

# DNA MARKER PANEL VALIDATION UPDATE BY NATIONAL BEEF CATTLE EVALUATION CONSORTIUM

## National Beef Cattle Evaluation Consortium

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### Commercial genetic test validations

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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

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Summary of NBCEC validations for commercially-available DNA-tests for complex (quantitative or multiplex) traits in beef cattle (note: validations do not include tests for "simple" traits such as coat color, horned/polled, AM status etc.)

Company	Test Name	Trait	Date of validation
iGenity <a href="http://www.igenity.com">www.igenity.com</a>	Profile <sup>®</sup>	Fat Thickness	12/2008
	Profile <sup>®</sup>	Marbling Score	12/2008
	Profile <sup>®</sup>	Quality Grade (% ≥ Choice)	12/2008
	Profile <sup>®</sup>	Rib Eye Area	12/2008
	Profile <sup>®</sup>	Yield Grade	12/2008
	Profile <sup>®</sup>	Postmortem Cold Carcass Weight	12/2008
	Profile <sup>®</sup>	Tenderness	12/2007
	Profile <sup>®</sup>	Residual Feed Intake (RFI) (for Bos indicus influenced cattle)	12/2007
	Profile <sup>®</sup>	Residual Feed Intake (RFI) (for Bos taurus cattle)	6/2008
	Profile <sup>®</sup>	Drumstick index (DMI) (for Bos indicus influenced cattle)	12/2007
Pfizer Animal Genetics (Bovigen) <a href="http://www.bovigen.com">www.bovigen.com</a>	Profile <sup>®</sup>	Hole Pregnancy Rate	
	Profile <sup>®</sup>	Stability (longevity)	
	Profile <sup>®</sup>	Maternal Calving Ease	
	Profile <sup>®</sup>	Docility	
	GeneSTAR <sup>®</sup>	Tenderness MVP	2/2009
MMI Genomics <a href="http://www.mmi-genomics.com">www.mmi-genomics.com</a>	GeneSTAR <sup>®</sup>	Marbling MVP	2/2009
	GeneSTAR <sup>®</sup>	% IMF (feedlot cattle)	2/2009
	GeneSTAR <sup>®</sup>	Feed Efficiency MVP	2/2009
MMI Genomics <a href="http://www.mmi-genomics.com">www.mmi-genomics.com</a>	Tri-Mark <sup>™</sup>	Marbling Score and Quality Grade	
	Tri-Tenderness <sup>™</sup>	Tenderness	

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Summary

The GeneSTAR Tenderness MVP<sup>433</sup> was found to be significantly associated with a decrease in Warner-Bratzler shear force (WBSF) measurements (i.e. increased tenderness) at 14 d postmortem in two Bos taurus sample populations. Additionally this test was found to be significantly associated with a decrease in Warner-Bratzler shear force measurements at day 1 d postmortem, but not 14 d postmortem, in a Bos indicus-influenced population of 390 animals.

Significance of the GeneSTAR Tenderness MVP<sup>433</sup> (Molecular Value Prediction)

Population	TRAIT	Panel	b <sup>2</sup>	F	p	N
North American Angus validation population	WBSF <sup>433</sup> Tenderness (day 14 postmortem, kg)	Tenderness	0.665	4.2	0.021	462
North American Angus validation population	WBSF Tenderness (day 14 postmortem, lb)	Tenderness	0.328	14.33	0.00008	760
North American Bos indicus-influenced "Pilot C" validation population	WBSF Tenderness (day 1 postmortem, kg)	Tenderness	0.358	6.227	0.007	390
North American Bos indicus-influenced "Pilot C" validation population	WBSF Tenderness (day 14 postmortem, kg)	Tenderness	0.037	0.189	0.332	388

<sup>433</sup> Molecular prediction values (MVP) were provided by Pfizer Animal Genetics based on their 56 SNP panel for Marbling Score, Tenderness and Net Feed Intake (residual feed intake).

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**Summary**

There was no significant association of this test with the trait of Marbling Score in any of the validation populations. However, the GeneSTAR Marbling MVP<sup>1</sup> was found to be significantly associated with percent intramuscular fat (%IMF) in a *Bos indicus*-influenced, and one of two *Bos Taurus* populations. Additionally this test was found to be significantly associated with the quality grade (% choice or better) in the *Bos indicus*-influenced population of 794 animals, but not the *Bos taurus* "D" validation population.

**Significance of the GeneSTAR Marbling MVP<sup>1</sup> (Molecular Value Prediction)**

Population	TRAIT	Panel	b <sup>2</sup>	F	p	N
North American <i>Bos taurus</i> "Pfizer A" validation population	Marbling score <sup>2</sup>	Marbling	-0.267	3.15	0.081	595
	% IMF	Marbling	0.193	1.76	0.094	282
North American <i>Bos taurus</i> "Pfizer B" validation population	Marbling score	Marbling	.120	1.1	0.147	723
	% Choice	Marbling	-0.032	0.1	0.624	723
North American <i>Bos indicus</i> -influenced "Pfizer C" validation population	Marbling score	Marbling	0.312	5.26	0.011	785
	% Choice	Marbling	0.387	1.73	0.096	392
North American <i>Bos indicus</i> -influenced "Pfizer C" validation population	Marbling score	Marbling	0.276	3.68	0.028	392
	% IMF	Marbling	0.659	9.83	0.001	394

<sup>1</sup> Molecular prediction values (MVP) were provided by Pfizer Animal Genetics based on their 56 SNP panel for Marbling Score, Tenderness and Net Feed intake (residual feed intake).

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The GeneSTAR feed efficiency MVP<sup>1</sup> was found to be significantly and positively associated with residual feed intake (RFI) in a North American population of 671 *Bos taurus* cattle. No significant association was found between this MVP and feed efficiency in a North American population of 395 *Bos indicus*-influenced cattle.

**Significance of the GeneSTAR Feed Efficiency MVP<sup>1</sup> (Molecular Value Prediction)**

Population	TRAIT	Panel	b <sup>2</sup>	F	p	N
<i>Bos taurus</i> "Pfizer A" validation population	Residual Feed Intake (RFI; kg) <sup>2</sup>	Feed Efficiency	0.4	n/a	0.02	671
<i>Bos indicus</i> -influenced "Pfizer C" validation population	Residual Feed Intake (RFI; kg)	Feed Efficiency	-0.019	0.017	0.55	395

<sup>1</sup> Molecular prediction values (MVP) were provided by Pfizer Animal Genetics based on their 56 SNP panel for Marbling Score, Tenderness and Net Feed intake (residual feed intake).

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igenty

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**Igenty profile**

**Carcass Composition and Average Daily Gain**

The IGENTY profile was found to be significantly associated with marbling score, back fat thickness, quality grade, ribeye area, and yield grade carcass traits and average daily gain in a commercial predominately *Bos taurus* sample population of 1364 animals. This test was not evaluated on a *Bos indicus*-influenced or purebred *Bos indicus* population.

**Significance\* of the Igenty Molecular Breeding Values for Carcass Traits and Average Daily Gain**

Breed	TRAIT	Panel	b <sup>2</sup>	F	p	N
Commercial Validation population	USDA Marbling Score	MBS	0.76	28.6	0.0000001	1354
	Backfat Thickness	BFAT	0.81	12.46	0.0002	1354
	Quality Grade <sup>1</sup>	% ≥ CHOICE	0.73	14.06	0.00009	1364
	Ribeye Area	REA	1.01	10.99	0.0005	1354
	Yield Grade	YG	1.16	21.98	0.000002	1354
	Average Daily Gain	ADG	0.61	14.69	0.00007	1364

<sup>\*</sup> Molecular breeding values (MBVs) for each trait were provided by Igenty based on the various SNP panels for each trait.

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**IGENTY profile Feed Efficiency for *Bos taurus* cattle SUMMARY**

The IGENTY TAURUS feed efficiency MBVs were inconsistently associated with residual feed intake in the validation populations. In two populations there was a significant positive association of the MBV with the trait (North American *Bos Taurus*, CRC Temperate), but in the remaining four populations there was no significant effect and in both Angus populations the estimated association was negative, meaning that the results were associated in the opposite direction.

For further information on this validation contact Dr. John Pollak (607) 255-2846.


TEST DATASET	Trait	PANEL	b	P	N
TEMPERATE <sup>1</sup> (CRC1)	RFI	TAURUS	0.309	0.04	~546
SHORTHORN <sup>1</sup> (CRC)	RFI	TAURUS	0.393	0.17	~189
ANGUS (CRC1)	RFI	TAURUS	-0.426	0.96	~327
NORTH AMERICAN <i>Bos Taurus</i> <sup>2</sup>	RFI	TAURUS	0.351	0.085	~706
NORTH AMERICAN CHAROLAIS <sup>3</sup>	RFI	TAURUS	0.022	443	~393
NORTH AMERICAN ANGUS <sup>3</sup>	RFI	TAURUS	-0.217	0.89	~436

<sup>1</sup> Data analyses for these validation populations were performed by Dr. David Johnston, Animal Genetics and Breeding Unit, University of New England, Armidale, Australia (6/2006).

<sup>2</sup> Data analyses for this validation population was performed by Gordon VanderVoort, Dr. Matt Kelly, Duc Lu and Dr. Stephen Miller, University of Guelph (6/2006).

<sup>3</sup> Data analyses for these validation populations were performed by Dr. Denny Crews, Agriculture and Agri-Food Canada (6/2006).

Publishing traditional EPDs and marker information separately, as is currently the case, is confusing and can lead to incorrect selection decisions when marker scores predict only a small proportion of the genetic variance.



An increasingly relevant question in evaluating commercial DNA tests is *"What proportion of the additive genetic variation in the target trait is accounted for by the test?"*

## Estimation of the Proportion of Genetic Variation Accounted for by DNA Tests.

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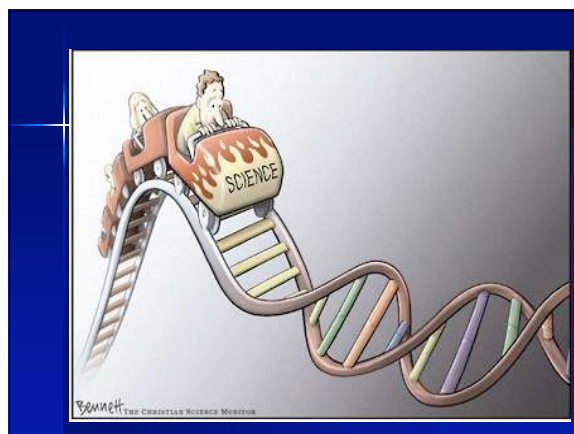
Advancements in Genetic Prediction Technical Keynote Session, Tomorrow (Saturday) afternoon in Room 203, Convention Center

The screenshot shows the Beef CRC website. The main content area is titled 'DNA markers' and features a photo of a person standing next to a herd of cattle. The sidebar on the right contains a search bar, a 'Subscribe to Recent Publications' button, and a 'Join the Forum Now' button. The website is designed with a blue and white color scheme.

The screenshot shows the Australian beef DNA results page. The main content area is titled 'Australian beef DNA results' and features a list of DNA markers and their associated results. The sidebar on the right contains a search bar, a 'Subscribe to Recent Publications' button, and a 'Join the Forum Now' button. The website is designed with a blue and white color scheme.

Table 3: Bivariate animal model results using all phenotypes and GenSTAR MVPs from the 56 marker pane Version January 2009. Results are from a data combining breeds and fitting breed in the model. The residual effect for the MVP was fixed at 0.001 and the residual correlation at 0.0.  $\sigma_p^2$  = phenotypic variance of the observed data after fitting the models,  $h^2$  = heritability of the trait, note MVP have a heritability of very close to 1.0,  $r_g$  = genetic correlation between MVP and target trait,  $r_g^2$  = % genetic variance explained by marker,  $b$  = regression coefficient of MVP on phenotype has been calculated as ratio of covariance over variance of MVP. Standard errors of estimates are in brackets.

Test	Trait	Data	N	$\sigma_p^2$	$h^2$ (se)	$r_g$ (se)	$r_g^2$	$b$ (se)
Pline MVP	IMF	Phenot =	3,594	2.035	0.39 (0.06)	0.054 (0.07)	0.1	0.255 (0.30)
		MVP =	703	0.035				
		Phenot =	3,524	0.978	0.37 (0.06)	0.064 (0.07)	0.4	0.231 (0.24)
		MVP =	668	0.027				
Pline MVP	MSA	Phenot =	876	0.767	0.23 (0.10)	0.011 (0.13)	0.0	0.028 (0.33)
		MVP =	253	0.026				
		Phenot =	878	0.717	0.37 (0.11)	0.121 (0.11)	1.5	0.415 (0.39)
		MVP =	225	0.022				
Pline MVP	MS	Phenot =	1,454	0.281	0.35 (0.09)	0.131 (0.12)	1.7	0.218 (0.20)
		MVP =	710	0.035				
		Phenot =	1,808	0.236	0.37 (0.08)	0.096 (0.08)	0.9	0.171 (0.15)
		MVP =	670	0.027				
Pline MVP	Tenderness	Phenot =	594	0.211	0.31 (0.13)	0.016 (0.14)	0.0	0.024 (0.22)
		MVP =	253	0.026				
		Phenot =	636	0.229	0.19 (0.11)	0.189 (0.17)	3.6	0.262 (0.23)
		MVP =	225	0.022				
Pline MVP	Feed Efficiency	Phenot =	3,322	0.433	0.08 (0.04)	0.170 (0.14)	2.9	0.109 (0.09)
		MVP =	639	0.088				
		Phenot =	3,254	0.612	0.30 (0.06)	0.283 (0.08)	8.0	0.301 (0.09)
		MVP =	585	0.180				
Pline MVP	NFI	Phenot =	783	0.658	0.36 (0.10)	0.126 (0.14)	1.6	0.137 (0.16)
		MVP =	253	0.142				
		Phenot =	782	0.871	0.31 (0.10)	0.547 (0.13)	29.9	0.747 (0.18)
		MVP =	225	0.079				
Pline MVP	Feed Efficiency	Phenot =	783	0.840	0.14 (0.11)	0.248 (0.15)	6.2	0.300 (0.13)
		MVP =	253	0.082				
		Phenot =	784	1.110	0.21 (0.25)	-0.044 (0.16)	0.2	-0.074 (0.27)
		MVP =	215	0.958	0.37 (0.26)	-0.053 (0.14)	0.5	-0.131 (0.33)



The diagram shows the evolution of cattle from 2003 to 2020. It is divided into four columns representing the years. Each column contains a list of genetic testing methods and marker panels. The methods evolve from single marker/single trait tests in 2003 to universal marker panels in 2020. The panels become more comprehensive over time, including more traits and markers.

2003	2008	2013	2020
<ul style="list-style-type: none"> <li>single marker/single trait</li> <li>reported genotypes</li> <li>single marker accounted for very small amount of genetic variation</li> <li>limited adoption</li> <li>technology oversold</li> </ul>	<ul style="list-style-type: none"> <li>multimarker tests for a few traits reported in a variety of formats</li> <li>no tie between DNA test results and national genetic evaluation</li> <li>tests accounted for small proportion of additive genetic variation</li> <li>limited validation</li> <li>technology not in a form producers could use</li> </ul>	<ul style="list-style-type: none"> <li>panels with hundreds of markers for many traits</li> <li>results reported in units of the trait</li> <li>incorporation of DNA information into national genetic evaluation</li> <li>DNA-based evaluations improve accuracy of EPDs</li> <li>large numbers of genotyped populations are available for validation</li> </ul>	<ul style="list-style-type: none"> <li>universal marker panel used by worldwide beef cattle community</li> <li>mandatory, seamless submission of genotype data to national genetic evaluation/breed associations</li> <li>cost is low and industry uses DNA information for herd management, feedyard sorting, and breeding.</li> </ul>