# QTL Detection in the UK Suffolk and Texel Sheep Sire Referencing Schemes

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**Introduction** Genomic research and the detection of quantitative trait loci (QTL) provide tools to enhance genetic progress and improve understanding of the biology of commercially important traits. The large sire reference schemes in UK terminal sire sheep breeds provide a unique opportunity to investigate QTL segregation within commercial populations. This study aims to identify QTL for performance traits in commercial Suffolk and Texel sheep.

**Material and Methods** Blood samples were collected from three sire reference scheme (SRS) Suffolk rams (S1-S3) and five SRS Texel rams (T1-T5) and a proportion of their commercial progeny. Progeny group size varied between 66-230 individuals. DNA was extracted from blood and sires were genotyped for up to 9 candidate regions on chromosomes 1, 2, 3, 4, 5, 6, 11, 18 and 20 based on current knowledge and other studies of the sheep genome. Markers heterozygous in each sire were genotyped in all their respective half-sib progeny. The probability of inheriting a particular sire chromosome at a particular position was calculated for each offspring at 1cM intervals, using the method of Knott *et al.* (1996). Phenotypic measurements of weight at 8 weeks of age (8Week) and ultrasonic scanning (ScanWT), ultrasonic muscle (Mus) and fat (Fat) depth at the third lumbar vertebra were obtained from Signet. Additionally, both muscle and fat depth were adjusted to correct for body weight (MusWT and FatWT). Phenotypes were corrected for fixed effects of flock-year, sex, birth-rearing rank and age of dam, estimated using ASREML (Gilmour *et al*., 1999). In addition, ultrasonic scanning traits were corrected for age at scanning. Each of the adjusted phenotypes was regressed on the inheritance probabilities, at each location along each chromosome for each family. For each regression an F-ratio of the model including the phase probability versus the same model without the phase probability was calculated. The best estimated position for a QTL in each family, for each trait, was taken to be the location with the largest F-ratio. Following the recommendations of Lander and Kruglyak (1995) for confirmed linkage, a threshold representing a nominal P value of 0.01 was used.

**Table 1** Summary of significant effects at the 1% nominal level. Effects given in kg for weight traits and mm for fat and muscle traits

| Chromosome | Sire | Trait | Position | Effect (se) | F |
|---|---|---|---|---|---|
| 1 | S1 | Mus | 200 | 2.28 (0.729) | 9.77 |
| | | MusWT | 200 | 1.62 (0.547) | 8.78 |
| 2 | T1 | Fat | 169 | 0.62 (0.170) | 12.85 |
| | | FatWT | 169 | 0.51 (0.160) | 9.94 |
| | T2 | MusWT | 59 | 1.24 (0.463) | 7.14 |
| | T4 | 8Week | 167 | 1.93 (0.617) | 9.78 |
| | | ScanWT | 165 | 2.74 (0.997) | 7.53 |
| 3 | S2 | FatWT | 80 | 0.44 (0.154) | 7.96 |
| | T3 | Mus | 13 | 1.54 (0.433) | 12.64 |
| | | MusWT | 18 | 1.25 (0.340) | 13.47 |
| 4 | T2 | FatWT | 43 | 0.75 (0.221) | 11.44 |
| 18 | S1 | 8Week | 98 | 2.59 (0.759) | 11.69 |
| | S2 | 8Week | 38 | 1.52 (0.572) | 7.05 |
| | | ScanWT | 44 | 2.10 (0.754) | 7.77 |
| | T2 | Mus | 85 | 1.82 (0.554) | 10.79 |
| | | MusWT | 88 | 1.26 (0.441) | 8.16 |
| | T5 | Fat | 75 | 0.77 (0.289) | 7.02 |
| | | FatWT | 76 | 0.69 (0.241) | 8.19 |
| 20 | T1 | Fat | 49 | 0.59 (0.182) | 10.44 |

**Results** Significant effects were detected in 6 different chromosomal regions. These are summarised in Table 1. Effects varied between 0.5-0.8 phenotypic standard deviations. Four of the regions contained effects only detected in individual sires. In contrast, the effects on chromosomes 2 and 18 were supported across 2 or 3 different sires. The data on chromosome 2 suggests 2 QTL (results not shown), one affecting muscle growth around 60cM and another affecting fat growth around 170cM. The fat QTL on chromosome 2 corresponds to the region of the myostatin locus responsible for double muscling in cattle. The effects on chromosome 18 on muscle in T2 are almost identical to the description of the Carwell gene, both in size of effect and chromosomal position, possibly suggesting the Carwell locus is segregating in UK Texel sheep.

**Conclusions** The study has been successful in detecting QTL in UK sire reference scheme sheep populations. The chromosomal candidate region approach is useful in populations where traditional QTL mapping methods e.g. diverse breed or line crosses, may not be feasible or appropriate. Future work aims to improve the resolution of position and effects detected in this study.

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