

Chromosomal localization of the callipyge gene in sheep (*Ovis aries*) using bovine DNA markers

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ABSTRACT A mutation causing muscular hypertrophy, with associated leanness and improved feed efficiency, has been recently identified in domestic sheep (*Ovis aries*). Preliminary results indicate that an autosomal dominant gene may be responsible for this economically advantageous trait. We have exploited the conservation in sequence and chromosomal location of DNA markers across Bovidae to map the corresponding callipyge locus to ovine chromosome 18 using a battery of bovine chromosome 21 markers. Chromosomal localization of the ovine callipyge locus is the first step toward positional cloning of the corresponding gene.

Increasingly, health concerns expressed by consumers determine the quality standards for meat. Currently, the fat content and lean composition of meat products are emphasized. In this work, we report the mapping of a gene affecting both the production efficiency and quality of meat in domestic sheep (*Ovis aries*). In 1983, a sheep producer identified a ram that possessed extreme muscling. The animal showed little external fat but had unusual muscling in its hind quarters. This phenotype was transmitted by the founder male to part of his offspring and to his descendants in later generations, suggesting an inheritable neomutation.

Subsequently, a study was initiated to more rigorously determine the segregation mode of this muscular hypertrophy condition (1). In the study, 150 Rambouillet ewes with normal phenotypes were mated to rams that showed the muscular hypertrophy phenotype; the rams were themselves offspring of crosses between normal ewes and muscular hypertrophy males. Of the 200 lambs produced from the ewes, 97 (48.5%) expressed the muscular hypertrophy phenotype and segregation of the muscular hypertrophy phenotype was equal between the sexes. These data indicate a single autosomal gene is responsible for the muscular hypertrophy condition. The name *callipyge* (from Greek *calli-*, beautiful; *-pyge* buttocks) and symbol *CLPG* are proposed for this gene, and the existence of two alleles, *CLPG* and *clpg*, is suggested; *CLPG/CLPG* and *CLPG/clpg* animals are heavy muscled and *clpg/clpg* animals are conventional in appearance.

Growth and carcass characteristics of animals expressing the callipyge trait were also analyzed in the study (2, 3). Birth weights, weaning weights, and rate of gain were not significantly different between the heavy muscled and normal phenotypes. However, muscle mass was 32.2% greater in lambs with muscular hypertrophy than in normal lambs. This increase in muscle mass was limited almost exclusively to the pelvic limb with little increase in the thoracic limb. Carcasses of heavy muscled animals were also remarkably lean, with 7.8% less fat than carcasses from normal animals.

To characterize this potentially advantageous gene, we sought to identify genetic markers linked to the *CLPG* locus. As relatively few markers have been mapped in sheep, contrary to the situation in cattle, we exploited the conservation in sequence and chromosomal location of markers across Bovidae and used a battery of bovine DNA markers to perform linkage studies in sheep.

MATERIALS AND METHODS

Pedigree Material. Our pedigree material was composed of two large kindreds segregating at the callipyge locus. Two heterozygous (*CLPG/clpg*) rams were mated to 24 (pedigree 1) and 57 (pedigree 2) conventional (*clpg/clpg*) ewes, yielding 35 and 98 offspring, respectively. These rams were at least five generations from the heavy muscled founder ram and were separated by four generations of breeding. Sixty-three of the offspring were born as single lambs, while there were 29 sets of twins and 4 sets of triplets. In cases of multiple offspring born to a dam, marker genotypes were used to check for monozygosity; there was no evidence of monozygosity in any of these lambs. There was evidence of leukochimerism in one muscular hypertrophy male born twin to a muscular hypertrophy female. Three alleles were detected for this animal for three of the markers. This lamb and its twin were dropped from all linkage analyses.

Offspring were scored as heavy muscled (genotype *CLPG/clpg*) or conventional (genotype *clpg/clpg*) by repeated visual examination starting at 3 weeks of age. Phenotypes of five offspring were ambiguous; these animals were dropped from the analyses. Segregation ratios at the *CLPG* locus did not deviate significantly from mendelian expectations in the remaining offspring; 21 heavy muscled versus 14 conventional offspring were identified in pedigree 1 ($P > 0.20$) and 44 heavy muscled versus 54 conventional offspring in pedigree 2 ($P > 0.35$). Moreover, mendelian proportions were respected in both sexes: in this flock, there were 26 heavy muscled versus 28 conventional male offspring ($P > 0.75$) and 39 heavy muscled versus 40 conventional female offspring ($P > 0.90$).

Markers and Genotyping. Bovine minisatellite markers included in this study (GMBT02, GMBT11, GMBT16, GMBT21, GMBT33, and GMBT36) and methods used for their analysis were as described (4). The bovine cosmid (MSBT29) as well as the corresponding hybridization conditions have been described (5). The origin of the microsatellite markers used (CSSM18, TGLA122, TGLA337, UWCA4, ETH131, and PBMS5) were described (6–10). Microsatellite primer sequences are reported in Table 1. Annealing temperatures for the PCR microsatellite reactions were reduced to 55°C when using bovine primer sequences for amplification of the homologous

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Abbreviations: lod, logarithm of odds; cM, centimorgan(s).
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Table 1. Primers based on bovine microsatellite sequences used for amplification of homologous loci in sheep

Microsatellite	Primer sequence
CSSM18.UP1	5'-AGGAATTCCTCTAGAAAAGCAGGC-3'
CSSM18.DN1	5'-TGTGCATAATTTGTGTCCGTCCGGA-3'
TGLA122.UP1	5'-CCCTCCTCCAGGTAAATCAGC-3'
TGLA122.DN1	5'-AATCACATGGCAAATAAGTACATAC-3'
TGLA337.UP1	5'-TTTGTAAAGGATAGTAGGCTACT-3'
TGLA337.DN1	5'-GCTCTTCCCTTGGTTTCCTTG-3'
UWCA4.UP1	5'-CAGCTTCAAATGAGTATGTCACC-3'
UWCA4.DN1	5'-CAACAAGAAAGCAGAGACTCC-3'

ovine loci. The Fib15 hybridization probe was previously described (11); hybridization conditions were as described for the minisatellite markers (4).

Linkage Analysis. Linkage analyses were performed using the ANIMAP (D.N. and M.G., to be published elsewhere) and LINKMAP (12) programs. To perform the analyses, our kindreds were converted to "perfect" half-sib pedigrees by assuming that individuals within full-sibships had unrelated dams. No information was lost using this procedure when analyzing linkage with the *CLPG* locus as all the segregation information for this locus is derived from the male meioses. However, some information was lost when performing linkage analyses among markers and it was not possible to estimate female recombination rates.

As all offspring were unambiguously informative for segregation at the *CLPG* locus, likelihoods were independent of *CLPG* allele frequencies. Allele frequencies for the marker loci were obtained from the sire and dam population by gene counting and used in the likelihood calculations. Penetrance of the muscular hypertrophy phenotype was set at 1.0,

compatible with the 1:1 segregation ratio of heavy muscled and conventional offspring.

RESULTS

The Ovine Callipyge Gene Is Linked to GMBT16. To map the *CLPG* locus, genomic DNA was collected from 172 animals within two paternal half-sib pedigrees. Each pedigree was composed of a muscular hypertrophy ram (genotype *CLPG/clpg*) mated to conventional females (genotypes *clpg/clpg*). The resulting 133 offspring were either heavy muscled or conventional, depending on the paternal allele inherited. A subset of 90 animals (19 in pedigree 1 and 71 in pedigree 2) was initially genotyped using four bovine minisatellite probes: GMBT02, GMBT11, GMBT16, and GMBT36. Pairwise linkage analysis was performed between these markers and the *CLPG* locus using ANIMAP programs. Surprisingly, while linkage was excluded for three of these markers, one of the markers, GMBT16, gave positive logarithm of odds (lod) scores in both pedigrees: 0.7 at 20% recombination in pedigree 1 and 3.7 at 20% recombination in pedigree 2. To verify this finding, 82 additional animals were genotyped for GMBT16 and added to the analysis. Lod scores increased in both kindreds: 3.4 at 10% recombination for pedigree 1 and 5.5 at 20% recombination for pedigree 2 (Table 1). Based on the combined maximum lod score of 8.6 at 20% recombination, we concluded that the GMBT16 locus is indeed linked to the ovine *CLPG* gene (Table 2).

When hybridized to *Hae* III-digested ovine genomic DNA, the bovine GMBT16 probe generates a variable multibanded, though locus-specific, pattern. Six alleles have been identified in sheep so far. It is noteworthy that the same probe reveals a very polymorphic multibanded, locus-specific pattern with *Mbo* I in cattle (4). These multibanded patterns are

Table 2. Pairwise linkage analysis between ovine chromosome 18 markers and the ovine callipyge locus

Pairwise linkage analysis*	Recombination fraction (ϕ)						
	0.00	0.01	0.05	0.10	0.20	0.30	0.40
<i>CLPG</i>-GMBT16							
Pedigree 1	$-\infty$	2.21	3.30	3.40	3.13	2.33	1.19
Pedigree 2	$-\infty$	-7.92	0.97	3.97	5.47	4.77	2.79
Σ	$-\infty$	-5.71	4.27	7.37	8.60	7.10	3.98
<i>CLPG</i>-CSSM18							
Pedigree 1	$-\infty$	3.04	4.3	4.11	3.55	2.59	1.31
Pedigree 2	$-\infty$	14.19	15.69	15.21	13.73	9.27	4.97
Σ	$-\infty$	17.23	19.99	19.32	17.28	11.86	6.28
<i>CLPG</i>-TGLA122							
Pedigree 1	$-\infty$	-3.88	0.00	1.56	2.09	1.83	1.02
Pedigree 2	$-\infty$	-4.04	5.13	7.94	8.72	7.11	4.07
Σ	$-\infty$	-7.92	5.13	9.50	10.81	8.94	5.09
<i>CLPG</i>-MSBT29							
Pedigree 1	$-\infty$	-13.56	-6.91	-4.03	-1.46	-0.39	-0.03
Pedigree 2	$-\infty$	-7.72	-1.28	1.01	2.41	2.30	1.36
Σ	$-\infty$	-21.28	-8.19	-3.02	0.95	1.91	1.33
<i>CLPG</i>-UWCA4							
Pedigree 1	$-\infty$	-14.81	-7.37	-4.39	-1.78	-0.64	-0.14
Pedigree 2	$-\infty$	-37.64	-18.07	-10.27	-3.58	-0.81	0.11
Σ	$-\infty$	-52.45	-25.44	-14.66	-5.36	-1.45	-0.03
<i>CLPG</i>-GMBT21							
Pedigree 2	$-\infty$	-39.43	-20.78	-13.00	-5.79	-2.29	-0.54
<i>CLPG</i>-GMBT33							
Pedigree 1	$-\infty$	-21.03	-10.82	-6.66	-2.51	-1.14	-0.26
Pedigree 2	$-\infty$	-54.04	-27.49	-16.70	-7.07	-2.64	-0.58
Σ	$-\infty$	-75.07	-38.31	-23.36	-9.58	-3.78	-0.84
<i>CLPG</i>-fibrillin							
Pedigree 1	$-\infty$	-11.01	-4.87	-2.42	-0.41	0.26	0.26

*Lod scores are summed over the pedigrees.

thought to reflect the presence of species-specific minisatellite variant repeats (13) within this minisatellite locus in cattle and sheep.

Construction of a Linkage Map for Sheep Chromosome 18 Using Bovine Chromosome 21 Markers. The GMBT16 locus has been mapped to the proterminal region of bovine chromosome 21 using somatic cell hybrids and *in situ* hybridization and to the proterminal region of ovine chromosome 18 by *in situ* hybridization (4). These two chromosomes are recognized as evolutionary homologs based on their similar banding patterns (14). In addition to GMBT16, at least nine other type II markers have been assigned to bovine chromosome 21: CSSM18, TGLA122, TGLA337, MSBT29, UWCA4, ETH131, PBMS5, GMBT21, and GMBT33 (4–10). A linkage map of bovine chromosome 21 has been previously constructed, with a marker order of GMBT16–CSSM18–TGLA122–UWCA4–ETH131 (6). These markers, as well as TGLA337, MSBT29, PBMS5, GMBT21, and GMBT33, were genotyped in large paternal half-sib cattle families (4, 15, 16) and the resulting linkage map is represented in Fig. 1. These 10 markers were also tested on sheep DNA as described above. Polymorphic locus-specific patterns were obtained in sheep with all three bovine VNTR-type (variable number of tandem repeats type) markers (GMBT16, GMBT21, and GMBT33), with the bovine cosmid (MSBT29), and with three of the six bovine microsatellite primer pairs (TGLA122, TGLA337, and UWCA4). Primer pairs originally described for the amplification of the CSSM18 microsatellite in cattle (6) did not work in sheep. However, because of the likely critical position of the CSSM18 locus with respect to the *CLPG* gene (Fig. 1), we designed a new set of oligonucleotides (Table 1) that amplified the homologous locus in sheep, based on the sequence of the bovine CSSM18 locus. Ram 1 proved heterozygous for GMBT16, GMBT33, TGLA122, UWCA4, and CSSM18, while ram 2 was heterozygous for GMBT16, GMBT21, GMBT33, TGLA122, UWCA4, and CSSM18. The respective pedigrees were genotyped for informative systems and pairwise linkage analysis was performed between all markers using ANIMAP. Corresponding lod scores among these markers are reported in Table 3. These markers fall into two linkage groups in sheep: group 1, GMBT16, CSSM18, TGLA122, MSBT29, and UWCA4 and group 2, GMBT21 and GMBT33. The most likely locus order and recombination rates between adjacent markers were determined by multilocus linkage analysis using ANIMAP. The following map was developed for the first linkage group: GMBT16 (17%)–CSSM18 (19%)–TGLA122 (15%)–MSBT29 (12%)–UWCA4. Odds versus alternative orders were >1200:1. The maximum likelihood recombination rate between the markers of the second linkage group, GMBT21 and GMBT33, was 19%. Although likely, this set of data does not allow us to conclude that the second linkage group is located on the same ovine chromosome (chromosome 18) as the first linkage group, although they are on the same chromosome (chromosome 21) in cattle. A graphical representation of the corresponding sheep map is shown in Fig. 1.

Placement of the Callipyge Locus on the Sheep Chromosome 18 Map. Based on the virtually telomeric location of GMBT16 on sheep chromosome 18 and the 20% recombination rate observed between this marker and the *CLPG* locus, we hypothesized that the most likely location of the callipyge gene was between GMBT16 and TGLA122, close to CSSM18. This hypothesis was confirmed by performing a multilocus linkage analysis in which the relative map locations of the type II markers were fixed, while the position of the *CLPG* locus was varied with respect to this marker map (Fig. 2). As predicted, a maximum lod score of 26.2 was obtained in the interval between CSSM18 and TGLA122 at 3 and 17.5 cM from these markers, respectively. Multilocus linkage analyses using ANIMAP indicated that the placement of the *CLPG* locus in the

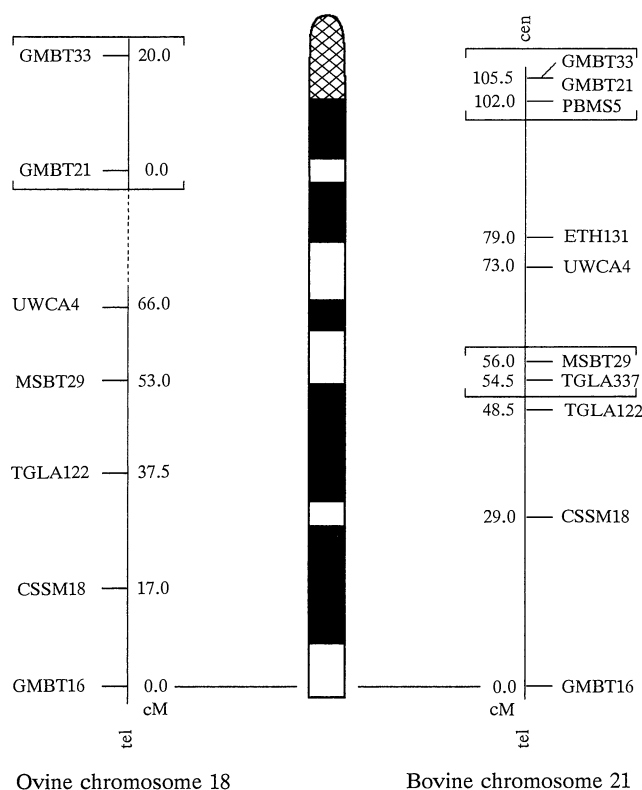


FIG. 1. Linkage maps of bovine chromosome 21 and ovine chromosome 18. Map positions are given in centimorgans (cM), starting from the proterminal GMBT16 marker. Recombination units were converted to cM using Kosambi's mapping function. The GMBT21–GMBT33 linkage group in sheep is treated independently, as the available data in sheep do not allow us to link it to the other ovine chromosome 18 markers. Brackets delineate marker groups for which odds versus alternative orders were <100:1.

CSSM18–TGLA122 interval is 3600 times more likely than placement in the adjacent GMBT16–CSSM18 interval.

DISCUSSION

In this study, we demonstrate that one can efficiently take advantage of a DNA marker map available in a given species (such as *Bos taurus*) to perform linkage studies in related species (such as *Ovis aries*). We tested six bovine VNTR markers and one bovine cosmid-based marker by Southern blot hybridization on ovine genomic DNA. All of these bovine probes gave locus-specific and polymorphic patterns in sheep. Our initial attempts to PCR-amplify six microsatellite loci in sheep using bovine primer sets were successful for three of these systems. These results corroborate our earlier finding of an $\approx 50\%$ success rate when using bovine primers to amplify the homologous ovine microsatellite sequence (17) and, as expected, indicate that PCR is more sensitive to mismatches than Southern blot hybridization. However, as shown for CSSM18, the amplification success rate can be increased by shifting the positions of the primers used for amplification. It is likely that with primer adjustments, it will be possible to amplify virtually all microsatellite sequences in a related species.

Marker GMBT16 had previously been mapped to the proterminal region of chromosome 21 in cattle and to the corresponding region of the evolutionary homologous ovine chromosome 18 (4). We demonstrate here that GMBT16, CSSM18, TGLA122, MSBT29, and UWCA4 belong to the same linkage group in cattle and sheep and that the most likely gene order is the same in both species. These results

Table 3. Pairwise linkage analysis among ovine chromosome 18 markers

Pairwise linkage analysis*	Recombination fraction (ϕ)						
	0.00	0.01	0.05	0.10	0.20	0.30	0.40
GMBT16-CSSM18	$-\infty$	-1.79	4.57	7.60	7.94	5.48	3.40
GMBT16-TGLA122	$-\infty$	-31.49	-12.71	-5.41	0.34	1.97	1.53
GMBT16-MSBT29	$-\infty$	-35.82	-19.22	-12.05	-5.34	-2.09	-0.48
GMBT16-UWCA4	$-\infty$	-36.32	-17.86	-9.69	-3.12	-0.46	0.32
GMBT16-GMBT21	$-\infty$	-28.57	-14.75	-8.99	-3.76	-1.34	-0.27
GMBT16-GMBT33	$-\infty$	-55.29	-28.43	-17.35	-7.33	-2.67	-0.56
GMBT16-fibrillin	$-\infty$	-2.82	-0.21	0.73	1.26	1.13	0.59
CSSM18-TGLA122	$-\infty$	-5.11	4.79	7.89	8.86	7.23	4.03
CSSM18-MSBT29	$-\infty$	-13.39	-3.99	-0.46	2.00	2.26	1.34
CSSM18-UWCA4	$-\infty$	-41.15	-12.17	-11.75	-4.43	-1.32	-0.16
CSSM18-GMBT21	$-\infty$	-32.50	-16.78	-10.33	-4.49	-1.74	-0.40
CSSM18-GMBT33	$-\infty$	-56.55	-28.66	-15.34	-7.26	-1.86	-0.56
CSSM18-fibrillin	$-\infty$	-6.15	-2.18	-0.68	0.41	0.61	0.34
TGLA122-MSBT29	$-\infty$	1.70	6.61	7.96	7.75	6.00	3.21
TGLA122-UWCA4	$-\infty$	-24.35	-7.40	-1.26	3.17	3.75	2.37
TGLA122-GMBT21	$-\infty$	-31.69	-15.91	-9.42	-3.64	-1.08	-0.10
TGLA122-GMBT33	$-\infty$	-66.08	-33.35	-20.04	-8.22	-2.91	-0.58
TGLA122-fibrillin	$-\infty$	-9.65	-4.21	-2.04	-0.27	0.29	0.25
MSBT29-UWCA4	$-\infty$	3.13	6.61	7.40	6.87	5.18	1.68
MSBT29-GMBT21	$-\infty$	-12.66	-5.87	-3.15	-0.84	0.01	0.15
MSBT29-GMBT33	$-\infty$	-30.92	-14.85	-8.26	-2.58	-0.31	0.29
MSBT29-fibrillin	$-\infty$	-11.66	-5.96	-3.54	-1.37	-0.43	-0.07
UWCA4-GMBT21	$-\infty$	-28.89	-15.09	-9.35	-4.09	-1.58	-0.36
UWCA4-GMBT33	$-\infty$	-46.17	-22.46	-12.95	-4.71	-1.13	-0.01
UWCA4-fibrillin	$-\infty$	-8.74	-3.98	-2.09	-0.52	0.02	0.09
GMBT21-GMBT33	$-\infty$	-3.69	2.01	3.92	4.73	3.99	2.29
GMBT33-fibrillin	$-\infty$	-14.81	-7.34	-4.32	-1.70	-0.57	-0.11

*Lod scores are summed over informative pedigrees.

demonstrate that a high proportion of type II DNA markers can be made to work in different but related species and that there is a high level of conservation of chromosomal location and order. However, genetic distance was not always conserved between these two species. Markers GMBT21 and GMBT33 are tightly linked in cattle (0% recombination in males); while these markers show clear evidence of linkage in sheep, the recombination rate is estimated at 19%. GMBT21 and GMBT33 have been assigned to chromosome 21 in cattle by virtue of their segregation pattern in somatic cell hybrids as well as their linkage with the other chromosome 21 markers. Although we have not yet been able to

demonstrate linkage between the second linkage group (GMBT33 and GMBT21) and the other ovine chromosome 18 markers, we predict that these two markers map to ovine chromosome 18 with a higher recombination rate between these markers and UWCA4 than in cattle.

The marker map of sheep chromosome 18, based on bovine chromosome 21 markers, was used to position the callipyge locus in the interval between CSSM18 and TGLA122. Chromosomal localization of the ovine *CLPG* locus is the first step toward positional cloning of the corresponding gene. The availability of a bovine YAC library (18) is expected to be invaluable for the identification of the callipyge gene. Given the fact that this YAC library represents ± 6 bovine genome equivalents with mean insert size of at least 800 kb and that only 3 cM separate CSSM18 from the *CLPG* locus, YAC walking starting from this marker may be sufficient to construct a contig spanning the bovine homologue of the *CLPG* locus. The clones composing this contig could in turn be used to generate additional markers in the region. Although these markers would be based on bovine sequences, we show in this work that the majority of bovine primers can be made effective in sheep.

The advantage of working with livestock species such as sheep is that large numbers of informative offspring can be bred with relative ease. Boehnke (28) recently showed that with 400 meioses, a number that should be easily obtainable with sheep, the expected distance between the two nearest crossovers flanking the trait locus of interest is 0.5 cM, with a 90% probability of being inferior to 1 cM. Assuming that enough markers have been generated in the region from an available contig, the distance between the two nearest flanking markers should only be slightly higher, of the order of 1 cM. A 1-cM region is expected to correspond to ≈ 1 million base pairs and to contain from 25 to 50 genes, by analogy with results from human research. As the expression pattern of the

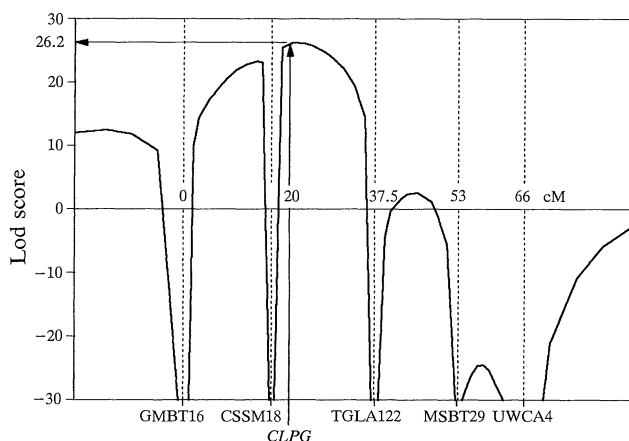


FIG. 2. Multilocus linkage analysis of the ovine callipyge locus. Recombination frequencies between GMBT16-CSSM18-TGLA122-MSBT29-UWCA4 were fixed at 16.6%, 19.2%, 15.2%, and 12.4%, respectively, while the map position of the callipyge locus was varied. Corresponding lod scores were calculated with LINKMAP. Recombination units were converted to cM using Kosambi's mapping function; map locations were centered around GMBT16.

CLPG gene is likely to be muscle-tissue specific, positional cloning of this gene seems to be a realistic endeavor.

Comparative anchor loci (19) known to reside on bovine chromosome 21 (B2M, FES, IGF1R, and CHGA) map to human chromosome 15 (B2M, FES, and IGF1R) or human chromosome 14 (CHGA). The IGF1 receptor should be considered as a plausible candidate gene for the ovine muscular hypertrophy phenotype. However, no polymorphisms have yet been identified for this locus in sheep (data not shown). A form of limb girdle muscular dystrophy, sometimes characterized by hypertrophy of the gastrocnemius muscle, has been mapped in man to 15q15-21 (20) and close to the fibrillin *Fib15* gene (11). Using a human *Fib15* probe that resolves a *Taq* I polymorphism in sheep, preliminary evidence indicates absence of at least tight linkage between the ovine callipyge and fibrillin loci (Table 2).

Muscular hypertrophy has been identified and selected for in other livestock species such as cattle and swine and is often referred to as "double muscling." The condition described in cattle is actually a muscular hyperplasia characterized by a generalized increase in muscle mass ($\pm 20\%$) with all other organs and tissues reduced in size, a 40% reduction in intramuscular fat and a 9% improvement in feed efficiency (21). Contrary to sheep, the bovine condition manifests itself at birth (if not *in utero*) causing a high incidence of dystocia. Moreover, the condition in cattle is due to a partially recessive allele at an autosomal locus (22, 23), while the hypertrophy-causing allele is dominant in sheep. A DNA fingerprint band showing evidence for linkage with the bovine double muscling condition has been previously described (24) but has been refractory to subsequent cloning (P. Hilbert, personal communication). Because the bovine and ovine muscular hypertrophy conditions manifest themselves quite distinctly, it seems unlikely that the same locus is involved in both traits. In pigs, the ryanodine receptor (*RYR1*) gene, or a very closely linked gene located on pig chromosome 6, has been shown to have a major effect on muscular development and carcass leanness (25). Animals homozygous for a T for C-1843 nucleotide substitution in the *RYR1* gene have a 2–3% increase in lean, dressed carcass weight. Animals heterozygous for the mutation have intermediate growth and carcass characteristics. The T for C-1843 mutation is linked to the occurrence of porcine stress/pale soft exudative meat syndrome and susceptibility to anesthetic-induced malignant hyperthermia (26). The *RYR1* gene has been mapped to bovine chromosome 18 (27), precluding a role for this gene in the ovine muscular hypertrophy condition.

The dominant nature of the callipyge gene lends itself to successful transfer into other meat-producing species, thereby extending the importance of identifying the causal gene. Dissemination of the muscular hypertrophy trait through a flock could occur in a single generation, as the mating of a *CLPG/CLPG* male to conventional (*clpg/clpg*) females would produce all heavy muscled lambs. However, this mating scheme requires the identification of homozygous rams. A genetic marker for the callipyge gene would provide a rapid and inexpensive method of confirming an animal's genotype for this trait.

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