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# The effects of penalization of FAMACHA<sup>®</sup> scores of lambs treated for internal parasites on the estimation of genetic parameters and prediction of breeding values

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### ABSTRACT

Internal parasite infestation in sheep can be practically assessed using a subjective score for the color of the inner eyelid (FAMACHA<sup>®</sup> score). Additive genetic variation for this trait would permit selection against internal parasite infection or for tolerance to internal parasites. However, medicated sheep have improved FAMACHA<sup>®</sup> scores shortly after treatment; use of these records could produce misleading breeding values. The objectives of this study were to (1) apply different penalties to FAMACHA<sup>®</sup> records of lambs that required treatment, and thereby generate distinct data sets associated with those penalties, and (2) estimate heritability and predicted breeding values for each data set under moderate and severe internal parasite challenge conditions. Two types of penalties were applied. The first penalty consisted of adding the average increase (worsening) in FAMACHA<sup>®</sup> score of untreated lambs to the records of the treated lambs in a given year. The second type of penalty was the assignment of a high value as the actual FAMACHA<sup>®</sup> score of treated lambs; in multiple analyses this value was 5 (which is the maximum possible FAMACHA<sup>®</sup> score), or increased to 6, 7, 8, 9, or 10. Single-trait animal models were employed in analyses of FAMACHA<sup>®</sup> scores in Merino lambs ( $n = 1671$ ) across 6 yr. Results indicated that, under both moderate and severe internal parasite challenge conditions, application of penalties increased the additive genetic variance (and therefore the estimated heritability) relative to analyses in which records of treated lambs were included without any modification or analyses in which they were excluded. Estimates of correlation coefficients of predicted breeding values for FAMACHA<sup>®</sup> score from the various analyses indicated that, in most cases, there were strong positive associations among those from the penalized data sets. Correlations of ranks of predicted breeding values were also strongly positive; however, those involving penalty values of 10 were lower, indicating some rank changes. Distributions of predicted breeding values indicated that in moderate internal parasite challenge conditions, the analyses of penalized data removed multi-modality, but resulted in highly leptokurtic distributions (many observations congregated at the mean). In the severe internal parasite challenge conditions, applications of penalties induced multi-modality. Penalizing records of treated lambs with a value of 5 appears to be a reasonable method for more closely estimating the additive genetic variance and therefore, the heritability, which may permit more useful genetic analyses. Excessive penalization of records of treated lambs appeared to be unnecessary at best, and at worst detrimental to genetic evaluation through rank changes of predicted breeding values.

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## 1. Introduction

Selection for improved resistance to or tolerance of gastrointestinal nematodes is a viable option for sheep breeders (e.g., Eady et al., 2003; Karlsson and Greeff, 2006). Implementation of a practical system for assessment of internal parasite burden based on visual appraisal of anemia in the ocular conjunctivae (FAMACHA<sup>®</sup>, Malan and Van Wyk, 1992; Bath et al., 1996) has facilitated accumulation of records. This method of assessment (FAMACHA<sup>®</sup>) appears to be strongly genetically correlated with other measures of internal parasite burden (Riley and Van Wyk, 2009). Effective treatment of a lamb immediately alters its infestation, and consequently, improves (lowers) its FAMACHA<sup>®</sup> score. This makes records subsequent to treatment inconsistent with the individual's genuine response to the parasite, and therefore, inappropriate for breeding value prediction. There may be a way to incorporate information from treated sheep that will enhance predicted breeding values. Bisset et al. (1996) adjusted all records for treatment status of the individual. Such an adjustment may be a less effective strategy than record penalization in genetic analyses (Riley and Van Wyk, 2009). It is not known how different methods of penalization of records of treated lambs or the severity of penalization will affect the distribution of predicted breeding values under different intensities of internal parasite challenge environments. The objectives of this study were to (1) apply increasingly heavy penalties (higher values of FAMACHA<sup>®</sup> scores) to records of lambs that required treatment, and thereby generate distinct data sets associated with those penalties, and (2) estimate heritability and predicted breeding values for each data set under moderate and severe internal parasite challenge conditions.

## 2. Materials and methods

The population and the data were described in detail previously (Riley and Van Wyk, 2009). In brief, records were obtained from weaned (at an average of 100 d of age) Merino ram and ewe lambs ( $n = 1671$ ) from a South African flock from 1999 to 2005. In addition to other traits, FAMACHA<sup>®</sup> scores (1–5; higher numbers indicate lighter color and increased anemia due to internal parasites [primarily *Haemonchus contortus*]) were recorded on all lambs approximately monthly through the duration of the internal parasite season (summer; approximately October through March of each year). Lambs were treated for internal parasites with Levamisole at 7.5 mg/kg body weight if they had a FAMACHA<sup>®</sup> score of 3, 4, or 5 at these monthly observations. Ultimately, the entire flock was treated when the farmer and veterinarians subjectively determined later in the season that the peak of the *Haemonchus* season had been reached.

The occurrence of treatments across time within each year was considered in the arbitrary identification of levels of internal parasite severity or challenge within the flock in the respective years. **Severe** internal parasite challenge corresponded to records obtained at the last observation, that is, when the decision was made to mass treat the flock for internal parasites. **Moderate** internal parasite challenge corresponded to records obtained approximately 1 month prior to mass treatment of the flock. The records analyzed in this study were from these two times only.

FAMACHA<sup>®</sup> records of treated lambs were analyzed in 9 separate analyses across both data sets (moderate and severe internal parasite challenge). When a penalty was applied, it was applied to records of lambs that had been treated at any earlier time in the season for reason of individual inability to manage current worm challenge unaided; that is, once a lamb was treated, all of its subsequent records were penalized. For both moderate and severe internal parasite challenge data sets, seven separate penalties were evaluated. A complete genetic analysis was conducted on each data set after application of each penalty. Penalties consisted of (1) assigning the maximum (or greater than maximum) value for FAMACHA<sup>®</sup>

**Table 1**

Simple statistics for FAMACHA<sup>®</sup> scores ( $n = 1671$ ) with different penalties for records of treated lambs ( $n = 53$ ) under moderate internal parasite challenge.<sup>a</sup>

Penalty for treated records	Mean	SD	Range	
None	1.42	0.6	1	4
Exclusion	1.41	0.59	1	4
Added average increase of nontreated lambs	1.45	0.64	1	4.48
<i>Assigned value of:</i>				
5	1.52	0.86	1	5
6	1.56	0.99	1	6
7	1.59	1.14	1	7
8	1.62	1.29	1	8
9	1.65	1.45	1	9
10	1.68	1.61	1	10

<sup>a</sup> Penalties for records of treated lambs: None: included without modification. Exclusion: excluded from analysis. Added average increase of nontreated lambs: the increase (worsening) in average FAMACHA<sup>®</sup> score of lambs that were never treated was added to each record of treated lambs. Actual FAMACHA<sup>®</sup> score of treated lambs was replaced with the maximum possible score of 5; then subsequent analyses replaced actual scores with values of 6, 7, 8, 9, or 10.

score to all records of previously treated lambs, that is, values of 5 (or, in turn, values of 6, 7, 8, 9, or 10), and (2) the algorithm of Riley and Van Wyk (2009): At each record date, simple means for treated and untreated animals were calculated for each trait. Using these means and means from the collection date immediately prior, when the mean FAMACHA<sup>®</sup> score of the untreated group worsened, this mean change was applied as a penalty to all previously treated lambs. Thus any average improvement (i.e., lower FAMACHA<sup>®</sup> score than that of the untreated lambs) of treated lambs was added to each individual record. When the mean of the untreated group improved, and the treated mean improved more than the untreated mean improvement, a penalty was applied to records of treated lambs to limit the improvement to that of the untreated group.

Additionally, for both data sets (moderate and severe internal parasite challenge), analyses were conducted in which records of treated lambs were included without modification or were simply deleted. These results were reported earlier (Riley and Van Wyk, 2009), and were included here to permit comparisons with results from the variety of penalization methods. Simple statistics for FAMACHA<sup>®</sup> score as it was used as the dependent variable (unmodified, or after penalization or exclusion) in moderate and severe internal parasite challenge conditions are shown in Tables 1 and 2, respectively. Except when the method of penalization caused some deviation from the discrete categories, FAMACHA<sup>®</sup> score was categorically distributed. These data were analyzed as continuously distributed variables. Linear and categorical genetic evaluations often perform similarly (Meijering and Gianola, 1985).

The fixed effect portions of models were built using the MIXED procedures of SAS (SAS Inst. Inc., Cary, NC) in both data sets (moderate and peak internal parasite challenge). Investigated effects included birth status (single or multiple birth), age of dam, age (as linear and quadratic covariates), gender-year combinations (contemporary groups), and interactions. Final models consisted of effects with  $F$ -ratios with  $P \leq 0.05$ .

Genetic analyses were conducted using animal models in MTDFREML (Boldman et al., 1995) with the fixed effects described above. The pedigree consisted of 2539 animals. All were single-trait analyses and modeled only the animal (additive genetic) effect. Estimates of additive genetic variance and heritability for FAMACHA<sup>®</sup> score were produced using both moderate and severe internal parasite challenge data for each analysis. Multiple starts at different initial values for variances were employed as an attempt to avoid convergence of equations to local maxima.

Breeding values were predicted for all individuals in the pedigree in both internal parasite challenge levels for each of the 9 data sets for penalization of the records of treated lambs using MTDFREML. Estimates of Pearson correlation coefficients of breeding values and Spearman correlation of ranks of predicted breeding values from the different analyses were generated using the CORR procedures of SAS. These estimates of correlation were obtained using predicted breeding values (1) for all individuals in the pedigree, and (2) for only the best (lowest numerically) 8% of the lambs with records ( $n = 144$ ). Because the 9 different analyses did not result in the same individuals with the best predicted values, the top 144

**Table 2**

Simple statistics for FAMACHA<sup>®</sup> scores of lambs ( $n=1604$ ) with different penalties for records of treated lambs ( $n=234$ ) under severe internal parasite challenge conditions.<sup>a</sup>

Penalty for treated records	Mean	SD	Range	
None	1.92	0.83	1	5
Exclusion	1.90	0.83	1	5
Added average increase of nontreated lambs	2.12	1.00	1	6.32
Assigned value of:				
5	2.36	1.33	1	5
6	2.50	1.64	1	6
7	2.65	1.96	1	7
8	2.79	2.28	1	8
9	2.94	2.62	1	9
10	3.09	3.00	1	10

<sup>a</sup> Penalties for records of treated lambs: None: included without modification. Exclusion: excluded from analysis. Added average increase of nontreated lambs: the increase (worsening) in average FAMACHA<sup>®</sup> score of lambs that were never treated was added to each record of treated lambs. Actual FAMACHA<sup>®</sup> score of treated lambs was replaced with the maximum possible score of 5; then subsequent analyses replaced actual scores with values of 6, 7, 8, 9, or 10.

predicted breeding values from each were used in turn with the predicted breeding values from the other 8 analyses that corresponded to those same individuals. This resulted in 9 sets of estimated correlation coefficients which varied slightly from each other. Therefore, the estimated correlation coefficients were averaged for tabular presentation. Estimates of skew and kurtosis for each distribution were produced using the UNIVARIATE procedures of SAS, and were tested for significance according to Snedecor and Cochran (1989).

### 3. Results

#### 3.1. Moderate internal parasite challenge

Estimates of heritability for FAMACHA<sup>®</sup> score in moderate internal parasite challenge conditions were essentially constant (Table 3) when records of treated sheep were assigned values of 5–10. This indicated that increasing the value of records by an increment of 1 for treated lambs increased both the additive genetic and phenotypic variances by the same relative amount. All of these estimates of heritability appeared to be larger than those from analyses of data sets where such records were included without adjustment, excluded, or penalized by adding

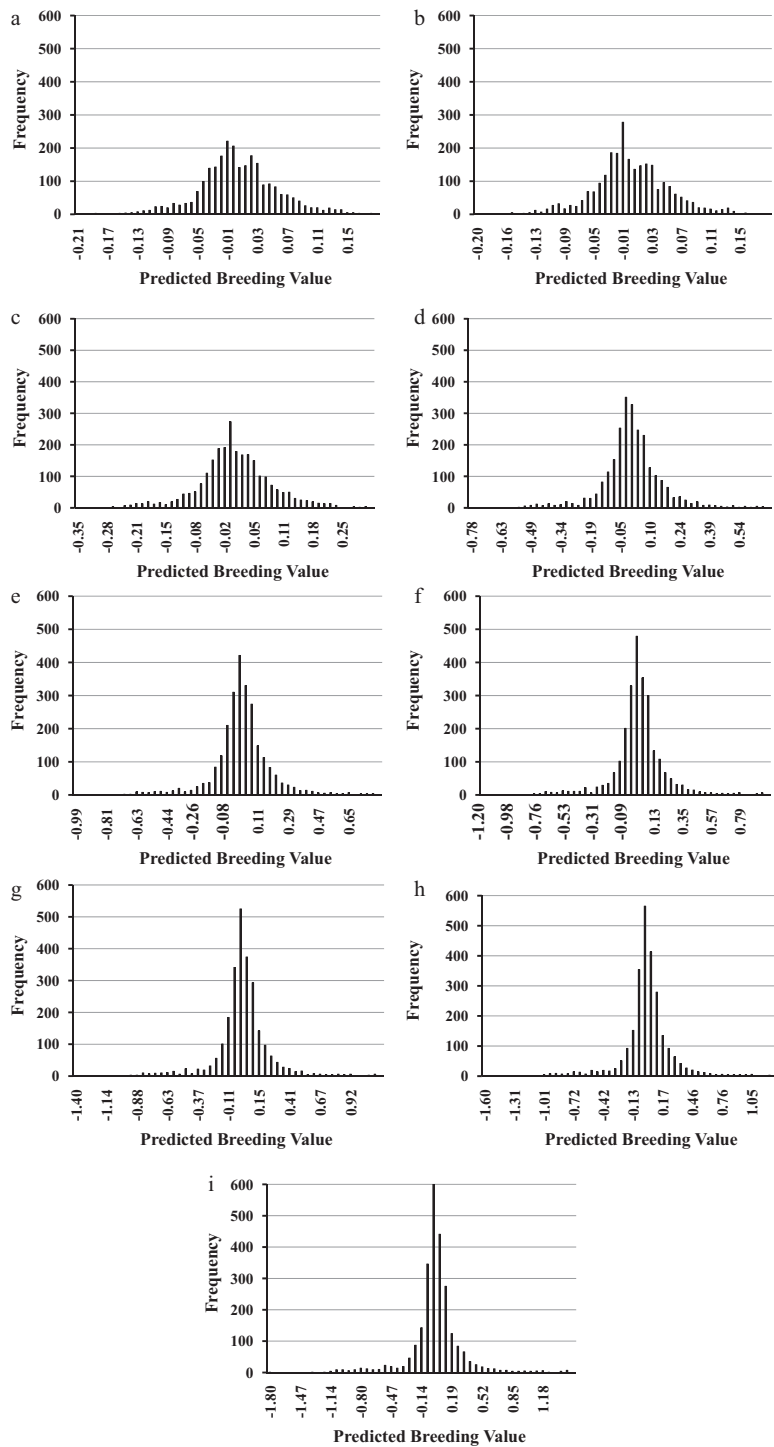
the average increase in FAMACHA<sup>®</sup> score for the lambs that were not treated. The range of predicted breeding values was smallest from results in which records of treated lambs were excluded and from results in which records of treated lambs were included without adjustment (differences between high and low breeding values were 0.39 and 0.4, respectively). This range increased for breeding values corresponding to increases in the value assigned to treated lambs. The correspondence (measured as Pearson's correlation coefficients) between breeding values for individuals that were produced from the different analyses ranged from 0 to 1.0 (Table 4). There were strong positive correlations ( $r>0.9$ ) for breeding values of the best 8% of the lambs produced from the analyses in which values of 5 through 10 were assigned as records of treated lambs. Although positively correlated with each other, predicted breeding values from analyses in which records of treated lambs were simply included without adjustment or excluded showed the lowest association with predicted breeding values of the other analyses. The rank correlation coefficients shown above the diagonal in Table 4 indicated substantial rank changes of predicted breeding values of the best 8% of the lambs from the analyses which utilized penalized records of treated lambs relative to those in which those records were included without modification or were excluded. Minimal rank changes of predicted breeding values were indicated by the near unity correlation coefficients for the predicted breeding values where the records of treated lambs were penalized by assigning values of 5–10. Histograms of the predicted breeding values from the nine data sets (Fig. 1) indicated that distributions from analyses in which records were included without adjustment or were excluded appeared to be bi- to multi-modal (Fig. 1a and b). In the analyses in which records of treated lambs were penalized, heavier penalties resulted in more peaked distributions, that is, predicted breeding values had greater frequencies near the mean. Significant positive estimates of skewness (ranged from 0.15 to 0.31; SE approximately 0.049) were detected for the breeding value distributions in which values of 6, 7, 8, 9, or 10 were assigned to records of treated lambs, although

**Table 3**

Estimates of additive genetic variance ( $s_a^2$ ), heritability ( $h^2$ ), and range of predicted breeding values for FAMACHA<sup>®</sup> scores of lambs with different penalties for records of treated lambs in moderate internal parasite challenge conditions.<sup>a</sup>

Penalty for treated records	$s_a^2$	$h^2$	Predicted breeding value	
			Range	
None	0.025	0.08 ± 0.038	−0.21	0.19
Exclusion	0.024	0.07 ± 0.039	−0.20	0.19
Added average increase of nontreated lambs	0.042	0.11 ± 0.041	−0.35	0.31
Assigned value of:				
5	0.099	0.15 ± 0.043	−0.78	0.68
6	0.135	0.16 ± 0.043	−0.99	0.84
7	0.178	0.16 ± 0.043	−1.20	1.01
8	0.228	0.16 ± 0.042	−1.40	1.18
9	0.286	0.16 ± 0.042	−1.60	1.35
10	0.351	0.16 ± 0.042	−1.80	1.52

<sup>a</sup> Penalties for records of treated lambs: None: included without modification. Exclusion: excluded from analysis. Added average increase of nontreated lambs: the increase (worsening) in average FAMACHA<sup>®</sup> score of lambs that were never treated was added to each record of treated lambs. Actual FAMACHA<sup>®</sup> score of treated lambs was replaced with the maximum possible score of 5; then subsequent analyses replaced actual scores with values of 6, 7, 8, 9, or 10.



**Fig. 1.** Distributions of predicted breeding values for FAMACHA<sup>®</sup> scores of Merino lambs in moderate internal parasite challenge conditions from analyses in which records of treated lambs were included without modification, excluded, or penalized. (a) Includes unmodified records of treated lambs. (b) Records of treated lambs excluded. (c) Records of treated lambs penalized with untreated average. (d–i) Records of treated lambs assigned values of 5, 6, 7, 8, 9, or 10, respectively.

the scale in Fig. 1 does not make this visually obvious. Estimates of kurtosis for all distributions were highly significant and ranged from  $1 \pm 0.1$  (records of treated lambs included without adjustment) to  $7.5 \pm 0.1$  (records of

treated lambs assigned values of 10), and increased as heavier penalties were assessed. All distributions were taller than normal distributions (leptokurtic) and had longer tails.

**Table 4**

Estimates of correlation of predicted breeding values and ranks of breeding values for FAMACHA<sup>®</sup> scores for the best (8%,  $n = 144$ ) Merino lambs under moderate internal parasite challenge conditions.<sup>a,b,c</sup>

Penalty for treated records	N	E	A	5	6	7	8	9	10
None (N)		0.99	0.76	0.38	0.26	0.16			
Exclusion (E)	0.99		0.74	0.35	0.22				
Average increase (A)	0.82	0.79		0.83	0.74	0.66	0.60	0.56	0.53
Assigned value of:									
5	0.39	0.35	0.81		0.98	0.95	0.92	0.90	0.88
6	0.25	0.21	0.72	0.99		0.99	0.97	0.96	0.95
7	0.16		0.64	0.96	0.99		0.99	0.99	0.98
8			0.59	0.94	0.98	1.00		1.00	0.99
9			0.54	0.92	0.97	0.99	1.00		1.00
10			0.51	0.90	0.96	0.98	0.99	1.00	

<sup>a</sup> Estimates of correlation coefficients for predicted breeding values shown below the leading diagonal; estimates of rank correlation coefficients shown above the leading diagonal.

<sup>b</sup> Penalties for records of treated lambs: None (N): included without modification. Exclusion (E): excluded from analysis. Added average increase of nontreated lambs (A): the increase (worsening) in average FAMACHA<sup>®</sup> score of lambs that were never treated was added to each record of treated lambs. Actual FAMACHA<sup>®</sup> score of treated lambs was replaced with the maximum possible score of 5; then subsequent analyses replaced actual scores with values of 6, 7, 8, 9, or 10.

<sup>c</sup> Estimates of correlation  $<|0.15|$  did not differ from 0 ( $P > 0.05$ ) and are omitted from this table.

### 3.2. Severe internal parasite challenge

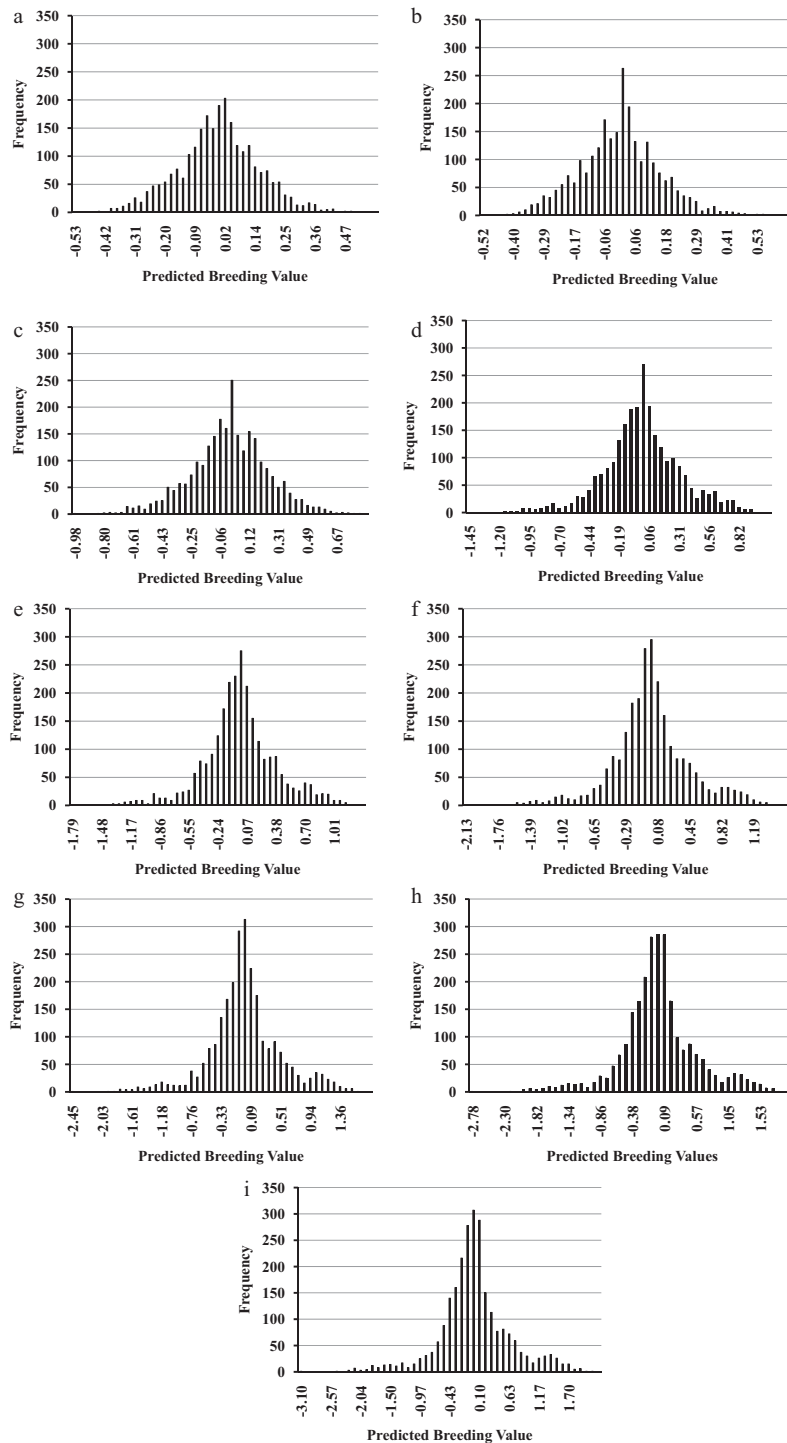
Estimates of heritability for FAMACHA<sup>®</sup> score appeared to be highest when penalties were applied to records of treated lambs at the lowest levels, that is, when values of 5 were assigned (Table 5). This indicated that the higher estimates of additive genetic variance from analyses with higher penalty values were accompanied by even higher estimates of phenotypic variance. The difference between the highest and lowest breeding values was lowest (1.11) in the results from analyses where the records of treated lambs were included without adjustment. That difference was highest (5.43) in breeding values produced when records of treated lambs were given a value of 10. Estimates of correlation coefficients between predicted breeding values for the best 8% of the lambs from the different analyses were generally large and positive (Table 6). The association of breeding values from the analyses in which records of treated lambs were included without modification or excluded had lower or no correlation with breeding values from all penalized record analyses (below leading diagonal in Table 6). Rank correlation coefficients (above the diagonal) were also positive. Substantial rank changes of predicted breeding values occurred as evidenced by the rank correlation coefficients involving those from unmodified values, excluded values, and assigned values of 10 for records of treated lambs.

Predicted breeding value distributions from the severe internal parasite challenge data are depicted in histograms in Fig. 2. Skew was not detected in any of these distributions ( $P > 0.1$ ). All distributions were leptokurtic ( $P < 0.01$ ); ranged from 0.36 for results where records of treated lambs were included without adjustment to 1.87 for results from analyses where treated lambs were assigned FAMACHA<sup>®</sup> values of 10; SE for each was approximately 0.1) but to a lesser degree than the distributions from moderate internal parasite challenge data, as can be visually noted by comparison of the histograms in Figs. 1 and 2. Also of note is the apparent multi-modality of the distributions of breeding values induced by assigning high values of FAMACHA<sup>®</sup> to records of treated lambs (Fig. 2, panels c–i).

### 4. Discussion

Penalization of records of treated lambs improved estimates of heritability for FAMACHA<sup>®</sup> score, but simply elevating the amount of the penalty did not increase estimates of heritability in either internal parasite challenge environment. Genetic variation was greater (as a proportion of phenotypic variance) in the more severe internal parasite challenge environment, which was consistent with previous results (Greeff et al., 1995; Woolaston and Windon, 2001; Riley and Van Wyk, 2009). Estimates of heritability increased to a plateau in analyses of data from both environments; that is, in both internal parasite challenge environments there appeared to be a threshold above which the increased penalization increased only the phenotypic variance. Estimates of additive genetic variance and heritability are possibly underestimated in the analyses in which treated records were either included without modification or were excluded; this especially appeared to be the case in the severe internal parasite challenge data. Penalization of records of treated lambs appeared to compensate somewhat for this underestimation. It must be concluded that indiscriminate intensification of penalties fails to recover additional additive genetic variance that might exist.

Correspondence between predicted breeding values for FAMACHA<sup>®</sup> score among the best (numerically lowest) was positive and strong when records of treated lambs were penalized in some way. Although numerically positive, association between breeding values produced from the penalty analyses with those from analyses in which records of treated lambs were either included without modification or were excluded were much smaller, especially in the severe internal parasite challenge environment conditions. Rank changes in predicted breeding values were substantial when considering the penalty results with the no penalty results. Among the predicted breeding values from analyses of penalized data in severe internal parasite challenge conditions, the simple associations and the associations among ranks of breeding values were much weaker when the penalty was assignment of a value of



**Fig. 2.** Distributions of predicted breeding values for FAMACHA<sup>®</sup> scores of Merino lambs in severe internal parasite challenge conditions from analyses in which records of treated lambs were included without modification, excluded, or penalized. (a) Includes unmodified records of treated lambs. (b) Records of treated lambs excluded. (c) Records of treated lambs penalized with untreated average. (d–i) Records of treated lambs assigned values of 5, 6, 7, 8, 9, or 10, respectively.

10. This indicates that application of heavier penalties to treated records not only fails to add benefit (in the form of increased heritability estimates) but creates potentially misleading results.

As estimates of heritability became more or less constant with higher penalty values, the ranges of predicted breeding values continued to increase. All of the distributions of breeding values appeared to differ from a normal

**Table 5**

Estimates of additive genetic variance ( $s_a^2$ ), heritability ( $h^2$ ), and range of predicted breeding values for FAMACHA<sup>®</sup> scores of lambs with different penalties for records of treated lambs in severe internal parasite challenge conditions.<sup>a</sup>

Penalty for treated records	$s_a^2$	$h^2$	Predicted breeding value	
			Range	
None	0.101	0.17 ± 0.049	−0.53	0.58
Exclusion	0.110	0.19 ± 0.055	−0.52	0.64
Added average increase of nontreated lambs	0.208	0.23 ± 0.053	−0.98	0.86
Assigned value of:				
5	0.372	0.23 ± 0.051	−1.45	1.07
6	0.533	0.22 ± 0.05	−1.79	1.32
7	0.729	0.21 ± 0.049	−2.13	1.55
8	0.961	0.20 ± 0.049	−2.45	1.79
9	1.225	0.20 ± 0.048	−2.78	2.01
10	1.525	0.19 ± 0.048	−3.10	2.23

<sup>a</sup> Penalties for records of treated lambs: None: included without modification. Exclusion: excluded from analysis. Added average increase of nontreated lambs: the increase (worsening) in average FAMACHA<sup>®</sup> score of lambs that were never treated was added to each record of treated lambs. Actual FAMACHA<sup>®</sup> score of treated lambs was replaced with the maximum possible score of 5; then subsequent analyses replaced actual scores with values of 6, 7, 8, 9, or 10.

**Table 6**

Estimates of correlation of predicted breeding values and ranks of breeding values for FAMACHA<sup>®</sup> scores for the best (8%,  $n = 144$ ) Merino lambs under severe internal parasite challenge conditions.<sup>a,b,c</sup>

Penalty for treated records	N	E	A	5	6	7	8	9	10
None (N)		0.87	0.73	0.51	0.40	0.34	0.29	0.25	0.22
Exclusion (E)	0.90		0.57	0.36	0.23				
Average increase (A)	0.76	0.62		0.88	0.82	0.77	0.74	0.71	0.69
Assigned value of:									
5	0.53	0.41	0.89		0.98	0.96	0.94	0.92	0.90
6	0.44	0.29	0.84	0.99		0.99	0.98	0.97	0.96
7	0.37		0.80	0.97	1.00		1.00	0.99	0.98
8	0.32		0.76	0.95	0.99	1.00		1.00	0.99
9	0.28		0.73	0.94	0.98	0.99	1.00		1.00
10	0.26		0.71	0.92	0.97	0.99	1.00	1.00	

<sup>a</sup> Estimates of correlation coefficients for predicted breeding values shown below the leading diagonal; estimates of rank correlation coefficients shown above the leading diagonal.

<sup>b</sup> Penalties for records of treated lambs: None (N): included without modification. Exclusion (E): excluded from analysis. Added average increase of nontreated lambs (A): the increase (worsening) in average FAMACHA<sup>®</sup> score of lambs that were never treated was added to each record of treated lambs. Actual FAMACHA<sup>®</sup> score of treated lambs was replaced with the maximum possible score of 5; then subsequent analyses replaced actual scores with values of 6, 7, 8, 9, or 10.

<sup>c</sup> Estimates of correlation  $<|0.15|$  did not differ from 0 ( $P > 0.05$ ) and are omitted from this table.

distribution, primarily because of significant kurtosis in the moderate internal parasite challenge data for the various analyses indicated extensive congregation of breeding values around the mean. This should not be surprising, since only 3% of records were penalized in any analysis and the estimates of heritability were low.

The occurrence of multi-modality in the various distributions may be due to the categorical nature of this trait. Penalization of records of treated lambs appeared to have distinct effects on this multi-modality contingent upon the internal parasite challenge environment. Penalization appeared to remove the slight multi-modality that was characteristic of distributions of predicted breeding values in the analyses of moderate internal parasite challenge data in which records of treated lambs were included without modification or were excluded. In the distributions of predicted breeding values from analyses of severe internal parasite challenge data, application of heavier penalties appeared to induce multi-modality (Fig. 2, panels d–i). These departures from normality in these distributions may not be a source of serious concern for the effectiveness of the breeding values themselves.

In genetic analyses of FAMACHA<sup>®</sup> score, penalization of the records of treated lambs appears to be preferable to

either inclusion of such records without modification or excluding them. Based on the current results, assigning a value of 5 to records of treated lambs appears to be the preferable method of penalization. This method would be a simple, quick implementation of a penalty relative to the average advantage removal method, which requires multiple steps and data handling. It appears that use of this penalty would accomplish the recovery of at least some of the additive genetic variance that is absent when records of treated lambs are included in the analyses without modification.

Some additional investigation of the practicality of assessing genetic variability under moderate challenge of internal parasites would be helpful. As of now, phenotypes obtained under severe challenge conditions appear to be the most useful for selective improvement of resistance or resilience.

Genetic analyses with threshold models or analyses that incorporate different distributions and link functions should be considered for modeling of such data. These alternative approaches must still consider the problem that the inclusion of records of treated lambs presents. Larger data sets would be helpful; perhaps it could be confirmed that estimates of heritability decrease with increasing val-

ues of penalties, as they appeared to do in the present study. In remote regions that lack structure for large national or regional genetic evaluations, it may be that data sets of smaller size provide the only information available for prediction of breeding values. Evaluations of a practical, relatively easily obtained phenotype like FAMACHA<sup>®</sup> score combined with simple penalties may permit rapid within-flock genetic evaluations. These could offer producers the ability to select from candidate sires and dams using ranked predicted breeding values for FAMACHA<sup>®</sup> scores to improve internal parasite resistance and (or) tolerance, with the ultimate objective to have sheep that are better able to live and produce under conditions of relatively severe internal parasite challenge.

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