

STORELINK

**MEAT & LIVESTOCK AUSTRALIA /
NSW AGRICULTURE**

PROJECT M726C

**Final Report
July 1999**

Individual Sire Identification Project



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1. EXECUTIVE SUMMARY

The original aim of the Sire Identification subproject was to evaluate the alternative techniques for identifying progeny of different sires. The commercial use of various alternatives will be dependent on the accuracy of the technique and the cost of implementation. High accuracy is attainable with all techniques provided certain guidelines are observed. The most costly technique – DNA typing – is currently cost efficient only in stud cattle breeding situations, but is likely to become much more attractive if demand is sufficient.

In the course of the project, we have put more weight on consideration of other areas relating to the use or identification of individual sires. These include the prediction of response in relation to the estimated genetic merit of sires, and the measurement of responses and differences between groups in relation to the sizes of the groups of interest. We have therefore developed a discussion of this aspect and provided a kit of tables that deal with factors affecting the outcome of using selected sires. An important aspect of this area is an appreciation of some of the statistical (mathematical) issues involved. We have attempted to provide some fairly simple explanations of such issues. These are not intended to fully school the reader in mathematical procedures, as this is not necessary, but rather to provide an awareness of the underlying principles at a level that will help to clarify some of the reasons why certain outcomes are more or less predictable.

We have also looked at two applied situations within two Storelink Demonstration Groups at Moree and Albury. For a herd within the Moree Group we have calculated the cost of actually providing individual sire identification for progeny by single sire joining and compared that to the actual advantages. In the Albury group herd we have determined what could be reasonably invested in individual sire identification by determining the differences in financial returns from sire progeny groups finished in a feedlot.

2. TECHNIQUES AVAILABLE FOR INDIVIDUAL SIRE IDENTIFICATION

Options are available to industry to get accurate sire identification (ID) in commercial herds. We reviewed a number of these options — they were:

Single Sire Matings

The constraint to using this option is the provision of secure mating groups to restrict mating to specific single sires. Thus the physical requirements of separate paddocks and maximum possible separation between paddocks will determine the feasibility for any particular property. It is likely that additional capital costs will be incurred in subdivision to provide sufficient paddocks for group sizes much smaller than normal management groups.

Synchrony would have to be staggered if used, to avoid excess mating load.

Pregnancy testing would be essential with this option if the same sires were not used for each group throughout the joining season.

There is also a high risk of unintended matings (bulls jumping fences, etc.)

Alternate Breed Group Joining

This may be a feasible option for group joinings using 2 or more sires with clearly identifiable characteristics in the progeny that differ due to the breed of sire. However there are few heritable characteristics that are definitive enough to give positive identification of parentage. Only dominant traits would be useful in this regard, since we need expression of clear differences in all progeny of the sires compared.

Some dominant traits that could be used would be:

- white face (for Hereford-sire progeny)
- breed coat colour
- polled or horned

The use of coat colour may be reliable only for extreme comparisons (eg. Angus-sired vs charolais). Polled is considered to be a dominant trait in most breeds having it as the normal phenotype.

This could be a low cost option, but limited to small numbers of sires per mating group and also requiring strict separation restrictions.

The situations where this would be applicable are limited.

AI

Synchronised AI provides a fully controlled system, and the accuracy of progeny parentage is basically a function of the accuracy of records.

There are several synchrony systems available, based on control by prostaglandin, progesterone, oestrogen, gonadotrophins and various combinations of these. There are options for insemination at fixed times or detected oestrus and the AI may be done by contractors or the producer. Thus there are a wide variety of scenarios that will affect the cost for any particular operation. The suitability of various synchrony regimes according to the resources, status of the animals and nutritional conditions is considered in a

separate review exercise - "COWSYNC" (Wilkins and Hoffman), which will be used as the guide for demonstration programs. There is wide variation in cost of programs (\$13 - \$50 excluding semen cost). Budgets for a range of AI programs is attached as Appendix 1.

Fully synchronised programs would be necessary if using contractors, but it would be possible to use modified systems, or even unsynchronised AI, if the producer can do the AI himself. However this is an unlikely option.

Pregnancy testing for confirmation of conception to AI would be necessary to eliminate uncertainty.

DNA Typing of Progeny

This is an option where individual identification is required following multiple sire mating. The cheapest DNA typing test currently available costs \$35/sample laboratory fee, but extra costs involved in sampling (say \$2-\$5), would increase this to around \$40/sample. Several alternatives are possible for the future to lower costs, but these essentially depend on large volume if demand greatly increases. This option does not require synchrony. Pregnancy testing is not essential but desirable to aid management.

Prior screening of sires before mating can aid definition of test results on progeny. Some limitations in accuracy and proportions of sire allocation apply.

General Considerations

Synchronisation (of oestrus) will assist management and pregnancy diagnosis with all options, if it is not essential for the particular one used. High mating loads restrict use to AI or small groups only with natural mating.

Pregnancy diagnosis will aid general nutritional and calving management/separation of time of calving groups. In particular, the separation of cows into groups on cycle of successful conception will in some cases be essential for sire ID - eg. where different sires (by either AI or paddock mating) are used in successive cycles. This would be best done with ultrasound, but not readily available in the short term. Diagnoses with palpation should be accurate (dependent on operator) but would require stringent timing strategies for this purpose.

Calving dates will assist ID to some extent but must be used with great caution. Variation in gestation length results in considerable spread in calving dates for cows inseminated on the same day (see example Figure 1). Any use of calving dates must account for this variation.

With any system, progeny of uncertain matings may have to be excluded unless checked with DNA typing (adding to the cost).

3. IMPROVEMENTS IN DNA TECHNOLOGY

Vankan and Burns (1997) presented the use of DNA markers for sire identification with its use and limitations. This is an improvement on the previously used blood typing technique, being more accurate at similar cost. There is also the possibility of making collection and handling of samples easier and less costly than the blood sampling used to date (Demeny et al., 1997).

We have examined the use of hair and blood samples for DNA typing.

3.1 Methods

We used samples from steers and heifers that were slaughtered as the end point for an experiment conducted by Helen Hearnshaw of NSW Agriculture at Grafton. The parentage of these animals was known prior to this exercise, so that the accuracy of the test results could be checked. The animals were killed at Casino abattoir on 10/6/97 and 16/6/97, and the following samples were taken along the slaughter chain :-

- blood from the jugular after the throats were severed at the start of the slaughter chain
- section of the tail after removal from the body

A sample of the whole blood (several drops to give a blot area of about 2 x 3 cm) from each animal was put onto separate strips (10 x 3 cm) of special filter paper (Schleicher & Schuell – No 2992), as described by Demeny et al. (1997). These were air-dried before storage for dispatch. About 20 hairs were pulled with tweezers from each of the tail pieces, making sure that they had follicles on their ends. These were put into separate "snap-lock" plastic bags for dispatch.

Samples were processed and analysed with the standard techniques at the Qld DNA typing Laboratory.

3.2 Results

There were 28 whole blood samples sent for analysis. Of these, 24 also had samples prepared as filter paper blots. Hair samples sent for analysis had problems as described below.

The samples were from progeny of 4 sires, 2 that had previous DNA typing results, and 2 others that were tested on this occasion from semen straws. A few samples were included with sires other than these 4, as a false identification check.

Whole blood and filter blot

All samples for both whole blood and filter blot were correctly identified to sire, including those with no record of sire available. Some of the filter blot samples did not yield suitable DNA extract because they must have been incompletely dried before submission.

Hair samples

We had problems with the hair samples. The laboratory was unable to attend to them till several weeks after arrival and by then most were in a poor state, unsuitable for DNA extraction. This was due to the method of collection – in this case from the tail pieces removed on the chain at the abattoir. The samples were wet or at least moist when brought back for preparation, and the hairs were apparently not completely dry before being put in the plastic bags for dispatch. Hair samples are normally taken from live animals and would not have any problems of moisture.

3.3. Conclusions

This exercise has confirmed previous reports of the accuracy of the DNA typing test, which was not really in question. The filter paper blot technique was shown to be quite a viable alternative and has several attractive features, with the ease of storage probably the most useful.

The problems of moisture in samples (both hair and filter paper) sent to the lab were a valuable warning to demonstrate the degree of care needed in preparation of such samples. For this reason, staff at the laboratory have been keen to recommend veterinary involvement in collection of samples, but this is expensive. We have agreed in discussions that adequately trained technical staff can do the job when made fully aware of all the pitfalls, but considerable effort would need to be put into training if producers were to collect their own samples.

Goddard and Goddard (1997) pointed out that the extreme offspring (best and worst) of a mating are the most informative for estimating EBVs. They therefore suggested that the cost of DNA testing to identify sires and estimate EBVs in multiple sire matings could be greatly reduced.

DNA testing is also being evaluated for its cost/benefit in Merino ram breeding (Barnett et al., 1997; Parsons et al., 1997).

The concept of SMART breeding — use of Selection with Markers and Advanced Reproductive Technologies has recently been proposed as the way for the future by integrating a variety of molecular and novel reproductive technologies (Davis et al., 1997).

4. ECONOMIC GENETIC GAINS –what are we aiming for?

To realise economic gains by sire selection, the traits considered must be:-

- Heritable
- Of economic significance in the sale product

Largest profits will be gained by realising large differences in bulk of saleable product in the progeny (eg. by increasing carcass weight) and/or achieving differences in traits of high value (eg. marbling). Gains could also be made by increasing efficiency of feed conversion.

Estimation of breeding value or ranking, by identification of progeny to sires, can be used to determine:-

- Future use of those particular sires in the breeding program
- Use of current progeny
 - selection of animals for finishing
 - selection of females for future breeding
- Culling of female relatives to improve the genetic merit of the current breeding herd

The amount of money that can be spent on sire ID obviously depends on the value of the improvement that can be made by using the information. This will be a function of the size and value of the response in targeted trait(s) in any group of progeny, and the number of animals affected by the improvement. There may be cumulative effects to be considered, since sires, and their progeny as sires, affect production into the future. The cost of getting the information depends largely on how many progeny must be tested to get a "reasonably accurate" estimate of the breeding values or ranking of the sires.

Information generated to estimate breeding value of sires will have more economic benefit (to the industry) than that immediately obvious in the current herd, if the genetic gains are transferred to other herds. This has always been the case at the stud level, but we could see an increase in transfer of better genotypes among commercial producers if sire evaluation is economic at that level.

4.1 Making the "black-box" more transparent

Issues relating to genetic responses, estimated breeding values (EBVs) and the like often have a "black-box" air about them because of their apparent complexity and difficulty of explanation. We have therefore attempted to clarify a few of the important areas to give users a better appreciation of what is involved and what can be expected. Issues such as numbers of progeny, accuracy of estimates, response that can be expected in progeny groups in commercial herds. The latter is an important issue for the awareness of producers since the actual gains are affected, not only by the estimated merit of the sire, but also by the sample size of the groups where they are measured. We will attempt to provide as much assistance as possible to producers in making the "black box" more transparent, when applying genetic theory to practical production situations.

4.2 "Accuracy" of EVBs

The genetic merit of an animal, as indicated by EBV for various traits, is the best estimate that can be made from the available data, which will have some level of reliability attached to it. This is the "accuracy" value that appears with the EBV. The size of this (accuracy) depends on the heritability of the trait and the amount of information that was used to calculate the EBV. An explanation of this is often given with the publication of EBVs as in the Breed Sire and Dam summaries provided by the breed societies. The visual presentation of EBVs and their accuracy for various traits, as presented in the "Diamond Select" format, developed by the Western Angus Group of Victorian breeders, is an excellent way to provide an appreciation of these concepts. We are grateful to this group of innovative breeders for permission to reproduce their format (shown in the following figure) to demonstrate its "user friendliness". The visual concept of the

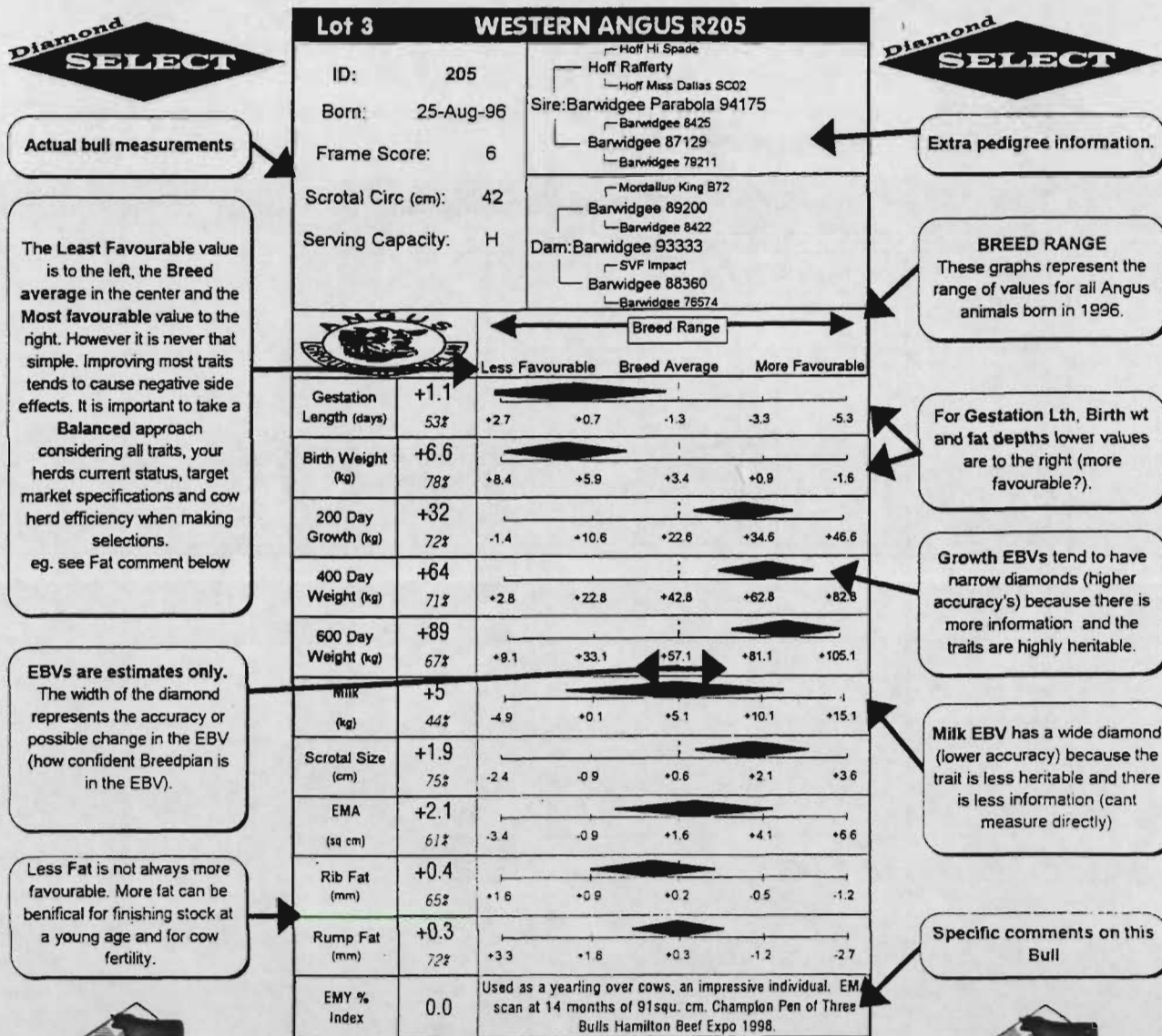
“diamond” provides any easy way to portray the accuracy (thus possible change) of the value of EBVs for various traits.

Catalogue Presentation for BREEDPLAN

Many people have sought over the years, better ways to present BREEDPLAN EBVs and their accuracies. I'm pleased to help publicise this great new idea from a group of Victorian breeders - Western Angus. Their trademark is Diamond Select. As shown below, the centre of the diamond shows the location of EBVs in the breed percentile table. The width of the diamond shows the possible spread - decreasing as you go from the most likely estimate. I'm told Simon Gubbins had the initial idea and David Kelly worked out the presentation on his computer.



Western Angus breeders Alec & Jo Moore, Mark Gubbins, David & Wendy Kelly, Simon Gubbins and John Sambell.



Purchaser _____

Price _____

4.3 Cost of estimating genetic merit in relation to accuracy

There are direct relationships in the accuracy (or predictive value) of estimates of genetic parameters with the amount of data used to generate them. The "accuracy" figures given with EBVs for various traits, as calculated in BREEDPLAN, result from the number of records from progeny and related individuals that contribute to the calculations. The situations we are now considering are those where we may have access to records from progeny only, and producers need to appreciate the scale of numbers and accuracy that will apply, when estimates of breeding merit or rankings are made in this way. For example, it has been calculated that for say 400 day weight, which has a heritability of around 0.3, data on 10 progeny will give an estimate of the sire's EBV with an accuracy of 67% - this is probably too low an accuracy to justify the cost of getting the information - we would need to get data from 50 (or more) progeny to increase the accuracy to 90%. In commercial situations, we may not be making the actual mathematical calculations to quantify EBVs, but will more likely be ranking sires. However, the same principles apply to the accuracy of the estimates made. Table 1 shows the relationship between numbers of progeny and accuracy of estimates for a range of parameters. These accuracy figures are a direct reflection of the standard errors of the EBVs, which determine how well we can predict the performance of the progeny the next time that sire is used. Increasing accuracy of the EBV means smaller standard errors and better prediction of performance. There is a large effect in reducing the standard error of the estimated EBVs as you move from say 70% to 90% accuracy and again large as you go from 90% to 99% - but there are large differences in the numbers of progeny required to make these shifts (as shown in Table 1), which therefore increases costs.

Table 1. Accuracy (%)[#] of EBV estimates using data on variable numbers of progeny, for traits with a range of heritabilities.

Heritability (example traits)	No of progeny tested					
	10	15	20	30	50	100
0.1 days to calv. calv. ease	45	52	58	66	75	85
0.2 200 day wt gest. length	59	66	72	78	85	92
0.3 400, 600 wt P8 fat	67	74	79	84	90	94
0.4 birth wt scrot. size	73	79	83	88	92	96

these calculations of accuracy of EBV estimates are based on the records from the progeny only (and assuming no more than half-sib relationship among progeny) – accuracy will be improved by additional records if available.

4.6 Detection of differences between groups

When making comparisons between means of groups (like sire progeny groups), we need to know the size of the difference that can be safely declared “significant”. “Significant” simply means that we have satisfied some statistical (mathematical) test of the data. There are 2 commonly used procedures to examine such differences. These are the “t” test and the calculation of the “least significant difference” (LSD). If the “t” value or the difference between group means satisfies the test (ie differences at least as large), we can be confident that it was due to the effect (like sires) being tested, and not to some other chance effect. We can put a value on the level of certainty about these tests, which is called the “level of probability”, and commonly set at 5%. This means that there is only a 5% chance of being wrong, or a 95% certainty of being correct, that the difference was due to the effect examined. The factors that are important in calculating such differences are the sizes of the groups compared and the variation in the trait being considered. An estimate of the variation in the trait for a specific set of data is calculated in performing the “t” test or from the procedure called “analysis of variance”. Alternatively, a value from other similar data may be used.

The following example considers the comparison of mean weaning weights for groups of progeny by 2 different sires, when tested by the “t” test. For a weaning weight (or 200 day growth) of around 200 kg, we find a standard deviation (a measure of variation) of around 20 kg in data from commercial herds. This ratio of standard deviation to the mean (called the “coefficient of variation”) of around 10% is a value commonly found in traits like growth and weight. Table 3 shows the size of differences required for progeny groups compared by the “t” test.

Table 2. Detectable differences ($P < 0.05$) in mean weaning weights of calves for various sample group sizes using the “t” test comparison.

Group size	Std. error of the mean	Detectable difference
10	6.3	19.0
20	4.5	13.4
30	3.7	11.0
40	3.2	9.5
50	2.8	8.5
100	2.0	6.0

Calculations for this example used a mean of 200 kg, and standard deviation (sd) of 20 kg.

Table 3 shows that for a sample size of 20 progeny, we would need a difference of 13.4 kg (or larger) between pairs of progeny group means for statistical significance. To get a difference of this size in the progeny means, we would need twice that difference in the sire EBVs (i.e. 26.8 kg). The practical implication of these numbers is that small differences in sire EBVs are not able to be detected or demonstrated (with statistical significance) in commercial herds unless quite large numbers of progeny are available, or

conversely, that only large differences in EBVs can be detected in progeny groups of small to moderate size. Using data from a GROUP BREEDPLAN sire summary to illustrate this point, there was a difference of 20.3 kg in 200 day growth EBVs for sires in the top 10% (+ 21.5 kg) compared to the bottom 10% (+ 1.3) for the 1996 born animals (average + 11.0). Thus, even such a fairly extreme difference in 2 sires would not have been detectable with progeny groups of 20. This does not imply pessimism in the use of EBVs – for the example we are working backwards from limited numbers of progeny to estimate EBVs (in fact differences) in their sires, whereas the normal consideration is the genetic gain likely to be made using sires that have EBVs provided, given reasonably high accuracies.

Table 3 shows calculations using the LSD procedure. These have been generated from a spreadsheet routine that allows us to have varying sized groups, of equal or unequal numbers, and with any nominated variability for the trait considered. The values for the differences shown in Tables 3 and 2 are slightly different, with the former being more conservative.

To find the LSD for a comparison using Table 3, select the row and column appropriate to the numbers of individuals in the groups being compared. The cell at the intersection contains the value of interest.

Table 3. Least significant differences for the trait weaning weight, when comparing groups of varying sizes, using a set value for the variation in the trait, and setting the level of significance at 5% (or 95% level of confidence).

	Group 1										
	10	15	20	25	30	40	50	75	100	150	200
Group 2											
10	17.5										
15	16.0	14.3									
20	15.2	13.4	12.4								
25	14.7	12.8	11.8	11.1							
30	14.3	12.4	11.3	10.6	10.1						
40	13.9	11.9	10.7	10.0	9.5	8.8					
50	13.6	11.5	10.4	9.6	9.1	8.3	7.8				
75	13.2	11.1	9.9	9.1	8.5	7.7	7.2	6.4			
100	13.0	10.9	9.6	8.8	8.2	7.3	6.8	6.0	5.5		
150										4.5	
200											3.9

This issue, of statistically significant differences in relation to sample sizes, is relevant to the practical demonstration of genetic gains by selection on EBVs (or alternatives).

5. PREDICTION OF WEANING WEIGHTS IN COMMERCIAL HERDS BY SIRE EBVS – what can we expect to see in the paddock?

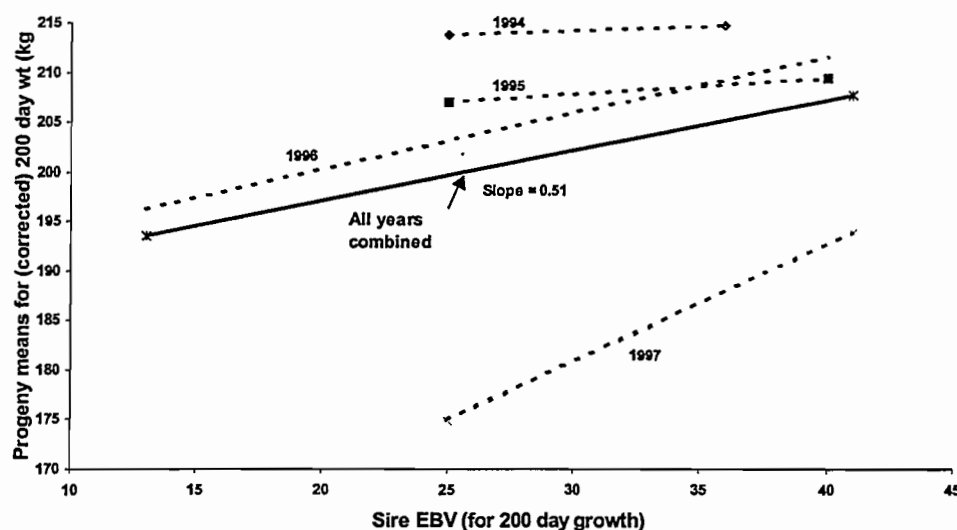
Commercial beef producers have now had access to EBVs for production traits for some time, to assist them in achieving the breeding objective(s) for their herd. However, increases in production due solely to genetic improvement, as predicted from genetic theory, can be difficult to demonstrate. This is because of the other influences of environment and management that will affect the outcome (in a trait like liveweight) that we see and measure. These influences are hard to control, even in a research situation, and more so in commercial herds. In this exercise we examined the weaning weights of calves of individual sires, bred and managed under commercial conditions, to compare the actual performance with that predicted by their sire's EBVs.

The study used data from a commercial Hereford herd at Mallanganee, in northern NSW. Cows were mated by AI over 4 years and managed in a single group. The weights of the calves at weaning were "corrected" by 2 methods. The first method adjusts for the different ages of the calves (weaning date minus birth date), and then gives them a "standardised" 200 day weight. These weights were then examined by statistical tests (least squares analysis of variance; Harvey, 1990) to estimate the effects of sire, sex, age of dam, and a seasonal effect (within years) due to cycle of conception. This allows us to isolate the effect due to the sires alone, when we account for the other influences that we can identify. However there is no guarantee that we have identified and accounted for all the effects that might have operated. In the second method of correction, we calculated an adjusted 200 day weight by the formulas used in BREEDPLAN. The BREEDPLAN calculations apply standard corrections that are particular to breed (Hereford in this case) for sex of calf, and age of dam, and also adjust to a common age of 200 days (David Johnston, pers.comm.).

For progeny groups within years, the rankings of the means for sire groups, and differences between them, were compared to their sires' EBVs for 200 day weight. The data were also analysed as a total block over all years to see the overall trend of the relationship between progeny means and sire EBVs. This analysis accounted for the year effects, since the growth of the calves differed between years, as expected. The different methods of correction gave essentially the same outcome, and the results presented in Figure 1 are those using the BREEDPLAN calculations.

Given that animals get half of their genes from their sire, we expect that half of the difference between sires will be expressed as a difference between progeny groups. Thus we expect that the slope of the relationship between sire EBV and the mean for the progeny group should be 0.5. The slopes for individual years varied considerably - 0.11, 0.17, 0.57 and 1.19. However, when the data were combined over all years, the analysis showed a slope of 0.51 (Figure 1) – right on the theoretical prediction. Other scientists have shown similar validation of this relationship when sufficiently large numbers of progeny were examined within years or accumulated over time (eg analysis of MRC Project M112 by Johnston, Graser and Goddard; and analysis of the CRC data from the Queensland herds by Newman).

Figure 1. Relationships between the mean 200 day weights for progeny groups and their sire's 200 day growth EBV over 4 separate years, and the overall trend with the data for all years combined.



Rankings of weaning weights were reasonably well correlated with sire EBVs, although none reached statistical significance due to small sample sizes. However, in two of the years, there was little difference in the means of the progeny of sires over the complete range in EBVs (25-36 and 25-40, Figure 1). The extremes were nearly always well predicted, but those in the middle of the range sometimes varied in their rankings. This demonstrates that progeny groups will not always perform exactly as expected from sire EBV predictions in any single year. However this does not question the validity of the genetic predictions, but demonstrates that at least one variable affecting the outcome is the need to have a sufficiently large sample size to allow the mean effect to be accurately expressed. Another variable affecting the outcome is the accuracy of the EBVs at the time of making the comparison.

Table 4 shows the change in the values of the EBVs over time for sires that were used over several years. This is the result of recalculation (increasing accuracy) with the accumulation of more data from the progeny of successive seasons, and will account for some of the change in rankings and departure from the predicted slope seen in Figure 1. Table 4 shows that some of the sires had considerable changes over time.

Table 4. Change in EBV for 200 day growth for the 17 sires used over the 4 years of data collection in the above study.

	Sire	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Estimate																		
1st		15	43	27	45	29	34	34	27		27	28	27	33	35			
2nd		13	38	26	40	32	34	38	31	31	25	35	30	28	36	41	34	38
3rd(1999)		7	33	27	35	25	24	36	26	28	19	30	24	25	33	37	30	37

The results of this exercise illustrate that producers need to be aware of the various factors that may affect the response they see in the progeny of different sires. Sires with EBVs of high accuracy can be used with confidence of improving the average genotype of their herd, but year to year variation and restrictions of group size may mask the overall response to selection in the short term.

6. CASE STUDIES TO ASSESS THE VALUE OF SIRE DIFFERENCES

Case studies used demonstration groups at 2 locations (one at Moree and one at Albury) to examine the actual value of differences between sires in the carcasses of their progeny. These were based on retrospective analysis of data sets from the abattoir feedback information. It was intended to have a second group in the Moree area, but the data from this property proved unsuitable for analysis.

Case Study 1

MOREE STORELINK DEMONSTRATION SITE

THE “DUNBEACON” CASE STUDY

Co-authors:

David Llewelyn

John Wilkins and

Ian McDouall

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Acknowledgements

We would like to thank Bob Gahan, Breed Development Officer, Tamworth and Helen Hearnshaw, Snr. Research Scientist, Grafton, for reviewing text and data respectively in this case study and Julie Gearing, Moree, for typing it.

COSTS & RETURNS FROM PROPERTY SUB-DIVISION TO ALLOW FOR SINGLE SIRE JOININGS AND FEEDBACK APPRAISAL ON A BEEF PROPERTY IN THE UPPER HORTON DISTRICT OF NORTHERN NSW

1. Aim

The aim of this project was to document the value and costs involved with identifying sires of steers sold out of a commercial herd to see if commercial benefits could firstly be identified and secondly be substantiated.

2. Purpose

In the intensive beef cattle areas the most practical way of matching steer progeny to their sire is to subdivide the property into sufficient joining paddocks so that bulls can be mated singly and their progeny identified early in life. When on-animal identification is carefully maintained and matched with carcass body numbers, then feedback appraisal can occur.

The number of commercial beef properties conducting single joinings is in fact very small. However, there is a percentage of intensive well developed properties in endowed areas who could further subdivide to allow for single joinings if there was shown to be substantive benefits.

The purpose of this investigation was to monitor both costs and returns from one such property where single sire joinings were practised and feedback appraisal was valued.

3. Case Study Description

As part of the M.L.A. funded Storelink project, NSW Agriculture officers examined feedback records from 380 rising 2 year old steers turned off "Dunbeacon" over a 5 year period. The steers were all bred on the property (2,024 ha) and grown out on improved temperate pastures prior to turnoff as heavy feeder steers, in truck lots. They were predominantly fed at one feedlot and killed exclusively at one abattoir following an average of 200+ days on feed.

Ten breeder paddocks of approximately 100 ha., had been previously established with the aid of electric fencing, thus allowing single sire joinings and subsequent sire identification of all calves at branding, using specially coloured Allflex button tags. Approximately 60 cows were run with each bull in a total herd of 600 cows and 10 bulls.

Feedlot, slaughter floor and chiller assessment data was all re-entered from paper records for statistical analysis and correlation purposes. Only data suitable for analysis was used in lot and sire comparisons.

An appraisal of the actual on property cost of obtaining this information was compared with projected dollar benefits from potential herd and management improvements.

4. Costs of Property Subdivision

Added Costs

Fencing sub-divisions

2350 m of 4 wire electric fence	\$ 7,087.60
1600 m of single wire offsets	360.00
1800 m of double wire offsets	805.00
2700 m of single electric in regular fence	1,234.00
3 mains units @ \$350	<u>1,050.00</u>
Total fencing costs (written off over 20 yrs)	\$10,516.00

i.e. Annual fence costs	\$ 525.83
Care and upkeep of electric fences 2 hrs/wk @ \$15/hr	\$ 1,500.00

Watering Points

N.B. The Dunbeacon philosophy of having two watering points in each paddock virtually eliminated the need for more dams when paddocks were sub-divided

\$ 00.00

Tags

600 Allflex maxi tags @ 63c	\$ 378.00
600 coloured button tags @ 29c	\$ 174.00

Tattooing pliers 1 roller tattoo set @ \$ 500.00 (written off over 10 years)	
Annual cost of pliers	\$ 50.00
Extra labour at branding time	
Tattoo and tag (\$15/hr., 1 calf/minute)	
600 calves @ 25c/head	\$ 150.00

Recorder identifies individual tag records at branding, weaning, classing and final weighing
i.e. 4 operations @ 25c/head
600 animals @ \$1 /head

\$ 600.00

Additional Station Bookwork

1 hour for each mob handled @ \$20/hr.	
10 mobs x \$20	\$ 200.00
3 additional lots of weighing records	\$ 600.00

Chasing, compiling, collating and interpreting feedback

Travel to abattoir (3,000 km @ 30c/km)	\$ 900.00
Accommodation	\$ 300.00
Extra phone calls	\$ 100.00
4 days extra office work	\$ 400.00

Professional Services	
Re-entering data	\$ 1,000.00
Statistical analyses	<u>\$ 2,000.00</u>

\$ 8,877.83

5.1. Costs Saved

2 less bulls required @ \$3,000	\$ 6,000.00
2 broken down bulls avoided @ \$3,000 (under single joinings, losses are nil)	\$ 6,000.00
1 station hands wages	<u>\$ 22,022.00</u>
(electric fencing sub-divisions reduced time spent on)	<u>\$ 34,022.00</u>
a) fixing fences	
b) returning strays to proper paddocks	
c) mothering-up cows and calves which become boxed	
d) maintenance for flood fences	

5.2. Returns

On this property we have found that gains made through Sire I.D. have been most valuable. The owners have in fact been more than happy to spend the extra \$8,877 to identify sires to their progeny since this cost was negated upfront by less bull costs, an increased efficiency of joining and also of running the property. Any improvements in steer performance is therefore viewed as a positive return on investment. We expect these sort of efficiencies would be reproducible elsewhere in similar circumstances.

From a breeding standpoint, the main value of sire I.D. in a commercial herd is to be able to confidently choose the next bull or bulls to follow on in that herd and so add value to subsequent turnoff progeny.

Where progeny performance is accurately identified through feedback this allows for the culling (although belatedly) of poor performing sires and sire lines. Conversely, by identifying high performing registered sire lines, more use could be made of them in the herd using A.I., or closely related bulls such as paternal half-sibs could be selected as future sires. However, where full performance information on the traits of interest is available on bought in sires it would be preferable to use this information to aid selection in the first instance.

A combination of these approaches will likely be needed for some years yet. The amount of genetic improvement that will occur in any herd is a function of both the accuracy and intensity of selection.

In this case study, the following breeding value benefits are assumed. Growth is valued at current commercial per Kg rates for longfed feeder steers. Reduced fat cover and increased marble score are valued as additional benefits on top of the base price as indicated in this case by the abattoir performance payment system.

Present base	600 day wt EBV +24 (breed average)	Rump (P8) fat 27mm	Marble Score 2.7
Purchased Sires	+54 (difference 30 kg.) pass 15 kg to progeny @ 1.30	enable 5mm reduction @ \$5 per mm 360kg carcass (200+ days on feed) worth \$25	increases 0.2 score @ 20c per score on 360 kg carcass (200+ days on feed) worth \$14.40
=	\$19.50		
=	say \$50 per steer progeny in one generation		
=	\$10 per year (5 year generation)		
=	+ \$2,850 for the herd per year	(600 breeders 95% branding equal ratio steers to heifers = 285 steers)	

N.B.

This budget supposition doesn't take into account the value of any genetic improvement in the female sale progeny nor second generation effects such as enhanced maternal abilities or simply building the herd asset value over time.

Nor does it put a figure on environmental management improvements which may well occur as a result of knowing and managing the herd more closely. These could easily be the most rewarding paybacks in the system and of course need to be further evaluated.

The sums do however assume that the identification of sire lines within the herd will enable a balanced breeding program, whereby compensatory matings will occur, thus enabling a tighter trait profile and therefore a reduced percentage of downgradings at abattoir level due to 'spread' within lots.

For example, in the herd of study high growth, low fat sires would be joined to high fat lower growth females and so on for other breeding trait combinations as well.

Another point is that hidden benefits are there that really only become apparent as the program progresses.

e.g. Further benefits found (but not yet evaluated) at Dunbeacon included:

- the easy identification of sire's background when classing heifers

- picking up any deleterious effects in progeny which could be traced to the sire
- identifying by sire background tail end steers, or for that matter leader steers turned off in the first draft, showing good growth and early maturity pattern
- optimising rate of growth at critical times and adjusting steer turnoff age so as to improve marbling expression in carcasses

Not all benefits are equally applicable to all situations because herd and property goals differ.

6. Overview

The figuring on costs and returns relates here to one NSW property with specific breeding aims, their own property enterprise structure and a single market outlet.

While the costs are actual, the returns projected are best bet estimates based on expected breeding values for a herd of this type, or have been assumed from E.B.V. - commercial feedback benchmarks derived from within the herd.

Since in reality, the sub-division costs are outlaid well before the breeding returns are likely to eventuate, we should consider adjusting the results back into net present (discounted) dollar values.

However, due to the substantial cost savings incurred in this program right at the outset (ie. less bull costs and less labour costs) we have not pursued this line of thinking further in this paper.

7. Analysis

The study group(s) consisted of 17-21 month feeder steers. These were long-fed in a feedlot, for 190-270 days, for the Japanese market. The steers were all killed at one meatworks, in similar lots according to their time of induction to the feedlot. We have analysed carcass value information within sire progeny groups. Traits affecting carcass value - such as dressing percentage and marbling ability - were analysed for their effect on the differences (in final value) between sire progeny groups, and these differences were also compared to those between lots (kill groups). Data were analysed using the Harvey program of least squares analysis of variance. The main effects examined were those of sires and lots, while also accounting for the effects of different times of days on feed and different induction weights.

There were totals of 10 different sires and 9 different kill lots in the analysis. There were statistically significant differences ($P < 0.05$) between lots for the traits of dressing percentage, marbling, average daily gain on feed, P8 fat depth and eye muscle area (EMA). There were also significant differences between sires for all those traits except for EMA.

Results are summarised below and the following diagrams (Figures 2-7) illustrate the size and value of the differences in particular carcass traits.

WITHIN HERD

*VALUE DIFFERENCES FOR TURNOFF LOTS AND SIRES USED

	Lot	Sire	
A.D.G. in feedlot	\$36.82 (0.35 kg/d)	\$19.74 (0.17 kg/d)	Assumes 10% more feed intake from best to worst sires / lots
Dress %	\$46.31 (2.74%)	\$34.14 (2.02%)	Calculated at \$16.90 per percent difference
Finish	\$38.72 (7.8 mm)	\$56.84 (11.2 mm)	Calculated at \$5.00 per mm above 12 mm
<hr/>			
#Marb.	\$118.93 (1.03 score)	\$89.10 (1 score)	Marbling values are based on raw means and calculated according to the abattoirs performance rating system - see Fig. 3 header

*Value Differences are best to worst within type, with actual variation in brackets

Includes premiums and discounts which are non-linear

Figure 2. Differences in marble scores (LSM) for progeny from different sires

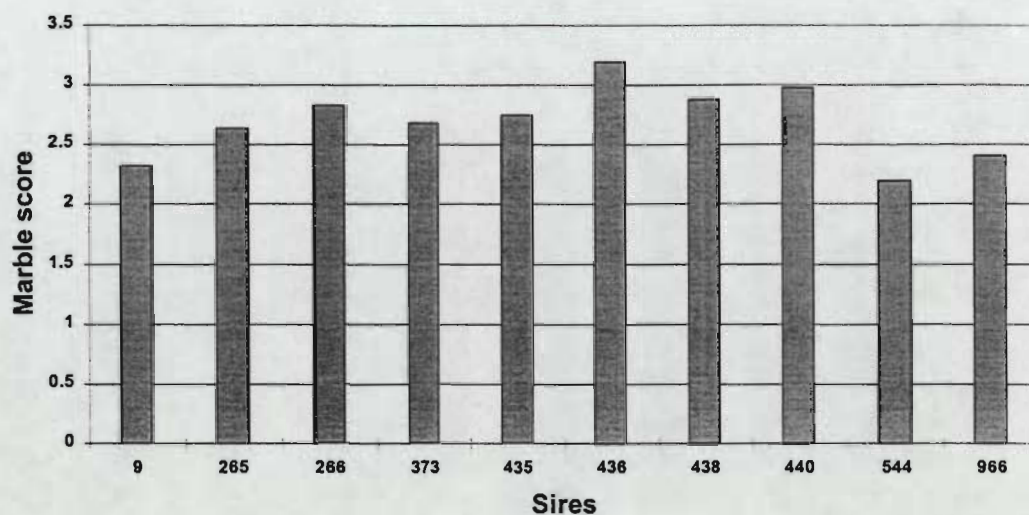


Figure 3. Differences in carcass value (\$) of progeny from different sires (carcass premium or discount due to marbling in c/kg x carcass weight) (raw means). Marble score '2' at the base price, with score '1' having a discount of 40c/kg, score '3' a premium of 20c/kg, with each additional score worth an additional 20c/kg premium.

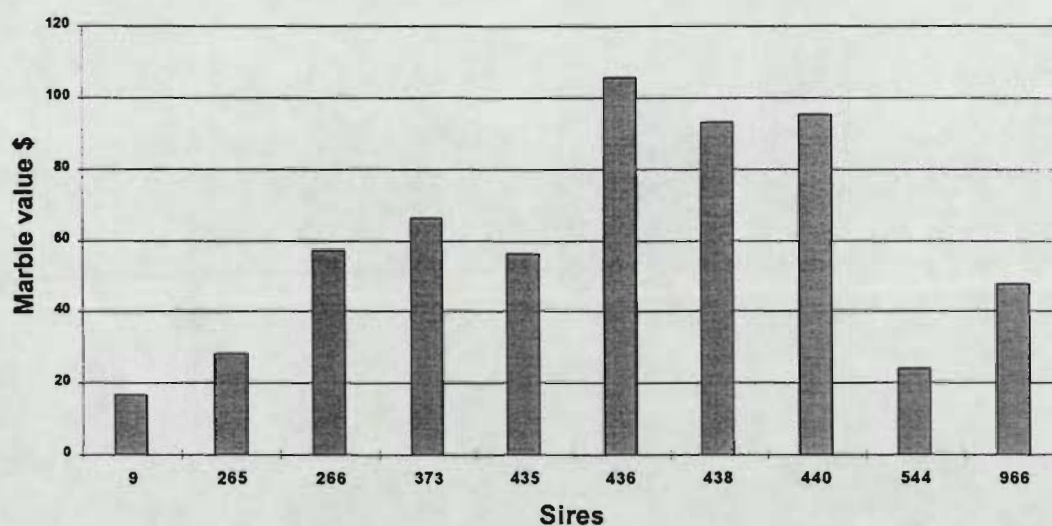


Figure 4. Differences in marble scores (LSM) for different turnoff lots

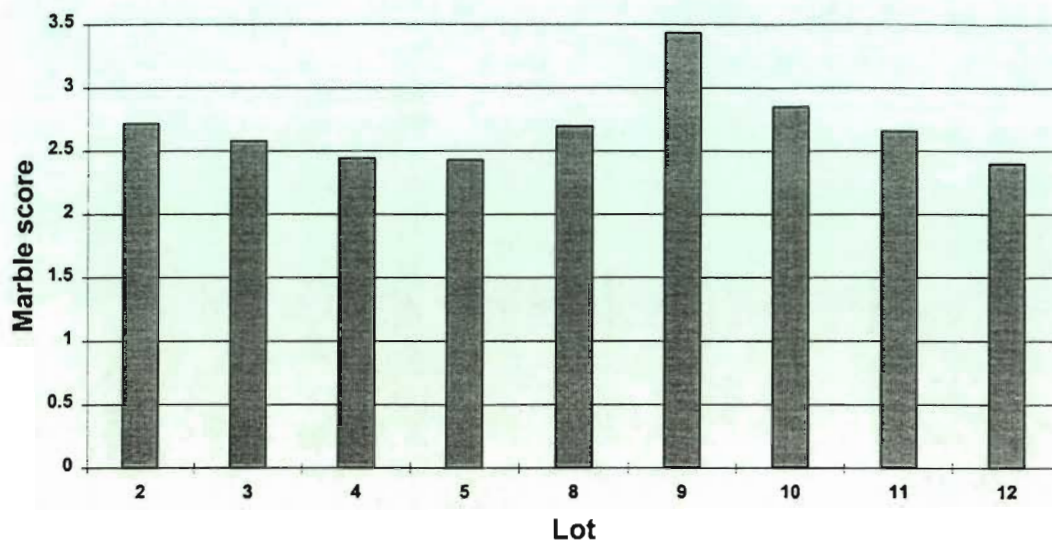


Figure 5. Differences in carcass value (\$) of different turnoff lots (carcass premium or discount due to marbling in c/kg x carcass weight), (raw means). Marble score '2' at the base price, with score '1' having a discount of 40c/kg, score '3' a premium of 20c/kg, with each additional score worth an additional 20c/kg premium.

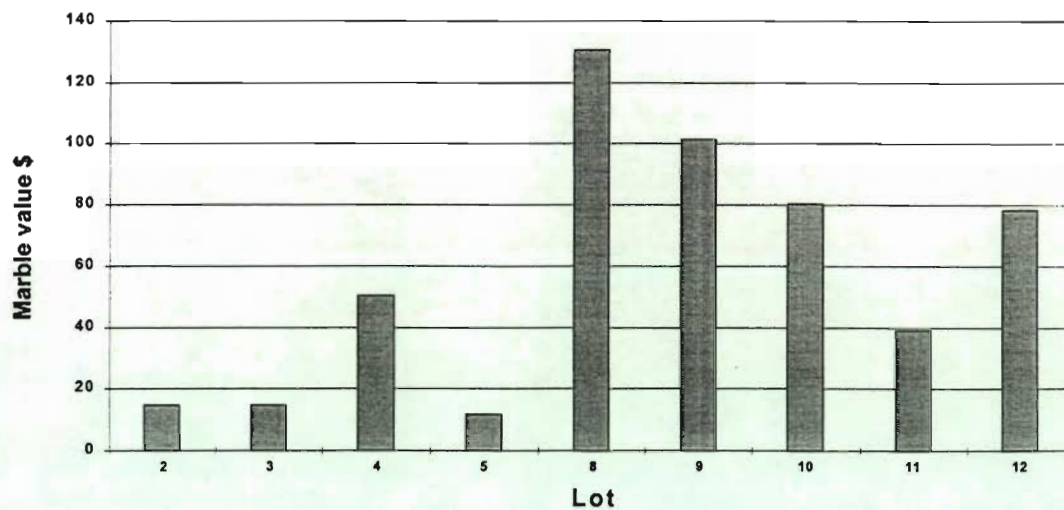


Figure 6. Differences in dressing percentage (LSM) for progeny from different sires

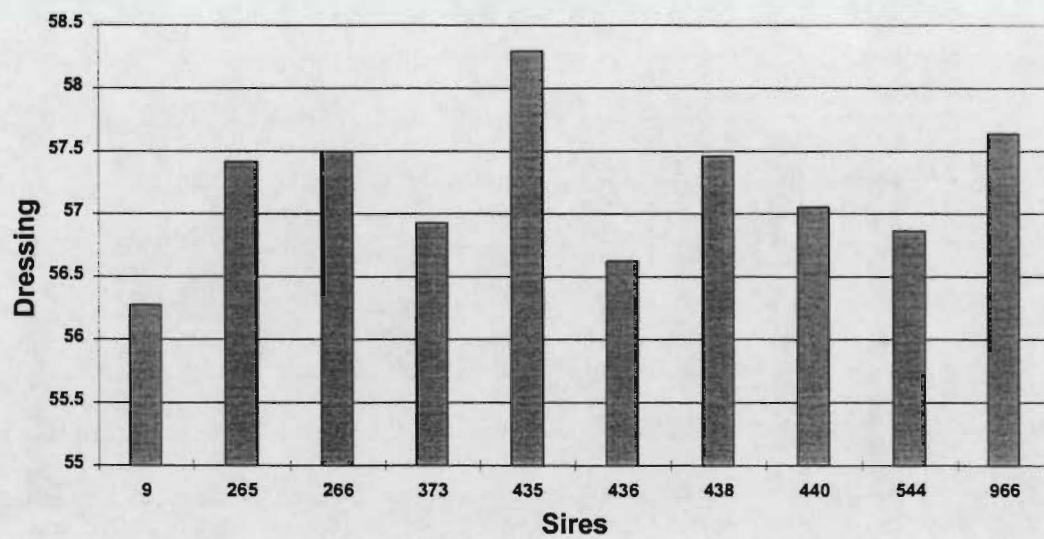


Figure 7. Differences in dressing percentage (LSM) for different turnoff lots

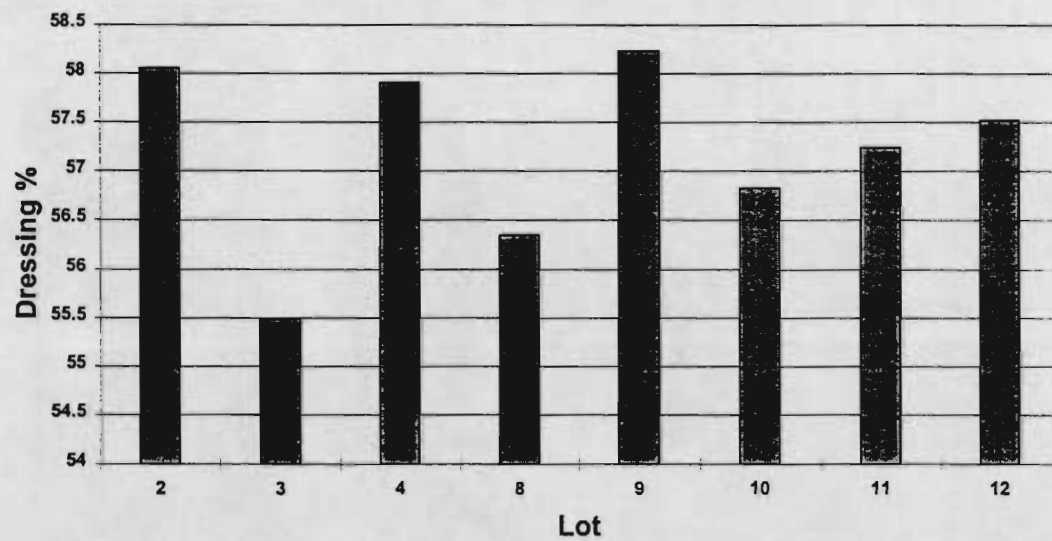


Figure 8. Differences in subcutaneous fatness at the P8 site (mm) for progeny from different sires

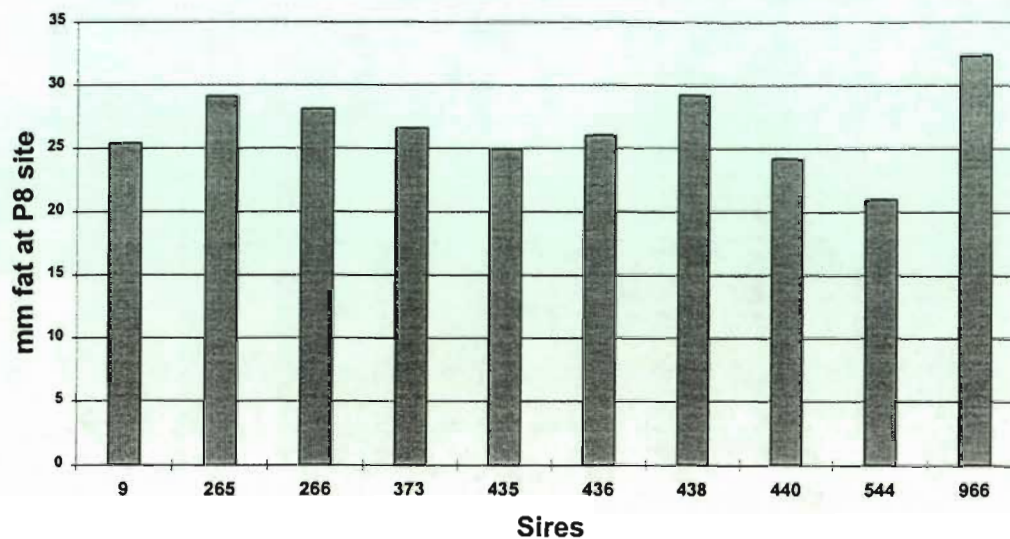


Figure 9. Differences in subcutaneous fatness at the P8 site (mm) for different turnoff lots

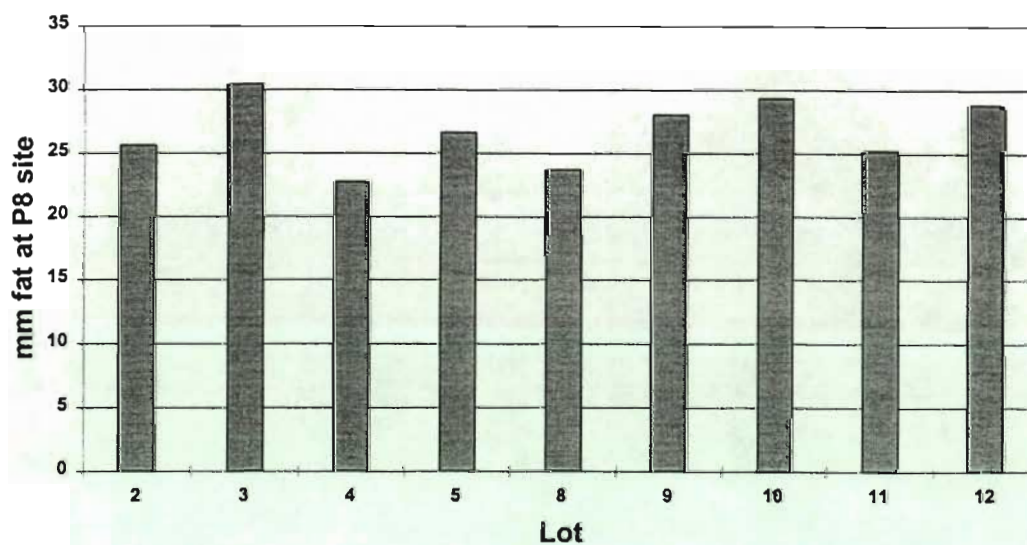


Figure 10. Differences in average daily gain in the feedlot (LSM) for progeny from different sires

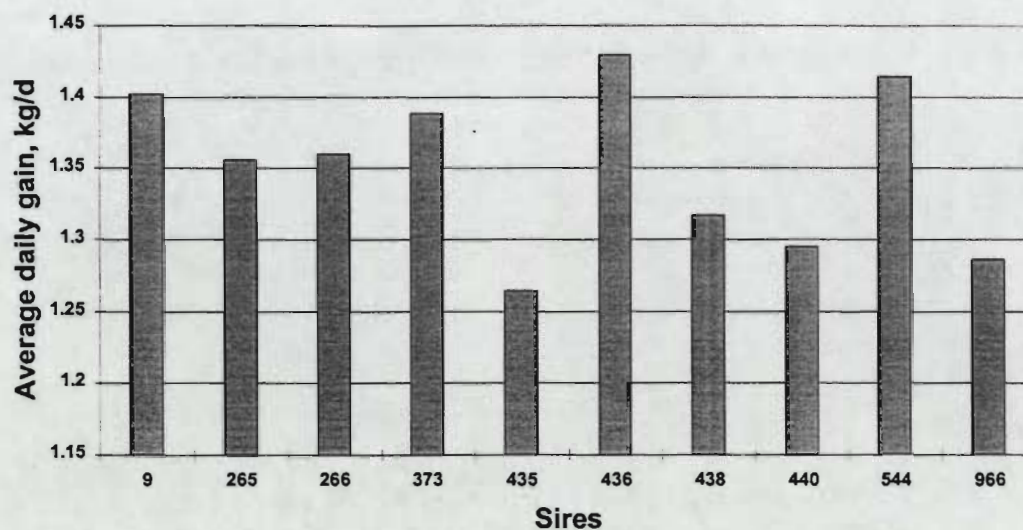
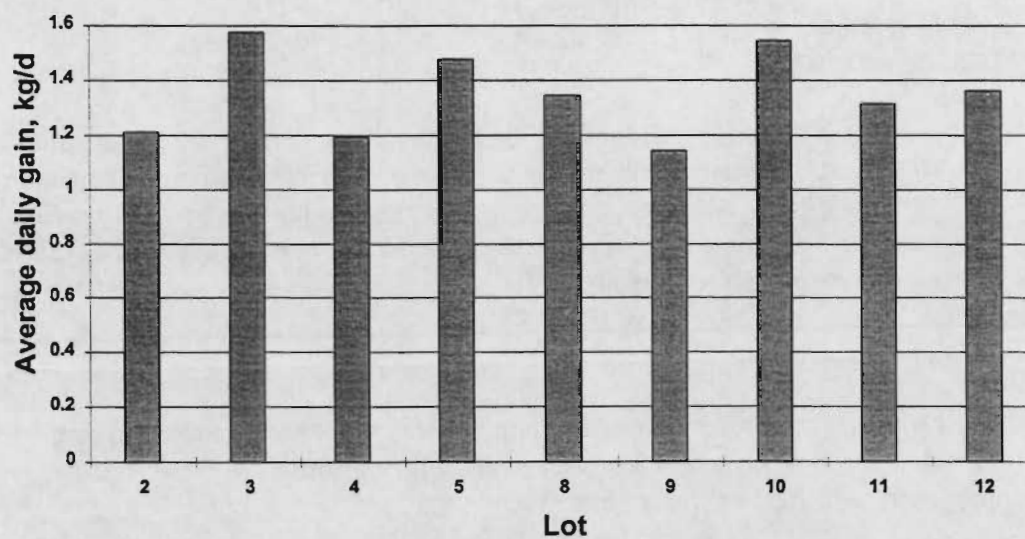


Figure 11. Differences in average daily gain (LSM) for different turnoff lots



8. Some Conclusions on the Value of Sire ID in Commercial Herds

With Sire I.D.

What Do We Know?

1. That the current battery of herd sires have progeny variances that are statistically different, i.e. there are genetic herd differences existing.
2. Areas/traits current sires are deficient in.
3. Areas/traits current sires are good in, i.e. performing well.
4. The trait variance within herd and therefore likely impact of further selections for those traits.

Therefore,

- We can compensatory mate to develop a balanced breeding program and increase our consistency of turnoff by controlling the desirable spread of trait values, i.e. reduce the percentage of downgradings at abattoir level.
- We can start to subtract genetic differences from the total environmental influences, thus developing a clearer picture of what scope there is for improving management aspects at the same time.

Without Sire I.D.

What Do We Know?

1. A general turnoff profile can still be attained through feedback but profiled feedback on specific traits may or may not be attributable to breeding - and if it is we don't know which sires have progeny with good results / which ones are causing the poor results. Therefore we are unable to make appropriate joining decisions for future generations.

Selection Scenarios in Practice

Once a specific trait profile is worked up for a commercial herd, a selection emphasis can be developed for immediate sire replacements allowing consolidation of the most appropriate gains in subsequent progeny.

This is achieved by benchmarking your trait profile directly against your target market preferences, working on the areas of deficiency and being careful to maintain the high performing attributes of your herd.

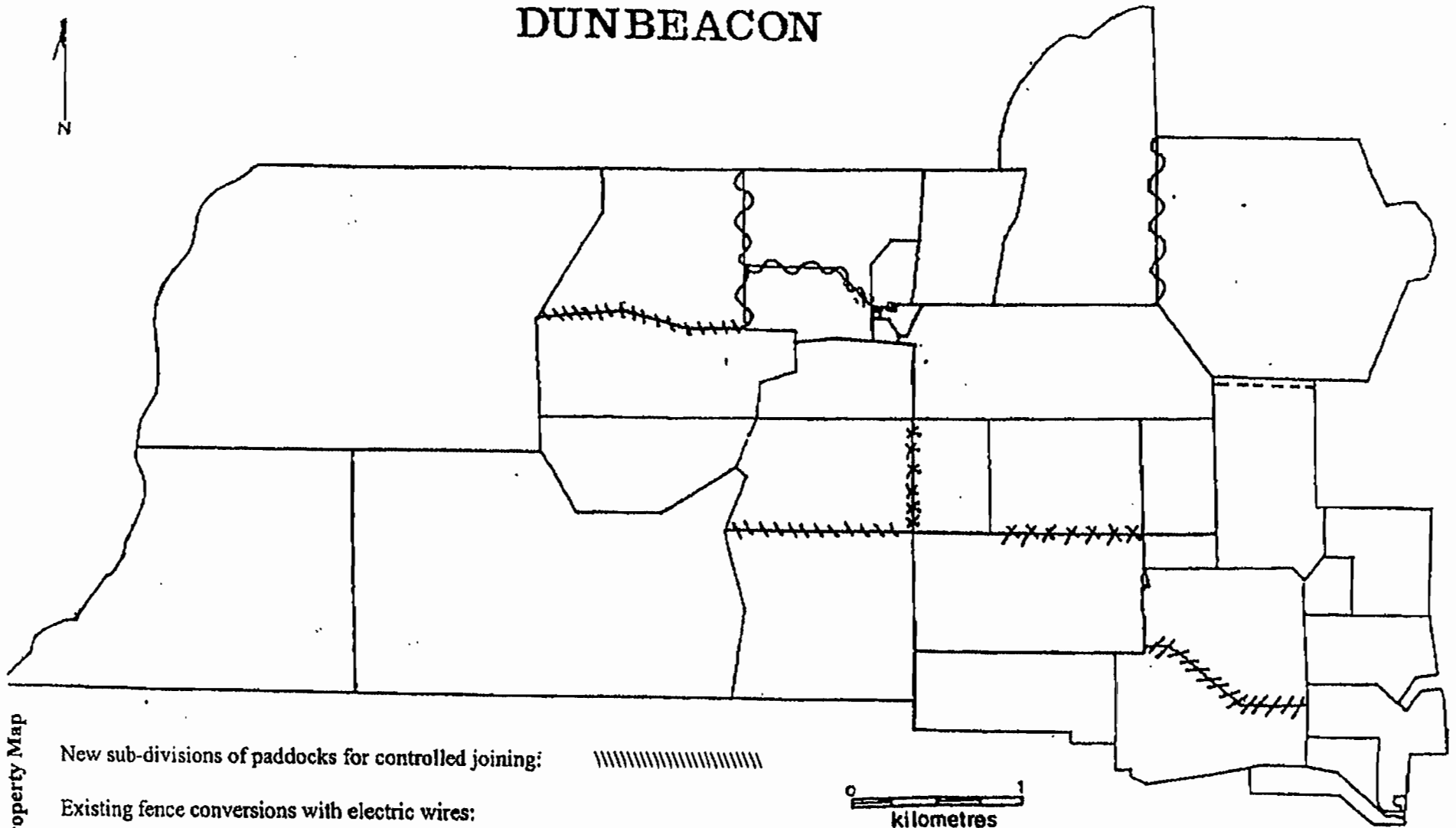
If most emphasis is placed on the major shortfall traits in value terms, then the best financial advantage can be built in to the herd, again assuming good management and production practices are maintained and that the traits are at least moderately heritable.

In the light of results obtained in this case study, we suggest that further theoretical and practical modelling examples be developed to assist commercial breeders and their seedstock base to take advantage of abattoir feedback. It will be necessary to do some figures on herd benefits per generation, then per year, based on assumptions.

1. No. of traits to be improved
2. Heritabilities
3. Outlay on sires (\$)
4. Within breed / across breed spread of trait ranges
5. Accuracy of performance or progeny information on sires available for purchase
6. Reliability (i.e. group breedplan data)

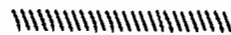
This is especially important if N.L.I.S. devices (connected to accurate feedback) become readily available in the near future.

DUN BEACON



Appendix (i) Property Map

New sub-divisions of paddocks for controlled joining:



Existing fence conversions with electric wires:

Double offset:

Single wire in fence (plastic insulator):



Single offset:

Single wire in fence (porcelain insulator):



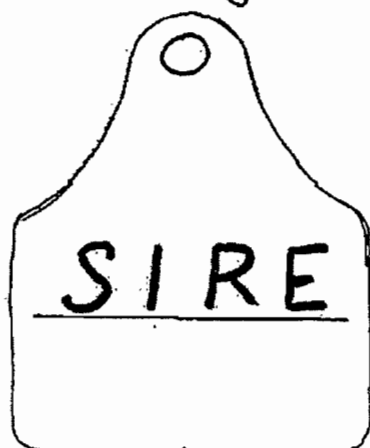
Appendix (ii)

Sire I.D. tags

Front Tag



Back Tag.



Appendix (iii)

Fencing Subdivision Costs

(a) Upgrading existing fencing:

Type 1

Single wire offsets: 1600m at 0.0875 m = \$ 140.00

Type 2

Double wire offsets: 1800m at 0.1750 m = \$ 315.00

Type 3

Single wire in fence:

Porcelain insulators: 1250 m at .27072 m = \$ 338.40

Single wire in fence:

Plastic insulators: 1450 m at .16372 m = \$ 237.39

(b) New Fencing: 2350 m at 2.016 m = \$4,737.60

Fencing Labour

(a) Upgrading existing fencing

Single offset: 1600 m at .1375m = \$ 220.00
½ of double offset

Double offset: 1800 m at .244 m = \$ 440.00
2 men for 2 days at 110 per man per day

Single line in fence: 2700 m at .244 m = \$ 658.00
Equivalent to double offset

4 wire electric fence 2350 m at 1.00 m = \$2,350.00
110 per day per man
21 working days

CASE STUDY 2

ALBURY STORELINK DEMONSTRATION SITE

Co-authors:

**Brian Cumming
and
John Wilkins**

Demonstration design

This study comprised a group of steers and heifers, custom fed in a feedlot for varying periods (up to 130 days), at Regmont feedlot, Albury. These animals were the progeny of 5 different sires, with 21 – 40 animals from each sire. They were finished in the feedlot and killed in separate runs. The object of this demonstration was to evaluate the differences in value of the end products of each progeny group to determine how much money we could have invested to trace backwards for sire identification if it was unknown. There needs to be sufficient differences in value of the progeny to justify costs associated with determining genetic merit. In fact for this exercise, it was necessary to actually do the traceback, since the accuracy and cost of doing the tests is not in question, and we already had the necessary sire ID and EBVs.

We had GROUP BREEDPLAN EBVs for 4 these sires and initially examined the ranking of the 4 sires for 400 and 600 day weight EBVs, in relation to the weights at feedlot entry. The results are shown in Table 1.

Table 1 Sire 400 and 600 Day EBV's and Feedlot Entry Weights for Progeny

Sire No.	400 day EBV (kg)	600 day EBV (kg)	Adjusted Feedlot Entry Wt. (kg)	
			Steers	Heifers
66	44	60	402	417
227	49	65	408	414
88	51	62	409	402
224	52	80	423	405

The “adjusted” weight at feedlot entry accounted for the differences in the times of entry and between steers and heifers.

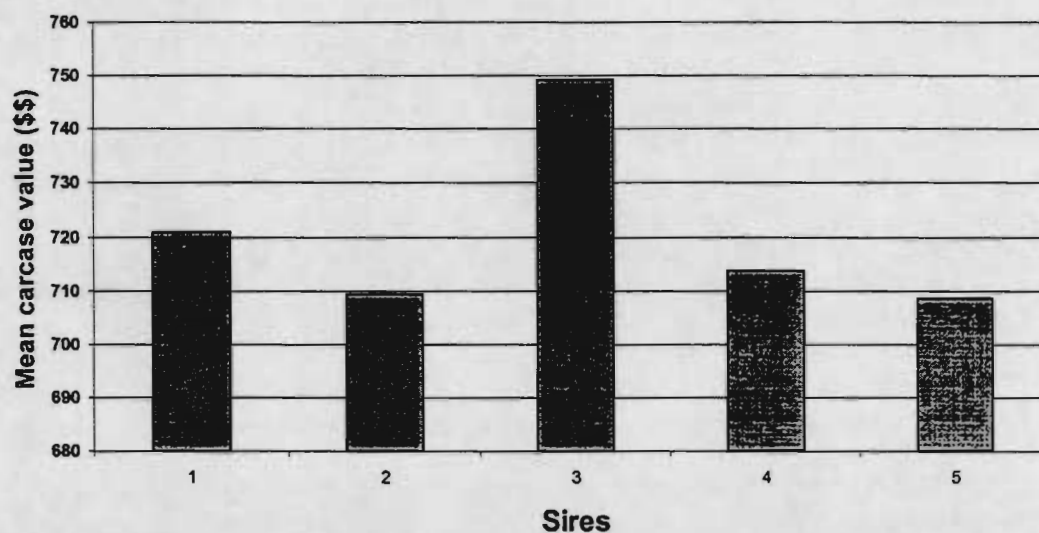
The ranking of the entry weights for the steers was as predicted by the 400 day EBVs, and in fact the difference between the extremes was larger than would have been expected. The larger than expected difference may have been due to sample size, but could also reflect the accuracy levels for these EBVs, which was only around 75% and therefore could cause considerable departure from expected performance in the progeny. The poor agreement of rankings for the heifers is likely a result of smaller sample sizes (only 4 and 7 animals for 2 of the sires).

Results of carcase traits and values

The differences in marble scores and dressing percentages between sire groups were not significant. The mean values of the carcasses for different sire progeny groups were calculated from the price paid per kg of hot standard carcase weight, as determined by the grading of the carcasses. These prices ranged from \$2.22 to \$2.51, between the different carcase grades and different times of kill. The mean differences in carcase value due to sires, accounting for the variation between times of kill, and adjusting for differences between sexes, are shown in Figure 8. These are also adjusted for differences in entry weight for different sires, which gives a conservative estimate of the differences in value. The difference in value between the best and the worst performing sire groups was

\$40.48. This was increased to \$62.12 if differences in entry weights were ignored. In fact the differences in entry weights may be considered as part of the sire effect, but use of the higher value figure would have to be made with caution, as there may have been several factors independent of sires that could also have affected entry weights.

Figure 8. Differences in mean carcase value between sire groups.



The carcase value differences show in Figure 8 indicate how much money can be spent on the exercise of sire ID, while still giving a worthwhile return for investment.

In this case there is a \$40.48 per head advantage in favour of the progeny of Sire No. 3 compared to Sire No. 5. That means that there would be a significant financial incentive to identify the sires of those progeny group if they were coming from an unidentified background such as multi-sire joinings. If the cost of obtaining individual sire identification was less than 440.48 for these two groups, it would be a worthy financial investment.

References

Goddard, M.E. and Goddard, D.E. (1997). Using DNA fingerprinting of extreme offspring to progeny test sires. *Proc. Assoc. Advmt. Anim. Breed. Genet.* 12:438-441.

Vankan, D.M. and Burns, B.M. (1997). DNA fingerprinting — how it works and applications for the beef industry. *Proc. Assoc. Advmt. Anim. Breed. Genet.* 12:433-437.

Parsons, Y.M., Fricke, B.L., Fleet, M.R., Franklin, I. And Cooper, D.W. (1997). DNA pedigreeing of commercial flocks. *Proc. Assoc. Advmt. Anim. Breed. Genet.* 12:270-272.

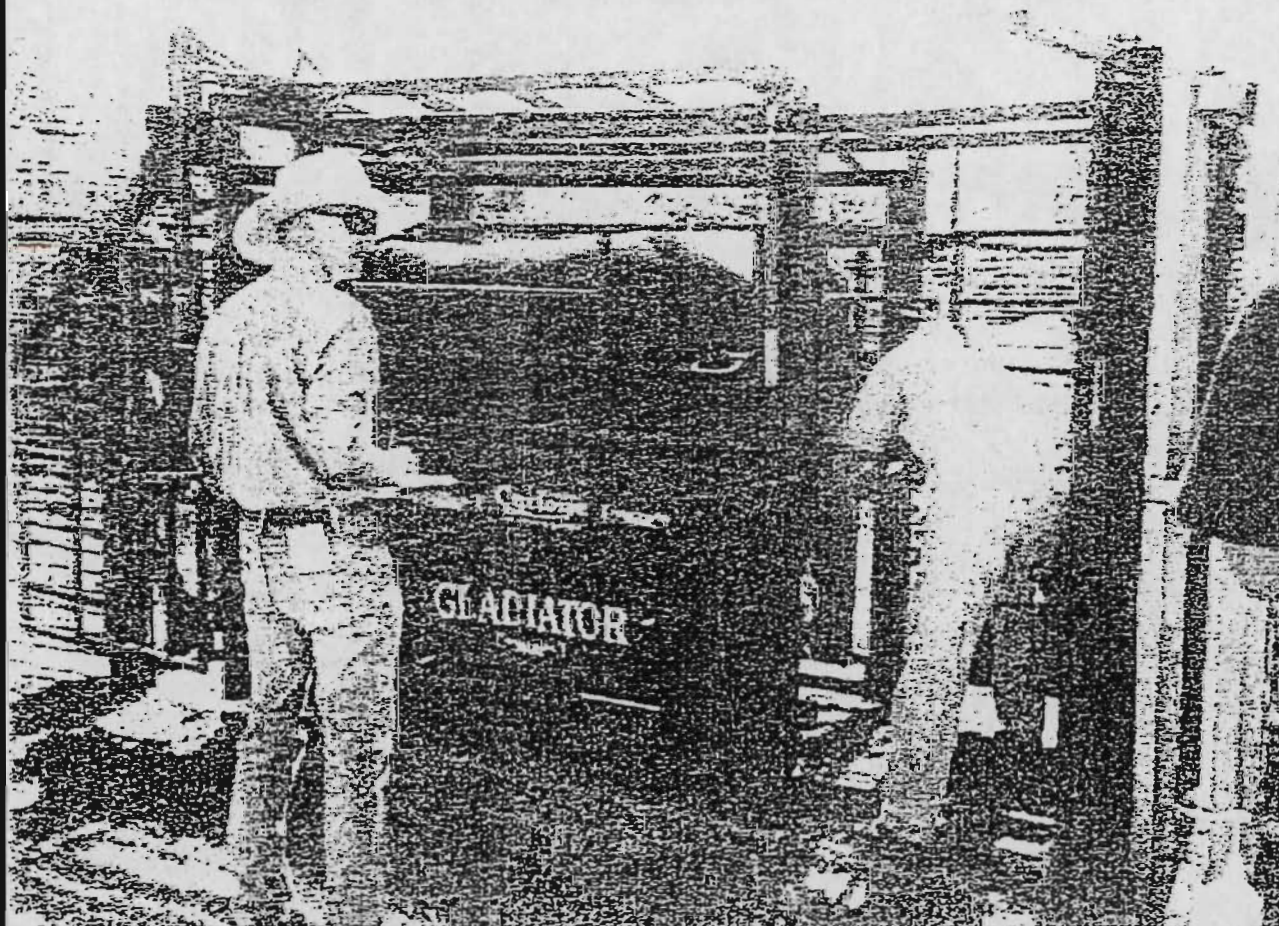
Demeny, D., Parsons, Y.M., Franklin, I. And Cooper, W. (1997). Low cost sampling method for DNA based testing. *Proc. Assoc. Advmt. Anim. Breed. Genet.* 12:265-269.

Barnett, N.L., Purvis, I.W., Stewart, V.A.M. and Franklin, I.R. (1997). At what price is DNA pedigreeing cost effective for Merino breeders? *Proc. Assoc. Advmt. Anim. Breed. Genet.* 12:425-428.

Davis, G.P., D'Occhio, M.J. and Hetzel, D.J.S. (1997). SMART BREEDING: selection with markers and advanced reproductive technologies. *Proc. Assoc. Advmt. Anim. Breed. Genet.* 12:429-432.

Proceedings from a Seminar in Albury
26 March 1998

ADVANCES IN BEEF CATTLE ARTIFICIAL INSEMINATION



CATTLE AI PROGRAMMES

SOME OPTIONS AND COSTS

1. No synchrony.
2. Some prostaglandin options.
3. Progesterone options.
4. Some new developments.
5. Comments.

Some considerations when selecting an AI programme to suit your individual requirements:

- Facilities.
- Labour.
- Time restrictions.
- Cost of semen.
- Back up bull options.
- DIY or employed AI technician.
- Cows or heifers.
- Previous AI results.

No Synchrony.

1. Inseminate of natural heats.

- No synchronising drug requirements.
- Useful if small groups of cattle can be observed and identified from the "kitchen window" and DIY (Do it yourself).
- Has been successfully used in large herds with heat detectors on horseback and portable yards in the paddock.
- Good conception rates with good heat detection.
- AI over 21 days.
- High labour costs.
- Good heat detection required.
- Dont get the concentrated calving pattern that synchronised programmes can provide.

Semen costs. ?

Drug costs.

Tail paint	\$15.00 / 100 head.
OR Kamar	\$140.40 / 100 head.
	(Available in boxes of 25)

Labour costs.

DIY	Allow for 4 hours per day for heat detection, mustering and inseminating over a 21 day period.
Consumables;	
Gloves	\$29.00 / 100 head.
Lubricant.	\$8.00 / 100 head.
AI sheaths.	\$6 / 100 head.
AI technician.	
	Allow for 5 cows per day at \$25 / cow.

Failure costs. Minimal if heat detection is good.

Prostaglandin options.

- Slightly better conception rates to AI Vs Progesterone programmes.
- Greater spread in synchrony.
- More suited for the DIY operator.
- Poorer submission rates (lactating cows).

Drugs available:

Estroplan	Parnell Laboratories.
Estrumate	Jurox P/I
Juromate	Jurox P/L
Lutalyse	Upjohn P/L
Prosolvin	Intervet Aust. P/L

2.1. Double Injection Programme.

Day 0	PG all cows or heifers.
Day 11	PG all cows or heifers.
Day 13	Inseminate on heat detection.

- The majority of heifers will cycle on days 13 and 14.
- The majority of cows will cycle on days 13, 14 to 16.
- Can delay second injection till day 14.
- Inseminations all done over one period.
- Good conception rates with good heat detection.
- Slightly poorer submission rates to programme 2.2
- Submission rates with lactating cows can be disappointing.

Semen costs.	?
Drug costs.	Prostaglandin x 2 injections . \$900 / 100 head.
	Tail paint \$15 / 100 head.
	OR Kamar \$140.40 / 100 head.
Labour costs.	Allow 4 hours for two treatment yardings.
	Allow 16 hours for heat detection, yardings and DIY inseminating.
	Consumables
	Gloves \$29.00 / 100 head
	Lubricant. \$8.00 / 100 head.
	AI sheaths. \$6 / 100 head
AI technician costs.	
	Allow \$9 / head.
Failure costs.	
	Drug costs with poor submission rates.

2.2 Heat detection following single PG injection.

Day 0 PG all females.
Day 0-5 Inseminate ot heat detection.
Day 7 PG all females not yet inseminated.
Day 9-12 Inseminate to heat detection.

- Reduced drug costs as only 30% - 50% are given a second injection.
- Slightly better submission rates than programme 2.1
- Total programme time is condensed.
- Insemination and heat detection is done over longer periods.
- Can increase the time between the two injections to give two distinct heat detection and AI windows.
- Requires good records and identification to avoid giving the second injection to females that have been inseminated as this will cause them to recycle.
- Requires more labour time in heat detection.

Semen costs. ?

Drug costs. Prostaglandin Inj. x 145 \$652.50 / 100 head.
Tail paint \$15 / 100 head.
OR Kamar \$140.40 / 100 head.

Labour costs. Allow 4 hours for two treatment yardings.
Allow 32 hours for heat detection, yarding and DYI

Consumables

Gloves \$29.00 / 100 head.
Lubricant. \$8.00 / 100 head.
AI sheaths. \$6 / 100 head.

AI technician costs.

Allow \$10 / head.

Failure costs.

Drugs with poor submission rate.

2.3. Heat detect then PG programme.

Day 0 Apply Kamar or tail paint in evening.
Day 1 Commence inseminating all cows on detected heats.
Day 7 PG all unmated cows and continue to inseminate on detected heats.

- Inexperienced operator gets a chance to "warm up" prior to the bulk of the females being inseminated.
- You get a chance to observe how the herd are cycling prior to PG injection.
- Greater PG use on non-cyclers than programme 2.4.
- Total programme completed in approx. 10 days.
- Single PG injection on less than total herd.

Semen costs. ?

Drug costs.	Prostaglandin x 66 Inj.	\$297 / 100 head.
	Tail paint	\$15 / 100 head.
	Kamar	\$140.40 / 100 head.

Labour costs.

Allow 4 hours for two treatment yardings.
Allow 36 hours for heat detection, yarding and DYI

Consumables:

Gloves	\$29.00 / 100 head.
Lubricant.	\$8.00 / 100 head.
AI sheaths.	\$6 / 100 head.

AI technician costs.

Allow \$10 / head.

Failure costs.

2.4. The Why Wait Programme.

Day 0- day 11 Detect and record cows on heat.

Day 12 Commence mating on heat detection.

PG cows that were on heat from day 0 to day 5.

Day 18 PG cows that were on heat day 6 to day 11.

-The aim is to inseminate all cycling cows over a 10 to 12 day period.

-PG is used efficiently as only cows with previous heats are injected.

-Gives the inexperienced operator a chance to "warm up" prior to the bulk of the females are inseminated.

-Heat detecting prior to insemination is required.

-Are heat detecting for almost 21 days.

-May still be a useful programme if expensive semen is being used and a contract inseminator employed.

Semen costs. ?

Drug costs. Prostaglandin x 50 Inj. \$225 / 100 head.

Tail paint \$15 / 100 head.

OR Kamar \$140.40 / 100 head.

Labour costs. Allow 4 hours for treatment yardings.

Allow 60 hours heat detection, yarding and DIY

Consumables:

Gloves \$29.00 / 100 head.

Lubricant. \$8.00 / 100 head.

AI sheaths. \$6 / 100 head.

AI technician costs.

Allow \$10 / head.

Failure costs.

Progesterone Options.

- Slightly poorer conception rates to AI Vs prostaglandins.
- Increased drug costs.
- Tighter synchrony Vs prostaglandins.
- Better submission rates (lactating cows) vs prostaglandins.
- Decreased labour hours.

3.1 CIDR B Inter Ag (NZ) (Available in packets of 10)

Requires good hygiene when inserting device.

Heifer programme.

Day 0	Insert CIDR B (Capsule with CIDR or Inj. Oestradiol benzoate 2 mg)
Day 6	Inject PG
Day 10	Remove CIDR and tail paint or KAMAR.
Day 12	AI on heat detection or blanket AI well grown heifers at 48-50 hours post CIDR withdrawal.

Cow programme.

Day 0	Insert CIDR B (Capsule with CIDR or Inj. Oestradiol benzoate 2mg)
Day 6	Inject PG
Day 8	Remove CIDR B Apply tail paint or KAMAR
Day 9	Inject Oestradiol benzoate (1mg) if females are under stress or poor cycling performance is suspected.
Day 10	Inseminate on heat detection.

Semen Costs ?

Drug Costs CIDR B @ \$10.90 \$1090 / 100 head.
 Oestradiol Capsule @ \$1.60 \$160 / 100 head.
 OR Oestradiol benzoate Inj 2mg. \$200 / 100 head.
 Prostaglandin x 100 Inj. \$450.00 / 100 head.
 Tail paint \$15 / 100 head.
 OR Kamar \$140.40 / 100 head.

Labour costs. Allow 7 hours for three treatment yardings.
 Allow 10 hours for heat detection, yarding and DYI

Consumables

Gloves \$29.00 / 100 head.
Lubricant. \$8.00 / 100 head.
AI sheaths. \$6 / 100 head.

AI technician costs.

Allow \$7 / head.

Failure costs.

-Drug costs.
-Loss of production.
-Back up bull requirements.

Resynchrony programmes.

Reapply KAMAR or re-tailpaint and reinsert CIDR B 18 days following removal of the first device and leave in for five days.

-Inseminate to heat detection post CIDR withdrawal.
-To get maximum number of cows pregnant to AI.
-Reduce the pressure on back up bulls.
-Reuse the CIDR's from the first insertion.

Semen costs. Allow for 35-40 doses / 100 head programme.

Drug costs. Tail paint \$15 / 100 head.
 Kamar \$140.40 / 100 head.

Labour costs. Allow 4 hours for yardings and treatments.
 Allow 14 hours for heat detection, yarding and DYI

Consumables:

Gloves \$11.60 / 40 head.
Lubricant. \$3.20 / 40 head.
AI sheaths. \$2.40 / 40 head.

AI technician costs.

Allow \$8 / head.

Failure costs.

-Drug costs.
-Loss of production.
-Back up bull requirements.

3.2 Crestar. Intervet (Aust) P/L
(Available in boxes of 25)

Requires good facilities to immobilize females head to insert Crestar.

Day 0	Crestar implant in outer surface of the ear. Inject 2ml Oestradiol valerate.
Day 7	PG injection. (Can be optional when used with dry cows)
Day 9	Remove implant. Inject PMSG 400IU. (Not necessary when used with heifers that are cycling well) Apply tail paint or KAMAR
Day 11	AI at 48 hours post implant removal for heifers. AI at 54-56 hours post implant removal for cows.

- The PMSG can be deleted in heifers that are cycling well.
- Meat withholding of 51 days.
- Not registered for use with lactating dairy cows.
- Can do fixed time insemination but not recommended with lactating cows.

Semen costs.	?
Drug costs.	Crestar and Oestradiol Inj. \$1140 / 100 head.
	Prostaglandin \$450 / 100 head
	PMSG 400IU x100 \$300 / 100 head.
	Tail paint \$15 / 100 head.
	OR Kamar \$140.40 / 100 head

Labour costs. Allow 9 hours for two treatment yardings and
increased hours if treatment options are taken up.
Allow 10 hours for heat detection, yardings and DYI

AI technician costs.
Allow \$7 / head.

Failure costs.

- Drug costs.
- Loss of production.
- Back up bull requirements.