

TARGETING MULTIPLE END-USES IN BEEF CATTLE BREEDING PROGRAMS

B.P. Kinghorn¹, A.L. Van Eenennaam², and M.D. MacNeil³

¹University of New England, Armidale, Australia ²University of California, Davis, USA

³Delta G, Miles City, Montana

Introduction

The beef cattle breeder must juggle many issues when making decisions resulting in implementation of the breeding program, including concerns about breeding objectives, genetic gains, crossbreeding, inbreeding, logistical constraints, and various types of operational costs.

One approach to solving these problems is to follow sets of guidelines recommended by experts and respected practitioners, together with the desires and experiences of the breeder. Guidelines are developed that cover a range of issues, for example:

- Rank on index and choose the best as parents
- Avoid extensive use of any one sire or any one sire family
- Avoid full-sib matings
- Do not use carriers of genetic defects, or at least do not mate carriers
- Use Breed X sires to mate cows and Breed Y sires to mate heifers
- Perform corrective mating for a given trait Z

These guidelines are then followed as closely as possible. However, given that some guidelines are antagonistic or competitive with others, they can be difficult to integrate and compromise must be made to achieve good overall outcomes. For example, theories and rules about selection, crossbreeding and inbreeding have been developed largely in isolation from each other, such that it is difficult to mix them in real applications, and we are likely to miss the best overall strategy. Moreover, the task of trying to integrate rules can be tedious and somewhat arbitrary.

Mate Selection (i.e. selecting the best combination of sires and dams to mate with each other) is an approach that can be used both to integrate all the key issues facing animal breeders, and to implement the program *tactically*. This means that the outcome of the mate selection analysis directly determines the actions to take; the result is essentially a mating list.

Mate selection incorporates decisions on mate allocation as well as animal selection. Because selecting the best animals depends on the pattern of mate allocation, and vice versa, we can best make these decisions simultaneously as mate selection; we just decide what mating pairs and groups to make.

Moreover, there can be added advantages in making decisions tactically, rather than following a pre-set strategy. This is because a tactical approach will make use of knowledge of the full range of actual animals available for breeding at the time of decision making, as well as other factors such as availability of mating paddocks, current costs of specified semen, current quarantine restrictions on animal migration, current or projected market prices, etc. Tactical implementation of breeding programs gives the power to capitalize on prevailing opportunities - opportunities that would often be missed when adhering to a predetermined set of rules.

Such tactical mate selection systems have been used in the key domestic species for over 15 years (Kinghorn et al., 2002; Kinghorn, 2011a) using computer programs called Total Genetic Resource Management (TGRM), GenMate and Matesel. This paper will illustrate the use of mate selection to implement a beef cattle breeding program with special emphasis on targeting multiple “end-uses”.

In addition to the nucleus breeding program matings, the seedstock breeder might want to make matings to give progeny that are not targeted for use in the breeding program, but for another end-use such as:

- To contribute to a multiplier or commercial herd with the same breeding objective as the seedstock producer
- To contribute to a multiplier or commercial tier with a different breeding objective
- To produce some bulls for specific crossing duties
- To target a specific market end-point, such as extreme marbling.

It is also possible that the breeder seeks genetic diversity for a specific set of traits within the main breeding program, in order to give future flexibility to satisfy different groups of customers or to change direction of the breeding program. This could mean, for example, the targeting of a line of animals within the main breeding program that are of exceptional merit for marbling.

In this paper we use the targeting of two end-uses reflecting two sets of bull-buying customers:

Terminal: Customers who buy bulls for producing slaughter progeny alone

Maternal: Customers who buy bulls that will sire replacement heifers for cow-calf production

This means that there are three selection indices to be used for the three end-uses – a combined index for the ongoing nucleus seedstock program, a terminal index to target the customers that are producing slaughter progeny alone (i.e. not retaining replacement heifers), and a maternal index to accommodate customers that are retaining replacement heifers.

Data for the study

A dataset from an Angus beef herd pedigree was used for this study. It consisted of 169 female selection candidates, 85 male selection candidates, and a total of 1128 records including ancestors. This data set included Angus EPDs for a range of traits.

Following Van Eenennaam and Kinghorn (2014), SNP genetic markers were simulated into this dataset as loss of function (**LOF**) loci. This was done to mimic the presence of a number of lethal recessive fertility reducing loci, where the homozygous offspring (“aa”) die during embryogenesis. These LOF loci therefore play a role in assessing female fertility, and their presence is being actively investigated by several groups globally. Genotypes for 100 rare lethal SNP mutations were simulated, and genotype probabilities were calculated for all loci based on DNA test results of 95 animals with simulated genotypes. This resulted in a predicted average of 4.58 lethal mutations carried (i.e., animals were “Aa” at an average of 4.58 loci) per animal, with embryo mortality rate predictions averaging 8.6% (\pm 3.01%), ranging 1.4% to 26.3% across all 1128 animals. Of course this is mortality rate per fertilization, and with second joining of females that return to estrus, the average effect of embryo mortality on fertility is only

0.83%. This means that the biggest impact of reducing embryo mortality by managing LOF alleles is in giving a tighter pattern of calving.

Selection Indices

Table 1 shows economic weights that were available for some of the traits in the dataset. The Terminal Index was derived by MacNeil and Herring (2005), and the Maternal Index by MacNeil (2015).

Table 1. Economic weights used to generate Nucleus, Terminal and Maternal selection indices Maternal traits are in bold.

Trait	Nucleus Index	Terminal Index	Maternal Index
Calving ease direct	0.950	0	1.900
Birth weight	-0.930	-1.860	0
Weaning weight direct	0.655	0.900	0.410
Average Daily Gain	0.318	0.286	0.351
Heifer pregnancy	0.805	0	1.610
Calving ease maternal	0.950	0	1.900
Weaning weight maternal	-0.055	0	-0.110
Marbling score	15.920	13.540	18.300

Maternal traits (bold in Table 1) attract a zero weighting in the Terminal index, as expected. The economic weights for the nucleus index are simply the average of the Terminal and Maternal indices, assuming equal importance of these end-uses for the main breeding program.

Unfortunately, availability of EPDs and economic weights were such that many Terminal and Maternal specialized traits had very few records in this dataset, and are not included in Table 1. This means that the indices used were rather similar – the Terminal and Maternal indices being correlated 91.4% and 96.2% respectively with the Nucleus index. This gave little opportunity for these data to give strong results, such that the results given are illustrative rather than evaluative.

In particular, only 18 EPDs for heifer pregnancy were available. Accordingly, EPDs for heifer pregnancy were replaced by predictions of the impact of simulated LOF loci on pregnancy rate, through predicted impact on embryo loss from lethal recessive (“aa”) expression in the embryonic progeny, as indicated in section “Data for the study”. This resulted in proxies for heifer pregnancy values averaging 91.4% (i.e. 100% - 8.6%), with a standard deviation of 3.01%. In other words, heifers carrying fewer LOF alleles (Aa) had higher heifer pregnancy values than those carrying a lot of LOF alleles. In the worst case, one animal carried so many LOF alleles that she had a pregnancy value of only 73.7%, as on average her embryo mortality rate was predicted to be 26.3% when mated within this population. Accordingly, she would be penalized heavily when using the Maternal index considering the high economic weighting given to heifer pregnancy (Table 1). Conversely, no penalty is given to the average progeny heifer pregnancy weight in the Terminal index as all of those animals are targeted as parents of slaughter animals. As a result, it might be expected that high genetic merit animals carrying a lot of LOF alleles

would be used more in producing bulls for Terminal customers than in producing bulls for Maternal customers who buy bulls that will sire replacement heifers for cow-calf production.

Overview of mate selection analyses

Two key outcomes in any breeding program are the levels of genetic gain and genetic diversity, as indicated by predicted mean progeny index (\$Index; Y axis) and parental coancestry (X axis), respectively (see Figure 1). The most aggressive breeding program will use the highest EPD stock available with no regard to diversity, possibly covering the whole female herd with semen from the very best bull. This is represented by the “0 degrees” point in the top right corner of Figure 1. The most conservative breeding program will use as many bulls as required to maximize genetic diversity, with more matings to bulls that are less related to the female herd. This is represented by the “90 degrees” point in the bottom left corner of Figure 1.

For high-end beef breeding programs, importing outside stock to generate diversity and avoid longer-term inbreeding might be seen as a big compromise in genetic merit. For these programs, a moderate policy of about 25 degrees (see the green line in Figure 1) is probably appropriate. However, for most breeding programs, 10 degrees may be more appropriate to maximize the rate of genetic gain (i.e maximize the predicted progeny mean index) while giving some consideration to genetic diversity.

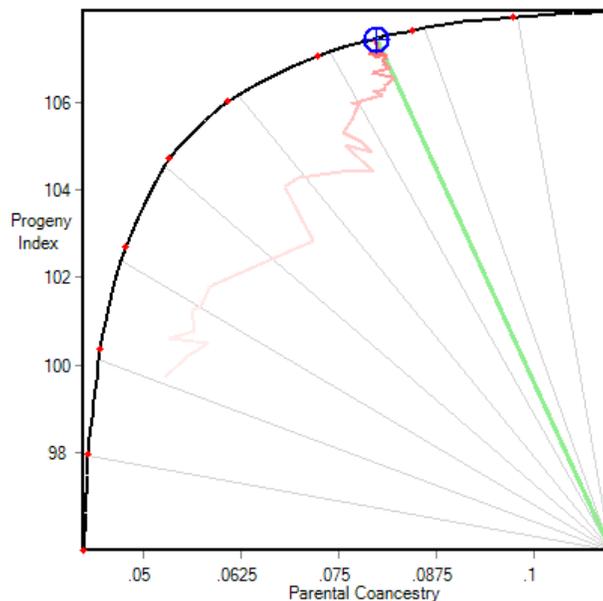


Figure 1. A response frontier. The curve is the frontier of optimal contributions (or optimal number of matings allocated to each candidate), where each point on the frontier represents an optimal mating list for the corresponding relative emphasis on progeny index and parental coancestry. The top-right of the frontier is 0 degrees, with full emphasis on progeny index (genetic gain), and the bottom-left is 90 degrees, with full emphasis on lowered parental coancestry (increased genetic diversity). The solution has settled on the frontier at the 25 degree ‘target’ line. Where other issues (such as trait distributions and progeny inbreeding) are given sufficient emphasis, the solution will move away from this frontier, downwards (lower genetic gain) and/or to the right (lower genetic diversity). From the Matesel instruction manual available at the following website: <http://www-personal.une.edu.au/~bkinghor/matesel.htm>.

The best choice also depends on the shape of the frontier curve, which in turn depends upon the animals that are available for selection. Where there are many lowly related male candidates of similar high index value, greater diversity can be achieved at little loss in genetic gain simply by including more of these males in the mating list. This is seen in the shape of the frontier, and a higher-degree solution is warranted. Conversely, where there are only a few candidates of notably high index value, spreading contributions to give lower coancestry results in rapid loss in genetic merit. This is typical where there is one legacy sire, and the next best candidates are his sons; we have to move out of that high-merit family line to get new diversity. Kinghorn (2011b) shows how these factors can be handled automatically.

Method

The current analyses use the “Multiple EndUses” feature of Matesel (<http://www-personal.une.edu.au/~bkinghor/matesel.htm>). There were three end-uses: Nucleus, Terminal commercial and Maternal commercial, with the indices used to select for these end-uses coming from Table 1.

For the treatment analyses, the total number of matings to be made was set at 125, with 75 of these being dedicated Nucleus matings (i.e., producing animals that are targeted to return to the seedstock nucleus herd), plus 25 targeted to produce offspring for the customers that are producing slaughter progeny alone, and an additional 25 targeted to customers who buy bulls that will sire replacement heifers for cow-calf production

The overall weighting for these three groups were set at 1, 0.85 and 0.85, ensuring that the nucleus end-use attracts the best candidates mated in the best manner to maximize the nucleus index for these 75 matings. This does not mean that the nucleus has been reduced from 125 to 75 females, as all resulting progeny will be candidates for selection into the nucleus. However, what we have done is to increase the chances that we will have more appropriate bulls available for sale to Terminal and Maternal customers, by targeting 25 matings at each of these specific outcomes.

Essentially we direct the head of the breeding program at our long-term genetic goals for the nucleus, and we direct the tail of the breeding program at our customers’ needs.

Control analyses were also run with just two end-uses, Nucleus and General commercial, with 75 and 50 matings generated. These both used the same Nucleus index, such that there was no Terminal and Maternal specialization targeting commercial customers. In this case, the outcome is expected to be the same for the Nucleus end use as achieved in the treatment analyses, but the commercial end-use is expected to have outcomes intermediate between the Terminal and Maternal outcomes in the treatment analyses with three end-uses.

Results

Mate selection runs were first run with full emphasis on genetic gain, corresponding to 0 degrees in Figure 1. Figure 2 shows that the Nucleus (black) consistently gives very much better genetic gain as indicated by the value of the mean progeny index than any of the other end uses, as expected. For the non-nucleus matings, the control analyses (lightest grey) using the same Nucleus index for all matings gives results that are always intermediate between the Terminal and Maternal outcomes. This means that the Terminal end-use matings are on average

substantially better than the control for the Terminal index, and similarly for the Maternal end-use index.

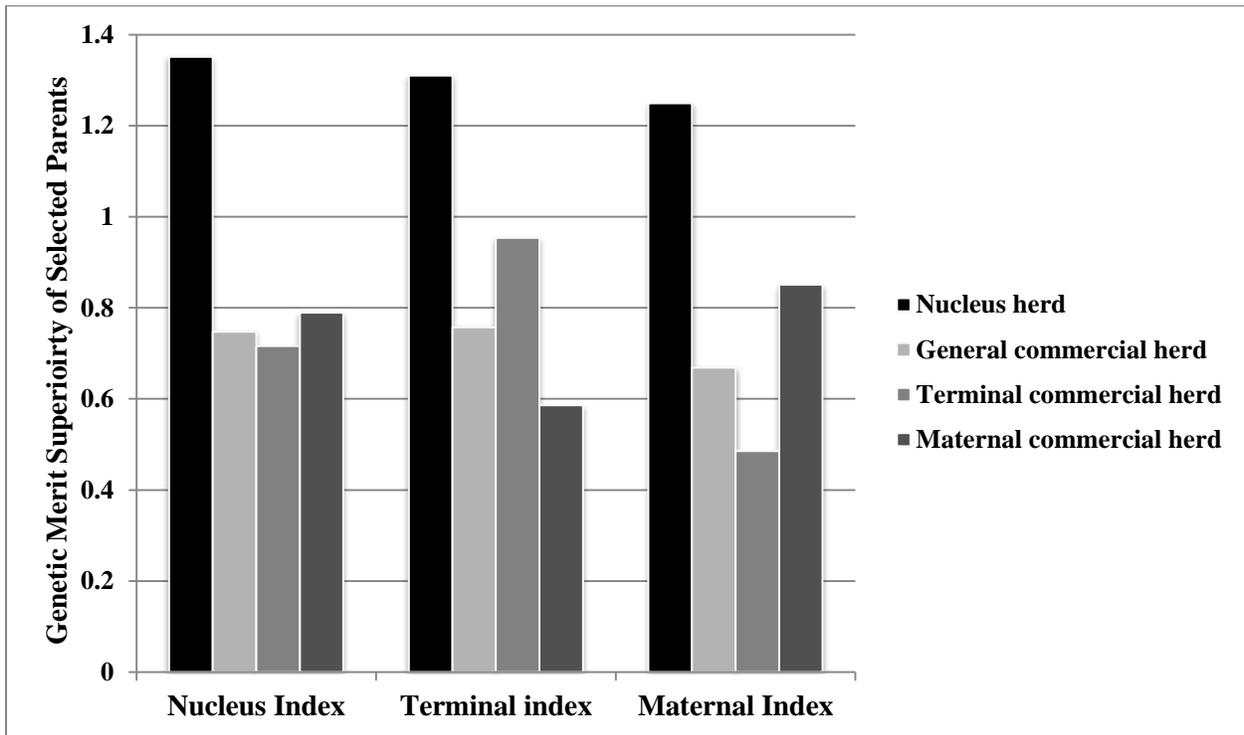


Figure 2. Mean genetic merit under each of the three selection indices for each end use group. Genetic merit is given in standard deviation units superiority of selected parents as deviated from the mean index of the available candidates. For these runs, target degrees was set to zero, giving full emphasis to genetic merit in progeny.

Strong emphasis on maintaining genetic diversity in the nucleus was used for results shown in Figure 3, with target degrees set at 45 (refer to Figure 1). This results in lower response in the Nucleus end-use (compare the black bars in Figure 3 to those in Figure 2), but actually higher responses in the Terminal and Maternal end uses compared to full emphasis on genetic gain. This is because genetic diversity is of little value to bull-buying commercial customers, and this is recognized by the method in Matesel, which only calculates and accommodates parental coancestry values as expressed in the Nucleus (EndUse 1) matings. Under this conservative policy, high genetic merit individuals are used less in the Nucleus matings, and are now available for increased use in the commercially-targeted matings which results in a higher average genetic merit of the Terminal and Maternal end-use matings.

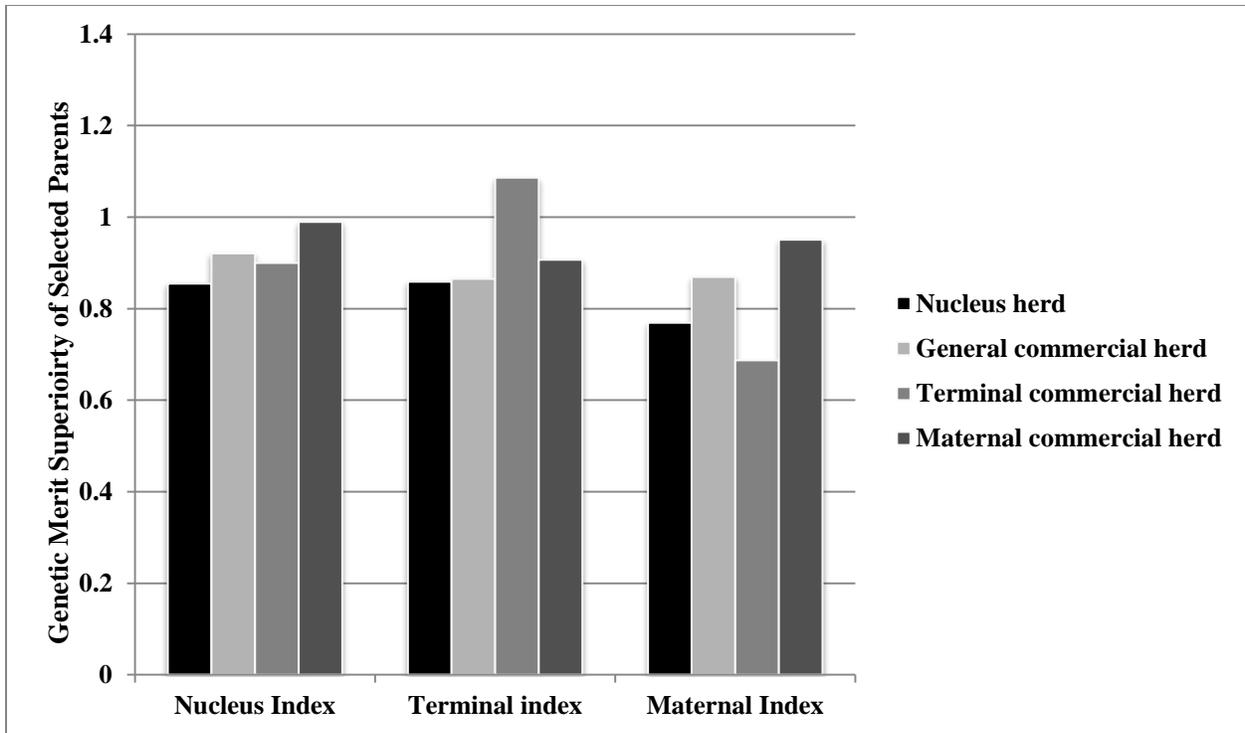


Figure 3. Mean genetic merit under each of the three selection indices for each end-use group. Genetic merit is given in standard deviation units superiority of selected parents as deviated from the mean index of the available candidates. For these runs, target degrees was set to 45, giving strong emphasis to genetic diversity at the cost of genetic merit in progeny.

Discussion

Results suggest that targeting multiple end uses in the manner presented gives outcomes that reflect the desire to satisfy multiple targets. These results are likely moderate compared to what might be expected in practice, given the availability of a more complete range of economic weightings and corresponding EPDs.

Of course, the results relate to *predicted* progeny merit, as we are in the process of selecting parents from candidates, and the actual outcome of these decisions must wait until progeny are born and tested. At this later stage, the value of individual progeny will be newly evaluated, and their fate (nucleus use, commercial sale, or cull) determined accordingly. Variation in merit within the allocated end-uses, both predicted and realized, will affect assessment of the method described here. However, the increased specialization evident in Figures 2 and 3 where 25 matings were each specifically targeted to Terminal and Maternal outcomes is likely to lead to a real increase in the ability of the breeder to produce seedstock (or indeed product) suitable for diverse customer needs.

In the context of LOF lethal recessive fertility reducing loci, it is important to appreciate that this is an key consideration for Maternal customers who are producing replacement heifers, but is of little importance to Terminal customers who are producing progeny for slaughter alone. This is perhaps best illustrated in Figure 3 where the average genetic value of the Terminal index increases substantially for the Terminal commercial herd when allowed to use the high genetic

merit parents that were being discounted by both the Maternal and Nucleus indices due to the economic weighting associated with the trait of Heifer pregnancy in those two indices, and the fact that there was no discount associated with that trait in the Terminal index.

As indicated previously, the best index or indices and policy to use in practice depend on the position of the seedstock breeding in the industry (i.e. what is target market) and breeder attitude to genetic progress versus genetic diversity. However, most breeders are unlikely to be as conservative as the example in Figure 3 with a target degrees set at 45 (i.e., very high value given to genetic diversity). For most breeding programs, 10 degrees may be more appropriate to maximize the rate of genetic gain (i.e, maximize the predicted progeny mean index) while giving some consideration to genetic diversity.

Acknowledgements

The authors acknowledge Mike Kasten and the American Angus Association for herd and pedigree data; and funding support from the National Research Initiative Competitive Grant no. 2013-68004-20364 from the USDA National Institute of Food and Agriculture.

References

- Kinghorn, B.P.; Meszaros S.A.; Vagg, R.D. 2002: Dynamic tactical decision systems for animal breeding. Proceedings of the 7th World Congress on Genetics Applied to Livestock Production. 33: 179-186. [CD-ROM communication n° 23-07. ISBN 2-7380-1052-0]
- Kinghorn, B.P. 2011a. An algorithm for efficient constrained mate selection. Genetics Selection Evolution. 43:4. <http://www.gsejournal.org/content/43/1/4>
- Kinghorn, B.P. 2011b. Automated mate selection analyses. Assoc. Advmt. Anim. Breed. Genet. 19:15-22.
- MacNeil, M.D. and W.O. Herring. 2005. Economic evaluation of genetic differences among Angus bulls. Proc. West. Sec. Amer. Soc. Anim. Sci. 56:87-90.
- MacNeil, M.D. 2015. Value of genomics in breeding objectives for beef cattle. Presented at 52nd Annual Meeting Brazilian Society of Animal Science, Belo Horizonte. July 20-23, 2015
- Van Eenennaam, A. L. and Kinghorn, B.P. 2014. Use of mate selection software to manage lethal recessive conditions in livestock populations. Proceedings, 10th World Congress of Genetics Applied to Livestock Production. Paper 408, https://asas.org/docs/default-source/wcgalp-posters/408_paper_9819_manuscript_1027_0.pdf?sfvrsn=2