

GENETIC, PHENOTYPIC AND ENVIRONMENTAL CORRELATIONS BETWEEN FOOTROT AND FLEECE TRAITS IN SHEEP

M. Abdelsayed¹, P.C. Thomson¹ and H.W. Raadsma¹

¹ReproGen Animal Bioscience group, Faculty of Veterinary Science, University of Sydney, Camden, NSW, 2570

SUMMARY

This study provides insight on the relationship between footrot susceptibility and fleece traits in Merino sheep, and predicts how selection for one will impact on genetic change in the other. A large pedigreed resource flock of 4,800 half-sib progeny was divided into two groups, challenged and non-challenged with footrot. Four fleece traits, greasy fleece weight (GFW), clean fleece weight (CFW), fibre diameter (FD), and clip yield (YLD) were measured over 10, 16 and 22 months of age. Various univariate and bivariate animal models were fitted to the data using combinations of phenotypes of fleece traits adjusted and unadjusted for footrot where variance and covariance estimates were obtained using ASReml-R to calculate quantitative genetic parameters. Heritability estimates for fleece traits were in the range of 0.17 to 0.69 with no impact of adjustment for footrot. Genetic, phenotypic and environmental correlations between fleece traits and footrot are generally low over the two challenges (-0.03 and 0.18). Overall, footrot is unlikely to have an adverse genetic effect on CFW and selection for either footrot or CFW is unlikely to lead to correlated responses in the other trait, and breeders can select both for animals that have higher fleece weights and improved resistance to footrot.

INTRODUCTION

Ovine footrot is a serious disease for the sheep industry and one of the most common causes of lameness with significant impacts on the welfare of sheep (Green *et al.* 2006). Footrot is a disease which may cause severe economic losses from reduced body weight and growth, decreased wool production, mortality and restrictions to marketing opportunities and causes disruptions to normal farm operations (Raadsma and Egerton 1991). With higher labour costs associated with controlling footrot, increased pressure to reduce costs and to avoid environmental contamination, the need for a long term and sustainable solution is required. One such solution is genetic selection of animals resistant to footrot (Patterson and Patterson 1989; Raadsma *et al.* 1994). The exploitation of genetic variation for resistance to footrot has been undertaken in Australia, New Zealand and the USA since the 1980s in different breeds of sheep (Bulgin *et al.* 1988; Patterson and Patterson 1989; Raadsma *et al.* 1994; Conington *et al.* 2008) and has been shown to be a cost-effective and sustainable option for the control of footrot.

In order to effect selection for increased resistance to footrot, estimates of economic losses are required to obtain relative economic weightings for resistance, and appropriate estimates of genetic variance and covariance between footrot and all traits included in the breeding objective (Marshall *et al.* 1991). One set of the production traits that is of interest to the sheep industry are fleece traits. Fleece traits are the easiest to genetically improve of all the important economic traits in sheep as they generally have a moderate to high heritability and are easy to measure (Taylor and Atkins 1997). To date no estimates of genetic relationships between resistance to footrot and fleece traits are available to predict if selection for either footrot or fleece traits will impact on genetic change in the other.

MATERIALS AND METHODS

This study uses data from an existing experimental resource collected over four years between 1988 and 1991 which has been described in detail by Raadsma *et al.* (1994).

Experimental sheep and management. At 10 months of age 4,800 lambs were allocated to two groups, an experimental group to be challenged with footrot (1,082 wethers, 480 ewe lambs) and a breeding replacement group (1,123 ewes, 227 ram lambs) which remained free from footrot. All experimental weaners were shorn at 10 months of age and the fleece traits: greasy fleece weight (GFW), clean fleece weight (CFW) fibre diameter (FD) and clip yield (YLD) were measured before challenge with footrot.

Footrot challenge I: induced challenge. The lambs from the experimental group were firstly experimentally challenged with the bacterial isolate *Dichelobacter nodosus* (VCS 1006, serogroup B), in an animal house. Sheep were then transferred to pasture after 2 weeks and remained on pasture for a further 6 months in their respective challenge groups. All sheep were inspected for footrot at 3, 6, 9, 12, 15, and 27 weeks following initial footrot challenge. After final inspections for footrot and the conclusion of the induced challenge (Challenge I), both the experimental progeny group and the non-challenged replacement breeding group were subsequently shorn at 16 months and fleece trait measurements were obtained.

Footrot challenge II: natural challenge. After 6 weeks from the final inspection of the induced challenge, all experimental sheep in the challenged group at 16 months of age were exposed to infection at 16 months of age by grazing on an irrigated paddock containing donor sheep that had previously been infected with virulent isolates of footrot causing bacteria *D. nodosus*. Sheep were then kept on non-irrigated pasture and were then inspected 6, 9, 12, 15 weeks after initial introduction on the irrigated paddock. Following the final inspection for footrot in the natural challenge (Challenge II), once more the experimental (challenged) and breeding replacement (non-challenged) groups were shorn at 22 months of age and fleece trait measurements were obtained.

At each inspection for both Challenges I and II, all feet from each sheep were scored for the presence and severity of footrot using a scoring system from 0-5 of increasing severity (Raadsma *et al* 1994).

Resistance traits-fleece traits. Overall there are three repeated measures within each of the fleece traits CFW and FD for the challenged group which include 10 months (no footrot), 16 months challenged and 22 months challenged. For the non-challenged group there were only two repeated measures within each of the fleece traits CFW and FD at 16 and 22 months. These repeated measures of CFW and FD will be examined at each point in time separately as individual traits.

Resistance traits-footrot traits. There are seven individual scores of footrot for Challenge I (induced) and for Challenge II (natural) there are five individual scores of footrot. For Challenge I and II an average was taken of the overall seven scores and overall five scores to provide two resistance traits namely Overall I and Overall II.

Statistical and genetic analyses. The following animal model was fitted for each of the fleece traits and footrot traits analysed at each point of time in the challenged and non-challenged groups:

$$Y = \mu + \text{Year} + \text{Flock} + \text{Sex} + \text{BrType} + \text{DamAge} + \beta_1 \text{DayBorn} + \beta_2 \text{BirthWt} + \text{Animal} + \epsilon$$

where Y = CFW, FD trait or footrot trait at the chosen time; the fixed effects in the model were Year, Flock, Sex, BrType (birth rearing type), DamAge (age group of dam), DayBorn (day of year

born covariate), and BirthWt (birth weight (kg), covariate). The random effects in the model were Animal (polygenic term incorporating pedigree structure) as well as ϵ , a random error term.

In addition to the above univariate model structure, overall footrot scores for Challenge I and Challenge II were fitted as covariates in the univariate animal models in order to test for the significance of footrot on fleece weight and FD. Bivariate and multivariate animal models were also fitted to the data using various combinations of fleece traits (CFW, FD) and footrot traits using ASReml-R (www.vsni.co.uk) where variance and covariance estimates were obtained in order to calculate heritabilities, genetic, phenotypic environmental correlations and estimated breeding values.

RESULTS AND DISCUSSION

Genetic parameters: fleece traits with and without footrot as a fixed effect in the univariate animal models. For animals challenged with footrot, heritability estimates for CFW were moderate (Table 1), and high for FD (Table 2). There was no clear change in heritabilities when footrot was included as a fixed effect in the model (comparable estimates are CFW16c/FR 0.23±0.07, CFW22c/FR 0.48±0.09, FD16c/FR 0.70±0.08, FD22c/FR 0.68±0.1). Should the presence of footrot have had a major environmental impact on CFW and FD, we would have expected a higher heritability for CFW and FD when variation due to footrot was accounted for, compared with a model that did not have footrot as a term in the model. Clearly this is not the case, and is in part confirmed by similar genetic and environmental variance components for CFW and FD under both models, suggesting that effectively the same degree of genetic variation in the fleece traits is expressed when footrot is or is not accounted for in the model. Similarly the heritability estimates for both CFW and FD were almost identical to estimates derived from the animals challenged with footrot compared to the animals which were not challenged with footrot (Table 1 and Table 2 challenged (c) and non challenged (nc) respectively). This is also evident by the high genetic correlations between challenged and non-challenged expressions of fleece traits as shown in Tables 1 and 2 for CFW and FD respectively. Furthermore the impact of FR on EBVs of fleece traits is minimal by the near identical rankings of sires when data from either the challenged and non-challenged progeny groups is used in the EBV estimation (data not shown). The challenge of footrot is confounding the expression of fleece traits in non-challenged animals and as a result phenotypic and environmental correlations cannot be estimated (* Table 1 and 2). The results suggest that expression of either CFW or FD under either an environment in which footrot is expressed or not, the genetic and environmental variation is the same in both fleece traits leading to the conclusion that no major effect of genotype by environment interaction is evident.

Table 1: Genetic parameter estimates for clean fleece weight (CFW) at 10, 16, 22 months of age challenged with footrot (c) and non-challenged-free of footrot (nc). Genetic correlations below diagonal, phenotypic correlations above diagonal, with environmental correlations in parentheses, and heritabilities ± S.E. on diagonal. * = cannot be estimated

	10nc	16c	22c	16nc	22nc
10nc	0.22 ± 0.06	0.36 (0.17)	0.47 (0.36)	*	*
16c	0.96	0.21 ± 0.06	0.55 (0.37)	*	*
22c	0.72	0.94	0.49 ± 0.09	*	*
16nc	0.86	0.98	0.85	0.30 ± 0.06	0.60
22nc	0.62	0.89	0.73	0.89(0.42)	0.37 ± 0.07

Table 2: Genetic parameter estimates for fibre diameter (FD) at 10, 16, 22 months of age challenged with footrot (c) and non-challenged-free of footrot (nc). Genetic correlations below diagonal, phenotypic correlations above diagonal, with environmental correlations in parentheses, and heritabilities \pm S.E. on diagonal. * = cannot be estimated.

	10nc	16c	22c	16nc	22nc
10nc	0.55 \pm 0.07	0.72 (0.39)	0.62 (0.20)	*	*
16c	0.93	0.71 \pm 0.08	0.74 (0.32)	*	*
22c	0.85	0.92	0.69 \pm 0.14	*	*
16nc	0.99	0.91	0.99	0.60 \pm 0.06	0.69
22nc	0.88	0.86	0.99	0.93(0.43)	0.58 \pm 0.13

Table 3: Genetic (r_g), phenotypic (r_p) and environmental (r_e) correlations between fleece traits clean fleece weight (CFW) and fibre diameter (FD) and footrot challenges.

Trait	r_g	r_e	r_p
16c CFW and Overall FR score at Challenge I	-0.05	0.07	0.05
22c CFW and Overall FR score at Challenge II	-0.23	0.05	-0.05
16c FD and Overall FR score at Challenge I	0.11	-0.07	0.00
22c FD and Overall FR score at Challenge II	-0.28	0.20	-0.04

Genetic parameters: bivariate analysis between fleece traits and footrot. Genetic, phenotypic and environmental correlations between the economical important fleece traits CFW and FD and footrot are generally low and negative as shown in Table 3. The findings indicate that fleece traits and footrot resistance are unlikely to be influenced by the same genes. The neutral to low genetic correlations between fleece traits and footrot resistance will allow for selection of both traits simultaneously in a designed breeding program if both traits were included in the selection index.

CONCLUSION

From this study we can conclude that footrot is unlikely to have an adverse genetic effect on fleece traits and selection for either footrot or any of the fleece traits examined are unlikely to lead to correlated responses in the other trait. The impacts of these findings on a selection program are found to be neutral where breeders can select both for animals that have better fleece characteristics and improved resistance to footrot.

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