Rates of genetic progress being achieved throughout the New Zealand ram breeding industry

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ABSTRACT

Changes in the rate of genetic progress in the New Zealand sheep industry since 1990 are linked to structural aspects of breeding scheme design and to major industry sheep breeding initiatives. Data was sourced from the December 2007 SIL-ACE genetic evaluation for 140 recorded Dual Purpose flocks and 62 recorded Terminal Sire flocks. Genetic trends in both of these flock types approximately doubled after the introduction of Sheep Improvement Ltd. and there was a further incremental increase of similar magnitude after the introduction of the Central Progeny Test and SIL ACE. Substantial variation in the magnitude of genetic trends was observed across flocks within and between breeds. Large numbers of flocks average less than 50 cents gain in index per year, while significant numbers of flocks are achieving in excess of 150 cents gain per year. Flocks with higher rates of genetic gain tended to be using superior rams introduced from other flocks, while flocks with lower rates of genetic gain tended to be repeatedly using older sires of lower genetic merit. The implications of these results for industry sheep genetic improvement initiatives are discussed.

Keywords: sheep; genetic improvement; recording; breeding scheme.

INTRODUCTION

There is ongoing substantial investment by a wide range of public and private entities in genetic improvement within the New Zealand sheep industry. This includes a substantial investment of time and commitment by performance recording sheep breeders. After ten years of structured industry investment in the form of Sheep Improvement Ltd. (SIL), it is timely to reflect on the impact it has had on genetic progress. By taking a critical retrospective view of what has been achieved, it is likely to provide insights on how to extract maximum industry benefits from future investment.

Undoubtedly, productivity gains within the New Zealand sheep industry over the past 30 years have been sensational (Cocks & Brown, 2005). It is extremely unfortunate that the benefits of these massive productivity gains are often hidden by the ongoing fluctuations and deterioration in product prices. Many interest groups and entities can, and do, lay claim to the responsibility for these gains. Establishing concrete foundations to support their claims is often problematic.

With appropriate storage and recording of data, it is possible to partition phenotypic changes in the performance of flocks into component trends associated with genetic improvement, versus component trends associated with systematic and random changes in management and the environment. This is achieved using a statistical procedure known as best linear unbiased prediction (BLUP) of animal genetic merit, and quantifying systematic changes in animal genetic merit over time (Henderson, 1973). The SIL database contains information on performance and pedigree for flocks dating back to the earliest days of performance recording by New Zealand sheep breeders.

The objective of this paper is to describe an analysis of a subset of SIL data to evaluate genetic trends. Particular attention is paid to identifying underlying characteristics of the flocks and their recording patterns in an attempt to better understand the variability among flocks for rates of genetic change. Genetic trends are evaluated over time periods defined by the introduction of new initiatives in sheep genetic improvement in New Zealand.

DATA AND METHODS

Data were sourced from the SIL-ACE (Advanced Central Evaluation) across flock and breed genetic evaluation, run in December 2007. A wide range of traits are evaluated (Growth, Meat, Wool, Reproduction, Facial Eczema, WormFEC) in SIL-ACE, although many of the flocks have no data for the less commonly recorded traits. In the SIL-ACE evaluation, all breeds, across the Dual Purpose, Terminal Sire and Mid Micron groupings, are included in a single analysis with across breed and across flock genetic links. These links are strengthened through the three contributing research flocks at Woodlands (Southland), Ashley Dene (Lincoln) and Poukawa (Hawkes Bay) which comprise the Meat and Wool New Zealand Central Performance Test (Young & Newman, 2009).

Flocks represented in this dataset are likely to be more innovative on average than those New Zealand flocks that are not represented. However, there are a number of high genetic merit or high genetic progress flocks that are not included in this sample, either because their linkage is insufficient,

FIGURE 1: Classification of Dual Purpose flocks into four subgroups based on average index trend and average index merit.
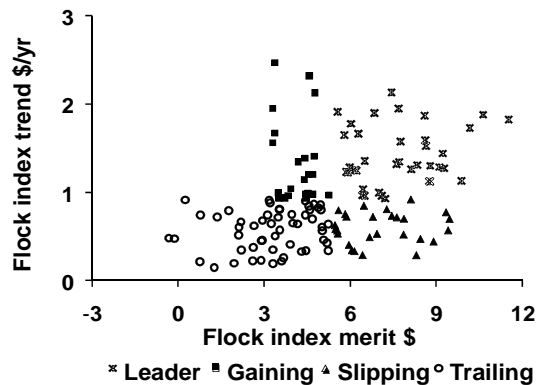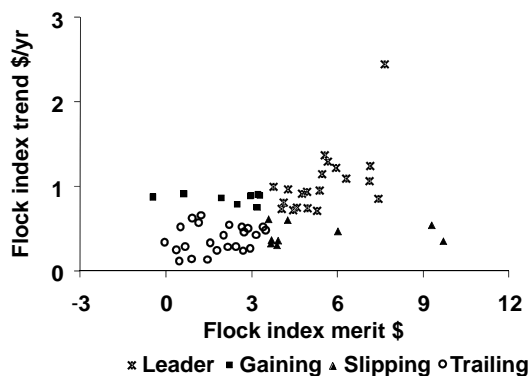

FIGURE 2: Classification of Terminal Sire flocks into four subgroups based on average index trend and average index merit.

their data is not available to SIL, or because they choose not to have their data included.

In order to preserve confidentiality, an initial summary analysis was run on SIL computers using SAS software command scripts developed by AbacusBio. The summary analysis captured a wide range of information for each flock-year combination including breeding values and overall economic indexes (Amer, 2000) for various classes of animals including sires and dams, ages of animals at recording, extent of trait recording and numbers of animals born and weaned. Flock identifiers were coded randomly to a sequence of integers, before flock-year summary files were created to preserve anonymity. Data were then released for further analysis.

The evaluation period for the SIL-ACE evaluation incorporated records from animals born between 1990 and 2006. There were approximately 1.4 million Dual Purpose or Mid Micron animals and approximately 200,000 Terminal Sire type animals with weaning weight records included in the analyses. For the 2004 to 2006 birth year period, a total of slightly fewer than 600,000 animals were

born in 140 recorded Dual Purpose flocks, 24,000 were born in recorded Mid Micron flocks, and 98,000 in 62 recorded Terminal Sire flocks.

Data were partitioned into four time intervals, and results reported by time period. Two periods 1990 to 1994, and 1995 to 1998, span the period prior to the development of SIL. The period from 1999 until 2003 spans the period under SIL, but prior to the establishment of the CPT and SIL-ACE evaluation. The remaining most recent period is from 2004 to 2006. All available data from within these time periods were captured for the included flocks.

Flocks were classified into four subgroups each for Terminal Sire, and for Dual Purpose breeder types with a view to clustering results across the large number of flocks available. The four subgroups were defined as follows:

1. Leader – Above average for current average genetic merit (average of industry overall index excluding survival and disease traits for 2004 to 2006 born animals) and also for recent genetic trend in the industry overall index (based on average trend between 2004 and 2006);
2. Gaining – Below average for current average genetic merit but above average for recent genetic trend;
3. Slipping - Above average for current average genetic merit but below average for recent genetic trend;
4. Trailing - Below average for current average genetic merit and below average for recent genetic trend.

A number of additional flock characteristics were evaluated including the flock size, sire and dam ages at birth of lambs. These determines generation interval, whereby long generation intervals slow down the rate of genetic progress. Also evaluated was the degree of use of rams from outside flocks, the merit of rams used from outside flocks relative to the merit of homebred rams, the degree of repeated use of the same rams over years, the relative genetic merit of repeatedly used rams and the proportion of lambs born where the parents of the lambs are unknown.

RESULTS

Figures 1 and 2 show differences among flocks for recent levels of genetic merit and annual rates of genetic progress for terminal sire and dual purpose breed types respectively. Four categories of flocks are marked on each figure. The Leading (37 flocks) and Trailing (54 flocks) quadrants are more represented than the Gaining (22) and Slipping (27) quadrants. This reflects an overall skewing of the distribution where there are smaller numbers of very elite flocks, based on index merit and trend, leading the industry

and a larger number of flocks clustered around or just below the average based on trend and merit.

Tables 1 and 2 show annual rates of genetic response in the SIL overall industry indexes, as well as in two component sub-indexes of the overall indexes for Dual Purpose and Terminal Sire flocks respectively. Rates of genetic progress are shown by time period and flock type. A marked acceleration in the rate of genetic progress is apparent across successive time periods. Across all groups of dual purpose type flocks, rates of genetic progress were 23, 29, 54 and 84 cents in the overall economic index across the 1990 to 1994 (pre SIL), 1995 to 1998 (pre SIL), 1999 to 2003 (post SIL) and 2004 to 2006 (post SIL-ACE) respectively. Across all groups of terminal sire flock types, rates of genetic progress were 23, 20, 35 and 48 cents in the overall economic index across the same time periods respectively.

For the Dual Purpose flocks, not all responses in the overall indexes can be explained by the two sub-indexes of growth and reproduction. The balance of the overall index response was attributable mainly to economic improvements in wool traits. Genetic progress in the reproduction sub index reflects progress solely in the trait number of lambs born per ewe lambing and was negligible prior to 1999. Since 1999, the reproduction sub-index has made up a higher proportion of gain in the Leading and Gaining flock types than in the Slipping and Trailing flock types. Dual Purpose flocks recording for Facial Eczema and internal parasite resistance have achieved higher rates of genetic progress than industry averages. However, the majority of their extra genetic progress comes from improvements in non-disease traits.

For Terminal Sire flocks, progress in the meat and growth sub-indexes have contributed relatively equally to overall progress across time periods and flock types.

In general, flocks with higher rates of genetic gain tended to be using superior rams introduced from other flocks, while flocks with lower rates of genetic gain tended to be repeatedly using older sires of lower genetic merit. There was no clear evidence that the flocks with lower rates of genetic progress in the economic indexes had fundamental deficiencies in the structure or design of their breeding programs. A more likely explanation is that flocks where there are lower rates of genetic progress place more selection emphasis on physical attributes of the animals than on economic indexes.

DISCUSSION

This paper formally quantifies marked improvements in the rate of genetic progress in traits of direct economic relevance, firstly following the introduction of Sheep Improvement Ltd. (Young & Wakelin, 2009), and second, following the joint introduction of the Meat and Wool New Zealand Central Performance Test and the SIL-ACE across breed genetic evaluation (Young & Newman, 2009). The sample of flocks analysed here is not fully representative of the New Zealand sheep breeding industry. Therefore, extrapolation of these results to aggregate total economic benefits requires assumptions about the market share of national ram

TABLE 1: Annual rates of genetic response in the overall economic index and in two component economic sub-indexes across all Dual Purpose flocks participating in the SIL ACE evaluation.

Time period	Overall index ($)				Growth sub-index ($)				Reproduction sub-index ($)			
	Trailing	Slipping	Gaining	Leader	Trailing	Slipping	Gaining	Leader	Trailing	Slipping	Gaining	Leader
2004-2006	0.57	0.60	1.34	1.41	0.42	0.36	0.74	0.82	0.12	0.18	0.47	0.46
1999-2003	0.47	0.75	0.51	0.71	0.34	0.48	0.38	0.42	0.09	0.17	0.11	0.18
1995-1998	0.14	0.49	0.08	0.45	0.16	0.42	0.15	0.28	-0.03	0.06	-0.09	0.09
1990-1994	0.17	0.30	0.11	0.39	0.16	0.26	0.18	0.38	-0.01	0.04	-0.08	-0.03

TABLE 2: Annual rates of genetic response in the overall economic index and in two component economic sub-indexes across all Terminal Sire flocks participating in the SIL ACE evaluation. There was insufficient (n = 1) of the flocks classified as Gaining with animals present in the 1990 to 1994 time period to calculate a trend for this period.

Time period	Overall index ($)				Growth sub-index ($)				Meat sub-index ($)			
	Trailing	Slipping	Gaining	Leader	Trailing	Slipping	Gaining	Leader	Trailing	Slipping	Gaining	Leader
2004-2006	0.38	0.44	0.86	1.05	0.24	0.24	0.38	0.46	0.14	0.20	0.49	0.59
1999-2003	0.27	0.55	0.66	0.71	0.17	0.28	0.37	0.36	0.10	0.27	0.29	0.34
1995-1998	0.19	0.32	0.53	0.33	0.03	0.08	0.37	0.15	0.17	0.24	0.16	0.18
1990-1994	0.19	0.46		0.14	0.11	0.14		0.07	0.08	0.32		0.06

sales for the flocks included and was beyond the scope of this analysis. Such an analysis based on the methodology of Meikle and Amer (2003) is being undertaken as part of a separate independent study. The industry benefits are expected to be substantial and to far outweigh the magnitude of industry funded investment in structures underpinning genetic improvement.

These results demonstrate substantial opportunities for further improvement. Of particular concern is the large number of flocks performing well within the potential rates of genetic progress demonstrated by other flocks. Another area of concern is the one–dimensional nature of genetic improvement, it being largely focused on growth rate, particularly in dual purpose type flocks. While genetic progress in litter size has contributed significantly, there are typically decreasing returns to additional incremental gains in litter size (Amer *et al.,* 1998) and there are significant numbers of sheep farmers that feel that they are at or approaching their optimal litter size. While increases in growth rate allow farmers to exploit seasonal price premiums and reduce lamb feed demand from times when pasture is most scarce, they also result in increases in breeding ewe mature weights, which offsets some of the benefits.

There is a need for new selection criteria that are not excessively costly and impractical in order to broaden the directions of genetic progress. Research into genetic markers continues to hold muchpromise and the advent and recent rapid adoption of genome wide selection tools in dairy cattle suggests that new breakthroughs in this area for sheep may not be far away. This would provide sheep breeders with the option to select for a broader range of economically important traits at a young age, if genetic merit can be assessed using genetic markers with reasonable accuracy without detailed pedigree and performance recording, new models of sheep breeding programmes may evolve. In these, larger numbers of potential selection candidates might be generated, but the assessment of genetic merit via genetic marker tests would be restricted to those candidates that are deemed to be physically acceptable to commercial ram buyers. It is apparent from this study that selection for physical attributes remains a substantial drain on the genetic progress within a substantial proportion of performance recording breeder flocks under the current breeding structures.

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Trans-Tasman genetic evaluation of sheep – spreading the net wider

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ABSTRACT

At the instigation of local breed groups, Sheep Improvement Ltd. (SIL) and Sheep Genetics (SG) exchanged flock data and conducted genetic evaluations on the combined dataset. Results from each system show only modest changes in breeding values compared to analyses of their respective within country datasets. Correlations of breeding values (BVs) were 96 to 100% for weaning weight, autumn live weight, ultrasonic muscle, ultrasonic fat, fleece weight and number of lambs born. Correlations between BVs generated by the two systems from the same datasets were less strong but still good at 69 to 89%, for most traits. This was attributed to differences in parameters used by the two analysis systems and to some measurements being taken at different ages. The weakest correlations occurred for ultrasound scan traits at 14 to 65% since SG adjusts these to constant 'carcass' weight but SIL does not. It is concluded that the best option for breeders seeking superior genetics internationally is to facilitate data exchange and have analysis and reporting done within their own country.

Keywords: genetic evaluation; sheep; across-flock; international; Sheep Improvement Ltd; Sheep Genetics.