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Making better use of the SIL genetic engine

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ABSTRACT

Developments in genetic evaluation techniques used in the SIL genetic engine have increased the accuracy with which estimated breeding values are calculated and have provided maternal breeding values for growth and survival traits. Although these will assist progressive breeders, a considerable number of breeders would gain greater benefits from improvements in data recording techniques to more fully utilise the potential of the SIL genetic engine to identify genetically superior animals. In particular, reproductive and survival data are often recorded less than optimally. Ewes culled at pregnancy scanning, barren ewes, lambs born dead and lamb deaths from birth to weaning require particular attention.

Keywords: sheep; breeding values; genetic evaluation; reproduction; lamb survival.

INTRODUCTION

Genetic improvement is just one of many methods available to sheep producers to enhance the performance of their animals. Genetic improvements have the advantage of being permanent, cumulative, sustainable and cost-effective. The Sheep Improvement Limited (SIL) redevelopment of sheep performance recording in New Zealand allowed many advances in computing and genetics to be incorporated into the new system (Newman *et al.*, 2000). The SIL system offers all breeders Best Linear Unbiased Prediction technology (BLUP), providing the ability to compare animals across sexes and age classes, as well as across flocks, where appropriate. Recent developments within the SIL system have added breeding value information for maternal traits for weaning weight and lamb survival.

However, many New Zealand flocks using 'state of the art' genetic evaluation procedures are still not achieving anywhere near their potential rates of genetic progress for economically important traits (Amer, 2002a). There are a number of possible reasons, including poor breeding practices, such as use of older rams and ewes when superior and younger selection candidates are available, poor linkage between groups within a flock or between flocks in a joint analysis, and incomplete data recording procedures. Identifying and rectifying such deficiencies has the potential to substantially increase the rate of genetic progress in the New Zealand sheep flock. Recent developments in the SIL genetic engine provide a range of tools that can assist in the identification of deficiencies in a specific breeding programme.

DEFICIENCIES AND DEVELOPMENTS

Accuracy of pedigree information

BLUP uses all pedigree information to increase the accuracy of prediction of breeding values (BVs). Screened-in ewes lack pedigree information and cannot be accurately described genetically. As a result, they tend to be lowly ranked until they, or at least their progeny, prove their genetic merit. Given that accuracy of identification of genetically-superior ewes from unrecorded-flocks is low, screening in ewes reduces the accuracy of genetic selection through culling recorded

ewes of above average genetic merit to make way for the screened-in ewes. This is because the reduction in pedigree information reduces the accuracy of BV estimation for subsequent generations and can also obscure real levels of inbreeding. Rates of genetic improvement will always be sub-optimal if known pedigree / performance data are rejected in favour of unproven genetics, unless screening is to increase the size of the recorded flock, or (in some circumstances) to record a wider genetic base for a "new" trait.

Linkage (connectedness)

Lack of adequate genetic linkages, sometimes called connectedness, between groups reduces the accuracy with which breeding values can be estimated. Sire referencing and group breeding schemes rely on effective genetic linkages between contemporary groups. BLUP genetic evaluation procedures account for biases in animal performance caused by environmental effects unique to specific contemporary (management) groups by comparing the performance of related individuals within any pair of groups. Genetic links between groups contribute to a data structure which allows statistics to partition differences between contemporary groups into environmental and genetic components when evaluating the genetic merit of individuals. The effectiveness of genetic links depends on the number, and types, of relatives between two groups. Linkage is only created by recording of relevant traits; if no daughters of a sire have lambed in a flock there will be no linkage for reproduction traits. Similarly if there are no data for ultrasound scanning there will be no linkage for meat traits.

It is useful to distinguish between two types of linkage. First, there is direct linkage, where a parent has progeny in the two contemporary groups under question. These are usually known as link sires. The two contemporary groups are therefore linked, with the strength of linkage depending on the number of progeny in each contemporary group. The second type of linkage is indirect linkage, where two contemporary groups without any direct linkages between them may still be linked if they are both linked to a third flock. Two contemporary groups may have both direct and indirect linkages between

them, and when taken together, the two types of linkage make up overall linkage.

Relative types other than having a shared parent can also create linkages between flocks but in many cases, the power of linkage is not necessarily proportional to the degree of relationship among the animals in the two contemporary groups. For example, it is helpful to consider two flocks which have used two rams extensively. The rams are full brothers, with one ram used exclusively in Flock A, while the other ram is used exclusively in Flock B. Overall, a large number of animals in Flock A are cousins of animals in Flock B. Relatedness of the two rams creates a small amount of linkage but there is a danger in relying on this sort of linkage. If, for example, the brother used in Flock A had received a much better sample of genes from his parents than the brother used in Flock B, then the better performance of his progeny would not be a reflection of a better environment for Flock A; rather it would be due to the genetic superiority of the ram. In this situation BLUP is unable to distinguish between genetic and environmental differences unless the genetic differences between the two rams have been evaluated quite accurately somewhere other than in flocks A and B. As a consequence, purchasing a breeding ram from another flock will not create good links unless the ram had already been used as a sire in the original flock.

SIL has developed a method based on cluster analysis that graphically illustrates the extent of direct linkages between contemporary groups (Figure 1). Cluster analysis results provide a means to summarise the complex web

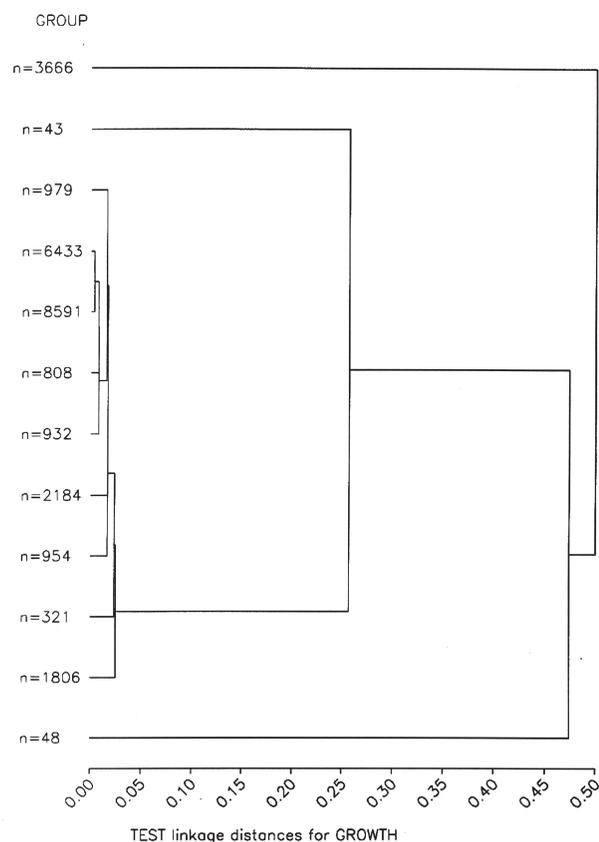


FIGURE 1: The degree of linkage between flocks declines as the connecting line between the flocks moves to the right.

of linkage information among all combinations of groups into a simple tree diagram (Amer, 2002b). The further to the right the line connecting any two groups goes, the weaker the linkage between them.

For an across flock assessment of linkage, contemporary groups are defined as groups of animals belonging to a common birth flock. Only a short bracket of years, 3 to 5 years, should be considered when completing an across-flock analysis of linkage. If more years are considered, historical linkages have too much emphasis and linkage is overestimated. For a within-flock assessment, contemporary groups are defined as belonging to a common birth flock, birth year, sex and management group.

Data Integrity - recording birth and dam fates

Data relating to reproduction and birth are often incomplete. This has adverse effects on breeding value estimation for reproduction and survival traits. Breeders frequently do not record ewes that are barren (dry) at lambing or ewes culled as dry at pregnancy scanning. This has the effect of overestimating ewe reproductive performance. For example, a ewe that had two sets of twins and was then culled as dry would have a reproductive record of 220 or 22 depending on whether dry ewes are recorded or not by the breeder. The correct average number of lambs born (NLB) for the ewe is 1.33 (four lambs in three matings) but if dry ewes are not recorded, it may be treated as 2.00 (four lambs in two matings). Over estimation of the breeding value of the individual ewe is one effect, but more significant is the effect on her living relatives in the flock.

This type of error has been particularly obvious in recording of hogget lambing performance. If a breeder mates his hoggets but only records those that lamb, then the average reproductive ability of the flocks is inflated, e.g. nine hoggets of which three have twins, three have singles and three are dry, then the correct average number of lambs born is 1.00 lamb/ewe (nine lambs from nine ewes). However, if dam fates were not correctly recorded the apparent average is 1.5 lambs (nine lambs from six

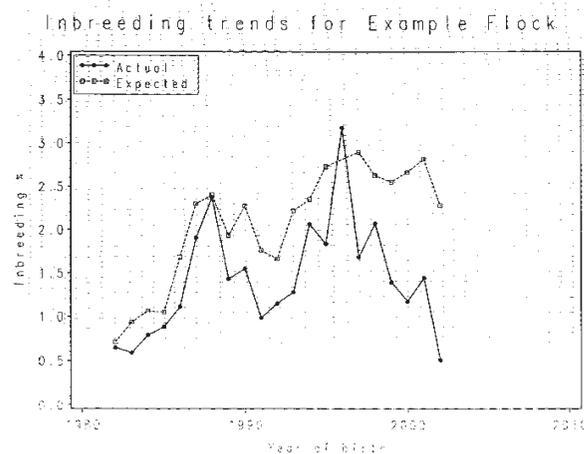


FIGURE 2: A graph of expected and actual inbreeding is one of the figures and tables used to summarise a flock's breeding programme structure.

TABLE 1: Revised growth and survival sub-index components for dual-purpose and terminal sire sheep breeds (from Amer, 2002c).

Goal trait group	Objective trait	Economic weight	
		Dual-purpose (cents)	Terminal sire(cents)
Growth	Carcass weight (kg)	199	158
	Weaning weight direct (kg)	134	66
	Weaning weight maternal (kg)	112	
	Ewe weight (kg)	-105	
Survival	Lamb survival direct (per lamb)	6329	4110
	Lamb survival maternal (per lamb)	6371	

ewes), so ewes with one lamb are below average in the absence of data to show otherwise.

Diagnosics

Genetic evaluation tools, such as genetic-trends graphs, are becoming increasingly sophisticated, but they do not provide specific reasons for low rates of genetic progress in any particular situation. Identification of deficiencies in a specific breeding programme can involve long discussions with the breeder, followed by detailed manual investigation of the breeder's data. The associated costs and time delays associated with this mean that many deficiencies remain uncorrected.

To overcome this problem, a set of tools has been added to the SIL system that checks for a wide range of potential problems within the structure and operation of a breeding flock. For any population, a series of reports are generated, with each report focussing on a particular aspect of the breeding flock. Diagnostics cover generation interval, selection differentials, traits recorded, mating ratios, merit of retained sires, frequency of animals with unknown parentage (screened in animals), number of animals in key fixed effect categories, as well as the incidence and historic patterns of inbreeding (an example of inbreeding trends is shown in Figure 2). These reports are useful for an SIL advisor to become familiar with flock breeding programme structure, or to answer breeder queries relating to genetic trend performance in their flock. In some instances they can also be used to explain unexpected breeding values for specific animals.

Maternal breeding values

Estimates of the direct genetic and maternal breeding value components for weaning weight and survival are now available. However before these are promoted, care needs to be taken to ensure that breeders understand when consideration of maternal breeding values is important. Maternal breeding values describe the performance of the female offspring of a sire. For terminal-lamb production systems where all lambs are slaughtered, maternal breeding values are of no relevance in the selection or purchase of rams as none of the progeny will be used as dams (Amer, 2000). In contrast, dual-purpose sheep

breeders will keep female replacements and so the genetic maternal ability of rams which sire replacement ewes is of interest. This is reflected in the different indexes calculated for dual-purpose and terminal sire animals (Table 1).

CONCLUSIONS

Developments in genetic evaluation techniques used in the SIL genetic engine have increased the accuracy with which estimated breeding values are calculated. Calculation of direct and maternal breeding values for weaning weight and survival enables breeders to identify animals best suited to the needs of their individual breeding programmes. Progressive breeders will benefit from ongoing advances in computing and genetics being incorporated into the SIL genetic engine. However many breeders would also gain from improvements in data recording techniques to more fully utilise the potential of the SIL genetic engine to identify genetically superior animals. User-friendly summaries of a range of aspects of a breeding programme have been developed and are available to assist breeders and consultants to identify possible problem areas which might contribute to their failure to achieve potential rates of genetic progress. SIL advisors have an important role in assisting SIL users to understand developments and how they can best be utilised.

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