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Short communication

Preliminary association of microsatellite heterozygosity with footrot in domestic sheep

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ABSTRACT

Genetic heterozygosity in wild, unmanaged animal populations is often associated with protection against infectious disease. However, little is known about the relationship between heterozygosity and disease susceptibility in domesticated livestock, where disease resistance has the potential to improve animal welfare and productivity. We have investigated whether susceptibility to footrot, an important cause of poor welfare and reduced productivity in sheep, is associated with heterozygosity at 14 candidate microsatellite loci. Heterozygosity at locus BMC5221 was associated with resistance to footrot ($P=0.0034$). This locus was selected based on a gene ontology classification of 'response to Gram-negative bacteria'. Sheep homozygous at BMC5221 were at increased risk of virulent footrot (OR = 4.8, 95% CI = 1.5–15.3), with a dose response relationship between homozygosity and disease severity. A highly significant homozygote deficit was observed in sheep without virulent footrot (observed = 4, expected = 21, $\chi^2=13.76$, $P=0.0002$) but not in sheep that had clinical disease, suggesting homozygotes were disproportionately likely to contract virulent footrot. Our results indicate that genetic heterozygosity might be important for healthy immune function in domesticated livestock. The use of gene ontology codes might prove a useful strategy to target selection of candidate markers in future studies.

1. Introduction

Over 95% of sheep flocks in the UK have sheep with footrot (Kaler and Green, 2008) and farmers estimate that 8–10% of sheep in a flock are affected at any one time (Kaler and Green, 2009). The disease presents with a range of severities, from mild interdigital inflammation (interdigital dermatitis; ID), to separation of the hoof horn from the foot (Beveridge, 1941), and all severities are associated with lameness (Kaler et al., 2010). The causative agent, *Dichelobacter nodosus* is an obligate anaerobe that can survive off the host for 7 days (Whittington, 1995). Such a survival interval should be sufficient to allow all sheep in an infected population to be exposed, yet the majority does not develop disease, suggesting there is host variation in susceptibility.

Resistance to footrot varies between populations and phenotypes, and where heritability has been estimated, the majority of values lie in the range 0.10–0.20 (Nieuwhof et al., 2008), indicating the potential for effective selection for resistance. Indeed targeted breeding of sheep has led to a reduction in susceptibility to footrot in Corriedale sheep in New Zealand (Skerman and Moorhouse, 1987). However, footrot is not in performance recording schemes, and recording and reporting occurrence of disease is not something all sheep breeders are keen to do. The identification of markers for resistance/susceptibility to footrot would therefore be a useful addition to conventional breeding (Nieuwhof et al., 2008). One such marker has been developed, based on haplotypes around the *DQA2* locus of the major histocompatability

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complex (MHC), an important component of the immune system (Ennen et al., 2009; Escayg et al., 1997). Unfortunately such markers often appear population-specific, and this test is not effective in the breeds tested in the UK.

One promising avenue for the development of genetic markers for footrot is suggested by a host of recent studies that report heterozygosity-fitness correlations (HFCs). Here, heterozygosity measured at a small number of microsatellite markers often predicts measures of fitness, including disease susceptibility. However, most research on genetic heterozygosity and disease resistance has focused on natural populations of animals, with high genetic heterozygosity generally associated with a reduced risk of infectious disease (Luikart et al., 2008; Rijks et al., 2008). Thus, individuals that are relatively homozygous at a panel of presumed neutral microsatellite markers tend to be at greater risk of infection and disease, with higher parasite loads and greater mortality risk (Rijks et al., 2008). Examples include bacterial and nematode parasites in sea lions and tuberculosis in wild boar (Acevedo-Whitehouse et al., 2005, 2006). Although originally the underlying mechanism was thought to operate through inbreeding depression, recent theory and empirical studies suggest that in most cases the HFCs result through chance linkage between one or more of the markers and gene(s) with dominant or overdominant gene action (Balloux et al., 2004; Slate et al., 2004).

Unfortunately, there has been little research to date on domesticated populations (Kashtanov et al., 2003) where herd management and artificial selection impact on genetic variability. Thus the aim of the present study was to investigate whether genetic heterozygosity influences susceptibility to footrot in sheep. Using a targeted approach, we selected genetic markers specifically on the basis of proximity to genes that might be expected to play a role in resistance to infection. A panel of 14 candidate loci were developed and genotyped in a cohort of mule ewes (i.e. F1 crossbred animals) from one flock that was under constant observation for two years as part of a clinical trial of the management of lameness (Wassink et al., 2010).

2. Materials and methods

2.1. Study population and sampling

A lowland commercial flock from Oxfordshire, England, was studied from May 2005–December 2006. The flock consisted of crossbred animals, with no information available on the parental population, or specific sires. Ewes were inspected twice each week, their locomotion observed (Kaler et al., 2008), and sheep lame with locomotion score ≥ 2 were diagnosed and the cause of lameness recorded. A sheep was defined as having virulent footrot when there was separation of the hoof horn from the sensitive tissue of the foot with a characteristic smell. A sheep was defined as having interdigital dermatitis (ID) when the skin between the claws was reddened and moist. In 2006, a blood sample was collected into EDTA tubes under Home Office license and stored at −20 °C from all ewes that were present on the farm and had been in the study for both years.

There were 191 blood samples from crossbred mule ewes with phenotypic data available for two years selected for analysis in two stages. In the first stage, sheep with maximally contrasting disease presentations were screened at 14 loci. This represented half the study population and included approximately equal numbers of case and control sheep. Cases included the most severely affected individuals (defined as those affected with footrot in both years) and sheep affected in one year only. Control sheep were selected to match the proportions of the case sheep, so approximately the same number of 'extreme' sheep (no ID, no footrot) were selected as there were sheep with footrot in both years, with the remainder made up of sheep with ID but not footrot. The resultant sample set consisted of 48 sheep with virulent footrot (CASES; 16 with virulent footrot in both years and 32 with virulent footrot in one year) and 47 sheep with no virulent footrot (CONTROLS; 15 with no signs of ID or virulent footrot and 32 with ID but not virulent footrot). The remaining, less contrasting samples were genotyped at the locus identified as most significantly associated with virulent footrot in the first analysis. This consisted of 44 case individuals (1 with virulent footrot in both years and 43 with virulent footrot in one year) and 52 control individuals (21 with no virulent footrot and no ID and 31 with ID but not virulent footrot).

2.2. Marker selection

Fourteen candidate microsatellite loci were selected. These included markers which correspond to regions in the human genome where homozygosity has been associated with increased risk of mortality to bacterial disease (BMS1248, MCM148, ILSTS102; (Lyons et al., 2009)); markers located in the ovine MHC (OLADRBPs (Crawford et al., 1995)) and markers associated with other livestock diseases (CP26: tuberculosis (Acevedo-Whitehouse et al., 2005); INRA111 and INRA131: bovine mastitis (Schulman et al., 2004); MCMA16 and MCMA53: ovine scrapie (Luhken et al., 2007); TCRG4: ovine parasitism (Luikart et al., 2008); SHP4: ovine eczema (Phua et al., 1999); BL4: IgA QTL (Davies et al., 2006)). Two additional markers (TGLA48 and BMC5221) were chosen by identifying markers in the same linkage group as genes with the gene ontology (GO; www.geneontology.org) code for 'defence response to Gram-negative bacterium'. The locations of all non-ovine markers were aligned to the bovine genome using the comparative genomics function of the UCSC genome browser (http://genome.ucsc.edu/). Corresponding ovine loci were subsequently determined by alignment of the bovine and ovine genomes using the sheep comparative maps CMap site (http://chimaera.vet.unimelb.edu.au/cmap/).

2.3. Microsatellite genotyping

Genomic DNA was extracted from frozen blood samples using a DNeasy blood and tissue kit as recommended by the manufacturer (Qiagen, Crawley, UK). All loci were amplified using previously published and validated polymerase chain reaction (PCR) primers (see Supplementary data file 1 for details), as described in detail previously (Hoffman and Amos, 2005). Briefly, PCR reactions were carried out in 12 μL volumes containing 2μL template DNA (minimum of 10 ng/μL), 1× Buffer A [10 mM Tris–HCl (pH 8.3), 50 mM KCl, 1.5 mM $MgCl_2$, 0.01% Tween 20, 0.01% gelatin, 0.01% NP40], 1.0 mM

$MgCl_2$, 0.2 mM each of dATP, dGTP and dTTP, 0.01 mM dCTP, 2 μM of each primer, 0.25 U Taq polymerase and 0.01 μCi [α^{32}P]-dCTP. Loci were amplified using standard PCR cycling conditions of 94 °C for 4 min, 35 cycles of 45 s at 94 °C, 30 s atT_1, 30 s at 72 °C, and a final extension step of 72 °C for 5 min. PCR products were resolved by electrophoresis on standard 6% polyacrylamide sequencing gels, and detected by autoradiography. All gels were initially scored by one researcher (EMS) and checked for errors by a second investigator (JIH). Primer sequences, genomic locations and annealing temperatures (T_1) of all markers are presented in Supplementary data file 1.

2.4. Statistical analyses

Observed and expected heterozygosity was calculated for each locus using 'Genepop on the Web' (Raymond and Rousset, 1995). Deviations from Hardy–Weinberg equilibrium were assessed using Fisher's Exact Tests, with correction for multiple testing applied using the false discovery rate (FDR) implemented in Q-value (Storey and Tibshirani, 2003). Multilocus heterozygosity was quantified for each individual using the measure internal relatedness (IR; (Amos et al., 2001)), while for each marker it was scored as a binary measure (0 for homozygotes and 1 for heterozygotes). The association between heterozygosity and disease status in the first sample set (n = 95) was investigated using generalised linear models (GLMs) in R2.7.2 (http://www.r-project.org). We initially tested whether IR was significantly associated with footrot disease status (positive (n = 48) or negative (n = 47)); then we tested the association at each locus individually. To compensate for overdispersion, significance testing was carried out using F-tests. Overdispersion is the norm for GLMs in which the response is modelled using the binomial. It is relatively simple to apply a conservative correction to take this into account by using F-tests rather than Chi-square tests. Resulting *P*-values were corrected for multiple tests using the FDR implemented in Q-value (Storey and Tibshirani, 2003).

After the second stage of genotyping, the association between heterozygosity and disease was calculated as described above in the full study population (n = 175 successfully genotyped sheep), because joint analysis of two-stage data is more efficient than replication analysis (Skol et al., 2006). We also investigated replication of the association in two cohorts containing equal proportions of sheep in each disease state (Table 1).

The risk of footrot for homozygotes at BMC5221 was determined by calculation of odds ratios (OR; (Bland and Altman, 2000)), with analyses based on the full population dataset (n = 175). The population was classified into four disease states: 1-virulent footrot in both years (n = 15); 2-virulent footrot in one year (n = 65); 3-ID but not virulent footrot (n = 61); 4-no sign of ID or virulent footrot (n = 34). The proportion of homozygotes at the associated locus in each of the four disease categories was calculated. The baseline for comparison was no sign of ID or virulent footrot. The overall OR was also calculated for the risk of footrot based on the binary disease classification (i.e. category 1 + 2 (n = 80), compared with 3 + 4 (n = 95)). The 95% OR confidence intervals were calculated as described previously (Bland and Altman, 2000).

Table 1
Distribution of sheep in each disease state in the matched cohorts.

Disease status	Cohort 1	Cohort 2
Footrot in both years	7	8
Footrot in one year	33	32
ID, no footrot	31	30
No ID, no footrot	17	17

The observed and expected genotypic distribution at the associated locus was calculated using 'Genepop on the Web' (Raymond and Rousset, 1995) with analyses based on the full population dataset (n = 175). The probability that the distribution deviated from expectation was assessed using Chi-square (χ^2) tests and the CHIDIST function in Microsoft Excel.

Locus-specific signatures of selection were tested using an F_{ST}-outlier approach implemented in LOSITAN (Antao et al., 2008). F_{ST}-outlier tests are able to detect the majority of selected loci between populations in reasonably realistic conditions (Beaumont and Balding, 2004). The initial population genotyped at all 14 loci was divided into two cohorts for analysis: virulent footrot positive (n = 48) and virulent footrot negative (n = 47). We ran 15,000 simulations as recommended (Antao et al., 2008) to achieve smoothing of confidence interval contours. Data were analysed using the infinite alleles model, a confidence interval of 0.95 and FDR of 0.1. High F_{ST} at an individual locus compared to a simulation assuming neutrality would potentially indicate divergent selection whereas low F_{ST} suggests balancing selection.

3. Results

3.1. Association between homozygosity and footrot

The genotypes of all markers were in Hardy–Weinberg equilibrium. Observed heterozygosity ranged from 0.26 to 0.95 with an average of 6.6 alleles per locus (range 2–12; Table 2). Overall there was a non-significant negative association between heterozygosity, estimated as internal relatedness (IR) (Amos et al., 2001) and footrot disease status ($F_{[94]} = 1.35$, $P = 0.25$). However because we specifically targeted functional loci, further experimental effort is required to fully evaluate genome-wide effects of heterozygosity. We next tested each locus separately for individual association between heterozygosity and disease status. We found significant associations at two loci: TGLA48 ($F_{[91]} = 4.42$, $P = 0.036$) and BMC5221 ($F_{[90]} = 8.35$, $P = 0.0039$). Both of these loci were initially selected using gene ontology (GO) codes for response to Gram-negative infection (*D. nodosus* is Gram-negative). Following correction for multiple testing using the false discovery rate (FDR) (Storey and Tibshirani, 2003), BMC5221 remained significantly associated with virulent footrot ($Q = 0.03$; Table 2). However, using the F_{ST}-outlier approach we were unable to detect any evidence of selection at the tested loci (see Supplementary data file 2), and all loci clustered around neutral F_{ST}.

Following the completion of the second round of genotyping, BMC5221 retained its strong association with virulent footrot ($F_{[174]} = 8.59$, $P = 0.0034$; n = 175). Moreover, in the full sample set of 175 animals, homozygosity at BMC5221

Table 2
Description of loci and results of GLMs of the effect of heterozygosity on footrot disease status.

Name of locus	Reason for selection	Number of alleles	Observed heterozygosity	*F* value	*P* value	*Q* value[a]
SHP4	Ovine eczema	8	0.89	0.00	0.96	0.51
BMS1248	Human infection	9	0.70	0.00	0.95	0.51
TCRG4	Ovine parasitism	4	0.57	0.17	0.68	0.42
OLADRBPs	Ovine MHC	12	0.95	0.29	0.59	0.40
ILSTS102	Human infection	4	0.67	0.34	0.56	0.40
INRA131	Bovine mastitis	8	0.79	0.37	0.54	0.40
MCMA53	Atypical scrapie	7	0.71	0.39	0.53	0.40
MCMA16	Atypical scrapie	4	0.52	0.67	0.41	0.40
INRA111	Bovine mastitis	2	0.26	0.91	0.34	0.40
MCM148	Human infection	3	0.68	0.91	0.34	0.40
CP26	Porcine tuberculosis	6	0.78	0.92	0.34	0.40
BL4	IgA QTL	7	0.71	1.66	0.20	0.40
TGLA48	GO ontology	7	0.54	4.42	0.036	0.13
BMC5221	GO ontology	12	0.89	8.35	0.0039	0.03

[a] Significance value adjusted for multiple testing using the false discovery rate implemented in Q-value (Storey and Tibshirani, 2003).

decreased progressively from 26.7% in sheep with virulent footrot in both years of the study to 2.9% in sheep that had no clinical signs of virulent footrot or ID (Fig. 1). The association was replicated when the population was analysed as two cohorts matched for disease status (cohort 1: $F_{[87]}=4.36$, $P=0.037$; cohort 2: $F_{[86]}=4.23$, $P=0.040$; Table 1).

3.2. Risk of footrot based on genotype

Based on analysis of the full population dataset, compared to sheep never having clinical signs of footrot (n = 34), sheep homozygous at BMC5221 (n = 15) had an odds ratio (OR) of 12.0 (95% CI = 1.2–119.1; Fig. 1) for having virulent footrot in both years. This fell to an OR of 6.0 (0.7–49.0, n = 65) for footrot in one year, and 1.7 (0.2–17.1, n = 61) for having ID but not virulent footrot. Overall the OR for having virulent footrot if homozygous at BMC5221 was 4.8 (95% CI = 1.5–15.3) compared with ID or no clinical signs of disease.

3.3. Genotype distribution

Notwithstanding the lack of data on specific sire genotypes, which may have had varying levels of influence on our study population; the crossbred sheep in this flock which did not have virulent footrot were significantly more likely to be heterozygous at BMC5221 than expected (73 expected, 90 observed, $\chi^2=3.94$, 1 d.f., $P=0.04$). The number of homozygotes for individual alleles was too small to draw strong conclusions about specific allele effects. However, relative to Hardy–Weinberg expectations, there was a large deficit of individuals homozygous for allele 9 in both cases and controls (17 expected, 3 observed, $\chi^2=11.53$, 1 d.f., $P=0.0007$; Table 3). This contributes to the highly significant homozygote deficit in control sheep (21 expected, 4 observed, $\chi^2=13.59$, $P=0.0002$; Table 3). Among the cases, there were almost exactly the predicted number of homozygotes (15 expected, 14 observed, $\chi^2=0.08$, $P=0.78$; Table 3). However the distribution of these homozygotes differed from expectation ($\chi^2=35.32$, 7 d.f., $P=9.7\times10^{-6}$), with an excess of rare alleles, and only one at the commonest allele, allele 9 (Table 3).

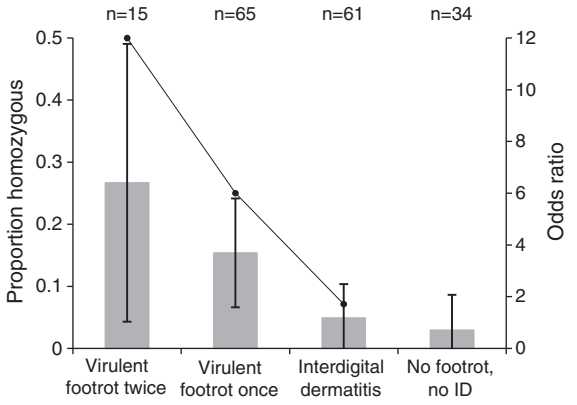

Fig. 1. Proportion of homozygous individuals (grey bars), and the odds ratio (points) of disease, at BMC5221, by disease level.The numbers above each category are the total numbers of sheep in that category; error bars represent 95% confidence intervals; ID: interdigital dermatitis.

4. Discussion

The aim of the present study was to investigate whether genetic variation influences susceptibility to footrot in domestic sheep. We have tested for possible associations between footrot in a flock of sheep examined several times each week over two consecutive years, and microsatellite homozygosity. We studied a commercial crossbred sheep population rather than a research flock to give our work a broader appeal; however without further testing we cannot guarantee that the population dynamics of this flock are representative of the UK sheep population. As such these results are provisional, but we would encourage the analysis of BMC5221 in any future research into the genetic basis for footrot susceptibility.

We were unable to detect a correlation with multilocus heterozygosity, or evidence for selection at any of the tested loci. However two putative associations were detected with individual markers, both of which were initially chosen for their proximity to genes involved with the response to Gram-negative bacteria. Despite a modest sample set, one of these markers, BMC5221, appears robust both to correction for multiple tests and to the inclusion of a second round of genotyping of relatively mildly affected individuals. It is perhaps unsurprising that there was no evidence of selection in

Table 3
Differences between observed and expected numbers of homozygote individuals at locus BMC5221 in sheep with and without virulent footrot.

Allele	Sheep with virulent footrot				Sheep without virulent footrot			
	Observed	Expected	χ^2	*P* value	Observed	Expected	χ^2	*P* value
1	5	3.08	1.20	0.27	1	2.49	0.89	0.35
2	0	0.00			0	0.00		
3	0	0.06	0.06	0.80	0	0.15	0.15	0.70
4	3	4.60	0.56	0.46	1	6.03	4.20	0.04
5	4	1.43	4.59	0.03	0	0.64	0.64	0.42
6	0	0.06	0.06	0.80	0	0.00		
7	0	0.22	0.22	0.64	0	0.35	0.35	0.55
8	1	0.04	24.85	6.2×10^{-7}	0	0.01	0.01	0.94
9	1	5.61	3.79	0.05	2	11.12	7.48	0.01
10	0	0.00			0	0.00		
11	0	0.00			0	0.03	0.03	0.86
12	0	0.00			0	0.00		
All	14	15.11	0.08	0.78	4	20.82	13.59	2.3×10^{-4}

our population. F_{ST} measures the reduction in heterozygosity in a subpopulation due, for example, to genetic drift and ranges from zero (no subdivision) to one (extreme subdivision). Our study sheep, in effect, formed an F_1 population where there has been no opportunity for genetic drift to occur, and the two cohorts analysed were drawn from the same overall population.

The observed genotype distribution at BMC5221 does not fit with a simple model where lambs are born with genotypes in Hardy–Weinberg Equilibrium and homozygotes preferentially contract footrot. Instead, disease-free animals exhibit a strong heterozygote excess not present in case animals. The most likely explanation for this is that selection of distantly related rams (mule ewes are cross-bred) for breeding artificially inflates heterozygosity above Hardy–Weinberg expectations. Consequently, a heavily used sire with a rare allele would have undue influence on subsequent populations. An alternative, hypothesis may be that there is disproportionate mortality in homozygotes in early life, for example because of other infectious diseases. In practice these alternative hypotheses are difficult to distinguish without testing the impact of breeding practices on heterozygosity.

The locus that was significantly associated with virulent footrot following correction for multiple testing (BMC5221) has characteristics that one might expect of a locus linked to a gene associated with disease susceptibility. Linkage disequilibrium should lead to genotypic disequilibrium between cases and controls, although not necessarily a pure 'heterozygote is good' signal. This is what we find, with both cases and controls deviating from Hardy–Weinberg expectations, though in different directions. The controls have a deficit of homozygotes, while the cases have the expected total number of homozygotes but not at the commonest alleles expected under Hardy–Weinberg equilibrium.

The strongest deviation from Hardy–Weinberg expectation involved a large deficit of allele 9 homozygotes in both case and control sheep. This might be due to purifying selection, though the implied mortality would have to be very high. As two of the three allele 9 homozygotes are present in the disease-free group, this genotype appears not to be associated with virulent footrot, but may impact on other diseases. Arguably, and more likely, is that allele 9 is present at a much higher frequency in one of the parent breeds compared with the other. This would facilitate the high allele 9 frequency in our population, and the low frequency of homozygote individuals. Why homozygotes for allele 5 are absent from the disease-free group (Table 3) is unclear, but this may again reflect a breed-specific allele frequency or, speculatively, linkage to a deleterious recessive allele.

The association between heterozygosity and disease is supported by the observed dose response relationship (Fig. 1). Stratifying the data according to disease severity reveals a pattern where the association with homozygosity is at its highest among animals with the most severe symptoms and declines as the symptoms become weaker. This is exactly the pattern expected if disease severity reflects a balance between both genetic and non-genetic risk factors such that the most severely affected animals have a higher probability of carrying susceptible genotypes compared with those showing intermediate symptoms. This may also suggest that susceptibility to footrot and interdigital dermatitis is linked.

BMC5221 was selected because it is linked to the region containing the chromogranin precursor A gene (*CHGA*) on ovine chromosome (OAR) 18 (Maddox et al., 2001). However the genomic separation between *CHGA* and BMC5221 is quite large and the marker is actually located in a mitochondrial oxodicarboxylate carrier (*SLC25A21*), 11.5 Mb upstream of CHGA (Dalrymple et al., 2007). OAR 18 is approximately 120 cM long (Maddox et al., 2001), or, in terms of physical size, 72.5 Mb, giving an average of 1.65 cM/Mb. This suggests the separation between BMC5221 and CHGA is approximately 19 cM. Whilst linkage disequilibrium (LD) patterns are breed-specific, 25% of microsatellite markers on OAR 18, separated by 10–20 cM are in significant LD in Australian cross-bred sheep (Merino × Border Leicester) (Meadows et al., 2008). However, the proportion of markers in significant LD increases as the genetic distance separating them decreases, with 61% of markers separated by up to 5 cM in significant LD (Meadows et al., 2008). In view of this, we used the virtual sheep genome (v.2; http://www.livestockgenomics.csiro.au/perl/gbrowse.cgi/vsheep2/) and bovine genome annotation to identify any other biologically plausible candidate genes in the region (Dalrymple et al., 2007). We identified two potential positional and functional candidate genes of interest: *NFKBIA* (nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha) which is 1.6 Mb upstream of BMC5221; and *PSMA6* (proteasome subunit α type 6)

located 1.7 Mb upstream of BMC5221. *NFKBIA* inhibits *NF-κB* (nuclear factor kappa-light-chain-enhancer of activated B cells), which plays a key role in regulating the immune response to infection (Silverman and Maniatis, 2001). It is activated following Toll-like receptor 4 (*TLR4*) recognition of Gram-negative bacteria (Beutler, 2000), and so potentially has a role in the control of infectious disease. *PSMA6* also influences *NF-κB*, with increased *PSMA6* expression apparently enhancing inflammation through activation of *NF-κB* (Ozaki et al., 2006). Future studies should aim to characterise polymorphisms within these genes in sheep, and investigate associations with footrot.

Our approach of choosing candidate markers for footrot in domestic sheep in the UK has successfully identified at least one, and possibly two, novel loci associated with this disease. A variety of criteria were used to select markers initially, with the use of GO codes apparently proving successful. The focus on heterozygosity differs from previous investigations of genetic factors influencing susceptibility to footrot, which tend to search for heritable differences in susceptibility (Nieuwhof et al., 2008). Although effective at identifying additive genetic variability, such methods may overlook loci where heterozygosity is important, because heterozygosity is largely non-heritable. In this sense, our study complements existing techniques and also uncovers novel regions. Moreover, heritability studies of footrot often use clinical signs such as interdigital inflammation with no under-running of the hoof horn and so include a combination of footrot and ID (Nieuwhof et al., 2008), whereas we considered these presentations separately and detected a dose effect. By focusing on each trait it is possible that a purer genetic signal might be detected.

Although heterozygotes do not breed true, a genotype test could be used either to guide targeted mating, or to inform extra scrutiny of homozygotes. Thus, depending on the cost of a test and the economic benefits likely to accrue, it might be worthwhile testing sheep to ascertain whether they are lower risk (heterozygote) or higher risk (homozygote), with scrutiny and (possibly) prophylactic treatment being directed more towards the latter. In terms of breeding, heterozygotes would be allowed unrestricted mating, since they will produce 50% heterozygous offspring regardless of their mate's genotype, whereas homozygotes could be matched to complementary homozygotes.

The phenotypic data used to characterise sheep in this study were more detailed than are usually available for investigations into the heritability of, or genetic susceptibility to, footrot in sheep. This was because of a two-year longitudinal epidemiological study of lameness in sheep that would be both costly and time-consuming to repeat. The data result in a high level of confidence in our phenotypic assignment of disease state. By restricting our analyses to a single sheep population, we also minimised genetic stratification in our sample. While future studies should aim to investigate greater numbers both of sheep and markers, it will be difficult to obtain such detailed phenotypic data for a large number of sheep.

5. Conclusion

We have identified a novel locus and two putative functional candidate genes associated with footrot in domestic sheep. So far we have examined relatively modest numbers of markers and sheep. However, the GO code system could potentially be used to identify many more candidate loci. Greater knowledge of genetic susceptibility to ID and footrot could potentially be used to understand the pathogenesis of the disease and to guide breeding programmes to produce sheep with a naturally lower risk of disease.

Supplementary materials related to this article can be found online at doi:10.1016/j.livsci.2011.10.009.

Conflict of interest statement

The authors report that there are no conflicts of interest relevant to this publication.

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