Innovations in sheep performance recording in new zealand

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Abstract

Sheep performance recording in New Zealand commenced in the late 1950s and early 1960s with a sole focus of producing genetic improvement in the national flock. The first selection index was produced in 1961. Since that time, New Zealand has operated a number of national sheep recording schemes with the current "Sheep Improvement Limited" (SIL) service operating since 1998. This service is now incorporated into B+LNZ Genetics, a subsidiary of the farmers' levy-funded organisation, Beef + Lamb New Zealand.

In 2014 B+LNZ Genetics commenced a substantial programme to upgrade the SIL system, to improve accuracy of data collection through electronic identification and in-field recording tools, to increase size of the genetic evaluation, and to integrate the use of SNP data into a single-step breeding value calculation.

New web and mobile tools are being developed to encourage better use of genetic information by commercial farmers and livestock agents, supported by an extension programme. New mobile and in-field data collection tools are being developed to streamline the process of performance recording by breeders. Research work is being undertaken to improve the prediction of lean meat yield and to include ewe longevity (stayability) and maternal body condition score (BCS) in the traits evaluated.

Background

The first release of sheep into New Zealand was in 1773 by the explorer James Cook. Released to run wild in the forest, it is likely these animals died within days. Ruminant livestock farming started in 1814 with the importation of sheep and cattle from Australia to support missionary endeavours. Performance recording for genetic improvement started in the 1960s, with the first selection index calculated in 1961 (Dalton, 2014) and the first national sheep scheme in 1968 (Clarke and Rae, 1977).

Performance recording and selection for genetic improvement has made a substantial contribution to the performance of the New Zealand flock. Genetic trends from 1995 to 2014 show improvement in average genetic merit for number of lambs born (NLB) of 0.13 lambs, for weaning weight (WWT) of 2.7kg, and for carcass weight (CW) of 1.6kg. Figure 1 illustrates the trends for NLB and WWT.

A key measure is the delivery of the genetic improvement to the national flock. Sheep numbers in New Zealand have declined markedly from a high of 70 million wintered in the early 1980s to 29 million in 2014, as shown in Figure 2. During that time, meat and wool production have remained close to static, reflecting the productivity benefits of improved livestock genetics, nutrition and pasture genetics, and animal health.
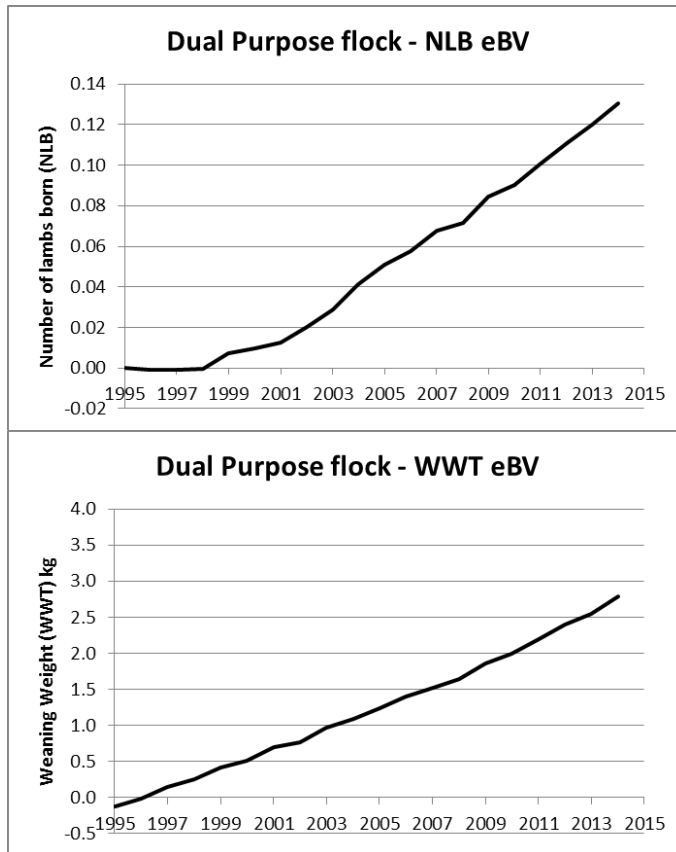
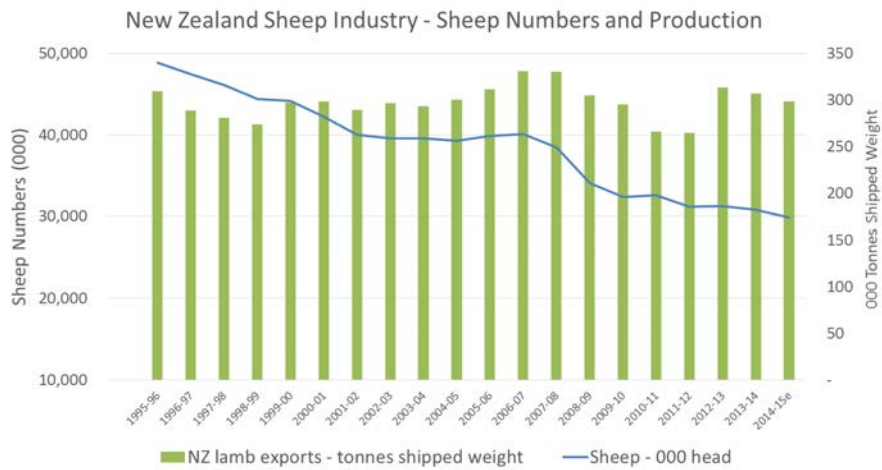Figure 1. SIL ACE Dual Purpose Genetic Trends for NLB and WWT.

Figure 2. New Zealand Sheep Numbers (wintered) and lamb production (source: Beef + Lamb New Zealand).

In 2014 B+LNZ Genetics, a wholly-owned subsidiary of Beef+Lamb New Zealand was formed, bringing together the genomic research and development performed by Ovita, the SIL sheep performance recording system, and the B+LNZ Central Progeny Test.

B+LNZ Genetics is commencing a five-year programme to improve the rate of genetic gain in New Zealand performance recorded flocks and to increase the effective adoption of improved genetics by the wider sheep industry. It will do this by a number of means, but one of the key mechanisms is a set of improvements to the SIL performance recording system, focusing on:

- Improved accuracy of recording through better data collection and increased use of DNA parentage;
- Improving the accuracy of breeding value estimation by using a single-step genetic analysis incorporating increasing quantities of genotype data;
- Delivering better tools to breeders and commercial farmers enabling them to understand and make selection decisions and informed ram purchases.

The existing Sheep Improvement Limited (SIL) performance recording system and database was developed in 1999 based on system designs from the early- and mid-1990s. It is a traditional performance recording system based on animal identification and phenotype observations collected by breeders. These observations were manually recorded on paper forms, and sent to a regional bureau operator to be entered into the computer system. These bureau operators would also produce selection index reports and pre-lists for breeders "on demand", sending these out in paper form (and more recently, as PDF documents that breeders could print). Figure 3 demonstrates the flow of information in this system.

Existing workflows and outputs

Some interesting characteristics of the current New Zealand SIL system are:

- Animals are identified by a "Birth ID" which consists of the flock registration code, year of birth, and a unique number assigned within that flock and year of birth. If animals are transferred to another flock they may be re-tagged for convenience, but the official identifier from the flock of birth remains. An ICAR identifier is not used. Radio-frequency identification (RFID or EID) tags have been adopted only recently and are not yet used by all breeders. New Zealand does not currently operate a national individual animal identification and traceability system for sheep, although it does for cattle and deer.
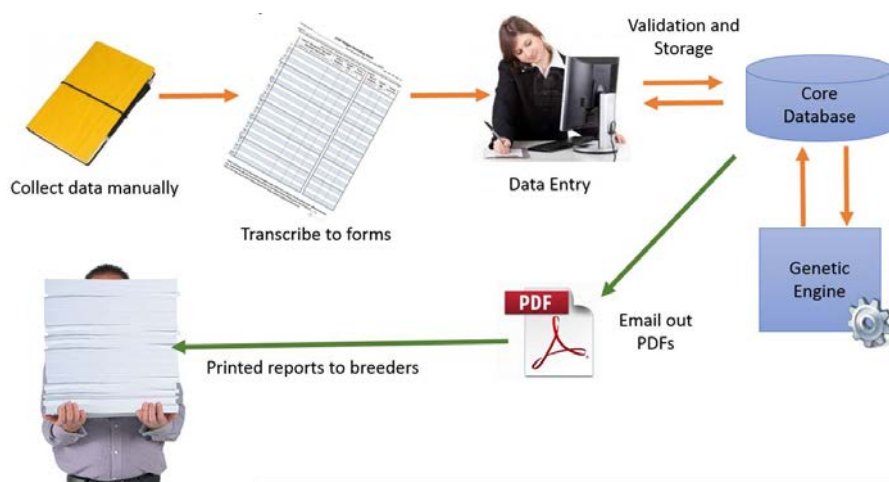

Figure 3. Data flows through the current SIL system.

- Genetic evaluation was carried out primarily using separate "within-flock analyses", with some collaborative breeding groups carrying out across flock-evaluations, until the SIL-ACE across-flock evaluation was instituted in 2004 (Young and Newman, 2009). SIL-ACE is still an "opt-in" analysis in which over 300 flocks now participate (representing 55% of SIL flocks and 78% of new animals born). However, not all flocks record all traits, and some are not well connected.

A feature of the original within-flock analysis model that appealed to breeders was that they could request an updated analysis at any point in time, and so did not have to return their data by a specific deadline. A weakness of this flexibility was that bureau operators and the SIL system were expected to respond to at-times unreasonable demands where a breeder submitted their data and then expected a new within-flock analysis and report the next day.

- Genotype data has been managed entirely separately, being delivered from the laboratory to a research provider to generate breeding values, which are then combined with the SIL breeding values for reporting.

- The SIL database system was built using a unique object-oriented database system called JADE (www.jadeworld.com). The JADE database system allows animals and their relationships to be modelled as entities using object-oriented design principles and then stores these directly without attempting to map them to a relational database. This is a strength when collecting, editing, and manipulating records of individual animals, but object-based systems tend to be slower when attempting to carry out set-oriented update or processing operations on thousands or millions of records.

Next generation workflow and analysis

As part of the B+LNZ Genetics development programme, new information technology tools and processes are being implemented in the core SIL system and extended to the wider set of tools used by industry to support adoption of improved genetics. The resulting system model is illustrated in Figure 4, and includes:

- Changes to the core SIL database, including migration from JADE to a SQL database and new software tools will facilitate more rapid development of new services.

- Genotype data will be moved into the core database, storing processed allele data from the laboratory as well as its FImpute (Sargolzaei *et al.,* 2014) format to enable rapid extraction for analysis. Genotype service providers (retailer and laboratory) are separate organisations that will connect to deliver data (and retrieve lists of animals) through an integration interface (Application Programming Interface or API).

- A single-step across-flock analysis (Aguilar *et al.,* 2010) will replace the current within-flock and across-flock analyses. This analysis could be run as frequently as weekly to maintain much of the flexibility from which breeders currently benefit. Pedigree, phenotype trait observations, and genotype data will be delivered from the SIL database to the genetic analysis system using automated routines.

- In-field data collection tools utilising smartphone and wireless technology, and connecting to weigh-scales, tag readers, and auto-drafters will encourage adoption of electronic animal identification, streamline the process of capturing data, and remove transcription errors. Our analysis of farmer demographics suggests that a number of breeders will continue to use traditional data entry services, particularly in smaller flocks, and breeders will be able to separately contract organisations to provide this data entry on their behalf.

  As well as providing a set of in-field data collection tools, the SIL system will provide a full integration interface (API) that allows third-party developers to create and provide other tools which breeders may elect to use.

- A new web-based user-interface will allow breeders to directly review their own data to see validation errors or warnings and approve its submission into the core database. Alternatively they may prefer to delegate this task to an expert or advisor who can undertake this process on their behalf. Breeders and advisors will be able to interactively request reports utilising standard templates with support for flexibility in the columns of data shown and the filtering that can be applied. These reports will be able to be downloaded in a range of formats for printing or use by other tools.
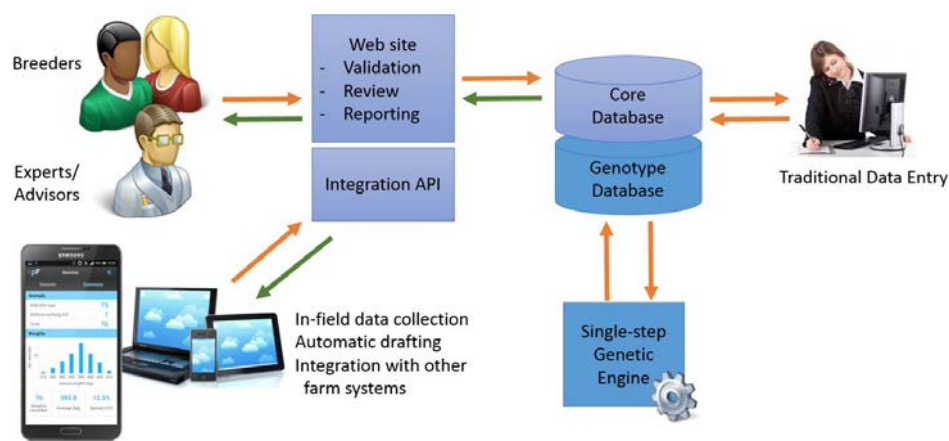

Figure 4. Data flows in the next-generation SIL system.

B+LNZ Genetics is also investing in the creating of a range of tools that will support commercial farmers in their application of improved sheep genetics.

Next generation tools

The first of these tools, the B+LNZ Genetics FlockFinder is a mobile application intended for primary use by commercial farmers, livestock agents, and others who assist farmers with ram selection or purchasing. Illustrated in Figure 5, the application works on Android and iOS smartphones and can be downloaded from the Apple store or Google Play. It allows farmers to choose a breed of animals, region, and the goal traits that the breeder is recording for. The application returns a list of registered SIL breeders and provides contact details as well as showing these on a map.

Other tools planned will allow breeders to understand how their flock compares to its peers in average flock index merit and rate of genetic gain, and to present SIL information to commercial farmers in a way that supports ram buying with more emphasis on using a relevant index and eBVs.

Tools for commercial farmers will allow them to assess the performance of their current or intended ram team in the light of their farm goals. This sort of tool will link to other industry benchmarking tools currently being developed by Beef + Lamb New Zealand.
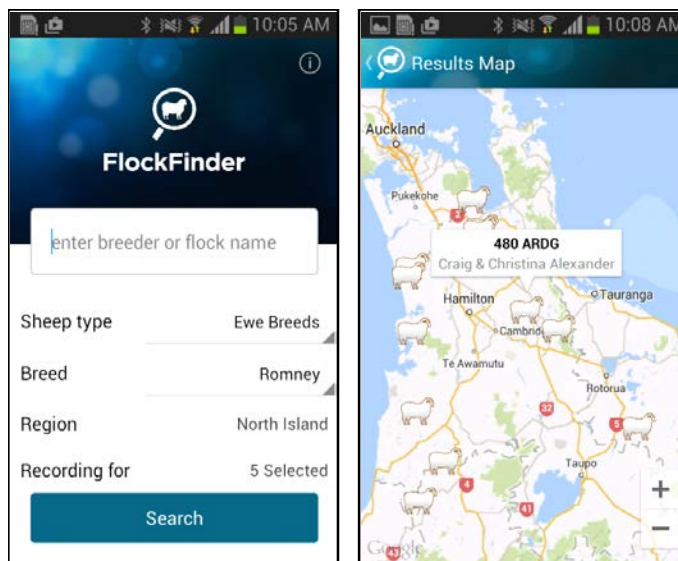
Figure 5. B+LNZ Genetics FlockFinder application.

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