Value Of DNA Information For Beef Bull Selection

A.L. Van Eenennaam[*], J.H. van der Werf [†], and M.E. Goddard[‡]

Introduction

The value of genomic selection to the dairy industry was immediately apparent due mainly to the gains associated with the early selection of A.I. sires in the absence of progeny test information, and theoretical simulations of benefit to the breeding sector (Schaeffer, 2006) were followed by swift industry adoption (Hayes et al., 2009). Few studies have examined the economic implications of using DNA marker information in the beef cattle breeding sector which is characterized by a large number of seedstock herds specializing in the production of yearling bulls for sale to commercial producers. From the perspective of a seedstock breeder, the response to selection and therefore the value associated with the use of a DNA test is dependent upon how much the DNA information improves the accuracy of genetic evaluations at the time of selection, and the value of a unit of genetic improvement.

The objective of this work was to estimate the economic value of using DNA test information to increase the accuracy of sire selection in a closed seedstock breeding program. A selection index model was used to predict the response to selection based on conventional performance recording and on selection with additional DNA information. The expected selection differential of bulls when selected on the basis of DNA test and performance recording information was determined, and the returns associated with the selection of the top 3% of the bull calves as stud sires, and the top half of the remaining bull calves as commercial sires was calculated.

Material and methods

Breeding objectives and index accuracy. Breeding objectives were developed for both maternal (self-replacing) and terminal 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 and marbling has a high value (FEEDLOT). The traits that were included in the breeding objective and associated economic values (Figure 1A) were derived using Version 4.2 of BreedObject software (Barwick and Henzell, 2005). Because a gene flow method was used to derive disocunted gene expressions, the economic values were derived without any discounting (Barwick, personal communication). Selection criteria (Figure 1B) were those currently recorded by BREEDPLAN, the national genetic evaluation system for beef cattle in Australia. Key genetic and phenotypic parameters were based on the estimates for *Bos taurus* breeds detailed in Archer et al. (2004). Selection index theory was used to predict index accuracy when informed by conventional performance recording alone, or in combination with DNA test information, following the approach described by Lande and Thompson (1990). The proportion of additive genetic variance explained by the DNA test was set to the heritability of selection criteria (Figure 1B).

[*] Department of Animal Science, University of California, Davis, CA, 95616 USA
[†] School of Environmental and Rural Science, University of New England, Armidale, Australia
[‡] Victorian Department of Primary Industries and University of Melbourne; and Chief Scientist, CRC for Beef Genetic Technologies, Australia

A. Trait	Unit	Economic value (AU$ per unit)			
		GRASS INDEX		FEEDLOT INDEX	
		Terminal	Maternal	Terminal	Maternal
Sale liveweight – direct	kg	1.388	1.040	1.154	0.810
Sale liveweight – maternal	kg	0	1.040	0	0.810
Dressing %	%	11.653	8.990	16.077	12.880
Saleable meat %	%	9.308	7.188	13.292	10.736
Fat depth (rump)	mm	0.869	0.866	0	0
Marbling score	score	0	0	82.072	66.117
Cow weaning rate	%	0	2.576	0	4.590
Cow survival rate	%	0	6.080	0	6.789
Cow weight	kg	0	-0.194	0	-0.254
Calving ease – direct	%	1.739	1.886	2.024	2.256
Calving ease – maternal	%	0	0.753	0	0.902

B. Selection Criteria	Unit	Heritability
Birth weight	kg	0.39
200 d Weight	kg	0.18
400 d Weight	kg	0.25
600 d Weight	kg	0.31
P8 fat	mm	0.41
RIB fat	mm	0.34
Eye Muscle Area	cm^2	0.26
Intramuscular Fat	%	0.25
Scrotal Size	cm	0.39
Days to Calving	days	0.07
Mature Cow Weight	kg	0.41

Figure 1. A) Traits in the breeding objectives examined, unit definitions, and economic value and B) selection criteria, unit definitions, and heritabilities.

Structure of the seedstock herd. A simple two-tier industry example was modeled where the seedstock breeder was incurring the costs of DNA testing to improve the accuracy of bull selection. In this example the seedstock tier consisted of a closed nucleus of 600 breeding females. It was assumed that in the absence of DNA test information, breeding value estimates on young, untested bulls were informed by their own performance records on selection criteria (Figure 1B) along with those of their sire, dam and 20 paternal-half sibs. Each year the top 8 bulls were selected to be stud sires, and 125 (remaining bulls from the top half of the calf crop) were made available for sale to commercial producers. Commercial sires were then used to sire four calf crops at a mating ratio of 25 females: 1 male.

Economic analyses. The discounted gene flow method of Hill (1974), which tracks gene flow in populations with overlapping generations, was used to compute the number of Cumulative Discounted Expressions (CDEs) derived from the selection/ purchase of a genetically superior bull using the biological parameters, discount rate and planning horizon outlined in Table 1. CDEs were multiplied by the economic value associated with each trait in the breeding objective and summed to determine the value associated with the use of DNA testing to select genetically superior stud and commercial bulls. These values were then compared to selection based on performance recording alone as a baseline. It was assumed that all of the bulls in the annual cohort were DNA tested to enable selection of the best 3% as stud sires, and 50% as sale bulls. The extra cost of using

Parameters	Value
Number of live stud calves available for sale/selection per exposure	0.89
Stud cow:bull ratio	30
Number of stud cows	600
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)
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
Planning horizon	20 years
Discount rate for returns	7%
Maximum age of commercial sire	5 (4 breeding seasons)
Commercial cow:bull ratio	25
Number of commercial females	9225

Table 1. Biological and economic parameters of the modeled seedstock herd

DNA testing was assumed to be only the cost of the test, and resulting benefits were expressed on a per DNA test basis (Table 2).

Results and discussion

Genetic improvement on commercial beef ranches is largely realized through the purchase of yearling bulls (Amer et al., 2007). DNA testing using a hypothetical DNA test panel associated with 7-41% of selection criteria additive genetic variance (depending upon the heritability of the selection criteria; Figure 1B), increased overall selection response between 20-41% over that obtained with performance recording along, depending upon the traits included in the breeding objective (Table 2).

Variable	Unit	Information available	GRASS INDEX		FEEDLOT INDEX	
			Terminal	Maternal	Terminal	Maternal
SD of Breeding Objective	(AU$)		31.97	33.35	47.29	54.08
SD of Selection index (Index σ_{GI})	(AU$)	Performance records	14.62	9.07	11.94	10.40
		Records + DNA test	17.62 (+20%)	11.40 (+26%)	14.85 (+24%)	14.64 (+41%)
Accuracy of Index	r	Performance records	0.46	0.27	0.25	0.19
		Records + DNA test	0.55	0.34	0.31	0.27
Value of ΔG in commercial sires selected from top half of stud herd	(AU$/ bull)	Performance records	301	318	245	345
		Records + DNA test	363	396	306	480
Value of ΔG in stud sires selected from top 3% of stud herd	(AU$/ bull)	Performance records	17899	15922	14579	16751
		Records + DNA test	21617	19724	18211	23110
Increased value derived from ΔG in commercial sires	(AU$/ DNA test)	Records + DNA test	31	39	30	67
Increased value derived from ΔG in stud sires	(AU$/ 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**

Table 2. Standard deviation of breeding objective, selection index standard deviation, and improvement (%) over performance recording alone, accuracy of index, value of genetic gain in commercial and stud sires, and overall value derived per DNA test.

The value of this improvement relative to that obtained using traditional performance recording ranged from AU$61-135 for commercial bulls, and AU$3,632-6,359 for stud bulls. Assuming that the entire bull calf crop (n = 267) was tested and that the top 3% (n=8; i=2.27) bulls were selected as stud sires, and the remaining top half of the bulls (n=125; i = 0.8) were sold as commercial sires, the breakeven value of the genetic gain derived from DNA testing ranged from AU$139-258 per test.

These values assumed commercial producers were willing to pay a price premium for genetically-superior bulls, and some form of industry vertical integration or profit sharing between sectors such that the rewards for improvement in processor traits (e.g. dressing %, marbling score etc.) were transferred along to commercial producers and breeders. The value of DNA tests for selection critieria to improve traits of direct value to commercial cattle enterprises (e.g. cow weight) would be less than that calculated for the total industry merit indexes modeled in this study. For example, 69% of the returns from including DNA data in commercial sire selection for the terminal feedlot index were derived from improved dressing %, saleable meat %, and marbling score traits of value to the processing sector.

In this study, the proportion of additive genetic variance associated with the DNA test was set to the heritability of all selection criteria. This value was chosen as a reasonable approximation of the accuracy that might be expected when phenotypic information was available on a genotyped discovery population of approximately 2,500 genetically homogeneous animals (van der Werf 2009). This approximation is dependent upon the effective number of QTL contributing to the additive genetic variance (Goddard 2009). Unlike the dairy industry, there are relatively few high accuracy A.I. beef sires available for marker discovery. Phenotypic records will therefore likely form the basis of beef cattle discovery populations.

In the future it is likely that DNA tests will be available for economically-relevant traits which are difficult to measure and for which no good selection criteria exist (e.g. residual feed intake). Evaluating the value of DNA tests for these traits will be dependent upon their inclusion into breeding objectives along with the concurrent development of the appropriate economic values. DNA testing may also have other potential benefits to different sectors of the beef industry (e.g. reducing the risk associated with the purchase of a commercial sire, marker-assisted management in the feedlot) that were not considered in the present study.

Conclusion

The increased selection response and value associated with the use of DNA marker tests in beef cattle breeding programs will be dependent upon a number of factors including the accuracy of the DNA test and both individual herd and overall industry structure. From an industry wide perspective DNA testing could be beneficial, but the commercial viability will strongly depend on price signalling throughout the production chain.

Acknowledgement

The authors thank Steve Barwick from the Animal Genetics and Breeding Unit of the University of New England for providing selection index economic parameters. This project was supported by National Research Initiative competitive grant no. 2009-55205-05057 from the USDA National Institute of Food and Agriculture Animal Genome Program.

References

Amer, P.R., Nieuwhof, G.J., Pollott, G.E. et al. (2007). *Animal* 1:1414-1426.

Archer, J.A., Barwick, S.A., and Graser, H.U. (2004). *Aust. J. Exp. Agric.* 44:393-404.

Barwick, S.A. and A. L. Henzell. (2005). *Aust. J. Exp. Agric.* 45:923-933.

Goddard, M. (2009). *Genetica 1*36:245-257.

Hayes, B.J., Bowman, P.J. Chamberlain, A.J. et al. (2009). J. Dairy Sci. 92:433-443.

Hill, W. G. (1974). *Anim. Prod.* 18:117-139.

Lande, R., and Thompson. R. (1990). *Genetics* 124:743-756.

Schaeffer, L. R. (2006). *J. Anim Breed. Genet.* 123:218-223.

van der Werf, J.H. (2009). *Proc. Assoc. Advmt. Anim. Breed. Genet.* 18:38-41.