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Mapping of multiple quantitative trait loci for growth and carcass traits in a complex commercial sheep pedigree

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Abstract

The confirmation of the segregation of experimentally discovered quantitative trait loci (QTL) in a variety of commercial populations is required before their commercial significance can be fully realized. The use of complex pedigrees in the design of such confirmation experiments has the potential to increase the probability of the QTL segregating within the pedigree while maintaining the power to detect this segregation. Here a QTL analysis is applied across candidate chromosomes of a complex pedigree of 570 Charollais sheep from commercial flocks in the UK. This pedigree also contained a moderately sized half-sib family which was analysed separately. Two QTL significant at the 5% chromosome-wide level were detected in the half-sib analysis and seven were detected in a maximum likelihood variance component analysis of the complex pedigree using identity-by-descent values estimated by Markov chain Monte Carlo methods. The estimation of QTL effects was achieved by fitting all QTL for a specific trait simultaneously, reducing the large upward bias observed in the single QTL models. Both methods of analysis detected QTL for live weight, although these mapped to different regions, and the variance components method detected QTL for ultrasonically measured fat depth. This analysis demonstrates the viability of applying a variance component analysis to large pedigrees with the presence of considerable inbreeding.

Keywords: *carcass composition, Charollais, fat thickness, QTL, variance components.*

Introduction

The last decade has seen a large number of experiments to discover quantitative trait loci (QTL) of commercial benefit segregating in livestock populations. Generally, these experiments have met with success in terms of identifying regions containing QTL, but the variants underlying the discovered QTL have been discovered in very few cases (e.g.Grobet *et al*., 1998; Kim *et al*., 2000; Wilson *et al*., 2001; Grisart *et al*., 2002). Therefore, direct evaluation of the importance of the discovered QTL in (other) commercial populations is usually not possible. Instead, further QTL experiments need to be performed on candidate chromosomal regions in the commercial populations of interest (e.g.Nagamine *et al*., 2003; de Koning *et al*., 2003; Walling *et al*., 2004).

Animals in national improvement schemes provide opportunities for the evaluation of the importance of QTL as these animals typically have good pedigree and phenotypic information. The widespread use of artificial insemination in these populations typically creates large half-sib families, thus potentially providing study designs similar to those used in experimental populations. However, such designs are not necessarily optimal for the confirmation of a QTL segregating in a population of interest. For the genotyping of a fixed number of individuals, there is a trade off between the probability of having a QTL segregating in a half-sib family and the power of detection of the QTL (Weller *et al*., 1990). This potential pitfall can be reduced by the use of a large number of related families, where the relationships between families can be used to mitigate some of the power lost due to increasing the probability of observing QTL segregation (Williams *et al*., 1997; Slate *et al*., 1999).

The analysis of complex pedigrees suffers from the computationally demanding nature of the calculations involved. However, their use is becoming increasingly widespread in populations where experimental intervention is not practical. George *et al*. (2000) demonstrated a two-step procedure for variance component interval-mapping in complex pedigrees that contain missing marker information. Firstly, the proportion of genes identical-by-descent (IBD) between all individuals is estimated at each chromosomal location using a Markov chain Monte Carlo (MCMC) sampling procedure. Then the contribution of the chromosomal location to the phenotypic variance is assessed using restricted maximum likelihood (REML). This approach has been used to map QTL in humans (Visscher *et al*., 1999), wild deer populations (Slate *et al*., 2002) and commercial pig populations (de Koning *et al*., 2003). Here, this methodology

is used to investigate growth and carcass traits in a complex pedigree from a commercial sheep population.

Material and methods

Animals

A selection of 570 related sheep from the United Kingdom Charollais Sire Referencing Scheme formed the basis of the pedigree to be analysed. Animals were chosen on the basis of being the descendants of five widely used sires. Emphasis was placed on identifying sheep that derived from mating between the descendants of these sires. A total 406 sheep from this pedigree were genotyped, with the majority of ungenotyped sheep being ancestors in the pedigree. This pedigree contained evidence of inbreeding with 70 loops in total. Each animal was weighed at 8 weeks of age (EWW) and at ultrasonic scanning (SCW) undertaken at approximately 20 weeks of age. At scanning, muscle depth (MUS) and fat depth (FAT) at the third lumbar vertebra were recorded. Both muscle and fat traits were also analysed following correction for live weight giving two further traits (MWT and FWT, respectively).

Selection of chromosomes

Chromosomes to be genotyped were selected based on previous studies in sheep or other livestock species showing the likely presence of major QTL for traits related to the growth and carcass traits being analysed. Chromosome 1 has been shown to contain growth effects around the transferrin gene (Kmiec, 1999a and b). Chromosome 2 contains muscling effects near the myostatin gene (Marcq *et al*., 1998; Broad *et al*., 2000; Walling *et al*., 2001). Chromosome 3 is syntenic to the region around insulin-like growth factor-1 (IGF-1) that shows growth effects in cattle (Moody *et al*., 1996; Stone *et al*., 1999; Casas *et al*., 2000; Machado *et al*., 2003). Chromosome 18 contains the *callipyge* gene (Cockett *et al*., 1994; Freking *et al*., 2002) and the Carwell rib eye muscling locus (Nicoll *et al*., 1998), which are possibly allelic. Chromosome 20 contains the MHC locus that has been shown to affect growth traits in sheep (Paterson *et al*., 1998; Bot *et al*., 2004) as well as cattle (Elo *et al*., 1999) and pigs (Jung *et al*., 1989).

Genotyping

The five chromosomes were genotyped at a total of 69 markers chosen for having a polymorphic information content (PIC) greater than 0·6. This gave an average marker spacing of approximately 17 cM. Entire chromosome lengths were covered, allowing confidence intervals for QTL position to be constructed and compared to the candidate regions. Marker order was checked against that given by Maddox *et al*. (2001) using Cri-Map (Green *et al*., 1990). Updated map distances from the map given in Maddox *et al*. (2001) were used in the analyses due to the comprehensive nature of their data set (Maddox, 2003).

Preparation of phenotypic data

The phenotypic measurements were corrected for known fixed effects and covariates using a dataset of approximately 42000 sheep which had been measured in the Charollais Sire Referencing Scheme. Pre-correction of phenotypes was chosen over the simultaneous analysis of all effects as the latter option would require the inversion of a 42000 by 42000 matrix of IBD probabilities at each chromosomal position examined in the variance component analysis. More accurate estimates of fixed effects are obtained by pre-correcting the phenotypes using the larger data set and the smaller standard errors obtained have no effect on further results as only residuals from the models are used in the QTL mapping. All traits were corrected for the sex of the sheep, year of birth, the flock that they were raised in, their birth-rearing rank and the linear effect of the age of their mother. SCW, MUS and FAT were further corrected for the linear effect of age (in days) at the time of scanning, while MWT and FWT were corrected instead for the linear effect of weight at scanning. All models were fitted using ASREML (Gilmour *et al*., 2002) and residuals were checked for normality.

Heritability estimation

Heritabilities of the adjusted traits were estimated using the animal model approach (Lynch and Walsh, 1998). Briefly, this model is written in matrix notation as

$$\mathbf{y} = \mu + \mathbf{Zu} + \mathbf{e}$$

where $\mathbf{y}$ is an ($n \times 1$) vector of phenotypes, μ is the mean of the phenotypes, $\mathbf{Z}$ is an ($n \times q$) incidence matrix relating animals to phenotypes, $\mathbf{u}$ is an ($q \times 1$) vector of additive polygenic effects and $\mathbf{e}$ is the residual vector. The random effects $\mathbf{u}$ and $\mathbf{e}$ are assumed to be uncorrelated and distributed as multivariate normal densities as follows : $\mathbf{u} \sim N_q\left(0, \mathbf{A}\sigma_u^2\right)$ and $\mathbf{e} \sim N_q\left(0, \mathbf{I}\sigma_e^2\right)$ where $\mathbf{A}$ is the standard additive genetic relationship matrix and $\mathbf{I}$ is the identity matrix. The estimation of the variance components was done using ASREML (Gilmour *et al*., 2002) and the heritability of a trait, h^2 was calculated as

$$h^2 = \frac{\sigma_u^2}{\sigma_u^2 + \sigma_e^2}$$

Pedigree error assessment

The probability of an incorrectly assigned parent-offspring trio having inconsistent genotypes at a marker locus was calculated as

$$Q_l = 1 - 2S_2 + S_3 + 2S_4 - 2S_2^2 - 3S_5 + 3S_3S_2$$

where

$$S_t = \sum_i p_i^t$$

and p_i is the frequency of allele i at the locus (Dodds *et al*., 1996). The distribution of the number of inconsistent genotypes expected for an incorrectly assigned parent-offspring trio was approximated using a binomial distribution with n = 69 and probability Q = 0·4938 being the average of Q_l over all loci l. From this approximation, 99·5% of all pedigree errors involving parent-offspring trios will have greater than 23 mismatches. A similar calculation was performed for parent-offspring pairs using

$$Q_l = 1 - 4S_2 + 4S_3 - 3S_4 + 2S_2^2$$

(Dodds *et al*., 1996) which gave an average Q = 0·3289. Using the binomial approximation, 99·5% of all parent-offspring

pairs will have greater than 12 inconsistencies. Offspring in pairs with more than 12 inconsistencies had their parent set to unknown in the pedigree. When parent-offspring trios had more than 23 inconsistencies, each parent was tested individually to check if the inconsistency could be assigned to one parent and the appropriate parent(s) was set to unknown in the offspring's pedigree entry. All other inconsistent parent-offspring genotypes were removed. More complex genotype inconsistencies were removed using PedCheck (O'Connell and Weeks, 1998). The above thresholds cannot be applied to these complex inconsistencies but cases that showed repetitive inconsistencies of the same type (e.g.more than four alleles in a full-sib family with two ungenotyped parents) occurred in only a few clear-cut cases.

Half-sib analysis

The genotyped pedigree contained a half-sib family with 51 progeny. This was analysed with a regression based interval-mapping method, developed from the method of Knott *et al*. (1996), using QTL Express (Seaton *et al*., 2002). Briefly, the corrected phenotype is regressed upon the conditional probability that a particular haplotype is inherited from the sire. The test statistic is an F ratio with 1 and $n-2$ degrees of freedom where n is the size of the half-sib family. To allow comparison with further analyses, the F statistic was transformed into a likelihood-ratio statistic by

$$LRT = \begin{cases} (n-1)\ln\left(\frac{n-2}{n-1}+\frac{F}{n-1}\right)-\ln(F); & F>1 \\ 0; & F\le 1 \end{cases}$$

(Baret *et al*., 1998). Chromosome-wide significance of possible QTL were determined by permutation testing (Churchill and Doerge, 1994) and confidence intervals for QTL location were constructed by bootstrap analysis (Visscher *et al*., 1996). Other half-sib families in the pedigree were considered too small for the detection of QTL at a moderate power.

Variance component analysis

The complete 570 sheep pedigree was analysed using the two-step approach proposed by George *et al*. (2000). Firstly identity-by-descent (IBD) coefficients between all individuals were determined using LOKI (Heath, 1997) at 1-cM intervals along the chromosomes. IBD coefficients were calculated from the mean of samples taken every 10 iterations after a 1000-iteration dememorization period. Chromosomes 1, 2, 18 and 20 required 10 000 samples to obtain good concordance between repeated runs of LOKI and chromosome 3 required 100 000. The QTL effect at each chromosomal location was modelled as

$$\mathbf{y} = \mu + \mathbf{Zu} + \mathbf{Zv} + \mathbf{e}$$

where **y**, **Z**, **u** and **e** are as defined in the estimation of heritability and **v** is a $(q\times 1)$ vector of additive QTL effects. The distribution of **v** is assumed to be $\mathbf{v} \sim N_q\left(0, \mathbf{G}\sigma_v^2\right)$ where **G** is the $(q\times q)$ (co)variance matrix for the additive QTL effects, represented by the proportion of alleles IBD. At each step along the chromosome the variance explained by the QTL effect is tested for significance by

$$LRT = -2\ln\left(L_0 - L_1\right)$$

where $L_1$is the log-likelihood of the model including the QTL effect and L_0 is the log-likelihood without the QTL effect. Likelihoods were calculated using ASREML (Gilmour *et al*., 2002). For a single chromosome location, the likelihood-ratio statistic is distributed as a 50 : 50 mixture of a point mass at 0 and a X_1^2 distribution. Due to the computationally demanding nature of variance component QTL mapping, the chromosome-wide significance of the QTL effect cannot be directly computed. However, simulation studies show the chromosome-wide test statistic to be distributed between a X_1^2 distribution and a X_2^2 distribution (Xu and Atchley, 1995; Grignola *et al*., 1996). Here, a X_2^2 distribution was assumed for stringency.

Results

The trait data are summarized in Tables 1 and 2. From the differences between the standard deviation for the raw and corrected data, known environmental effects are estimated to account for between 37% and 68% of the variation in trait values demonstrating the importance of the pre-correction of trait data. All traits showed a significant heritability with lowest estimated heritability being 0·25 for FAT and the largest 0·31 for MWT. As expected from the nature of the traits being analysed, there were significant phenotypic correlations among corrected traits. The largest of these correlations occurred between the pairs of traits corrected from the same raw phenotype (i.e. FAT with FWT and MUS with MWT) and the two live weight traits (EWW and SCW). The lack of significant correlation between weight-corrected traits (FWT, MWT) and SCW is expected, as SCW was included as a covariate in the correction of these traits.

Table 1 *Summary of measured trait data*

Trait†	Mean	s.d.	Residual s.d.‡	Heritability estimate (s.e.)
EWW	22·3	4·68	3·70	0·25 (0·011)
SCW	50·7	10·1	5·78	0·27 (0·012)
FAT	3·61	1·77	1·29	0·25 (0·013)
FWT			1·12	0·27 (0·013)
MUS	28·2	3·57	2·60	0·25 (0·013)
MWT			2·21	0·31 (0·014)

† EWW = live weight at 8 weeks old; SCW, FAT and MUS = live weight, fat depth and muscle depth, respectively at ultrasonic scanning (approx. 20 weeks old); FWT and MWT = FAT and MUS respectively, after correction for live weight.
‡Standard deviation of the phenotypic residual values after correcting for fixed effects and covariates included in the model.

Table 2 *Phenotypic correlation matrix of corrected trait data*†

	Trait				
Trait	EWW	SCW	FAT	FWT	MUS
SCW	0·65***				
FAT	0·28***	0·50***			
FWT	-0·05***	-0·00	0·87***		
MUS	0·31***	0·53***	0·33***	0·07***	
MWT	-0·03***	0·01	0·08***	0·09***	0·85***

† See Table 1 for trait definitions. Significance values are for the comparison to a correlation of 0.00.

Analysis of genotyped animals revealed 16 sheep with inconsistent parental information. If this sub-population is representative of the population as a whole, this indicates that up to 6·5% of parent-offspring pairs in the United Kingdom Charollais Sire Referencing Scheme are incorrectly assigned. The map order of the markers used in the Charollais sheep population agreed with the published international mapping flock (Maddox *et al*., 2001) except for a small region of chromosome 1 where the ordering of markers MCM137 (232·6 cM) and BM6506 (234·8 cM) relative to their flanking markers was significantly different. Due to these markers being tightly linked, the order used in the analysis had little effect on the QTL profiles (data not shown) and as such the map order given in Maddox *et al*. (2001) was used for consistency.

Half-sib analysis

Chromosome 1 contained QTL significant at the 5% chromosome-wide level for the two weight traits, EWW and SCW. The information content for the half-sib family across chromosome 1 is displayed in Figure 1. The lack of information about 150 cM is a result of using markers chosen for overall polymorphic information content (PIC) rather than being heterozygous in the half-sib family. Approximately 70% (16 out of 23) of markers genotyped on chromosome 1 were heterozygous in the half-sib family providing good agreement with the selection criteria that required a PIC greater than 0·6. Figure 1 also shows the QTL profiles for SCW and EWW on chromosome 1. The peak for SCW occurs at 148 cM (between heterozygous markers MCM58 at 112·9 cM and ILSTS04 at 175·1 cM) in the middle of the area with low information content. The 95% bootstrap confidence interval for QTL position is 70 to 239 cM. The effect of allelic substitution is 1·21 residual standard deviations (s.e. = 0·36). The QTL for EWW is estimated to be at 202 cM (between CSSM04 at 199·8 cM and BMS4000 at 203·0 cM) with a 95% confidence interval of 24 to 291 cM. This allele substitution effect of this QTL is 0·56 residual standard deviations (s.e. = 0·19). A further significant QTL effect was observed on chromosome 18

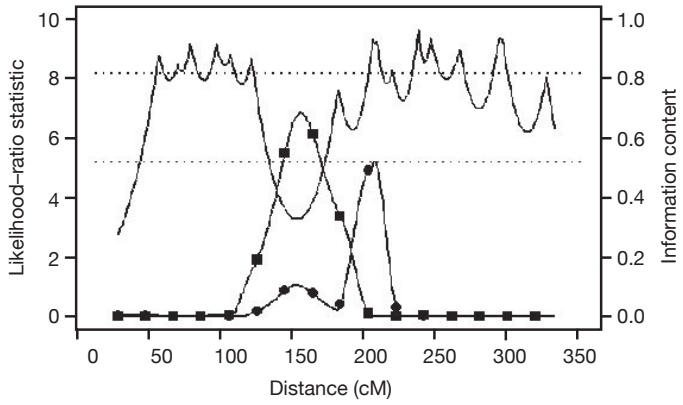

Figure 1 QTL profiles and information content for half-sib analysis on chromosome 1. Significant QTL were detected for live weight at ultrasonic scanning at approximately 20 weeks of age (SCW, -■-) and 8-week weight (EWW, -●-). Chromosome-wide significance thresholds (0.05 and 0.01) are given as dashed lines. The information content (solid line) shows a large drop at around 150 cM due to markers being chosen for their average information content rather than heterozygosity in the common sire.

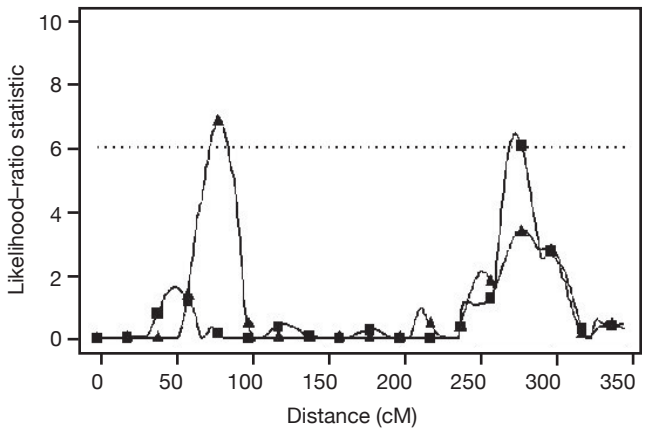

Figure 2 QTL profiles from the variance component analysis of fat depth (FAT, —▲—) and live weight at scanning at approximately 20 weeks of age (SCW, -■-) on chromosome 1. The dashed line indicates an approximate 5% chromosome-wide significance threshold.

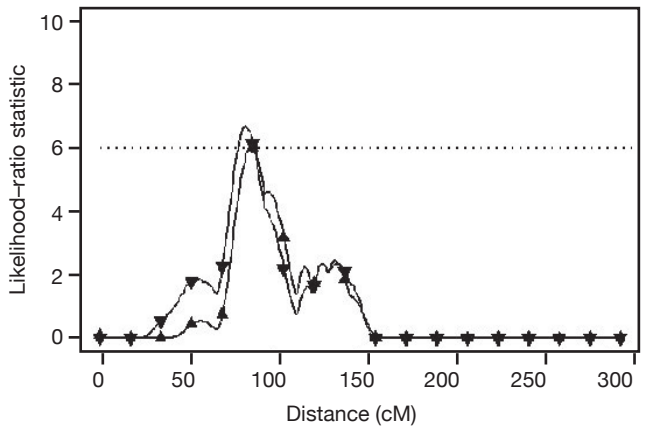

Figure 3 QTL profiles from the variance component analysis of fat depth (FAT, —▲—) and live weight-adjusted fat depth (FWT, -▼-) on chromosome 2. The dashed line indicates an approximate 5% chromosome-wide significance threshold.

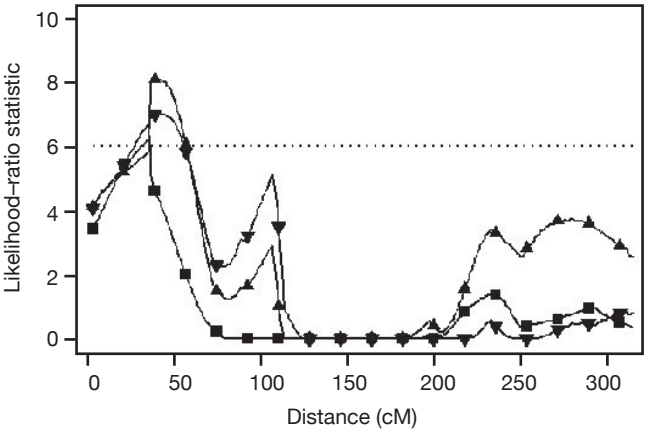

Figure 4 QTL profiles from the variance component analysis of fat depth (FAT, —▲—), live weight adjusted fat depth (FWT, -▼-) and live weight at scanning at approximately 20 weeks of age (SCW, -■-) on chromosome 3. The dashed line indicates an approximate 5% chromosome-wide significance threshold.

for SCW (F = 5·28, $P<0·05$ chromosome-wide). However, only two markers on this chromosome were heterozygous in the common sire (MCMA25 at 96·5 cM and OY5 at 118·0 cM), so the localization of QTL peak is unreliable and gives a 95% bootstrap confidence interval spanning the entire chromosome.

Variance component analysis

A total of seven trait × chromosome combinations reached the approximate 5% chromosome-wide significance level in the variance component analyses, two on each of chromosomes 1 and 2 and three on chromosome 3 (see Figures 2 to 4). The majority of these QTL were for the two traits derived from fat depth measurements with QTL for FAT on chromosomes 1, 2 and 3 and QTL for FWT on chromosomes 2 and 3. The QTL for FAT and FWT on chromosomes 2 and 3 map to very similar positions, 89 cM (1 LOD support interval = 74 to 115 cM) and 86 cM (71 to 109 cM) for FAT and FWT respectively on chromosome 2 and 36 cM (0 to 63 cM) for FAT and 34 cM (0 to 54 cM) for FWT on chromosome 3, indicating these are probably the same QTL. The QTL for FAT on chromosome 1 maps to 81 cM (62 to 96 cM). The remaining QTL were for SCW on chromosome 1 at 276 cM (258 to 315 cM) and at 32 cM (0 to 73 cM) on chromosome 3.

The estimates of the proportion of additive genetic variance explained by each QTL ranged from approximately 0·60 to 0·90, giving the total proportion of the additive genetic variance explained by the QTL detected for each of these traits of greater than 1·00. This upwardly biased nature of the estimates of effects determined at the QTL peak has previously been observed by others using this QTL mapping method (George *et al*., 2000; Göring *et al*., 2001). The biased nature of QTL effect estimates is a general problem due to the estimation of effects at the QTL peak where the estimate is the greatest and is particularly strong when the power to detect the QTL is low (Lynch and Walsh, 1998). However, as the nature of the bias is consistent among QTL, the relative proportion of variance explained by each QTL can be estimated by including multiple QTL effects in the variance component model. In this way the proportion of the total additive genetic variance explained by the QTL for FAT on chromosomes 1, 2, and 3 were estimated as 0·429, 0·207 and 0·364 respectively. The QTL for FWT on chromosomes 2 and 3 explained 0·560 and 0·440 of the genetic variance respectively and the QTL for SCW explained 0·571 and 0·429 on chromosomes 1 and 3 respectively. As these proportions sum to 1·00, it follows that the remaining polygenic variance was estimated as zero in all cases. This is not surprising given how large QTL effects were when estimated individually. Multiple QTL models also allow for the testing of the significance of each QTL in the presence of the others. Only the QTL for FAT on chromosome 2 fell below significance at a nominal 5% level indicating this QTL did not explain a significant amount of trait variation given the other QTL. However, this is likely to be due to a lack of power for the detection of three QTL simultaneously as the QTL for FWT in the same region remains significant in the presence of the other FWT QTL. As such the QTL for FAT on chromosome 2 should not be discounted as a false positive.

Discussion

The investigation of the presence of previously discovered QTL in a variety of commercial populations is an important step in the understanding of the commercial relevance of QTL discovered in experimental studies. This approach is facilitated by the use of genetic improvement schemes in which large numbers of animals are routinely produced and have relevant data collected. The pedigrees available from such schemes provide an inexpensive resource for QTL mapping. Also, any significant results are immediately applicable for marker assisted selection schemes.

Typically, with a large amount of pedigree and phenotype data available, the major constraint in the detection of QTL in commercial populations will be the cost of genotyping. This can be reduced by only considering chromosomes with experimental evidence of QTL for similar traits in other populations. However, the appropriate study pedigree needs to be selected from the available data in order to maximize the power of QTL detection. The use of half-sib families is an attractive option given the widely available resources for the analysis of such data due to its frequent use in experimental populations. However, the detection of QTL in such designs requires the QTL to be segregating in the common parent. In the best-case scenario where the QTL has allele frequencies of 0·5 for each state, approximately 50% of animals will be segregating for the QTL (under idealized population conditions). Thus five families will be needed to provide a greater than 95% chance of having at least one parent segregating for the QTL. However, if the QTL alleles have frequencies of 0·1 and 0·9, a case that is more realistic for highly selected traits, 17 families are required for a similar probability of QTL segregation. With a fixed genotyping budget, increasing the number of families rapidly decreases the power to detect the segregation of QTL in each family. This problem can be potentially reduced by the use of related families where the additional relationships can be used to provide an increase in power to detect QTL (Williams *et al*., 1997; Slate *et al*., 1999). Although the analysis of complex pedigrees is comparatively very computationally demanding, the use of such designs is becoming possible even with moderately large pedigrees containing substantial inbreeding.

Chromosome 1 was chosen because of the presence of the transferrin gene at 299 cM, which has been shown to be associated with growth effects (Kmiec, 1999a and b). Four QTL were found to be segregating on chromosome 1 of the UK Charollais sheep population, two with the half-sib analysis and two by variance component analysis. The half-sib analysis found significant QTL for SCW and EWW at 148 and 202 cM respectively. The power of the half-sib analysis to distinguish between one and two QTL was reduced due to the selection of markers for information content in the whole pedigree. This resulted in a region of low information content in the centre of chromosome 1 for the half-sib analysis and large overlapping confidence intervals for SCW and EWW whose peaks occurred around this region. However, both confidence intervals for the QTL position exclude the transferrin gene. The variance component analysis found QTL for FAT and SCW with peaks at 81 and 276 cM respectively. The one LOD support interval for the SCW QTL overlaps the

transferrin gene indicating this as a potential candidate gene. The one LOD support interval for the SCW QTL detected in the variance component analysis does not overlap the 95% confidence interval for the SCW QTL detected in the half-sib analysis. However, one LOD support intervals have been shown to be smaller than their respective 95% confidence intervals (Van Ooijen, 1992; Mangin *et al*., 1994) and the more appropriate two LOD support interval for SCW covers the entire chromosome. Thus there is not enough evidence from this study to conclude that there is more than one QTL for SCW on chromosome 1. Discrepancies between result from the half-sib analysis and the variance component analysis such as observed here appear to be common even when analysing half-sib families using both methods (Slate *et al*., 2002; de Koning *et al*., 2003). Here, QTL found using the variance component analysis but not in the half-sib analysis are likely to be due to the QTL alleles not segregating in the common parent of the half-sib family.

Significant QTL were found on chromosome 2 for the two traits derived from fat depth measurements, FAT and FWT. Given the high correlation between these traits and the similar QTL profiles, it is likely that there is one underlying QTL affecting both traits. Chromosome 2 was chosen for the mounting evidence of one or several QTL for carcass composition segregating around the myostatin locus (Marcq *et al*., 1998; Broad *et al*., 2000; Walling *et al*., 2001). However, the regions covered by the one LOD support intervals for both traits are approximately 90 cM proximal from the region around myostatin in which growth effects have been observed. Three QTL were found with the variance component analysis of chromosome 3, one for each of FAT, FWT and SCW. The confidence intervals for these traits cover the proximal 70 cM of chromosome 3, again excluding the candidate IGF-1 locus at 227 cM. No significant QTL were found on chromosomes 18 and 20, apart from a significant effect for SCW on chromosome 18 in the half-sib analysis which provided little information due to lack of segregating markers in the common parent.

The use of a candidate region approach to detect QTL in the Charollais sheep population has not been successful in the detection of QTL previously observed in other livestock populations. Of the nine significant QTL detected in this study, only one maps to a candidate region (SCW on chromosome 1). This is currently being confirmed in a larger sample from the Charollais sheep population before marker assisted selection is implemented. Confirmation studies are essential before any of the QTL detected in this study can be used in a marker assisted selection scheme. The upwardly biased estimates for QTL size suggests selecting only on the marker information with no additional phenotypic selection as the residual additive variance is estimated to be zero. However, unbiased estimates of QTL sizes can be obtained by estimating at the current QTL estimate position in the verification study population. The discovery of QTL in regions not generally recognized as important for the traits analysed indicates that the understanding of quantitative genetics of important traits in a variety of commercial populations needs to be improved. It is realistic to assume that QTL of major effect on the trait undergoing selection are likely to have become close to fixation through the intense selection based on phenotype (or estimated breeding value) that occurs in commercial populations. Thus, QTL with an estimated smaller effect in experimental populations using wide crosses may be more commercially important than those of large effect.

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