Genomics
Explanation Leaflet

The sheep genome was first sequenced in 2014 and since then great progress has been made in the study of its molecular genetics. As a result it is now becoming possible to use information about an individual animal's genetic makeup to enhance more traditional estimates of breeding value. This means in practical terms that more informed decisions can be made on difficult and hard to measure traits earlier in an animal's life, something that can have a huge impact on the efficiency and profitability of any livestock business.

This leaflet explains some of the background, benefits and implications of this emerging technology.

What is Genome-Wide Selection (GWS)?

Genomic selection refers to the use of genetic information as well as the traditional pedigree and performance records to predict an animal's breeding value. Breeding values produced in this way are referred to as GEBVs (Genomic Estimated Breeding Values) rather than the EBVs we currently have.

How is it done?

An individual animal's DNA (Texel Sheep Society use a nasal swab sample) is compared to a DNA SNP key which is developed from a reference population within the breed which is made up of several thousand of the most informative animals whose DNA has also been collected. Using GWS, areas of the genome are identified that are closely linked to differences in performance in the traits of interest e.g. growth, health, meat eating quality.

What is a SNP?

A SNP (pronounced 'snip') is the piece of information from the DNA available at that point on the sheep genome. SNP's are taken at equal spacing across the entire sheep genome and are contained in Chips which can be used to assess genetic variation.

What is a SNP chip?

Chips vary in size and the larger (more dense) they are, the greater the amount of information reported and the higher the cost.

The Texel Society reference population has been founded on the 50,000 (50K) and the 700,000 (700K) chip, which represents a £350,000 investment. Future samples will be reported using a lower density chip, the 15K and all male registrations are now routinely tested on this Chip.

Imputation

A major breakthrough in genomic science is the use of a technique called imputation. This allows lower cost (lower density) chips to be used routinely. With a mathematical calculation, using algorithms, to fill in the missing information, i.e. between the 15K chip and the 50K chip.

This allows a more affordable chip to be used routinely but it still offers the power of information that can be created by using the more expensive 50k or 700K chips. Whilst imputation will be used for the majority of animals the Texel Society still has the option to use the 50k chip on strategically important and informative sires in the Breed.

The results from the comparison between the individual animal and the breed's SNP key are then used to produce a variety of different GEBVs for the traits of interest.

Are GEBVs more accurate than current EBVs?

The accuracy of breeding value estimates for unproven lambs can be enhanced by as much as 30% using GEBVs, and can be as accurate as progeny testing but this does depend on:

- The heritability of the trait in question (less to gain in traits that are well recorded, have high heritabilities etc than those that are difficult to record with low heritability's) but benefits can still be provided.
- The population in which the trait is being evaluated
- The quantity and quality of the pedigree and performance records
- The quality of the SNP key

GEBVs are particularly useful for measuring "Hard To Measure" (HTM) low heritability traits such as mastitis, foot rot, meat eating quality etc.

So will we need to keep collecting on-farm performance records?

Yes, as without the ongoing collection of phenotype data from a well connected population accuracy would suffer which will affect the accuracy and value of both EBVs and GEBVs. The more information collected from across the population the greater the accuracy and reliability of the breeding values.

An important aspect of "SNP key" technology is regular validation of the SNP key against the actual performance of the population/breed. This means that the key has to be regularly examined in relation to possible genetic change going on within the population/breed so that Geneticists are confident it is correctly identifying variation.

For this purpose performance recorded flocks are of vital importance as they collect valuable data for traditional traits such as growth, including ultrasound/CT scan data for muscling and meat yield. However in addition the Texel Society has established a network of "Phenotype Farms" who serve as a constant 'reference population' of ~2500 genotyped animals that are or have been fully recorded on-farm for specific "hard to measure" health related traits such as mastitis and foot rot.

All of these records form the basis of the validation process to ensure the key remains relevant in the face of genetic change.

So what are the benefits?

Genome-wide selection has three main benefits:

1. **Speed**: Genotypes can be obtained shortly after a lamb is born, thereby enhancing the accuracies of genetic merit predictions much quicker than performance recording alone. This allows for faster rates of genetic improvement resulting from shorter generation intervals and is particularly valuable for traits that can only be measured later in life such as maternal ability, growth rate and carcass traits.
2. **Improved accuracy** of low heritability traits/traits that are difficult to record: Breeders should experience greater response to their breeding decisions on traits with low heritability if the accuracy of the predictions is higher using genome-wide selection. It also offers opportunities to predict the breeding values of traits that are difficult to measure such as health, fertility, meat quality, greenhouse gas emissions etc.
3. **Lower Cost**: Because accuracies are enhanced much more quickly using genome-wide selection compared to collecting records on-farm (depending on the trait) there can be less cost involved in getting breeding value estimates to similar levels of accuracy. (Compare the cost of genotyping a ram lamb to the costs of having to wait until it has become a sire and amassed performance recorded progeny in a number of flocks to reach the same levels of accuracy).

Is Genome-Wide Selection the same as the Gene Tests currently available?

They are similar but different!

Genome-Wide Selection – referred to throughout this leaflet, is a technique that uses a key with many thousands of SNPs (small bits of DNA) on it to compare individual DNA samples against and predict genetic merit. The density of SNP keys range from 15,000 SNPs per key to 700,000 SNPs, each SNP identifying an area of genetic variation.

Gene Tests – These are DNA tests currently available to the industry to identify either a) a specific gene or genes whose location within the DNA is known (such as scrapie genotype)

The potential for genetic change that can be gained through Genome-Wide Selection is typically by far greater than the use of standalone Gene Marker tests since most traits of interest are affected by many genes having a small effect, rather than a single gene having a big effect. These many genes are more likely to be found by a SNP key that identifies many thousand areas of variation than a Gene Test that identifies just a few. In instances where single genes are known to have significant effects, however, the opposite will be true.

How soon will GEBVs be available?

The Texel Society will be publishing GEBVs for mastitis and foot rot initially in a limited way to the participating phenotype farms in late 2016. The Kimbolton flock will be amongst the first flocks to benefit from these.

The opportunity to submit DNA for testing for these traits will then be widened out to the entire membership as a part of an initial rollout hopefully in 2017/18. Full details and timings can be found in the Texel Society Breed Development Strategy document.

Development of this technology in the UK for is in its early stages and the Texel Society is leading the sheep Industry on this topic. A recent project award will see the continuation of the Phenotype Farm initiative and ensure that a significant and up to date reference population of several thousand well-recorded animals is maintained for traits of commercial influence.

In addition further projects will see SNP keys being developed for Meat Eating Quality (MEQ), carcass traits and further health traits based on abattoir condemnation data.

Conclusion

The myth surrounding this emerging technology is that it will mean an end to on-farm recording and that all our questions about an animal's genetic merit will be simply answered by a blood test, a nasal swab or a tissue sample.

This isn't the case! It should be remembered that the enhancement of EBV accuracy will vary according to the trait in question and the type of animal being evaluated (Ram lamb, Aged Ram etc.).

Once in place, it will only be breeders and through the support of Organisations like the Texel Society, that can collectively make Genome-Wide Selection work via effective knowledge transfer and by ensuring high-quality on-farm records continue to be collected.

Sources

Genome-Wide Selection – The Answer to All Our Prayers? Signet, Alison Glasgow