eSearch – Better Access To Genetic Information For New Zealand Sheep

M.J. Young[*], S-A.N. Newman[†], S. McIntyre[*]

Introduction

Sheep Improvement Limited (SIL) provides a performance recording and genetic evaluation service to the New Zealand sheep industry. Since being set up in 1999 it has grown (Newman *et al.* 2010) and across-flock genetic analyses have become common for most flocks where previously within flock evaluations were more common. SIL conducts a large scale, across flock, across breed genetic evaluation every two months called SIL-ACE.

Across-flock evaluations provide the opportunity for valid comparison of animals on the basis of genetic merit. However, not every buyer of "genetics" is looking for the same thing. Therefore new tools are needed to search large datasets like SIL-ACE for animals with particular combinations of genetic merit. ***eSearch* for SIL-ACE** is a powerful search tool to help industry locate animals with the genetic merit to meet their needs.

SIL-ACE

SIL-ACE evaluations were first run in 2004 for 1.2 million animals in 151 flocks. Initial analyses were run twice per year and generated 16 breeding value (BV) traits for Growth, Meat (carcass quality), Reproduction and Internal Parasite Resistance. A key factor in making this possible was between breed connectedness generated by the Alliance Central Progeny Test (CPT, McLean *et al.* 2006) set up in 2002. Initially the CPT focused on carcass traits but it has expanded to consider all major traits assessed by SIL and is now known as the Meat & Wool New Zealand Central Progeny Test. This expansion delivers much greater connectedness for maternal traits (Young & Newman 2009). Results of the CPT are published on two websites (www.sil.co.nz and www.meatandwoolnz.com).

Evaluations are now run every two months with data from 3.2 million animals in more than 330 flocks (Young & Newman 2009). 78 million breeding values are generated for 22 traits in the standard SIL goal trait groups for Growth, Meat (carcass quality), Wool (production), Reproduction, Lamb Survival, Internal Parasite Resistance and Facial Eczema Tolerance. These traits are described in detail in documents on the SIL website (www.sil.co.nz).

Other features of SIL-ACE

For one trait, Lamb Survival, a lot of historic data in some flocks is incomplete (i.e. >90% survival to weaning compared to 80-85% in SIL flocks with comprehensive data). Where

---

[*] Address for correspondence - SIL, Meat & Wool New Zealand, PO Box 39-085, Christchurch 8545, New Zealand
[†] AgResearch, Invermay Agricultural Centre, Private Bag, Mosgiel 9007, New Zealand

SIL considers that a high proportion of lamb deaths have not been reported, it excludes that flock-year birth cohort from the analysis of Lamb Survival.

For other traits, not all SIL-ACE participating flocks collect key predictor traits for all the goal traits evaluated. In some cases this is because they have to be registered for some traits where there are specific recording protocols that must be followed which are monitored by a 3rd party service provider.

These factors impact on flock connectedness (Newman 2003). Sires must come from, or been used in, flocks genetically connected to the largest group of SIL-ACE flocks in order to be listed on the across-flock sire leader lists for traits and indexes published on the SIL-ACE website (www.sil.co.nz/Latest-reports/SIL-ACE.aspx). This requirement means that comparisons made between animals on these lists are valid. Flock connectedness is also reported on the SIL-ACE website.

SIL-ACE results

Up to 2010, Leader Lists for the top rated 200 sires used in connected flocks were produced for all traits evaluated and for a range of indexes that comprised different combinations of these traits. This limited reporting was due to the agreement entered into with flock owners – that only animals in the top 25% would be reported on for any trait or index. The top 200 sires is actually equivalent to the top 5-10% of sires. For each list sires had to have been used in flocks genetically connected for the component traits, but within flock reports could be made without the constraint of connectedness.

Limitations of previous SIL-ACE reporting

These Leader Lists limited the value that could be obtained from the large scale SIL-ACE genetic evaluation. Firstly, they rank animals on only one criterion and, secondly, they don't report on performance for other traits or indexes. So an animal highly rated on SIL-ACE for Growth may have no information available for Reproduction or Survival because it does not appear on those Leader Lists.

Perhaps the greater problem lies where one is looking for animals that have very good merit (say in the top 25%) across a range of traits, most will not appear because these lists only report the top 5-10%. Only rarely is a sheep highly rated across four or more different traits. Many SIL breeders select for four or more different goal traits.

A related criticism is that some animals in the top 5% have such extreme merit that breeders want to avoid the use of such genetics because they are not seeking such a big lift in performance from genetics for that trait. So users may want to look for BVs or indexes within a certain window of the range available.

SIL has developed an on-line search tool, ***eSearch***, to address these issues. Participating breeders agree to allow this tool to search through SIL-ACE results of all their animals.

eSearch – an on-line tool to search SIL-ACE results

eSearch is a powerful search engine (www.sil.co.nz/esearch.aspx) used over the internet that finds animals meeting criteria specified by the user. Two viewpoints are targeted.

Firstly, for ram buyers, there is ***FlockFinder***, to identify flocks that have genetic information for traits a ram buyer is seeking to improve. This does not identify individual animals. Rather, it lists flocks collecting the data that SIL-ACE uses to produce estimates of genetic merit which a buyer can use to discriminate between animals when buying rams from that flock. Flock contact information is easily accessible from this listing.

Secondly, with a ram breeder focus, there is ***RamFinder***, a tool that allows detailed specification of a range of criteria including BVs, indexes, birth years and genotype. It produces lists of individual animals meeting the search criteria. Genetic merit is depicted visually for individual animals using bar graphs to aid quick comparison of animals (see Figure 1). Such graphs make use of the speed with which the human eye and brain can assess shape as opposed to reading a series of numbers.

Defining genetic merit

Modern genetic evaluation systems can provide accurate estimates of genetic merit which can lead to rapid genetic change. This makes the definition of genetic goals critical. In addition, the landscape of domestic animal production is changing as pressures increase with regard to food quality, animal welfare and environmental stewardship. This means the selection objectives of tomorrow are likely to differ from those of day, perhaps dramatically. Having tools that allow users to look at different definitions of genetic merit can help identify genetics of the future. ***eSearch*** provides the opportunity to look for different combinations of genetic merit using data we currently produce and can improve understanding of how genetic traits are inter-related.

Currently, many “different” breeds or genotypes make use of the same selection tools aimed at the same selection goals. Often genetic change is seen as a measure of success. This will not always be the case. Some genotypes may choose to differentiate themselves from others by defining their genotype objectively in terms of genetic merit for particular traits and a position on a particular scale.

In New Zealand we are seeing an increasing number of ram breeders and their clients questioning the pursuit of more lambs and of carcass leanness to the point of very low fat, in ewe breeds. Knowing the SIL system, these breeders target less extreme merit for these traits in animals they use. ***eSearch*** provides the opportunity to “window” some traits while focusing on gain in other traits in a breeding programme.

The future for *eSearch*

SIL will add other traits to ***eSearch*** as demand requires. As genomic BVs are added to SIL (Newman *et al.* 2010) these can be incorporated into the underlying ***eSearch*** database.

SIL is committed to work that makes genetic information relevant, accessible and easy to understand. ***eSearch*** was designed with these goals in mind. Usage of the system, and user feedback, will shape its development.

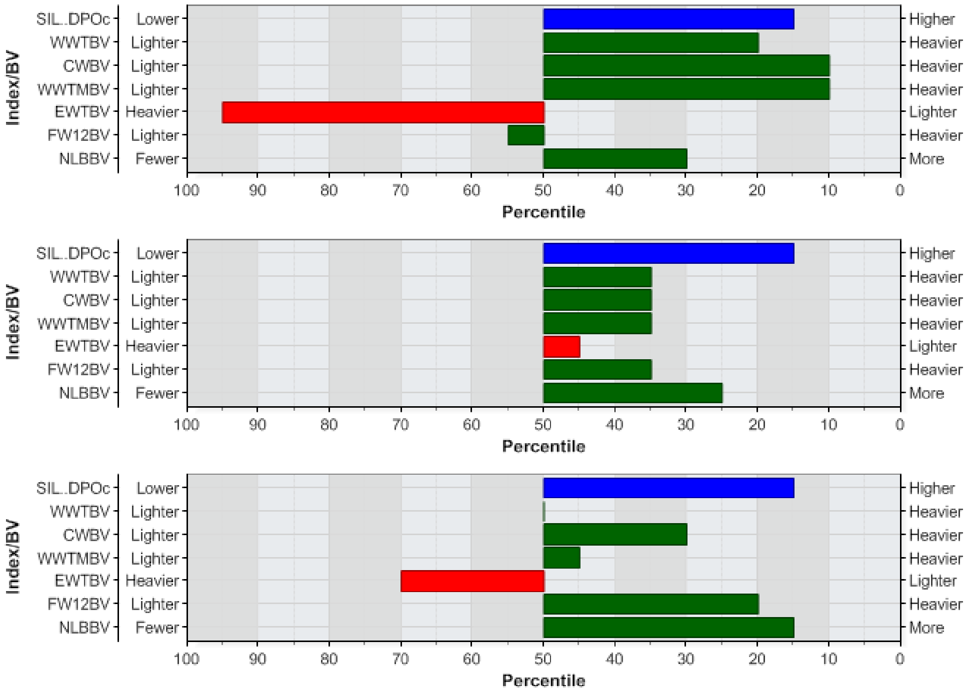

Figure 1. Visual depiction of genetic merit for three sheep based on SIL-ACE percentile bands for a Dual Purpose sheep index and breeding values (BV). All three sheep have similar overall indexes (DPOc). The first sheep has high merit for lamb growth and milking ability (WWTM) but is penalized for adult ewe size. The second sheep has above average performance for all traits while the third sheep has superior performance for wool production and number of lambs born.

Note. Dual Purpose sheep produce lambs for carcass production with some ewe lambs kept as flock replacements. BVs are listed for weaning weight (WWT), carcass weight (CW), weaning weight maternal (WWTM), adult size (EWT), wool production (FW12) and number of lambs born (NLB).

References

McLean, N.J., Jopson, N.B., Campbell, A.W. *et al*. (2006). In *Proc. NZ Soc. An. Prod.* 66:368-372.

Newman, S-A.N. (2003). In *Proc. NZ Soc. An. Prod.* 63:194-196.

Newman, S-A.N., Young, M.J. and Amyes, N.C. (2010). In *Proc. 9th WCGALP*, 4pp.

Young, M.J. and Newman, S-A.N. (2009). In *Proc. NZ Soc. An. Prod.* 69:153-154.