

Simultaneous genetic improvement of Facial Eczema tolerance and maternal traits in sheep

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Summary

Tolerance to the toxin sporidesmin, which causes Facial Eczema (FE) in grazing livestock, is known to be moderately to highly heritable. However, given reliable phenotyping of the trait requires use of a commercially offered testing service that is expensive, genetic selection for tolerance to FE is carried out through two-stage selection by the majority of breeders, using the estimated breeding values of retained sires to determine which should be phenotyped. A group of five Romney breeders in the north of the North Island of New Zealand, an area prone to high sporidesmin counts, have been using the commercial testing service since the early 1980's. The rate of index gain they have achieved in the FE (DPX) and industry New Zealand Maternal Worth (NZMW) index are explored relative to known changes in their breeding programmes design. In their early period of FE testing, they predominately focused on the DPX index, however, from 2008 they expanded to include the NZMW index, which is reflected in increased genetic gain in the NZMW index being achieved, but with little loss in their rate of progress in the DPX index. From 2012, they have incorporated genomic testing into their breeding programme and use it as an additional tool in their two stage selection procedure. Whilst it is only early days for incorporation of genomics into their breeding programmes, since 2012 their rate of gain has almost doubled for both the NZMW and DPX indexes. The genetics trends of this group will continue to be monitored with additional years of data to determine the benefits of genomic selection on index gain.

Keywords: facial eczema, disease tolerance, genetic improvement, genomic selection

Introduction

Facial eczema (FE) is a disease observed in grazing ruminants and is caused by ingestion of the toxin sporidesmin, produced from the fungus *Pithomyces chartarum*. Throughout the world there are different strains of the fungus but the most common strains in New Zealand, which proliferate under warm, humid conditions, produce the toxin (di Menna *et al.* 2009). There is evidence that as a result of climate change, an increasing geographical area of New Zealand is experiencing elevated *P. chartarum* proliferation in more years than has been historically observed (Johnson *et al.* 2017). Ingestion of the toxin results in damage to the liver, which in the first instance results in sub-clinical depressed production, but if prolonged and severe enough, can result in clinical symptoms that are mediated by photosensitivity and include skin lesions, which is where the name FE stems from.

Genetic tolerance to FE has been demonstrated to be a moderately to highly heritable trait in New Zealand maternal sheep (Morris *et al.* 1999, 2012 & McRae *et al.* 2016).

However, because exposure to the toxin has only sporadically occurred in terms of the frequency and severity of exposure, genetic selection for tolerance in a systematic way using natural challenge has not been possible. To address this, a commercial testing procedure, Ramguard™, was launched in 1988 (Towers *et al.* 1990), which involves artificially dosing animals, under veterinary supervision, with known amounts of the toxin. Twenty-one days after dosing, serum gamma-glutamyltransferase (GGT21) levels are measured on each animal, as GGT levels are associated with liver damage (Towers & Stratton 1978).

Because the fungus historically only proliferated in relatively specific geographical regions of New Zealand (di Menna *et al.* 2009), only a limited number of New Zealand ram breeders have applied selection pressure on FE tolerance. However, a number of breeders within this region have now been testing for thirty years using the Ramguard™ service, with some also testing for four years previous to this in a research setting. The resulting FE phenotypic data is entered into the Sheep Improvement Limited (SIL) database (Newman *et al.* 2009) and breeding values for GGT21 are generated and incorporated into selection indexes alongside other maternal and growth traits in New Zealand Maternal Worth (NZMW) index + FE (DPX) index. The NZMW is a combination of growth, reproduction, survival and wool indexes (<https://www.sil.co.nz/technical>). The DPX index is derived from the FE breeding value using an economic value in cents (<https://www.sil.co.nz/technical>). Amyes & Hawkes *et al.* (2014) reviewed ram breeder industry usage of Ramguard, including using the example of the Auckland Romney Development Group (ARDG) to demonstrate the genetic gain that they have achieved for GGT21 breeding values since the development of their breeding group in 1984. Of all traits recorded in SIL for which there is a selection index, GGT21 has the smallest number of records, with the number of rams commercially tested through the Ramguard programme very low, even within the likes of the ARDG because of the cost of measurement (>\$NZ300 per ram). Amyes & Hawkes (2014) included estimated breeding value data up until the born 2012 lamb crops for the ARDG breeding group. Since this time, a number of genomic tests (different genotyping densities) have been commercially launched in New Zealand, which has enabled the generation of genomic EBVs for GGT21 and other maternal traits, which can be used by the likes of ARDG to enable better informed selections of which rams should be tested through the Ramguard programme.

This paper presents updated (from Amyes & Hawkes, 2014) trends for ARDG for the DPX index and the NZMW index, relating results to changes implemented in their breeding programmes.

Materials and methods

The average genetic merit per year from 1995 for the five ARDG flocks (SIL Flock IDs: 406, 480, 630, 1645 & 2529) was obtained from SIL for the DPX and NZMW indexes. The NZMW index combines sub-indexes for growth, reproduction, survival and wool. The equivalent averages for reported national dual purpose flocks were also obtained. The data was split into blocks of four years (the first block was five years) and the rate of gain in the respective indexes (cents/year) within each time block was calculated by regressing average index values on year (0-5 within each block).

Results and discussion

Table 1 summarises the size of the ARDG group in terms of the number of phenotypes that

are captured across the five flocks for number lambs born, weaning weight, and GGT21 on an annual basis. Of note from Table 1 is that the number of GGT21 phenotypes is only a very small proportion of the animals that have a weaning weight phenotype. With the exception of years in which natural challenge data was collected, the approach taken by breeders to generate GGT21 EBVs is to carry out a two-stage selection programme, as is commonly used for traits that are expensive or hard to measure (Jopson *et al.* 2004). Compared to other two-stage selection programmes, selection of animals for the expensive to measure GGT21 trait is based on the knowledge of the estimated genetic merit of the animal (to be discussed further below), as opposed to a cheaper proxy measure. Specifically, for the cohort of ram lambs that are retained through to approximately a year of age, a subset of ram lambs are selected based on EBVs and phenotyped through the Ramguard™ programme.

The rate of genetic gain achieved for the DPX and NZMW indexes for the ARDG group is summarised and compared to all dual purpose flocks in New Zealand in Table 2 and graphically in Figure 1. The decision was made not to contrast to other flocks that are GGT21 phenotyping, as the purpose of this paper is not specifically promote the group, rather report on genetic trends of the group, and how they relate to selection decisions made by the group. In the first three time periods reported, through to 2008, selection was based on both the NZMW and DPX indexes (or equivalent forms at the time) but relatively more emphasis being placed by the group on DPX. This is reflected in the flocks being below industry average gain for the NZMW index during this time. However, in 2008 the decision was made by the group to increase selection pressure on the NZMW index, and from this time point their annual rate of gain for the NZMW index has surpassed the industry average rate of gain. A further change in the breeding programme has been the use of genomic technologies, with molecular breeding values being generated for the flocks for the DPX and NZMW indexes since 2012. The group has been using the molecular breeding values to aid in their two stage selection process, in choosing which rams to Ramguard phenotype. Whilst there was also one flock that added additional natural challenge GGT21 phenotypes (Table 1) during this time period, previous inclusion of natural challenge phenotypes (in 2008 and 2009) did not significantly impact on rates of genetic gain. Whilst it is only evidence from one time period and reserved interpretation is needed, nearly two fold rates of increase in genetic gain compared to what they had previously achieved have been observed for both the FE and maternal indexes since 2012. This level of improvement is consistent with the potential improvement through use of genomic selection modelled by Pickering *et al.* (2013), which specifically considered the NZMW index.

Conclusions

The purpose of this paper was to investigate realised genetic (index) gain being achieved by a group of ram breeders that have applied a large amount of selection pressure towards selection for tolerance to FE, selection that relies on a two-stage selection procedure. The results reflect this pressure up until 2008, when they revised their breeding goals to increase emphasis on the NZMW index, and they subsequently have been able to achieve significant genetic gain in both indexes (albeit not at the maximum rates theoretically possible). Although it is based on only one period of time, it appears that the flocks have seen significantly increased rates of index gain since 2012, when they included genomic testing as part of their two-stage selection procedure. These trends will continue to be monitored as a realised example of the benefits of the inclusion of genomic testing within ram breeding operations.

Table 1. Summary of the number of phenotypes per year entered into Sheep Improvement Limited for five genetically linked flocks (Auckland Romney Development Group), including gamma-glutamyltransferase measured after artificial dosing of animals with a known amount of the sporidesmin toxin (GGT21)

	Count of Phenotypes Entered in to Sheep Improvement Limited			
	Survival	Weaning Weight	GGT21	% GGT21 ¹
1995	4581	3545	66	1.9
1996	4621	3633	64	1.8
1997	4691	3666	243 ²	6.7
1998	4479	3425	74	2.2
1999	3566	2719	71	2.7
2000	2874	2542	68	2.7
2001	3433	3067	71	2.3
2002	3463	2999	69	2.3
2003	3741	3213	72	2.2
2004	3696	3223	70	2.2
2005	3581	3121	68	2.2
2006	3547	3119	72	2.3
2007	3479	3036	70	2.3
2008	3190	2651	250 ²	9.4
2009	3616	3039	306 ²	10.1
2010	3074	2494	74	3.0
2011	3187	1936	82	4.2
2012	3301	2419	81	3.3
2013	3071	2622	80	3.1
2014	2940	2575	93	3.6
2015	3058	2561	403 ²	15.7
2016	3100	2098	53	2.5

¹% of animals with GGT measurements relative to weaning weight records

²In these years, one flock measured and included GGT levels measured after a natural challenge of sporidesmin

Table 2. Average gain in Sheep Improvement Limited Facial Eczema and Maternal Worth Indexes (NZMW) for five genetically linked flocks (Auckland Romney Development Group) and for all recorded dual purpose flocks

Year	Average Gain in Index (cents/year)			
	Facial Eczema Index		Maternal Worth Index	
	Industry	ARDG	Industry	ARDG
1995-2000	3	62	46	20
2000-2004	3	69	39	33
2004-2008	4	57	54	21
2008-2012	6	63	80	97
2012-2016	14	109	87	157

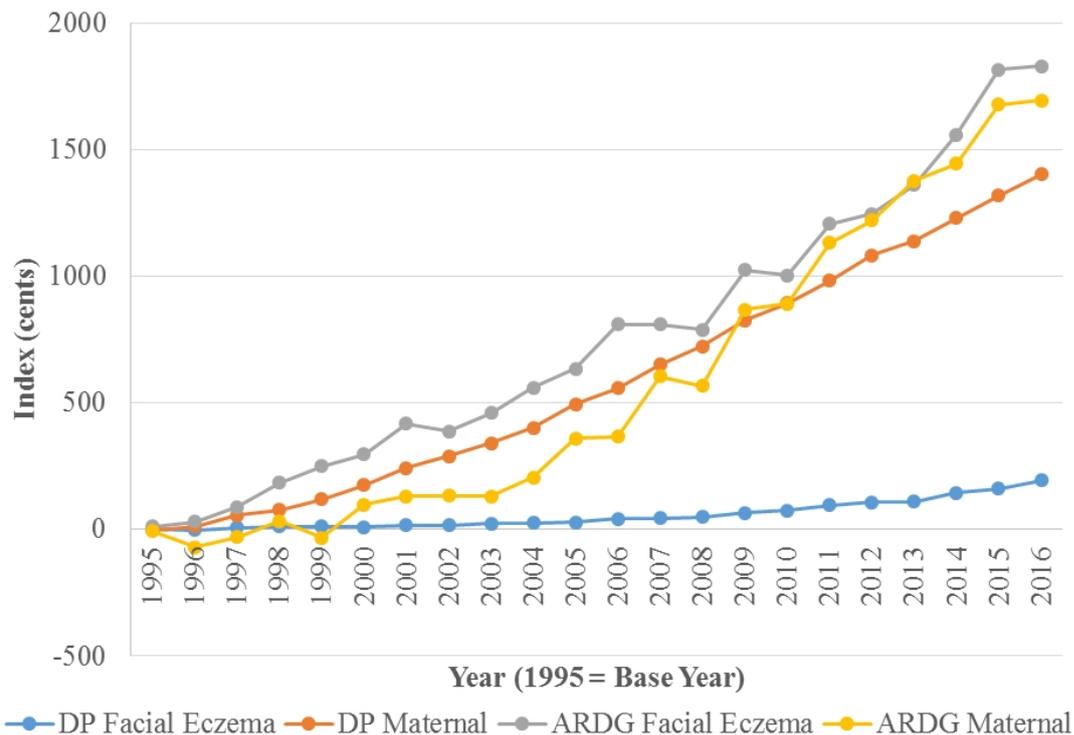


Figure 1. Index gain in Sheep Improvement Limited Facial Eczema and Maternal Worth Indexes (NZMW) for five genetically linked flocks (Auckland Romney Development Group) and for all recorded dual purpose flocks

List of References

- Amyes N.C & A.D. Hawkes 2014. Ramguard – Increasing the Tolerance to Facial Eczema in NZ Sheep. Proc. NZ Soc. Ani. Prod. 74: 154-157.
- Di Menna M.E., B.L. Smith & C.O. Miles 2009. A history of facial eczema Res. NZ J. of Agr. Res. 52: 345-367.
- Johnson P.L., C.A. Cameron, H.V. Henderson, and N.G. Cullen 2017. Brief communication: Hot years in history and facial eczema. Proc. N.Z. Soc. Anim. Prod. 77: 107-109
- Jopson, N.B., P.R. Amer, & J.C. McEwan 2004. Comparison of two-stage selection breeding programmes for terminal sire sheep. Proc. N.Z. Soc. Anim. Prod. 64:213–216.
- McRae, K.M., N.G. Cullen, N.C. Amyes, & P.L Johnson 2016. Brief communication: An update on genetic parameters for facial eczema tolerance in sheep, 76: 43-45.
- Morris C.A., N.C. Amyes, S.M. Hickey & D.B. Binnie. 1999 Genetic progress in a Romney Group Breeding Scheme. Proc. NZ Soc. Ani. Prod. 59: 117- 120.
- Morris C.A., S.H. Phua, N.G. Cullen & N.R. Towers NR 2012. Review of genetic studies of susceptibility to facial eczema in sheep and dairy cattle. NZ J. Agr. Res. 56: 156-170.
- Pickering, N.K., K.G. Dodds, B. Auvray, J.C. McEwan. 2013. The impact of genomic selection on genetic gain in the New Zealand sheep dual purpose selection index. Proc. Ass. Advance. An. Breed. Gen. 20: 175-178.
- Newman S-AN, J.C. McEwan & M.J. Young 2009. A decade of Sheep Improvement Limited (SIL). Proc. Ass. Advance. An. Breed. Gen. 18: 624-627.
- SIL, 2017. <https://www.sil.co.nz/technical> [Accessed 01 September 2017]
- Towers N.R., & G.C. Stratton 1978. Serum gamma glutamyl transferase as a measure of sporidesmin induced liver damage in sheep. NZ Vet. J. 26: 109-112.