

BENEFITS OF STATISTICALLY EFFICIENT DESIGNS FOR GENETICS RESEARCH PROJECTS

D. L. Robinson

Animal Genetics and Breeding Unit*, NSW Agriculture & CRC for the Cattle and Beef Industry,
University of New England, Armidale, NSW 2351

SUMMARY

A suite of computer programs (Robinson 1995) was used to find the most balanced and efficient ways to assign the different treatment combinations to the offspring of each sire. If instead, offspring of each sire had been allocated to treatments by a simple rotational system, 3.5 % more animals would have been required to achieve the same accuracy of estimating sire effects, and 5-10 % more animals to achieve the same accuracy of estimating effects of market, finish, nutrition and other treatments within intake groups. For the 9,677 straight and crossbred animals involved, a 5-10 % increase corresponds to 484 to 968 additional animals, which would have required additional expenses of at least \$145,150-\$290,300 simply for purchase, transport and feeding. Including all costs and overheads, a 5-10 % increase in information collected might be valued at \$0.5 to \$1.0 million.

Keywords: Beef cattle, statistical design, efficiency

INTRODUCTION

Breeding to meet market specifications is a complex issue. Profitability may depend on knowing the suitability of seedstock for different markets and their performance under different feeding regimes. The Co-operative Research Centre (CRC) for the Cattle and Beef Industry (Meat Quality) was set up to obtain this important information for industry. Objectives included developing an understanding of the genetic basis of cattle growth and development, finding genetic markers and estimating genetic parameters for carcass, meat quality and growth traits, in order to construct a comprehensive package of breeding strategies to meet the range of value-added markets. Obtaining information on genetics, markets, pasture vs feedlot finishing, hormone implant, grow-out nutrition and other treatments, as well as breed and sire effects and G x E, requires data from animals of different breeds and sires born and raised under different climatic and management/nutritional regimes. This paper discusses how statistically efficient designs have been used in the CRC to increase the number of treatments considered, and provides estimates of the monetary cost of the additional numbers of progeny per sire required to achieve similar accuracy if animals had simply been allocated to treatment combinations using a simpler system.

METHODS

In the CRC straightbreeding project, one set of core cattle was available for use by the Growth and Nutrition, Meat Science, Genetics and all other programs to estimate the effects of market, finish, nutrition, management and treatment on all traits of interest, as well as effects of tropical and temperate environments, genetic parameters and G x E interactions. A summary of breeds, years

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and intake groups, market, finish, nutrition and other treatments, as well as numbers of animals by breed type and sex are given in Table 1.

Table 1. Market, finish, nutrition and treatments & numbers of animals by breed type and sex

	Temperate	Tropical	Crossbred - Brahman dams x
Breeds:	Angus, Hereford, Murray Grey	Brahman (B), Belmont Red (BR),	Angus, Brahman, Belmont Red, Charbray,
Sex:	(MG), Shorthorn (S)	Santa Gertrudis (SG)	Charolais, Hereford, Limousin, Santa,
Birth Herds:	3518 steers, 440 heifers	2218 steers, 1605 heifers	Shorthorn sires
	11 Ang, 6 Her, 3 MG, 3 S	3 (linked) B, 3 BR, 4 SG	972 steers, 924 heifers
Years/ Intakes¹	94W ¹ , 95S&W ¹ , 96S&W, 97S&W, 98S&W	94W ¹ , 95W, 96W, 97W, 98W	2 birth herds for all animals 95W ¹ , 96W, 97W, 98W
Growout treatment	Steers only: 3 nutrition treatments; 3 nutrition + minimal handling for 95W & 96W	Tropical/temperate location (also nutrition treatments - first intake of straightbred steers and last group of straight and crossbred steers & heifers; hormone implant treatment - crossbred steers; nutricharge treatment - animals sent south)	
Finish	Pasture or Feedlot	Pasture (tropical) or Feedlot (Tropical or Temperate)	
Slaughter	Domestic (400 kg liveweight; feedlot entry 300 kg), Korean (520 kg liveweight; feedlot entry 400 kg) or Japanese markets (steers only; 600 kg liveweight; feedlot entry 400 kg).		

¹S = Summer intake (January-February); W = Winter intake (April - June for temperate breeds; May - November for tropical breeds, which were sometimes split into late and early management groups)

Use of integrated, statistically efficient designs means the same animals can be used for more than one purpose with only a small loss of efficiency for each single use. In addition, integrated design enables interactions between uses to be estimated. For example, it is important to know how the effect of grow-out nutrition differs according to market or finishing system, and the size of genotype x environment interactions between the different markets and finishing systems, as well as how nutrition treatments affect feed efficiency, fatness, meat quality and general performance in the feedlot.

However, to achieve these aims, care and effort is required with the design. If the offspring of one sire were distributed predominantly to one particular market, finish or treatment type (or specific combinations thereof), it would be difficult to determine how much of the apparent effect were due to that particular sire, and how much to treatments. For some applications, eg variety trials or multi-factorial experiments, catalogues of designs have traditionally been available. Nearly always, a high degree of balance is required. Examples would be three or four replicates of 100 varieties in 10 incomplete blocks (where every variety occurs in every replicate and near perfect balance is achieved over incomplete blocks), or a fractional replicate of a factorial design, where all main effects are observed the same number of times, as are higher order interactions.

For genetic experiments, exact balance over sires is not possible, because the numbers offspring produced may differ considerably, and discarding animals bred specifically for the CRC would be exceedingly wasteful. In fact, numbers of offspring per sire in CRC data ranged from 1 to 76. Table 2 gives the number of animals, sires, treatment combinations and intake cohorts for straightbred

temperate breed animals. Animals were allocated to treatment combinations (**Design A**) according to the procedures described by Robinson (1995). To estimate the efficiency of this method, a second, simpler allocation method (**Design B**) was devised for comparison. This involved sorting animals by sire within birth herd and then allocating the first animal to the first treatment combination, the second animal to the second combination and so on. This leads to approximately equal numbers of animals for each treatment combination. However, if the treatment combinations were ordered in a systematic way (eg DP1, DP2, DP3, DF1, DF2 ...; for D = domestic market, P = pasture, F = feedlot and 1, 2, 3 represent nutrition or other treatments), sires with only a few offspring would all end up in the same market, which would be highly inefficient. To avoid this, order of treatment combinations was randomised before assignment to the offspring of each sire.

Evaluation of Efficiency. Two models were fitted for each straightbred breed. The first model, estimating variance of sire estimates for the entire breed was: sire + cohort.treatment_combination + cohort.herd (**Model 1**). Here, cohort refers to management group, a combination of sex and intake group, of which there were generally one or two per year (Table 1). This model can be estimated only if at least one link sire is present in all cohort.herd combinations. Those without a link sire were therefore omitted from the analysis. The second model was used to compare the variance of treatment effects (which differed from year to year) for steers within a cohort, evaluated at 3 markets, 2 finishes and 3 or 4 nutrition treatments. This model was: sire + herd + market + finish + nutrition + market.finish + market.nutrition + finish.nutrition + market.finish.nutrition (**Model 2**). Linkage was again checked. If any cohort had one unlinked herd, that herd was deleted from the analysis. For simplicity, if a cohort had more than one unlinked herd, the entire cohort was omitted. Once animals have been allocated, the variance of differences between predicted means for any treatment or treatment combination is essentially a fixed property of the design (**V**). For any trait analysed, the observed variance can be expressed as $V\sigma^2$, where σ^2 is the residual variance of the trait. Using Model 1, the mean variance of the difference between estimated sire effects was calculated under Designs A and B. For Model 2, variances of the differences between predicted means were calculated for sire effects as well as main effects of market, finish and nutrition and their interactions.

Table 2. Numbers of straightbred animals, sires, animals in linked herds, and efficiency of designs A and B for sire effects, estimated by variance of differences between sires

Breed	Number of Animals				No of sires	Numbers of				Model 1		Loss from B (%)
	Total	Dead/Invalid	Valid & linked			Treat comb	Herds	Cohorts	Herd x Cohorts	Var(sire diffs)		
			Steer	heifer						A	B	
Angus	1849	43	1515	227	111	177	11	13	44	0.402	0.414	3.0
Hereford	1138	38	970	130	58	159	6	12	26	0.141	0.142	1.1
Shorthorn	513	14	499	0	35	166	3	9	12	0.537	0.561	4.5
M.Grey	458	7	340	73	19	74	3	6	10	0.139	0.144	3.4
Total	3958	102	3324	430	223	576	23	40	92	1.218	1.261	3.5

Table 3. Mean within-cohort variances of differences between all pairs of treatment or treatment combinations under Designs A and B, and loss from using Design B, for steer cohorts with adequate linkage, evaluated at 3 markets, 2 finishes and 3 or 4 nutritions

	Mean variance (V) of difference between predicted means ¹							Sires
	Market	Finish	Nut	M.F ²	M.N ²	F.N ²	M.F.N ²	
Angus (4 cohorts, 16 herd x cohorts, 709 steers, 66 sires)								
Var A	0.145	0.097	0.167	0.294	0.513	0.338	1.053	2.859
Var B	0.155	0.104	0.184	0.313	0.541	0.36	1.080	2.942
Loss %	6.7	7.1	10.4	6.4	5.6	6.5	2.6	2.9
Hereford (5 cohorts, 13 herds x cohorts, 778 steers, 66 sires)								
Var A	0.267	0.178	0.286	0.537	0.868	0.576	1.778	1.589
Var B	0.278	0.193	0.31	0.565	0.925	0.617	1.841	1.656
Loss %	4.3	8.8	8.3	5.1	6.6	7.2	3.5	4.2
Shorthorn (6 cohorts, 6 herds x cohorts, 394 steers, 48 sires)								
Var A	0.658	0.436	0.718	1.339	2.234	1.458	4.638	3.128
Var B	0.720	0.526	0.851	1.478	2.72	1.766	5.343	4.019
Loss %	9.5	20.5	18.6	10.4	21.8	21.1	15.2	28.5
Murray Grey (3 cohorts, 5 herd x cohorts, 340 steers, 28 sires)								
Var A	0.162	0.108	0.199	0.325	0.610	0.402	1.250	0.862
Var B	0.171	0.116	0.216	0.345	0.646	0.426	1.290	0.925
Loss %	5.7	8.0	8.2	6.2	5.8	6.0	3.2	7.4

RESULTS AND DISCUSSION

Table 2 gives mean variances of estimated sire differences from fitting Model 1 to the entire dataset (excluding unlinked herd.cohort combinations). 3.5 % more animals would be required to achieve the same accuracy using Design B. Table 3 provides results for the within-cohort analysis (Model 2). Apart from the Shorthorn breed, where, after deleting one totally unlinked herd, the number of animals in each cohort averaged 66, between 5 % and 10 % more animals would be needed for the same accuracy with Design B. Assuming results for straightbred temperate breed animals are similar to those for straightbred and crossbred tropical breeds, a 5-10 % increase out of a total of 9677 animals corresponds to 484 to 967 additional animals, which would have involved additional expenses of at least \$145,150 - \$290,300 simply for purchase, transport and feeding. Including all costs and overheads, a 5-10 % increase in information collected might be valued at \$0.5 to \$1.0 million.

REFERENCE

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