

UPDATE ON SHEEP GENOMICS AND GENETICS

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Background

In recent years, the majority of genetic and genomic research in livestock has focused on species of larger economic value such as dairy cattle and swine. As genetic and genomic technologies drop in price more industries, including sheep, are trying to take advantage of these data for use in their breeding systems. Sheep genetics research has generally taken a single candidate gene approach to identify polymorphisms responsible for major differences in important traits such as ovulation rate, scrapie resistance, and color. Complex traits such as out of season lambing, feed efficiency, and meat quality have not been researched extensively yet because they are polygenic and difficult to measure consistently. These complex traits are more important to producers and are what producers want genomic solutions to.

Most shepherds in the U.S. have not yet taken advantage of classical genetic selection due to a variety of reasons. Because of this, there are not large reference populations for sheep genomics research within the U.S like there are in Europe, Australia, or New Zealand. In order for producers to fully utilize genetic and genomic selection, shepherds must begin to consistently record economically important traits. Despite this genetic and genomic research has provided some advances to the industry.

Genomic & Genetic Technology

As technology advances and prices for genetic technology decreases more researchers and producers are seeking to evaluate and reap the benefits of marker assisted selection and genomic selection of complex traits. Some of these methods include High-Density single nucleotide polymorphism (SNP) microarrays, Genotyping-by-Sequencing, and Whole Genome Sequencing. Each technology has their benefits and drawbacks depending on the application of the project and financial constraints.

Genomic Selection

In order to use genomic selection within the sheep industry, the effect of SNPs need to be determined to incorporate them into the evaluation model. Reliable record keeping must occur across the industry in traits that are economically important. Reference populations are needed to combine genotype and phenotype information to determine the effect of these SNPs. Ideally a different reference population would be used for each breed but because of the diversity of sheep breeds present in the US this poses a logistical and financial challenge to attain the sample size needed for accurate estimated breeding values (EBVs).

Genomic selection can increase the accuracy of EBVs, reduce generation interval length, and improve selection in complex traits allowing the industry to produce more efficiently.

Scrapie Resistance

Scrapie has been almost eradicated within the United States through the use of monitoring tools and genetic selection towards less susceptible genotypes. Most shepherds are using genetic

selection to test their sheep for codons within the *PRNP* gene associated with scrapie susceptibility, the most commonly tested being codon 171, 154, and 136. This research was conducted in the major commercial breeds.

While shepherds utilize codon testing as a selection tool, there are some misinterpretations of what the genotypes actually mean and their importance in less studied sheep breeds. Currently these tests are run as individual tests which reduce the efficiency of testing many individuals. Because shepherds utilize codon testing, which is marker assisted selection, it should be fairly straightforward to convey to shepherds the principles of genomic selection.

Parentage

In recent years, determining parentage in sheep and goats has increased in importance leading to the development of new parentage panels. Prior to these developments, most parentage panels used approximately twenty microsatellite markers, short regions of repeated DNA. With the ability to genotype hundreds and thousands of SNPs on a single microarray for less expense than microsatellites, several companies and research groups have published smaller (approximately 100-300 SNPs) marker sets that provide greater than 99% accuracy in parental assignment (Heaton *et al.* 2014; Clarke *et al.* 2016).

In order to use genomic selection efficiently, parentage assignment is vital to properly assign breeding values with a high accuracy to the correct sheep. If large farms wish to use genomic selection towards a variety of traits, parentage assignment will be necessary if multi-sire breeding groups are used to reduce management costs.

Dairy Sheep Genomics

To date numerous genetic studies attempted to map major Quantitative Trait Loci (QTL) related to milk yield, protein composition, somatic cell score, and other dairy related traits in sheep (Barillet *et al.* 2001; Giambra *et al.* 2014). These studies yielded some major QTLs but a large portion of the variance remained unexplained, leading to the conclusion there are a large number of small effects as opposed to a small number of large effects. These small SNP effects can be incorporated into genomic selection equations. As of this writing, none of these major QTLs are offered commercially.

Majority of dairy sheep genomic selection research has originated from France with the Lacaune breed. Progeny testing and estimated breeding values are utilized in France for milk production and composition and have been since the 1980s. Using Genomic Estimated Breeding Values (gEBVs) resulted in a higher accuracy in younger animals for lowly heritable traits and faster rate of genetic gain (Duchemin *et al.* 2012). New Zealand sheep research has also utilized genomic selection within one of their dairy flocks. Using genotyping by sequencing technology they were able to generate gEBVs for several dairy traits in a reasonable amount of time and at an inexpensive cost without any traditional breeding values previously calculated. This technique holds promise for the US dairy sheep industry to generate gEBVs.

Future Directions

Sheep genomes are being sequenced at a faster rate which is allowing researchers to identify variants responsible for a wide variety of phenotypes. Most of these are outside the U.S. but as technology improves and prices decrease for whole genome sequencing, genotyping by sequencing, and SNP chips the overall benefit to the US Sheep industry will be greater. As SNP effects are determined it is likely that specific panels will be developed for specific breeds or breed

groups within the industry. Genotyping by Sequencing is being used extensively in the New Zealand sheep industry to reduce costs while providing the same amount of information that SNP chips provide. This technology is still improving but could be used in the US Sheep industry to generate gEBVs.

References

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