THE EFFICIENCY AND PLACE OF MULTI-HERD ANIMAL EVALUATION PROCEDURES FOR BEEF CATTLE

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SUMMARY

Multi-herd evaluation procedures for beef cattle are reviewed. These include the formal establishment of genetic links across herds through the use of AI reference sires, the conduct of central performance testing and the participation in co-operative nucleus breeding schemes. The advantages, limitations and problems of each of these procedures are discussed. The primary and most limiting factor for the use of field data for multi-herd animal evaluation is the extent of genetic ties across herds. Even the most sophisticated analytical procedure cannot properly account for poor connectedness amongst herds. Central performance tests are often limited by poor representation of individuals from contributing herds, the influence of pre-test environmental effects and differences between the test and commercial environments. Co-operative nucleus breeding schemes may provide suitable population structures for multi-herd evaluation, although further work is required to examine the impact of unbalanced data structures on the accuracy of evaluation.

INTRODUCTION

Since the very beginnings of the application of genetic principles to livestock production, animal breeders have been concerned with the evaluation of animals both within and between herds. This evaluation is a fundamental component of any breeding programme and the search for optimum evaluation procedures has received a great deal of emphasis in animal breeding research. In particular, there has been much deliberation on the role and efficiency of various procedures for multi-herd animal evaluation.

It is well recognised that the rate of genetic improvement is directly related to the selection intensity applied when choosing replacement stock. The principal constraint to the rate of genetic improvement within many beef cattle enterprises is the limitation on the intensity of selection, due to small herd size. In an attempt to overcome this limitation many breeders look beyond their own herd and obtain at least a proportion of their replacements from an outside source. A further motivation for the introduction of outside genetic material is the fear of inbreeding within the closed herd and subsequent reduction in performance due to inbreeding depression.

Many beef cattle populations consist of a hierarchical structure, with a small number of 'elite' herds which provide breeding stock to 'multiplier' and 'commercial' herds. Within the 'elite' sector there is often vigorous competition which results in breeders continually seeking the most
fashionable genetic material, often from outside their own herd. Similarly the 'multiplier' herds choose replacement sires from the 'elite' sector and these in turn provide sires for the 'commercial' sector. This exchange relies on the evaluation by breeders of the relative merit of animals from different herds. Consequently, multi-herd evaluation, whether based on subjective appraisal, intuitive judgement, objective measurement, or a combination of these, forms an integral part of the exploitation of available genetic resources.

A major problem associated with multi-herd evaluation is to adequately account for the influences of genetic and non-genetic differences between herds. Variation in the performance of animals in different herds may be partly due to real genetic differences, but a large proportion of the variation is due to differences in climate, nutrition, management or other environmental factors peculiar to each herd. Further biases may be introduced from differing mating and selection strategies between herds. Consequently direct comparisons of the performance of animals reared in different herds can be misleading. Various strategies have been adopted to overcome this problem including the formal establishment of genetic links across herds through the use of common AI sires (reference or marker sires), the use of central performance testing and the participation in co-operative nucleus breeding schemes. Each of these strategies involve particular organizational and technical difficulties, and each have certain advantages and limitations. Along with the evolution of these strategies has been the development of more sophisticated analytical procedures and advances in computing power which enable more efficient utilization of available information.

In this paper we shall review the advantages and limitations of the various procedures used for multi-herd animal evaluation and identify problem areas which require further study.

MULTI-HERD EVALUATION USING FIELD DATA

With the increased activity in performance recording of beef cattle during the 1960's and 70's it was generally emphasised that such records should be used strictly for comparisons of animals managed within the same contemporary group, within a herd. At the same time, the success of dairy cattle populations in producing across-herd evaluations for sires used in artificial insemination (AI) led to strong pressures for the organisation of similar programs for beef cattle. The major limitation to the development of these programs was the very low usage of AI in most beef cattle enterprises.

Warwick (1980) reviewed the history of the establishment of national sire evaluation programs in the USA. He noted that the first critical examination of such programmes was undertaken by a committee of the Beef Improvement Federation in 1968. This committee recognized that problems in accounting for between-herd differences were a hinderance to valid comparison of sires used in different herds. The use of reference sires to establish genetic ties between herds was mentioned but the concept was not elaborated. General recommendations included the need for greater use of AI and the combined use of performance records from the individual, its ancestors, collateral relatives and progeny, as key components of a national sire evaluation programme.
The first real opportunity for the establishment of multi-herd evaluation programmes based on field data in the USA coincided with the introduction of exotic European breeds. Imported bulls were few in number and most were used through AI across many herds. In addition, performance recording was enthusiastically supported and in some cases a prerequisite for registration. This combination, providing both genetic ties among herds and a large volume of performance data, enabled multi-herd sire comparisons using adaptations of dairy sire evaluation methods (Warwick, 1980). Those established breeds in which little AI was used did not have a suitable distribution of sires across herds for the use of routine field data for multi-herd evaluation. Consequently organised field tests were introduced in which minimum numbers of progeny in each contemporary group included in the analysis had to be sired by a designated reference sire. With the rapid expansion of the number of bulls available for natural mating the extent of AI declined in the newly introduced breeds and these also placed greater emphasis on the use of designed field tests for sire evaluation.

The development of multi-herd evaluation programmes based on the use of field data in the extensive beef industries in other countries (eg. Canada, Australia, New Zealand) followed a similar history to that experienced in the USA. The introduction of the exotic genotypes was usually associated with widespread use of AI and the establishment of ties between herds. This was followed by the increased availability of sires for use in natural mating, a reduction in the extent of AI usage and a greater reliance placed on designed field tests. In Europe, specialized beef enterprises are generally smaller with more intensive management and a greater use of AI. Nevertheless, a large proportion of the cow population is still bred by natural service and much emphasis is placed on the establishment of systematic connections between herds by the specification of minimum requirements for reference sire usage (Foulley and Sapa, 1982).

Data Structure

The suitability of field records for use in multi-herd animal evaluation is dependent on the extent of genetic links (connectedness) among the herds from which the data is collected. Connectedness among sires can arise either directly by having progeny in the same contemporary group, or indirectly by having progeny linked through a common sire with progeny in many contemporary groups. Although there is a general appreciation of the importance of an appropriate data structure for the prediction of differences between animals, the specification of optimum designs for the establishment of systematic connections among herds has received limited attention. Those studies which have been reported generally relate to specific population structures and concentrate on the optimisation of the distribution of progeny among home sires and reference sires to achieve a specified degree of accuracy of across-herd evaluation.

Connolly and Cunningham (1976) examined the efficiency of a range of allocation of resources to test sires and reference sires for the evaluation of test sires in different AI centres. The efficiency of any particular data structure was based on the variances of comparisons between sires, calculated by least squares methods. They found that the level of reference sire replication at centres was critical. Foulley and Clerget-Darpoux (1978) and Foulley et al. (1983a) developed expressions for the relationship between the accuracy of across-herd evaluation and the distribution of progeny among home sires and reference sires. These expressions were derived from the algebraic manipulation of the mixed model equations corresponding to a specific data
analysis model appropriate for beef cattle breeds involved in organised sire evaluation programs in France. The predicted accuracy of a sire evaluation using this approach was lower than that obtained from classical selection index theory, because of the error involved in the estimation of contemporary group differences. The magnitude of this error was shown to be dependent on the number of reference sire progeny and number of home sire progeny per contemporary group. Foulley and Clerget-Darpoux (1978) found that a fairly wide range of variation in progeny distribution between reference sires and home sires resulted in a similar accuracy of across-herd selection among home sires. In particular, it was possible to substantially reduce the number of reference sire progeny in each herd without having a significant impact on the accuracy of evaluation. This was an important finding as the achievement of a sufficiently high rate of reference sire usage (via AI) was a major limitation to the application of this system.

Nielsen (1974) examined several data analysis procedures for the estimation of the additive genetic value of sires from simulated data sets. These data sets represented a range of data structures with different numbers of progeny by reference sires and non-reference sires within herds. Whilst there was little difference between the analytical procedures examined, data structure did have a significant impact on the correlation between the true and estimated genetic values. With the same total number of reference sire progeny within a herd, fewer reference sires each with more progeny appeared to be the best structure. Hudson et al. (1980) also used simulation to examine the impact of the distribution of reference sire usage across herds on the expected average standard error of prediction for young bulls. Designa were simulated and mixed model equations formed using data from the Canadian National Sire Monitoring Program. Depending on the acceptable level of accuracy required, it was found that from 10 to 20 percent of matings to reference sires was sufficient to provide adequate connectedness between herds.

Several strategies have been proposed for determining the degree of connectedness among subclasses within large unbalanced data sets. Schaeffer (1975) noted that relative to the total numbers of sires and herds represented in a dairy or beef cattle data set, the number of filled sire-herd subclasses is usually less than one percent. These subclasses are connected if differences between all pairs of sires and between all herds are linearly estimable. Disconnectedness results in groups of subclasses where the sires cannot be compared with the remaining sires, nor the herds compared with remaining herds. Essentially there are independent subsets of the data which should not be analysed collectively. Petersen (1978) and Fernando et al. (1983) have developed algorithms for identifying connected subsets of data in a two-way classification (eg. herds and sires). Foulley et al. (1983b) described an index for assessing the degree of connectedness between pairs of sires. The value of this index is determined from the prediction error variances of the two sires and has values ranging from 0 and 1, the value diminishing with the deterioration of the degree of connectedness. A value of 0 represents the situation where estimation is not possible, whilst a value of 1 represents a balanced distribution of progeny between the sires. These index values can be included in a cluster analysis to identify groups within the data set such that the index value between any two sires within a group is higher than that between either of those sires and any other sire in another group.
Analytical Models

The value of field records for multi-herd evaluation is dependent on the use of an appropriate analytical model. Early models were based on adaptations of simple procedures for ranking dairy sires used extensively across many herds through AI (e.g., Regressed Contemporary Comparison). These procedures assumed a random distribution of progeny across herds, no genetic trend and random sampling of mates of each sire within each herd. More recently the application of mixed-model procedures (e.g., Henderson, 1973) has lead to the adoption of more sophisticated and complete models for the analysis of unbalanced data structures. Eriksson (1983) reviewed the many studies which have compared various mixed-model approaches for beef sire evaluation. He noted that the general flexibility of this approach enables the specification of a model which fulfils both the statistical requirements and the computational limitations imposed.

Berger (1983) outlined the methodology recommended for national sire evaluation programs in the USA. The basic mixed-model included fixed contemporary group and random sire and residual error effects. More complete models included various combinations of additional fixed and random effects (e.g., maternal grandsires, dams, genetic groups) and interactions between these effects. The inclusion of additive genetic relationships among sires (and maternal grandsires or dams, if these are included in the model) increases the accuracy of evaluation, provides greater connectedness among the data and aids in accounting for genetic trend in the population. Recent applications have included individual performance along with sire and dam effects to provide across-herd evaluations for yearling bulls and heifers which have no progeny records (Wilson et al., 1985). The reduced animal model (RAM) proposed by Quaas and Pollak (1980) for within-herd evaluation has been recently applied for across-herd evaluations in the USA (e.g., Benyshek et al., 1985) and Australia (K. Hammond, pers. comm.). The later application uses a multi-herd RAM, including relationships among all animals and traits. A valuable consequence of the use of the RAM for genetic evaluation is the potential to accurately estimate the genetic and environmental trends in the population over time.

It is apparent that with the continual development of more efficient computing strategies and increases in computing power, the focus is shifting from obtaining simple methods of computation to defining more appropriate models for analysis. Nevertheless, as pointed out by Eriksson (1983), not even the most sophisticated evaluation procedure can account for poor distribution across herds of animals to be evaluated. He suggested that a well designed program of sire usage is still a very powerful base for a good evaluation procedure.

Consequences of genotype by environment interactions

The existence of genotype by environment interactions can have important consequences for the use of field records in the evaluation of animals across herds. It is common for multi-herd evaluation programmes to encompass herds over a wide geographical area, with a range of climatic conditions, nutritional environments and management practices. An interaction may result in a change in the magnitude of differences between animals from one production environment to another and in extreme situations may result in a re-ranking of genotypes between environments. Varying degrees of interaction have been identified for a number of performance traits, both within industry field records and designed experimental evaluations. Interactions may be
present at each of the levels of sire by region, sire by herd within region and sire by contemporary group within herd. A number of strategies have been devised to detect and account for these in the design and analysis phases of evaluation programmes.

The majority of studies which have examined field records for the existence of sire by environment interactions have involved an analysis of variance with the inclusion of interaction components in the model. Nunn et al. (1978) and Buchanan and Nielsen (1979) observed significant sire by region interactions for weaning weight in American Simmental field data. However, Tess et al. (1979) found that when sire by herd, within region and sire by region interaction were both included in the analysis then the sire by region interaction was no longer an important source of variation. Bertrand et al. (1985) found that sire by herd within region and sire by contemporary group within herd interactions were both significant sources of variation for weaning weight in Polled Hereford field data collected in the USA. Buchanan and Nielsen (1979) observed a significant sire by region interaction for birth weight in American Simmental field data whilst Burfening et al. (1982) found no significant sire by region interaction for calving ease score or birth weight, but did detect significant sire by herd within region interactions for both traits. Whilst each of these studies found varying degrees of interaction at each level of the data structure it would appear that sire by herd or contemporary group interaction is potentially the cause for most concern. In some cases the proportion of the total variation explained by this interaction was much larger than the estimated variance due to sire effects.

Henderson (1974) discussed the inclusion of sire by herd interaction in the mixed-model analysis of field data. A simulation study by Nielsen (1974) confirmed that when a significant sire by herd interaction existed, the accuracy of sire evaluation was increased by including an interaction effect in the model. None of the data structures examined were adequate when an interaction was present, as each structure involved single herd progeny testing of sires with varying degrees of reference sire usage. If it is considered necessary to account for interaction effects in multi-herd sire evaluations then multiple herd progeny testing of each individual sire is required. Bertrand et al. (1985) noted that the general consequence of including a sire by herd (or contemporary group) interaction term in the analytical model is to reduce the emphasis placed on subclass means with large numbers of observations, thus reducing the interaction effect particular to any one contemporary group. Including an interaction effect in the model will also account for the distribution of progeny across herds such that a sire used in only a few herds will have a low accuracy of evaluation. However, as pointed out by Benyshek (1980), the increased accuracy of multiple herd progeny testing compared to single herd testing of sires, with the use of reference sires to link herds, may be completely negated because of the reduction in the total number of sires evaluated. Consequently, the overall genetic change in the population may be greater if a larger number of sires were evaluated in single herd tests.

CENTRAL PERFORMANCE TESTING

As the term suggests, central performance testing involves the evaluation of the performance of a group of animals under uniform conditions at a single location (central test station). In principle, it is a means of 378
removing the confounding due to differences in environment and management when comparisons are made among individuals originating from different herds. Central performance testing has been used extensively for many years as an important part of industry breeding programmes throughout Europe (Andersen et al., 1981) and North America (Wilton and Batra, 1972). More recently, it has been adopted to a limited extent in Australia and New Zealand (Dalton and Morris, 1978) and it currently receives much emphasis in South Africa (Bosman and Hunlun, 1984). There has been considerable debate over the value of central performance testing as a strategy for the evaluation of potential breeding animals. In particular, the influence of pre-test environmental effects on subsequent performance at the central test station and the often poor association between the test environment and the commercial production environment have been recognised as potential problems.

A wide range of testing strategies exist throughout the countries in which central performance testing is conducted. Differences exist in the age at which animals enter the test, the length of the test period, the nutritional regime, the feeding policy (restricted or ad libitum), the number of individuals included in each test and the traits recorded. Testing can be either continuous, where animals are compared against a rolling average, or in batches, with contemporary comparisons made within the batch. Because of the expense involved in conducting a central performance test the procedure has been restricted largely to the evaluation of the individual performance of bulls. The concept of central progeny testing, where groups of progeny of a number of sires are tested under uniform conditions, has generally been considered impractical because of the cost involved and the limited number of sires which can be adequately tested. Nevertheless, this system has been adopted in some European countries as part of the evaluation of dual-purpose bulls prior to widespread usage through AI (Menissier, 1976).

A potential advantage of the concentration of resources for central performance testing is that it may provide the opportunity for the recording of additional performance characteristics which may not be practical to measure at the individual herd level. For example, at central test stations where animals are intensively housed it is not uncommon for individual feed intakes to be recorded for each animal in the test group. Combined with the recording of weight gain over the test period, feed intake data can be used to estimate feed conversion efficiency for each individual on test. The use of ultrasonic equipment for the estimation of subcutaneous fat depth or more complex devices for the assessment of body composition on the live animal (e.g. computerised tomography) may be feasible at a central test station, even though these facilities would usually not be available in individual herds. In addition to the potential genetic benefits of central performance testing the procedure has received considerable support and acceptance for its role in breed and herd publicity, in promotion of the concept of objective performance testing and as a tool for the marketing of animals. In particular, the high sales potential of superior ranking bulls from central performance tests has encouraged ready acceptance by many breeders (Dalton and Morris, 1978).

The high cost of testing and limited capacity of central test stations often means that very few animals are tested from each herd. Consequently there is usually little potential for indirect comparisons amongst those animals in each contributing herd which are not submitted for testing. In addition to differences in pre-test environment and management there is frequently a range of selection strategies adopted by individual breeders when choosing animals for testing. Even if representative sampling from each
contributing herd could be achieved a very sophisticated analytical model would be required for valid evaluation of all animals.

**Effectiveness of central performance testing**

Despite the fact that central performance testing is considered an important part of beef cattle improvement programmes in many countries, there has been little published on the effectiveness of the technique. Perhaps the time and cost involved have been the main reasons for this neglect (Dalton and Morris, 1978). Further clarification will be possible as more data is collected in those populations in which both central testing and field evaluation programs are conducted (e.g. Wilton and McWhir, 1985). Among those studies which have been reported in the literature, there has often been conflicting results. If central performance testing is to be an effective means of identifying genetically superior individuals there should be a high positive association between the test results and subsequent evaluations based on progeny test data.

Baker et al. (1984) summarised the results of earlier studies which had used progeny testing to investigate the accuracy of central performance testing. They also reported the results of a comprehensive evaluation of the technique, conducted in New Zealand. A total of seven previous studies were cited, of which four involved testing of bulls following weaning at about 6 to 8 months of age (Shelton et al., 1958; Kincaid and Carter, 1958; Carter, 1971 and Smith et al., 1979). The remaining three studies involved tests starting much earlier, from 30 to 90 days of age (Lessells and Francis, 1968; Averdunk et al., 1980 and Dee Roo and Finland, 1983). The small data sets reported by Carter (1971) and Smith et al. (1979) were too limited to assess the value of these particular tests, although Carter (1971) warned that the disappointing results should dictate caution in advocating central performance tests in New Zealand. The studies reported by Shelton et al. (1958) and Kincaid and Carter (1958) were American experiments both showing positive relationships between performance and progeny test results. Bulls and all progeny in one experiment (Shelton et al., 1958) and male progeny in the other experiment (Kincaid and Carter, 1958) were fed high energy diets post weaning in feedlots. Heifer progeny in the later study were fed at pasture. Although feeding regime was confounded with sex differences, these results suggested that the effective heritability of the performance tests was lower under pasture feeding than in the feedlot. The studies reported by Lessells and Francis (1968), Averdunk et al. (1980) and Dee Roo and Finland (1983) all showed favourable relationships between performance and progeny test results. These results emphasize the importance of starting bulls in performance test at a young age to minimize pre-test environmental effects.

The New Zealand study reported by Baker et al. (1984) involved a series of central performance tests with Hereford bulls from about 10 to 19 months of age at pasture. A representative sample of these bulls was subsequently used through AI in dairy herds and their crossbred progeny were assembled and reared together at pasture. Regressions of progeny growth traits on performance traits of their sires were in almost all cases not significant and the effective heritabilities, from offspring-sire regression, were much lower than expected for both final weight and post-weaning gain (0.07 and 0.09, respectively). It was concluded that the central performance tests had been of limited value for ranking bulls on breeding value for growth. The influences of pre-environmental effects and the relatively late age of animals at the start of the test were suggested as critical factors in explaining these results.

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In contrast to the findings of the New Zealand study, Wilton and McWhir (1985) reported results of a Canadian trial which suggested that central performance testing could result in moderately accurate estimates of subsequent progeny performance. This study utilised data on Hereford sires and their sons tested for growth rate in test stations. Some sires also had subsequent progeny proofs in performance recorded herds. Correlations between individual performance compared to contemporaries at the station and subsequent progeny performance for post-weaning gain and yearling weight were close to expectation (0.16 and 0.20 respectively) based on numbers of progeny, levels of heritability and genetic correlations appropriate to field conditions. The correlation for weaning weight (0.20) was higher than expectation. Nevertheless, progeny performance under field conditions did not appear to be as closely related to individual test station performance as did progeny performance in test stations.

**Influence of pre-test environmental effects and age at start of test**

Several factors have been identified as contributing to the poor relationship found in some studies between central performance test and field progeny test results. A number of these can be grouped under the general classification of pre-test environmental influences and include nutrition and herd of origin effects due to climatic, seasonal and management factors.

Herd of origin effects have been found to account for a large proportion of the total variation in growth and efficiency of bulls in central performance tests (eg. Morris, 1981; Collins-Lusweti and Curran, 1985). Morris (1981) suggested these herd effects could originate from either non-genetic differences among herds having a carryover effect on performance during test, or genetic differences due to sampling of the sires and dams of the particular bulls being tested. Limited New Zealand data suggested that the genetic effect is probably small. Nevertheless, significant herd genetic differences for weaning and yearling weight have been reported for Hereford and Angus cattle in the USA (Cundiff et al., 1975).

Dalton and Morris (1978) reviewed a number of New Zealand studies in which the effects on subsequent growth of differences induced by early feeding treatments were compared. They found variable degrees of compensatory growth following periods of under-nutrition. The influence of the animals nutritional environment prior to 3 to 4 months of age often had a lasting effect on subsequent growth performance. They suggested that considerable caution was required when interpreting data influenced by compensatory growth because of differences in level and duration of under-nutrition and in length of the re-alimentation period. Compensatory growth during the test period will introduce a negative environmental correlation between start weight and subsequent rate of gain (eg. Morris, 1981; Tong, 1982). Real genetic differences between animals in rate of gain would result in a positive correlation between start weight and subsequent gain on test. Baker et al. (1984) argued that since the phenotypic correlation consists of these two opposing effects, it is of little value for determining the relative merits of gain on test and final weight for ranking animals.

In a report by a working group of the European Association of Animal Production on performance testing of bulls, Andersen et al. (1981) recommended that in tests for dairy and dual purpose breeds, calves should be assembled at the test centre as soon as possible after receiving colostrum (ie. from 4 days of age) and certainly no later than 6 weeks of age. In addition, it was suggested that calves should undergo an adaptation period
minimum of 3 weeks) to introduce them to the test environment and to overcome as far as possible the influences of pre-test environmental differences. The same report recommended that beef bulls which had been suckled prior to starting the test should be assembled at the test centre as early as possible and not older than 7 months of age. Again, they recommended an adaptation period of at least 4 weeks prior to the start of the test.

Simm et al. (1985) compared testing systems in which bulls were either reared artificially from birth to 84 days of age, or reared on their own dam to 84 or 168 days of age, to examine whether non-genetic effects on performance could be reduced by early weaning. All bulls were performance tested on ad libitum feeding from 200 to 400 days of age. Artificial rearing was not effective in reducing environmental variation in performance. The influence of year-season of birth and dam age was reduced for some traits, but additional environmental variation was introduced due to the restriction of pre-test growth rate. It was considered that the low growth rate of artificially reared bulls would not be acceptable to breeders submitting bull calves for testing. Additionally, artificial reared bulls had a mortality rate twice that of naturally reared bulls. Bulls reared naturally to 84 days of age were least affected by dam age and year-season of birth and performed as well as those weaned at 168 days of age. Simm et al. (1985) concluded that earlier weaning of bulls entering central performance tests (ie. 2-3 months of age) would reduce pre-test environmental effects on performance, and may increase the accuracy of identifying genetically superior bulls. It was noted by Willis and Preston (1970) that early weaning of calves had been practised in Cuba, with bulls from a number of beef breeds and crosses starting on test at 90 days. However, in many situations, serious cattle management and sociological problems need to be overcome before convincing breeders of beef bulls to wean at an early age.

Influence of test environment

There is considerable variation in the conditions under which central performance tests are conducted, both within and between countries. The majority of testing centres in Europe, North America and South Africa are managed under semi-intensive conditions, with the feeding of complete rations. In New Zealand and Australia, tests are often conducted at pasture with varying degrees of supplementation. Ideally, there should be a close correspondence between the test environment and the commercial production environment in which subsequent progeny are managed. On the other hand, provided that genotype by environment interactions are not important, the heritability of a trait may be increased under a more favourable test environment.

Testing under semi-intensive conditions has obvious benefits in enabling the close monitoring of performance and offers the opportunity to record individual feed intake. In addition, it ensures that the conditions during the testing period are as uniform as possible so that each animal has an equal opportunity to express its genetic potential. Feeding regimes vary from ad libitum feeding to restriction on age or weight. Diets may contain different levels of concentrate (energy and/or protein) and roughage. If complete high energy diets are fed ad libitum then daily gain is limited only by the growth potential of the animal in that environment. Maximising growth rate may reduce the time required for testing and consequently reduce costs. In addition, recording of feed intake is simplified and the determination of feed conversion efficiency is possible (Krausslich, 1974).
Andersen et al. (1981) suggested that it is possible to alter the relative expression of various components of growth rate by regulating the level of feeding. At a low feeding level, variation in growth rate was considered to be largely a function of variation in residual efficiency (maintenance requirement, heat loss related to growth, and the efficiency of digestion) between animals. They hypothesised that variation in growth rate at a higher level of feeding was a function of variation in residual efficiency and lean tissue growth capacity. Genetic variation in appetite (physically and/or physiologically regulated) will only affect growth rate if the level of feeding is above the maximum intake of some animals. The choice of feeding system should depend on the ultimate breeding objective but more commonly it is dictated by considerations of ease of management and the desire to maximise the rate of gain on test. Andersen et al. (1984) noted the need for further research into determining the genetic correlations between feed efficiency measured on performance tested bulls and feed efficiency in their progeny as growing animals and breeding females.

The test period should be sufficiently long to provide the opportunity for individuals to express their performance potential for those traits on which evaluation is based. Management considerations generally tend to impose tests of fixed duration, even though in some circumstances it may be desirable to test to a constant degree of maturity or finish. Such a strategy would result in a range of ages and weights at the end of the test (Krausslich, 1974).

NUCLEUS BREEDING SCHEMES

A nucleus breeding scheme is a hierarchical breeding system in which a 'nucleus' herd is established to breed replacement sires for both itself and an associated 'base' population. Whilst this structure can be adopted in a single herd, the majority of nucleus breeding schemes involve a number of cooperating breeders and are essentially multi-herd breeding programmes. A nucleus breeding scheme may consist of more than two levels, with the intermediate levels acting as multipliers of stock obtained from the nucleus. In some situations the nucleus is a closed herd, providing all its own replacements as well as sires for use in multiplier and base herds (closed nucleus system). Alternatively, the nucleus may be an 'open' herd obtaining a proportion of its replacements from lower levels of the hierarchy (open nucleus system). In either case, the systematic transfer of breeding stock between the nucleus and base generates a network of direct and indirect genetic links among the participating herds. The pattern and extent of these links determines the possibility for obtaining accurate and precise genetic evaluation across all herds.

The concept of co-operative nucleus breeding schemes has received greatest acceptance amongst breeders in the extensive beef cattle industries in New Zealand, Australia and South Africa. Dodd et al. (1982) surveyed the major group breeding schemes operating in New Zealand. Several large schemes were in operation with a range of population structures and selection priorities. Nicoll and Johnson (1986) reported that the estimated rate of genetic improvement in one large scheme was comparable to that achieved in a number of long-term single-trait selection experiments.

A number of theoretical studies have attempted to define optimum designs for nucleus breeding schemes, particularly in terms of maximising genetic
responses across the population (James, 1977; Hopkins, 1978; Mueller, 1984; Mueller and James, 1984). The concepts and theory developed for the evaluation of open nucleus breeding schemes could be utilised more widely in the investigation of designs for multi-herd breeding programmes. Hopkins (1978) noted that there may be benefits in considering large-scale AI progeny testing schemes as open nucleus systems. Proven bulls selected after progeny testing and highly selected bull dams could be regarded as the nucleus, whilst those animals not used to breed young bulls for progeny testing could be regarded as the base. The model used by Mueller and James (1984) is sufficiently general for the study of designs for structured populations of this kind.

Each of the above mentioned studies have concentrated on the development of prediction models for determining the sensitivity of genetic gain to variations in population structure and selection strategies. There has been little attention given to the problems associated with the evaluation of animals across the different herds and levels of a scheme. Mueller (1984) and Mueller and James (1984) did investigate the effects of changes in accuracy of selection based on different indices. As more advanced analytical procedures are adopted for the evaluation of animals in open nucleus systems the importance of data structure will become more evident.

The major constraints to the establishment and implementation of cooperative nucleus breeding schemes have generally been organisational rather than technical. Perhaps the principal limitation to the adoption of cooperative schemes in many beef cattle populations has been the poor definition of industry breeding objectives. This results in a diverse array of production characteristics receiving varying degrees of selection emphasis by different breeders. As the definition of breeding objectives becomes clearer and breeders obtain a greater realisation of the benefits of cooperative breeding schemes, then the rate of adoption of this strategy will undoubtedly increase. In addition, the application of advances in artificial breeding technology such as superovulation and embryo transfer (eg. Land and Hill, 1975) in the nucleus may increase the potential advantages of these schemes.

CONCLUSIONS

Multi-herd animal evaluation has become an important component of industry breeding programmes in many beef cattle populations. The major problem in making comparisons among individuals from different herds is to adequately account for the genetic and environmental differences between herds. Various strategies have been adopted to overcome this difficulty including the formal establishment of genetic links across herds through the use of AI reference sires, the conduct of central performance testing and the participation in co-operative nucleus breeding schemes.

Field performance records can be used for multi-herd animal evaluation, provided genetic connections exist among the herds as a result of the widespread use of common sires through AI. The level of AI usage in most beef cattle populations is generally low and the extent of connectedness among herds is often very limited. Consequently, before multi-herd evaluations can be conducted it is often necessary to establish additional genetic links among the herds through the organised use of designated reference sires. A number of studies relating to specific population
structures and analytical models have demonstrated the importance of adequate connectedness among herds in determining the accuracy of across-herd selection. Further work is required to examine the impact of unbalanced data structures for a wider range of situations. Even the most sophisticated analytical procedure cannot make up for a lack of genetic ties over space and time.

There has generally been little emphasis placed on the examination of alternative designs for multi-herd breeding programs which incorporate field data for animal evaluation. Both deterministic and simulation approaches can be used to examine designs for particular situations (eg. Morris et al., 1980; Parnell et al., 1984). Whilst the rate of genetic progress is limited by the accuracy of evaluation, all major components influencing progress should be considered simultaneously in the definition of optimum designs.

In principle, a central performance test provides a means of removing the confounding due to differences in environment and management when comparisons are made amongst individuals originating from different herds. Despite the widespread adoption of central performance testing there is conflicting evidence as to its effectiveness for genetic evaluation. A number of studies have found poor relationships between individual test station performance and subsequent progeny performance. It has been shown that unless testing commences very early in an individual's life, the carryover effect of pre-test environment can have a major influence on the performance test results. In addition, the number of individuals tested from each contributing herd is often too few to obtain an evaluation of remaining animals in those herds.

The systematic transfer of genetic material among herds in a cooperative nucleus breeding scheme may provide a suitable data structure for valid multi-herd animal evaluation. A number of studies have examined predicted genetic responses for various designs and selection strategies in nucleus breeding schemes. Nevertheless, further work is needed to determine the impact of the resultant population structures on the accuracy of selection among participating herds.

As beef cattle breeders become more aware of the potential benefits of using superior bulls through AI the level of participation in designed field evaluation programmes will undoubtedly increase. In addition, continued developments in AI technology, data analysis procedures and design specifications will make these programmes more attractive. The future role of central performance testing is less certain, particularly in those populations for which there are large differences in pre-test environment and where the test and commercial environments differ markedly. It is likely that in many situations central performance testing will be superseded by the widespread establishment of organised field evaluation programs.

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REFERENCES


