

Value of DNA information for beef bull selection

A.L. Van Eenennaam¹, J.H. van der Werf², M.E. Goddard³

¹ Cooperative Extension Specialist Animal Biotechnology and Genomics University of California, Davis

² University of New England Armidale, NSW, Australia

³ Victorian Department of Primary Industries and University of Melbourne, VIC, Australia





Objective

Estimate the value of using DNA test information to increase the accuracy of beef bull selection in a seedstock breeding program

- The expected returns from using a commercial sire sourced from a seedstock herd using DNA testing
- Additionally, the value of marker information in the selection of replacement stud males to be mated in a seedstock breeding program was also estimated.



The following seedstock operation was modeled

Parameters	Value
Number of stud cows	600
Number of bulls calves available for sale/selection	267 (all get tested with DNA test)
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 commercial sire	5 (4 breeding seasons)
Commercial cow:bull ratio	25
Number of commercial females	9225
Planning horizon	20 years
Discount rate for returns	7%
Number of live stud calves available per exposure	0.89
Stud cow:bull ratio	30
Cull for age threshold of cow	10
Age structure of breeding cow herd (2-10 yr)	0.2, 0.18, 0.17,0.15, 0.12, 0.09, 0.05, 0.03, 0.01
Bull survival (annual)	0.8
Age structure of bulls in stud herd (2-4 yr)	0.41, 0.33, 0.26
Age structure of bulls in commercial herd (2-5 yr)	0.34, 0.27, 0.22, 0.17

EXAMINED 4 BREEDING OBJECTIVES: PROFIT DRIVERS





Materials and methods

- Selection index theory was used to predict the potential benefit of including DNA information in selection decisions.
- Information from DNA test information was modeled as a molecular breeding value (q_i) explaining a proportion (ρ) of the additive genetic variance (σ_{ai}^2) in trait i; $V_{qi} = \rho . \sigma_{ai}^2$, as described by Lande and Thompson (1990).

DEVELOPED TEST USING 2500 RECORDS ON CORRELATED TRAIT PERFORMANCE RECORDS

Selection Criteria	<u>Heritability</u>
Birth weight	0.39
200 d Weight	0.18
400 d Weight	0.25
600 d Weight	0.31
P8 fat	0.41
RIB fat	0.34
Eye Muscle Area	0.26
Intramuscular Fat	0.25
Scrotal Size	0.39
Days to Calving	0.07
Mature Cow Weight	0.41

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Effect of trait heritability on theoretical proportion of trait genetic variation explained by DNA tests trained in populations of 1000 (\blacktriangle) or 2500 (\bullet) individuals with phenotypic observations*.



* Effective population size (N_e) = 100, length of bovine genome (L) = 30 M, effective number of loci (M_e) = 2NeL, and a normal distribution of QTL effects were assumed. Derived from the formula of Goddard (2009).



Materials and methods (continued)

- Indexes were constructed and index accuracies were calculated when information source included DNA test information from one of the two DNA panels **and** performance recording, over that derived from performance recording alone.
- Discounted gene flow methodology (Hill, 1974) was used to calculate the value derived from the use of superior bulls selected using DNA test information **and/or** performance recording. Results were ultimately calculated as discounted returns per DNA test purchased by the seedstock operator.

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Variable	Unit Informa availa	Information	GRAS	s Index	FEEDLOT INDEX	
Variable		available	<u>Terminal</u>	Maternal	<u>Terminal</u>	<u>Maternal</u>
Accuracy of the index	r	Performance Records	.50	.29	.26	.19
	Records + DNA test	.58	.35	.32	.27	

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Results



Value of genetic improvement (AG) per bull derived from performance recording and DNA testing to increase the accuracy of COMMERCIAL BULL selection in a closed seedstock breeding program

Variable	Unit	Information available	Gras	s Index	FEEDLOT INDEX	
			<u>Terminal</u>	Maternal	<u>Terminal</u>	<u>Maternal</u>
Value of ∆G in commercial	٨١١٣	Performance Records	301	318	245	345
selected from top half of stud herd	/bull	Records + DNA test	363	396	306	480



Most of the value from DNA testing for the Feedlot indexes was derived by the processing sector (i.e. Dressing %, Saleable meat %, Marbling score)







Value of genetic improvement (ΔG) per bull derived from performance recording and DNA testing to increase the accuracy of SEEDSTOCK BULL selection in a closed seedstock breeding program

Variable	Unit	Information available	GRAS	s Index	FEEDLOT INDEX	
			<u>Terminal</u>	Maternal	<u>Terminal</u>	Maternal
Value of ΔG in stud sires selected	AU\$ /bull	Performance Records	17899	15922	14579	16751
from top half of stud herd		Records + DNA test	21617	19724	18211	23110



COMBINED VALUE PER DNA TEST

Variable	Unit	Information available	GRAS	s Index	FEEDLOT INDEX	
			<u>Terminal</u> <u>Maternal</u> <u>T</u>		Terminal	<u>Maternal</u>
Increased value derived from ∆G in commercial sires	AU\$/ DNA test	Records + DNA test	31	39	30	67
Increased value derived from ∆G in stud sires	AU\$/ DNA test	Records + DNA test	111	114	109	191
Total value per test to seedstock operator	AU\$/ DNA test	Records + DNA test	143	153	139	258

VALUE DERIVED PER DNA TEST ASSUMING A PERFECT MARKET

		Information	GRASS INDEX		FEEDLOT INDEX	
Variable	Unit	available	Terminal	Maternal	Terminal	Maternal
Selection response	%	Performance records	285		*)	.+
from DNA testing		Records + DNA test	20%	26%	24%	41%
Value of ΔG in	(AU\$/	Performance records	301	318	245	345
from top half of stud herd	bull)	Records + DNA test	363	396	306	480
Value of ΔG in stud sires	(AU\$/ bull)	Performance records	17899	15922	14579	16751
selected from top 3% of stud herd		Records + DNA test	21617	19724	18211	23110
Increased value derived	(AU\$/	Performance records		(41)	¥1	8
from DNA testing commercial sires	DNA test)	Records + DNA test	31	39	30	67
Increased value derived	(AU\$/ DNA test)	Performance records		14.3	*	(1
from DNA testing stud		Records + DNA test	111	114	109	191
Total value per DNA test	(AU\$/ DNA test)	Performance records		242		
to seedstock operator		Records + DNA test	143	153	139	258



To determine the value of a multi-trait DNA test you need to know

- 1. Selection objective being targeted
- 2. Heritability of the analyzed trait (h²)
- 3. Accuracy of genetic estimates already available to inform selection decisions
- 4. Genetic correlation between MVP and the trait (r_q)
- 5. Genetic variances and covariances for selection index calculations
- 6. Regression coefficient of phenotype on MBV (b)
- 7. Biological attributes and structure of stud and commercial herds
- 8. Selection intensity of replacement stud sires and bulls for sale (and females)
- 9. Number of calves per exposure
- 10. Type of herd (terminal, maternal)
- 11. Value derived from accelerated genetic progress
- 12. Sector where value is derived and how that is value is shared
- 13. Cost of test, and which animals are being tested
- 14. Planning horizon etc., etc., etc.

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Implications



- Value of DNA testing will be enterprise dependent
- DNA information clearly has the potential to provide value to seedstock producers if it is meaningfully incorporated into national cattle evaluations
- It is difficult to make optimal selection decisions or even estimate the value of multi-trait DNA tests in the absence of information on their accuracy, and the incorporation of their target traits into breeding objectives and selection index calculations
- This will likely require the development of multi-trait selection indexes for breeding objectives of relevance to U.S. beef production systems.

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