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Associations of *PrP* genotype with lamb production traits in three commercial breeds of British lowland sheep

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The Ram Genotyping Scheme was launched in Great Britain in 2001 as part of the National Scrapie Plan and was devised to reduce and eventually eradicate classical scrapie susceptible genotypes from the national pedigree flock. Anecdotal claims from breeders suggest that sheep with more resistant PrP *genotypes may have inferior phenotypes. In this study, we test this possibility for lamb production traits in three breeds of lowland sheep: Charollais (22 752 lambs), Poll Dorset (22 589 lambs) and Texel (23 492 lambs). Data were received from 50 breeders and comprised weights at birth, 8 weeks and scanning (from which average daily weight gain was derived), and ultrasonic muscle and fat depths. Animal (direct) genetic effects and up to three maternal effects were fitted in linear mixed models for each trait. Fitting either* PrP *genotype or number of copies of individual alleles carried as fixed effects allowed potential associations with the* PrP *gene to be assessed. There were no significant associations seen in the Poll Dorset breed; however, significant associations were found with the number of allele copies carried in the other two breeds included in this study. Charollais lambs carrying one copy of the* VRQ *allele had significantly (*$P < 0.01$*) greater ultrasonic muscle depth (0.58 mm) and fat depth (0.2 mm) than non-carriers. In the Texel breed, lambs with one* ARR *allele were significantly heavier than those with two or zero* ARR *alleles; heterozygous* ARR *lambs were 0.07 kg heavier at birth (*$P < 0.05$*), 0.42 kg heavier at 8 weeks (*$P < 0.01$*) and 0.17 kg heavier at scan weight (*$P < 0.01$*), than non-carriers. After Bonferroni corrections to adjust significance thresholds to account for the large number of independent comparisons made, all significant results remained so at* $P < 0.05$ *or greater, except for the* ARR *allele effect on birth weight in the Texel breed, which was no longer significant. These results compare favourably with others from studies on many continental breeds of sheep, published in recent years, and add credence to the conclusion that selection on* PrP *genotype is unlikely to have any noticeable impact on the measured growth and carcass traits in sheep.*

Keywords: sheep, scrapie, *PrP*, prion protein, transmissable spongiform encephalopathy

Implications

Using data collected on commercial farms, we describe outputs from a large study investigating potential associations between lamb performance and *PrP* genotype in three British lowland sheep breeds (Texel, Charollais and Poll Dorset). The lowland sector is the most important contributor of genes to the slaughter generation of lambs in the British sheep industry and this is the most comprehensive study of possible *PrP*/trait associations in these breeds, to date. Although significant associations were sometimes seen, there was little pattern across breeds. Therefore, selection on *PrP* genotype is unlikely to have marked impacts on lamb performance traits in these breeds.

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Introduction

Following the outbreak of Bovine Spongiform Encephalopathy in the 1990s and the threat it posed to human health (Ironside *et al.*, 1996; Bruce *et al.*, 1997), industry-wide initiatives were put in place to control the prevalence of scrapie in sheep and goats in Great Britain. With the eventual aim of eradicating the disease from the national sheep flock, the National Scrapie Plan of Great Britain (NSP) was established in 2001. As part of the NSP, the Ram Genotyping Scheme (RGS), a selective breeding programme, was designed to take advantage of *PrP* allele mutations on chromosome 13. Variants from the wild-type (*ARQ*) at codons 136, 154 and 171 give rise to four commonly seen alleles (*ARR*, *AHQ*, *ARH* and *VRQ*) that can encode up to 15 different genotypes (Baylis and Goldmann,

Table 1 *The structure of the dataset*

Breed	No. of flocks	Total no. of lambs	No. of genotyped lambs	% of lambs with genotypes	Year range
Charollais	19	22 752	11 934	52.4	1997–2006
Poll Dorset	9	22 589	7111	31.5	1997–2006
Texel	22	23 492	10 588	45.1	1998–2005

2004), offering differing levels of susceptibility to classical scrapie in sheep (Hunter *et al*., 1994). Animals carrying the *VRQ* allele are the most susceptible, whilst homozygous *ARR*/*ARR* are the least susceptible.

Of concern at the commencement of the NSP were anecdotal claims from sheep breeders that animals with the *ARR*/*ARR* genotype had inferior performance to those with more susceptible genotypes. This led to the initiation of a research project in which potential associations between *PrP* genotype and performance and survival traits were investigated in a variety of sheep breeds from all sectors of the sheep industry in Great Britain. Results for hill breeds have now been reported (Man *et al*., 2006; Sawalha *et al*., 2007a; Pritchard *et al*., 2008; Moore *et al*., 2009), with the general conclusion being that although significant associations between *PrP* genotype and lamb performance are occasionally seen, these are generally small in magnitude and not consistent across breeds. However, the majority of British slaughter lambs are sired by terminal sire (i.e. lowland) breeds (Pollott *et al*., 2006), and it is in this sector that associations between *PrP* genotype and performance traits, if they exist, would have the largest impact. Currently, no large-scale investigations of such associations under commercial conditions in these breeds have been reported. This paper describes an analysis of lamb production traits in three lowland sheep breeds, comprising two terminal sire breeds and one self-contained breed, in which possible associations with *PrP* genotype were assessed.

Material and methods

Datasets and traits

Commercially reared and performance-recorded Charollais, Texel and Poll Dorset flocks were invited by the Meat and Livestock Commission (MLC) to take part in the research. A total of 50 pedigree breeders who agreed to participate provided varied sized data for the analyses. Nineteen Charollais and nine Poll Dorset flocks supplied data from 1997 to 2006, while 22 Texel flocks supplied data from 1998 to 2005. In total, this contributed 68 833 lamb records and included 29 633 lambs with *PrP* genotype information. The number of recorded lambs differed per breed, with the proportion of lamb records that could be unambiguously matched to *PrP* genotype ranging from 32% to 52% (Table 1).

Pedigree structure and data integrity were examined prior to recoding of animal identifiers using the R'Tools suite of programmes (Pong-Wong *et al*., 2001). Six traits were analysed: weights at birth, 8 and 20 weeks of age (scan weight), average daily weight gain from 8 to 20 weeks, and ultrasonic muscle and fat depths. Birth weight was recorded at or within 24 h of birth. Ultrasonic muscle and fat depths were measured at the level of the third lumbar vertebra. Fat depth data were right-skewed from the standard normal distribution curve and the analyses were performed on square-root transformed data that were closer to being normally distributed. The number of records, basic statistics and number of sires are shown by breed in Table 2. Datasets from each breed were well balanced, with similar numbers of trait observations by year, except birth weight, where data were available only from a subset of breeders.

PrP *genotypes*

The NSP Administration Centre (NSPAC) supplied *PrP* genotypes obtained using a variety of proprietary commercial genotyping methodologies, chiefly SNP assays. In all cases, the ovine *PrP* gene was genotyped at polymorphic codons 136(A/V), 154(R/H) and 171(Q/R/H) to discriminate between the five major alleles: *ARR*, *ARQ*, *ARH*, *AHQ* and *VRQ*. *PrP* genotypes were merged with performance datasets and cleaned using SAS software version 9.1 prior to analysis.

Statistical methodology

Mixed model univariate analyses were performed for all traits, using ASReml version 2.0 (Gilmour *et al*., 2002). Models included direct (animal) genetic effects and up to three maternal traits (maternal genetic, permanent environmental and temporary (litter) effect), as well as appropriate fixed effects including *PrP* genotype (described below) and were of the form:

$$y = Xb + Z_1a + Z_2m + Z_3l + Z_4pe + e,$$

where y is the vector of observations for each trait, b is the vector of fixed effects, a and m are vectors of random direct and maternal additive genetic effects, l and pe are vectors of random maternal temporary and permanent environmental effects, e is the vector of random residual effects and X, Z_1, Z_2, Z_3, Z_4 are design matrices relating fixed and random effects to observations. Fixed effects included were consistent across breeds and traits, and were flock-year, sex, maternal age, litter size or type of rearing, and all two-way interactions. Additionally, covariates of birth date and age at which measurements were obtained, i.e. age at weighing and age at scanning were also fitted. Random effects contributing significantly to the global model fit, as

Table 2 *Summary statistics for each trait and breed*

Trait	Breed	*N*	Mean	CV	Min	Max	No. of sires
BWT (kg)	CH	12 421	4.95	19.9	1.0	9.5	348
	PD	9568	3.99	20.0	150	8.5	156
	TX	16 248	4.60	24.5	1.0	9.5	490
W8W (kg)	CH	22 750	26.9	24.8	5.4	56.2	605
	PD	20 860	22.8	24.0	5.0	48.0	280
	TX	23 489	25.5	25.5	2.0	54.0	598
SWT (kg)	CH	14 796	53.2	18.0	13.0	90.0	557
	PD	8502	39.5	23.9	12.5	82.0	258
	TX	20 867	43.1	21.3	12.0	83.5	589
ADWG (kg/day)	CH	14 471	0.310	26.2	0.080	1.370	543
	PD	7855	0.200	49.0	0.145	0.875	245
	TX	20 856	0.237	31.5	−0.070	0.741	588
UMD (mm)	CH	13 924	29.7	11.5	14.0	45.0	545
	PD	8153	26.9	14.5	12.0	41.0	254
	TX	19 412	28.1	13.5	12.0	44.0	576
UFD ($mm^{0.5}$)†	CH	13 924	2.01	22.3	0.69	3.91	545
	PD	8154	1.94	23.1	0.32	3.78	254
	TX	19 406	1.55	25.3	0.10	3.46	577

BWT = birth weight; W8W = 8-week weight; SWT = scan weight; ADWG = average daily weight gain from 8 to 20 weeks; UMD = ultrasonic muscle depth; UFD = ultrasonic fat depth; CH = Charollais; PD = Poll Dorset; TX = Texel; CV = coefficient of variation (%).
†Square root transformed. Minimum, mean and maximum values on the observed scale were 0.47, 4.04 and 15.29 for CH, 0.10, 3.76 and 14.29 for PD and 0.01, 2.40 and 11.97 for TX.

assessed by the likelihood ratio test, were included in the final model. In all cases the most economical (parsimonious) model was selected. This resulted in slightly random different models, sometimes being fitted for the same trait in different breeds; however, the primary aim was to define the best fitting model for the purpose of assessing *PrP* effects, rather than to estimate variance components. Variance components and derived genetic parameters are not discussed further, other than to note that for all breeds and traits they were in general agreement with previously published studies, giving confidence in the integrity and structure of the datasets.

Testing for associations with PrP *genotype*

The potential associations of *PrP* genotype with each trait were assessed by including the *PrP* genotype as a fixed effect in the linear models, described above, by one of the two following methods. First, animals were classified based on their *PrP* genotype; i.e. *ARR*/*ARR*, *ARR*/*ARQ*, *ARR*/*AHQ*, and so on. The number of genotypes ranged from six to nine across breeds. Secondly, in a separate set of analyses, animals were classified according to the number of copies of each of the *PrP* alleles carried (i.e. 0, 1 or 2), e.g. *ARR*/*ARR*, *ARR*/xxx and xxx/xxx, where xxx represents non-ARR alleles, etc. Each allele was examined in turn by this method. Only a proportion of the animals in each dataset was genotyped, therefore the significance of the *PrP* genotype or the allele effects was assessed after fitting a fixed effect of 'genotyped or ungenotyped'. For most traits, genotyped lambs had superior trait values relative to ungenotyped lambs, possibly reflecting preferential genotyping of better performing lambs by breeders.

Exploration of *PrP* associations in these analyses involve a large number of independent comparisons, i.e. three breeds and several traits, hence there is an increased risk of obtaining apparently significant results by chance alone. A conservative means of adjusting for this is the Bonferroni correction in which the significance level is adjusted to $[1 - (1 - a)^{1/n}]$, where there are n independent comparisons (hypotheses) being made. Correcting for three independent datasets, the *P*-value necessary to attain 0.05 significance becomes 0.017; for three datasets and two independent traits per dataset (body size and carcass composition) the value is 0.0085; and for three datasets and three traits per dataset (body size, fat and muscle depth) the value is 0.0057.

Results

PrP *allele distribution*

PrP allele frequencies in each breed are shown in Figure 1. All five common *PrP* alleles are present in the Texel dataset; however, the Charollais and Poll Dorset dataset show less *PrP* allele diversity, being dominated by the *ARR* and *ARQ* alleles. The most frequent allele in all breeds was *ARR*, ranging in frequency from 0.56 in Texel to 0.83 in Charollais. The *ARQ* allele was present at a similar frequency in all breeds, ranging from 0.11 in the Texel to 0.17 in the Poll Dorset. Substantial differences between the breeds were apparent in the relative frequencies of the *ARH*, *AHQ* and *VRQ* alleles. Only in the Texel dataset were *ARH* and *AHQ* alleles present, with the *ARH* allele being the second most common allele. All three breeds had very low frequencies of the *VRQ* allele, ranging from 0.01 to 0.05. It was most

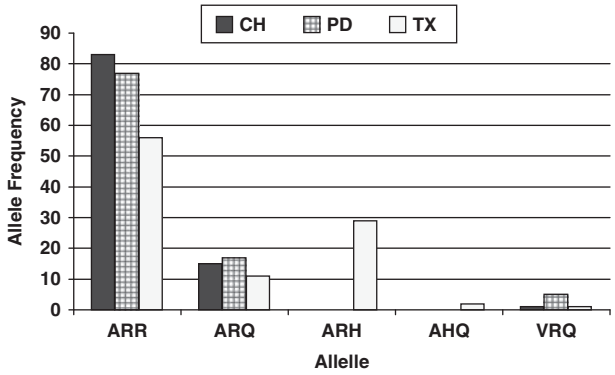

Figure 1 PrP allele frequencies for the Charollais (CH), Poll Dorset (PD) and Texel (TX) datasets.

common in the Poll Dorset dataset, this being the only dataset with homozygous *VRQ* genotypes present ($n = 25$). Allele frequencies for these three breeds are similar to previously published breed-level *PrP* allele frequencies obtained from NSP data (Eglin *et al*., 2005).

PrP *associations with performance traits*

The significance of the association between performance traits and *PrP* genotype or the number of copies of each *PrP* allele, is shown in Table 3 for every trait and every breed. Results for the number of copies of each allele are presented as histograms in Figures 2 to 7, for the *ARR* and *VRQ* alleles.

Birth weight

The only significant association of *PrP* genotype or the number of specific *PrP* alleles with birth weight was seen in the Texel breed (Table 3), where lambs with one *ARR* allele were significantly heavier by 0.08 kg than those with no *ARR* alleles ($P = 0.013$) (Figure 2). However, after Bonferroni correction, this result is of marginal significance, depending on the stringency of the correction made.

Eight-week weight

No significant associations of *PrP* genotype with 8-week weight were detected in either the Charollais or Poll Dorset lambs. However, analyses of the Texel data revealed significant effects of both *PrP* genotype ($P = 0.003$) and the number of *ARR* alleles carried ($P < 0.001$) (Table 3, Figure 3). Lambs with one *ARR* allele had significantly higher weights than lambs with either two (0.40 kg) or zero *ARR* alleles (0.42 kg). A significant association was also seen in *ARH*-carrying lambs ($P = 0.04$), due to high 8-week weights in a group of 129 *AHQ*/*ARH* lambs. The *ARR* allele association, but not the *ARH* association, remained significant ($P < 0.01$) after Bonferroni correction for nine independent tests.

Scan weight

Scan weight results were similar to those for 8-week weight. Once again, no significant associations were detected in Charollais or Poll Dorset lambs. However, an *ARR* allele effect ($P < 0.001$) was seen in the Texel breed where lambs with one *ARR* allele had significantly higher scan weights (0.42 kg greater) than lambs with two copies (Table 3, Figure 4).

Table 3 *Tests of significance (*P *values*[1]*) for different traits and analyses differing in genotypic classifications for the three breeds*

Classification	Breed	BWT	W8W	SWT	ADWG	UMD	UFD
PrP genotype	CH	0.43	0.86	0.59	0.79	0.07	0.36
	PD	0.91	0.54	0.83	0.95	0.56	0.34
	TX	0.25	**0.003**	0.15	0.47	0.49	0.61
ARR carriers	CH	0.83	0.83	0.97	0.52	0.54	0.79
	PD	0.98	0.33	0.70	0.77	0.79	0.65
	TX	**0.013**	**<0.001**	**<0.001**	0.31	0.25	0.51
ARQ carriers	CH	0.53	0.94	0.78	0.47	0.68	0.96
	PD	0.86	0.91	0.94	0.82	0.46	0.27
	TX	0.71	0.78	0.90	0.62	0.96	0.77
ARH carriers	CH[†]	–	–	–	–	–	–
	PD[†]	–	–	–	–	–	–
	TX	0.28	**0.04**	0.06	0.34	0.16	0.92
AHQ carriers	CH[†]	–	–	–	–	–	–
	PD[†]	–	–	–	–	–	–
	TX	0.35	0.16	0.42	0.51	0.80	0.42
VRQ carriers	CH	0.92	0.36	0.48	0.69	**0.001**	**0.05**
	PD	0.50	0.62	0.83	0.77	0.26	0.60
	TX	0.81	0.09	0.92	0.26	0.99	0.22

BWT = birth weight; W8W = 8-week weight; SWT = scan weight at ~20 weeks; ADWG = average daily weight gain from 8 to 20 weeks; UMD = ultrasonic muscle depth; UFD = ultrasonic fat depth; CH = Charollais; PD = Poll Dorset; TX = Texel.
Values in bold represent significant results.
[†]Alleles are not present in this breed.
[1]The *P* values presented in this table do not show Bonferroni corrections.

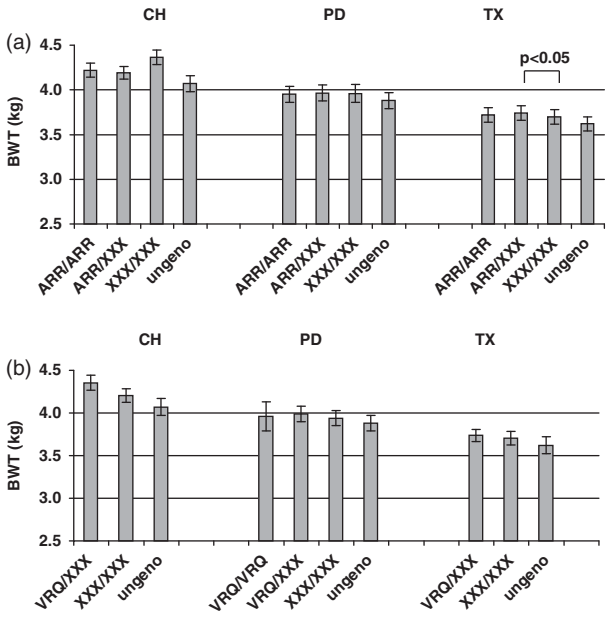

Figure 2 Least squares means (and standard errors) for birth weight (BWT) of animals classified by the number of copies of (a) *ARR* and (b) *VRQ* alleles for the Charollais (CH), Poll Dorset (PD) and Texel (TX) datasets. Significant genotype contrasts and their *P*-value are indicated in the figure.

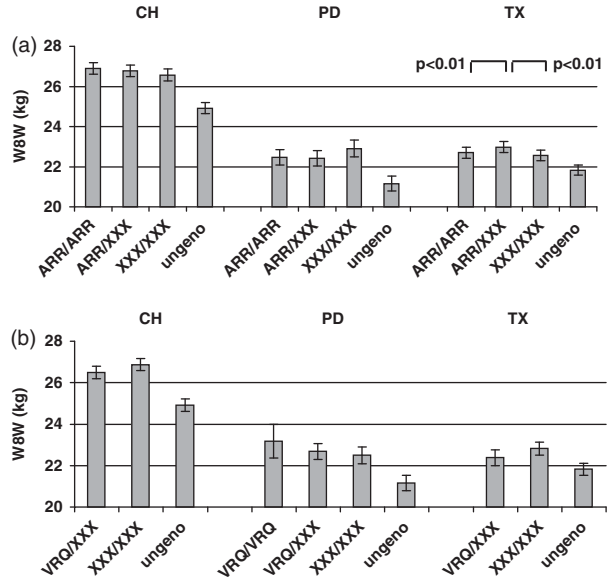

Figure 3 Least squares means (and standard errors) for 8-week weight (W8W) of animals classified by the number of copies of (a) *ARR* and (b) *VRQ* alleles for the Charollais (CH), Poll Dorset (PD) and Texel (TX) datasets. Significant genotype contrasts and their *P*-value are indicated in the figure.

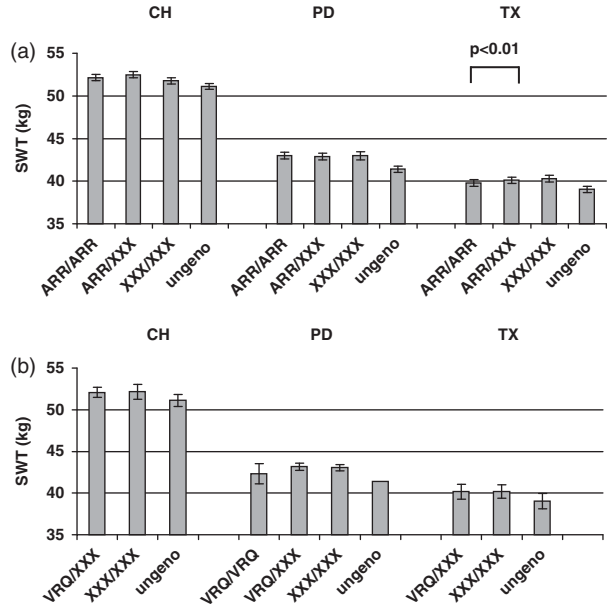

Figure 4 Least squares means (and standard errors) for scan weight (SWT) of animals classified by the number of copies of (a) *ARR* and (b) *VRQ* alleles for the Charollais (CH), Poll Dorset (PD) and Texel (TX) datasets. Significant genotype contrasts and their *P*-value are indicated in the figure.

This association remained significant ($P < 0.01$) after Bonferroni correction for nine independent tests.

Average daily weight gain

No significant *PrP* genotype effects were seen for average daily weight gain (Table 3, Figure 5). The absence of an *ARR* allele effect in the Texel breed is simply reflective of the fact that the association affected growth rate prior to, rather than subsequent to the 8-week weight.

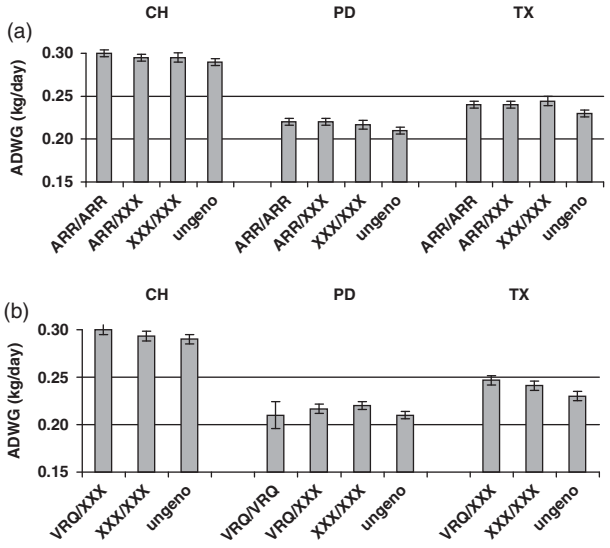

Figure 5 Least squares means (and standard errors) for average daily weight gain (ADWG) of animals classified by the number of copies of (a) *ARR* and (b) *VRQ* alleles for the Charollais (CH), Poll Dorset (PD) and Texel (TX) datasets. Significant genotype contrasts are indicated in the figure.

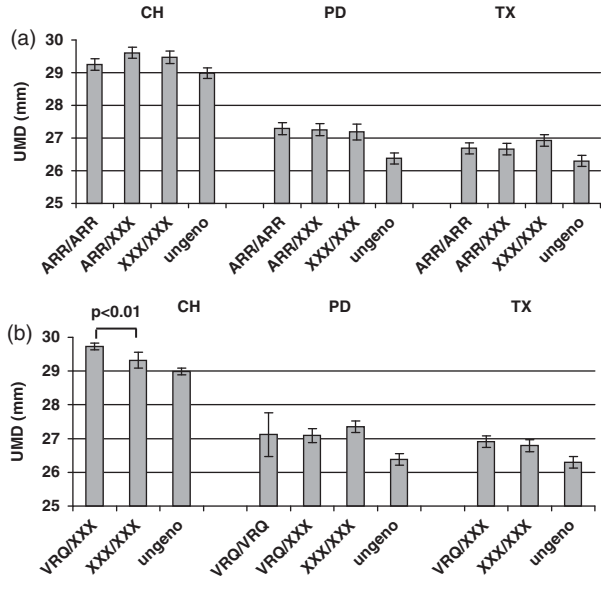

Figure 6 Least squares means (and standard errors) for ultrasonic muscle depth (UMD) of animals classified by the number of copies of (a) *ARR* and (b) *VRQ* alleles for the Charollais (CH), Poll Dorset (PD) and Texel (TX) datasets. Significant genotype contrasts and their *P*-value are indicated in the figure.

Ultrasonic muscle depth

No association was detected between muscle depth and *PrP* genotype in Poll Dorset or Texel lambs. However, a highly significant association ($P < 0.001$) was found for Charollais in the analysis of number of *VRQ* alleles (Table 3), and this result remained significant ($P < 0.01$) after Bonferroni correction for nine independent tests. Lambs with one copy of the *VRQ* allele had 0.58 mm (approximately 2%) deeper muscle than those with zero copies (Figure 6). Correcting muscle depth for scan weight

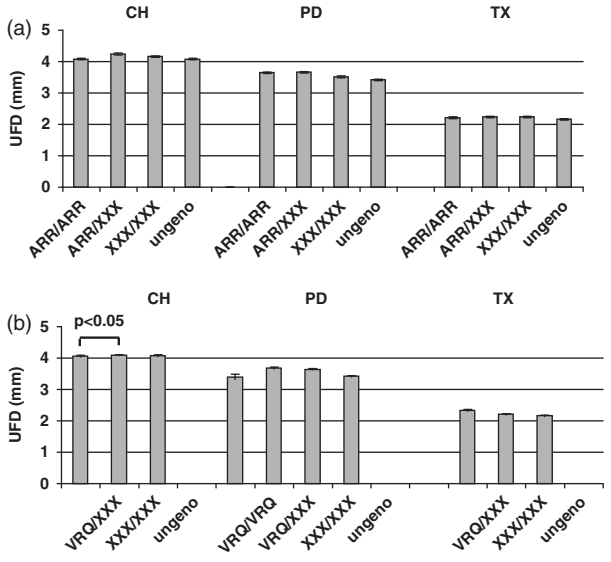

Figure 7 Least squares means (and standard errors) for ultrasonic fat depth (UFD) of animals classified by the number of copies of (a) *ARR* and (b) *VRQ* alleles for the Charollais (CH), Poll Dorset (PD) and Texel (TX) datasets. Significant genotype contrasts and their *P*-value are indicated in the figure.

did not alter the magnitude or significance of the association (results not shown).

Ultrasonic fat depth

No significant associations were found between *PrP* genotype and ultrasonic fat depth in Texel or Poll Dorset lambs. However, in Charollais lambs a significant association of number of *VRQ* alleles ($P = 0.045$) and ultrasonic fat depth was observed (Table 3, Figure 7). After back-transformation to the observed scale, this equated to 0.22 mm (approximately 5%) extra fat in *VRQ*-carrying lambs, a result that is similar to that seen for muscle depth. However, the number of *VRQ*-carrying lambs was small (Figure 1), and although the magnitude of the effect was large it did not retain significance after the Bonferroni correction.

Discussion

A small number of significant associations between *PrP* genotype and lamb performance traits were detected in two of the three lowland breeds included in this study. The Charollais and Texel breeds revealed results that are of relevance to the sheep industry, although in reality the impacts might be slight, as discussed below. No significant associations were found with any trait in the Poll Dorset breed.

In the Charollais breed, lambs carrying one *VRQ* allele had significantly greater muscle and fat depths than lambs without this allele (there were no lambs present in this dataset with two *VRQ* alleles). Thus, in principle, decreasing the frequency of the *VRQ* allele could result in a reduction of muscle and fat in Charollais lambs at scanning. Whilst loss of muscle depth may be considered an adverse effect, this would be offset by the concurrent reduction in fat depth that could be seen to be advantageous as continual effort is required to keep fat depths at acceptable levels to reach industry carcass specifications. However, it must be kept in mind that the frequency of this allele is very low in our dataset ($n = 168$ heterozygotes, less than 2.5% of lambs). If our dataset is representative of the breed, the effects on individual flocks and therefore industry as a whole are likely to be minor.

In direct contrast to our study, Sweeney and Hanrahan (2008), found that carriers of the *ARR* allele in the Charollais breed showed increased muscle depths relative to the *ARQ* allele, while the same study showed results in the opposite direction for these two alleles in the Suffolk breed. Studies on the German Black-Headed Mutton breed (de Vries *et al*., 2004) also showed reduced muscle depths with *ARR*-carrying animals compared with non-carriers of this allele. A study on three UK hill breeds by Moore *et al*. (2009), showed that only the Welsh Mountain breed had any associations with ultrasonic traits in which the *ARR* and *AHQ* alleles were associated with lower muscle depths, while *VRQ* carriers were associated with more fat than other genotypes. In the same breed, Pritchard *et al*. (2008) observed a contrasting result in which *ARR* homozygous lambs had significantly greater muscle depth than *ARR* heterozygous lambs. Extensive studies failed to show any significance of *PrP* genotype in determining the depth of muscle or fat in many other European sheep breeds (Roden and Haresign, 2001; Prokopova *et al*., 2002; de Vries *et al*., 2004; Vitezica *et al*., 2005; Isler *et al*., 2006; Man *et al*., 2006; Sawalha *et al*., 2007a; Sweeney and Hanrahan, 2008). Thus, there is no clear pattern of association emerging between ultrasonic muscle depth and *PrP* genotype, and there are no other reports of fat depth associations of this type.

Significant associations with weight traits at all ages and number of copies of the *ARR* allele carried were found in the Texel breed in our study. Lambs with one *ARR* allele had consistently higher birth, 8-week and scan weights than lambs with two or zero alleles. The body size effect was largely present by 8 weeks of age, as no significant associations were seen with 8- to 20-week average daily weight gain. The observation that the body size advantage is associated with *ARR* heterozygous lambs, rather than *ARR* homozygous lambs, means that the benefits of increasing *ARR* allele frequency will depend on the actual allele frequency. As the allele frequency increases beyond the approximate value, 0.5, observed in this dataset, the live weight advantage associated with *ARR* heterozygous lambs will decline. As well as the direct benefits of lambs being heavier, birth weight is also an important factor in lamb survival, although an intermediate optimum birth weight is often seen (Sawalha *et al*., 2007b; Gubbins *et al*., 2009). Therefore, bearing in mind the small absolute effect of *PrP* genotype on birth weight and the complex relationship with *ARR* allele frequency, expected impacts on lamb survival are likely to be trivial. As the Texel breed is one of the few major breeds in which substantial numbers of *ARH* alleles are present, the beneficial association with 8-week weight observed in the Texel breed may help to explain its continuing presence in this breed.

Several other studies have been carried out on the Texel breed and associations with weight traits and the *PrP* gene (Brandsma *et al*., 2004; de Vries *et al*., 2004; Brandsma *et al*., 2005; Sweeney and Hanrahan, 2008); however, only that of Brandsma *et al*. (2004) showed any significant findings. Again, these were in direct contrast with our study, showing that *VRQ* carriers were approximately 1 kg heavier than *ARQ* homozygotes at 135 days of age (equivalent to scan weight in this study), based on the reported differences in estimated breeding value.

For weight traits, associations with the number of specific *PrP* alleles have been seen in other studies, although not in the consistent manner of the *ARR*-carrying lambs in the Texel breed. For example, a significant positive association was seen between birth weight and *AHQ*/*AHQ* in North Country Cheviot (Hill) lambs; however, this association became negative in the same lambs at 8 weeks (Moore *et al*., 2009). In the same study, the *VRQ* allele was associated with higher 8-week weights while the *ARR* allele was associated with significantly lower predictions for 8-week weight, scan weight and average daily weight gain in the Welsh Mountain breed. In the Swaledale breed (Man *et al*., 2006), significant associations were found with the number of *ARR* alleles carried, with *ARR* heterozygotes outweighing non-carriers by 0.44 kg at weaning. In the Scottish Blackface breed (Sawalha *et al*., 2007a), the number of copies of *AHQ* and *ARQ* alleles carried give rise to significant associations with slaughter weight, where *AHQ* heterozygotes were 0.5 kg heavier than non-*AHQ* carriers and *ARQ* homozygotes were 0.4 kg lighter than either *ARQ* heterozygotes or non-carriers. The same study found that the number of copies of the *ARQ* allele carried were important, with heterozygous *ARQ* lambs being significantly heavier at birth by 0.04 kg than homozygous *ARQ* lambs.

Also in direct comparison with our study, Tongue *et al*. (2006) reported positive associations with birth weight and *PrP* genotype in the Dorset breed, where *VRQ* carriers had a disadvantage of 0.6 kg at this age over *ARQ* heterozygotes.

Other studies on important European sheep breeds have failed to show positive associations between lamb weight and growth traits and *PrP* genotype (Roden and Haresign, 2001; Prokopova *et al*., 2002; de Vries *et al*., 2004; Alexander *et al*., 2005; Moussaoui *et al*., 2005; Vitezica *et al*., 2005; Isler *et al*., 2006; Tongue *et al*., 2006; Casellas *et al*., 2007; Sweeney and Hanrahan, 2008), thus leading Sweeney and Hanrahan (2008) to conclude that there is no compelling evidence to reject the null hypothesis that there is no association between *PrP* genotype and lamb growth traits.

Despite the lack of consistent associations across breeds, it is difficult to ignore the observation that the *PrP*-trait significant associations seen in the Charollais and Texel breeds were highly significant in this study. It is possible that these are false positive results arising from insufficient stringency in the significance testing or factors in the datasets that we have not accounted for adequately.

In summary, there is little evidence of consistent relationships between *PrP* genotype and lamb performance traits across sectors or even between breeds within the same sector. The conclusion of Sweeney and Hanrahan (2008) that there is little evidence to support the anecdotal evidence from breeders that superior *PrP* genotypes had inferior phenotypes also applies to this study. Although this study revealed some apparently relevant associations of *PrP* genotype with performance traits, in reality their practical impact will be slight.

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