Best foot forward

The resistance to footrot of fine-wool wethers is partly determined by their sire.

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Introduction

Footrot continues to have a major impact on the sheep industry in New Zealand. This is particularly true in the fine-wool industry because Merino sheep tend to be more pre-disposed to footrot than most other breeds. However, within the Merino population in New Zealand, there is genetic variation in resistance to footrot which can be exploited to breed more resistant animals.

The focus of the initial FeetFirst project at Winchmore was to find fine-wool rams that were resistant to footrot. These resistant rams, and a selection of progeny-tested sires, were then used in the Merino central progeny test (CPT). Footrot outbreaks in the male progeny of the CPT provided an opportunity to investigate the sire effects on resistance to footrot in each sire's progeny.

In addition, this data set provided an opportunity to investigate the correlation between the Lincoln Footrot Gene Marker Test (LFGMT) result of a sire, and the prevalence and severity of footrot within progeny groups in the CPT.

Methods

i)Winchmore trial

The initial trial took place at Winchmore, where a mixture of Merino (678), Polwarth (21) and Corriedale (7) two-tooth rams were purchased from 22 different studs. Using a mixture of rams from different farming environments allowed investigation into the variability in resistance in the current fine-wool population. The rams were transported to AgResearch's Winchmore research farm between February and April 2013, and were run there until April 2014.

The rams were exposed to sheep carrying footrot in conditions that were conducive to transmission. Every week for approximately twelve months the rams were inspected for footrot. Any ram with a footrot score of 4 in any hoof (under-running of the hoof material, based on the 0 to 5 scale outlined by Mulvaney (2013)) was removed from the flock, treated for the disease, and sent to the works for processing. At the conclusion of the Winchmore trial, the rams that were found to have footrot resistance had their semen collected for use in the CPT. The aim: to assess the resistance of their progeny to footrot.

ii) Merino central progeny test

Over the next two years, Merino ewes were mated to a total of 80 sires by artificial insemination. The ewes were randomly assigned to each sire. The sires used were mainly Merinos, but also included Quarterbred, Halfbred, Corriedale, SAMM and Dohne rams. The resultant progeny were weaned and separated based on gender. The mobs were then run under normal grazing conditions and measured for a range of production traits.

The females were deliberately kept clear of footrot so that their performance across other traits could be measured without impediment. The castrated male progeny (wethers) were deliberately grazed in conditions where footrot was known to exist. The number of wethers involved was 752 in 2013 and 679 in 2014.

The purpose of this trial was to generate footrot infection data for the progeny against their sires. This data was used to validate the LFGMT and to assist with the development of a new genomic breeding value (gBV) for footrot resistance in fine-wool sheep. It also allowed the performance of siblings with and without footrot challenge to be compared.

In each year, when a footrot outbreak occurred, the sheep were inspected immediately prior to treatment being instigated. At this time, the severity of footrot in each foot was assessed by a trained operator, using the same 0 to 5 scale used in the Winchmore trial. This data was used to generate estimated breeding values (EBVs) using ASREML.

Of the rams that were used in the CPT, 59 of them had been tested using the LFGMT provided by Lincoln University. These rams included 49 Merinos, four Quarterbreds, three Corriedales, one Halfbred, one SAMM and one Dohne. An additional analysis was completed on these rams to investigate the relationship between the sire's LFGMT score and the prevalence and severity of footrot in his male progeny. There were a total of 978 animals that were scored and included in the analysis. The average number of wethers per sire group was 17.

The average footrot score for an individual was calculated based on the scores given to each foot. In calculating the average footrot score, the score of each foot had to be collected. This enabled a range of analyses to be undertaken: 1) maximum footrot score; 2) average footrot score; 3) sum of footrot scores; 4) footrot as a binomial trait (4=1, <4=0); and 5) number of feet with score 4. The results of these different analyses demonstrated that the traits are highly correlated, and using an average footrot score for an individual was a reliable predictor of footrot susceptibility.

The data was analysed using Restricted Maximum Likelihood (REML) with LFGMT allele code fitted as a fixed effect, and drop, sire breed (nested within drop) and sire (nested within sire breed) fitted as random effects. This statistical analysis was performed using GENSTAT (VSN International 2012).

Results & Discussion

i)Winchmore trial

Of the 678 Merino rams taken to Winchmore, only 33 remained at the end of the trial period. The other rams developed a footrot score of 4 in at least one foot and were removed from the trial. There was one Merino ram that survived the whole trial without contracting footrot at all, whereas the other 32 Merinos that survived the challenge had become infected and reached a footscore of 3 before recovering.

The best of the remaining rams were retained and semen collected for use in the CPT. The Merino rams remaining were from 11 different studs. All seven Corriedale rams remained at the end of the trial, as none had reached a footrot score of 4. The genetic resistance of this flock was previously verified in experiments at AgResearch Wallaceville.

The rate of footrot infection differed considerably between ram sources (studs), as shown in Figure 1. These differences may be a result of differences in genetic resistance to footrot or a level of immunity developed from a previous footrot infection.

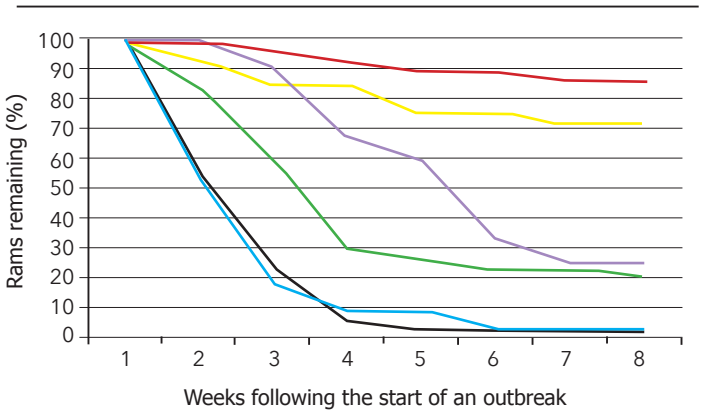

Figure 1: Proportion of rams from six sources remaining in the weeks following April 26th 2013.

There was sufficient variation in terms of resistance to footrot within the trial mob of rams to do a comparative analysis using the LFGMT. The LFGMT partly explained the likelihood of a ram remaining free of footrot. Rams that had a 1 as the first digit of their LFGMT score (first "allele") were more likely to remain free of footrot (Table 1). This was significantly better than the rams that had a 3 as the first digit (P=0.013). While rams that had a 2 or 4 as the first digit tended to be more likely to get footrot, this difference was not statistically different.

Table 1: Number of Merino rams challenged with footrot and surviving the challenge at Winchmore, when pooled across source and intake, according to the first allele from the LFGMT.

First 'allele'	Number challenged	Survived challenge	Percent survival
1	232	19	8.2
2	92	4	4.4
3	270	8	3.0
4	71	2	2.8
Total	665	33	5.0

Of the rams with a 1 as the first digit of their LFGMT test result, the ones that also had a 1 as their second digit were more likely to remain free of footrot (Table 2). However, this difference was only statistically significant between groups 1,1 and 1,5 (P = 0.032).

Table 2: Number of Merino rams challenged with footrot and surviving the challenge at Winchmore, when pooled across source and intake, according to the second allele from the LFGMT, where the first allele was reported as 1.

Genotype	Number challenged	Survived challenge	Percent survival
1,1	30	4	13.3
1,2	25	1	4.0
1,3	114	9	7.9
1,4	61	5	8.2
1,5	3	0	0.00
Overall	230	19	8.26

Of the rams that were retained at the end of the trial, seven of them were used in the Merino CPT to assess the footrot resistance of their progeny. Thirty-three additional sires from the industry were also progeny-tested at the same time.

The rams from the Winchmore trial performed better than average and were among the top performers in terms of their progeny's resistance to footrot (Figure 2). That is, the average foot scores of their progeny were lower and these sires had lower breeding values for footrot resistance.

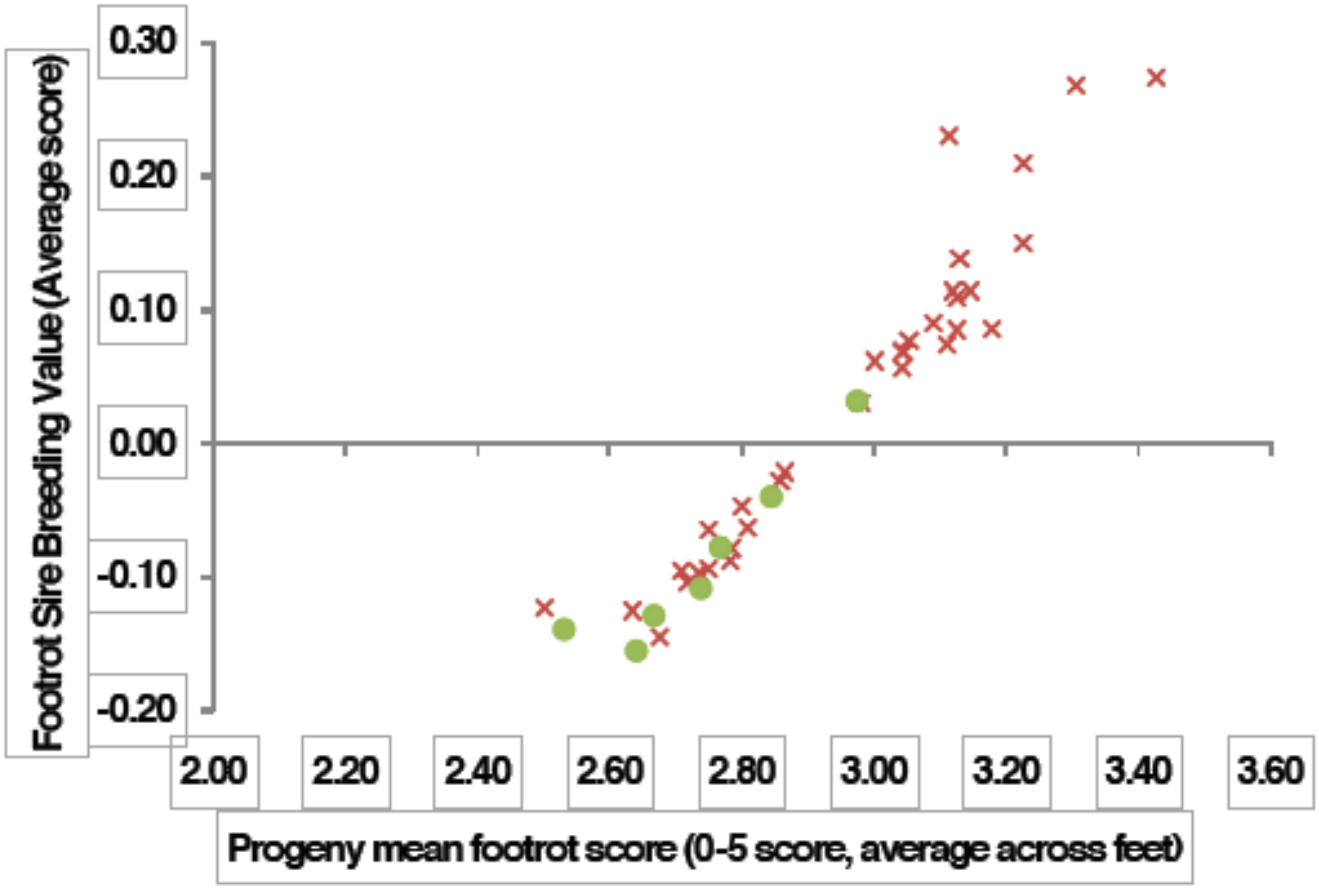

Figure 2: Progeny mean footrot score and footrot EBVs for sires discovered during the Winchmore trial (green dots) and other sires nominated from industry (red crosses). Animals in the bottom left of this graph are more genetically resistant to footrot.

ii) Merino central progeny test

Sire effect and estimated breeding values

The 2013 and 2014 drop wethers both experienced significant footrot outbreaks when conditions were conducive to its spread. The outbreak in the 2014 drop wethers resulted in significantly higher footrot scores than that in the 2013 drop animals.

The breeding values calculated for the sires reflect the genetic variation in the population of animals studied (Figure 3). Each dot on the graph shows the average footrot score for the progeny of individual sires. For example, sire 1 (indicated by the green arrow) had an EBV of -0.55 and his progeny had an average foot score of approximately 1.1, compared to sire 2 (indicated by the orange arrow), which had an EBV of 0.48 with an average progeny foot score of 3.0.

On this scale, the lower the breeding value (i.e. the more negative), the more resistant the sire is to footrot. Conversely, high positive numbers reflect sires that are highly susceptible to footrot. One sire was used in both drops and is represented here as a green triangle. This shows that although the progeny had higher footrot scores in 2014 for this sire, the breeding value does not change (as the increase in footrot score is a result of a higher environmental challenge, not a change in the genetic potential of the sire).

This is an important aspect of genetic tolerance to diseases; the sire will always have the same EBV, but the effect of the disease in their progeny will be associated with the degree of challenge. The key benefit is that the progeny from sires with good EBVs will always be better than those from sires with poor EBVs under any level of challenge.

This and previous analyses demonstrate that the heritability of resistance to footrot is approximately 25%. That is, 25% of the variation between individuals in a mob can be explained by differences in their genes.

This is similar to the heritability of resistance to worms. A heritability of this magnitude means that useful rates of genetic gain toward resistance to footrot should be able to be achieved by breeders as long as they place selection pressure on the trait. Evidence that this is achievable comes from the Broomfield Corriedales that were developed by culling animals susceptible to footrot. When sires from this strain were mated to randomly chosen ewes and compared with control Corriedale sires, the prevalence of the disease was significantly lower in the offspring of the Broomfield sires (Skerman and Moorhouse, 1987).

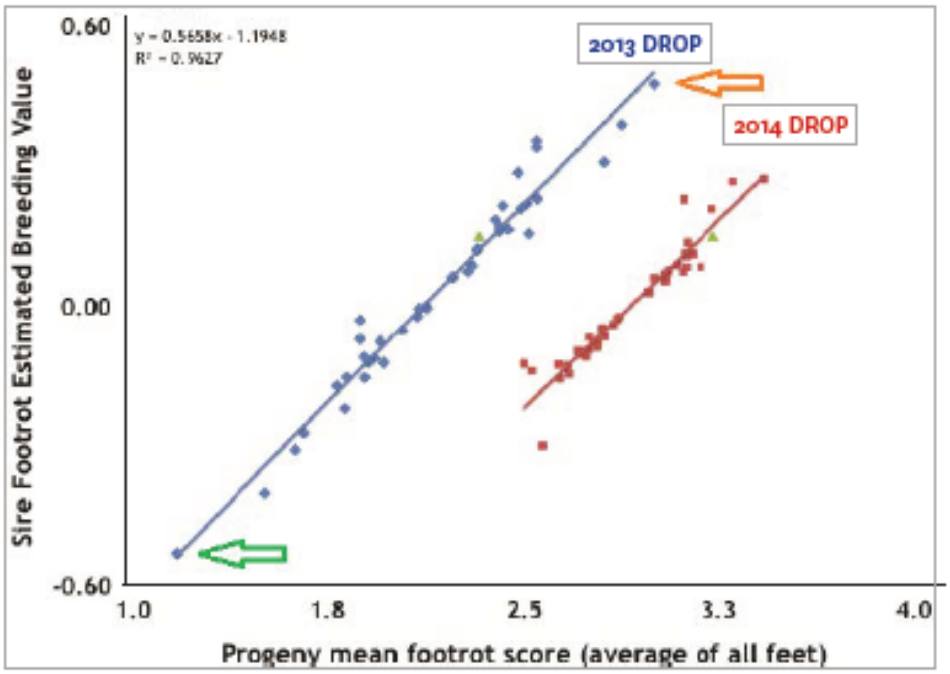

Figure 3. Progeny group average footrot score from sires with a calculated estimated breeding value for footrot. Each dot represents the average of all the progeny of an individual sire. Progeny were born in 2013 (blue diamonds) and 2014 (red squares). One sire was used in both years (green triangles).

Correlation between LFGMT score and progeny foot score.

The average foot score for the progeny of sires with different LFGMT results are shown in Table 3. Whatever the score, there was no significant difference in the progeny.

Footrot gene-marker test of sire	Number of sires	Average progeny footrot score
1,1	11	2.7
1,2	7	2.7
1,3	17	2.7
1,4	6	2.6
1,5	1	2.5
2,2	2	3.3
2,3	6	2.9
3,3	5	2.8
3,4	2	2.7

Table 3: The LFGMT score of sires and the mean footrot score of their wether progeny averaged across two years.

When the average footrot scores of progeny groups are plotted in their groups based on the LFGMT, it is obvious why there was no statistical correlation between the LFGMT and the prevalence or severity of footrot in this data set (Figure 4). Importantly this data set is across two years with two distinctly different footrot outbreaks.

In this analysis there were 11 rams with an LFGMT score of 1,1. The average footrot scores in their progeny ranged between 1.2 and 3.2, similar to the progeny of sires with an LFGMT score of 3,3.

It is clear from Figure 4 that the LFGMT results of the rams tested here do not represent a normal distribution. The rams tested have a bias toward the more favourable LFGMT results. This reflects the industry uptake of the LFGMT, which has resulted in the culling of animals with unfavourable LFGMT results over time. However, based on the results achieved here, it is extremely unlikely that the inclusion of more rams with unfavourable test results would have changed the outcome determined here.

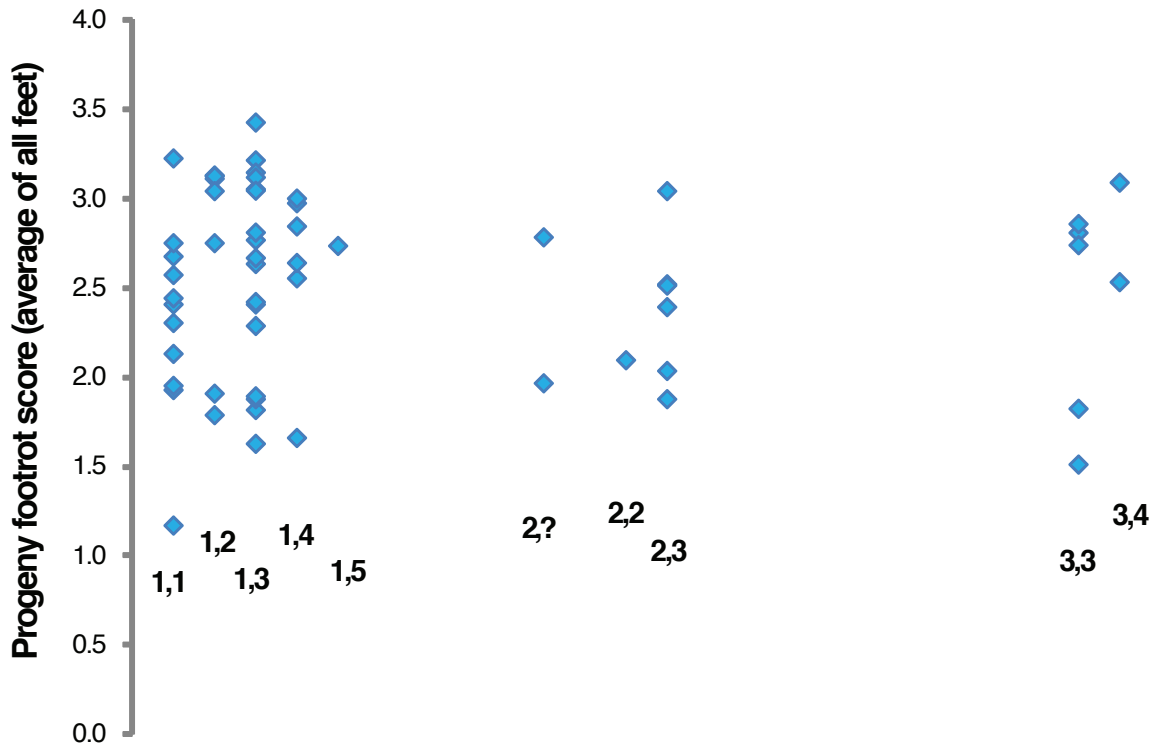

Figure 4: Progeny group average footrot score, grouped according to the sire's LFGMT score. Each dot represents the average of all the progeny of an individual sire.

Conclusions

These trials were principally about finding a group of rams that survived a significant footrot challenge and to determine whether their advantage was genetic or not. The results set out here confirm that there is exploitable genetic variation in the resistance to footrot within the New Zealand fine-wool sheep population. This variability, combined with the level of heritability of the trait, provides confidence that genetic selection can be used successfully to breed for increasing tolerance to footrot.

The other aspect of the trials was to see if there was an association between the LFGMT score of a ram and the resistance of his progeny to footrot. The low correlation between the LFGMT of an individual ram and the foot score of his progeny under a footrot challenge is a strong indication that the test has some significant limitations as a tool for predicting genetic tolerance to footrot.

However, looking to the future, these results confirm that breeding from rams with low breeding values for footrot will result in progeny with a lower likelihood of developing the disease. It also provides confidence that culling sheep that develop footrot infection will improve the rate of genetic improvement in resistance to the disease. In addition, the availability of a genomic breeding value (which is currently under development) will mean that sheep can be assessed for their genetic resistance to footrot without having to expose all sheep to a footrot challenge.

The combination of these strategies is expected to significantly decrease the impact of the disease on the fine-wool industry.

REFERENCES

Moorhouse SR and Skerman TM (1988) A genetic approach to footrot control *Proceedings of the New Zealand Society of Animal Production* 48, 139-142.

Mulvaney C (2013) A guide to the management of footrot in sheep (The New Zealand Merino Company Limited: Christchurch, New Zealand) 26-29.

VSN International (2012) 'GENSTAT for Windows' 15th edition (VSN International: Hemel Hampstead, United Kingdom).

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