A Nuffield Farming Scholarships Trust

Report

Award sponsored by

The South of England Agricultural Society

Sheep genomics: the future of profitable performance prediction

Robert Hodgkins

August 2013

NUFFIELD UK

A Nuffield (UK) Farming Scholarships Trust Report

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"Leading positive change in agriculture.
Inspiring passion and potential in people".

Title	**Sheep genomics: the future of profitable performance prediction**
Scholar	Robert Hodgkins
Sponsor	The South of England Agricultural Society
Objectives of Study Tour	• To establish the current state of sheep genomics, in terms of both research and practical applications. • Asses the applications of new technology and determine if we can apply to our ram selling operation.
Countries Visited	• Australia (New South Wales) • New Zealand (Both North and South Islands) • Scotland (United Kingdom)
Findings	• Genomic research in sheep has advanced rapidly in the southern hemisphere and is now in a marketable (New Zealand) /near marketable (Australia) state. • Currently only European flocks with a high percentage of southern hemisphere genetics and who record on southern hemisphere recording systems can make use of this technology. • "Pure" genomic results do broadly correlate with the observed raw measurements **but** to maximise their value it needs to be combined with eBV (estimated breeding values) data. • Significant further research is needed to validate difficult to measure phenotypes within European based flocks. • Used properly genomics can be a powerful aid to speed up genetic gains in a flock, by allowing sires with high eBV but poor accuracy scores to be used in your breeding programmes with greater confidence. • Genomics could also be used to accelerate the improvement of a stabilised NZ Romney based cross.

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Background

Ours is a large, family run commercial sheep farm with a large commercial ram selling operation called "WairereUK". My parents, Chris and Caroline, my brother Andrew and I are equal partners. I completed a degree in mechanical engineering, went to work for 'Caterpillar' designing turbochargers, then 'Visteon' writing the code to control engine fuel maps, and finally worked for 'Ford' where I designed the latest generation of Ford Transit dual mass flywheels and clutches. After several years I grew tired of office based work and yearned for the outside and the freedom farming has to offer, so I left engineering to re-join my family farm.

We run around 3,000+ New Zealand (NZ) Romney ewes on a spread out unit (25 miles round trip to visit every flock), on good to poor grassland in the south of England. We operate a single breed, closed flock and take great care and interest in selecting future progeny to make shepherding as enjoyable and stress free as possible. We are one of the largest 'Signet' recorded flocks in the country and single-sire mate and record around 1,500 ewes and their progeny. In addition, since completing this Nuffield Farming Scholarship, we now record all our sheep on the New Zealand performance recording system (SIL). We sell high quality, NZ Romney rams and females and on a typical year we will sell around 110 two-tooth (shearling) rams and all the breeding females that are not required for our own replacements.

In 2011 at the Sheep Breeders Round Table event we heard a presentation from Dr Alex Ball explaining the current state of research into the genomic selection programme which was taking place in the southern hemisphere. The money and scientific minds being thrown

Me, Rob Hodgkins

at the problem were formidable and I listened intently to the details of the project and the expected benefits it would bring.

During the question and answer session a point was raised about the possibility of transferring the technology to Europe. To heavily paraphrase Dr Ball he explained that because cross breed analysis was not accurate and the need for a fully referenced and performance recorded population of at least 5,000 sheep all with DNA testing, there was no chance this technology would be available in Europe . . . . "*Unless you flew your own New Zealand flock over here, or had a half million £s to research the locations of the genes for your own phenotypes".*

Well, that single throwaway line was to radically alter the next few years of my life. Since 2005 we had been importing Romney semen and pre-impregnated Romney

embryos from New Zealand and in 2006 we had flown into Europe, from New Zealand the first live rams to be imported for almost 25 years (we have since imported another 22). This meant that we could be one of the very few farms, outside New Zealand and Australia, to take advantage of genomic technology.

That evening whilst discussing using the technology to aid the selection within our own flock, my father mentioned there was a grant given by a body called Nuffield that paid for people to look into projects like this. Having looked at their website I realised I had five days before applications closed for that year so I took the plunge and sat down to write out my application form.

My Nuffield Farming Scholarship project into genomic selection has seen me travelling half way across the world, spending eight weeks in the southern hemisphere investigating the technology and its current applications. The Nuffield name opened doors into some of the world's most advanced research labs and I got to talk to some of the world leaders in this field. I saw an 'Illumini I-Scan' read DNA from over 300 sheep on a single chip. In Australia I got the opportunity to spend a day doing a lambing round on a Merino stud with a farmer, discussing the gains genomics will make for his farm in his project to breed a more maternal Merino ewe.

The first half of this report will explain how this technology works and what the likely benefits are to the countries investing in it. The second half of this report details the experiences I have had bringing this technology into the UK and what (if any) benefits I can report from it.

One of the first NZ tups bought across, pictured with UK ewes (picture circa 2006)

Disclaimer

The views expressed in this report are my own and not necessarily those of the Nuffield Farming Scholarships Trust or of my sponsor - The South of England Agricultural Society, WairereUK or any other sponsoring body.

Introduction

I believe the New Zealand Romney has a huge part to play in the future of British farming and my ambition is to present it as a possible solution to the several big problems affecting British farming today. The average age of a British farmer is said to be 55 and rising; if we were to look at the sheep sector it would probably be even higher. I am sure you could write an entire report on how to lower this but, like any industry, to be attractive to the right people, you need to stick to the basics and create an attractive business model:

More money (A) + Less work (B) = higher quality candidates

A. *Make sheep farming as financially rewarding as possible by producing your product for the lowest possible price. In my eyes that means a forage based animal requiring low levels of labour input with minimal interference. A robust selection of stock with the right genetics is key to a viable sheep farming sector, which in these times of global markets and harvests needs to be protected from global market price fluctuations in sheep meat and feed prices by producing animals at the lowest cost of production possible.*

B. *Significantly decrease how labour intensive sheep farming can be, via use of a maternal ewe with the capacity to look after herself - including lambing outside (cold weather tolerance genes) with high disease resistance (e.g. foot rot resistance genes) and significantly reduced shepherding requirements.*

My project was to investigate the use of genomic selection to aid in this.

Section One : Performance Recording and Genomics

In order to understand this report it's necessary to understand the concepts behind both performance recording and genomics.

The main factors that will dictate how quickly lambs grow and thus how profitable your sheep enterprise is, are:

a) Environment
b) Genetics

The general consensus in the industry around meat and growth traits seems to be: 70% environment and 30% genetics.

Genetics can only influence about 30% of a flock's potential; given enough favourable inputs even the worst sheep (genetically) can be given high growth rates through additional feeding, more intensive rearing etc. The key to a profitable enterprise is keeping those (expensive) inputs to a minimum and ensuring the sheep are working as hard for you as you are for them. We can do this by selecting animals with the traits most suited to our farming system.

Over time in any wild population natural selection will favour those individuals most suited for the climate. Larger populations produce a greater degree of variations but smaller populations adapt more quickly as competition for resources is usually fiercer, meaning only the very best survive. i.e. in a situation where there is an abundance of resources even animals less well suited will survive. However if there is very limited resources and a small population then change will occur rapidly as only the very, very fittest will survive and breed. Effective performance recording should aim to combine the best elements of both by having the variations inherent in a large population, but ensuring only the very best go forward (like a small population). It can be shown that the very worst case in terms of genetic improvement is having a small population, putting no selection pressure on it and not monitoring performance.

Performance recording has the power to "skew" the normal distribution curve by picking only those animals with superior traits and integrating them into a breeding programme. Further selection pressure can also be applied through changes to the environment e.g. recording animals that need assistance at lambing and culling them out of the population, meaning greater improvement can be made.

In summary, performance recording is a process designed to increase the rate of "genetic gain" within a breeding population. We can do this by using large populations to produce more variation, then selecting which genetics go forward to the next generation.

This can be expressed thus:

$$\text{Genetic gain} = \frac{\text{Selection intensity} \times \text{Selection accuracy} \times \text{Genetic heritability}}{\text{Generational interval}}$$

Where:

Selection intensity = how many dams and sires are involved *(the size of the population and the mating ratios of those animals selected for breeding)*

Selection accuracy = how accurate the existing data on dams and sires is *(the accuracy level of the eBV)*

Genetic heritability = A measure of how inheritable the trait is and the level of

genetic variation *(heritability varies considerably between traits – see section on "heritability")*

Generation interval = how quickly the population moves *(e.g. chickens lay eggs once a day and reach sexual maturity in a short time frame, ewes only lamb once a year and take 8 months before being ready for (seasonal) mating, so faster gains can be made in chickens).*

The simplest recording system

A good simple example of performance recording would be to ear notch at birth all male ram lambs born from twins - high fertility is *somewhat* heritable so twins are slightly more likely to produce twins. By keeping back only ear-notched rams as replacements, over time you should increase the lambing percentage (assuming equal environmental conditions).

Taking a step further, if you weigh all those ear-notched rams and only kept the heaviest back for breeding, over time you would expect the flock to become faster growing and more likely to bear twins.

The problem with this approach is two-fold:

a) Doesn't take into consideration other factors. Consider the following scenario: what if one lamb died soon after ear-notching? Its sibling would then be raised a single, meaning its growth rate would be much higher as it is not competing for milk. You would naturally weigh it and, not knowing it had been raised a single, probably pick it for breeding. That ram may not have good growth ability and if the mother has lost a lamb she may be more likely to have poor mothering ability.

   An extreme consequence of this would be you are introducing average growing and poor mothering ability into the flock!

b) Changes to the environment - for example what if half the flock had access to high sugar ryegrasses with clover and the other half had access to a bare hill with virtually no grass. The results would not be representative of the genetic potential of the animal, because of the very different diets they have been exposed to.

Simple systems give simple results but, to fully understand the flock's genetics and to make data-based decisions to avoid the scenarios listed above, you need to individually record the performance of each animal. Then blend data from multiple streams i.e. weight gain data from siblings, half siblings, fathers and grandfathers to try and eliminate environmental factors as much as possible.

In short, to produce accurate data-based decisions you need to be measuring multiple traits and producing "Estimated Breeding Values" (eBV) for your sheep.

Estimated breeding values (eBVs)

Every country has its own recording system. The UK uses "Signet", Australia uses "Lambplan" and "Merinoselect" and New Zealand uses "SiL". There are differences between them which aren't really within the scope of this report to examine - suffice to say they all record data from an animal's life.

Most systems would record <u>at least</u> the following:

- Born type (single, twin or triplet)
- Mothering ability
- Birth weight
- Weight at 8 weeks
- Weight at 20 weeks or at weaning

with more advanced measurements being:

- Eye muscle depth (ultrasound measured)
- Fat depth (ultrasound measured)
- Ewe mature weight
- Faecal egg counts
- Feedback of carcase quality and weight from abattoirs

This information is sent to a central computer database and, for each eBV, a variety of information is "blended" together, including performance of siblings, half siblings, sires and dams etc. See figure 1.

This process is called Best Linear Unbiased Prediction (BLUP)

Heritability

Heritability is a measure of how likely it is for a trait to be passed down into the next generation. Traits are often not expressed in the next generation - short parents do not always have short children - every trait has a level of heritability.

Some traits are highly heritable (25% or greater chance of being passed down) making animal selection for this trait effective which can result in easy economic gains for the flock. Some traits are reasonably heritable (10-25%). Progress in your flock with these is still possible by selection but improvements

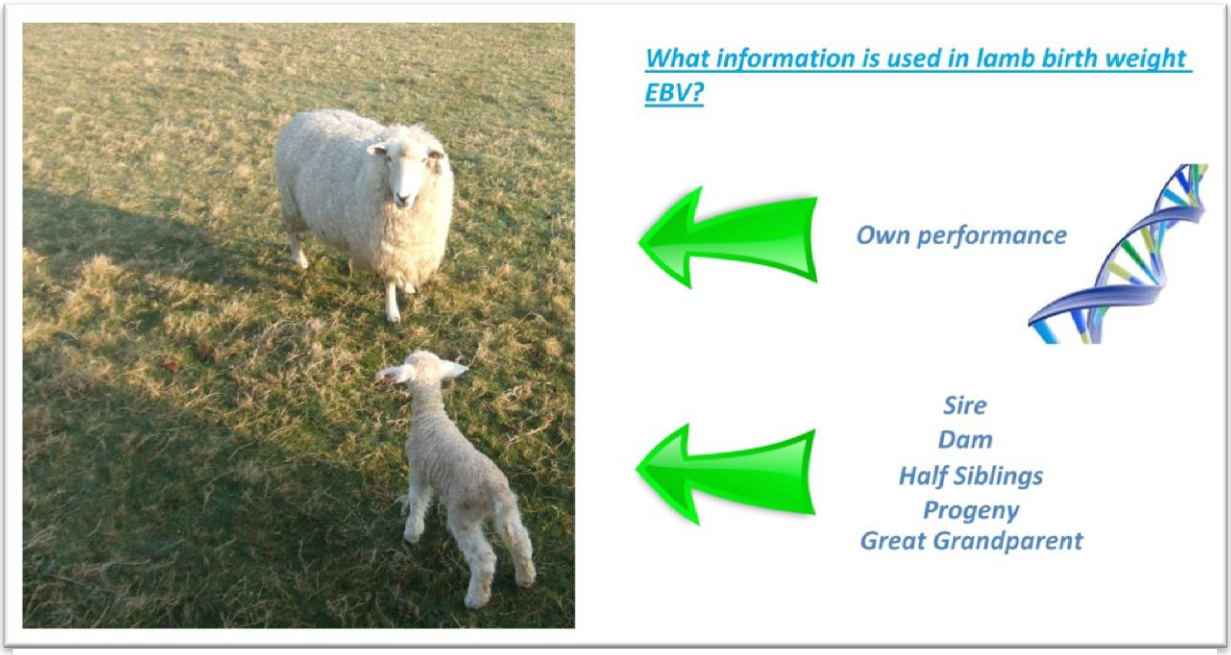


Figure 1: How to create an eBV

will be slower. Some traits are not very heritable (10% or lower). With such small values, making progress will be difficult and a large population will be required, if only 10% of the offspring are displaying the trait required, then the number of suitable sires for the next generation will be small, and the traits will take many generations and significant effort to be established in your flock.

The importance of eBV

The effect of eBV, recording, selecting and buying the right sheep cannot be overstated as a major profit driver in sheep businesses. EBVs work to increase the "selection accuracy", one of the main components in the equation for increasing genetic gain. They also work to validate heritability and understand the degree that the traits you are breeding for have been passed down.

EBVs take this into account by giving every animal an accuracy score, showing how much data is available to authenticate that score. More information means more accuracy. Information from siblings and half-siblings can be used to increase accuracy. This again links back to our equation, with a high accuracy meaning a higher genetic heritability.

Accuracy

For every eBV there is an accuracy figure to go with it. This is defined as the correlation between the BV (the "true" Breeding Value) and the eBV. The accuracy is given as a percentage (0% to 100 %). The closer to 100% the more the estimated breeding value becomes the actual.

Take LW8 (lamb weight at 8 months) as an example. A ram with an eBV showing high LW8, with 100 siblings also all displaying very high 8 month weights, will have a very high accuracy behind its LW8 eBV – *there is evidence that it is likely to be passing that trait down*. However a ram with only 10 siblings will still have a low accuracy behind its 8 month weight – *there is not enough proof yet that it is passing that trait down.*

Accuracy is also higher for those traits with higher heritability. However it would be wrong to conclude that in a breeding programme only the animals with the highest accuracy should be used. All breeding programmes need to balance accuracy with the time between generations and the advantages of using less accurate ram lambs to push forward genetic gain. *What is needed is a means to increase trait accuracy at a very young age. Or, to link back to the equation earlier, we need to alter our "generational interval."*

Practical example of why to use eBV

Which set of genes would you like to be breeding from?

Consider figure 2 (below) with the example of ewes B25 and B104. As can be seen from the picture they both look very much the same with similar body weight (74kg and 76kg respectively) and condition scores, and each had twins in 2010 and 2011. At a glance they would appear to be identical sheep. However a closer look at their performance figures on

Figure 2: Which are the best sheep?

the table to the right reveals a different story. Let's look in depth at one eBV, LW8, for these two ewes.

LW8

This is a useful economic indicator as a higher weight will mean a lamb finishes faster if going to market or, if being kept for breeding stock, it will mean that lamb will be more likely to hit 42kg and be suitable for a ewe lamb mating. LW8 units are kilograms i.e. an eBV of 4kg means that an animal in identical environmental conditions will grow a lamb 2kg heavier than the average flock animal (4/2 = 2). *You would divide by 2 as the lamb only gets half the genetics from its mother's side.*

The figures show that the ewe B25 has a score of 3.77, meaning - through a combination of her weight and information from her relatives' weight - she will pass on genes capable of producing lambs 1.8kg (1/2 set of genes from each parent) heavier than the average. Compare that to ewe B104 who would produce lambs -0.43kg lighter than the average.

To try and quantify this let us take these two sheep and *hypothetically* mate each of them with the very best ram we have for LW8 (number 4685 with an eBV of 5.62) and the very worst ram we have for LW8 (number 1031 with an eBV of -1.22).

Equation

$$\frac{Ewe\ Lw8\ eBV\ +\ Ram\ LW8\ eBV}{2} = Per\ lamb\ increase\ /decrease\ from\ flock\ average$$

B104 (worst) + 1031 (worst)

$$\frac{-0.86 + \ -1.22}{2} = -1.04$$

B104 (worst) + 4685 (best)

$$\frac{-0.86 + \ 5.62}{2} = 2.38$$

B25 (best) + 1031 (worst)

$$\frac{3.77 + \ -1.22}{2} = 1.28$$

B25 (best) + 4685 (best)

$$\frac{3.77 + \ 5.62}{2} = 4.69$$

Ignoring other environmental factors, the difference between the worst combination and the best combination at 8 months is a difference per lamb of 5.73 kg (live weight).

Or, to put it another way, assuming each ram sires 100 identically average ewes (and maintained Wairereuk weaning average of 162 lambs) then ram 4685 at 8 months would have had the potential to have produced an additional (3.42kg x 162) = 554kg of live weight, in his progeny.

To put some figures around this, the live weight price in November 2012 (8 months from birth) was £1.60 per kilo.

5.73 x £1.60 = £9.17 (difference per lamb sired between "best" and "worst" rams)

£9.17 x 162 (lambs per mating) = £1,485.54

£1485.54 x 6 (no. of mating in his lifetime) = **£8,913.24!!**

Relatively modest investments in high yielding genetics can make a huge difference to your profitability.

Genomics

Below is a very simplified explanation of genomics. This report will not go into depth but it will give a very brief overview of the science.

Genomics is the study of the genes an animal is carrying. Genes control every aspect of us from how tall we are likely to grow through to our eye colour right through to how likely it is we will suffer from a certain disease. If we knew what genes control the traits we want we could test each animals DNA and know if that animal has the traits we need to make the farm profitable.

Figure 3 shows a breakdown of one of our rams into his component parts.

So how do we use this knowledge in a practical way?

As farmers we don't have to understand every last detail but we do need to understand enough to ensure we utilise the technology to ensure the most profitable outcome.

Consider the hypothetical and extremely simplified situation in figure 4. We know from weight records that Romneys A, B and C all exhibit huge growth rates (*called a phenotype*).

We send DNA samples to the lab and an area of the DNA between point A and B (*called a single nucleotide polymorphism, or SNP*) is found to be common on all three animals. We now know that between those points

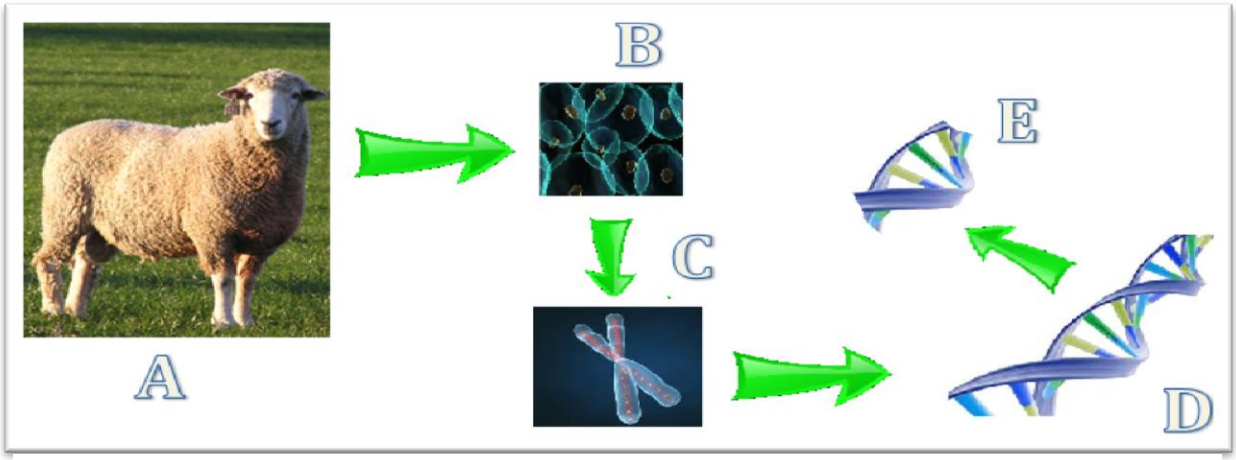


Figure 3. Breakdown of a Romney ram

WairereUK stud animal 1378 ***(A)***

is made up of cells ***(B)***

Every cell has a nucleus (the yellow part of the cell structure). Within that nucleus there are 54 chromosomes ***(C)***

and each chromosome is a single piece of (very long) DNA ***(D)***

A gene ***(E)*** *is a small section of that very long piece of DNA that controls something like wool colour or growth rates. The sheep genome is all 54 chromosomes together.*

somewhere lies one of the genes for high growth rate, so we can now test Romney D and know *from the moment it is born, without any performance recording*, that if it shares that common point, then it will have the gene for high growth rates.

In reality there is a lot more complexity with multiple genes needing to be switched on and off in order to "switch on" a specific trait and instead of 3 Romneys you would need to test around 5000 to gain enough confidence.

So genomics is really the science of taking a DNA sample from an animal and being able to

tell - just from that sample - huge amounts of information about the genetic potential of that animal, commercially it can be used in

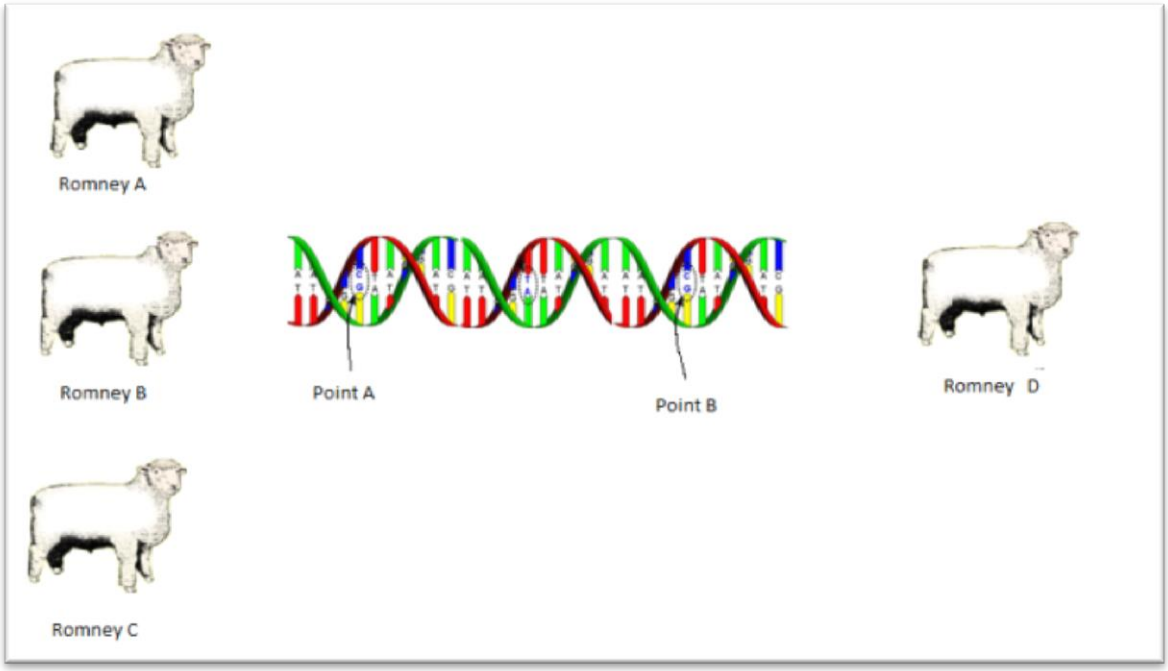


Figure 4. Genes control traits

several ways:

A. As per figure 4 use genomics to get an idea of the likely performance of non-recorded stock, saving years of recording its performance.
B. Use genomics on very young recorded stock, or stock with not much progeny, to increase accuracy of eBV.
C. Use genomics to identify difficult, expensive, or time consuming traits that you want to breed **in** or **out** – e.g. the genes responsible for internal parasite resistance or increased likelihood of twins.

Zoetis Animal Health

'Zoetis' (formally known as Pfizer) is a large multinational firm which, together with partners (AgResearch Ltd and Beef and Lamb NZ), marketed the world's first commercial genomics test for sheep. This was built on the knowledge gained from the International Sheep Genome project. The International Sheep Genomics Consortium is a partnership of scientists and funding agencies from Australia, Austria, Brazil, China, Finland, France, Germany, Greece, India, Iran, Israel, Italy, Kenya, New Zealand, Norway, Spain, Switzerland, Turkey, United Kingdom and United States to develop public genomic resources that researchers can use to find genes associated with production, quality and disease traits. The project commenced informally in 2002, and was built on an existing collaboration for the International Mapping Flock that was created nearly a decade earlier.

Zoetis currently market two different types of test: the first is a trait specific test, and the other is a complete multi-gene analysis.

Single trait analysis (focus on a small part of the DNA strand)

Examples include:

MyoMAX a DNA test for a double muscling gene which increases carcase weight and lean meat yield

LoinMAX a DNA test for a gene which increases loin muscling

WormSTAR a DNA test which identifies animals that shed less eggs onto pasture (parasite resistance) and animals that grow well in the presence of parasite challenge (parasite resilience)

Shepherd a DNA based parentage system that provides pedigree information and eliminates the need for tagging at birth and single sire mating.

Farms already use these tests to identify key traits that are important to them and they have been in use around the world for a number of years.

The 50K SNP chip (complete DNA strand analysis)

See figure 5 below

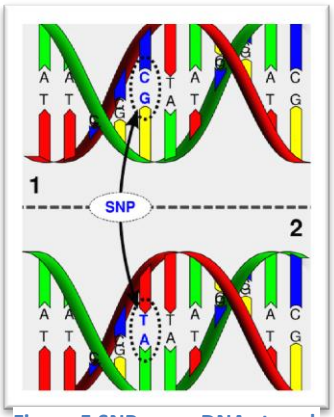


Figure 5 SNPs on a DNA strand

When cell division occurs the DNA strand is split to produce two versions. Occasionally this process goes wrong and a small change is introduced. This small change is called a Single Nucleotide Polymorphism, or SNP (pronounced "snip") and this change is what the genomics test is looking for. The SNPs give scientists the opportunity to 'cut up' the DNA strand into much smaller 'chunks' and allow us to compare 'chunks' of DNA across sheep. So by going back to figure 4 if 2 chunks of DNA are the same in two different sheep we will know they are carrying the same genes.

Consider this analogy: a complete DNA strand might be a considered a map with no road or street names and a gene as an individual house you are looking for. SNPs act as road names allowing you to break up the map into different sections so in "blue eye street" you know there are 6 houses and a church – you don't know which of the 6 houses are causing blue eyes but you do know that if you look at another map in the same location and you see a street with 6 houses and a church you can guess that street will be "blue eye street."

SNPS are inheritable, if there is no genetic link then SNPS will be in different places. So an English Romney and a New Zealand Romney may have very similar DNA but because there SNPS are in different locations the 'maps' are different you cannot locate your '6 houses and a church' because the 'streets' end and begin in different places.

In summary: SNP's acts as a marker to locate a gene in a DNA sequence.

Through comparing the genetic code of a variety of breeds from around the world, including Texel, Romney, Merino and Polled Dorset, many SNPs were identified. The most relevant SNPs were included in developing the SNP chip which contains 50,000 individual SNPs covering the entire sheep genome (hence the "50K" Chip). A SNP chip can identify many thousands of individual genes for a single animal.

Calibration flocks

In figure 4 there was a simplified example of how animals could be examined via genomics. In reality to start understanding even basic traits *(or in technical terms "Phenotypes")* you need a reference population of at least several thousand recorded, genotyped animals, all with genetic links to one another,

with at least another 1,000 animals tested per year to ensure the genomic predictions remain calibrated.

Every generation the DNA alters slightly as it splits and, as small changes creep into the DNA strand, the population drifts further away from the original reference population. The location of the genes moves over time and the computer has to be calibrated to look for the new location for these genes. Fully recorded reference populations have to be maintained and measured to ensure the accuracy of the test. In New Zealand, these flocks take rams from major breeders across the country to ensure the genetics the test is being based on are representative of the genetics seen in the wider industry.

The world's first commercially available SNP Chip

Zoetis lays claim to having the world's first commercially available SNP chip, which was released late in 2010. Through DNA analysis it was able to offer values for the following key performance traits, with more expected to be introduced each year:

Figure 6. DNA Strand

PRODUCTION

- ✓ Carcase Weight (CWT)
- ✓ Liveweight at 8 months (LW8)
- ✓ Weaning Weight (WWT)
- ✓ Liveweight at 12 months (LW12)
- ✓ Ultrasonic Eye Muscle Area (EMAC)
- ✓ Adult Ewe LiveWeight (EWT)
- ✓ Eye Muscle Area (EMA)
- ✓ Number of Lambs Born (NLB)

WOOL

- × Lamb Fleece Weight (LFW)
- × Fleece Weight 12 Months (FW12)
- × Ewe Fleece Weight (EFW)

MEAT YIELD

- ✓ Fat Lean Yield (FATY)
- ✓ Shoulder Lean Yield (SHLY)
- ✓ Loin Lean Yield (LNLY)
- ✓ Hind Quarter Lean Yield (HQLY)
- ✓ Lean Yield Weight Adjusted (LEANY)

HEALTH

- × Facial Eczema (FE)
- ✓ Faecal Egg Count 1 (FEC1)
- ✓ Faecal Egg Count 2 (FEC2)*
- ✓ Adult Faecal Egg Count (AFEC)*
- ✓ Lamb Dag Score (LDAG)*
- ✓ Adult Dag Score (ADAG)*

* *There is uncertainty as to whether NZ parasites are the same as those in the UK*

× *Items marked as a cross would not be considered a priority in the UK at present.*

What does the SNP Chip bring us?

The long term expectation for the technology is to be able to look at DNA sequence in greater detail through the use of higher rated SNP chips with the next generation technology looking at 700K (meaning 700,000 markers). Currently genomic tests are able to, in conjunction with traditional recording systems, increase the accuracy figure of eBV.

So to recap: A ram with 100 progeny all displaying very high 8 week weights will have a very high accuracy behind its 8 week eBV – there is good evidence that it is passing that trait down. However a ram with only 10 siblings will still have a low accuracy for its 8 week weight – there is not enough data yet

that it is passing that trait down reliably. But the ram that has only 10 half-siblings AND was gene tested and shown to carry the genes responsible for high weight gain will also have an improved accuracy.

To show that the results have been obtained by blending recorded performance data with genomic data, Estimated Breeding Values (eBV) are replaced with Genomic Breeding Values (gBV).

Estimated Breeding Value (eBV) = Traditional breeding value based on measurements taken on whole flocks and combined via BLUP. (Best Linear Unbiased Prediction)

Molecular Breeding Value (mBV) = Breeding values taken solely from the DNA of the animal, by identifying key genes responsible for desirable traits.

Genomic Breeding Value (gBV) = A combination of eBV and mBV designed to give more accurate results earlier on in the animal's lifecycle than eBVs can deliver by themselves.

In Simple Summary:

eBV + mBV = gBV

eBV, mBV and gBV are not currently directly comparable. Work is on-going to try and calibrate the results so you can compare them.

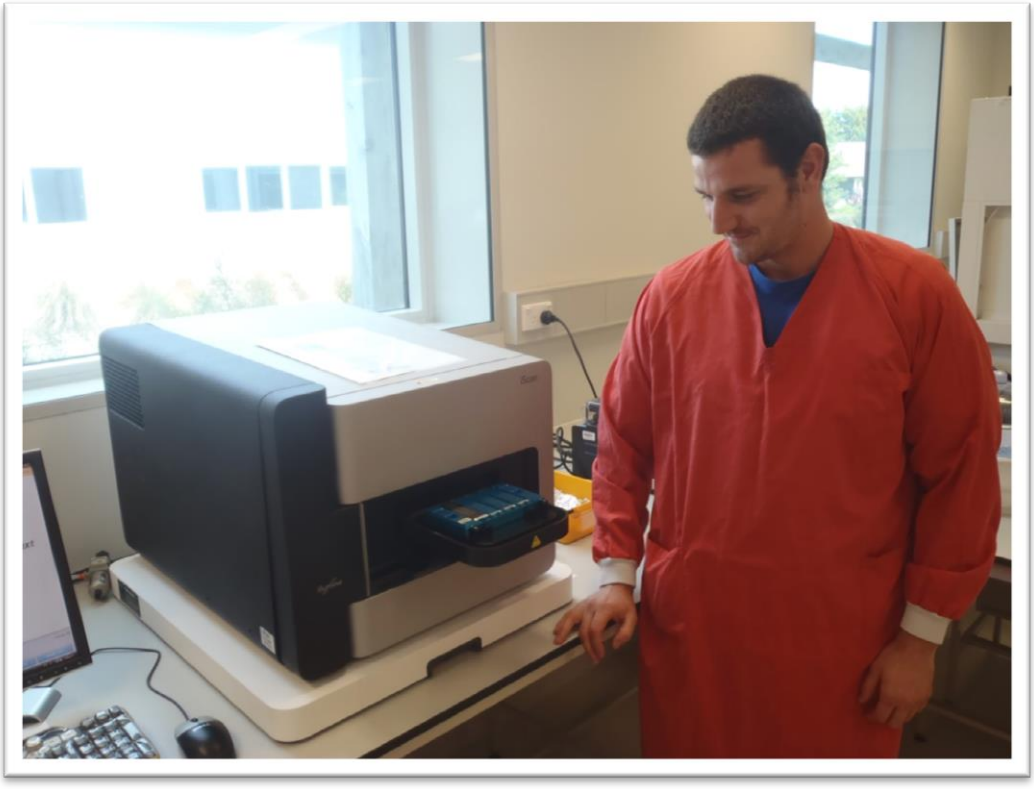


Figure 7. Me looking at an Illumini I-Scan reading sheep DNA in New Zealand

Section Two: Genomics in action

Introduction

Having explained in Section One a little about performance recording and genomics, in this Section (Two) we will look at the current state of genomics around the world and how it is being applied. Although the mapping of the sheep genome was an international collaboration there are only two countries (Australia and New Zealand) currently trialling/releasing commercial tests for sheep based on genome-wide analysis. On October 28th 2012 I left the UK to spend 8 weeks travelling around the southern hemisphere.

My findings are detailed below but the overriding impression I had throughout the trip was how focused the farmers I met were on genetic improvement and profitability; how an animal "looked" was completely irrelevant unless it was linked to a profit driving trait (and obviously structurally sound). I kept thinking back to a previous Scholar's report and a quote attributed to an unknown Australian farmer

"If an animal is making you money you will soon learn to like the look of it."

I saw first-hand farmers putting this message into action.

Australia

Ovine Genome development in Australia

In Australia the first visit I made was to the University of New England (UNE) to visit the sheep Co-operative Research Centre's (CRC) programme.

The Sheep CRC is a partnership of Australia's leading sheep industry organisations. Briefly; it is a government led initiative to bring key players from industry, science and academia together to work to create value and solve specific problems for the Australian industry.

The sheep industry won a CRC contract and has since set about researching key areas of the sheep genome and trying to link it back to desirable performance traits.

> …. how focused Australian and NZ farmers were on genetic improvement and profitability. How an animal "looked" was completely irrelevant if not linked to a profit driving trait.

The nucleus of the group was based on a number of calibration flocks totalling 5,000 ewes located at eight research sites in widely differing environments around Australia. The work aimed to:

a) Enhance the accuracy of Australian Sheep Breeding Values (ASBVs) for current traits
b) Contribute to the development of ASBVs for new traits
c) Validate molecular markers for current and new traits
d) Develop breeding values that

Figure 8: University of New South Wales

combine phenotypic and DNA based information

The technology is still not commercially available, with Australia careful about releasing the technology until fully validated. The programme is also able to test four separate breeds of sheep - Merino, Border Leicester, Poll Dorset and White Suffolk, so has cross-breed capability with a very wide range of traits having been identified: around 260 – compared to New Zealand's current tally of 22.

Market reaction

Having visited several farms across the region - some that are using a pre-production version of this technology and some very traditional large breeders opposed to it - I can say reaction to it has been mixed. Those who are using it and are widely supportive of it are pushing for the next stage of full commercialisation of the technology in the New Zealand style. However there are also pockets of serious resistance to genomic technology with many believing it is a technology that promises much and to date has delivered very little. Indeed just before I visited the country there was fierce debate raging after Australian Wool Innovation (AWI) pulled their funding for the Merino nucleus flock (the "calibration" flock for the Merino breed of sheep) with AWI chairman Wal Merriman commenting that "science had little to offer Merino breeding", and AWI chief executive Stuart McCullough saying there was "an insufficient bridge between science and commercial reality" to justify the funding.

There is still a commitment from Meat and Livestock Australia (MLA) to the flock, having approved a further $2.2 million to maintain the research flock until 2014. But without AWI support it is likely that testing for wool-related traits (a particular focus for Merino breeders) will eventually cease to be published.

It was my view that scientists were slightly losing sight of the commercial reality of sheep farming; a large numbers of traits were interesting but you cannot breed a sheep whilst trying to control and measure 260 variables.

An example of this would be the recently discovered genes responsible for zinc content in muscle. Whilst this was an interesting discovery, I couldn't really see a way to commercialise the data. The fact is most meat is sold through supermarkets at the present time. Supermarkets are interested in carcase weight and confirmation, they are unlikely to pay any additional money for the zinc content. (Red meat is a major source of zinc in our diets. It is vital for many human functions and lack of zinc in diets has been shown to have adverse effects – hence the interest in producing *"vitamin enhanced"* meat). Certainly the supermarkets would not currently pay the kind of premium that would mean breeders choose eatability phenotypes over say, number of lambs born (NLB) or weaning weight (WWT).

The idea in Australia currently was to "band" meat into five levels of quality with lamb sired from a ram with high zinc content, or other desirable eatability phenotypes, being a 5* product and lambs from unknown sires being a 1* product. My concern is that consumers may already be confused over labelling and options and any additional levels of complexity may not be in anyone's interest.

New Zealand

I arrived in the South Island of New Zealand on the 16th November 2012 and headed further south to Zoetis NZ headquarters to look at how they are using the technology.

History of Genome development in New Zealand

In 2002, the Ovita consortium was formed with the stated intention of increasing New Zealand sheep farmers' productivity and profitability.

It was a partnership between Beef + Lamb New Zealand, AgResearch and the New Zealand government, who together funded scientific research into sheep genomics.

Zoetis Animal Genetics is the commercialisation partner, having bought the technology from Ovita and in 2010, released the first genomics test for ovine application. As the uptake has increased, the costs of the tests have decreased, with more traits being released every year (current 2013 traits are listed in section titled The world's first commercially available SNP Chip).

Market reaction

In New Zealand the farmers' reaction to the technology was much like the Australia's, very mixed. It was my view that the technology was probably rushed into the market too early to try and recoup the money Zoetis had invested and big promises were made about the technology being able to replace performance recording completely and the accuracy of the tests was possibly overstated. The tests were also very expensive at the beginning. All this meant that the credibility of the tests suffered in the early days and people are only now beginning to get an understanding of what the test can bring to their breeding programmes, plus its limitations in use. Adoption has also been improved by the unit price having reduced by 60% since its 2010 introduction.

Summary : Australia and New Zealand

Both countries believe that genomics is going to play a significant role in upping productivity from sheep. New Zealand had focused its efforts on a small number of traits within a single breed of sheep (Romney and Romney-based crosses). By selling their government and farmer-levy-owned research to a commercial enterprise they got the benefit of it being first to market, but suffered early problems with over-promises from the commercial partner, as they rushed to recoup their investment.

Contrast that to Australia which has examined a larger number of breeds and as they have not sold the rights to a commercial partner, they have not had to rush an untested product onto the market. This means they have had opportunities to further refine that product through increased identification of traits. However, being removed from commercial reality has meant the research has possibly been focused on the advancement of science rather than the advancement of the product. Having already lost the support of AWI, the CRC does risk losing famer support unless industry-wide benefits are realised and the technology is released to a wider range of farmers.

Case Study – Nithdale Genetics, New Zealand

Nithdale Genetics is a Romney and Suffolk Stud owned by Heather and Andrew Tripp. The farm covers an area of around 1,450ha with an effective grazing area of 1,400ha, carrying around 7,300 sheep with a separate dairy herd and parlour.

The Tripps have invested substantial capital in new DNA technology. For example although they lambed commercial ewes on the hill un-shepherded for a number of years, until 2009 they had lambed their stud ewes in the lowland paddocks so as to tag lambs and thus determine the parentage.

Because they could use DNA technology to identify parentage they were able to change to an extensive system by lambing on the hill un-shepherded. By blood testing sires and dams they were enabled to determine the parentage of the lambs through their own

Figure 10. Nithdale Romney rams carrying MyoMax gene

DNA. This approach reflected what many of Andrew's clients were doing (i.e. lambing un-shepherded) while still enabling performance recording of stock to occur.

The obvious disadvantage is that because the lambing is unsupervised, you lose information on NLB (number of lambs born) relying completely on scanning results and not knowing if or why young animals perished (predation, disease etc). There is no way to accurately work out the ratio of NLB to NLW (number of lambs weaned). The other disadvantage is when working out growth rates or daily live weight gains, how do you know what day it was born?

As mentioned previously there is a gene predominately in the Texel breed, that has been shown to increase lean meat yields on a carcase. In 2005 after extensive research the gene responsible was discovered and a blood test called 'MyoMAX' was released.

Sheep identified with the MyoMAX gene tend to display increased muscling in the leg and loin, less carcase fat and an improved carcase weight compared to their contemporaries. A lamb that receives one copy of the gene will have 5% more muscling in the leg and loin and 7% less carcase fat. An animal with MyoMAX from both parents (termed a double copy) will have up to 10% more muscling and 14% less carcase fat.

In 2007 Nithdale began work to introduce the MyoMAX genes into the Romney breed to increase its attractiveness as a dual purpose animal whilst retaining the core Romney traits of high maternal ability and lowered shepherding requirements. In other words, a sheep that effectively has the all the traits traditionally bred for in the Romney with some of the meat traits of the Texel. Because all lambs were being DNA tested for parentage anyway it was only a small incremental cost to apply the MyoMAX test as well.

A MyoMax–carrying Texel was crossed with high index Romney ewes and all the progeny

Figure 9. Rams being bought in for sale

were blood tested to see who was carrying the gene. Those who were carriers were bred

back to a Romney and again the progeny was tested. The objective was to breed an animal that is 7/8th - 15/16th Romney with two copies of the MyoMAX gene.

This process was expected to take at least 17 generations as to move forward, each generation had to not only carry a copy of the gene but be tested for maternal ability, also for survival in the harsh climate and for minimal shepherding environment to ensure the cross had lost none of its maternal traits.

Since the launch of the Zoetis 50K chip in 2010, rams carrying the MyoMAX gene are routinely tested via the 50K chip. By increasing the accuracy on desirable traits, rams fulfilling the criteria can be identified much earlier in their life, meaning earlier selection of which rams to use and by being able to use them as ram lambs, you can effectively gain an extra generation of progeny from them, confident that that progeny will likely have high eBV scores in maternal traits. It also means you are less likely to use rams that are not suitable due to poor core Romney traits.

To summarise: using genomic selection to increase their eBV accuracy via the Zoetis 50K SNP has enabled the Tripps to significantly reduce the amount of time they believe they will need to fully integrate the MyoMAX gene. Superior ram lambs – thus identified – can be used much earlier in their life to speed up genetic gains and thereby take an expected 5-8 years off the process.

Summary of Section two : Genomics in action

In summary every technological advance - from the introduction of machines powered by steam, through to GM crops - has encountered sceptics. This technology is no different and it will take time to prove its influence on profit and thus gain market acceptance. Although this technology is working in the southern hemisphere there are considerable challenges to making it work in Europe and these must not be underestimated.

What would it take for the UK at large to adapt this technology

The southern hemisphere is in a very different situation to Europe with two big factors playing in their favour:

a) Having vastly fewer breeds of sheep – *the sheep in Australia and New Zealand, which are relatively young countries, were introduced from Europe, and the expense and limitations of transport space meant only a few breeds went across and even fewer survived the harsh environment.*
b) An unsubsidised farming system - *farmers are much more profit-aligned, and are only prepared to pay for equipment or genetics proven to make a difference to their cost of production. (Farming operations are usually bigger with tradition taking a back seat to profitability).*

> Unfortunately, I believe that the cost of implementing this technology is at present too high for the UK.

In the southern hemisphere genomic technology is being used to tease out an additional few percentage points in terms of performance in an industry that, from 30 years of market force is already very effective at producing meat. Consider the fact a farm on the other side of the world can produce meat, chill it, send it in a ship 12,000 miles across the ocean to us, and still sell it more

cheaply than can a farm ten miles down the road, where the meat is produced with the aid of a government subsidy.

Show ribbons, and rams whose stellar growth rates are based on additional concentrate feeding, are not a good start from which to base your flock.

I believe, unfortunately, that the cost of implementing this technology is at present too high for the UK. It would require an investment of hundreds of thousands of pounds and a willingness on the part of UK sheep farmers to adopt 4-5 common breeds of sheep. As an industry there are a lot of changes we can make that would be a much better return on our investment. The most fundamental point is that we need a shift in our thinking, show ribbons and rams whose stellar growth rates are based on additional concentrate feeding are not a good start from which to base your flock. The New Zealand industry realised this 30 years ago when commercial sheep operations started recording their own flocks and realised their genetics were far more suitable than anything they could buy in.

We also need to get away from cross breed rivalries by ensuring all sheep breeds are recorded in the same way via a simple "terminal" and "maternal" index. This would put a lot more pressure on the breeders to ensure the stock they are selling is focused more on commercial sheep breeders than the show ring.

Finally more people need to recognise the value in performance recording and make decisions for their flock based on solid scientific reasons, not on the physical appearance of the animal (provided of course it is structurally sound). Long ears, bloom dipped fleeces and baby oiled faces should not be profit drivers.

Barriers to UK/rest of world adopting existing technology

The barriers to the rest for the world using the Zoetis-derived test are considerable (note all these points will apply equally for any future Australian-based test as well).

a) The test will only give valid results for a New Zealand-derived Romney as no calibration flocks exist for any other breed or for any other countries.
b) The results have to be blended with the SIL performance recording system – no other recording system currently can handle genomic inputs.
c) As explained, the location for traits on the genes "drifts". If you want to use the test on multiple generations of animals you have to be continually using New Zealand-sourced genetics, from studs that contribute to the calibration flock.

Section Three : Implementation

Background

Having read a number of Nuffield Farming Scholarship reports I always find the "practical" reports the most interesting i.e. where information gathered from travel is applied to the Scholar's farm or business and the results are shared. Having already – on the previous pages - detailed the barriers to adopting genomic technology in the UK my own family farm business is in a very fortunate position to possibly be one of the very few farms in the northern hemisphere able to use this technology to advance our own flock.

On my arrival back from my Nuffield travels we took the decision as a family to invest a substantial amount of capital in genotyping our entire New Zealand stud ram flock on the Zoetis 50K system, as well as one possible replacement stud ram born in the UK, converting most of the farm to a gBV based system and looking for ourselves at the benefits this technology could bring our flock.

Introduction

The main factors that will dictate how quickly lambs grow and the profitability of your sheep enterprise are:

a) Environment
b) Genetics

General consensus around meat and growth traits seems to be that they are due 70% to the environment and 30% to genetics.

As explained previously our farm's environment is largely dictated to us by higher level stewardship (HLS) and entry level stewardship (ELS) requirements dictated to us by DEFRA and our landlord, so the ability to influence environment through higher yielding/more palatable rye grasses or extensive use of legumes (e.g. clover) is limited. Therefore our focus on the farm must be on improving the genetics within the flock and I believe these tests can prove a useful tool in ensuring those animals most likely to improve the bottom line are selected. Their influence over profitability will be felt in several ways:

Benefits to our flock

A. Faster genetic gain by using higher accuracy ram lambs on main recorded flock.
B. Increased accuracy for SIL traits on the ram lambs, meaning a higher degree of accuracy when culling on trait ratings.
C. More accuracy for our customers buying 2-tooth (shearling) rams – these will have gBV and the increased levels of accuracy over eBV will mean the rams are more likely to deliver on the traits they were purchased for.
D. Access to difficult-to-measure traits – although a lot of further work is needed to validate them we now have detailed data on wool and meat yields.
E. Marketing – potentially being the only flock in the northern hemisphere capable of doing this will gain us valuable exposure both for our product and for what a Nuffield Farming Scholarship can help to achieve.

Figure 12 DNA sample next to two pence piece

Although, as mentioned, the test is still somewhat in its infancy I believe it has a valuable part to play in increasing the profitability of our farm that, in the medium to long term, will more than offset the cost of carrying out the tests. The nucleus of our entire breeding programme is currently 18 New Zealand born sires. These have all had DNA samples taken. Because all the younger animals on the farm will have one of these sires as a father we can convert most of the flock straight away to a gBV-based system, and we intend to purge the older, less capable animals. The timing on this has been fortunate; at this stage of the stud's development we are maintaining an unusually young average age flock and have a very high replacement rate for our ewes. The reason for this is we have seen over the last 7 years of performance recording steady gains and improvement in the newer generations; therefore younger animals will always get preference over older animals that have a higher amount of UK genetics.

Again, linking back to the equation at the beginning of the report, by mating ewe lambs we are trying to modify the "generational interval" as well as encouraging and selecting for the maternal phenotype and getting an extra lambing out of that ewe's lifetime.

Passing down genomic information

As explained previously, during reproduction the DNA strand splits in half and the offspring gets half its DNA from the sire and half from the dam. If the sire or dam has been subjected to genotyping, then that genetic information can be used to provide their siblings with genomic breeding values as well.

The information can be passed down one generation only, i.e. the lamb will pass down eBV data only.

As mentioned we have also had our top ranked English born ram lamb from the 2012 crop tested. Although he would have had enhanced accuracies from the fact his sire was genotyped, we felt having an English born ram

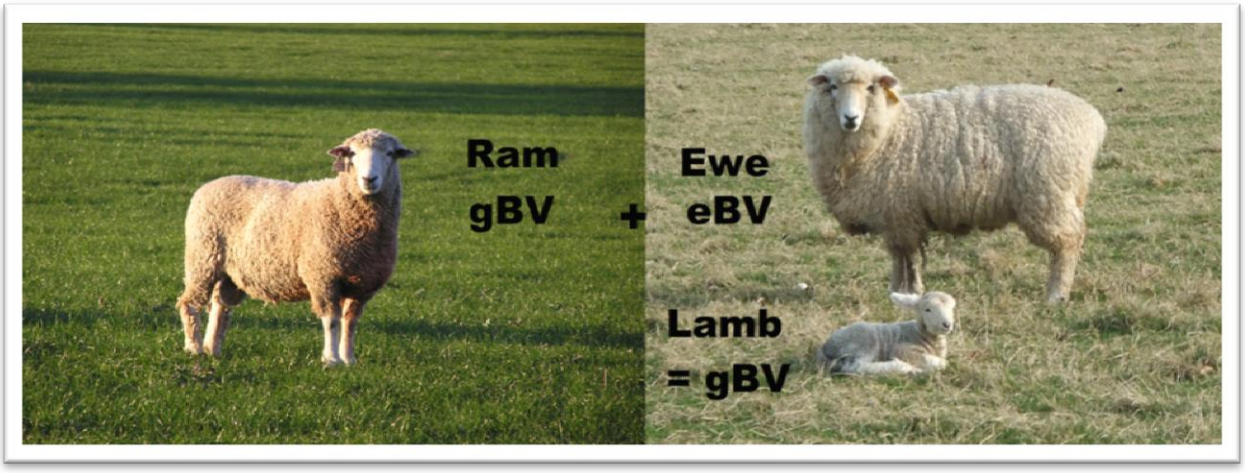


Figure 11: Creating a gBV

tested was important because:

a) He is likely to become a stud ram. UK 0263523 08147 has achieved our highest ever SIL ranking of 1517 (only around 2% of our lambs currently exceed an eBV of 1000 and is also the top ranked ram within our flock on the Signet system with a score of 340. With this potential he is being kept back from sale. We needed to have him tested so his progeny would have gBV as well.
b) Having a successful test on a UK-born ram has provided powerful proof that we have "true" New Zealand genetics on the farm. The test would only have worked if the ram has around 15/16th NZ Genetics. He is the first ever sheep born outside NZ to be given a genomic breeding value on the sheep 50K system and the results helped to ensure he will be staying on as the first English born sire in our flock's history.

Thanks to this is there will be three countries in the world currently pursuing breeding programmes using genomic information: Australia, New Zealand and the UK.

Collecting the samples

DNA samples were obtained through ear tissue samples. A German company, Caisley, provided the pliers and I acquired the ear tags from a company called Allflex whilst travelling through New Zealand. The ear tag was clipped into the ear and a sliver of ear tissue was punched through and captured in a small test tube.

Sending the samples

Samples were sent to Zoetis for analysis on the 1st March, 2013, with data being returned around six weeks later. We initially received mBV for all samples sent.

Example of data returned

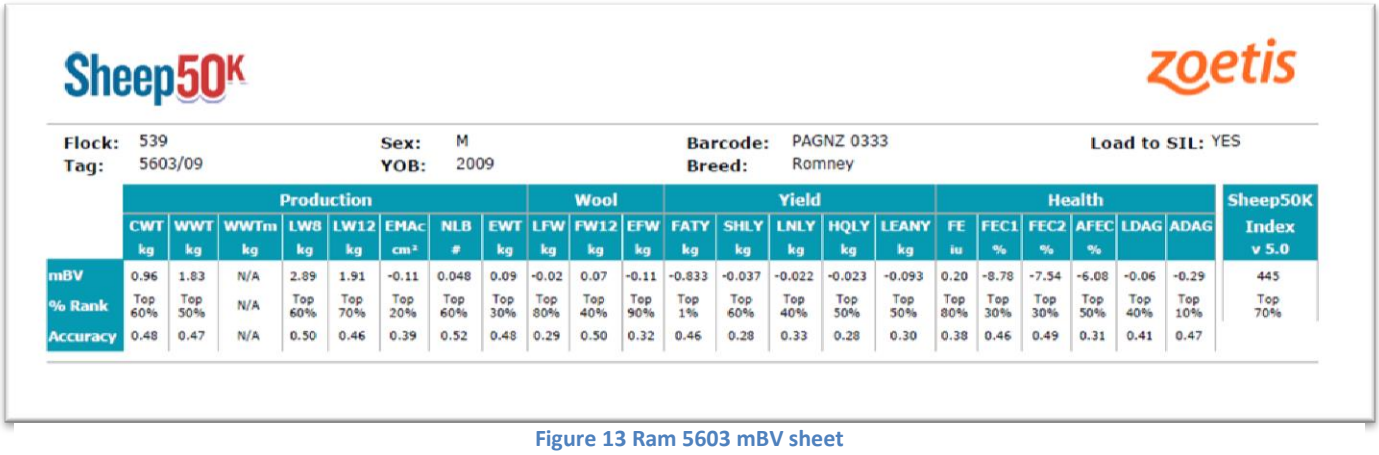
Below is the mBV set for our ram 5603 (for breakdown of abbreviations see section "The world's first commercially available SNP Chip).

The percentage rank is a cross flock analysis meaning he has been judged across every animal ever tested on the sheep 50K system.

This is a fairly low ranking animal with very low scores for wool traits and below average scores for LW8 and LW12. It does have exceptional scoring for fat yield producing a very lean carcase and could prove a useful animal for crossing with animals with high fat scores (highlighted with purple rings in the table below). Based on his indices and now his genomic ranking we will feel confident in removing him from the Stud flock, confident that there are now 'proven' better animals like 8147 coming through.

The sheet on next page shows:

a) Our flock's performance – labelled "Customer Job mBVs - (min, average, max)"
b) The breed average mBV (min, average, max)

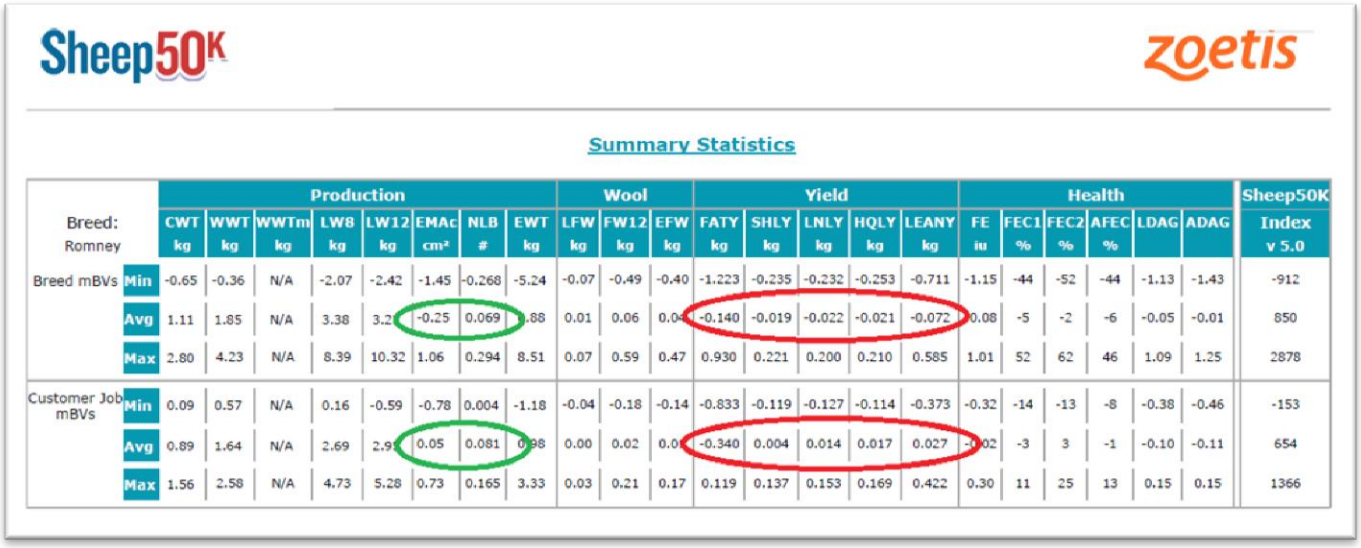


Sheep50K zoetis

Flock: 539 Sex: M Barcode: PAGNZ 0333 Load to SIL: YES
Tag: 5603/09 YOB: 2009 Breed: Romney

	Production								Wool			Yield					Health						Sheep50K
	CWT kg	WWT kg	WWTm kg	LW8 kg	LW12 kg	EMAc cm²	NLB #	EWT kg	LFW kg	FW12 kg	EFW kg	FATY kg	SHLY kg	LNLY kg	HQLY kg	LEANY kg	FE iu	FEC1 %	FEC2 %	AFEC %	LDAG	ADAG	Index v 5.0
mBV	0.96	1.83	N/A	2.89	1.91	-0.11	0.048	0.09	-0.02	0.07	-0.11	-0.833	-0.037	-0.022	-0.023	-0.093	0.20	-8.78	-7.54	-6.08	-0.06	-0.29	445
% Rank	Top 60%	Top 50%	N/A	Top 60%	Top 70%	Top 20%	Top 60%	Top 30%	Top 80%	Top 40%	Top 90%	Top 1%	Top 60%	Top 40%	Top 50%	Top 50%	Top 80%	Top 30%	Top 30%	Top 50%	Top 40%	Top 10%	Top 70%
Accuracy	0.48	0.47	N/A	0.50	0.46	0.39	0.52	0.48	0.29	0.50	0.32	0.46	0.28	0.33	0.28	0.30	0.38	0.46	0.49	0.31	0.41	0.47	

Figure 13 Ram 5603 mBV sheet



Sheep50K zoetis

Summary Statistics

Breed: Romney		Production								Wool			Yield					Health						Sheep50K
		CWT kg	WWT kg	WWTm kg	LW8 kg	LW12 kg	EMAc cm²	NLB #	EWT kg	LFW kg	FW12 kg	EFW kg	FATY kg	SHLY kg	LNLY kg	HQLY kg	LEANY kg	FE iu	FEC1 %	FEC2 %	AFEC %	LDAG	ADAG	Index v 5.0
Breed mBVs	Min	-0.65	-0.36	N/A	-2.07	-2.42	-1.45	-0.268	-5.24	-0.07	-0.49	-0.40	-1.223	-0.235	-0.232	-0.253	-0.711	-1.15	-44	-52	-44	-1.13	-1.43	-912
	Avg	1.11	1.85	N/A	3.38	3.2	-0.25	0.069	1.88	0.01	0.06	0.0	-0.140	-0.019	-0.022	-0.021	-0.072	0.08	-5	-2	-6	-0.05	-0.01	850
	Max	2.80	4.23	N/A	8.39	10.32	1.06	0.294	8.51	0.07	0.59	0.47	0.930	0.221	0.200	0.210	0.585	1.01	52	62	46	1.09	1.25	2878
Customer Job mBVs	Min	0.09	0.57	N/A	0.16	-0.59	-0.78	0.004	-1.18	-0.04	-0.18	-0.14	-0.833	-0.119	-0.127	-0.114	-0.373	-0.32	-14	-13	-8	-0.38	-0.46	-153
	Avg	0.89	1.64	N/A	2.69	2.9	0.05	0.081	0.98	0.00	0.02	0.0	-0.340	0.004	0.014	0.017	0.027	-0.02	-3	3	-1	-0.10	-0.11	654
	Max	1.56	2.58	N/A	4.73	5.28	0.73	0.165	3.33	0.03	0.21	0.17	0.119	0.137	0.153	0.169	0.422	0.30	11	25	13	0.15	0.15	1366

Figure 14: WairereUK flock average and breed overall average

The breed mBV is a record of every Romney animal ever tested on the system. Comparing the two average rows it is pleasing to note the highlighted areas showing (*in green)* that for eye muscle area and number of lambs born we are significantly above the New Zealand average values and showing *(in red)* meat yield is above average as well. Our overall index average value is lower, but this does give us an excellent starting point for how well our flock is currently performing and helps to provide a roadmap of the areas where we need to strengthen our selection criteria to ensure we are delivering a world class Romney animal.

We shall start to correct for lower scorings in our 2013 joinings and in future genetics bought across from New Zealand.

Section Four: Data verification of genomics

Introduction

I thought it was important at this point to do some study work on the results received back from Zoetis on the ram's likely performance. It is worth repeating that, because this is just mBV data, Zoetis themselves caution against making any judgments on this alone without blending with eBV and producing gBV.

Nevertheless, I feel it's a useful first step to look at just how closely mBVs tie up with real world data before studying gBVs. This is a validation *on our flock only* and is in no way an attempt to build or detract from the detailed work and research AgResearch and Zoetis have done. It is simply what is being observed in our own flock.

Points to note:

As stated, 70% of the ewe's potential is influenced by the environment. This can very effectively hide genetic effects.

Data is from one year only as eleven of the stud rams only arrived in 2011 and so we have no Signet information. As more year-on-year data becomes available more accurate analysis can occur. Below is a table of data we have available at this present time for analysis.

The rams from New Zealand have been selected for over 60 generations on key performance traits and so, unlike a wild population where we would expect to see large differences between the top and bottom, in such a controlled population the difference between a high and low eBV animal will be small.

I have tried to show this in the graph at the top of the next page; this is what we would expect to see when comparing data between a high mBV ram and a low mBV ram. You would expect to see the sire's offspring producing a naturally distributed curve around that trait (assuming a random population of females), as per figure 15.

	SiL eBV	SiL mBV	SiL gBV	Signet eBV
Stud sires (Inc. replacements)	✓	✓	✓	✓
2012 born lamb crop	✓	✓	✓	✓
2013 lamb crop	× (due soon)	× (due soon)	× (due soon)	× (due soon)
Recorded dams	✓	✓	× (due soon)	✓
Commercial unrecorded flock	×	×	×	×

Table of data available for analysis from our own flock

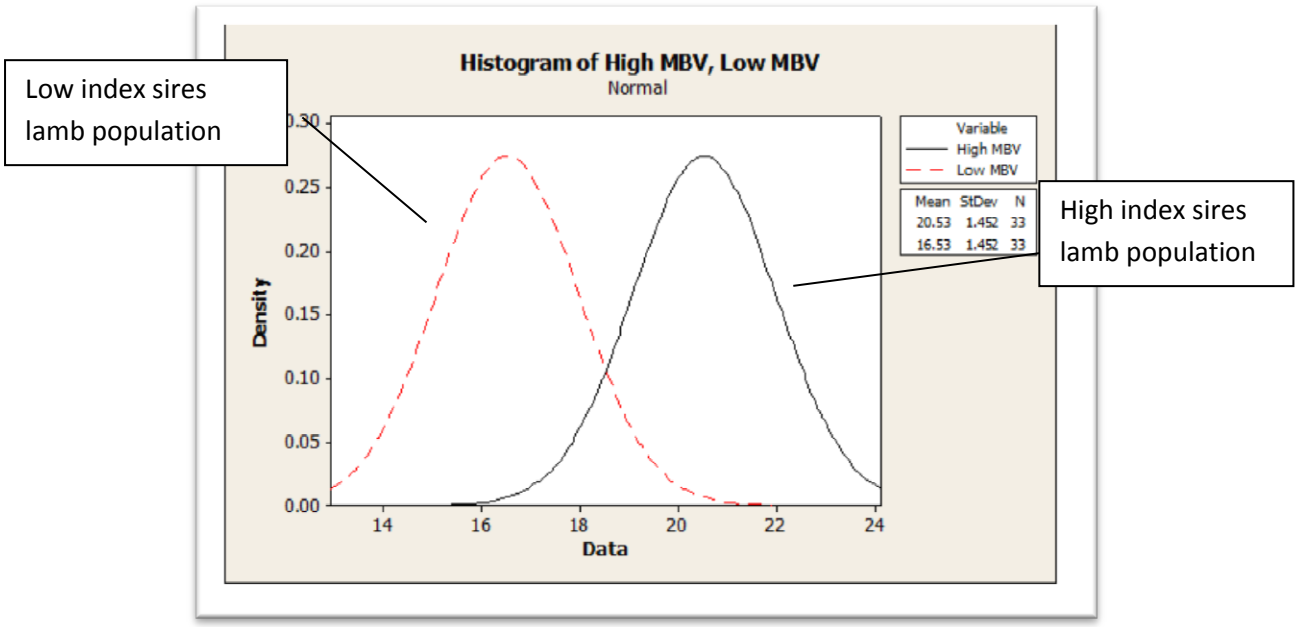


Figure 15: Two populations of lambs from 2 different sires

You only keep back for breeding rams at the top end of your population ensuring only the best genetics go forward for breeding (figure 16).

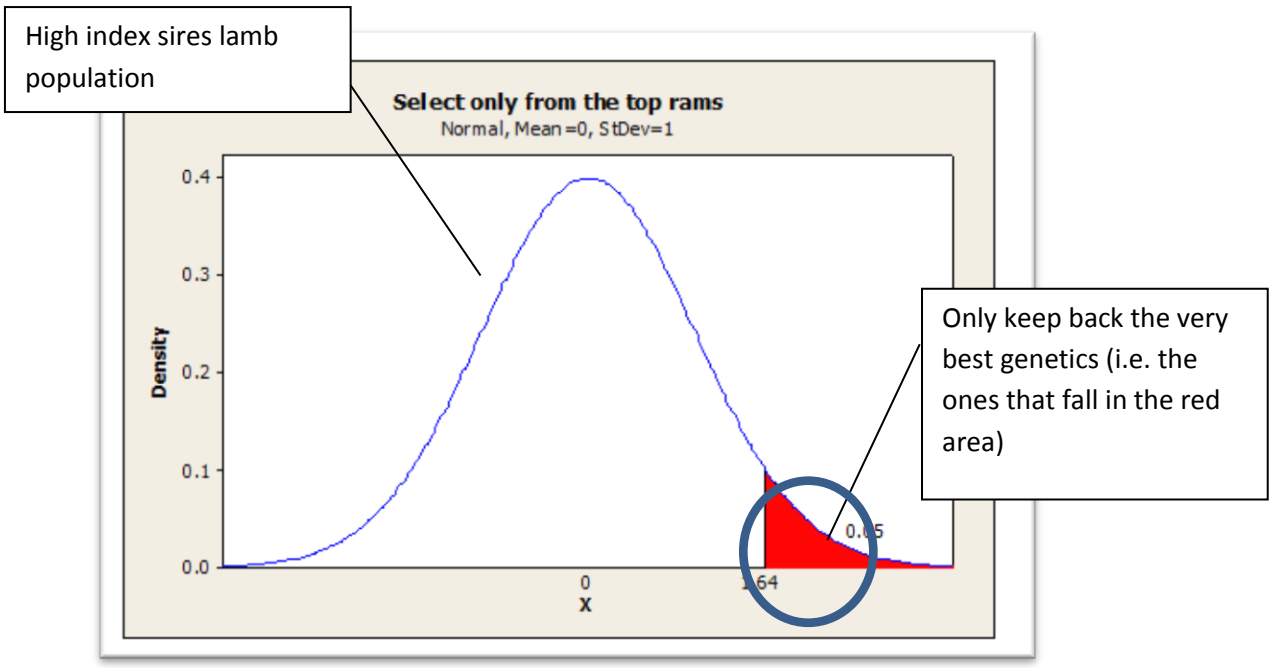


Figure 16. Only select animals from the top % of the higgest ranking sire

Over time, by actively selecting only superior genetics, the red curve shifts right. How quickly this shift occurs can be modelled by the equation given at the beginning of this report. Higher accuracy or greater population numbers will mean the red curve moves more quickly.

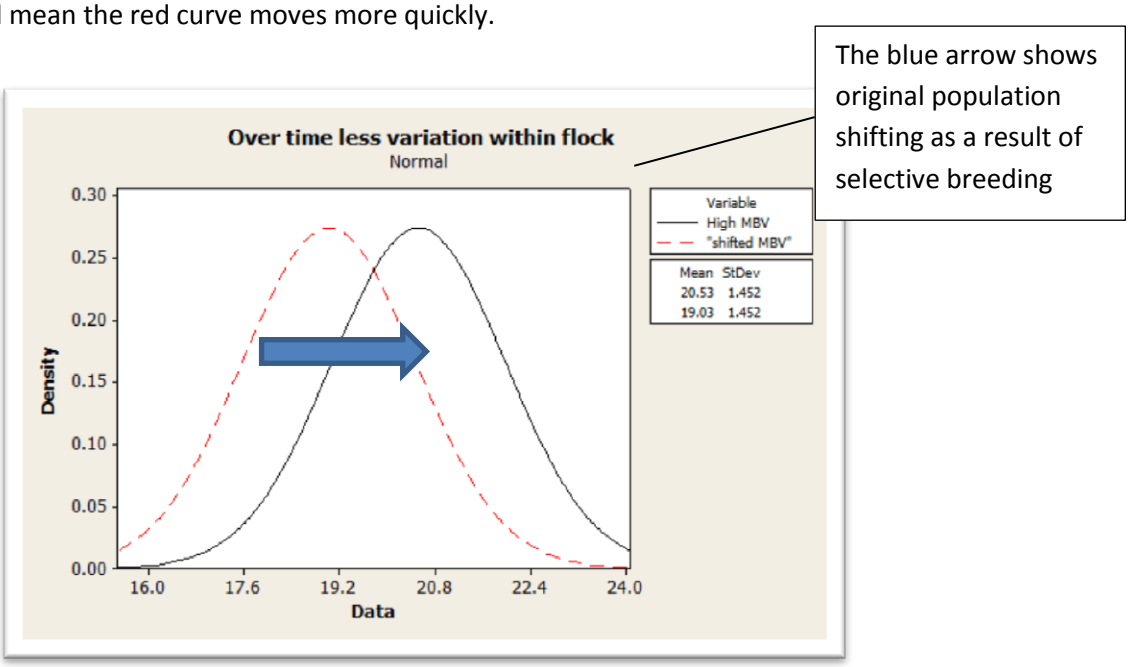


Figure 17: Over time low scores are culled out and the population curve moves right

If your breeding programme is successful the difference between your best and worst animals will decrease to a point where the population curves are very close together (figure 17).

On the next page is real data from our flock showing two populations of lambs' weaning weights (WWT) with our very best mBV score (2947) and our very worst scoring sire (3873) respectively note that 60 years of selective breeding in NZ has meant there is a small difference in the worst and best animals for WWT (figure 18).

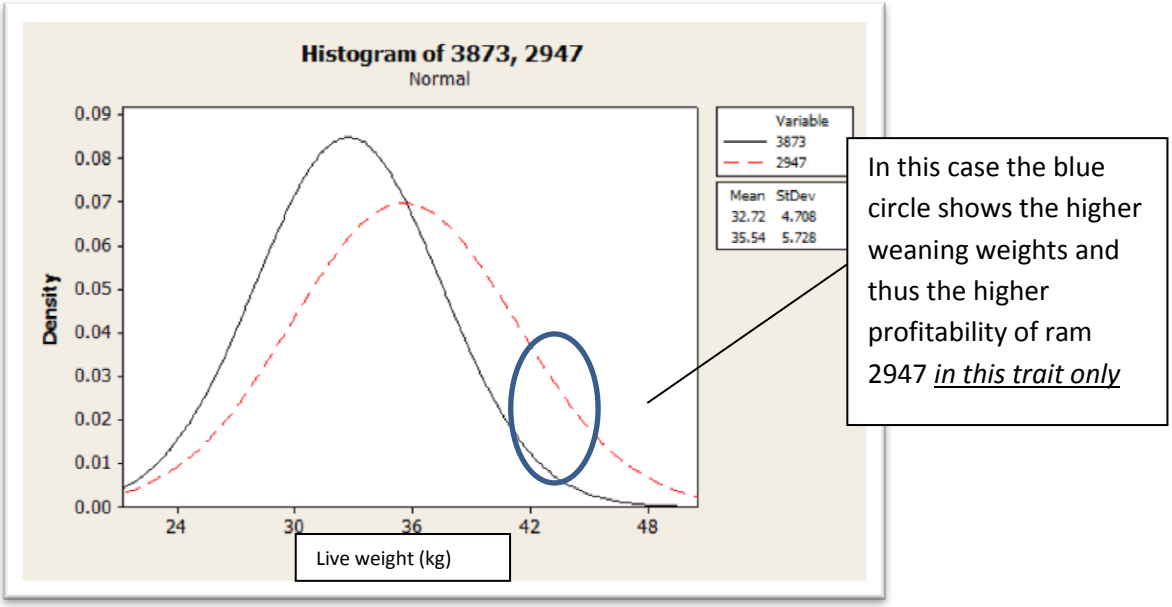


Figure 18: Weaning weights from lamb population of best and worst sires

It is important to take a broad view and not chase single traits. The danger in this example would be the better ram could (although I hasten to add hasn't!) have a lower NLB rating and thus be siring more singles that, with less competition for milk, would naturally grow faster.

To mention again something stated in Section 3 (the importance of eBV): even a small difference in eBV can make a big impact on your bottom line so everything we can do to increase the eBV is maximising the return you get from an investment in your genetics.

MBV Weaning weight

Weaning weight is the term given to the weight of the animals measured at around 100-120 days, a typical time frame for weaning. The raw data is normalised by working out their exact age, looking at their daily live weight gain, and adjusting the real "weighed" value to a date range common across the whole flock (in this example 100 days).

So if an animal weighs 40kg at 120 days - meaning a live weight gain of about 300g per day - its 100 day normalised value therefore is (100 x 0.3g) = 33.3 kg

The plot of best mBV versus worst mBV weaning weight was shown in the introduction to the data verification section and so I don't propose to repeat it. Instead the next plot compares the mean average distribution of weaning weight between the two extreme rams. The graph shows a clear difference between the two sets of animals, with the higher mBV animals having a higher average weaning weight on their lambs (32.48kg versus 34.77kg) and, as shown by the curve, a higher proportion of their overall lambs in the higher end of the spectrum.

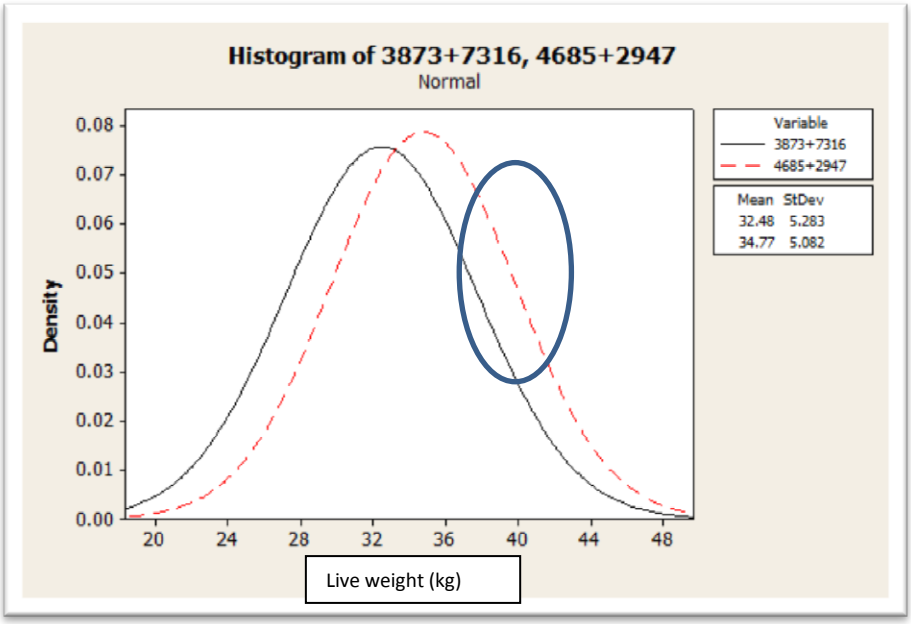


Figure 19: Natural distribution curve of progeny weaning weight comparing high and low mBV rams

Summary of graph indications

Graph title: natural distribution curve of progeny weaning weight comparing high and low mBV rams

Graph X,Y axis: Frequency of Progeny weaning weight versus weaning weight

What this graph is telling us: For this trait high mBV values for WWT seem to match with higher actual weaning weights

MBV LW8

LW8 means liveweight at 8 months and the data was collected from female lambs only and was taken to determine suitability for ewe lamb mating. If the animal weighed over 40kg she was put into a mating group. Because each animal was weighed several times the data was normalised using average liveweight gain to adjust every animal's weight to a standard time period (in this example 240 days old).

The black line denotes the worst two rams (in pure genomics) and the red line denotes the best two rams. It shows that a higher mBV in this case produces a narrower range of animals that have a high concentration around the mean and a decreased number of animals in the lower weight range.

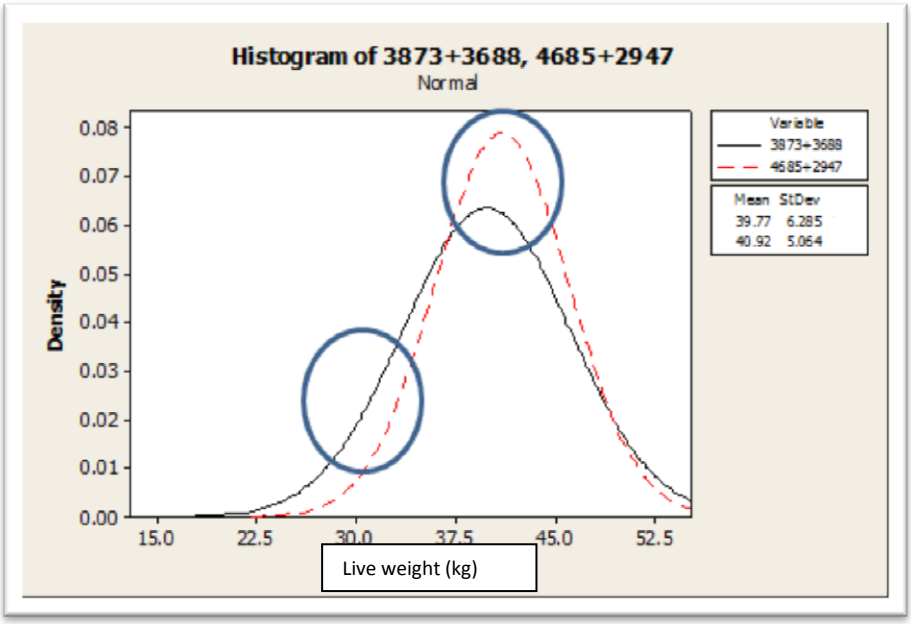


Figure 20. Natural distribution curve of progeny LW8 weight comparing high and low mBV rams

Summary of graph indications

Graph title: Natural distribution curve of progeny LW8 weight comparing high and low mBV rams

Graph X,Y axis: Frequency of Progeny weaning weight versus 8 month weight

What this graph is telling us: For this trait high mBV values for LW8 mean less lower weight animals and a smaller spread with more animals concentrated around the mean value.

Overall mBV value Vs Overall eBV value

To look at this data in a slightly different way we can use a scatter graph to plot each ram's SIL eBV Vs mBV i.e. data recorded from the flock over many years and subjected to BLUP analysis (the red line), mBV prediction of that animals performance (the black line), versus average progeny LW8 weight. This shows an interesting fact: that both eBV and mBV predict the performance of two rams in the green circle quite closely yet both track well away from those rams' actual performances: the top point underperforming and the bottom point massively over performing.

The only explanation I can give is differing environmental factors, access to grass etc. Unfortunately we don't keep enough detailed records to determine where those lambs were and in what groups they were in, and that is a lesson to be learnt for next year's crop.

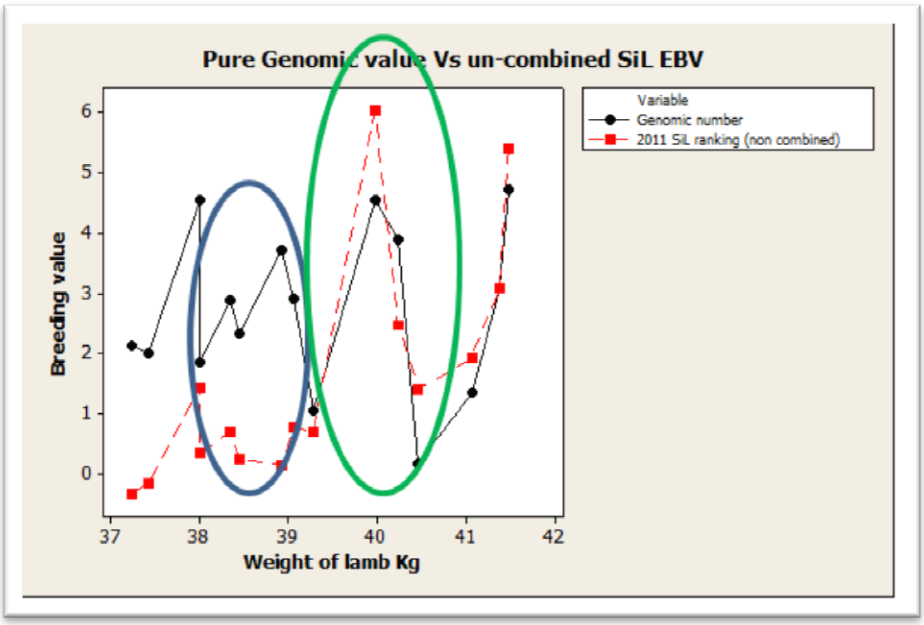


Figure 21. Scatterplot of SIL eBV of rams (Black line) and gBV (Red line) plotted against the average progeny LW8 weights

Summary of the graph's indications

Graph title: Scatterplot of SIL eBV of rams (Black line) and gBV (Red line) plotted against the average progeny LW8 weights.

Graph X,Y axis: eBV and mBV of rams Vs average progeny LW8 weights.

What this graph is telling us: mBV and eBV data correspond closely before being combined into gBV, the SIL data has been collected over the last 7 years of recording and before that combined with the rams history before he left NZ.

mBV Lamb dagginess (LDAG)

Figure 22: Cull lamb suffering Dagginess

This data was taken from the 2013 lamb crop when they were brought in for EID tagging and 8 week weight. A record was kept of any lambs that had “dags.” The plot below shows the number of lambs and who the sire was.

The sires are arranged by mBV (1373 having the worst score).

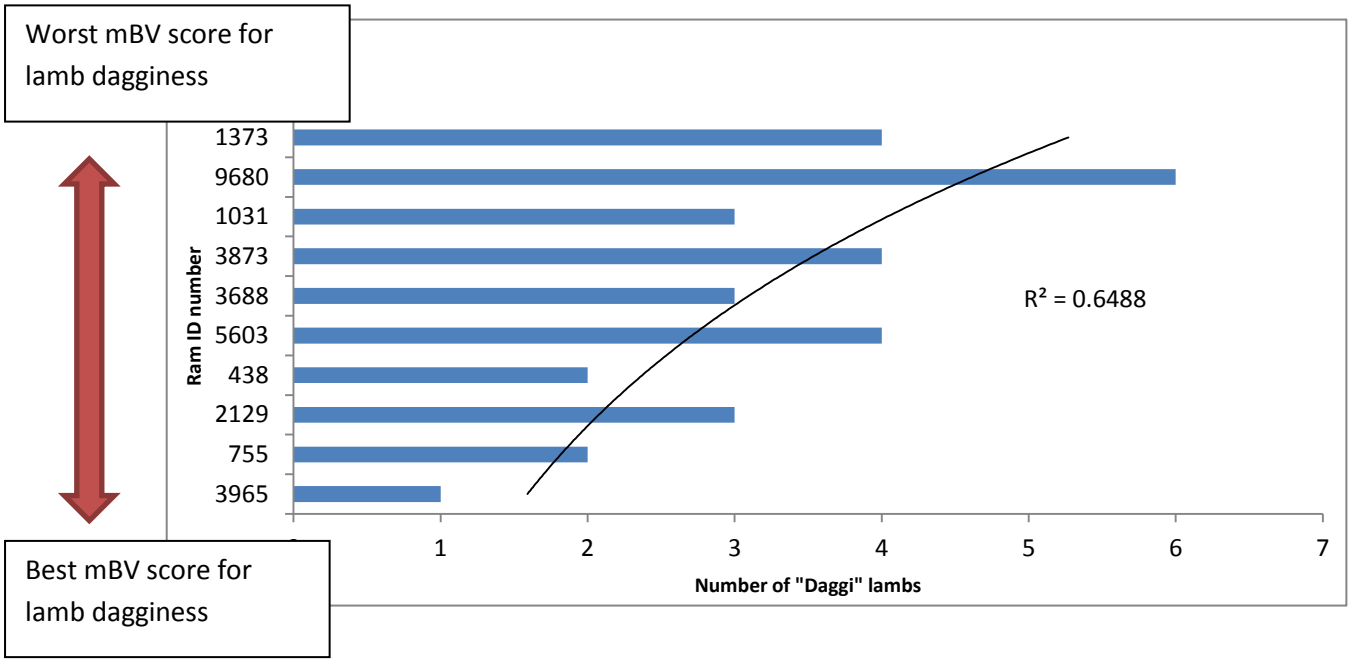


Figure 23: Bar chart showing number of Daggy lambs

Graph title: Bar chart showing number of Daggy lambs

Graph X,Y axis: Number of daggy lambs versus Ram ID number arranged by mBV score

What this graph is telling us: mBV score show a strong correlation with the number of dirty lambs.

GBV, mBV and raw data comparisons

At this point I am aware of a comment made about report writing that states your readership drops by half with every equation and graph you include!

I have tried to keep graphs to a minimum and hopefully it can be seen that, although genomics is not accurate enough by itself to be a reliable predictor of performance, I do feel - and hopefully have proven - that it will predict "bad" "good" and "excellent" animals. With the best animals always outperforming the worst animals I am also aware that showing data from a few traits out of the 22 being predicted is in no way conclusive proof but hopefully you can understand my reasoning – I would like to have a few readers left at the end of this report!

Where this technology will really make a difference is with this data being combined with eBV data to allow higher than average accuracies. What I propose to do now is plot raw data versus gBV versus Signet data (eBV) for each animal. Because SIL gBV are made up from SIL eBV, plotting one against the other would not reveal a great deal. Comparing gBV to an entirely unrelated data set measuring the same trait seemed to make sense. Being Signet recorded we are in the fortunate position that we have a completely independent data set we can measure against. (Although Signet and SIL do not use the same equations to calculate their eBV).

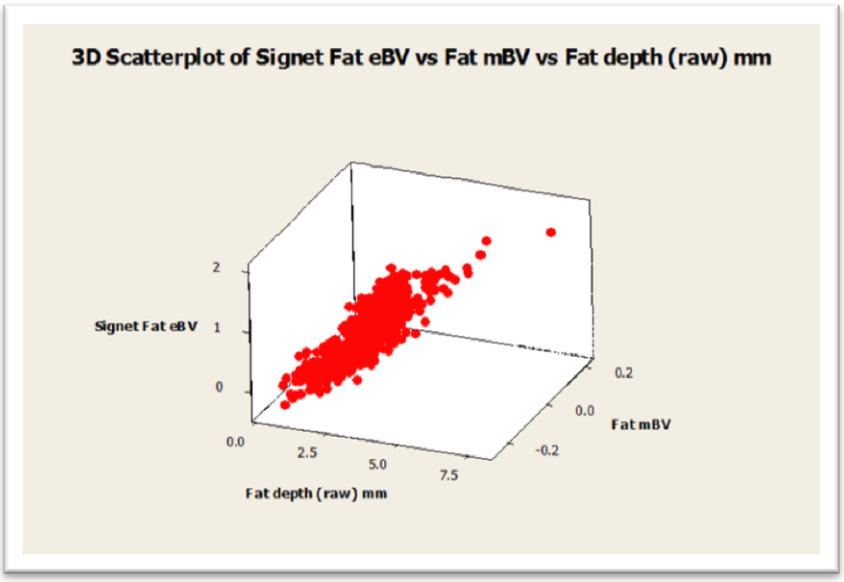


Figure 24: Signet eBV Vs Genomic mBV versus raw fat depth

Summary of graph's indications

Graph title: Signet eBV Vs Genomic mBV versus raw fat depth

Graph X,Y,Z axis: Signet eBV versus Genomic mBV versus raw fat depth

What this is graph is telling us: The reasonably straight line cut through three dimensional space show low fat depth, low Signet eBV and low mBV are correlated this is continued throughout the range of fat depth.

Figure 25: The eye muscle

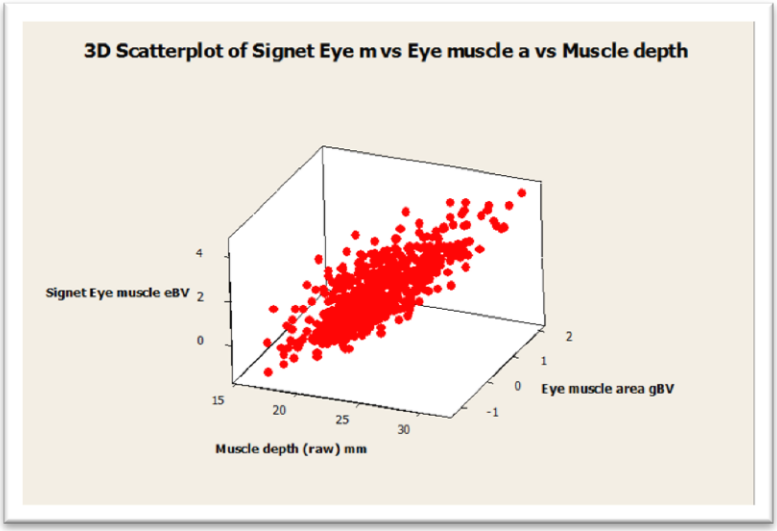


Figure 26: Eye muscle - Signet eBV versus SIL gBV versus actual muscle depth

Summary of graph's indications

Graph title: Eye muscle - Signet eBV versus SIL gBV versus actual muscle depth

Graph X,Y,Z axis : actual muscle depth (mm), SIL gBV, signet eBV

What this graph is telling us A wider spread of data between the combined SIL eBV and mBV vs the signet data shows a less commonality between the 3 sets of data (when compared to raw muscle depth in mm)

Figure 27: Back fat/eye muscle scanning 2013 born WairereUK rams

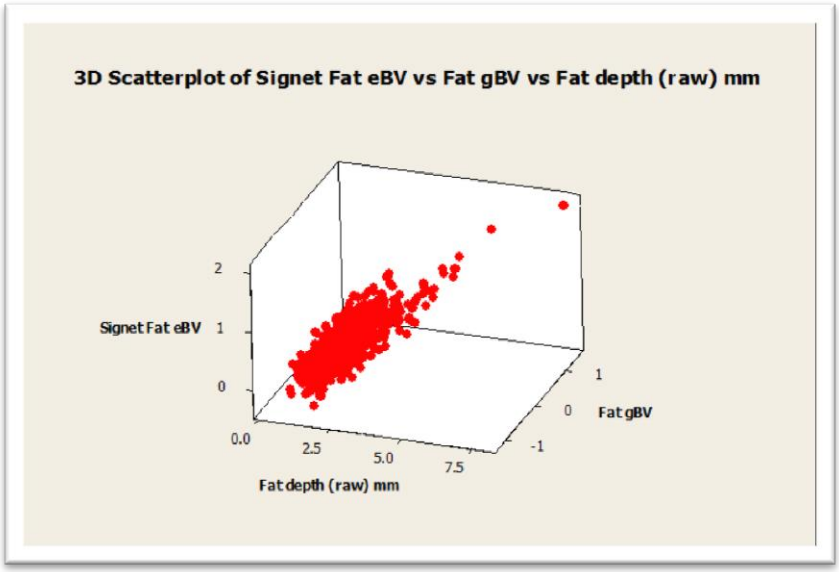


Figure 28: Signet eBV versus SIL gBV versus actual fat depth

Summary of graph's indications

Graph title: Fat - Signet eBV versus SIL gBV versus actual fat depth

Graph X,Y,Z axis : actual fat depth (mm), SIL gBV, signet eBV

What this graph is telling us The trend of the graph does show that the results match up well, this can be shown particularly well by the outlining data point that has a high fat depth, a high signet eBV and a high SIL gBV

Section Five: Conclusions

1. Although genomics is well established in the pig, dairy and poultry sectors as an accepted way to ensure only the best of the breed go forward, until recently the sheep industry has lagged behind.

2. Advancements in regard to the sheep industry have hitherto been limited to Australia and New Zealand. Europe is hampered by its large number of different breeds and further disadvantaged by the distortion effected by the subsidy system.

3. Initial test work shows correlation between genomics and traditional recording but further research is needed.

4. Care must be taken not to overstate the benefits of genomics until there is a level of evidence that stands up to scrutiny.

5. The technology offers the opportunity to use a Romney in an accelerated breeding programme to produce stabilised crosses.

6. My own business will continue to use both SIL and Signet systems both for recording animals and for proving genomic selection.

Commentary on my Conclusions

Genomics will be a focus for us in the future and is something we will continue to work with as another tool in the toolbox to improve the flock. We need to be very careful not to overstate its benefits and be extremely cautious about inferring anything from the gBV until we have a level of evidence that stands up to scrutiny. We can be confident that the gBV also have measured data in them - like NLB or weight - are likely to be good to use, as the measured data will counteract any erroneous mBV results.

My concerns are still very much with gBV where no previous data exists. We will be very careful for example in using the FEC (faecal egg count) results until we have some on farm data to show that they are accurate. We are very pleased with the closeness of the results for lamb dagginess, although only a small number of lambs were found with the condition and further work year on year, will be needed before we are confident enough to start actively promoting those results.

We will continue to use both the SIL and Signet system for recording animals. We are faced with the problem that, because the two systems do not recognise each other, top genetics with outstanding SIL scores can be brought across; but when entered into the Signet system they have to start from a very low base line and "prove" themselves over several generations. It takes a lot of time and with the costs involved, time is always at a

premium. We cannot afford to discount entire generations of lambs waiting for the Signet system to reflect the sire's true genetic potential.

Although the SIL system does give more data and allows us to take advantage of the many years of recording already carried out in New Zealand, using Signet means we can keep abreast of the situation in the UK. Because some of our stud animals have been in the country for a long time the Signet scores are becoming more aligned with what we think they should be. As time goes forward - and we import less stock and breed in-house replacement stud animals - this will become less of a problem.

If we wish to continue to use genomics we will have to import genetics from NZ to ensure our flock remains calibrated to the reference population. The plan we have is - rather than live import - we may start going down the route of importing semen. Now the NZ genetic base in the flock is so high, we no longer need so many live rams to cover such a high number of ewes. Zoetis's recommendation was to aim to bring in 100 straws of semen every 2-3 years. With these importations we can also target those traits on which we are weak.

We will be getting back the initial SIL and Signet figures for the 2013 crop of animals in the next couple of months; we have an option of selecting one or two rams on which to run the 50K test with a view to single sire mating them as ram lambs. Our initial assessment is that we probably won't do this with the 2013 crop unless a very high index animal appears – we already have a high number of sires on the farm and we already have 8147 who will be single sire mated this year. Although because of regulatory hurdles it is not presently possible, our long term goal would be to send semen from it - or another animal born in the UK - back to NZ to be tested there to truly validate our breeding programme as producing Romneys that are as good as any found in NZ.

As explained before, because of the amount of new genetics we have bought in year on year from New Zealand, we will rely on SIL figures to base our own breeding decisions on. I believe there is no reason why we could not harmonise the two recording systems - we have huge amounts of data now for both SIL and Signet values on the same animal. In-house analysis has already confirmed strong correlations between the two systems (which is to be expected) which we would happily make available should SiL/Signet choose.

But this does bring us to an interesting point. That is: what information do you provide to your ram buying customers? Since starting this project we effectively have three sets of information for each animal born. Whereas we have traditionally recorded and priced rams based on Signet figures we now have (we believe) more accurate SIL eBV for them as well as SIL based gBV. In total we have around 40-50 individual breeding traits which are likely to lead to extreme customer confusion. I personally believe we need to display between five and ten breeding values for the customer and over the next months I will be in contact with several of our past customers to understand what breeding values are the key drivers for their business.

> It would be interesting to carry out research on how far we can dilute the percentage of NZ genetics before the test becomes meaningless.

The final conclusion is that this technology does offer the opportunity to use a Romney in a breeding programme to start to produce stabilised crosses - like the New Zealand Perendale or Coopworth - in a more reduced time frame than has traditionally been possible. In 2013 the 50K chip is being expanded to cover "Tefroms", a stabilised hybrid of NZ Texel, Romney and NZ Finn. I have not covered this possibility in detail as a very good report by Sam Boon on hybrids can be found in the Nuffield Farming Scholarships Archives[1] entitled: "The opportunity for composite flocks within the UK sheep industry." If anyone is thinking along these lines it is an excellent guide on making the most out of hybrid vigour.

Potential criticisms

A) Is this GM food?

There is nothing we are doing with this technology that you could not do with a pen and paper, good physical measurements and a lot of time. Selective breeding has been going on for centuries and virtually every domesticated population has traits that are very skewed from where natural selection would have them. Selective breeding applies to virtually every food source we consume - from beef to apples to grain. So I do not foresee any problems with this.

B) How can we apply this project to UK-derived sheep?

As we have shown, this test can work on New Zealand Romney flocks based in Europe. In New Zealand this test can also be used on populations that contain only a percentage of Romney genetics. It would be interesting to carry out research on how far we can dilute the percentage of NZ genetics before the test becomes meaningless. My guess would be you would need around 50% NZ genetics. This work would have benefits for the wider Romney community as well as for people trying to emulate well known composite flocks from NZ - like Perindales and Coopworths.

Perendale

A future possible work stream I have thought about is collaborating with people like the North Country Cheviot Breeding Society, or an interested lone breeder, to work at stabilising the cross and using genomics to accelerate that process.

English Romney

Try using higher accuracy rams to target key traits that traditionally have been viewed as less important in the native population. The higher wool price in NZ has led to much development work for this trait. With the increasing wool price in the UK we can use this work to maximise the value of this by-product.

Coopworth

There is also the possibility of collaborating with people like the Border Leicester Breeding Society, or an interested lone breeder, to work at stabilising the cross and using genomics to accelerate that process.

Texel

There is a stabilised hybrid of East Friesan, Romney and Texel called a "TEFROM". Again, should a European flock choice go down this route, genomics should help get them there a lot faster.

[1] This is a 2005 report and anyone interested in obtaining a copy would need to contact the Nuffield Farming Scholarships director, Mike Vacher. director@nuffieldscholar.org.
More recent Nuffield Farming reports can be seen on http://www.nuffieldinternational.org/reports/index.php

C) Cost effectiveness – what price should we put on increased accuracy?

This is a difficult question to answer and will vary depending on the farm. A breeder who is chasing a particular goal or trait and who has the ability to potentially sire an additional 80-100 ewes by using a ram lamb, would view the investment very worthwhile. Depending on the number of rams chosen it would only mean a unit increase in cost-of-production of around £3-£6 per ewe. You would also get the benefit of gBVs for the offspring as well – further accelerating your progress in genetic gain.

D) Differences in parasites between NZ and UK?

This is a good question with Dr Joanna Connington from SRUC having done work to prove resistance to one country's worms does not necessary mean resistance to another country's worms. However it is important to note the difference between resistance and resilience, i.e. sheep can have a high worm burden but still thrive. Resilience to worms may be transferable between countries as, although there are many species of worms, they operate or attack in similar ways.

Man's best friend

Recommendations

1. **Prove on-farm phenotypes:**

   a) Detailed measurements in wool weights and quality to verify mBV – approach British Wool Marketing Board, and maybe get a grader on-site during shearing to take measurements as wool is removed, or get analysis done on individual fleeces.

   b) Take bottom twenty and top twenty lambs for worm resistance and put them together in the same field. Measure weekly live weight gain and dagginess under a minimal/non-existent drench routine.

   c) CT scanning of lambs to prove meat yield data and carcase weight gBV.

2. **Promote the work done to a wider audience**

   a) Work closely with interested parties to align SiL and Signet scoring to allow easy passage and introduction of high value foreign genetics into flocks.

   b) Engage with breeding societies to see if a joint programme of stabilised hybrids holds any merit or interest.

   c) Continue to promote eBV as an essential part of any breeding programme.

After my Study tour

Having returned from my study it is clear to me that genomics will play an important part in sheep breeding in the next 20 years. You only need to look at the increase in productivity that the chicken and pig industries have achieved to understand the power and benefits in profitability that this technology can bring. I can also see that early adopters of this technology are going to reap the benefits by having a 10-15 years head start on the rest of the industry - in the same way that long time adopters of eBV have seen huge genetic gains in their flocks.

On a wider note my Nuffield Farming Scholarship has also opened my mind to the opportunities that farming has to offer. With a young father and two brothers all wanting to get into sheep farming, succession on the family farm has always been a little bit of an elephant in the room with the problem being acknowledged but no real actions put in place.

Having seen multiplier flocks in New Zealand operate has really made me realise you can operate the same farm over multiple sites even across fairly long distances. The advantages of this are that as a business, you can "experiment" in-house with selective breeding without affecting the products you offer to your customers. So it is with great excitement that I am preparing to start my own sister unit in North Hertfordshire to enable WairereUK to experiment with several ideas we have to improve the flock genetics and thus the products we offer to our customers. With different environmental factors it will also be a good indication of how our different blood-lines cope with varying environmental stresses.

It is absolutely due to the Nuffield Farming Scholarship experience that I have had the confidence to approach our succession problem head on. Without being exposed to the very best of the farming industry I believe I never would have had gained that self-belief that enables such radical decisions to be made.

Also if anyone does have blocks of grassland in the North Hertfordshire/Cambridge border area I would love to hear from you!! I can promise some very interesting and fairly advanced animals that would make very good use of it.

Rob Hodgkins

Mob: 07747 623124
Nuffield Farming Scholarship reports can be seen: www.nuffieldinternational.org/reports/index.php
More information on Rob's flock can be found at www.wairereuk.com

The main farm address:
Locks Farm
Washington
Pulborough, West Sussex. RH20 4AA

Multiplier farm address:
Lower Heath Farm
Odsey
Royston, Hertfordshire. SG7 6SE

Full details of the Zoetis 50K system can be found on the New Zealand section of the Zoetis website. The test is not currently supported by Zoetis UK, and there is no intention for that position to change.

Glossary

2 tooth = Animal that has broken its second teeth – also known as yearling, gimmer etc

BLUP = Best Linear Unbiased Prediction

BV = breeding value – the true breeding value of the animal – what all performance recording attempts to find out

Dagginess = How "dirty" at the back end an animal is

Dam = Mother (ewe)

eBV = estimated breeding value - traditional breeding value based on measurements taken on whole flocks and combined via BLUP.

FEC = faecal egg count

LW8 = lamb weight at 8 months

gBV = Genomic Breeding Value - a combination of eBV and mBV designed to give more accurate results earlier on in the animal's lifecycle (eBV + mBV = gBV)

Genomics = using DNA sampling to advance a breeding programme through identification of genes.

mBV = Molecular breeding value - breeding values taken solely from the DNA of the animal, by identifying key genes responsible for desirable traits.

Phenotype = would be a "trait" for example growth rates

SiL = NZ based recording system

Signet = UK based recording system

Sire = Father (ram)

Weaning weight = weight at the point a lamb is removed from its mother.

Acknowledgements and thanks

I am extremely grateful to so many people who helped me through my travels - from the many Nuffield Farming Scholars who generously gave up their time and spare bedrooms (listed in the second Appendix, two pages further on) through to the educational institutions who spent a long time explaining highly technical material to a very simple shepherd from the other side of the world.

A big thank to my family who quite happily covered while I was away and who have been so excited and supportive about the new business venture.

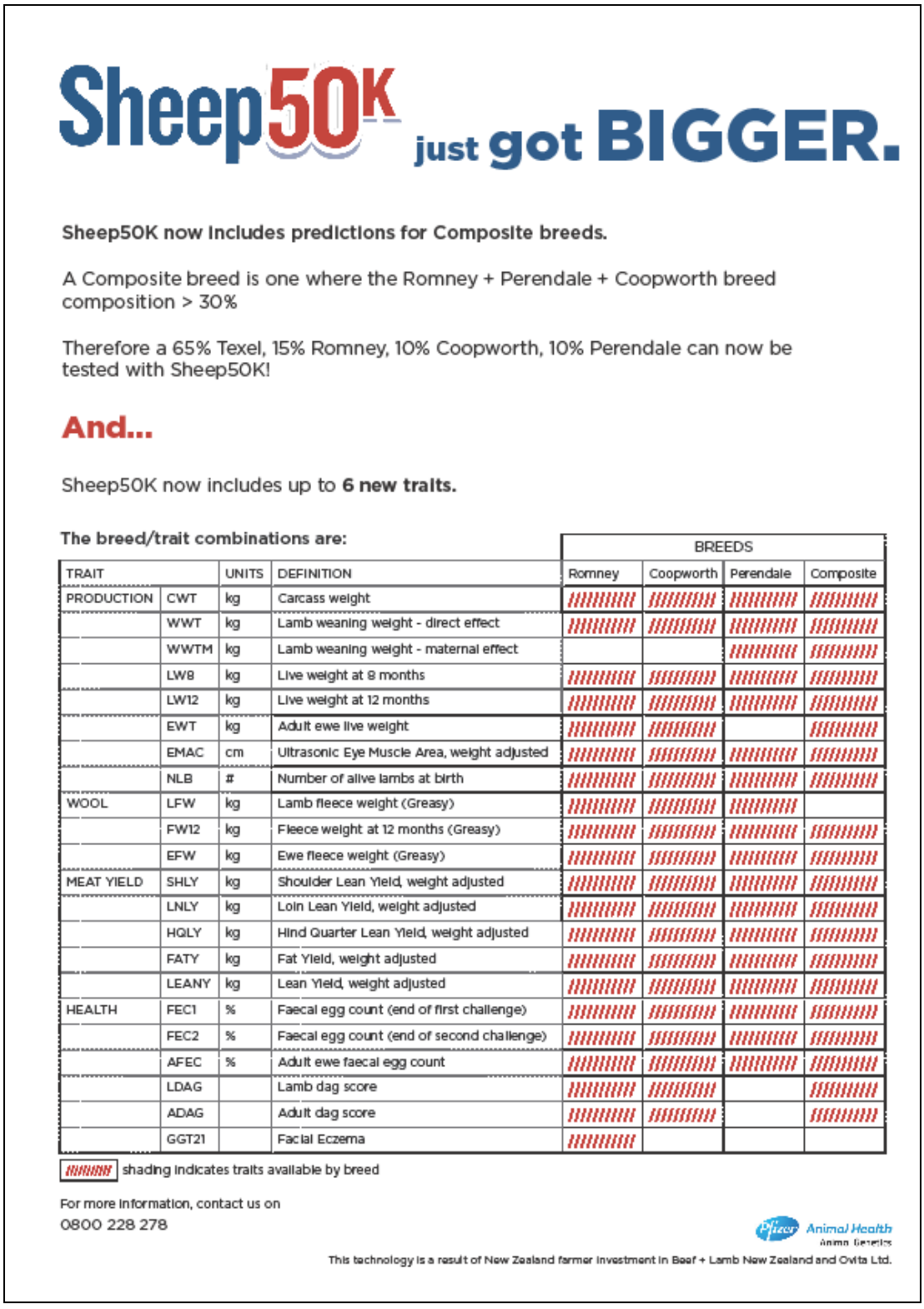
Finally the biggest thank you to Jo who in the last few months has gifted me the most wonderful example of genetic perfection in the form of our little baby girl Maggie Jasmine Hodgkins.

My own most wonderful example of genetic perfection - our baby daughter Maggie

Appendices

Sheep 50K (NZ) advert

see https://www.pfizeranimalgenetics.co.nz/Pages/Sheep%2050k.aspx



Sheep50K just got BIGGER.

Sheep50K now includes predictions for Composite breeds.

A Composite breed is one where the Romney + Perendale + Coopworth breed composition > 30%

Therefore a 65% Texel, 15% Romney, 10% Coopworth, 10% Perendale can now be tested with Sheep50K!

And...

Sheep50K now includes up to **6 new traits.**

The breed/trait combinations are:

TRAIT		UNITS	DEFINITION	BREEDS			
				Romney	Coopworth	Perendale	Composite
PRODUCTION	CWT	kg	Carcass weight	▨	▨	▨	▨
	WWT	kg	Lamb weaning weight - direct effect	▨	▨	▨	▨
	WWTM	kg	Lamb weaning weight - maternal effect			▨	▨
	LW8	kg	Live weight at 8 months	▨	▨	▨	▨
	LW12	kg	Live weight at 12 months	▨	▨	▨	▨
	EWT	kg	Adult ewe live weight	▨	▨		▨
	EMAC	cm	Ultrasonic Eye Muscle Area, weight adjusted	▨	▨	▨	▨
	NLB	#	Number of alive lambs at birth	▨	▨	▨	▨
WOOL	LFW	kg	Lamb fleece weight (Greasy)	▨	▨	▨	
	FW12	kg	Fleece weight at 12 months (Greasy)	▨	▨	▨	▨
	EFW	kg	Ewe fleece weight (Greasy)	▨	▨	▨	▨
MEAT YIELD	SHLY	kg	Shoulder Lean Yield, weight adjusted	▨	▨	▨	▨
	LNLY	kg	Loin Lean Yield, weight adjusted	▨	▨	▨	▨
	HQLY	kg	Hind Quarter Lean Yield, weight adjusted	▨	▨	▨	▨
	FATY	kg	Fat Yield, weight adjusted	▨	▨	▨	▨
	LEANY	kg	Lean Yield, weight adjusted	▨	▨	▨	▨
HEALTH	FEC1	%	Faecal egg count (end of first challenge)	▨	▨	▨	▨
	FEC2	%	Faecal egg count (end of second challenge)	▨	▨	▨	▨
	AFEC	%	Adult ewe faecal egg count	▨	▨	▨	▨
	LDAG		Lamb dag score	▨	▨		▨
	ADAG		Adult dag score	▨	▨		▨
	GGT21		Facial Eczema	▨			

▨ shading indicates traits available by breed

For more information, contact us on
0800 228 278

Pfizer Animal Health
Animal Genetics

This technology is a result of New Zealand farmer investment in Beef + Lamb New Zealand and Ovita Ltd.

Travel plan

28 October, 2012	Fly out from Heathrow
19th Octob34, 2012	Arrive Sydney
30th October, 2012	
31st October, 2012	Drive to Armidale
1st November, 2012	Meeting with Sam Gill
2nd November, 2012	Meeting with Julius Vander Werf
3rd November, 2012	Rest/options for local farmers known to S.G/JVW
4th November, 2012	Rest/options for local farmers known to S.G/JVW
5th November, 2012	Robert and Fiona Kelly
6th November, 2012	Drive to Parkes
7th November, 2012	Mark Swift NSch, Peak Hill
8th November, 2012	Andy and Mandy Bouffler
9th November, 2012	Tom Bull
10th November, 2012	Rest/look around Sydney
11th November, 2012	Rest/look around Sydney
12th November, 2012	
13th November, 2012	
14th November, 2012	Jim Litchfield
15th November, 2012	
16th November, 2012	Dr. Ben Haynes
17th November, 2012	
18th November, 2012	Fly Sydney to Christchurch
19th November, 2012	Jimmy Newport
20th November, 2012	Andrew and Heather Tripp
21st November, 2012	Luke Proctor – Pfizer Animal Genetics (Dunedin)
22nd November, 2012	Auurora Romney Stud, Palmerston
23rd November, 2012	Tan Bar, Andrew Chartres (manager)
24th November, 2012	Mckenzies, Ashburton
25-27th November, 2012	
28th November, 2012	Michael Taylor, Temuka
29th November, 2012	Drive to ferry point
30th November, 2012	Ferry crossing
1st December, 2012	Wairere – Masterton
2nd December, 2012	Wairere, Masterton
3rd December, 2012	OJ
4th December, 2012	
5th December, 2012	
6th December, 2012	Alexander Farming Genetics (Matamata)
7-8th December, 2012	
9th December	Fly to Dunedin
10th December, 2012	
11th December, 2012	Fly back to Auckland
12th December, 2012	Fly out of Auckland back home
13th December, 2012	In the air
14th December, 2012	Arrive home

Sheep 50K New Zealand farming articles

SCIENCE | GENOMICS

Predicting breeding merit

From the basic to the complex: **Russell Priest** reports on two presentations dealing with the technology involved in making genetic predictions.

The ultimate goal of being able to take some DNA from an animal and predict how that animal might perform is now not realistic.

So says renowned New Zealand-born geneticist Dr Dorian Garrick.

"The best we can expect now is to be able to predict breeding merit in close relatives within a breed and quantify the reliability of that prediction.

Garrick, who holds the Jay Lush chair in Animal Breeding and Genetics at Iowa State University and is also the director of the US National Beef Cattle Evaluation Consortium, delivered two papers at the Beef + Lamb Ag-Innovations event in Feilding.

His two presentations dealt with the technology involved in making genetic predictions about the performance of animals based on their DNA.

Basic genetic principles:

Garrick covered some basic background information on genetics before dealing with more complex issues.

He stated that most of what we know about the cattle genome has come about because scientists believe it might hold some useful information for human genetics.

"Genes have beginnings and ends and are part of structures known as chromosomes and they come in pairs; one of each pair comes from the father and the other from the mother," he said. "Humans have 23 chromosomes and cattle have 30, and there are approximately 30,000 genes in total.

"Only 2-3% of a chromosome is represented by genes and the rest is junk."

Genes are represented by base pairs and each chromosome has approximately 100 million of these.

"Only 2-3% of a chromosome is represented by genes and the rest is junk."

He explained that genes produce proteins such as enzymes and hormones that control all bodily functions and they also produce receptor cells. If the body is functioning properly the hormones and enzymes lock into their specific receptors in a similar manner to a key fitting into a lock.

Dorian Garrick: Several genes.

This then allows the particular bodily function to occur normally.

If there is a mismatch (the enzyme/hormone does not fit into its receptor), the bodily function is impaired, potentially leading to disorders like atrial fibrillation and cystic fibrosis in humans and mannosidosis and myophosphorylase in cattle.

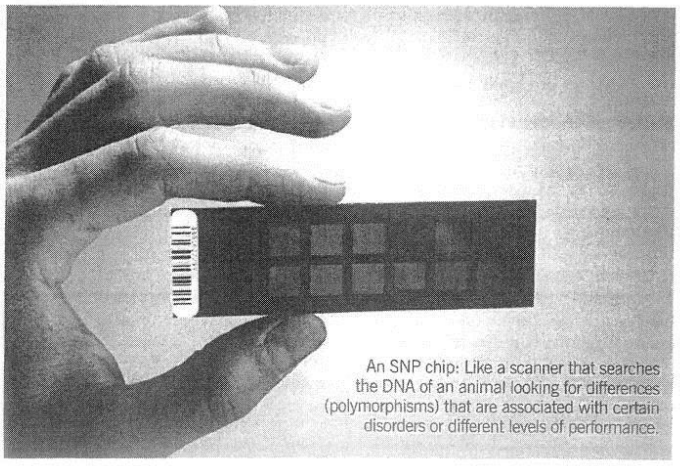
Applying DNA technology to the NZ beef industry

Beef breeders in NZ could benefit from:

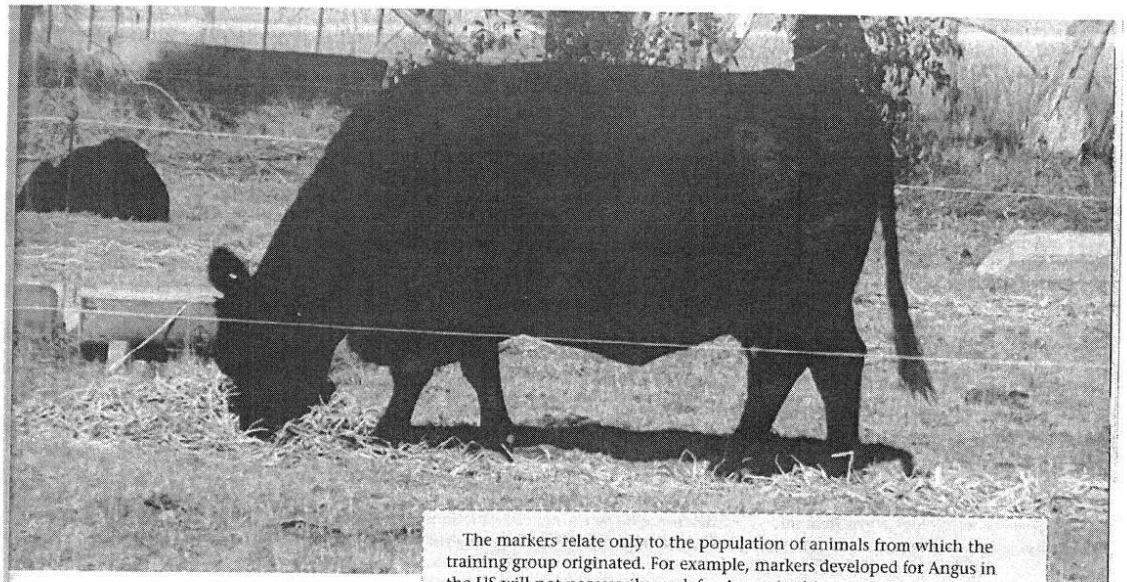
- Detecting the presence and frequency of broken genes
- Joint participation in one or more of the international genomics projects. This could help leverage additional funding from both participating countries
- A validation "experiment" involving at least 100 animals of any particular breed.

Genes that create these disorders are known as broken genes or mutations and result from mistakes made in the normal sequence of base pairs when they are being copied (a mistake is made about every 100 base pairs).

"Any mistakes are normally repaired by other genes, however, some slip through the cracks and remain unrepaired.



An SNP chip: Like a scanner that searches the DNA of an animal looking for differences (polymorphisms) that are associated with certain disorders or different levels of performance.



The markers relate only to the population of animals from which the training group originated. For example, markers developed for Angus in the US will not necessarily work for Angus in this country unless there are strong pedigree linkages between the two populations. Most major breeds in the US have developed marker tests. The breeds that have developed these using large training populations are the breeds that have the most accurate genetic predictions.

"Animals and humans have thousands of broken genes and they generally only create problems when two copies of the same broken gene occur in one individual. Broken genes can also have positive effects such as double muscling in cattle and the hairy N gene in Drysdale sheep.

"Besides producing human and animal disorders these mistakes, known as polymorphisms, create variation in performance between individuals. So in order to find out which animals are potentially more productive than others we need to know which polymorphisms are associated with high performance and which are associated with low performance."

Just because an animal has a high EBV for a particular trait does not mean all its genes are high-performing. A large percentage of them may be, but it can still have some low-performing genes, too.

Breeding high-performing animals involves capturing as many high-performing genes as possible in the next generation by mating parents with a background of high performance.

"To do this geneticists need thousands of animals that have been genotyped (their DNA has been tested) and have also been performance recorded," Garrick said.

"Using these two sources of information scientists can associate differences in performance with the genetic make-up of the animals. For example, the high-growth animals will have different polymorphisms to low-growth animals."

Few characteristics (traits) are controlled by one gene; most are controlled by several. Some exceptions to this are dwarfism, coat colour and horns in cattle. To find all the genes responsible for controlling a particular trait is not realistic, so what scientists do is look for genetic material (polymorphisms) close to major genes associated with a trait, then they map these.

These sites on the genetic map are known as gene markers and the template used to identify where these markers are on the map is called a SNP (single nucleotide polymorphism) chip. The closer these markers are to the gene(s) controlling the trait, the more accurate will be the prediction of the true breeding value of the animal.

SNP chips:

An SNP chip is like a scanner that searches the DNA of an animal looking for differences (polymorphisms) that are associated with certain disorders or different levels of performance.

Bigger (more dense) SNP chips will scan an individual's DNA a greater number of times, which means they are more likely to find polymorphisms than the smaller, less dense ones.

Not surprisingly, they are also more expensive. The first SNP chip to come on the market was a 50K one produced by a company called Illumina which scanned the genome 50,000 times and cost US$300. Nowadays there are several different SNP chips on the market and the cost has come down considerably. A 20K low-density SNP chip produced by a company called GeneSeek costs US$45 and it performs almost as well as a 50K chip using a technique called imputation.

The company also produces a 77K high-density chip costing US$75 which also has markers for some broken genes. The shelf life of these chips is not long, so when new markers are found they are added to the new chips.

Imputation:

This is a new piece of predictive technology that has enabled companies producing SNP chips to reduce their prices.

The technology uses our knowledge of how chromosomes are inherited and the power of the computer to predict (impute) the genetic make-up of sections of chromosomes. This effectively reduces the amount of scanning required and enables less dense and cheaper chips to be used.

The correlation between the accuracy of predictions using imputed genotypes and actual genotypes can be high.

Gene markers:

As mentioned, gene markers are developed by scanning the DNA of groups of thousands of animals.

These groups are known as "training" or "discovery" groups. It is an expensive

such large groups. Genotyping a group of 10,000 animals using a 20K chip would cost US$450,000, then the markers developed have to be tested to ensure they work.

Genomic verses pedigree-based predictions:

Several different genotyping tests have been developed and used by different breeds in the US to develop their genetic marker tests. All have proved to give better genetic predictions than traditional pedigree and performance-based systems.

The accuracy of the gene marker tests depends heavily on the size of the training populations of genotyped and phenotyped (performance recorded) animals.

Blending:

This is a technology where genomic information is combined with traditional pedigree and performance information to endeavour to improve the accuracy of the genetic prediction.

Garrick said four blending methods were used in the US and they all had serious problems. He believed none of them was going to work in the long term.

"Blending will only add to the accuracy of the prediction if the accuracy of the original information is very low.

If an animal is already accurately evaluated by using a progeny test, for example, then a genomic prediction will not improve accuracy."

Genes that create disorders are known as broken genes or mutations and result from mistakes made in the normal sequence of base pairs when they are being copied (a mistake is made about every 100 base pairs).

Big genes:

"There have been some major genes found that are causing large genetic variation and these are in similar chromosomal regions in several breeds," Garrick said. "Some of these same regions describe a lot of the genetic variation for weaning weight, yearling weight, marbling, rib eye area and calving ease.

"However, the 50K chip is not dense enough to be able to identify these gene effects."

The current status of DNA technology:

- Gene marker technology often achieves good predictions in close relatives but not in distant relatives
- The reliability of the predictions varies according to the trait being assessed and how closely the animals being predicted are related to the animals in the training group
- Imputation will make genomic prediction more affordable
- Characterisation of major gene effects will improve genomic predictions.

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Strategic grazing put to the test

An AgResearch study in South Otago has indicated that simple and low-cost management techniques can significantly reduce overland flow and contaminant losses from winter forage crop paddocks.

With the growth of dairy farming in Otago and Southland, there has been a corresponding increase in environmental concerns, particularly regarding nutrient loss, faecal microbes and sediment to waterways.

Winter forage grazing paddocks are believed to contribute a disproportionately large part of annual farm nutrient and sediment losses as a result of intensive stock grazing on soils with high moisture content.

The Dairy NZ-funded paired catchment study, which is part of the Pastoral 21 programme, was led by AgResearch Invermay-based senior scientist Ross Monaghan. The study was established at Telford dairy farm, just outside Balclutha. It has been investigating the effect of grazing strategy on overland flow and water quality when paddock soil type, topography, drainage and stock management were taken into account.

It was thought that strategic grazing of cows in a winter forage crop paddock could reduce overland flow and thus sediment and nutrient losses.

In the test two different types of management were used. There was a control group, with cows starting at the bottom of the hill, then strip grazing up the hill. There was no backfencing and the stream was unfenced and unprotected.

In the treatment catchment the cows enter at the top of the paddock, then strip graze in a downward direction. There was protection of the stream, back-fencing every four to five days, and finally restricted grazing of the area surrounding the stream if conditions were suitable, effectively offering the "last bite" of winter when conditions allow.

Monaghan says the trial has shown that strategic grazing of dairy winter forage paddocks can considerably reduce volumes of overland flow.

"By reducing overland flow, the yields of sediment and nutrients carried in the flow were also reduced considerably," he says.

"The strategic grazing method was a combination of protecting the critical source area (CSA) from stock by fencing, and grazing the least risky areas first and grazing towards the higher risk areas. This effectively left the most vulnerable areas with minimal soil damage for as long as possible throughout the winter season.

"Protection of the CSA, gullies and areas prone to soil saturation is a key part to reducing overland flow and sediment loss. Grazing the CSA can still occur, but only when soil conditions allow. These grazing managements are relatively simple to implement and low cost."

The trial is continuing in 2013, with the paddocks being swapped to see if the differences between the control and treatment grazing strategies continue to be seen.

This research is funded as part of the Pastoral 21 programme, a collaborative venture between DairyNZ, Fonterra, Dairy Companies Association of New Zealand, Beef + Lamb New Zealand and the Ministry of Business, Innovation and Employment.

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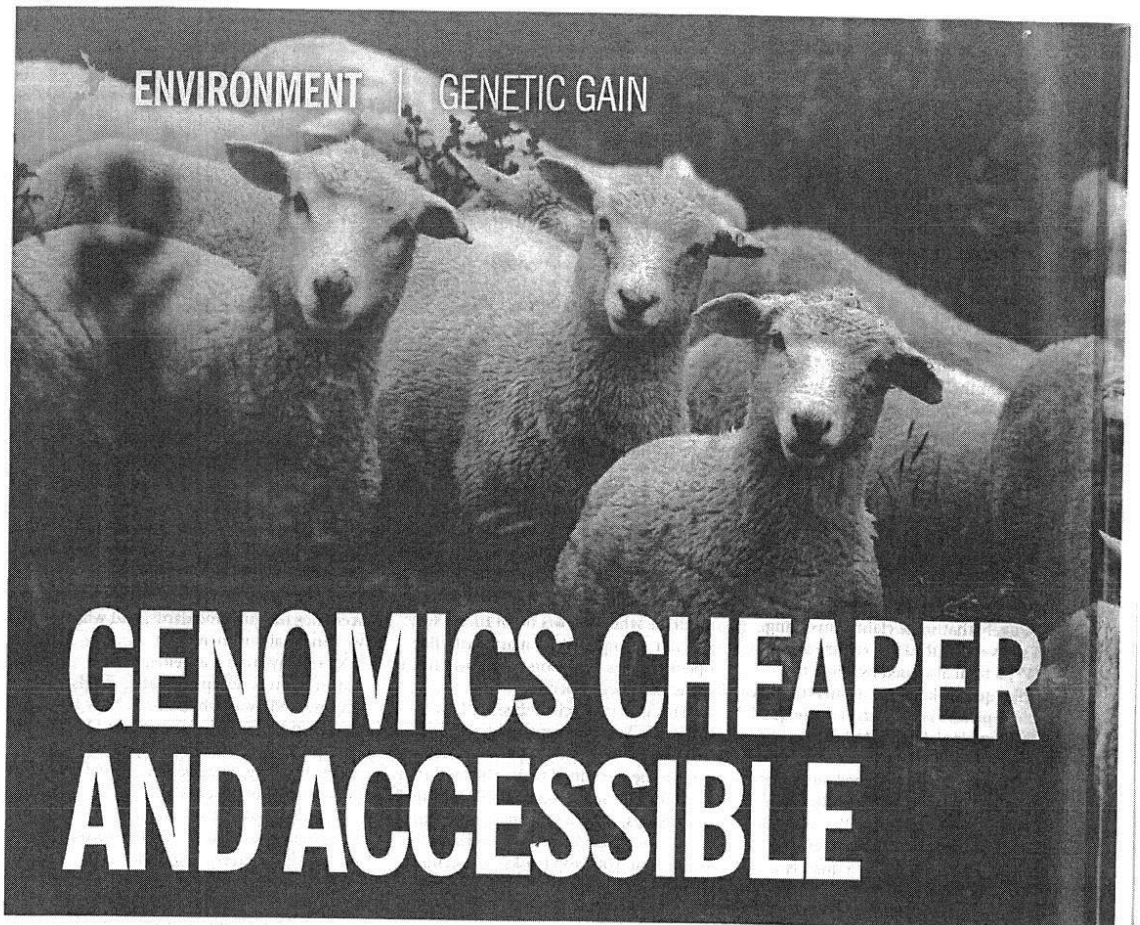


GENOMICS CHEAPER AND ACCESSIBLE

DNA testing is now 1000 times cheaper than it was six years ago. **Sheryl Brown** reports on what this means for farmers.

Combining genomic technology and reproduction techniques will accelerate genetic gain in the sheep and beef industries.

This is according to Dr Ben Hayes, Associate Professor at Australia's Department of Primary Industries' Biosciences Research Division.

He said the biggest influence on genomic technology in the past few years had been the rapidly declining cost. DNA testing was now 1000 times cheaper than it was six years ago, which meant it was cheaper and easier for scientists to access the data, and consequently, more economically viable for farmers to use in their businesses.

"It once cost $300 million to get a full genomic sequence, whereas now it is down to about $2000 to sequence a bull."

Hayes said the cost had spiralled downwards because of the enormous investment in human medicine, which had a spin-off for agriculture.

"People have seen the opportunity and have adapted the technology for cattle and sheep. The cost was astronomical, but it has come down more than a million-fold. So it's within the realms of possibility."

Hayes spoke at the recent Allflex Premium Primary Producers conference in Brisbane on genomic technology in agriculture and where the future lies for farmers in using the information.

To ensure the genomic breeding values are accurate, geneticists need large cross-reference populations to work with.

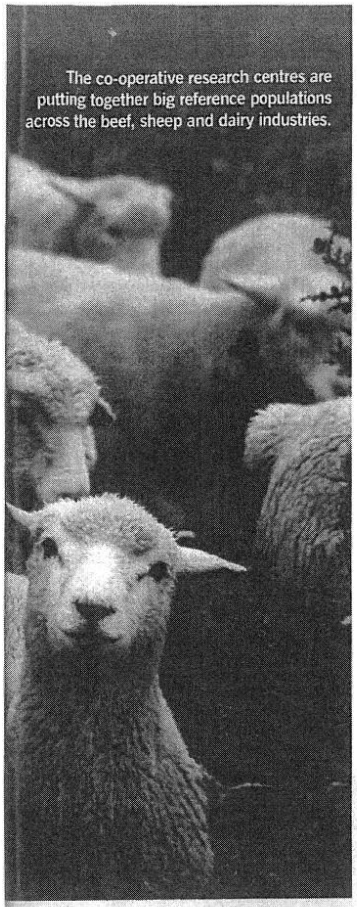
"We need masses of good trait data. The only way you're really going to make this work is if you've got a large reference population, where you have animals with the DNA profile that have been SNP chipped, and also have the trait really well-recorded."

Hayes said Australia had been fortunate as there had been significant investment in this space, with the co-operative research centres putting

Hayes said much effort had gone into getting genomic breeding values for feed conversion efficiency because it was a huge component when it came to the cost of running dairy and beef operations. The accuracy for feed conversion efficiency in beef cattle is 36%.

Higher accuracies in dairy genomic breeding values were reflective of the numbers of trait data available in the dairy industry, which is where the sheep and beef industries needed to get to. It was crucial to get higher accuracies of genomic breeding values across beef and sheep industries.

"The higher the accuracy, the better benefit you get back from the cost of genotyping, more genetic gain, more benefits."



The co-operative research centres are putting together big reference populations across the beef, sheep and dairy industries.

Accuracy needed

Various opportunities of how best to use the technology would exist in the future.

One big area livestock geneticists were working on now was breeding for traits previously difficult to breed for, such as meat quality and feed conversion efficiency.

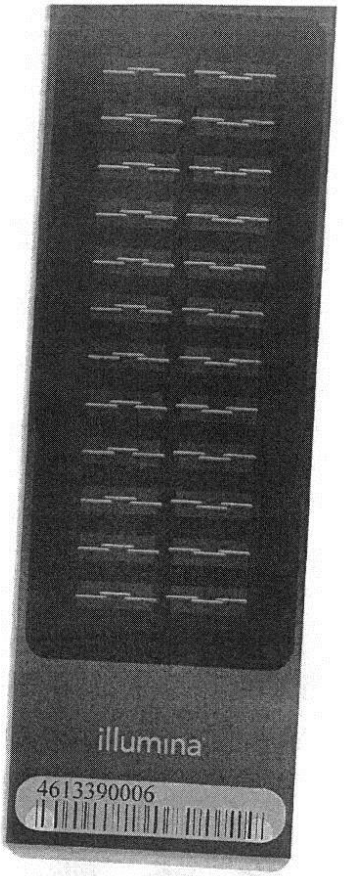
"That really was the dream eight years ago – can we take that technology and turn it into genomic breeding values for these hard-to-measure traits, or traits that come late in life so it's hard to make breeding decisions on animals early.

"Feed conversion efficiency is a really hard trait to breed for, unless you've got a bit of equipment like this. And it costs money to do it."

Hayes warned that to get the best out of the technology, it needed to be accurate: "The accuracy is the genomic breeding value versus the true breeding value.

"The currency of all breeding values is their accuracy. You have to have accuracy relevant to your population or breed you are using.

"The accuracy of the breeding values essentially tells you how quickly you're going to move in genetic gain."



Testing is now many times cheaper.

together big reference populations across the beef, sheep and dairy industries.

The Australian Beef Centre has almost 15,000 records, sheep more than 15,000, and dairy more than 20,000. With these numbers increasing, geneticists can begin assessing how accurate the genomic breeding values are.

The accuracy of the genomic breeding value for post-weaning weight, intra-muscular fat and meat quality in sheep and beef is moderate to low – between 25% and 35%. The accuracy for tenderness in beef is about 40%, so it was beginning to get interesting, Hayes said.

"We're getting towards something that would be economically beneficial to breed from."

Dr Ben Hayes: Key ancestors.

The Australian Sheep Centre has run several pilot projects where breeders can submit their DNA samples, get them genotyped, and they get back genomic breeding values.

The uptake of that has been good, which has helped increase the number of records, in turn helping with accuracy.

Some of the breeders were using the genomic technology with some advanced reproduction technologies, Hayes said.

"In sheep if you have a ewe lamb, there is a little window where the lamb is about six weeks of age where you can pick up the eggs, have the semen from the ram, put them together in a petri dish and get an embryo and implant that. That's called juvenile in-vitro embryo transplant.

"If you're running a programme like that, then the markers are a real benefit to you because they can tell you which ewe lambs to put into this programme."

Australia is working with other countries on the 1000 Bull Genomes Project to do full genomic sequences on key dairy and beef bull ancestors.

"Our strategy is to fully sequence all these key ancestors that capture our genetic diversity – the bulls that have contributed a lot of the genetics that are floating around in our populations today."

They will then be able to take DNA markers from cows and work out which chunk of the genome they received from these ancestors.

"Somewhere in that information are the genes that are affecting our traits today, which will lead to better accuracy of genomic breeding values.

"The focus was originally on dairy; we are now focusing on beef as well."

Genomics had an exciting future ahead, Hayes said, with one possibility being to create more accurate composite cattle. For example, you could take the good fertility genes from Brahman and the good meat quality genes from Shorthorn and put them together to get the ultimate composite.

"That's one possibility you could do in the future, but getting more traits into the database is critical."

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Report summary

Genomics is well established in the pig, dairy and poultry sectors as a cost effective method to ensure only the best of the breed goes forward. Until recently the sheep sector has lagged behind these other industries; it has neither the high unit cost per animal of cows nor the short generational gap of poultry. In the UK the large number of different breeds means that any collective industry research cannot usually be applied across flock and so little effort is made. Europe is also disadvantaged by the subsidy system which has distorted the market by de-coupling production and profit in such a way that farmers do not have high margins from their flocks.

The goal of my report was to investigate the current state of genomics research in the southern hemisphere and look at how they have overcome the problems the UK would face if we as an industry wanted to embrace it. I also wanted to research if, because of the high percentage of New Zealand genetics in our own flock, we could use technology. What I found was highly focused research which in most cases was targeted on maximising sheep value either through production traits like number of lambs born or through difficult-to-measure traits like internal parasite resistance. Some interesting work is also being done to improve meat quality in Australia with identification of genes for meat, zinc and iron content, shear strength of the muscle and values for tenderness.

Having returned to the UK we submitted DNA samples from our own imported NZ born rams, as well as one 2012 UK-born ram of outstanding merit. Through my Nuffield Farming Scholarship we have thus become the first flock outside New Zealand to test on the 50K platform, and the first flock outside New Zealand and Australia to have a selection criteria based on this type of information. Through analysis of our own data I have attempted to correlate the genomic predicted results with real data from our own flock. The results were broadly encouraging and whilst it would be wrong to say this is mature enough to be used as a standalone test, when used in conjunction with Estimated Breeding Values (eBV) it can prove a powerful tool in early identification of high quality genetics.