Ongoing Research & Development Projects

PROJECT TITLE: Breeding for resistance to Foot rot.

DURATION: 2005 - 2008.

PARTNERS: SLS Group, SAC Veterinary Services, Blackface Elite, MLC, CBS Technologies, Texel Society, ADAS, Rosemaund, Institute of Rural Sciences, Roslin Institute

FUNDING: This project was funded by EBLEX, QMS, HCC, SEERAD and Innovis through the SLP LINK programme with match funding from Defra

INTRODUCTION: The aim of this project, which has just started, is to develop robust procedures to identify individuals and family groups differing in their genetic resistance to footrot, to enable selective breeding for enhanced foot rot resistance. Using information from Blackface, Texel and Mule sheep, the project will use both molecular techniques and conventional animal breeding strategies to investigate the links between genetic susceptibility and phenotypic expression of foot rot. Together with a comprehensive assessment of the economic benefits of breeding for disease resistance, it will be possible to determine whether or not breeding for enhanced foot rot resistance is a practical and feasible option for the UK sheep industry.

This project will provide options to enable breeders to select animals for enhanced resistance to foot rot, combining both phenotypic measurement and molecular markers. Even in the event that the genetic markers are not sufficiently strongly associated with foot rot resistance in our breeds under UK environments, or they prove to be not economically *via*ble, breeders will still have the option of using Best Linear Unbiased Prediction (BLUP)-based selection to maximise the utility of information from foot rot scoring

FINDINGS: Foot rot project update – May 2007

The main aim of the project is to determine the 'best' way to breed foot rot-resistant sheep and this combines information gathered 'on the hoof,' together with molecular information generated from blood samples.

Foot scores and blood were collected on Texel sheep on 19 farms between July and October in 2006. The majority of the flocks scored reflected the geographical spread of performance-recording flocks (centred in the north of England and south of Scotland, with some notable exceptions, shown on the map). A total of 3,603 Texel sheep were scored, (farms shown in orange, red and green on the map below) as well as Blackface (blue and green) and Mule (red and pink) sheep, representing a total of 38,584 feet (as all feet were scored separately).

In the Texel breed, the prevalence of foot rot averaged 29% in 2006, however this varied considerably, being less than 1% for a couple of flocks and more than 59% for the worst-affected flock. Interestingly, the results from the questionnaire (sent out to all prospective Signet-recorded Texel sheep society members to identify suitable flocks for foot scoring) were not in accordance with results from the foot scoring, as the flocks that had the highest levels of foot rot did not feel they had a foot rot problem on their farm, whereas the farmer who had the least foot rot, indicated that he had a 'very bad' foot rot problem in his Texel sheep. Therefore, Texel breeders who recognise foot rot as the serious economic or welfare problem may be more likely to take measures to reduce the occurrence of the disease in their flocks and so have lower prevalence of the disease.

Breeding for resistance to footrot

Introduction

Footrot is the most common cause of lameness and is a major welfare problem in sheep. Lame sheep experience pain, discomfort and reduced mobility as well reduced milk supply, leading to a reduction in the live weight of their offspring. Also, affected sheep are more susceptible to other diseases because of their weakened condition. The causative organism is *Dichelobacter (Bacteroides) nodosus (D. nodosus),* is highly contagious, being easily transmitted from sheep to sheep *via* pasture, bedding or handling pens. Importantly, it can be spread by sheep that show no clinical signs of disease. Footrot is one of the top three diseases that farmers feel most affects the welfare of their sheep.

The control of footrot through management practices is usually an effective way to keep on top of the disease. The use of footbathing, foot paring, quarantine of affected animals, vaccinations and other methods such as the use of a 'snacker' feeder to avoid the concentration of sheep in one area are often used in a combination of ways that best suits the farm. However, with higher than ever labour costs associated with controlling the disease, increased pressure to reduce costs and to avoid environmental contamination, the need for sustainable and long-term solution is required, such as genetic resistance to footrot.

Aims of the project

Using a combination of quantitative and molecular genetic approaches, the overall aim of the project is to investigate the 'best' way to breed for footrot-resistance in UK sheep. Specifically, the main aims are to:-

1. To develop a repeatable and objective scoring system to qualitatively and quantitatively evaluate footrot in individual sheep
2. To investigate associations between footrot resistance and polymorphisms at the DQA2 gene (the 'New Zealand footrot genetic test') and other genetic markers within and close to the MHC region on Chromosome 20
3. Investigate if footrot is a heritable trait and estimate it's genetic associations with other traits of economic importance such as lamb weights and maternal characteristics
4. To predict the genetic, epidemiological and total financial benefits from breeding for footrot resistance

Methods

A Footrot Score validation flock of 100 ewes was used to test the efficacy of the footrot scoring method (Conington et al., 2008). The same method was then used to obtain 13,867 individual ewe records (55,468 hoof records) from Blackface, Texel and Mule sheep from 27 commercial farms and experimental flocks that had pedigree information for their sheep. Two trained footrot technicians scored all the sheep on all of the farms. Most of the flocks were part of the Signet Sheepbreeder recording scheme and so had additional information on their flock's performance. This comprehensive data set of footrot scores was used as a basis to answer most of the genetic questions arising from the project. In addition, we took blood samples from each of the animals and a subset of these were used for the molecular genetic analyses.

Results

Five footrot scores that largely describe the progression of footrot were used:-

NB PLEASE ALIGN THE DESCRIPTION OF THE CATEGORY BELOW WITH THE RELEVANT PICTURE IN THE ACCOMPANYING DOCUMENT 'CONINGTON_FIGURES.DOC'

0 = Normal hoof.

1 = Scald- confined to inter-digital skin

2 = More extensive interdigital dermatitis inflammation

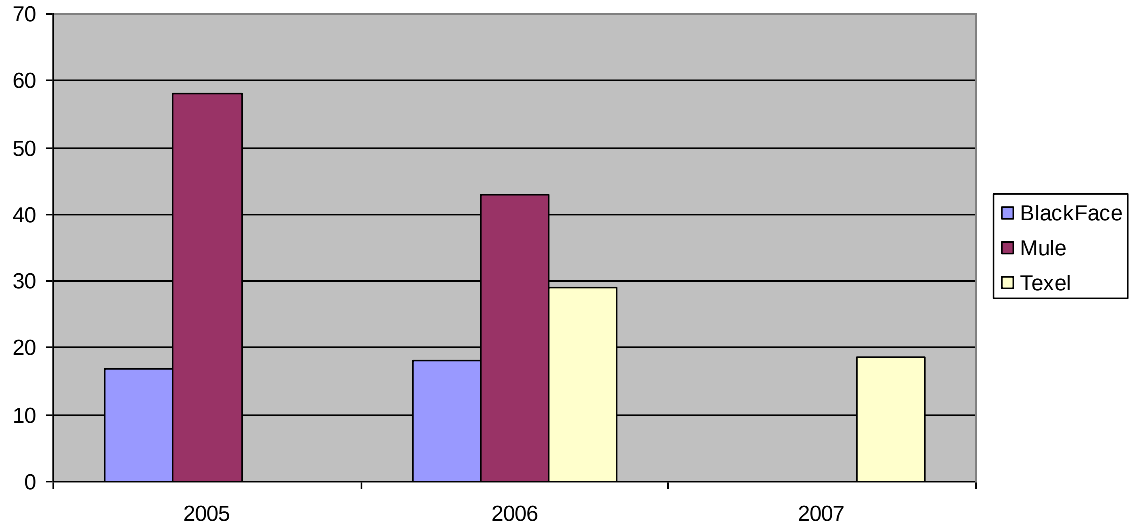
3 = Severe interdigital dermatitis and under-running of the horn of the heel and sole;

4 = As above with under-running extending to the walls of the hoof.

Footrot Prevalence

Figure 1 below shows the percent prevalence of footrot (scores 1-4) for the three breeds over the three year scoring period, 2005-2007. Note that this was not a breed comparison study, as the three breeds were reared in separate flocks with different management and environmental conditions (i.e the Blackface sheep were reared on extensive hill farms and the Texel sheep were largely reared on lowland farms). The graph illustrates the large differences that exist between average prevalence, ranging from 17% in the Blackface in 2005 to 58% for the Mules also in 2005. Large differences between average prevalence levels for individual farms were also seen, with less than 1% for a few farms to nearly 60% for another.

Figure 1: Footrot Prevalence of mixed age ewes following individual hoof inspection



Key factors affecting footrot scores

When comparing animals' performance within-breed, as for genetic analyses, it's important to understand the major influences on animals' performance. From the large quantity of data generated, we found that the major factors that affect footrot prevalence in ewes include the farm and management group, scorer, age of ewe (with older ewes having more footrot), and the number of lambs reared (with ewes rearing twins being at more risk than barren or single-rearing ewes). For lambs, male lambs had twice as much footrot than females, although there were no differences detected in whether lambs were reared as a single or twin.

Genetic aspects

The estimates of heritability were undertaken according to breed, type of animal (ewes or lambs), and also according to the prevalence of footrot on the flocks. The heritability of a trait (such as footrot) describes the degree to which it is under genetic control, on a scale of 0 to +1. The higher the heritability, the easier it is to change a particular trait through breeding methods. Typically, reproductive traits have low heritabilities (~0.1) and wool traits such as fleece weight have a high heritability (~0.6). The average estimate for heritability of footrot in ewes was 0.2, which means it has a low to moderate heritability. However, we estimated that for flocks with average prevalence levels of 30%, the heritability was 0.36, compared to 0.06 for flocks with an average prevalence level of 10%. This means that for flocks with high levels of footrot, the use of breeding methods to control footrot will be more effective than for flocks with low footrot levels. We estimated that it is more accurate to score ewes more than once. Typically, it is recommended that ewes be scored the same time each year and this is treated as a 'repeat measure' of the same footrot trait for the purpose of breeding value estimation. She and her relatives (including offspring) will be given breeding values based on these repeated measures.

Relationships with other traits and response to selection

It's important to understand what will happen to other traits in a breeding programme if selection for footrot resistance is undertaken. Using the estimate of genetic correlation, which measures the degree of association at the genetic level between two traits on a scale of -1 to +1, we can estimate the degree to which the same genes are responsible for two different traits. We found that for Texel lambs, footrot is not correlated strongly to live weight or muscle depth, but is moderately positively (0.27) correlated with fat depth. This means that reducing fatness in lambs through selection will also improve lambs' resistance to footrot. When genetic correlations were estimated among footrot and maternal performance data from Blackface ewes, favourable genetic correlations were estimated for footrot with ewe longevity, number of lambs reared and lamb survival. Depending on the original prevalence of footrot, in genetic terms we estimated that the prevalence of the disease can be reduced by 0.25 to 0.5% per year (e.g. from 10% to 9.5%, and so on) (Nieuwhof et al 2008a). So in general, selection to improve footrot in sheep is likely to bring both economic and animal welfare benefits. However, this estimate ignores the epidemiological benefits of reduced disease burden from having more resistant ewes to footrot.

Epidemiological benefits of breeding for footrot resistance

A model was developed (Nieuwhof et al., 2008b) to estimate the likely rates of improvement that could be made using genetic selection to control footrot in addition to the epidemiological benefits of the more resistant sheep having lower exposure to the disease. The model used both data generated from the project as well as published estimates for key model components such as the rate at which animals recover from infection, and the notional reproductive rate of the pathogen. The results from the model showed that the response would result in double the rate of progress to reduce footrot prevalence in the medium term (e.g. 2-5 generations) compared to predictions using the genetic models alone. This means that the use of breeding to control footrot is an effective and sustainable solution which is likely to lead to extra 'non-genetic' benefits of reduced pasture contamination of the key footrot pathogens.

Molecular genetic information

So that existing genetic tests can be validated in different sheep populations it is necessary to have foot scores on many different sheep with diverse genetic backgrounds as well as their DNA. The existing genetic marker test currently available in New Zealand is based on the DRB2 locus which is one of the genes involved with immune function located in the major histocompatibility complex (MHC) on Chromosome 20. In addition, we have developed a new multiplex of 18 separate markers along the length of Chromosome 20, to have much denser molecular information. The final results from these molecular studies will be known at the end of the year.

Acknowledgements

The research was funded by Defra, The Scottish Government, Eblex, HCC, QMS and Innovis, with grateful contributions from members of the Texel Sheep Society and Blackface Elite Sire Reference Scheme.

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Figures

Fig.1 *Mild interdigital dermatitis (scald).*

Fig. 2. *Score 2. More extensive interdigital dermatitis*.

Fig. 3. *Score 3. Severe interdigital dermatitis and under-running of the horn of the heel and sole*

Fig. 4 Score 4. *Severe interdigital dermatitis and under-running of the horn of the heel and sole*.

Fig. 5. *Drawing of scores 3 and 4* (Courtesy of Agnes Winter)