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Heterogeneous variances and genetics by environment interactions in genetic evaluation of crossbred lambs

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Short title: Heteroscedasticity and G×E in crossbred lambs

Abstract

Accounting for environmental heteroscedasticity and genetics by environment interaction (G×E) in genetic evaluation is important because animals may not perform predictably across environments. The objectives of this study were to evaluate the presence and consequences of heteroscedasticity and G×E on genetic evaluation. The population considered was crossbred lambs sired by terminal sires and reared under commercial conditions in the UK. Data on 6,325 lambs sired by Charollais, Suffolk, and Texel rams were obtained. The experiment was **conducted** between 1999 and 2002 on three farms located in England, Scotland, and Wales. There were 2,322, 2,137 and 1,866 lambs in England, Scotland and Wales, respectively. A total of 89 sires were mated to 1,984 ewes of two types (Welsh and Scottish Mules). Most rams were used for two breeding seasons with some rotated among farms to create genetic links. Lambs were reared on pasture and had their parentage, birth, 5 wk, 10 wk, and **slaughter** weights recorded. Lambs were **slaughtered** at a constant fatness, at which they were ultrasonically scanned for fat and muscle depth. Heteroscedasticity was evaluated in two ways. Firstly, data were separated into three subsets by farm. Within farm variance component estimates were then compared to those derived from the complete data (Model 1). Secondly, the combined data were fitted, but with a heterogeneous (by farm) environmental variance structure (Model 2). To investigate G×E, a model with a random farm by sire (F×S) interaction was used (Model 3). The ratio of the F×S variance to total variance was a measure of the level of G×E in the population. Heterogeneity in environmental variability across-farms was identified for all traits ($P < 0.01$). Rank correlations of sire EBV between farms differed for Model 1 for all traits. However, sires ranked similarly (rank correlation of 0.99) for weight traits with Model 2, but less so for ultrasonic measures.

Including the F×S interaction (Model 3) improved model fit for all traits. However, the F×S term explained a small proportion of variation in weights (less than 2%) although more in ultrasonic traits (at least 10%). **In conclusion,** heteroscedasticity and G×E were not large for these data, and can be ignored in genetic evaluation of weight but, perhaps, not ultrasonic traits. Still, before incorporating heteroscedasticity and G×E into routine evaluations of even ultrasonic traits, their consequences on selection response in the breeding goal should be evaluated.

Keywords: crossbred lambs, genetics by environment interaction, heterogeneous variances, sheep

Implications

Genetics by environment interaction (G×E) and heterogeneous environmental variances may impact genetic evaluation. Where appreciable, sheep reared in different environments may not perform predictably. Different variances across environments **were found**, with G×E more pronounced for ultrasonic than for weights traits up to **slaughter**. Still, their impacts were generally small. Genetic evaluation aims to assist livestock industries to achieve defined breeding goals; environmental heterogeneity and G×E can slow progress toward that aim. Although incorporating heteroscedasticity and G×E into genetic evaluation of ultrasonic traits may be justified, the utility of doing so must be considered within the framework of industry breeding goals.

Introduction

An animal's phenotype reflects a combination of its genetics and environment. Selection often takes place among animals that are reared in different climatic and

husbandry conditions, and animals (and their progeny) may not perform uniformly across them. None-the-less genetic evaluation programs often assume that animals will perform consistently across environments, and that variability in performance in different environments will be similar. A wealth of evidence has shown that is not the case, and that ignoring such effects had unfavorable consequences on genetic evaluation schemes (Robert-Graniè *et al*., 1999; Mulder and Bijma, 2005).

Differences in phenotypic variances across flocks can arise from differences in production conditions such as management, nutrition, and climate. Such environmental heteroscedasticity (sub-populations with different environmental variances) has been found in several livestock species for a multitude of traits (SanCristobal-Gaudy *et al*., 2001; Rowe *et al*., 2006; Nakaoka *et al*., 2007). Variable performance levels across flocks can also arise from sensitivities of genotypes to their environmental circumstances. Such genotype by environment interactions (**G×E**) have been observed in sheep and other species (e.g. Maniatis and Pollott, 2002; Pollott and Greeff, 2004; Steinheim *et al*., 2008).

Ignoring environmental heteroscedasticity and G×E can hinder the robustness of genetic evaluations. Accuracy of selection can be affected, leading to decreases in genetic response (Mulder and Bijma, 2005). Variance components may be poorly estimated and EBV biased, leading to re-rankings of animals (Hill, 1984; Garrick and Van Vleck, 1987). These effects often were greater when animals were selected on EBV derived from individual phenotypes, which remains the norm in livestock species, rather than on family mean performance (Hill and Zhang, 2004).

In the UK, 70% of the lamb crop has had terminal sire breeding, with Charollais, Suffolk, and Texel the predominant breeds used (Pollott and Stone, 2004). Environments in which lambs were reared also differ. By performance testing

terminal sire rams in several environments, the extent and consequence of heteroscedasticity and G×E on genetic evaluation can be examined. Such were the objectives of this study using a population of terminal-sire cross lambs reared under commercial conditions.

Material and methods

Animal care and use

The Animal Experiment Committees at the Institute of Biological Environmental and Rural Sciences (**IBERS**), the Scottish Agricultural College (**SAC**), and ADAS UK Ltd (**ADAS**) approved all procedures and protocols used in the experiment.

Animal resources

Data on 6,325 crossbred lambs sired by Charollais, Suffolk, and Texel rams were obtained. There were a total of 89 rams, which came from their breed's sire referencing schemes. These were cooperative breeding schemes where reference rams were shared among flocks to create connectedness and facilitate within breed genetic evaluation. The rams were selected according to a lean growth index designed to increase carcass lean growth, while constraining fat growth at a constant age end point (Simm and Dingwall, 1989). Sires were chosen from the top and bottom 5% of available rams based on index score and categorized as 'high' or 'low' lean growth index. High vs. low index rams differed in their EBV when evaluated at approximately 21 week-of-age. In high index rams, live weight EBV were 6.6 ± 0.5 kg greater, ultrasonic muscle depth (**UMD)** EBV were 2.3 ± 0.2 mm thicker, and ultrasonic fat depth EBV were 0.49 ± 0.12 mm thinner, than in low index rams (Márquez *et al*., 2012).

Lambs in this study came from mating of the terminal sires to Scottish or Welsh Mules. The Mule ewes were developed from the matings of Bluefaced Leicester rams with Scottish Blackface and (Welsh) Hardy Speckled Face ewes (van Heelsum *et al*., 2003; Mekkawy *et al*., 2009). Matings between Mule ewes and terminal sires took place between 1999 and 2002 on three farms in the UK (one each in England, Scotland, and Wales). Most sires were used for two breeding seasons and were physically moved between farms to create genetic links among farms and years (Márquez *et al*., 2012; 2013). Matings were designed so that the number of rams from high and low index categories, and from the three breeds, were balanced across farms, years and ewe breeds.

At birth, lamb parentage and weight (**BWT**) were recorded. Mule ewes were turned out to pasture within 48 hours of lambing with at most 2 lambs. Excess lambs were fostered to other ewes. Singletons and twins were grazed separately. Lamb's weights were further recorded at approximately 5 wk (**5WT**), and 10 wk (**10WT**) of age.

Once lambs were approximately 10 wk old they were evaluated subjectively for finishing condition every two weeks. This entailed lambs being restrained and assessed for fatness by palpation of the vertebral process and ribs. The fatness score ranged from 1 (devoid) to 5 (extreme), with L and H indicating 'low' and 'high' condition within a score, respectively. They were **slaughtered** once reaching a target finished condition of 3L fat score, which corresponded to approximately 11% subcutaneous fat (Kempster *et al*., 1986). Lambs were finished to a constant fatness so they could be compared at equitable levels of physiological maturity. Upon finishing, lambs' weights, henceforth referred to as **slaughter** weight (**SWT**), were obtained. The lambs were also ultrasonically scanned for muscle and fat depth. Their

UMD was measured at the deepest point of the eye muscle (longissimus lumborum) at the third lumbar vertebra. Ultrasonic fat depth was measured at the same location and at 1 and 2 cm lateral to it and averaged. When finished, lambs were processed at a commercial abattoir. Further details of design and husbandry were provided by Márquez *et al*. (2012; 2013).

Genetic groups

A pedigree was assembled, which consisted of 1,325,736 animals. There were six distinct (unrelated) breed types in the pedigree. Unknown parents for each breed were fitted as a genetic group: one for each terminal sire breed (the sires of the lambs), one for each Mule ewe breed types (the dams of the lambs), and one for the Bluefaced Leicester (the maternal grandsires of lambs). Across breeds the unknown parents were unrelated justifying their fit as separate genetic groups. Also, by fitting groups, differences in genetic means among breeds were accounted for, thereby reducing bias in the evaluation (Van Vleck, 1990).

Heterosis effects could not be explicitly fit in the analyses as performance and pedigree data on the hill breeds used to establish the crosses were unavailable. However, the combination of breed-types (½ terminal sire breed, ¼ hill breed, ¼ Bluefaced Leicester) was consistent for all lambs and therefore the expected levels of heterozgosity. Furthermore, by fitting genetic groups in the analyses, lamb EBV were adjusted for mean differences in parental breeds. All analyses in this study were performed using ASReml (Gilmour *et al*., 2009).

Heteroscedasticity

The traits investigated were BWT, 5WT, 10WT, SWT, UMD and log transformed ultrasonic fat depth (**logUFD**). Ultrasonic fat depth was transformed to

approximate normality. Analyses of the effects of index selection on these traits have been reported previously (Márquez *et al*., 2012; 2013).

Within farm. Heteroscedasticity due to farm was tested by creating three subsets of data based on where lambs were born and reared. There were 2,322, 2,137, and 1,866 lambs born in England, Scotland, and Wales, respectively. The model fitted was:

$$y_i = \mathbf{X_i}\beta_i + \mathbf{Z_{a_i}}a_i + \mathbf{Z_{d_i}}d_i + e_i \qquad \text{[Model 1]}$$

where y_i was a vector of observations, β_i was a vector of fixed effects coefficients, a_i was a vector of genetic animal effects, d_i was a vector of rearing dam effects, and e_i was a vector of random residual effects. The $\mathbf{X_i}$, $\mathbf{Z_{a_i}}$, and $\mathbf{Z_{d_i}}$ matrices were incidence matrices relating to observations in β_i, a_i and d_i, respectively. The *i* subscript referred to data from each of the three farms. Fixed effects were an overall mean, lamb sex (ewe or wether), age of dam (2 to 5-yr), and birth year (2000-2003). For all traits except BWT, a birth-rearing rank effect was fitted with four categories: single born/single reared, twin or more born/single reared, single or twin born/twin reared, and triplet born/twin reared. For BWT, birth rank (single, twin, or triplet) was fitted. Covariates for all traits except SWT and UMD were age at measurement. For SWT and UMD, the covariate was estimated subcutaneous fat percent at **slaughter**. Fat score was transformed to subcutaneous fat percent according to Kempster et al. (1986).

The (co)variance structure of this model was:

$$var\begin{bmatrix} a_i \\ d_i \\ e_i \end{bmatrix} = \begin{bmatrix} \boldsymbol{A}\sigma^2_{a_i} & 0 & 0 \\ 0 & \boldsymbol{I}\sigma^2_{d_i} & 0 \\ 0 & 0 & \boldsymbol{I}\sigma^2_{e_i} \end{bmatrix} \qquad \text{[Model 1]}$$

where **A** was the numerator relationship matrix among animals in the pedigree and **I** was an identity matrix of appropriate dimensions, $\sigma^2_{a_i}$ was the **additive** genetic

variance, $\sigma^2_{d_i}$ was the environmental rearing dam variance, and $\sigma^2_{e_i}$ was the residual environmental variance. Genetic groups were considered in **A**. Since the data were on crossbred animals, estimates of genetic variance were possibly increased by dominance effects. However, as noted earlier, it was presumed that heterotic effects were consistent among lambs in these data. Heritabilities were estimated within farm as the ratio of genetic variance to the sum of the total variances (i.e., $h^2_i = \sigma^2_{a_i}/(\sigma^2_{a_i} + \sigma^2_{d_i} + \sigma^2_{e_i})$).

A likelihood ratio test revealed that rearing dam did not explain substantial variation in **slaughter** traits (SWT, UMD, logUFD; $P > 0.2$), and therefore the rearing dam random effect was omitted for these traits. A maternal additive effect could not be fitted because of the lack of pedigree information on Scottish Blackface and Hardy Specked Face hill breeds, the dam breeds of the Mule ewes.

For each trait, log likelihoods for data from each farm were obtained. These were independent samples, and therefore the log likelihoods were summed and compared against a model fitted to the combined data. In the combined model, additional effects of farm and farm by birth year interaction were included. In the absence of heteroscedasticity, the sum of the log likelihoods from the independent samples and the log likelihood from the combined data would be expected to be equal. **A** likelihood ratio test with 2 degrees of freedom **was used** to test whether the sum of the log likelihoods from the independent samples differed from the log likelihood from the combined data. Rank correlations of EBV from the combined and within farm data were obtained to investigate any consequences of variance heterogeneity. Some sires did not have progeny on all farms. For those that did, re-rankings of sires were investigated, and correlations between EBV in the different farms were obtained.

Across farm. The second method to test variance heterogeneity was by fitting heterogeneous residual (farm) variances (Model 2). In this model, the combined data were used, but separate residual variances were estimated for each farm. The fixed effects of Model 1, in addition to farm, and farm by year interaction, were fitted to all the data with a modified (co)variance structure. The (co)variance matrix remained the same as in Model 1, except:

$$var\begin{bmatrix} a \\ d \\ e_1 \\ e_2 \\ e_3 \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & 0 & 0 & 0 & 0 \\ 0 & I\sigma_d^2 & 0 & 0 & 0 \\ 0 & 0 & I\sigma_{e\,1}^2 & 0 & 0 \\ 0 & 0 & 0 & I\sigma_{e\,2}^2 & 0 \\ 0 & 0 & 0 & 0 & I\sigma_{e\,3}^2 \end{bmatrix} \quad \text{[Model 2]}$$

where $\sigma_{e\,i}^2$ (i = 1,2,3) was the residual variance of farm *i.* Within farm heritabilities for this model were calculated as $h_i^2 = \sigma_a^2/(\sigma_a^2 + \sigma_d^2 + \sigma_{e\,i}^2)$.

The log likelihood for this model was obtained for each trait, and was tested against a null model with a single residual variance component, with a likelihood ratio test with 2 degrees of freedom. The consequences of heteroscedasticity were investigated by obtaining rank correlation of EBV calculated assuming either heterogeneous or homogeneous environmental variances.

Genotype by environment interaction

To investigate the presence of G×E, an animal model **was fitted** with a random farm by sire (**F×S**) interaction term. Fixed effects were the same as in Model 1. Random effects were animal, farm, F×S and a random residual. A random rearing dam was fitted for BWT, 5WT, and 10WT. The (co)variance structure for this model was:

$$var\begin{bmatrix} a \\ f \\ fxs \\ d \\ e \end{bmatrix} = \begin{bmatrix} \boldsymbol{A}\sigma_a^2 & 0 & 0 & 0 & 0 \\ 0 & I\sigma_f^2 & 0 & 0 & 0 \\ 0 & 0 & I\sigma_{fxs}^2 & 0 & 0 \\ 0 & 0 & 0 & I\sigma_d^2 & 0 \\ 0 & 0 & 0 & 0 & I\sigma_e^2 \end{bmatrix} \quad \text{[Model 3]}$$

where **A** was the numerator relationship matrix, σ_a^2, σ_f^2, and σ_{fxs}^2 were the variance components associated with animal (**additive genetic**), farm, and F×S, respectively. Other variance components were defined as in Model 1 and Model 2. The F×S interaction component would indicate the amount of G×E in a population (Dickerson, 1962). To test for its significance, a likelihood ratio test was performed by comparing it to a model without the random F×S interaction term. The ratio of F×S to total variance was calculated to quantify the extent of G×E in the population. The heritability was calculated as the ratio of genetic variance to total variance.

To investigate whether any G×E was caused by heterogeneous phenotypic variances, traits were standardized to their within-farm variance, and Model 3 was again fitted. Large differences in variance component estimates, and re-ranking of sires in standardized as compared to unstandardized data, would indicate the importance of variance heterogeneity.

Connectedness

In order to avoid biases in our EBV, the study was designed to establish sound genetic links, or connectedness, among farm locations within and across terminal sire breeds and index categories. The sufficiency of the design was explored by quantifying the strength of connections using prediction error correlations (Lewis *et al*., 2005; Kuehn *et al*., 2007; 2008). Using 5WT as the example trait, and a heritability of 0.20, connectedness correlations were derived among farms and

breed-index categories. The mixed linear animal model fitted included farm-year combination, sex-birth rearing type combination, and age of dam as fixed effects.

Results

Summary statistics for BWT, 5WT, 10WT, SWT, UMD and logUFD are provided in Table 1 relative to sire breed. As reported previously (Márquez et al. (2012; 2013), weights and ultrasound measures differed with respect to sire breed, although changes in means were generally proportional to changes in s.d. (similar CV across breeds).

Please place Table 1 about here

Within farm. When the data were separated by farm, likelihood ratio tests indicated the presence of heterogeneity in the environmental variance for all traits ($P < 0.01$). However, the estimates of total variance and heritability were similar for the combined data, and for within each subset of farm data (Table 2).

Please place Table 2 about here

Rank correlations between lamb EBV with the full data and farm subsets ranged from: 0.77-0.81 for BWT; 0.55-0.93 for 5WT; 0.57-0.74 for 10WT; 0.71-0.82 for SWT; 0.70-0.83 for UMD; and, 0.76-0.95 for logUFD. The rank correlations estimated within a particular farm were not consistently higher or lower than those in the other farms, nor were there clear patterns among correlations within farms. The rank correlations among lamb EBV were higher than those among sire EBV,

280 reflecting the fewer numbers of sires than lambs on individual farms (results not
281 shown).
282 *Across farm.* Allowing for heterogeneous environmental variances among
283 farms (Model 2) provided a better fit to the data for all traits ($P < 0.01$). However,
284 when comparing the genetic variances and heritabilities obtained from models with
285 heterogeneous vs. homogenous variance structures, they were within the standard
286 error for most traits (except SWT and UMD) (Table 3).
287
288 Please place Table 3 about here
289
290 Rank correlations between EBV obtained from the homogenous and heterogeneous
291 variance models were 0.99 for all weight traits (both animals and sires), and 0.88 and
292 0.84 for UMD and logUFD, respectively, among sires. These results indicate that re-
293 ranking only would be observed for ultrasonic traits, **although they** would not be
294 substantial. The across farm estimates of heritabilities were similar to the within farm
295 heritabilities of Model 1.
296 *Genotype by environment interaction*
297 For all traits, including a random F×S interaction in the model resulted in a
298 better fit ($P < 0.001$, except $P = 0.02$ for SWT). Heritabilities were similar to those
299 estimated in Models 1 and 2. The proportion of the F×S variance to total variance
300 was small for weight traits, but more pronounced for ultrasonic measures (Table 4).
301 Standardizing traits to a common within farm variance did not have an effect on
302 variance components or rankings (results not shown).
303
304 Please place Table 4 about here

Connectedness

Among farm locations, connectedness correlations were between 0.61 and 0.67. Between the high and low index category within a breed, these correlations ranged from 0.44 for the Suffolk to 0.53 for the Charollais. Values between breeds were only slightly lower (0.40). Correlations of 0.10 and above were shown to be indicative of strong connectedness (Kuehn *et al*., 2008). Although there were only 8 sires shared between Wales and Scotland, 14 between Wales and England, and 13 between Scotland and England, the rotation of rams among farms generated the well-connected design intended.

Discussion

Variance heterogeneity

Heteroscedasticity was present in this population, especially for ultrasonic traits. In the combined data, the additive genetic variance was similar to that estimated within farms (Model 1). These estimates changed little when fitting Model 2. Such was the case even when a homogeneous farm variance was assumed.

For both weight and ultrasound traits, accounting for heterogeneous variances improved model fit. However, for the weight traits, rank correlations between EBV obtained with homogenous and heterogeneous variances were near one. This suggested that any consequences of heteroscedasticity were not pronounced for weight traits, in agreement with previous results (Canavesi *et al*., 1995). Sire re-ranking was more evident for UMD and logUFD, suggesting heteroscedasticity would **have a greater** effect on the genetic evaluation of ultrasound traits.

Ignoring heterogeneous variances in genetic evaluation has risks. As observed in this study, animals may be incorrectly ranked resulting in lower selection response. Accuracies of EBV may also be affected. By fitting a heterogeneous variance model, EBV would be scaled, lessening the impact of inaccuracies in the estimation (Gianola, 1986). Given the presence of heterogeneous variances, several livestock breeds have developed genetic evaluation models that account for heteroscedasticity (Wiggans and VanRaden, 1991; Nakaoka *et al*., 2007).

An effective way to mediate bias in EBV due to heterogeneous variances would be to test progeny in different environments. In progeny testing of dairy cattle, ranking of bulls was not greatly affected by heteroscedasticity when their daughters were randomly distributed among farms with high and low variances (Winkelman and Schaeffer, 1988). Sire referencing schemes, such as those from which the rams used in this study were drawn, provide another way of distributing genetics of sires to many flocks. It has been reported that assumptions of homogeneity may not lead to substantial decreases in selection response when heritabilities are higher in more variable populations (Garrick and Van Vleck, 1987). No such pattern was found in these data.

Evidence for heterogeneity of variances within individual sheep breeds has been reported. SanCristobal-Gaudy *et al*. (2001) found that selecting for increased litter size led to increases in variability of the trait, and that using a heterogeneous variance model resulted in increased selection response. In a study comparing different breeds, Tosh and Kemp (1994) found variable estimates of heritability for weights up to 100 d in 3 breeds (Hampshire, Polled Dorset, and Romanov). They also report heterogeneous breed variances, and suggested accounting for breed

353 specific variance estimates may be necessary when comparing different breeds in an
354 across-breeds genetic evaluation.
355 *Genetics by environment interactions*
356 The ratio of F×S to total variance was shown to be indicative of the presence
357 and influence of G×E within a population (Dickerson, 1962; Meyer, 1987). For weight
358 traits, F×S explained approximately 1% of the total variation. For ultrasonic traits, this
359 percentage was greater (10 – 13%), indicating that G×E has a larger influence on
360 body composition traits. For weight traits, our results were similar to Maniatis and
361 Pollott (2002), also in sheep; however, they reported a lower proportion of variance
362 due to F×S in ultrasonic traits than in the current study.
363 In our case, including the F×S effect in the analyses decreased estimates of
364 heritability. Such was also the case for Maniatis and Pollott (2002). Here, as in their
365 study, ignoring F×S may have inflated estimates of **additive** genetic variance. They
366 hypothesized that some of the additive **genetic** variance was being partitioned into
367 the F×S variance component, yielding downwardly biased heritabilities. Shrunk
368 additive **genetic** variances were also found by Hagger (1998) for ADG in sheep
369 when fitting an F×S effect. Therefore levels of G×E in production traits appear to be
370 low but real in sheep populations.
371 Misztal (1990) suggested that an explanation for a significant F×S interaction
372 was poor representation of sires across-flocks, where genetic evaluations were more
373 severely regressed. In our study, sires were well represented across flocks, with a
374 proportion of sires having progeny in two of the three farms. The connectedness
375 among farms was also strong. Another reason for the F×S interaction may be
376 preferential treatment of some half-sib groups (Meyer, 1987). However, given the

377 design of this experiment, with management intentionally standardized across farms,
378 such would not be anticipated.
379 Ultrasonic traits had greater indication of heteroscedasticity than weight traits,
380 and also had a higher proportion of variation explained by the F×S interaction.
381 Dickerson (1962) and Canavesi *et al*. (1995) found that F×S interaction may be
382 caused by, or at least inflated by, heterogeneous variances. When **variances were**
383 standardized across farms, the variance component estimates, and the proportion of
384 F×S interaction variance to total variance, did not change. Notter *et al*. (1992) and
385 Maniatis and Pollott (2002) reported similar results.
386 *Effects on genetic evaluation*
387 Weight at **slaughter** reflects an animal's growth to a certain end point, such as
388 a target level of fatness. As such, it is a combination of the bone, fat, lean, and other
389 tissues deposited in an animal as it grows. **Evidence of** heterogeneity and G×E **was**
390 **not observed** in SWT, or in earlier weights, but **it was** in ultrasonic traits. Ultrasonic
391 measures were shown to be indicative of fat and lean tissue deposition in an animal
392 (Emenheiser *et al*., 2010), and therefore can be thought of as components of SWT.
393 Perhaps when considering the components rather than the culmination of growth,
394 heterogeneity and G×E become more apparent. Our findings indicate that accounting
395 for heterogeneity and G×E in genetic evaluation of ultrasonic measures, at least in
396 progeny of terminal sires, will reduce such bias.
397 In selection regimes, where animals were often reared in environments that
398 differed, ignoring G×E when estimating variance components in genetic evaluation
399 led to reductions in selection response (Garrick and Van Vleck, 1987; Mulder and
400 Bijma, 2006). Mulder and Bijma (2005) found that progeny testing schemes were
401 more robust to G×E than sib-testing schemes: when including information on

progeny, in the presence of any G×E, the rate of genetic change was greater. The current data were derived from a progeny testing scheme. **It was** therefore anticipated **that it would have** less of an impact of G×E than otherwise.

In the presence of G×E, the breeding objective of selection programs in different environments may differ. The construction of selection tools may also differ because genetic (co)variances between traits may vary across environments. With the presence of G×E, a way to optimize selection programs would be to have an overall breeding goal yet test progeny in more than one environment, as was **the case** in the current study.

Clearly the consequences of heteroscedasticity or G×E on genetic evaluation programs must be carefully considered before being incorporated into genetic evaluation. The limited extent of environmental heteroscedasticity observed in this study may justify it being ignored even for ultrasonic traits, as re-ranking of sires was trivial. Accounting for any G×E in the genetic evaluation of ultrasonic traits may be more important: the F×S random component explained at least 10% of the variation in these traits. Still, to robustly estimate the F×S effect, the number of offspring per sire needs to be large enough and connectedness among their offspring needs to be sufficient. Such was the case in this study but may not be so in industry breeding schemes.

Even where heteroscedasticity or G×E may be important, incorporating them into genetic evaluation schemes could be complicated. Firstly, environments must be delineated. In the current study this was straightforward; by its design, lambs were reared in three distinct locations within the UK. However, in genetic evaluation schemes, environments may be less easily distinguished, may overlap, and may vary

gradually across geographic regions and climates. Furthermore, environmental conditions would not be static over time, even on individual farms.

When deciding whether to incorporate G×E or heterogeneous variances into genetic evaluation, the efficacy of running such evaluations **also** deserves consideration. When fitting models with more random effects, solutions may be more difficult to obtain. Furthermore, the amount of data in current routine genetic evaluations would be large, with computational time a constraint. Therefore the costs of accounting for heteroscedasticity and G×E in routine, particularly multivariate, genetic evaluations need to be considered.

Conclusions

The aim of genetic evaluation programs is to assist livestock industries achieve defined breeding goals. The presence of environmental heterogeneity or G×E may hinder progress toward these goals. However, before incorporating such factors into routine genetic evaluations, their extent and consequence on reaching breeding goals need to be carefully evaluated. **In the present study, incorporating such comprehensive statistical models for weight traits was not warranted.**

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543 **Table 1.** Summary statistics for birth, 5 wk, 10 wk and **slaughter** weights, and for ultrasonic

544 muscle (UMD) and log-transformed fat (logUFD) depths, by sire breed.

Trait	Mean	s.d.	CV%	Minimum	Maximum
Birth weight (kg)					
Charollais	4.7	0.93	19.6	2.0	8.3
Suffolk	4.8	0.94	19.6	2.2	8.5
Texel	4.7	0.96	20.3	2.0	8.2
5 wk weight (kg)					
Charollais	16.3	3.69	22.6	5.8	31.5
Suffolk	16.9	3.68	21.8	5.5	28.8
Texel	16.6	3.85	23.2	5.5	29.5
10 wk weight (kg)					
Charollais	26.3	5.36	20.4	7.6	44.2
Suffolk	26.9	5.04	18.8	11.3	43.0
Texel	26.4	5.32	20.1	9.0	44.3
Slaughter weight (kg)					
Charollais	42.2	4.62	11.0	29.0	62.0
Suffolk	42.5	4.68	11.0	29.8	61.0
Texel	40.7	4.43	10.9	28.0	59.2
UMD (mm)					
Charollais	24.8	2.20	8.9	17.5	33.0
Suffolk	24.6	2.19	8.9	18.3	32.3
Texel	24.9	2.25	9.1	17.0	36.2
logUFD (mm)					
Charollais	1.4	0.31	22.6	0.2	2.4
Suffolk	1.3	0.29	22.2	0.4	2.2
Texel	1.3	0.30	22.8	0.1	2.5

545

546 **Table 2.** Estimates of genetic and environmental variance and heritability for growth and **slaughter** traits in sheep. Combined

547 model includes all data, and country subsets includes data only from farm in that country.

	Trait					
	BWT (kg^2)[1]	5WT (kg^2)	10WT (kg^2)	SWT (kg^2)	UMD (mm^2)	logUFD (mm^2)
Genetic variance						
Combined	0.110 ± 0.023	0.69 ± 0.15	1.68 ± 0.36	5.29 ± 0.64	1.33 ± 0.15	0.019 ± 0.003
England	0.094 ± 0.034	0.59 ± 0.24	2.01 ± 0.63	5.86 ± 0.95	1.31 ± 0.23	0.027 ± 0.004
Scotland	0.097 ± 0.033	1.25 ± 0.37	1.81 ± 0.63	6.46 ± 1.18	1.43 ± 0.24	0.015 ± 0.003
Wales	0.094 ± 0.034	0.67 ± 0.26	1.32 ± 0.53	4.39 ± 0.98	1.60 ± 0.29	0.027 ± 0.005
Environmental variance						
Combined	0.27 ± 0.02	3.61 ± 0.12	8.07 ± 0.26	10.67 ± 0.47	2.67 ± 0.11	0.046 ± 0.002
England	0.29 ± 0.01	2.89 ± 0.17	5.84 ± 0.41	7.61 ± 0.66	2.69 ± 0.18	0.035 ± 0.003
Scotland	0.26 ± 0.02	2.54 ± 0.21	5.73 ± 0.41	11.79 ± 0.89	1.96 ± 0.17	0.046 ± 0.003
Wales	0.29 ± 0.02	4.20 ± 0.23	9.73 ± 0.51	11.76 ± 0.81	3.19 ± 0.23	0.046 ± 0.003
Heritability[2]						
Combined	0.22 ± 0.04	0.13 ± 0.03	0.14 ± 0.03	0.33 ± 0.04	0.33 ± 0.04	0.30 ± 0.04
England	0.18 ± 0.06	0.12 ± 0.05	0.19 ± 0.06	0.43 ± 0.06	0.33 ± 0.05	0.43 ± 0.06
Scotland	0.20 ± 0.06	0.26 ± 0.07	0.17 ± 0.06	0.35 ± 0.06	0.42 ± 0.06	0.24 ± 0.05
Wales	0.18 ± 0.05	0.12 ± 0.05	0.10 ± 0.04	0.27 ± 0.06	0.33 ± 0.05	0.38 ± 0.06

[1]BWT= birth weight; 5WT = five week weight; 10WT = ten week weight; [1]SWT = **slaughter** weight; UMD = ultrasonic muscle depth; logUFD = log ultrasonic fat depth

[2]Heritabilities are without units

548

549 **Table 3.** Genetic and environmental variances and heritabilities for homogeneous and heterogeneous variance models for growth

550 and **slaughter** traits.

	BWT (kg^2)[1]	5WT (kg^2)	10WT (kg^2)	SWT (kg^2)	UMD (mm^2)	logUFD (mm^2)
Genetic variance						
HOM[2]	0.12 ± 0.03	0.91 ± 0.18	2.11 ± 0.41	6.01 ± 0.67	1.50 ± 0.16	0.024 ± 0.003
HET	0.13 ± 0.02	0.94 ± 0.19	2.14 ± 0.42	6.00 ± 0.67	1.34 ± 0.15	0.020 ± 0.003
Environmental variance						
HOM	0.27 ± 0.01	3.16 ± 0.12	6.87 ± 0.26	10.22 ± 0.49	2.58 ± 0.12	0.004 ± 0.002
England	0.28 ± 0.02	2.88 ± 0.16	5.85 ± 0.32	12.44 ± 0.66	2.02 ± 0.13	0.005 ± 0.002
Scotland	0.24 ± 0.02	2.73 ± 0.15	5.98 ± 0.32	7.72 ± 0.53	2.69 ± 0.14	0.004 ± 0.002
Wales	0.30 ± 0.02	3.96 ± 0.19	9.03 ± 0.43	10.82 ± 0.64	3.41 ± 0.17	0.053 ± 0.003
Heritability[3]						
HOM	0.24 ± 0.04	0.17 ± 0.03	0.18 ± 0.03	0.37 ± 0.04	0.36 ± 0.03	0.34 ± 0.04
England	0.24 ± 0.04	0.19 ± 0.04	0.20 ± 0.04	0.33 ± 0.03	0.39 ± 0.04	0.30 ± 0.04
Scotland	0.26 ± 0.05	0.20 ± 0.04	0.20 ± 0.04	0.44 ± 0.04	0.33 ± 0.03	0.33 ± 0.04
Wales	0.23 ± 0.04	0.16 ± 0.03	0.15 ± 0.03	0.35 ± 0.04	0.28 ± 0.03	0.27 ± 0.03

[1]BWT= birth weight; 5WT = five week weight; 10WT = ten week weight; [1]SWT = **slaughter** weight; UMD = ultrasonic muscle depth; logUFD = log ultrasonic fat depth
[2]HOM = homogeneous variances model; HET = heterogeneous variances model
[3]Heritabilities are without units

551

552 **Table 4**. Variance components estimates for the genetics by environment interaction **models for growth and slaughter traits**.

	BWT (kg^2)[1]	5WT (kg^2)	10WT (kg^2)	SWT (kg^2)	UMD (mm^2)	logUFD (mm^2)
Genetic variance	0.18 ± 0.03	1.02 ± 0.02	2.31 ± 0.53	6.60 ± 0.74	1.41 ± 0.20	0.026 ± 0.003
F×S[2] variance	0.009 ± 0.004	0.09 ± 0.04	0.19 ± 0.09	0.22 ± 0.14	0.47 ± 0.11	0.013 ± 0.002
Heritability[3]	0.30 ± 0.05	0.15 ± 0.05	0.15 ± 0.05	0.37 ± 0.04	0.30 ± 0.04	0.28 ± 0.05
G×E[3,4]	0.015 ± 0.007	0.013 ± 0.007	0.012 ± 0.007	0.012 ± 0.008	0.10 ± 0.02	0.13 ± 0.03

[1]BWT = birth weight; 5WT = five week weight; 10WT = ten week weight; [1]SWT = **slaughter** weight; UMD = ultrasonic muscle depth; logUFD = log ultrasonic fat depth
[2]F×S = sire by farm interaction
[3]heritability and G×E are without units
[4]G×E = genetics by environment interaction, defined as F×S variance as a proportion of total variance

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