4%	0.9%	8.0%	5.4%
3. *Bos taurus* x *Bos indicus*	0%	0%	1.6%	0%
4. *Bos indicus X* Brahman	1.5%	3.6%	29.9%	0%

Table 2. Estimates of additive genetic variance and heritability ($h^2 \pm SE$) for economically relevant trait marbling and indicators intramuscular fat percentage and molecular breeding value (on the diagonal), genetic covariances among traits (above diagonal), and genetic correlations ($r_g \pm SE$) derived from them (below diagonal).

Trait	MRB	IMF	MBV
Marbling score (MRB)	0.3812 0.48±0.03	0.1404	0.0179
Intramuscular fat (IMF)	0.56±0.09	0.1663 0.31±0.03	0.0253
Molecular breeding value (MBV)	0.38±0.10	0.80±0.22	0.0060 0.98±0.05

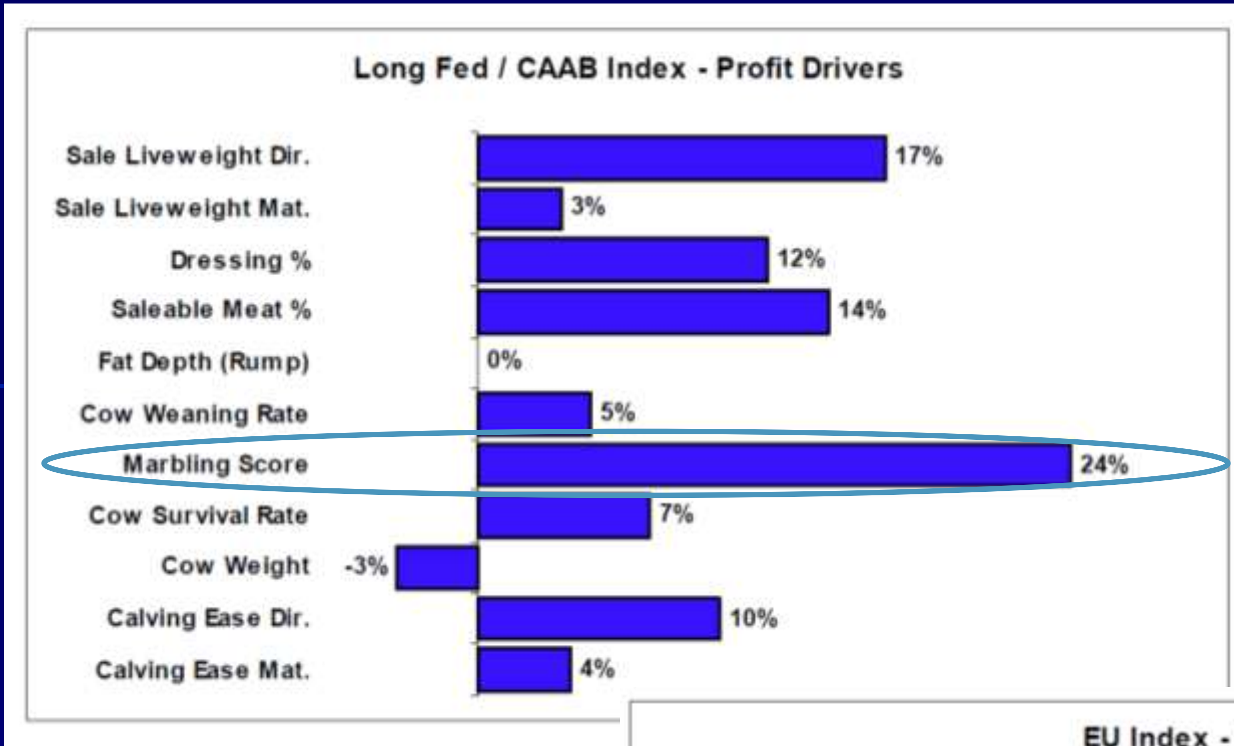
r_g = 0.38, so r_g^2 = ~15% for marbling score

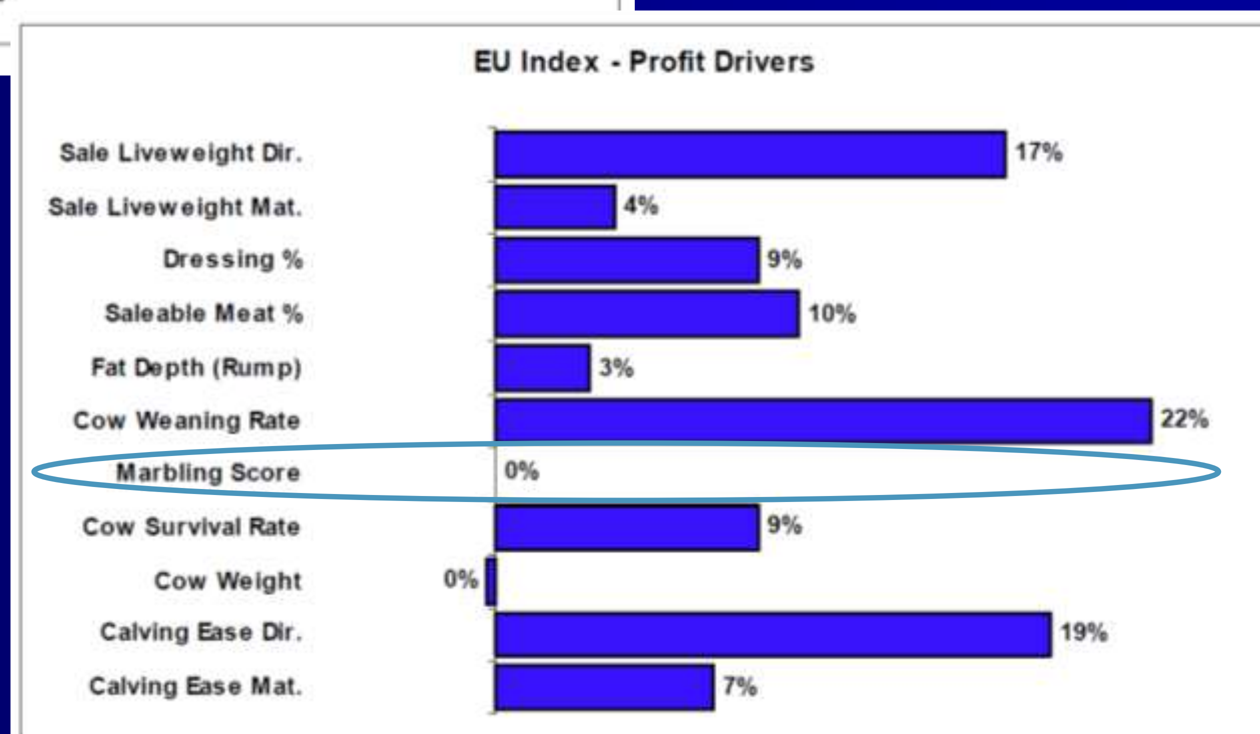
MacNeil, M. D., J. D. Nkrumah, B. W. Woodward, and S. L. Northcutt. 2009. Genetic evaluation of Angus cattle for carcass marbling using ultrasound and genomic indicators. J. Anim Sci. *In press*

What is the value of a genetic test that is associated with 15% of the genetic variation in marbling score?

The value of a genetic test will depend upon:

1. How much testing improves the accuracy of EBVs over the use of traditional phenotypes of individual and relatives
2. The proportion of genetic variation that is explained by the DNA test
3. The value of the trait in the selection objective!

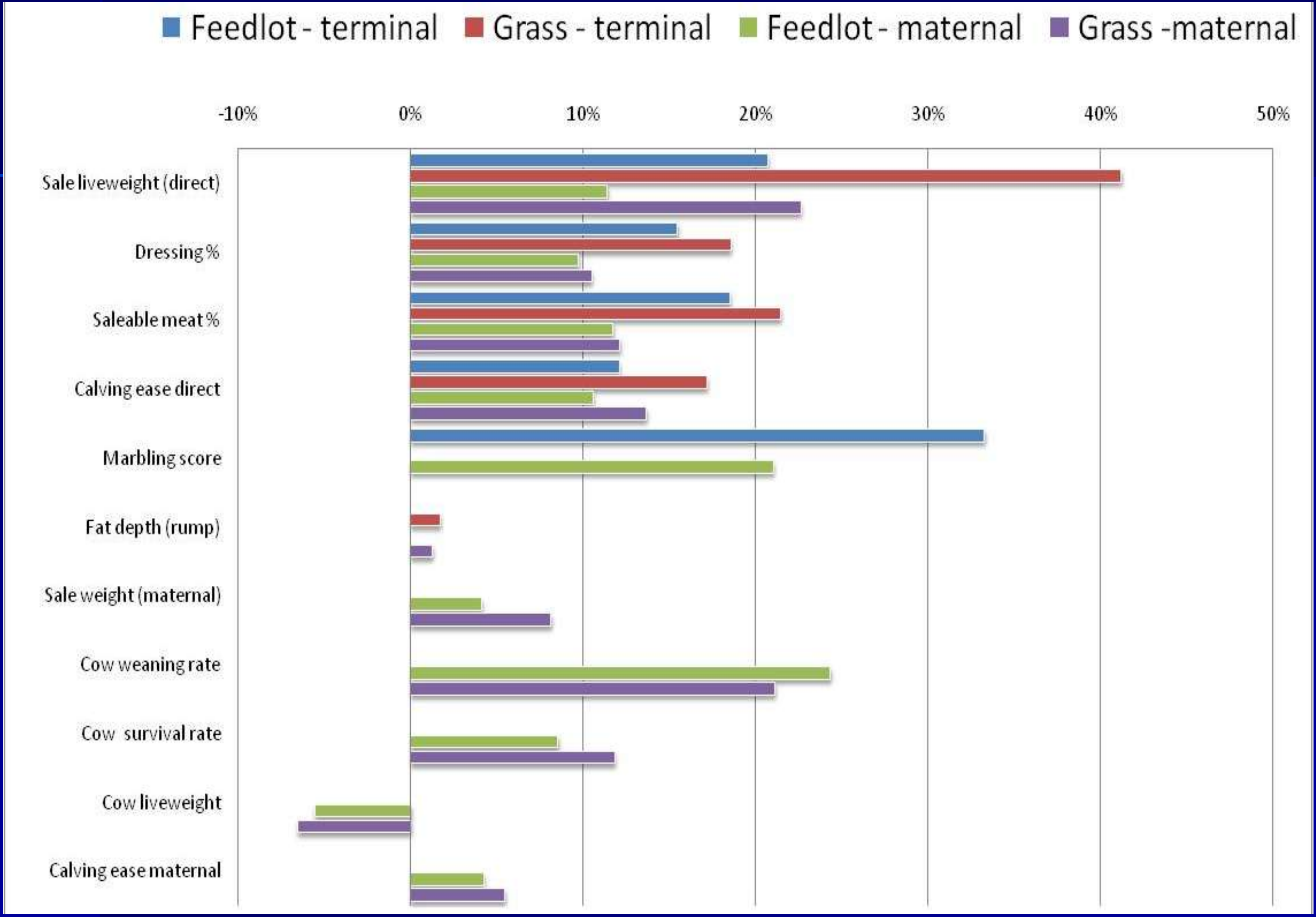

Long Fed / CAAB Index - Profit Drivers
Sale Liveweight Dir. 17%
Sale Liveweight Mat. 3%
Dressing % 12%
Saleable Meat % 14%
Fat Depth (Rump) 0%
Cow Weaning Rate 5%
Marbling Score 24%
Cow Survival Rate 7%
Cow Weight -3%
Calving Ease Dir. 10%
Calving Ease Mat. 4%


EU Index - Profit Drivers
Sale Liveweight Dir. 17%
Sale Liveweight Mat. 4%
Dressing % 9%
Saleable Meat % 10%
Fat Depth (Rump) 3%
Cow Weaning Rate 22%
Marbling Score 0%
Cow Survival Rate 9%
Cow Weight 0%
Calving Ease Dir. 19%
Calving Ease Mat. 7%

Biological parameters of the seedstock and commercial herd structure

Parameter	Value
Stud Herd	
Number of live yearlings per exposure	0.89
Number of stud females per stud male	30
Number of cows	600
Calf survival from birth to sale/selection	0.95
Number of bulls calves available for sale/selection	267
Number of stud bulls selected each year	8 (~3%; I = 2.27)
Number of bulls sold for breeding (annual)	125 (~50%; I = 0.8)
Maximum age of stud sire	4 (3 breeding seasons)
Average number of calves per stud sire surviving to sale/selection	65 (32.5 male; 32.5 female)
Planning horizon	20 years
Discount rate for returns	7%
Commercial Herd	
Maximum age of commercial sire	5 (4 breeding seasons)
Number of commercial females per male	100 (25 per year)

Relative importance of TRAITS IN THE BREEDING OBJECTIVES developed for terminal or self-replacing (maternal) herds targeting either the domestic Australian market where steers are finished on pasture (GRASS), or a high value market where steers are finished on concentrate rations in feedlots (FEEDLOT).



Herd using traditional performance recording was set as baseline profit

$T = \sum a_i g_i$

T is the profit from herd with BV = g

g_i is the BV for trait i

a_i is the economic weight for trait i (AU$/cow)

SELECTION CRITERIA, abbreviations, unit definitions, assumed phenotypic standard deviations, heritabilities, and records available on young bulls at time of selection/sale.

Criteria	Abbreviation	Unit	Heritability	Phenotypic SD	Own	Sire	Dam	Paternal half sib
Birth weight	BWT	kg/d	0.39	3.81	1	1	1	20
200 Day Growth	200	kg	0.18	22.36	1	1	1	20
400 Day Weight	400	kg	0.25	30.89	1	1	1	20
600 Day weight	600	kg	0.31	34.64	1	1	1	20
P8 (♀)	PHh	mm	0.41	1.98			1	10
P8 (♂)	PHb	mm	0.28	1.58	1	1		10
RIB (♀)	RIBh	mm	0.34	1.38			1	10
RIB (♂)	RIBb	mm	0.23	1.05	1	1		10
Eye Muscle Area (♀)	EMAh	cm2	0.26	5.25			1	10
Eye Muscle Area (♂)	EMAb	cm2	0.27	6.67	1	1		10
Intramuscular Fat (♀)	IMFh	%	0.25	1.00			1	10
Intramuscular Fat (♂)	IMFb	%	0.12	0.89	1	1		10
Scrotal Size (♂)	SS	cm	0.39	2.05	1	1		10
Days to Calving	DTC	days	0.07	23.49			1	
Mature Cow Weight	MCW	kg	0.41	46.90			1	

RECORDING COSTS OFF FARM

- 2007, 844 (18doa) registered calves,
- Angus society $15,871 (inc $2,473 DNA)
- Carcase scanning $9,813
- Structural assessment $6,318
- + other, total $34,058 = $41.23/hd

Slide courtesy of Lucinda Corrigan, Rennylea (www.rennylea.com.au)

RECORDING COSTS ON FARM

- 1 staff member PT recording, $35,000
- 1/10 labour unit calf recording, $5,616
- Labour, other data, ¼ unit, $20,022
- 4WMB inc running & depn $7,873
  computers & office costs $4,200
- TOTAL on farm $72,711
- Per head cost (on farm) $88.02

$/ head (on & off farm) <u>$129.26</u>

Slide courtesy of Lucinda Corrigan, Rennylea (www.rennylea.com.au)

Standard deviation of breeding objective (AU$), index standard deviation (Index σ_g) and improvement (%) over performance recording alone, and index accuracy when using a DNA test explaining 0, 5, 10 or 15% of the additive genetic variation for marbling score.

Unit	Trait	Percentage of additive genetic variance in MARBLING SCORE explained by DNA test	GRASS INDEX		FEEDLOT INDEX	
			Terminal	Maternal	Terminal	Maternal
SD Index Index σ_g (AU$)	SD of Breeding Objective (AU$)		31.97	33.35	47.29	54.08
	(performance recording information available)	1. None	16.15	10.03	12.23	11.50
		5. 5	16.15 (0%)	10.03 (0%)	14.20 (+16%)	13.06 (+14%)
		6. 10	16.15 (0%)	10.03 (0%)	15.94 (+30%)	14.45 (+26%)
		7. 15	16.15 (0%)	10.03 (0%)	17.50 (+43%)	15.72 (+37%)
Accuracy of Index	(performance recording information available)	1. None	.51	.30	.26	.21
		5. 5	.51	.30	.30	.24
		6. 10	.51	.30	.34	.27
		7. 15	.51	.30	.37	.29

What is the value of improving the breeding value of a commercial sire?

- The genetic superiority of a sire is expressed in the next, and subsequent generations in the case of sires breeding replacement females.
- The gene flow method of Hill (1974), which tracks gene flow in populations with overlapping generations, was used to compute the number of Discounted Gene Expressions (DGE_{CB}) derived from the selection/purchase of a genetically superior commercial bull at time 0 based on a gene flow matrix over a 20 year time frame

If cohort of yearling bulls improve the breeding value for a single trait – then the value of the increase can be calculated

$g_1 \alpha_1\ DGE_{CB1}$ / # bulls in age class x # cows in the herd

where

g_1 is the change in the breeding value for trait 1 ($\Delta G = \sigma_g$ x selection intensity)

α_1 is the economic weight for trait 1 (AU$/cow)

DGE_{CB1} = discounted genetic expressions in trait 1 from commercial bulls purchased in year 0.

Value of genetic gain in commercial sires, and value derived per DNA test explaining 0, 5, 10 or 15% of the marbling score additive genetic variation. Values are unique for the assumptions and hypothetical seedstock and commercial herd biological parameters modeled in this study.

Unit	Trait		Percentage of additive genetic variance in MARBLING SCORE explained by DNA test	GRASS INDEX		FEEDLOT INDEX	
				Terminal	Maternal	Terminal	Maternal
Value of ΔG in commercial sires selected from top half of stud herd	(AU$/bull)	(performance recording	1. None	515	424	389	458
			5. 5	515	424	453	510
			6. 10	515	424	508	557
			7. 15	515	424	559	600
Increased value of commercial sire per test	(AU$/ DNA test)		1. None	.	.	.	.
			5. 5	0	0	32	26
			6. 10	0	0	60	49
			7. 15	0	0	85	71

What is the value of improving the breeding value of a stud sire?

Selection of superior stud sires has a two-fold benefit to seedstock producers. Not only do these superior stud sires produce better bull offspring for the commercial sector, but they also increase the rate of genetic gain in the seedstock herd itself. In this case the DGE for a stud bull (DGE_{SB}) was calculated for age class 1 in the seedstock herd (i.e. DGE of yearling offspring in stud herd).

DGE_{SB} x selection intensity x Index σ_g x number of sale bulls x DGE_{CB1}

Value of genetic gain in stud sires, and overall value derived per DNA test explaining 0, 5, 10 or 15% of the marbling score additive genetic variation. Values are unique for the assumptions and hypothetical seedstock and commercial herd biological parameters modeled in this study.

Unit	Trait	Percentage of additive genetic variance in MARBLING SCORE explained by DNA test	GRASS INDEX		FEEDLOT INDEX	
			Terminal	Maternal	Terminal	Maternal
Value of ΔG in stud sires selected from top 3% of stud herd	(AU$/bull)	1. None	29608	18388	22421	21083
		5. 5	29608	18388	26033	23943
		6. 10	29608	18388	29223	26491
		7. 15	29608	18388	32083	28820
Increased value of stud sire per test	(AU$/ DNA test)	1. None	.	.	.	.
		5. 5	0	0	108	86
		6. 10	0	0	204	162
		7. 15	0	0	289	232
Total value per test to seedstock operator	(AU$/ DNA test)	1. None	.	.	.	.
		5. 5	0	0	140	112
		6. 10	0	0	264	211
		7. 15	0	0	374	303

The Power of the IGENITY® profile for Angus

The American Angus Association® through its subsidiary, Angus Genetics Inc.® (AGI), has a vision to provide Angus breeders with the most advanced solutions to their genetic selection and management needs.

Genomic-enhanced Expected Progeny Differences (EPDs) can now be calculated for your animals using the highly predictable American Angus Association database along with IGENITY® profile results to provide a more thorough characterization of economically important traits and improved accuracy on young animals.

Using the IGENITY profile for Angus, breeders receive comprehensive genomic results for multiple, economically important traits.

- **Marbling**
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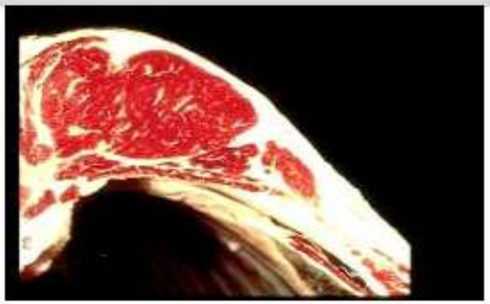
- **Fat Thickness**
- **Carcass Weight**
- **Tenderness**
- **Percent Choice**
- **Yield Grade**
- **Heifer Pregnancy**
- **Stayability**
- **Maternal Calving Ease**
- **Docility**
- **Average Daily Gain (ADG)**
- **Feed Efficiency**
- **Yearling Weight**

Additional tests available:

- **Arthrogryposis Multiplex (AM)**
- **Neuropathic Hydrocephalus (NH)**
- **Bovine Viral Diarrhea – Persistently Infected (BVD PI)**
- **Coat Color**

What traits are we working on?



- Feed efficiency
- Feedlot health index
- Post weaning gain growth
- Temperament index
- Days to spec
- Immunological factors

- Ribeye area
- Carcass weight
- % Red meat yield
- Marbling/IMF
- Tenderness
- Fatty acid profile
- Healthfulness of beef

http://www.pfizeranimalgenetics.com/sites/PAG/aus/Documents/GeneSTAR_MVP_Presentation_AUS.pdf

What traits are we working on?

- Heifer fertility
- Cow maintenance efficiency
- Longevity/Productivity
- Calving ease
- Bull fertility / libido
- Cow profitability index

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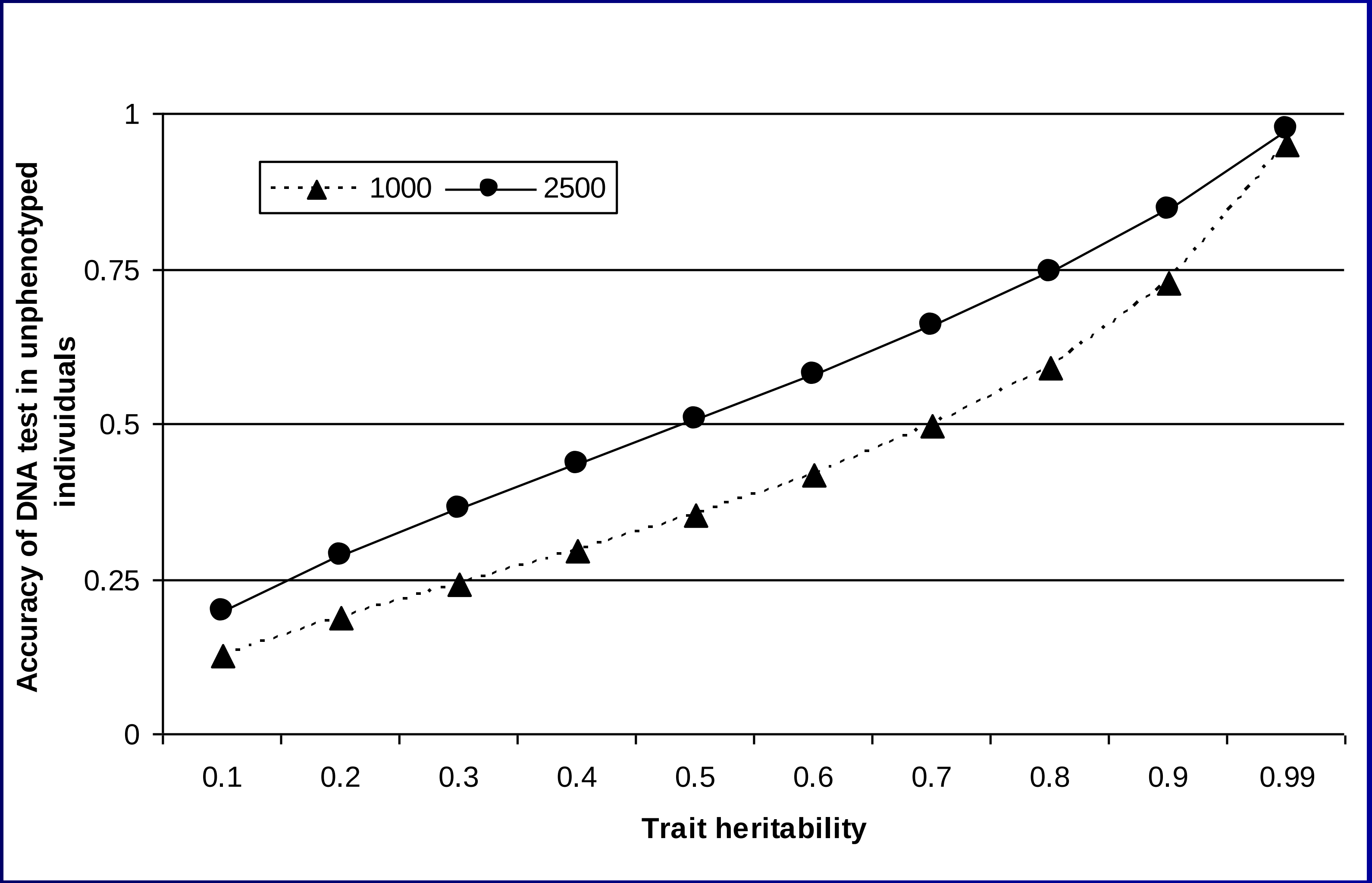
http://www.pfizeranimalgenetics.com/sites/PAG/aus/Documents/GeneSTAR_MVP_Presentation_AUS.pdf

Effect of trait heritability on accuracy of DNA tests trained in populations of 1000 (▲) or 2500 (●) individuals with phenotypic observations.



Standard deviation of breeding objective (AU$), index standard deviation (Index σ_g) and improvement (%) over performance recording alone, and index accuracy when using a DNA associated with specific additive genetic variation % of selection traits and/or criteria additive genetic variation

Unit	Trait	Percentage of additive genetic variance explained by DNA test	GRASS INDEX		FEEDLOT INDEX	
			Terminal	Maternal	Terminal	Maternal
Selection index standard deviation σ_g (AU$)	SD of Breeding Objective (AU$)		31.97	33.35	47.29	54.08
		1. None	16.15	10.03	12.23	11.50
		2. h^2 (criteria only)	19.37 (+20%)	12.05 (+20%)	13.66 (+12%)	15.38 (+34%)
		3. ½ h^2 (criteria + traits)	20.99 (+30%)	14.92 (+49%)	23.91 (+96%)	21.92 (+91%)
		4. h^2 (criteria + traits)	24.61 (+52%)	17.63 (+76%)	31.39 (+157%)	28.34 (+146%)
Accuracy of Index		1. None	.51	.30	.26	.21
		2. h^2 (criteria only)	.61	.36	.29	.28
		3. ½ h^2 (criteria + traits)	.66	.45	.51	.41
		4. h^2 (criteria + traits)	.77	.53	.66	.52

Value of genetic gain in commercial and stud sires, and overall value derived per DNA test. DNA tests explaining increasing percentages of selection traits and/or criteria additive genetic variation (case 1-4) were modeled.

Unit	Trait	Percentage of additive genetic variance explained by DNA test	Grass Index		Feedlot Index	
			Terminal	Maternal	Terminal	Maternal
Value of ΔG in commercial sires selected from top half of stud herd	(AU$/bull)	1. None	515	424	389	458
		2. h^2 (criteria only)	617	507	434	613
		3. ½ h^2 (criteria + traits)	670	630	764	858
		4. h^2 (criteria + traits)	786	744	1004	1113
Value of ΔG in stud sires selected from top 3% of stud herd	(AU$/bull)	1. None	29608	18388	22421	21083
		2. h^2 (criteria only)	35511	22091	25043	28196
		3. ½ h^2 (criteria + traits)	38481	27353	43834	40186
		4. h^2 (criteria + traits)	45118	32321	57548	51956
Increased value of commercial sire per test	(AU$/ DNA test)	1. None	.	.	.	.
		2. h^2 (criteria only)	51	42	23	78
		3. ½ h^2 (criteria + traits)	78	103	188	200
		4. h^2 (criteria + traits)	136	160	307	328
Increased value of stud sire per test	(AU$/ DNA test)	1. None	.	.	.	.
		2. h^2 (criteria only)	177	111	79	213
		3. ½ h^2 (criteria + traits)	266	269	642	572
		4. h^2 (criteria + traits)	465	417	1052	925
Total value per test to seedstock operator	**(AU$/ DNA test)**	**1. None**	.	.	.	.
		2. h^2 (criteria only)	**228**	**153**	**102**	**291**
		3. ½ h^2 (criteria + traits)	**344**	**372**	**830**	**772**
		4. h^2 (criteria + traits)	**601**	**577**	**1359**	**1253**

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The end


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