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MATE ALLOCATIONS IN BEEF CATTLE HERDS

W.H. Upton[1], S.A. Meszaros[2], S.A. Barwick[1] and B.P. Kinghorn[2]

[1]Animal Genetics and Breeding Unit, University of New England, Armidale, NSW 2351
[2]Department of Animal Science, University of New England, Armidale, NSW 2351

SUMMARY

BREEDPLAN, BreedObject and Total Genetics Resource Management (TGRM) offer the Australasian beef breeder the opportunity to apply genetic theory at a practical level. Application of these programs to three herds is used to demonstrate the potential for genetic improvement at the seedstock level.

Results for three Angus herds that have clearly made genetic improvement by using BREEDPLAN EBVs demonstrate the added value from the use of BreedObject and TGRM. Higher selection intensity combined with designed matings can more than double the rate of genetic progress in one year.

Keywords: Beef Cattle, selection, genetic improvement.

INTRODUCTION

Hammond *et al*. (1992) when describing the modern approach to animal breeding describes three primary components. These being the breeding objective, genetic evaluation and breeding program design. The breeding information systems described in this paper make available to beef cattle breeders, tools that allow the three steps to be applied at the practical level.

BREEDPLAN version 4.1 (Johnston *et al*. 1999) is the genetic evaluation system for the Australian beef industry that produces EBVs for most of the economically important traits. BreedObject Barwick *et al.* 1998) uses BREEDPLAN EBVs, the target market specifications and production details from a commercial beef herd to rank animals that will be most suitable for increasing profitability in that scenario. BreedObject defines the breeding objective and calculates appropriate weightings for EBVs (selection criteria). The selection index component of BreedObject formally links the genetic evaluation system, BREEDPLAN, with the breeding objective developed as the first part of BreedObject.

TGRM (Total Genetics Resource Management) (Meszaros 1999; Vagg *et al.* 1999) is a mating program designed to help achieve maximum genetic gain with a minimum of inbreeding. TGRM maximises the index value of the progeny within given constraints while controlling the rate of inbreeding.

This paper describes the genetic gains in three herds and illustrates predicted improvements from the use of BreedObject and TGRM.

MATERIALS AND METHODS

Data was used from three Australian Angus herds and the Angus published sire summary. The three herds were chosen because they had similar production and market objectives. BreedObject indexes were calculated for all animals within the three herds and all Angus sires.

Two of the herds in this study had previously organised for bull buying clients to complete BreedObject questionnaires to develop a breeding objective and selection index. The manager of the third herd completed the questionnaire on behalf of his bull buying clients. In each case the resulting index was very close to the standard Angus feedlot index and all herds opted to use the standard index.

The standard Angus index is designed for a production system that finishes cattle for approximately 200 days in a feedlot and the target market is Japan which pays a premium for marbling. This index has been developed over a number of years by the technical staff at the Angus Society with support from AGBU, using inputs from breeders and their commercial bull buying clients.

The standard Angus index was used as the primary trait on which TGRM allocated matings. Fifteen other EBVs were also available for consideration in the mate allocations.

Each herd nominated male and female candidates as parents of the next generation. In all three cases the first TGRM run used the highest 100 indexing male animals from the Angus database as prospective sires. This simulated a breeding program where unlimited use of AI was available.

Genetic progress monitored using the standard Angus BreedObject Japanese Longfed (B3) index as the measure of profitability was plotted for each of the three herds over years of birth (Fig 1). The index values for ancestral animals are calculated from EBVs assigned from pedigree information. Regression techniques were used to predict the index values for the 2000 born progeny assuming no change in selection policy.

TGRM was used to perform mate selections for each herd based on the index values for females within the herd and available males from the Angus population. Total cow numbers in the three herds was greater than 2700. Selection intensity in cows was low as the number available for selection was similar to the number of matings required.

RESULTS AND DISCUSSION

Trends in Figure 1 show that since the late 80s or early 90s the progress for the 3 herds who have extensively used BREEDPLAN figures as a guide to selection have made rapid improvement in index values. Regression coefficients for improvement since 1990 were \$2.87, \$3.09 and \$3.44 for herds 1, 2 and 3 respectively. Using these regression coefficients it was predicted that the 2001 born progeny would have average index values of \$55.56, \$52.65 and \$53.68 for herds 1, 2 and 3 respectively.

The allocation of mates using unlimited AI sets the genetic potential for a mating design with single use of females. For each herd the TGRM value showed considerable advantage over the current

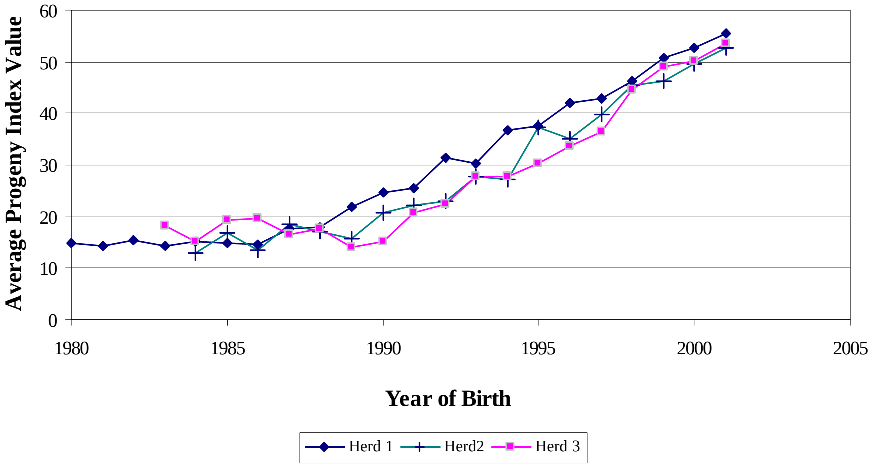

Figure 1. Genetic trends for three herds including regression estimates for 2001 born calves.

trend. The advantages were $16.80, $13.40 and $11.40 for herds 1, 2 and 3 respectively. These increases in average index values resulted in part from increased selection intensities on sires for the index. The average index values for the sires used in herds 1, 2 and 3 respectively were $92.6, $83.3 and $77.84. These compare favourably with the breed mean for 1999 born calves of $36.

In herds 1 and 3 the index values from TGRM will be an overestimate of what could be achieved even if the managers totally complied with the given mating plan as it assumes AI achieves 100% pregnancy. The average index value will be lower because a percentage of calves will be sired by naturally mated back-up sires with lower indexes. However herd 2 which relies on 100% AI for mating should be able to achieve close to predictions. There is no dilution of the predicted progeny with calves from back-up sires.

Herd 2 having been given the first TGRM mate selection list then imposed independent culling levels on some of the traits, limited the number of uses of some sires due to limitations in semen stocks or semen price and imposed ‘must use’ constraints on other sires. The second TGRM run had an average index value of $59.06. The actual mating plans for herd 2 were a slight modification of this second TGRM but the average index value was still approximately $59. Even after the additional constraints were applied the average index value still exceeded the regression value by more than $6.40.

The three herds in this study were chosen because it was demonstrated that they have similar breeding objectives and therefore a standard index can be used to make the results comparable across herds. The lack of vertical integration between the seedstock sector and the commercial breeder in the beef industry adds a level of complication as the seedstock breeder will generally supply genetic material to many commercial breeders and each of the commercial breeders could have a different breeding objective. The seedstock breeder must compromise and develop for himself a breeding objective that is appropriate for the majority of his clients. The alternative is to specifically target different customer groups and TGRM can accommodate this approach.

Development of standard indexes on a breed basis has been a digression from best genetic theory, but has been encouraged by the need to cater for multiple clients and the desire to rank animals across herds. Work in temperate Australia with breeders using the same breed and focusing on a similar market has generally shown high correlations between indexes. Standard indexes have also proven valuable to popularise the concepts of indexes, making them part of the language to describe animals.

TGRM mate selections attempt to maximise the index value in the progeny. Refinements in the outcome of individual traits can be applied at this level. Pressure can be applied to individual traits once the mid-parent values are calculated. Application of preferences at this level is not as severe as application at the parent selection level. Parents that may be discarded for an independent culling level on one particular trait may still be used when culling is done on expected progeny outcome given available parents of the opposite sex to complement the values of the first parent.

Applying independent culling levels at the predicted progeny level can extend economic merit beyond that of an index. This is true whenever the value of progeny merit is not linear. For example calving ease may have little economic value provided it is above the appropriate threshold for the herd in question. There is no need to move the average progeny value as long as the tail of the distribution can be ‘cut off’. Selection pressure can then be maintained on other traits that increase overall economic returns.

Experience with BreedObject indexes and TGRM in the three herds has demonstrated the potential to fast-track genetic improvement using these tools. It was not possible to separate the effects of the index and the TGRM mate allocation as the herds had not effectively been using the index for seedstock selection prior to the use of TGRM. Higher selection intensities on sires were a major contributor to the increased rate of genetic progress. The use of TGRM and BreedObject encouraged these higher intensities by focusing on traits of economic importance and accounting for inbreeding. As industry confidence in the tools increase and more features of TGRM are used, the TGRM-BreedObject breeding information system will have a major impact on the rate of progress in beef cattle herds by improved adoption of sound breeding principles.

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