SUMMARY

The effectiveness of within-flock genetic improvement programmes is reviewed with particular emphasis on breeding value estimation and genetic trend prediction and estimation. Some recent developments in improving accuracy of breeding value estimation in sheep are mentioned, while the need for precise genetic parameter estimates and appropriate accounting for the effects of selection in field data are highlighted. Realised rates of progress in sheep improvement programmes at the within-flock level have generally not been well documented. The methods available for evaluating genetic trends and the means for better servicing such evaluations in future are discussed.

INTRODUCTION

To fully discuss all aspects of the large number of sheep improvement programmes throughout the world is beyond the scope of this review and would repeat much that is already published. Descriptions of economic objectives and selection criteria for many such programmes can be found in Proceedings of the World Congresses on Sheep and Beef Cattle Breeding (1976, 1980, 1984) and Croston et al (1980). Improvement programmes are also undergoing continuing development, so that there is little point in attempting to describe operational procedures at any particular time. We will endeavour to use individual schemes to indicate more general trends occurring around the world.

The original stimulus for establishing sheep improvement programmes was to provide breeders with a more reliable measure of the performance of potential breeding stock. Apart from the dairy breeds, where progeny testing schemes similar to the dairy cattle schemes have been established for both sheep and goats, these early schemes often did little more than rank individuals on their measured performance for particular characters. Considerable attention was given to adjusting records for the effects of environmental factors, such as an animal’s age or the age of its dam. For the wool producing breeds such as the Merino, improvement programmes were often centred on wool testing laboratories where fleece samples were tested for the yield of clean wool and fibre diameter. But the clear initial aim in all of these schemes was to provide the breeder with more accurate information than could be obtained from the visual assessment of an animal’s merit.

More recently, improved methods of estimating breeding values have been increasingly incorporated into improvement programmes. For example, it was recognised that breeders required animals to be ranked simultaneously for more than one trait, since more than one character influenced overall returns and profitability. Prompted by theoretical developments in quantitative genetics and the increasing availability of computers, this trend has
accelerated. There is now increasing interest in including information on additional selection criteria both because of changes in breeding objectives and also as indicator traits. In addition, more widespread use of information on the relatives of potential breeding stock is now being attempted. These methods are aimed at improving the relevance and accuracy of breeding value estimation so increasing potential rates of response. Some recent developments in this area will be reviewed.

The success of an improvement programme depends on how well potential rates of response are translated into real genetic advances. The education of breeders and the rates of adoption within an industry are part of such an evaluation. Additionally, the efficiency with which individual breeders make selection decisions based on available data is an important component of actual genetic gain. Surprisingly little has been published on predicted and realised rates of change in sheep improvement programmes. Rae (1984), for example, has concluded that insufficient attention has been given to cost-benefit studies of sheep breeding programmes. Direct measures of genetic progress at the individual flock and industry level are a prerequisite for such economic analyses.

Production Systems and Objectives

Sheep production systems vary considerably in terms of their outputs. The relative importance of wool, meat and milk can vary from, for example, the Merino wool production systems, through dual purpose types, the specialist meat breeds to specialist dairy breeds. The perception of distinct objectives for different systems of production is often over-emphasised both at the international and national level. For example, Ponzoni (1982) has shown the relative contribution to overall economic returns in two breeds of sheep in Australia, the Merino, used largely for specialist wool production, and the Border Leicester, used as a sire of crossbred dams for lamb production. The relative contribution to economic returns of fleece characters, reproduction and body weights were 40, 46 and 14 percent for the Merino and 28, 48 and 24 percent respectively for the Border Leicester, showing a narrow range in the relative economic values that would be attached to these traits in a selection index. Yet the conventional wisdom concerning improvement programmes, even within Australia, would be that the Merino should be selected largely for wool production and the Border Leicester principally for increased reproduction rate with limited attention to wool. Similarly, Ponzoni and Walkley (1981) showed for the Dorset breed in Australia, which can be used as a crossing sire or as a terminal sire, that separate definitions of selection objectives were not warranted and that an objective related to its use as a crossing sire (dual purpose breed) was the most appropriate.

Sources of Information

Information on an individual's own measured performance can be the basis of an improvement programme using mass selection. For the major wool producing breeds in extensive conditions, reliance on mass selection is essential since pedigree records are rarely kept due to the substantial cost and labour required to identify parents and their offspring. In other breeds and production systems, pedigree records are routinely kept which then allows the programme to utilise information from relatives to predict breeding values. These relatives may include ancestors (such as a dam), collateral relatives (such as sire and dam half-sibs or, more rarely, full sibs) and
progeny in the case of progeny test schemes. For specific objectives or single traits, much has been published on the relative efficiencies of these sources of information for genetic improvement. The role of progeny testing in the improvement of growth rate and carcase characters in terminal sire breeds has been examined in detail (for example, Eikje 1978).

**BREEDING VALUE ESTIMATION**

**Multiple-trait evaluation**

We have seen that even in populations where a single trait may be thought of as of dominant importance, breeders must always consider several traits when adopting a breeding programme. The combination of specific selection criteria into a multi-trait selection programme can take a number of forms. Independent culling levels involving sequential culling on each trait is one alternative. Commonly, though, a selection index is computed, a trend that is becoming increasingly apparent. Theory has shown that selection on an appropriate single-stage selection index, is the most efficient form of multi-trait selection. Under many practical situations, however, breeders may prefer to use independent culling levels or multi-stage selection indexes. These may also be more cost effective by allowing breeders to cull a proportion of their young animals (particularly rams) as being unsuitable either as potential sires or potential sale rams and so eliminate the costs of retaining these animals until their conventional age of selection.

Multi-stage indexes have been adopted for sire selection in Norway (Gjedrem 1969) as a way of combining performance and progeny test data. Rams are initially chosen on their own growth performance and the best are then progeny tested for growth and carcase traits. Later, a proportion of these rams are further recorded for their daughters' producing ability. For early recognition of merit, though, multi-stage selection has not been highly promoted. Ponzoni (1981) described a possible two stage selection procedure in a pedigreed Merino flock. Initial selection was based on weaning weight and dam's reproduction performance with final selection made on first shearing information at 14-18 months of age. He showed that maximal genetic gain was reduced by less than 5 and 10 percent for reductions in population size at the first stage of 50 and 70 percent respectively. In this example, the two parts of the overall objective namely, growth and reproduction at stage one and wool traits at stage two were largely uncorrelated with each other (Ponzoni 1982). Substantial restriction of response through the use of independent culling levels, and by inference multi-stage selection indexes, is only likely to arise when the first trait (or group of traits) has a low heritability and/or genetic and phenotypic correlations with the second trait (or group of traits) that differ substantially in magnitude (Mortimer 1984).

**Genetic parameter estimates**

While the use of a formal index is likely to provide the most reliable basis of selection, its development does require accurate information on economic values and reliable estimates of both phenotypic and genetic variances and covariances. Hill (1981) reviewed the problems of inaccurate estimates of parameters on selection indexes and cautioned against the uncritical use of poorly estimated parameters. Hayes and Hill (1980) suggested procedures for examining the reliability of indexes and the
parameters on which they are based with a view to 'bending' the genetic estimates towards the phenotypic estimates in order to increase the accuracy of the computed index.

Genetic parameter estimates are commonly obtained from a population other than the one we wish to improve. For example, unselected flocks maintained by research organisations are often used to obtain efficient estimates of relevant parameters. Commercial flocks can and have been used to obtain information on genetic parameters, and, given the volume of data collected within improvement programmes, are likely to be used more widely for this purpose in the future. There are difficulties in using data of this sort. For example, accounting for the effects of selection and the use of males across levels of fixed effects (such as years) can present problems. Improved methods of variance component estimation such as REML procedures will be useful for such data analyses (Thompson 1982).

The need for accurate parameter estimates in a selection index has sometimes led to improvement programmes using a biological (or basic) index for an overall objective (Croston et al 1978) such as weight of lamb weaned in dual purpose sheep or lean tissue growth rate in terminal sire breeds.

The use of a basic index as a refuge from deciding upon appropriate parameters can sometimes appear more attractive than it really is. It is difficult to know in advance what emphasis is being given to the component traits since this depends on the variability of the component traits and the genetic and phenotypic relationships between them. Simm and Smith (1984) have shown that selection on lean tissue growth rate was largely equivalent to selection on growth rate alone. The cost of obtaining the measure of leanness may well be wasted by applying little effective selection pressure on that component. Similarly, weight of lamb weaned is a complex trait involving ewe fertility, litter size, and maternal and direct genetic effects on lamb survival and weaning weight (Eisen 1981). Binomial distributions of reproductive traits are also involved. Thus, basic or biological indexes do not overcome the problem of inadequate parameters, they simply ignore it by using an implied set of weights that are 'naturally' supplied.

**Information from relatives and repeated records**

Additional information from relatives can give useful improvements in accuracy of breeding values, particularly for traits with low heritability. For sex-limited traits, this may in fact be the only information available for one sex. To combine information from different sources for a particular trait requires knowledge of the correlations between relatives for the traits in question. However, the conclusion of Sales and Hill (1976a) that the relative magnitude of these correlations between groups of relatives is not too critical to the efficiency of the index is comforting. Repeated records can also make useful contributions to accuracy under similar conditions. The use of repeated records of dam's reproduction rate as a predictor of breeding value is well-established in dual purpose breeds. Martin and Smith (1980) have shown that additional information from half-sibs of the sire may increase rates of response in reproductive traits by 20-30 percent over dam's information alone.

Current interest in combined selection for both liveweight and measures of carcase composition in terminal sire breeds has resulted in a re-examination of the contribution of various sources of information in
assessment of breeding value. Rae (1984) reported the promising results obtained in New Zealand with live-animal predictors of fatness. Bennett and Clarke (1984) have extended the options by predicting selection responses for schemes involving an animal's own information, half-sib information (both live-animal and carcass measurements) and progeny information (both live and carcass measurements).

Indicator/indirect traits

The inclusion of information on traits which have no economic importance themselves but are potentially correlated with the objective is very sensitive to poor estimates of the genetic covariances between these traits and the objective (Sales and Hill 1976b). This has been an area of considerable research activity particularly for reproductive traits which have the dual problems of being sex-limited and binomially distributed. Walkley and Smith (1980) showed the potential rates of gain that could be achieved by a combination of direct (on relatives records) and indirect selection. The potential of indirect selection is dependent on the accuracy of selection already achieved for reproduction rate. Where all available information on relatives in a pedigreed flock is used, only marginal increases in accuracy will arise by including, for example, ovulation rate in females. Alternatively, in unpedigreed flocks, the possibility of using ovulation rate for selection represents the only available selection differential for reproduction rate apart from the small genetic covariances with traits such as fleece weight and body weight that are already included in the index (Ponzoni 1982).

Another aspect of indirect selection is the current interest in including aspects of disease resistance (or tolerance) into breeding objectives. Resistance to fleece rot and body strike have been shown to be moderately heritable in Australian Merinos under favourable conditions for their expression (McGuirk and Atkins 1984, Atkins, McGuirk and Thornberry 1980). In New Zealand, tolerance to facial eczema has also been found to be highly heritable (Rae 1984) and the response in plasma glutamyltransferase (GGT) levels to a challenge by the toxin involved has been shown to be a valuable indicator of tolerance (Towers et al 1983). The use of GGT response levels as a selection trait for potential sires is being promoted in areas where the disease is prevalent (Rae 1984). In both situations, the formal inclusion of such traits into an overall index relies on research generating the genetic covariances between the disease indicator and other traits in the selection objective. The relevance of recording schemes will be enhanced, in the long term, by expanding objectives to include such economically important traits to the breeder.

Age structure and parental selection

With a view to maximising the annual rate of genetic progress, considerable attention was given when establishing sheep improvement programmes to optimal age structures. Where individuals are assessed solely on their own performance, the optimum represents a balance between selection differential and generation length (see Turner and Young 1969). Studies in the Australian Merino indicated that rams, for example, should be used for no more than three years. In commercial ram breeding flocks, average age of rams was considerably greater than recommended (Savage and McGuirk 1976). Recently, more subtle effects of age structure on genetic progress have
been identified. Hopkins and James (1977) have shown the enhanced rates of response possible by selecting parents on the basis of breeding values in addition to selection of progeny. With complete pedigrees, estimated genetic trend and appropriate weightings for information from various sources (individual, parents, collateral relatives and progeny) the breeding value of each animal in the flock can be regularly updated and selection based on these breeding values regardless of age of the individual. Even in unpedigreed flocks, James (1981) showed that the principles of parent selection could be simply applied by keeping animals in the breeding flock for variable lengths of time dependent on their superiority in estimated breeding value at the time of selection. For example, rams could be chosen for use for 1 or 2 breeding seasons and ewes for between 1 and 6 breeding seasons (Hopkins and James 1977). The use of colour coded tags to indicate year of culling could be easily introduced in such flocks (James 1981). Such methods could increase genetic gain by 10 to 20 percent in unpedigreed flocks and by larger amounts in pedigreed flocks.

Best Linear Unbiassed Prediction (BLUP)

The theory of best linear unbiased prediction of breeding values has developed as an extension of the selection index. Its advantages include the simultaneous estimation of fixed effects and breeding values rather than the step-wise procedure used in least-squares procedures, the use of all information on relations through the specification of a matrix of relationships, and the estimation of breeding values for all animals in a flock incorporating the influences of selection and assortative mating. BLUP procedures do not remove the other assumptions in index selection methods, particularly those related to the adequacy of the assumed genetic parameters.

EVALUATION OF GENETIC PROGRESS

The measurement of genetic response in a flock over time may be based on either prediction or estimation methods. Prediction of genetic trend is the change in expected breeding values of the flock given an assumed set of genetic and phenotypic (co) variances while estimation of trend is the direct observation of response in the traits in the objective with no prior assumptions concerning genetic parameters.

Prediction of trend

An estimate of the phenotypic selection differentials in selected animals together with assumed genetic parameters can be used to predict the genetic selection differentials. From a knowledge of population structure, expected generation intervals can then be used to predict likely responses to selection.

(i) Single trait

For a single trait (or dominating objective), such as fleece weight in Merino sheep, such estimates of achieved selection differentials have been used widely. Commonly, the ratio of achieved to maximum selection differential (that is, the selection differential that could have been achieved by selecting an equivalent number of animals with fleece weight as the only criterion) has been estimated as an efficiency of selection (Riches and Turner 1957).
McGuirk, Rose and Scott (1982) examined the efficiency of sire selection in two large industry flocks of Merinos. In these flocks, as in other Australian Merino studs, rams are classed into three groups: potential sires, sale rams and visual culls. Unusually, though, production data were collected on all animals, whereas it is common for such data only to be collected on potential sires or potential sires and sale rams. The proportion of rams classed into each group and the production levels of these groups were compared (Table 1). In addition, information was also available on which rams were then chosen as stud sires. When expressed as sire selection efficiencies for clean fleece weight, an average of 86 percent was observed with a range between years from 82 to 93 percent (McGuirk and Swinton 1985). The high selection efficiencies represent an example of the way that aspects of traditional classing procedures and measured performance can be combined rather than being in competition. The achieved sire selection efficiencies are near maximal in that the objective, while dominated by fleece weight, also includes wool quality traits (fibre diameter and yield) and body characteristics.

The two studs examined by McGuirk, Rose and Scott (1982) were unusual in their extensive testing programme, and it is not clear to what extent their high selection efficiencies for fleece weight are common to other Merino studs. Beetson (1976) reported selection efficiencies among sires for a wide range of studs using fleece measurement services in Western Australia. He showed substantial variation in efficiencies although about half the breeders involved were achieving efficiencies of greater than 60 percent. However, only a proportion of the rams available in each flock were tested in the measurement service. Without knowing the selection differentials being applied to fleece weight prior to fleece sampling, little can be deduced on likely genetic trend.

(ii) Multiple traits

An equivalent form of retrospectively evaluating applied selection can be developed for a multiple trait objective. Since the index includes covariances between traits and information from relatives, genetic selection differentials can be expressed as the average superiority in estimated breeding value of selected animals both for the overall index and component traits. Dodd and Delahunty (1983) examined several large flocks in the New Zealand SHEEPLAN scheme in terms of the efficiency of selection of both sexes for the overall index and its component traits; number of lambs born (NLB), weaning weight (WW), hogget liveweight (HLW) and hogget fleece weight (HFW). Additionally, they estimated generation intervals in both sexes to predict expected rates of response for comparison with potential rates based on some assumed flock structures and a matrix of genetic parameters. Their results show a moderate efficiency of selection for the overall index (Table 2). There was considerable range in the efficiency of selection between flocks. For example, efficiencies for the index ranged from 44 to 87 percent for males and 17 to 56 percent for females. Intriguingly, the ranking of the breeders stated objectives were NLB, HFW, WW and HLW while the efficiencies of selection ranked in the reverse order (Table 2). The selection differential placed on NLB was substantially less than that expected either from perceived breeding objectives or from optimal use of the overall index. It should also be noted that the selection differentials computed by Dodd and Delahunty (1983) were not based on complete information from all progeny. On average across flocks, 35 and 31 percent respectively of all males and females weaned were not included on the two-tooth list which recorded the component traits and computed the index. The authors noted that this initial
selection was probably based on visual assessments of structural soundness which ranked high in breeders' nominated objectives. It is also likely that positive selection for weaning weight also occurred so that the true genetic selection differentials may have been underestimated, particularly for liveweight related traits.

The results of Dodd and Delahunty (1983) compare favourably with an earlier analysis of selection efficiency in a small number of flocks in New Zealand between 1968 and 1973, (Eikje and Clarke 1986). In the earlier analysis, efficiencies of selection on the index of 36 percent for rams and 41 percent for ewes were estimated, perhaps indicating more accurate selection on breeding value by breeders, particularly amongst potential sires, with more experience of the recording scheme.

(iii) BLUP prediction

For a fully pedigreed flock closed to outside introductions, BLUP procedures incorporating the full matrix of relationships between animals can generate a separation of genetic and environmental trend by utilising information from repeat matings, relatives' information and selection differentials. This estimate of genetic trend is still dependent on assumed parameter values but the population structure effects (for example, generation intervals) are accounted for in the trend estimator. Provided all information on which selection is based is included in the model, the effects of inbreeding, non-random mating of sires and dams, and selection effects are accounted for. There are problems, however, the most important for sheep programmes being the computational complexity. Blair and Pollak (1984) showed that even when using a reduced animal model (that is, one in which the equations for animals not leaving progeny were absorbed) mixed model, multiple trait equations can take several hundred rounds of iteration to converge, in a data set where adequate rankings of selection candidates were achieved in 100 or fewer rounds of iteration.

Estimation of trend

King and Smith (1982) reviewed available methods for estimating genetic change that are not dependent on a prior knowledge of genetic parameters. These can largely be grouped into two types: repeated matings of sires and/or dams, and some form of unselected control line.

(i) Repeated matings

The most common approach to estimating genetic trend from field data has been based on the regressions proposed by Smith (1962), whereby the performance of successive groups of progeny from individual parents is examined. Provided that all progeny are recorded, there is no selection among parents on progeny performance, and dams are randomly allocated to sires, the phenotypic changes in a trait with time can be separated into a genetic trend \( g \) and an environmental trend \( t \). The regression of performance on year of lambing represents the total trend, \( (g + t) \), whereas regressions within sires (or within dams) have expectations of only \( t + 0.5g \), since only one parent contributes to genetic progress. The regression within sire and dam has an expectation of \( t \) since progeny within a subclass have the same parents and are expected to have the same breeding value. These regressions can be combined in a number of ways to estimate the linear genetic trend (Powell and Freeman 1974). A variant of this method is the comparison of contemporaneous progeny from parents of differing ages (Dickerson 1969). The two methods lead to equivalent expressions for

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estimates of genetic trend and both are subject to the same biases from selection among parents and non-random allocation of sires and dams (Syrstad 1974). Powell and Freeman (1974) reviewed attempts in dairy cattle evaluations to remove or account for these biases in estimates of trend.

Eikje (1975) and Eikje and Steine (1976) estimated realised genetic trends for a number of important traits in the Norwegian sheep breeding scheme. The method used was the comparison of contemporary progeny from parents of different ages, but they included a grandsire effect in an attempt to reduce the possible effects of selection. The data came from progeny information on 40,000 progeny of 873 rams. Estimates of the linear genetic change per year and standard errors for the important traits in the scheme are shown in Table 3. These estimates of trend were close to expected responses particularly for the Index and weaning weight, the two major traits in the scheme. Kidney fat is included as a restricted trait so that response was expected to be zero while a positive response in fleece weight was expected but not achieved (Eikje 1975). An important aspect of the results was the relatively high standard errors about the estimates of trend for such a substantial data set. Dickerson (1969) showed that the sampling variances for such trend estimators are highly dependent on the difference in age between groups of parents. From the tables of Eikje (1975) the weighted average interval in age between groups of parents was only about 1.7 and 2.3 years for sires and dams respectively. This difference in age interval was reflected in the variances of the trend estimates since estimates from dams had a sampling variance of about 40 percent of that from sires (Eikje 1975).

To increase the precision of trend estimates requires the increased use of parents across many generations or increasing the interval between ages of parents producing contemporaneous progeny. Both, of course, are equivalent and have the dual disadvantages of increasing generation interval and reducing selection differential since the retention of older parents should not be related to progeny performance to avoid bias. The net result will be a substantially reduced rate of genetic progress. An attractive method of increasing the age interval between parents is the use of frozen semen (Smith 1977). The semen of selected sires in one year can be frozen and then used to inseminate ewes, say, 10 years later in a direct comparison with the selected sires from that year. The advantages of this approach are to increase the precision of trend estimation, reduce the risk of bias by establishing such comparisons infrequently and reduce the cost in genetic progress of generating comparisons in every year. The only disadvantage is that the selection intensity available among progeny in the year of comparison is prejudiced by the generation of a substantial number of progeny from inferior sires.

(ii) Control lines

The theory and design of a control line to measure genetic trend has been thoroughly summarised by Hill (1972). Estimates of genetic trend can be based on within-year deviations of the selected flock from the control. The accumulation of genetic drift will quickly result in the variance of the trend estimator being determined by the size of the control line, presuming that the control will always be a smaller flock (in effective population size) than the selected flock. Controls for individual industry flocks have rarely been considered because the size of the control required to estimate progress may result in some reduction in overall response. However, at least one large Australian Merino stud currently maintains an unselected control line.
An alternative form of control is an industry-wide, central control line as established in the South African Merino (van der Merwe and Poggenpoel 1977) and proposed for the Australian Merino (E.M. Roberts, pers. comm.). Samples of sires are obtained from the control line and used to generate progeny comparisons with home-bred sires within an industry flock. Such a control line can also be used to estimate between-flock genetic differences by comparisons with a common line (Erasmus 1976).

**DISCUSSION AND IMPLICATIONS**

The object of improvement programmes is to return intelligible results on the estimated breeding values of animals back to the breeder. These results must be in a form suitable for the breeder to make selection decisions and also to classify sale animals. The need to ensure that the measurements taken and the return of the results are compatible in timing with the management procedures of the breeder has been discussed by McGuirk (1982).

When developing improvement programmes, an essential prerequisite is the estimation of appropriate genetic and phenotypic parameters for the traits to be selected and the genetic relationships between these traits and the overall objective. To include indirect or additional traits we need to establish that they significantly improve the estimation of breeding values not just for the specific trait but, more importantly, for the overall objective. A similar procedure is required in establishing the benefits of using BLUP methodology. Rae and Anderson (1982) concluded that for within-flock selection, the need to estimate correction factors within flocks and to take account of genetic trend were reasons justifying BLUP rather than selection index techniques. To these might be added the use of more indirect relatives and selection for maternal genetic components. While such procedures can also be achieved by conventional selection indexes, the methods can become complex and are, perhaps, more easily specified with a BLUP model. It is important to establish that there are economic benefits. For example, the Sheepplan Technical Group Subcommittee (1985) predicted that the use of BLUP procedures in New Zealand would increase accuracy of prediction of index breeding values by 5 percent over present methods and by a further 15 percent by including the full relationship matrix. In addition, the incorporation of a maternal effects model for weaning weight and a more comprehensive model for lifetime lamb production were considered to be enhanced if BLUP procedures were utilised.

We have seen that a number of methods of predicting and estimating genetic progress are available for within-flock schemes, but that such methods seem to be only rarely used for routine monitoring. The specific advantages of monitoring genetic progress include:-

(i) The breeder can examine his selection decisions and the relative importance he is attaching to the various parts of his selection objective.

(ii) Soundly based predictions of genetic progress can be used to show a breeder's ram-buying clients and potential clients that his flock is making progress which will be expressed as an increase in merit of his sale rams with time.

(iii) Predictions of progress across many flocks gives a direct measure of the economic benefits of the recording scheme as a whole.
Estimates of progress at the individual within-flock level are potentially dangerous unless they are both precise and unbiased. A breeder's reputation and livelihood could be prejudiced by inappropriate estimates of his genetic progress. For this reason, the prediction of trend based on monitoring selection efficiencies is the area that improvement programmes should pay greater attention to in future.

For a closed flock with full pedigree information and all animals recorded, BLUP will yield the most precise predictions of genetic trend. There is a cost in computing complexity which must be weighed against the economic benefits of increased precision of prediction above that achieved by estimating genetic selection differentials within contemporary groups. For most current industry breeding schemes, though, flocks either consist of partly - or non-pedigreed individuals and/or only a portion of the population is recorded. There is an urgent need to encourage whole flock, or at least complete progeny, recording so that biases in the prediction of both breeding values and genetic trend can be reduced. There is natural resistance by breeders to retain animals (particularly males) that will be culled. A suitable compromise in many large Merino flocks in New South Wales has been accepted whereby the total number of culls is noted and a randomly chosen proportion of these are identified and left with the flock for subsequent measurement as being representative of the larger group. Where flocks have incomplete or no pedigrees there is often no information on which animals are chosen as parents. Thus, predictions of progress, based on estimated selection differentials, can only be made if the identities of selected animals are transmitted back to the database. Further refinements of genetic trend prediction in such flocks will rely on obtaining information on the later fate of selected individuals; that is, how many breeding seasons an animal remains in the flock.

Direct estimates of genetic trend at an industry level are rare. The analyses of Eikje (1975) and Eikje and Steine (1976) were concerned with total progress in the Norwegian breeding scheme rather than monitoring responses in individual flocks. The use of frozen semen and centralised control lines are important innovations in estimating trends that are not dependent on a set of known genetic parameters. However, since such direct trend estimators are relatively imprecise they can only be used infrequently (that is, a long time interval is required) and so they do not obviate the need for routine monitoring of model-dependent predictions of trend.

REFERENCES


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Table 1. Production levels of classed rams in a large Merino stud, from McGuirk, Rose and Scott (1982).

<table>
<thead>
<tr>
<th>Classing group</th>
<th>Relative Size of group (%)</th>
<th>Greasy fleece weight (kg)</th>
<th>Yield (%)</th>
<th>Clean fleece weight (%)</th>
<th>Fibre dia.(u)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Potential sires</td>
<td>12</td>
<td>4.24</td>
<td>69.9</td>
<td>2.95</td>
<td>20.7</td>
</tr>
<tr>
<td>Sale rams</td>
<td>68</td>
<td>3.58</td>
<td>69.5</td>
<td>2.48</td>
<td>20.5</td>
</tr>
<tr>
<td>Visual culls</td>
<td>20</td>
<td>3.20</td>
<td>68.7</td>
<td>2.19</td>
<td>20.2</td>
</tr>
<tr>
<td>Whole flock</td>
<td>100</td>
<td>3.67</td>
<td>69.4</td>
<td>2.54</td>
<td>20.5</td>
</tr>
</tbody>
</table>

Table 2. Average efficiencies of selection for an index and its component traits across several flocks in the New Zealand Sheepplan scheme, from Dodd and Delahunty (1983).

<table>
<thead>
<tr>
<th>Traits</th>
<th>Index</th>
<th>NLB</th>
<th>WW</th>
<th>HLW</th>
<th>HFW</th>
</tr>
</thead>
<tbody>
<tr>
<td>Rams</td>
<td>69</td>
<td>39</td>
<td>48</td>
<td>53</td>
<td>45</td>
</tr>
<tr>
<td>Ewes</td>
<td>36</td>
<td>17</td>
<td>27</td>
<td>30</td>
<td>24</td>
</tr>
<tr>
<td>Flock</td>
<td>62</td>
<td>34</td>
<td>45</td>
<td>49</td>
<td>41</td>
</tr>
</tbody>
</table>

* NLB = number of lambs born, WW = weaning weight, HLW = hogget liveweight, HFW = hogget fleece weight.

Table 3. Realised genetic progress in Norwegian scheme, from Eikje (1975) and Eikje and Steine (1976).

<table>
<thead>
<tr>
<th>Trait</th>
<th>Genetic change per year (± standard error)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ram index I</td>
<td>1.25 ± 0.51</td>
</tr>
<tr>
<td>Weaning weight (kg)</td>
<td>0.25 ± 0.10</td>
</tr>
<tr>
<td>Carcase weight (kg)</td>
<td>0.24 ± 0.16</td>
</tr>
<tr>
<td>Kidney fat weight (kg)</td>
<td>-0.01 ± 0.01</td>
</tr>
<tr>
<td>Fleece weight (kg)</td>
<td>-0.024 ± 0.021</td>
</tr>
<tr>
<td>Lambs born per ewe lambing</td>
<td>0.007</td>
</tr>
<tr>
<td>Lambs weaned per ewe lambing</td>
<td>0.023</td>
</tr>
</tbody>
</table>