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## Research

# Assessing the effect of the *CLPG* mutation on the microRNA catalog of skeletal muscle using high-throughput sequencing

Florian Caiment,<sup>1</sup> Carole Charlier,<sup>1</sup> Tracy Hadfield,<sup>2</sup> Noelle Cockett,<sup>2</sup> Michel Georges,<sup>1,3</sup> and Denis Baurain<sup>1</sup>

<sup>1</sup>Unit of Animal Genomics, Department of Animal Production, GIGA-R, and Faculty of Veterinary Medicine, University of Liège (B34), 4000-Liège, Belgium; <sup>2</sup>Department of Animal, Dairy and Veterinary Sciences, Utah State University, Logan, Utah 84322, USA

The callipyge phenotype is a monogenic muscular hypertrophy that is only expressed in heterozygous sheep receiving the *CLPG* mutation from their sire. The wild-type phenotype of *CLPG/CLPG* animals is thought to result from translational inhibition of paternally expressed *DLK1* transcripts by maternally expressed miRNAs. To identify the miRNA responsible for this *trans* effect, we used high-throughput sequencing to exhaustively catalog miRNAs expressed in skeletal muscle of sheep of the four *CLPG* genotypes. We have identified 747 miRNA species of which 110 map to the *DLK1-GTL2* or callipyge domain. We demonstrate that the latter are imprinted and preferentially expressed from the maternal allele. We show that the *CLPG* mutation affects their level of expression in *cis* (~3.2-fold increase) as well as in *trans* (~1.8-fold increase). In *CLPG/CLPG* animals, miRNAs from the *DLK1-GTL2* domain account for ~20% of miRNAs in skeletal muscle. We show that the *CLPG* genotype affects the levels of A-to-I editing of at least five pri-miRNAs of the *DLK1-GTL2* domain, but that levels of editing of mature miRNAs are always minor. We present suggestive evidence that the miRNAs from the domain target the ORF of *DLK1*, thereby causing the *trans* inhibition underlying polar overdominance. We highlight the limitations of high-throughput sequencing for digital gene expression profiling as a result of biased and inconsistent amplification of specific miRNAs.

[Supplemental material is available online at <http://www.genome.org>. The sequence and miRNA expression data from this study have been submitted to NCBI's GenBank (<http://www.ncbi.nlm.nih.gov/genbank/>) and Gene Expression Omnibus (GEO; <http://www.ncbi.nlm.nih.gov/geo/>) under accession nos. AF354168 and GSE24146, respectively. All new ovine miRNAs corresponding to the *DLK1-GTL2* locus also have been submitted to miRBase (<http://www.mirbase.org/>).

The callipyge phenotype is an inherited muscular hypertrophy of sheep. It is characterized by an unusual inheritance pattern referred to as polar overdominance: Only heterozygous individuals having received the *CLPG* mutation from their father express the phenotype (Cockett et al. 1996). The *CLPG* point mutation inactivates a muscle-specific silencer controlling the expression of a subset of imprinted genes in the *DLK1-GTL2* domain (i.e., the paternally expressed protein-encoding *DLK1* and *PEG11* [also known as *RTL1*] genes and the maternally expressed non-coding *GTL2* [also known as *MEG3*], anti-*PEG11* [also known as anti-*RTL1*], *MEG8* [also known as *RIAN*], and *MIRG* genes) (Charlier et al. 2001a; Freking et al. 2002; Smit et al. 2003). Hence, paternal heterozygotes ( $+^{Mat}/CLPG^{Pat}$ ) are characterized by ectopic expression of *PEG11* (Byrne et al. 2010) and *DLK1* (Davis et al. 2004) in skeletal muscle. *DLK1* is thought to contribute to the callipyge phenotype as its ectopic expression increases muscle mass in transgenic mice (Davis et al. 2004). Whether ectopic expression of *PEG11* is also involved in phenotypic expression remains to be established.

While showing increased levels of *DLK1* mRNA in muscle—like their  $+^{Mat}/CLPG^{Pat}$  counterparts—no *DLK1* protein is observed in muscle of *CLPG/CLPG* animals, accounting for their wild-type

phenotype (Davis et al. 2004). The absence of *DLK1* protein despite increased levels of *DLK1* mRNA in these animals is thought to result from the ectopic expression of the maternal noncoding RNAs, as this feature distinguishes *CLPG/CLPG* from  $+^{Mat}/CLPG^{Pat}$  individuals (Georges et al. 2003, 2004). The maternal long, non-coding RNA genes are hosting a large array of small C/D snoRNAs and miRNAs of unknown function (Seitz et al. 2004). We have postulated that these small RNAs are the mediators of the *trans* effect down-regulating *DLK1* in *CLPG/CLPG* animals thus causing polar overdominance (Supplemental Fig. 1; Georges et al. 2003, 2004). This hypothesis received strong support from the demonstration, in the same *DLK1-GTL2* locus, of RNAi-mediated *trans* inhibition of the paternally expressed *PEG11* by miRNAs processed from the maternally expressed anti-*PEG11* transcript (Seitz et al. 2003; Davis et al. 2005).

To identify small RNAs that might be involved in the *trans* inhibition of *DLK1* in skeletal muscle of *CLPG/CLPG* animals we have performed high-throughput sequencing (HTS) of small RNA libraries generated from skeletal muscle of sheep of the four possible *CLPG* genotypes. To qualify as mediators of the *trans* effect underlying polar overdominance (Georges et al. 2003, 2004), the corresponding small RNAs should (1) map to the *DLK1-GTL2* domain; (2) be imprinted with expression from the maternal allele; (3) be subject to the *cis* effect of the *CLPG* mutation (i.e., be ectopically expressed in skeletal muscle upon maternal transmission of the mutation); and (4) have the ability to guide the RISC complex to *DLK1* transcripts for inhibition.

### <sup>3</sup>Corresponding author.

E-mail [michel.georges@ulg.ac.be](mailto:michel.georges@ulg.ac.be); fax 32-4-366-41-98.

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## Results

### A catalog of miRNAs expressed in skeletal muscle of sheep

The callipyge phenotype is most pronounced in muscles of the hindquarters and manifests itself at ~1 mo of age. At 8 wk of age, DLK1 protein is detected in skeletal muscle of  $+^{mat}/CLPG^{pat}$  but not of  $CLPG/CLPG$  animals, suggesting that the *trans* effect operates at that stage (Davis et al. 2004). Thus, we elected to extract RNA from longissimus dorsi (LD) of two 8-wk-old animals per  $CLPG$  genotype. Small RNA (~18 to 30 bp) libraries were generated and sequenced on a Genome Analyzer I (Illumina). We obtained an average of 6,324,668 reads per animal (range: 5,222,920–6,685,342). Filtered, adapter-trimmed sequences (94.7%) were aligned to the bovine genome used as reference, with the exception of 390 kb of ovine sequence corresponding to the *DLK1–GTL2* domain (GenBank AF354168). The resulting alignments were used to predict miRNA precursors using miRDeep (Friedlander et al. 2008). This yielded 472 precursors, capturing 98.3% (range: 98.15%–99.32%) of trimmed reads. Sequence comparison with precursors in miRBase combined with mapping data indicate that 228 and 87 are the orthologs and paralogs, respectively, of previously reported bovine miRNAs (Glazov et al. 2009), while nine are the orthologs of miRNAs described in non-ruminant mammals. Thus, 148 precursors might correspond to previously unknown miRNAs (Supplemental Table 1). The chromosomal distribution of miRNA precursors is shown in Supplemental Figure 2. Chromosome 21, harboring the *CLPG* locus, stands out with 61 precursors (chromosomal average: 14.8).

As the genomic sequence of sheep is not completed, we used the bovine sequence as reference. The effect of this substitution was estimated by comparing the output of miRDeep using either the bovine or the ovine sequence of the *DLK1–GTL2* domain as reference. miRDeep predicts 49 precursors in this domain when using the ovine sequence, of which three are missed when using the bovine reference. Sensitivity is thus decreased by ~6%, but specificity does not seem affected.

We aligned all precursor pairs using BLASTN and used the bitscores (>35 bits) to identify precursor families using the MCL algorithm (Enright et al. 2002). The unique inflation parameter was set to the most aggregative value (2.0) for which the miR-376 family was recovered without contaminants (Seitz et al. 2004). Using this approach, 256 of the 472 precursors (= 54%) clustered in 62 families. The largest family (miR-2284 family) comprised 99 members. The remaining 61 families counted 2.6 members on average (range: 2–6).

While for 197 (= 41.7%) precursors we observed reads mapping either to the 5p or 3p arm of the pre-miRNA, both types of reads were observed for the remaining 275 (= 58.3%), jointly defining 747 distinct miRNA “species.” The fraction ( $F$ ) of 5p over total reads distinguishes five types of precursors (Landgraf et al. 2007): 5p-mature/3p-star ( $1 > F > 0.87$ ), 5p > 3p ( $0.87 > F > 0.50$ ), 5p = 3p ( $F = 0.5$ ), 5p < 3p ( $0.50 > F > 0.13$ ), and 5p-star/3p-mature ( $0.13 > F > 0$ ). The frequency distribution of  $F$ -values is shown in Supplemental Figure 3. The five types represent, respectively, 46.0%, 10.2%, 1.2%, 10.2%, and 32.4% of precursors. Precursors spawning miRNAs preferentially from the 5p arm were 1.4 times more abundant than those with 3p excess.

Aligning the reads with the identified precursors revealed considerable 3' length variability. As this might reflect trimming artifacts due to decreased sequencing fidelity toward the 3'-end, we will not elaborate further on it. 5'-Ends were in general more consistent, with nevertheless considerable evidence for the occur-

rence of isomirs (Morin et al. 2008). For 65% of the miRNAs,  $\geq 90\%$  of reads shared the same 5' extremity, for 27%,  $\geq 90\%$  of reads shared one of two 5' extremities, and for 6%,  $\geq 90\%$  of reads shared one of three 5' extremities. In general, more than 91% of alternative 5' extremities were within 4 bp of the most common one.

### Annotating miRNAs expressed from the *DLK1–GTL2* domain

Forty-nine of the precursors identified by miRDeep mapped to the *DLK1–GTL2* domain. Of these, 39 corresponded to known miRNAs reported in miRBase, while 10 were unknown. Detailed examination of the SOAP (Li et al. 2008) alignments revealed 5729 reads mapping to 14 regions not recognized by miRDeep as miRNA precursors. Six of these corresponded to miRNAs reported in miRBase and were included in the catalog. In addition, 487 reads mapped to 12 predicted C/D snoRNAs within *MEG8* (of note, bona fide C/D snoRNAs are ~80 bp long and would therefore have been excluded from the small RNA libraries). We found no reads for 14 miRNAs reported in human and/or in mice (of which five conserved in sheep).

5'-Ends showed the level of variability observed in the genome-wide catalog, that is, respectively, 58%, 34%, and 8% of miRNAs with one, two, and three isomirs representing  $\geq 90\%$  of the reads. Remarkably, 49 precursors (89.1% of the expressed precursors) had reads mapping to both 5p and 3p arms, to be compared with the genome-wide 58.3%.

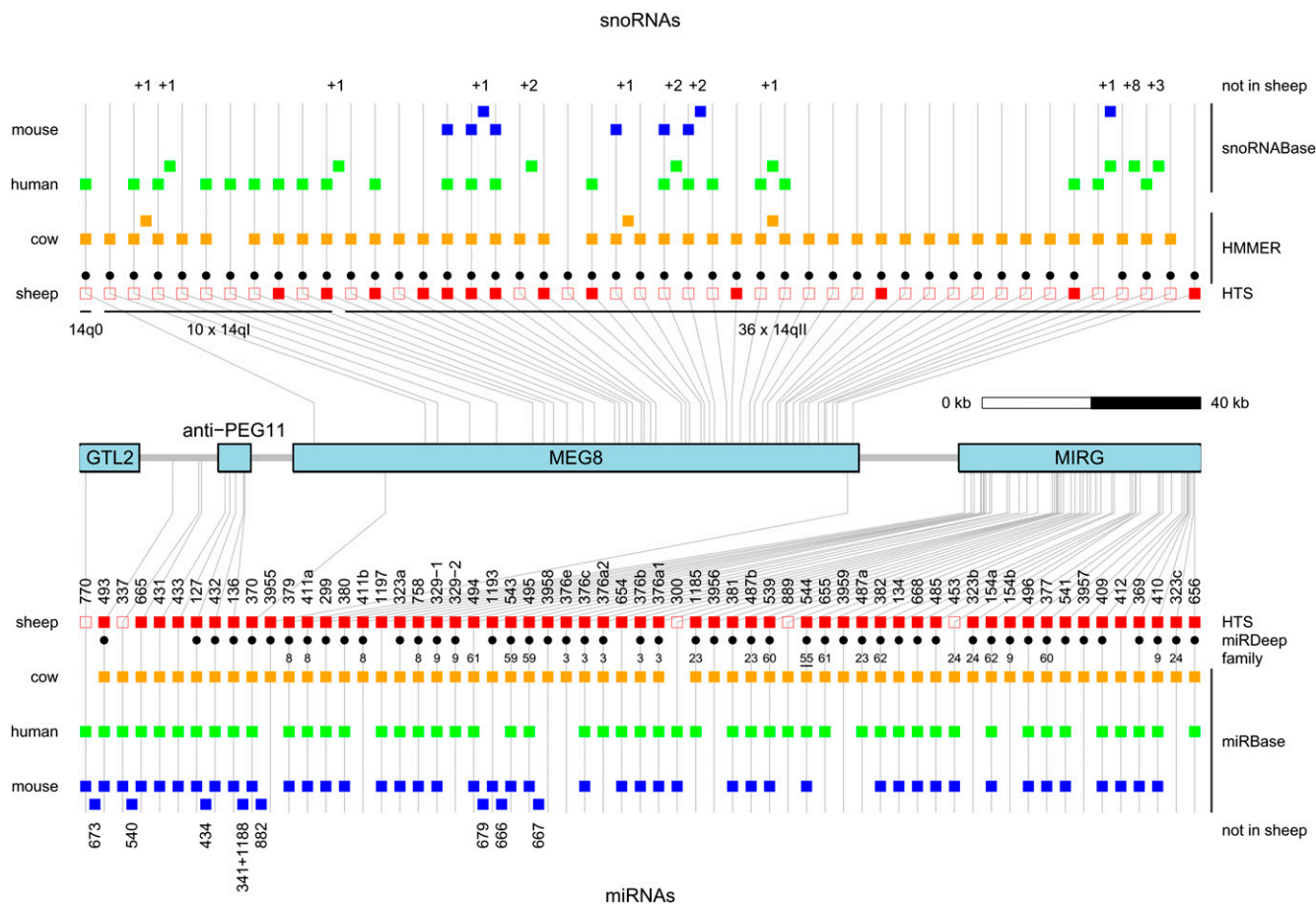
A summary of all miRNA precursors identified in the *DLK1–GTL2* domain is given in Figure 1. A total of 110 distinct small RNA species (not distinguishing isomirs) were identified, mapping to 61 miRNA and 12 C/D snoRNA precursors. All detected small RNAs derive from the same strand as *GTL2*, anti-*PEG11*, *MEG8*, and *MIRG*. Using a 10-way mammalian sequence alignment of *MIRG*, we generated a plot of sequence conservation within 8-nt windows (Supplemental Fig. 4A). We observed a striking coincidence between the peaks of conservation and the positions of the miRNAs, supporting miRNA generation as the primary function of *MIRG*. A similar colocalization of conservation peaks and C/D snoRNAs is not observed for *MEG8* (Supplemental Fig. 4B).

### Limits of HTS for the quantitative assessment of miRNA expression

Read numbers are assumed to faithfully reflect expression levels, allowing for accurate digital gene expression profiling. However, recent data indicate that the amplification steps during library construction may introduce substantial, protocol-specific biases (Linsen et al. 2009). To evaluate accuracy and precision of our HTS data in measuring miRNA expression, we (1) repeated the HTS experiment for seven of the eight animals (including RNA extraction, library construction, and sequencing on an Illumina GA-II instrument); (2) hybridized skeletal muscle (LD) RNA from the eight animals on Exiqon miRCURY LNA (Version 9.2—updated to miRBase 11.0) arrays (GEO GSE24146); and (3) performed QRT-PCR for eight miRNAs spanning a broad range of expression levels as determined by HTS. While the Exiqon arrays allow interrogation of 569 human miRNAs, we restricted the analysis to 265 for which the LNA probes were perfectly complementary to the orthologous ruminant miRNA.

The main conclusions of this experiment can be summarized as follows:

1. Spearman rank correlations ( $r_s$ ) between sequencing replicates were 0.80 on average, thus suggesting adequate reproducibility of HTS (Supplemental Fig. 5). Note that correlations were



**Figure 1.** Comparative map of the small RNA genes in the *DLK1-GTL2* domain: snoRNAs (upper panel) and miRNAs (lower panel). Square boxes correspond to small RNAs detected in sheep (red), cow (orange), human (green), and mouse (blue). Gray lines connect orthologs in the four species and indicate their chromosomal position with respect to the four long noncoding RNA genes in the domain: *GTL2*, *anti-PEG11*, *MEG8*, and *MIRG*. The position of precursors not detected in sheep is indicated by squares nested between vertical gray lines. The numbers above and below snoRNA and miRNA columns, respectively, correspond to numbers of additional paralogs for the snoRNAs (from +1 to +8) and names of additional miRNAs. The red squares are filled when reads for the corresponding small RNA were found in the conducted HTS experiments, empty when not. (Black dots) miRNAs predicted by miRDeep (Friedlander et al. 2008) in sheep. Numbers below the black dots identify the cluster/family to which the corresponding miRNA was assigned using the BLAST/MCL algorithm (Enright et al. 2002). The family number of miR-544 is underlined as the other members map outside of the *DLK1-GTL2* domain. (Black dots) snoRNAs predicted by HMMER (Durbin et al. 1998) in sheep. snoRNAs in mouse and human correspond to predictions made by Cavaille et al. (2002). snoRNAs in the cow were predicted by HMMER (Durbin et al. 1998). miRNAs in cow, human, and mouse were extracted from miRBase (Griffiths-Jones 2006).

slightly higher when comparing pairs of animals with the same *CLPG* genotype within sequencing runs (average  $r_s = 0.83$ ) (data not shown). Examination of specific miRNAs, however, highlighted limitations of digital expression profiling by HTS. Hence, while miR-127 accounted on average for 4% of reads originating from the *DLK1-GTL2* domain in the first experiment, its contribution increased to 25% on average in the second, pointing toward systematic discrepancies between the two experiments for some miRNAs. Moreover, while miR-1 represented  $\geq 83\%$  of reads (average 86%) in the first series of eight libraries, and  $\geq 80\%$  of reads (average 82%) in 5/7 libraries of the second series, it only reached 32% and 49% in the two remaining ones, thus showing substantial discrepancies even within an experiment. Finally, within sequencing experiments, the 5p/3p ratio differed significantly between individuals for nearly all miRNA precursors (chi squared test). In extreme cases, different individuals would appear to have inverted 5p/3p ratios despite sequence depths of hundreds and even thousands.

In no case were these opposite 5p/3p ratios confirmed in the second experiment. A representative example (miR-382) is shown in Supplemental Figure 6. Thus, while the repeatability of HTS may seem satisfactory in general, our findings suggest that amplification efficiency of specific miRNAs may vary considerably between experiments.

2.  $r_s$  values between expression levels (ranks) assessed using the Exiqon miRCURY LNA arrays averaged 0.86 between individuals of the same *CLPG* genotype. This value has to be compared with a value of 0.90 when restricting the HTS data to the 265 miRNAs interrogated with the Exiqon array. Thus, in these experiments, HTS and array hybridization were characterized by comparable reproducibility. Yet, when comparing ranks obtained with the two methods,  $r_s$  values dropped to 0.63 (first sequencing experiment) and 0.68 (second sequencing experiment) (Supplemental Fig. 7A,B). Supplemental Figure 7, C and D, illustrates the impact of this correlation drop in terms of probability of reversed rank order between alternative methods as a function of observed fold

difference in expression level: miRNA pairs showing a fivefold difference in expression level on the Exiqon arrays still have a probability of  $\sim 0.15$  to be ranked inversely by HTS. Of note, the RNAs hybridized on the arrays were not size-selected (thus potentially including pri-, pre-, and mature miRNA molecules), while the RNAs used to construct the libraries for HTS were size-selected to include only mature miRNAs.

- Given the observed discrepancies between the HTS and array-hybridization, we performed QRT-PCR for eight miRNAs (let-7d, miR-1, miR-206, miR-127, miR-382-5p, miR-382-3p, miR-3958, miR-3959) spanning a range of expression levels using the looped RT primer approach (targeting mature miRNAs) (Chen et al. 2005). QRT-PCR experiments were conducted in duplicate on the RNA samples used for HTS. Abundance of miRNA “*x*” relative to let-7d was estimated as  $\varepsilon_x^{C_{tx}} / \varepsilon_{let7d}^{C_{let7d}}$ , where  $\varepsilon$ 's are the experimentally determined amplification efficiencies and  $C$ 's the threshold exceeding cycle numbers. From these analyses it appeared that the QRT-PCR results were more consistent with the array-hybridization than with HTS in terms of expression ranks and estimated fold differences in expression levels (Supplemental Fig. 8A,B). Our data strongly suggest that some miRNAs undergo preferential amplification during the HTS procedure.

### Effect of *CLPG* genotype on relative expression levels of miRNAs in the *DLK1–GTL2* domain

The previous findings call for caution when interpreting variations in expression levels of individual miRNAs. To overcome this limitation, we examined the effect of *CLPG* genotype on the expression level of the miRNAs from the *DLK1–GTL2* domain considered as a group.

We first confirmed the previously described *cis* effect of the *CLPG* mutation on neighboring genes in the sequenced RNA samples. QRT-PCR experiments were conducted using primer sets specific for mature *DLK1* and *GTL2* transcripts, and for two internal controls (*RPLP0*, *RPS18*) selected with geNorm out of five housekeeping genes (Vandesompele et al. 2002). The expected *CLPG* effects were clearly observed (Supplemental Fig. 9). Expression levels of *DLK1* were increased  $\sim 12$ -fold and approximately fourfold in, respectively,  $+^{Mat}/CLPG^{Pat}$  and *CLPG/CLPG* animals when compared to  $+/+$ , while being slightly decreased ( $\sim 0.6$ ) in *CLPG*<sup>Mat/+Pat</sup>. Expression levels of *GTL2* were increased  $\sim 30$ -fold,  $\sim 14$ -fold, and approximately fivefold in *CLPG/CLPG*, *CLPG*<sup>Mat/+Pat</sup>, and  $+^{Mat}/CLPG^{Pat}$ , when compared to  $+/+$  animals. These results were undistinguishable from the ones that were previously reported using samples originating from other animals (Charlier et al. 2001a; Davis et al. 2004, 2005). The previously observed approximately fivefold increase of *GTL2* expression in  $+^{Mat}/CLPG^{Pat}$  when compared to  $+/+$  animals, and approximately twofold increase of *GTL2* expression in *CLPG/CLPG* when compared to *CLPG*<sup>Mat/+Pat</sup> animals remains particularly intriguing and points toward a *trans* effect of the padumnal *CLPG* mutation on the expression level of the madumnal non-coding RNA genes (Charlier et al. 2001a).

We then analyzed the HTS data. Read numbers corresponding to a given miRNA species (i.e., mapping either to the 5p or 3p arm of a precursor) were first adjusted to account for the different numbers of total “mappable” reads per individual. The relative expression level for a given animal was expressed as  $\log_2(i/m)$ , where  $i$  corresponds to the adjusted number of reads for that individual and  $m$  is the experiment-specific average number of adjusted reads for that miRNA across the seven individuals that were sequenced twice. Average  $\log_2(i/m)$  across miRNAs differed considerably be-

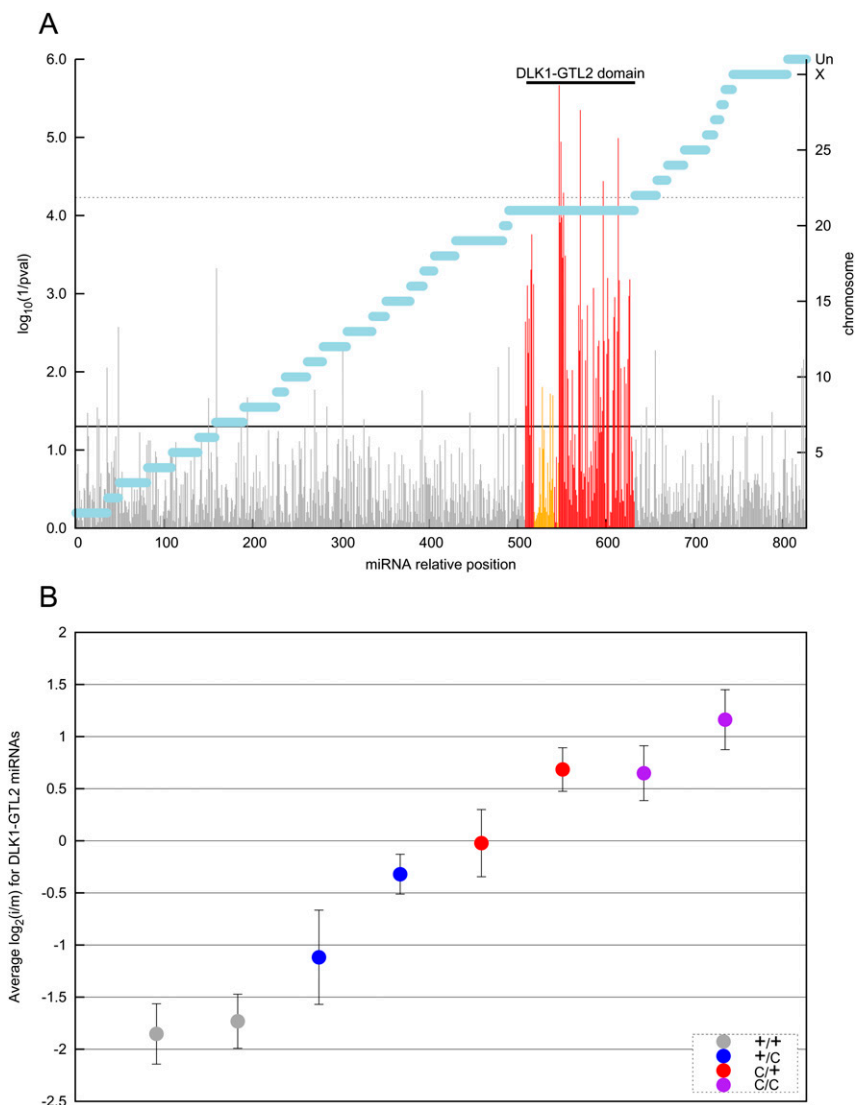
tween individuals, including for miRNAs outside of the *CLPG* locus. This was thought to reflect experimental issues rather than genuine biological differences (Supplemental Fig. 10). Therefore,  $\log_2(i/m)$  values were corrected for the average  $\log_2(i/m)$  value across miRNAs mapping outside of the *DLK1–GTL2* domain (for that individual). We then tested the effect of *CLPG* genotype on the corrected relative expression levels by ANOVA, using both sequencing experiments jointly. Figure 2A shows the corresponding  $\log(1/p)$  values. The effect of *CLPG* genotype on the relative expression level of miRNAs from the *DLK1–GTL2* domain is clearly visible from the localized cluster of significant  $\log(1/p)$  values. Six (miR-379, miR-411a, miR-495, miR-154b, miR-655, and miR-299) of the 99 “regular” miRNAs (i.e., excluding small RNAs derived from C/D snoRNAs) exhibited *P*-values  $< 6 \times 10^{-5}$ , corresponding to the Bonferroni-corrected 5% threshold, while 47 were characterized by nominal *P*-values  $< 0.05$ . Figure 2B shows, for each of the eight studied animals, the average relative expression levels over all “regular” miRNAs of the *DLK1–GTL2* domain. The order is identical to that observed for the long noncoding RNA genes including *GTL2*: *CLPG/CLPG*  $>$  *CLPG*<sup>Mat/+Pat</sup>  $>$   $+^{Mat}/CLPG^{Pat}$   $>$   $+/+$ . The magnitude of the effect, however, was smaller: Expression levels were increased  $\sim 6.4$ -fold,  $\sim 4.4$ -fold, and  $\sim 2.0$ -fold in *CLPG/CLPG*, *CLPG*<sup>Mat/+Pat</sup>, and  $+^{Mat}/CLPG^{Pat}$  when compared to  $+/+$  animals.

The previous figures pertain to “regular” miRNAs from the *DLK1–GTL2* domain. As can be seen from Figure 2A, the effect of *CLPG* genotype on the expression level of small RNAs derived from C/D snoRNAs were not significant, suggesting that *MEG8* might escape the *cis* effect of the *CLPG* mutation, contradicting previous findings (Charlier et al. 2001a). Examination of the effect of *CLPG* genotype on C/D snoRNA-derived small RNAs, however, revealed the expected trend in all but one  $+^{Mat}/CLPG^{Pat}$  individual (Supplemental Fig. 11). Expression levels of C/D snoRNA-derived species (average number of reads: 70; median: 6) were low when compared to miRNAs (average number of reads: 21,300; median: 249). Low levels, combined with the aberrant behavior of one individual, explain the nonsignificance of the *CLPG* effect on the expression level of small RNAs derived of C/D snoRNAs, which we nevertheless believe exists.

The effect of *CLPG* genotype on relative miRNA expression levels was also evaluated from the array data (Supplemental Fig. 12A,B). The effect of *CLPG* genotype was equally clear, manifesting itself as a clustered rise in  $\log(1/p)$  values. Expression levels were increased  $\sim 4.8$ -fold,  $\sim 3.1$ -fold, and  $\sim 2.2$ -fold in *CLPG/CLPG*, *CLPG*<sup>Mat/+Pat</sup>, and  $+^{Mat}/CLPG^{Pat}$ , when compared to  $+/+$  animals. Hence, the ranking was as expected (*CLPG/CLPG*  $>$  *CLPG*<sup>Mat/+Pat</sup>  $>$   $+^{Mat}/CLPG^{Pat}$   $>$   $+/+$ ), yet the magnitude of the effect was slightly lower than the HTS estimates.

### Imprinting status of miRNAs in the *DLK1–GTL2* domain

The obvious interpretation of miRNA expression levels in  $+^{Mat}/CLPG^{Pat}$  and *CLPG*<sup>Mat/+Pat</sup> intermediate between  $+/+$  and *CLPG/CLPG* (Fig. 2B) is that most miRNAs from the *DLK1–GTL2* domain are not imprinted, yet affected by the *CLPG cis* effect. All previous evidence, however, indicates that the maternally expressed non-coding RNA genes, including the embedded C/D snoRNA and miRNA genes, are exclusively expressed from the maternal allele. In the mouse, tested C/D snoRNAs and miRNAs from the *DLK1–GTL2* domain were expressed in mice with maternal uniparental disomies of chromosome 12 (mUPD12) but not with paternal UPD12 (Cavaille et al. 2002; Seitz et al. 2003, 2004). The same small RNA genes were expressed in mice inheriting a deletion of the



**Figure 2.** (A)  $\log_{10}(1/p)$  values of the effect of *CLPG* genotype on the expression level of 851 small RNAs in skeletal muscle of eight 8-wk-old sheep. Expression levels were estimated from the number of Illumina GA reads from two independent HTS experiments. The statistical significance of the *CLPG* effect was estimated by ANOVA. Gray vertical bars correspond to miRNAs outside of the *DLK1-GTL2* domain, red vertical bars to miRNAs from the *DLK1-GTL2* domain, and orange vertical bars to small RNAs derived from C/D snoRNA precursors. Horizontal black lines correspond to the nominal (plain line) and Bonferroni-adjusted (dotted line) 5% significance thresholds. Horizontal blue bars mark the different chromosomes (right Y-axis). (UN) Unassigned sequence contigs. (B) Average expression level, relative to the mean expression level of seven individuals sequenced twice (HTS1 and HTS2), of 99 “regular” miRNAs (i.e., excluding small RNAs derived from C/D snoRNAs) from the *DLK1-GTL2* domain in skeletal muscle of eight sheep sorted by *CLPG* genotype (gray: +/+; blue: +<sup>Mat</sup>/*CLPG*<sup>Pat</sup>; red: *CLPG*<sup>Mat</sup>/<sup>Pat</sup>; purple: *CLPG/CLPG*). Error bars correspond to  $1.96 \times$  the standard error of the estimate.

IG-DMR imprinting control element when on the paternal allele, but not when on the maternal allele (Lin et al. 2003; Seitz et al. 2004). In human, *MEG8* (also known as *RIAN*), from which the C/D snoRNA genes are processed (Cavaille et al. 2002), was not expressed in patients with pUPD14 (Kagami et al. 2008). We have previously shown that in sheep muscle, anti-*PEG11* and *MEG8* (hosting miRNAs and C/D snoRNAs, respectively) are exclusively expressed from the maternal allele, irrespective of *CLPG* genotype (Charlier et al. 2001a,b).

To more directly assess the imprinting of the miRNAs from the *DLK1-GTL2* domain in sheep and the effect of the *CLPG* mu-

tation on it, we searched for SNPs in the vicinity of pre-miRNAs for which at least one of the four studied *CLPG*<sup>Mat</sup>/<sup>Pat</sup> or +<sup>Mat</sup>/*CLPG*<sup>Pat</sup> animals would be heterozygous. We found nine such SNPs tagging six pre-miRNAs. Seven of these SNPs were within 160 bp from the corresponding pre-miRNA (miR-379, miR-134, miR-485, miR-453, miR-154b), one was in the loop (miR-453), and one was at position 20 of the miRNA\* (miR-377). One +<sup>Mat</sup>/*CLPG*<sup>Pat</sup> animal was homozygous for all SNPs and hence noninformative, but the other three were heterozygous for most (Table 1). For each SNP the allele associated with the *CLPG* mutation was determined by sequencing a *CLPG/CLPG* animal.

For miR-377 and knowing that the SNP mapped to the miRNA\*, we determined imprinting status from HTS data. We exclusively detected reads corresponding to the maternal allele, both in the *CLPG*<sup>Mat</sup>/<sup>Pat</sup> and +<sup>Mat</sup>/*CLPG*<sup>Pat</sup> animals, thus supporting tight imprinting, exclusive maternal expression, and no effect of *CLPG* genotype on imprinting. For miRNAs with SNPs lying outside of the mature miRNAs, we amplified the pri-miRNA with primers within 179 bp from the pre-miRNA, directly sequenced the resulting amplicons, and measured the allelic ratio using PeakPicker (Ge et al. 2005). For four of the five miRNAs, the results were identical to miR-377 (Table 1): tight imprinting, near exclusive maternal expression, and no effect of *CLPG* genotype. For miR-485, however, we observed relaxation of imprinting in one *CLPG*<sup>Mat</sup>/<sup>Pat</sup> animal and one +<sup>Mat</sup>/*CLPG*<sup>Pat</sup> animal, for which ~20% of transcripts were derived from the paternal allele. There was no evidence for relaxation of imprinting of miR-485 in the other informative *CLPG*<sup>Mat</sup>/<sup>Pat</sup> animal (Table 1). It is noteworthy that miR-134 located 588 bp upstream, and miR-154b located 4293 bp downstream of miR-485 did not show evidence for relaxation of imprinting in the same individuals.

#### Effect of *CLPG* genotype on absolute expression levels of miRNAs in the *DLK1-GTL2* domain

The previous analyses are not informative about absolute miRNA expression levels: Are they just present in minute, biologically irrelevant amounts? Or do they make a significant contribution to the pool of miRNAs in muscle? Analysis of the two sequencing experiments indicate that, after exclusion of miR-1 whose read numbers were inflated (see above), the percentage of reads originating from miRNA precursors in the *DLK1-GTL2* domain was 4% in +/+ animals, but increased to 10%, 11%, and 21% of the total in

**Table 1.** Imprinting status of miRNAs in the ovine *DLK1–GTL2* domain and effect of the *CLPG* genotype

	miRNA <sup>a</sup>								
	miR-379	miR-134		miR-485		miR-453		miR-154b	miR-377
	80 bp-5' <sup>b</sup>	3'-32 bp <sup>b</sup>	3'-160 bp <sup>b</sup>	3'-78 bp <sup>b</sup>	3'-94 bp <sup>b</sup>	57 bp-5' <sup>b</sup>	Loop <sup>b</sup>	69 bp-5' <sup>b</sup>	miR <sup>+b</sup>
<i>CLPG</i> :+ <sup>c</sup>	T:C	A:C	A:C	T:C	A:G	T:C	T:C	T:C	T:C
<i>(CLPG/+)</i> <sub>1</sub> <sup>d</sup>		100/0	100/0	100/0	98/2	99/1	99/1	97/3	14/0
<i>(CLPG/+)</i> <sub>2</sub> <sup>d</sup>		100/0	95/5	84/16	86/14	100/0		96/4	7/0
+/ <i>CLPG</i> <sup>d</sup>	98/2	94/6	97/3	83/17	88/12	95/5		98/2	46/0

<sup>a</sup>Name of the tested miRNA. miR-379 to miR-154b, percent of the madumnal/padumnal alleles found in cDNA; miR-377, number of HTS reads corresponding to the madumnal/padumnal allele.

<sup>b</sup>Position of the interrogated SNP with respect to the corresponding pre-miRNA.

<sup>c</sup>SNP alleles associated with the *CLPG* and + allele.

<sup>d</sup>*CLPG* genotype of corresponding animal.

+<sup>Mat</sup>/*CLPG*<sup>Pat</sup>, *CLPG*<sup>Mat</sup>/<sup>Pat</sup>, and *CLPG/CLPG* animals. The Exiqon arrays only measure the abundance of some miRNAs present in a tissue. However, as the proportion of miRNAs mapping to the *DLK1–GTL2* domain was virtually identical in the HTS (99/826 = 12%) and hybridization data (34/265 = 12.8%), the ratio of the sum of fluorescence intensities for miRNAs in the domain over the sum of fluorescence intensities over all miRNAs would also provide an estimate of the cellular abundance of miRNAs originating from the *DLK1–GTL2* domain. miRNAs from the domain accounted for 3.5%, 9.0%, 15.6%, and 22.3% of the Hy3 fluorescence on the Exiqon arrays in +/+, +<sup>Mat</sup>/*CLPG*<sup>Pat</sup>, *CLPG*<sup>Mat</sup>/<sup>Pat</sup>, and *CLPG/CLPG* animals. Both approaches thus provided comparable estimates, indicating that the *DLK1–GTL2* domain contributes a sizeable fraction of the miRNA population, especially in *CLPG/CLPG* animals in which they are predicted to mediate the *trans* inhibition of *DLK1*.

While claims about expression levels of individual miRNAs are hazardous for the reasons mentioned before, the QRT-PCR and array experiments strongly suggest that miRNAs from the *DLK1–GTL2* domain are characterized by an at least 30-fold range of expression levels (Supplemental Figs. 8, 13).

#### Effect of *CLPG* genotype on relative expression levels of miRNAs outside the *DLK1–GTL2* domain

Skeletal muscles that express the callipyge hypertrophy have a profoundly altered physiology. Ectopic expression of *DLK1* (Davis et al. 2005) triggers a cascade of secondary events leading to muscular hypertrophy (e.g., Vuocolo et al. 2007). These may involve altered miRNA expression. To detect such secondary miRNA perturbations, we tested the effect of *CLPG* genotype on relative expression levels of miRNAs outside of the domain. We first considered the HTS and array hybridization data separately. When accounting for multiple testing, no miRNA outside of the *DLK1–GTL2* domain appeared to be significantly affected by the *CLPG* genotype (Fig. 2; Supplemental Fig. 12). In an attempt to increase power, we combined HTS and array data for the 265 miRNAs with information on both platforms. Even then, no miRNA outside of the domain was significant (Supplemental Fig. 14). We conclude that the molecular events connecting ectopic expression of *DLK1* and muscular hypertrophy do not involve altered miRNA expression.

#### Editing of miRNAs from the *DLK1–GTL2* domain in skeletal muscle

It was recently observed that a cluster of miRNAs mapping to the *DLK1–GTL2* domain (human miR-368, miR-376a1 [5' and 3'],

miR-376b and miR-376a2 [5' and 3']; murine miR-376a [5' and 3'], miR-376b [5' and 3'], and miR-376c) undergo extensive A-to-I editing in human and mice, particularly in the central nervous system (Kawahara et al. 2007). The most extensively edited sites correspond to position "+3" or "+4" of the 5p miRNAs and position "+6" of the 3p miRNAs. Analyses performed in knockout (KO) mice suggest that 5p editing is ADAR2 (also known as ADARB1) dependent, while 3p editing is ADAR1 (also known as ADAR) dependent. Editing seemed not to affect processing, as equally high levels were observed in pri-miRNAs and derived mature miRNAs. By changing the seed, editing was predicted to alter the target spectrum.

As editing of miRNA seeds from the *DLK1–GTL2* domain in sheep may likewise alter affinity for *DLK1*, we systematically searched for it. We first examined whether the precursors of miR-376a,b,c undergo editing in skeletal muscle of mice. We RT-PCR-amplified the corresponding pri-miRNAs from cDNA of brain, kidney, and skeletal muscle (quadriceps femoris) from an FVB mouse and sequenced the corresponding PCR products. Strong (~80%) and moderate (~60%) editing of the "+44" 3p position (residue "+6" of the mature miRNA) was observed for the three studied miRNAs in, respectively, brain and kidney, hence recapitulating part of the results of Kawahara et al. (2007). Contrary to these investigators, we found no evidence for editing of the 5p arms, whether in or upstream of the mature miRNA sequence. No editing was observed in skeletal muscle of mice (data not shown).

We then scanned the pri-miRNAs corresponding to 56 precursors from the *DLK1–GTL2* domain using RNA extracted from skeletal muscle (LD) of one *CLPG/CLPG* and one +/+ sheep. Within the miR-376 cluster, we did observe substantial levels of editing of the "+44" 3p position (corresponding to position "+6" of the mature miRNA) of miR-376e (0%–25%), miR-376c (also known as miR-368; 5%–45%), miR-376a2 (0%–50%), miR-376b (0%–95%), but not of miR-654 and miR-376a1. No editing was observed in the 5p arm for any of these pri-miRNAs. Outside of the miR-376 cluster, we observed strong editing of three other pri-miRNAs: at the equivalent "+44" 3p position (corresponding in this case to position "+5" of the mature miRNA) for miR-381 (10%–82%), at 5p position "+5" (corresponding to position "+5" of the mature miRNA) for miR-411a (0%–20%), and at 5p position –4 outside of the mature miRNA sequence for miR-369 (0%–40%). Note that neither miR-381 nor miR-411a shows obvious similarity with members of the miR-376 cluster. Based on these results, we evaluated the level of editing of miR-376e, miR-376c, miR-376a2, miR-376b, miR-381, and miR-411a in 16 additional animals representing the four possible *CLPG*

genotypes at 2 and 8 wk of age. Editing of miR-376c, miR-376b, and miR-381 was observed in some of the new animals, but not of miR-376e, miR-376a2, and miR-411a. Unexpectedly, we observed a highly significant ( $p \leq 1.3 \times 10^{-5}$ ) effect of *CLPG* genotype on the level of editing of miR-376c, miR-376b, and miR-381: +/+ animals had markedly higher levels of pri-miRNA editing than the three other genotypes (Fig. 3A).

To verify whether editing of the pri-miRNAs resulted in equivalent proportions of edited mature miRNAs (as observed by Kawahara et al. [2007]), we evaluated the level of editing of mature miR-376e, miR-376c, miR-376a2, miR-376b, miR-381, and miR-411a in the HTS libraries (Fig. 3B). In general, editing levels of mature miRNAs were below 10%. For the three miRNAs with high levels of pri-miRNA editing (i.e., miR-376c, miR-376b, miR-381), levels dropped considerably in the fully processed miRNAs. This was most striking for miR-376b with virtually total absence of edited reads. For miR-376c and miR-381, editing levels dropped by a factor of  $\sim 10$  when compared to the precursors. Thus, for these miRNAs, editing either inhibits pri/pre-miRNA processing and/or reduces the stability of the miRNA. The effect of *CLPG* genotype on editing levels was still apparent for miR-376c and miR-381. For miR-376a2, editing levels appeared higher after than before miRNA processing (although still well below 10%). In this case, editing may thus promote processing and/or stability. Finally, for miR-411a, mature editing levels were consistently of the order of 1%, which was well above background (average of 0.02% across 14 5p miRNAs with an A residue at position "+5"). Such levels would not have been reliably detected at the pri-miRNA level.

### Evaluating the affinity of miRNAs in the *DLK1*–*GTL2* domain for *DLK1*

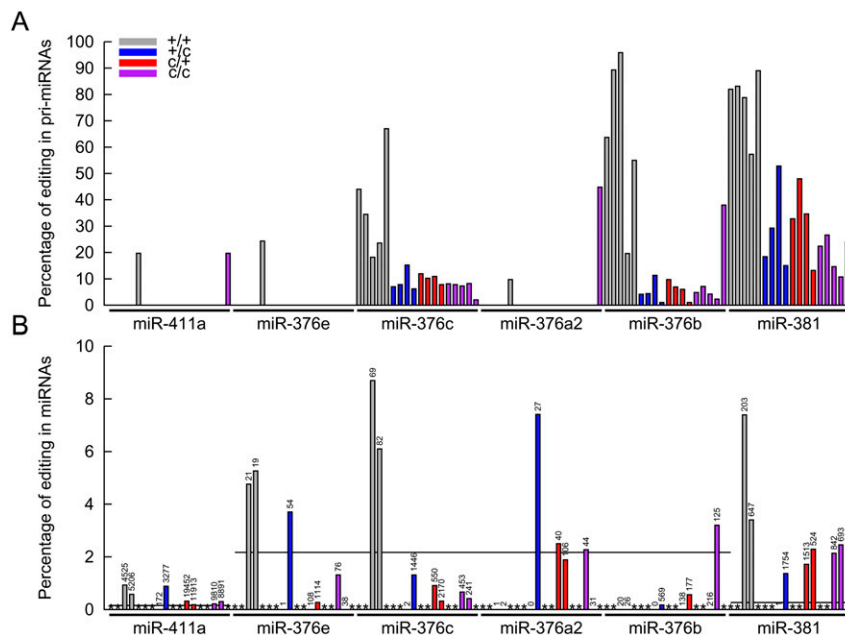
Having generated an exhaustive catalog of miRNAs expressed in skeletal muscle of *CLPG/CLPG* animals allowed us to test the miRNA-mediated *DLK1* *trans* inhibition hypothesis with unprecedented power.

For each of the 114 miRNA species from the *DLK1*–*GTL2* domain, we singled out the most abundant isomir (or pair of isomirs in *ex aequo* cases, leading to 127 distinct sequences) and quantified its affinity for *DLK1* using two established metrics. The first one ("G-species score") follows Grimson et al. (2007) and counts the occurrences of 6-mer (Watson-Crick [WC] reverse complement of miRNA residues 2 to 7), 7-mer-m8 (WC reverse complement of miRNA residues 2 to 8), 7-mer-A1 (WC reverse complement of miRNA residues 2 to 7 plus 3' A anchor), and 8-mer matches (WC reverse complement of miRNA residues 2 to 8 plus 3' A anchor) in *DLK1*. Thus, an 8-mer match would increase the "G-species score" by 4, that of a 7-mer (without 8-nt match) by 2, and that of 6-mer match by 1. The second one ("M-species score") sums scores ( $\geq 140$ ) obtained with the more liberal miRNA-target miRanda identification engine (John et al. 2004). G-species scores were summed to generate a "G-quadrille score," and "M-species scores" were summed to generate an "M-quadrille score." "Quadrille scores" evaluate the affinity for *DLK1* of the miRNAs considered as a team. Moreover, the same scores were generated for human and mouse (using species-specific miRNA sequences reported in miRBase), and corresponding scores were summed across species to generate "multiorganism (MO) scores." The latter should be more effective

at identifying an unusual affinity for *DLK1* if conserved across species. Whether the mechanisms underlying the *trans* inhibition of *DLK1* observed in sheep are shared with other species remains unknown.

To evaluate the statistical significance of the obtained metrics, we compared them with their distribution obtained on 10,000 random shuffles of the *DLK1* sequence. Shuffling was conducted such as to maintain the original trinucleotide composition of the target gene (cf. Supplemental Methods). While miRanda is expected to inflate the number of target predictions, their statistical significance should be well controlled by this approach (i.e., there is no reason why the true *DLK1* sequence should yield better miRanda scores than the shuffled sequences).

We first tested the approach using the *PEG11* ORF as positive control (1000 shufflings). *PEG11* is indeed targeted by at least six miRNA species derived from five pre-miRNAs in anti-*PEG11* in ovine, human, and mouse (miR-431, miR-433, miR-127, miR-432 [human and sheep], miR-434 [mouse], miR-136) (Davis et al. 2005). The targeting of *PEG11* by these miRNAs is "plant-like," relying on WC complementarity over the entire length, resulting in target slicing (Davis et al.



**Figure 3.** (A) Percentage of A-to-I editing of pri-miRNAs at the "+5" position (pre-miR-411a) or "+44" position (pre-miR-376e, pre-miR-376c, pre-miR-376a2, pre-miR-381) in longissimus dorsi of 18 animals representing the four possible *CLPG* genotypes [gray: +/+ (5); blue: +<sup>Mat</sup>/*CLPG*<sup>Pat</sup> (4); red: *CLPG*<sup>Mat</sup>/<sup>Pat</sup> (4); purple: *CLPG/CLPG* (5)]. The first two animals of each *CLPG* genotype were analyzed at 2 wk, the others at 8 wk. (B) Percentage of A-to-I editing of mature miRNAs at position "+5" (miR-411a = 5p), "+6" (miR-376e, miR-376c, miR-376a2, miR-376b = 3p), and "+5" (miR-381 = 3p). Animals are ordered as in A. (\*) Animals without HTS data. The numbers above each column correspond to the total number of reads (edited + non-edited) available for analysis. The black horizontal lines correspond to the average level of A-to-C substitution observed for miRNAs derived from the 5p arm at position "+5" (miR-411a), from the 3p arm at position "+6" (miR-376e, miR-376c, miR-376a2, miR-376b), and from the 3p arm at position "+5" (miR-381).

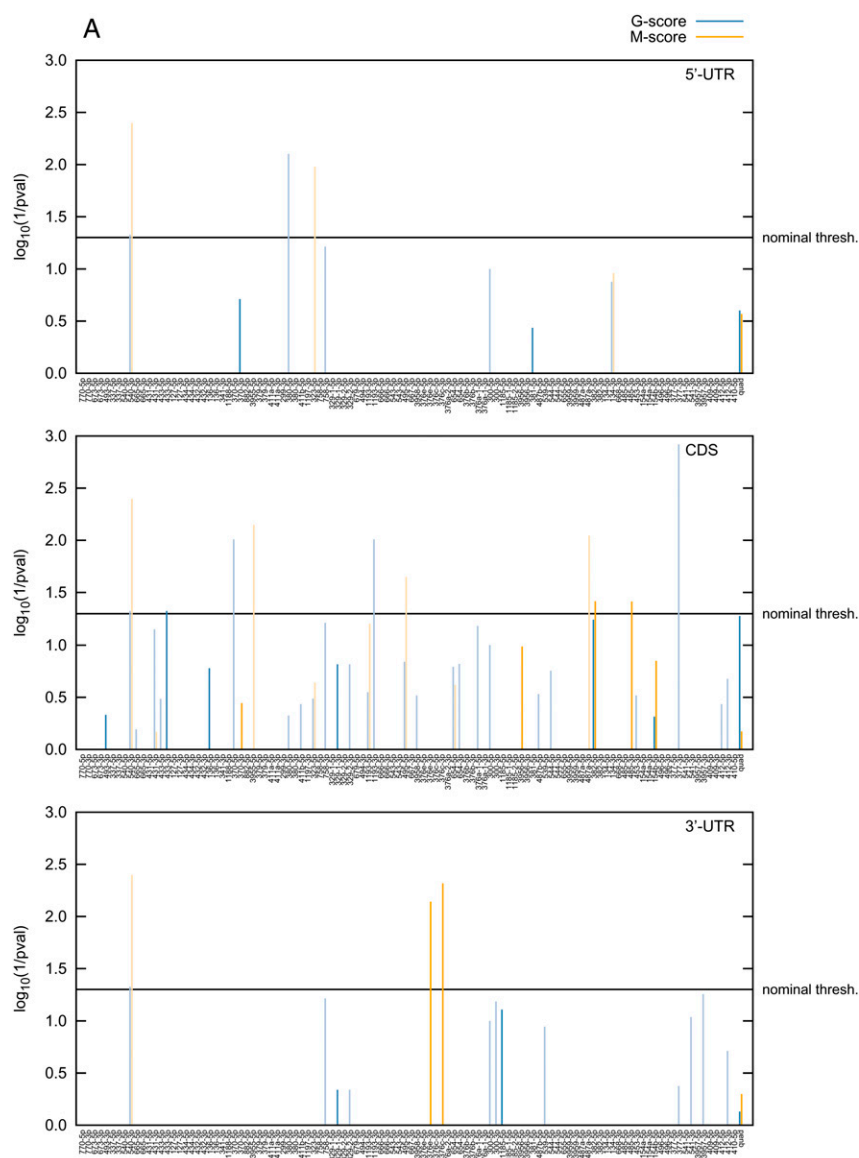
2005). For proper comparison with the presumably “animal-like” situation of *DLK1*, we only considered the miRNA seed sequences (residues 1 to 8) when computing the G-species scores (replacing the 3' A-anchor constraint [applying to 8-mer and 7-mer-A1 matches] by 3' W&C complementarity). miRanda scores were computed as before. When considering the ovine sequence (ORF) alone, both quadrille scores were significant (G:  $p = 0.003$ ; M:  $p = 0.025$ ), hence detecting the presence of one or more miRNAs targeting *PEG11*. Considered individually, however, none of the miRNA exceeded the Bonferroni-corrected 5% threshold. Two (of 12) miRNAs processed from anti-*PEG11* (miR-431-5p and miR-136-3p) achieved nominal significance ( $p = 0.003$ ) for both G- and M-species scores. Intriguingly, the ovine-specific miR-3959-3p, although processed from *MIRG*, achieved equivalent significance ( $p = 0.003$ ) (Supplemental Fig. 15A). When considering the three species simultaneously (hence exploiting evolutionary conservation known to exist), the significance of the two quadrille scores increased (G and M:  $p < 0.001$ ). Moreover, six (of 12) miRNA species processed from anti-*PEG11* yielded the highest possible signal (nominal  $p < 0.001$ ; Bonferroni-corrected  $p \sim 0.10$ ). Interestingly, miR-411a-5p processed from *MIRG* achieved the same top score, while the signal for miR-3959 remained essentially unchanged (nominal  $p = 0.003$ ) as this Laurasiatheria-specific miRNA is not shared with human and mouse (Supplemental Fig. 15B). The high miR-411a scores reflect one 7-mer and 10 6-mer matches in mouse, one 7-mer and six 6-mers in human, and two 7-mers and two 6-mers in sheep. Three matches were conserved in the three species, and one in two species. The high ovine miR-3959 score is due to one 8-mer and one 7-mer match. Thus, application of our method to *PEG11* indicated that (1) significant quadrille scores, but not species scores, could be obtained without exploiting evolutionary conservation; (2) significant quadrille and species scores could be obtained when exploiting conservation. Most interestingly, this analysis strongly suggests that the paternally expressed *PEG11* is not only targeted by fully complementary miRNAs processed from the maternally expressed anti-*PEG11*, but also by miRNAs processed from the maternally expressed *MIRG* pri-miRNAs, which recognize their target via seed-dominated complementarity.

We then applied the same approach to *DLK1* including the 5'-UTR, ORF, and 3'-UTR as it is established that miRNAs may target these different gene compartments (Baek et al. 2008; Selbach et al. 2008; Tay et al. 2008; Chi et al. 2009). When relying solely on ovine information, the most noteworthy result was the nearly significant G-quadrille score ( $p = 0.052$ ) on the *DLK1* ORF, hence suggesting an unusual affinity of the ovine miRNA team

for this segment of *DLK1* (Fig. 4A). This signal was primarily driven by miR-377-3p (nominal  $p = 0.0012$ ; one 8-mer and two 7-mer-m8 matches), miR-1193-3p (nominal  $p = 0.0098$ ; one 8-mer and two 7-mer-m8 matches), and miR-370-5p (nominal  $p = 0.0098$ ; one 8-mer and one 7-mer-m8 match; Fig. 4B). Note that none of these miRNAs achieves Bonferroni-adjusted significance. There was no convincing evidence for miRNA targeting of the *DLK1* 5'- or 3'-UTR.

When adding the human and murine information, the significance of the MO G-quadrille score for the ORF increased slightly ( $p = 0.036$ ), although none of the individual miRNAs clearly stood out (Fig. 4C). When applied to the 3'-UTR, the MO M-species score for miR-376c-3p achieved Bonferroni-corrected significance (nominal  $p = 0.0004$ ; Bonferroni-corrected  $p = 0.05$ ). This signal was due to a miRanda target site shared between mouse and sheep (Fig. 4C).

Weighting miRNA scores by expression level estimated from HTS reads and including all isomirs in such analyses did not yield stronger signals (data not shown).



**Figure 4.** (Continued on next page)



We find that the miRNAs from the *DLK1–GTL2* domain are affected by the *CLPG* mutation in the same manner as the maternally expressed long noncoding RNA genes (Charlier et al. 2001a). The main effect is in *cis* causing an  $\sim 3.2$ -fold increase in miRNA expression from a *CLPG* versus wild-type maternal chromosome ( $[CLPG^{Mat}/+^{Pat}]/[+/+] \approx 3, 7$ ;  $[CLPG/CLPG]/[+^{Mat}/CLPG^{Pat}] \approx 2, 7$ ). As for the other genes affected by the *CLPG* mutation, this is thought to result from the inactivation of a muscle-specific *cis*-acting silencer element. In addition, we confirm a *trans* effect consisting in the  $\sim 1.8$ -fold higher expression of miRNAs from the maternal al-

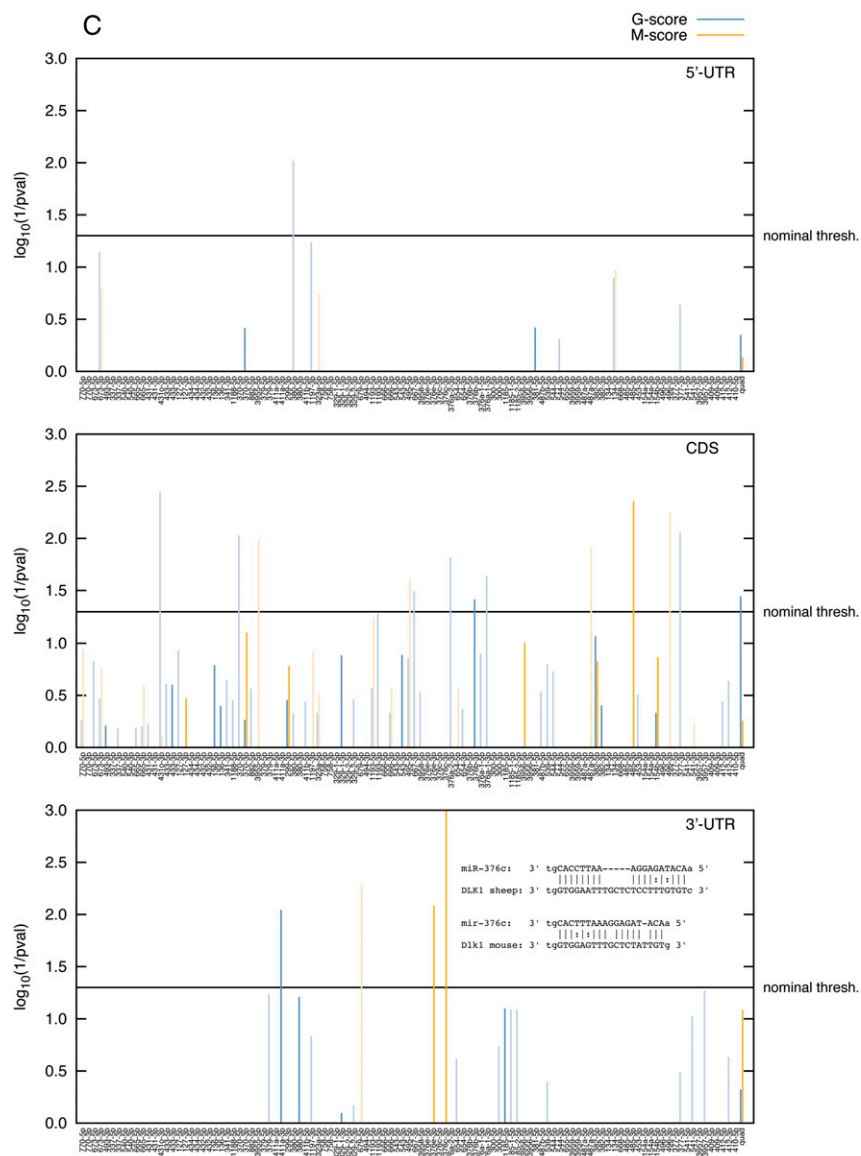
lele when the paternal allele is *CLPG* versus wild type ( $[+^{Mat}/CLPG^{Pat}]/[+/+] \approx 2.1$ ;  $[CLPG/CLPG]/[CLPG^{Mat}/+^{Pat}] \approx 1.5$ ). While the *MAT*  $\rightarrow$  *PAT* *trans* effect is known (*PEG11*) (Davis et al. 2005) or hypothesized (*DLK1*) (Georges et al. 2003, 2004) to reflect miRNA-mediated *trans* inhibition, the molecular mechanisms underlying this *PAT*  $\rightarrow$  *MAT* *trans* effect remain elusive. One possible explanation is that the silencer element that is inactivated by the *CLPG* mutation has the capacity to exert its effect in *trans* on the homologous chromosome. Such mechanisms have been attributed to enhancers in *Drosophila* and other organisms and may underlie transvection (Kennison and Southworth 2002).

The *cis* effect on miRNA expression is consistent with that observed for the long noncoding RNA genes but is considerably weaker ( $\sim 3.2$ -fold vs.  $\sim 9.5$ -fold). The reason for this difference is unknown. An explanation might be the saturation of the miRNA processing machinery.

Although HTS-based digital expression profiling may not be as quantitative as initially assumed, the combined HTS, array, and QRT-PCR data strongly suggest that miRNA expression levels differ at least  $\sim 30$ -fold. This could be due to differential processing efficiency of the precursors and/or stability of the processed miRNAs, but may also reflect the dependence on distinct promoters of unequal strength. The latter hypothesis is supported by the miR-485 imprinting data (see above), as well as by the recent identification of private host-gene-independent promoters for intronic miRNAs (Ozsolak et al. 2008).

Contrary to skeletal muscle of mouse, we observed substantial levels of A-to-I editing for 4/6 pri-miRNAs from the miR-376 family (miR-376e, miR-376c, miR-376a2, miR-376b) and for three unrelated pri-miRNAs (miR-381, miR-411a, miR-369) from the *DLK1–GTL2* domain in skeletal muscle of sheep. We noted a significant effect of *CLPG* genotype on pri-miRNA editing. Editing in *+/+* animals, characterized by the lowest miRNA expression levels, was  $\sim 4.2$ -fold higher than in the other genotypes. The reasons underlying this observation remain unclear, but could involve saturation of the editing machinery or down-regulation of components of the editing machinery by miRNAs from the domain. Contrary to Kawahara et al. (2007), editing levels were lower in the mature miRNA population when compared to precursors: Edited molecules never made up  $>10\%$  of reads.

The primary aim of this study was to lay the grounds for the identification of miRNAs that might account for the translational down-regulation of *DLK1* observed in *CLPG/CLPG* animals, that is, the *MAT*  $\rightarrow$  *PAT* *trans* effect. We approached



**Figure 4.** (A) Statistical significance [ $\log(1/p)$ ] of the affinity of ovine miRNAs in the *DLK1–GTL2* domain for the 5'-UTR, coding sequence (ORF), and 3'-UTR of the ovine *DLK1*. The affinity was measured using either G- (blue) or M-scores (orange) as defined in the text. Bars are dark colored for highly expressed and light colored for lowly expressed miRNAs. The last pair of bars ("quad") at the right of the graph corresponds to the quadrille scores, the remaining bars to the species scores and are labeled accordingly. *P*-values were determined using the sequence-shuffling test described in the text. Species scores require a Bonferroni correction for 127 independent tests. (B) Position in the *DLK1* mRNA of target sites (8-mers, 7-mers, and 6-mers as defined by Grimson et al. [2007]) for the same set of miRNA species. (C) Same as in A except that the scores are "multiorganism (MO) scores" combining information from sheep, human, and mouse.

this by posing that if an exceptional affinity of miRNAs from the *DLK1-GTL2* domain for *DLK1* could be clearly demonstrated in silico, this would very strongly support the hypothesis. The absence of such statistically significant affinity does not preclude actual interaction in vivo, but is neutral with respect to the hypothesis. We would not pretend that our data reveal an unambiguous affinity of the *DLK1-GTL2* miRNAs for *DLK1*, yet it is intriguing that both the G-quadrille score for the ORF and the miR-376c-3p MO M-species score for the 3'-UTR achieved 5% significance. This suggests that the *DLK1-GTL2* miRNAs might, indeed, effectively down-regulate *DLK1* in *CLPG/CLPG* animals. It is worthwhile re-stating in this regard that miRNAs from the domain account for an estimated ~20% of cellular miRNAs in these animals. We are in the process of testing this prediction biochemically using both reporter assays and AGO-based (also known as EIF2C) target coimmunoprecipitation (e.g., Takeda et al. 2010), prioritizing miRNAs on the basis of the results presented in Figure 4.

While miRNAs from the domain are strong candidate direct mediators of the MAT → PAT *trans* effect on *DLK1*, alternative possibilities should not be excluded. Among those figure (1) an indirect effect of the miRNAs from the domain, as well as (2) miRNA-independent mechanisms. It is interesting with regard to the latter that no clear function has yet been assigned to *GTL2*.

Individual miRNAs are predicted to target 200 to 300 genes on average (Grimson et al. 2007). What are the targets of the highly conserved miRNAs in the *DLK1-GTL2* domain? To start addressing this question, we assembled the list of 2832 bovine genes having at least one conserved 8-mer or 7-mer target site in their 3'-UTRs for any of the 24 out of 153 "conserved miRNA families" with representatives in the *DLK1-GTL2* domain (Friedman et al. 2009). We then looked for the enrichment of specific gene ontology (GO) terms among these genes (Ashburner et al. 2000). To that end, we randomly sampled 10,000 (GO Slim analysis) or 200,000 (whole GO analysis) sets of 2832 genes from the complete TargetScan list of 8458 bovine miRNA-targeted genes and compared the hit number of each GO term for the list of target genes of the *DLK1-GTL2* miRNAs with the distribution of hit numbers across the 10,000 (respectively, 200,000) random sets of genes. The resulting *P*-values were Bonferroni-corrected for the 6930 terms sampled out of the whole GO graph, or for the 55 terms of the GO Slim graph. Supplemental Table 2A shows the eight most enriched terms in both analyses, corresponding to a Bonferroni-corrected *P*-value  $\leq 0.027$  for the GO slim analysis, or a nominal *P*-value  $\leq 10^{-4}$  for the GO whole analysis. The outcome of this analysis strongly suggests that the miRNAs from the *DLK1-GTL2* domain are devoted to the targeting of regulators of the gene circuitry operating at the transcriptional, translational, and post-translational level, primarily in the nervous system. The list of genes corresponding to these top hits is provided in Supplemental Table 2, B and C.

## Methods

### Construction of small RNA libraries and high-throughput sequencing

Small RNA libraries were constructed using the "Small RNA sample preparation kit" following the instructions of the manufacturer (Illumina). Briefly, 10  $\mu$ g of total RNA extracted with TRIzol (Invitrogen) was size-fractionated by denaturing polyacrylamide gel electrophoresis (PAGE; 15%), and molecules ranging from 18 to 30 nt were eluted. RNA adapters were successively ligated to the 5'- then 3'-end of the isolated small RNAs, and ligation products of the desired length (40–60 bp then 70–90 bp) were recovered

by sequential PAGE (15% then 10%). Small RNAs appended with 5' and 3' adapters were reverse-transcribed with Superscript II (Invitrogen) and amplified with Phusion DNA polymerase (Finnzymes Oy). Resulting amplicons were PAGE (6%) gel-purified, hybridized on a flow cell lane, clustered, and sequenced (36 cycles) using standard procedures (Illumina). Libraries corresponding to eight animals (two of each *CLPG* genotype) were first sequenced on a GA-I (Illumina) by Fasteris SA. The experiment was subsequently repeated for seven animals using a GA-II instrument (Illumina) at the GIGA-R core facilities.

### Bioinformatics analysis of small RNA reads

The bioinformatics procedures applied for preprocessing of HTS reads; prediction, curation, and annotation of miRNA precursors; prediction of C/D snoRNAs in the *DLK1-GTL2* domain; gene annotation and conservation analyses in the domain; quantitative analyses of HTS reads; comparison of HTS, Exiqon, and TaqMan data; analysis of non-miRNA HTS reads; evaluation of miRNA affinity for *DLK1*; and GO analyses of targets of miRNAs encoded in the domain are described in detail in the Supplemental Methods.

### Exiqon array hybridization

Skeletal muscle RNA samples from the same eight animals (two of each *CLPG* genotype) extracted with TRIzol (Invitrogen) were hybridized on Exiqon miRCURY LNA Arrays (v.9.2) at Exiqon (Vedbaek). Briefly, RNA quality was evaluated on an Agilent Bioanalyzer 2100. Individual samples were labeled with Hy3 using the miRCURY Hy3/Hy5 power labeling kit, and cohybridized on the arrays with a Hy5-labeled equimolar mix of the eight samples. Arrays were scanned in an ozone-free environment. Fluorescence intensities were normalized with the global Lowess (LOcally WEighted Scatterplot Smoothing) regression algorithm using all probes except those corresponding to miRNAs from the *DLK1-GTL2* domain.

### Quantitative RT-PCR

QRT-PCR analyses of miRNAs were conducted using predesigned (miR-1, miR-127, miR-206, miR-382, miR-382\*, let-7d) or custom (miR-3958 and miR-3959) TaqManMicroRNA assays (ABI) on an 9700HT (ABI) instrument. Assay-specific amplification efficiencies were determined using serial RNA dilutions.

### Editing

The level of pri-miRNA editing was determined by sequence analysis of genomic- and cDNA-derived PCR products. Genomic DNA and total RNA were extracted using TRIzol (Invitrogen). Reverse transcription was carried out using Superscript III (Invitrogen) on 1  $\mu$ g of total RNA pre-treated with Turbo DNase (Ambion) and cDNA PCR-amplified using GOLD Taq (ABI; 35 cycles). The primer sequences used for mouse and sheep are provided in Supplemental Table 3. Amplicons were sequenced on a 3730 instrument (ABI), and the degree of editing was estimated from the electropherograms using PeakPicker (Ge et al. 2005).

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