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Leptin is required for hypothalamic regulation of miRNAs targeting POMC 3′UTR

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The central nervous system (CNS) monitors modifications in metabolic parameters or hormone levels and elicits adaptive responses such as food intake regulation. Particularly, within the hypothalamus, leptin modulates the activity of pro-opiomelanocortin (POMC) neurons which are critical regulators of energy balance. Consistent with a pivotal role of the melanocortin system in the control of energy homeostasis, disruption of the POMC gene causes hyperphagia and obesity. MicroRNAs (miRNAs) are short noncoding RNA molecules that post-transcriptionally repress the expression of genes by binding to 3′-untranslated regions (3′UTR) of the target mRNAs. However, little is known regarding the role of miRNAs that target POMC 3′UTR in the central control energy homeostasis. Particularly, their interaction with the leptin signaling pathway remain unclear. First, we used common prediction programs to search for potential miRNAs target sites on 3′UTR of POMC mRNA. This screening identified a set of conserved miRNAs seed sequences for mir-383, mir-384-3p, and mir-488. We observed that mir-383, mir-384-3p, and mir-488 are up-regulated in the hypothalamus of leptin deficient ob/ob mice. In accordance with these observations, we also showed that mir-383, mir-384-3p, and mir-488 were increased in db/db mice that exhibit a non-functional leptin receptor. The intraperitoneal injection of leptin down-regulated the expression of these miRNAs of interest in the hypothalamus of leptin deficient ob/ob mice. In summary, these results suggest that leptin modulates the expression of miRNAs that target POMC mRNA in hypothalamus.

Keywords: microRNA, melanocortin, hypothalamus, leptin, food intake

Introduction

The control of energy homeostasis is finely tuned by endocrine and neural mechanisms that cooperate to maintain the balance between caloric intake and energy expenditure. In this respect, the central nervous system (CNS) continuously monitors modifications in metabolic...
parameters (blood glucose) and/or hormones (insulin or leptin) and elicits adaptive responses such as food intake regulation and autonomic nervous system modulation (Cowley et al., 2001; Ibrahim et al., 2003; Plum et al., 2006; Mounien et al., 2010). It is now clearly established that specific neuronal networks of the hypothalamus play a pivotal role in energy homeostasis regulation (Morton et al., 2006). For instance, within the arcuate nucleus of the hypothalamus, pro-opiomelanocortin (POMC) neurons are critical regulators of energy balance and glucose homeostasis (Porte et al., 2002; Mounien et al., 2005, 2009, 2010; Parton et al., 2007; Hill et al., 2010). In accordance with this aspect, it has been shown that the disruption of the POMC and melanocortin receptor 4 (MC4R) genes in mice models causes obesity (Huszár et al., 1997; Yaswen et al., 1999), while MC3R gene-deficient mice have normal food consumption but accumulate fat (Chen et al., 2000). In humans, obesity can result from genetic deficiencies which produce a lack in the leptin receptor, POMC, or MC3/4R (Lee, 2009).

One important goal of current research is to identify the molecular mechanisms involved in the control of the expression of genes that are important to maintain energy homeostasis. It has long been acknowledged that the leptin acts as a key regulator of hypothalamic genes expression via different signaling cascades (Morton et al., 2006). For instance, when the leptin binds to the extracellular domain of its receptor (LepR), it recruits and activates the Janus kinase (JAK). JAK binds to and phosphorylates LepR at the same time. This mechanism activates signal transducer and activator of transcription 3 (STAT3). Once phosphorylated, STAT3 binds to POMC promoters, stimulating POMC expression (Morton et al., 2006). Interestingly, mice with genetic inactivation of STAT3 gain body weight (Gao et al., 2004). Altogether, the above collected data strongly suggest that the stability of energy homeostasis during environmental variation requires metabolic adjustments that are achieved through a fine regulation of gene's expression.

Because microRNAs (miRNAs) have been depicted to be another layer of gene regulation, it is not surprising that they are also involved in leptin-regulated gene expression. The miRNAs are endogenous, single-stranded, small, ~22-nucleotides noncoding RNAs, and are generally regarded as negative regulators of gene expression because they inhibit translation and/or promot mRNA degradation by base pairing to complementary sequences within the 3′untranslated region (3′UTR) of protein-coding mRNA transcripts (Bagga et al., 2005). Several studies identified miRNAs that are differentially expressed in the liver, pancreas, and adipose tissue of leptin-deficient (ob/ob) or leptin receptor-deficient (db/db) mice compared to the control animals (Lovis et al., 2008; Li et al., 2009; Nakanishi et al., 2009; Xie et al., 2009). Among these miRNAs, it has been shown that the pancreatic expression levels of mir-375 are aberrant in ob/ob mice, indicating that they contribute to insulin resistance in this model (Poy et al., 2009). Additional studies provide evidence for the involvement of mir-335 in lipid metabolism of the liver and the adipose tissue of ob/ob and db/db mice (Nakanishi et al., 2009). In the context of CNS, it has been shown that mir-200a, mir-200b, and mir-429 are up-regulated in the hypothalamus of ob/ob and db/db mice (Crépin et al., 2014).

Recently, it has been shown that conditional deletion of the RNAse III ribonuclease Dicer (involved in miRNAs maturation) from POMC-expressing cells results in obesity and diabetes which is associated with a neurodegenerescence of POMC neurons in the hypothalamus (Schneeberger et al., 2012; Greenman et al., 2013). These observations strongly suggest that miRNAs are important regulators of POMC neuron activity. In this context, the characterization of the miRNAs that target directly POMC mRNA and their interaction with the leptin signaling pathway remain unclear.

In the present study, we focused our attention on the specific miRNAs targeting POMC 3′UTR. Based on bioinformatic predictions of their involvement in POMC-signaling pathway and their conservation among vertebrates, the expression of mir-383, mir-384-3p, and mir-488 were investigated in models of obesity characterized by a decrease of POMC mRNA expression and leptin insufficiency (ob/ob) or leptin insensitivity (db/db) (Mizuno et al., 1998). Then, we further analyzed the role of leptin on the expression level of these miRNAs using different models of leptin-treated mice.

Methods

Animals

Experiments were carried out on different types of mice: C57BL/6, ob/ob, and db/db mice were purchased from Charles River (France). Fluorescence in situ hybridization (FISH) experiments were performed using male POMC-Tau-Topaz GFP transgenic mice developed by Pinto et al. (2004). To assess GFP expression in POMC-Tau-Topaz GFP mice, we carried out PCR on tail genomic DNA. GFP transgene was detected using the forward primer 5′-GCCACAACTTCAAGGTGTCG-3′ and the reverse primer 5′-GCTTCTCTGTTGGGTGCCT-3′, with the following PCR conditions: 5 min at 95°C, 36 cycles at 95°C for 30 s, 64°C for 30 s, and 72°C for 40 s, followed by a final step at 72°C for 7 min. The amplicon size was 573 bp.

All animals were individually housed in a pathogen-free facility at controlled temperature on a 12/12 h light/dark cycle (lights from 0700 to 1900 h) with standard pelleted diet (AO4) and water available ad libitum. All experiments were conducted in conformity with the rules set by the EC Council Directive (2010/63/UE) and the French “Direction Départementale de la Protection des Populations des Bouches-du-Rhône” (License no. 13.435 and no. 13.430). Protocols used are in agreement with the rules set by the Comité d’Ethique de Marseille, our local Committee for Animal Care and Research. Every precaution was taken to minimize animal stress and the number of animals used.

miRNA Prediction

To search for miRNAs that might regulate mouse POMC expression, we used the following public prediction algorithms and database: Targetscan (http://www.targetscan.org/) and miRanda (http://www.microrna.org/microrna/home.do). Using these different algorithms, we selected the miRNAs that are conserved among the vertebrates (Targetscan) and that have a good mirSVR scores (miRanda).
Surgery and Injections
For the intraperitoneal injection (i.p.), ob/ob, and C57BL/6 mice were injected between 1100 and 1200 h with recombinant murine leptin (Peprotech, France) (n = 5, 5 mg/kg) or saline. Mice were sacrificed 4 h after i.p. injection.

Intracerebroventricular (i.c.v) cannula placement and injections were performed as described previously (Girardet et al., 2011). Animals were anesthetized by an i.p. injection of ketamine (100 mg/kg; Imalgem 1000, Merial, France) and xylazine (6 mg/kg; Rompun, Bayer, France), and placed in a digital stereotaxic apparatus (Model 502600, WPI) coupled to the neurostar software (Neurostar GmbH, Germany). A 26-gauge stainless steel cannula was implanted into the lateral ventricle at the following coordinates: 0.3 mm posterior to bregma, 1.1 mm lateral to the midline, and 2.6 mm ventral to the skull surface. The correct cannula positioning was checked for each animal at the end of the experiment by cresyl violet staining of brain sections (Supplementary Figure 1).

The exogenous leptin was detected in the hypothalamus of ob/ob and C57BL/6 mice after i.p. and i.c.v injection by western blotting (Supplementary Figure 2 and Supplementary Material).

Quantitative RT-PCR (qRT-PCR) Analysis
Mice were killed by decapitation and the different brain regions were collected and frozen in liquid nitrogen and stored at −80°C until protein or RNA extraction. Total RNA was extracted with TRI Reagent (Sigma-Aldrich, France). For RNA quantification, cDNA was synthetized by 2 µg total RNA with M-MLV Reverse Transcriptase (Promega Corporation, WI, USA). For miRNAs quantification, cDNA was synthetized by 1 µg total RNA by the qScript microRNA Quantification System (Quanta Bioscience, MD, USA). For real-time PCR, we used LightCycler 480 (Roche, Germany). We used Pomc forward primer 5'-TGAACATCTTTTGCCCAGA-GAGCTCA-3' and reverse 5'-TGCA-GAGGCACCCAGATTGGCTTTACAAAGC-3'; β-Actin forward primer 5'-GATCTGGCACCACCCTCTCTAC-3' and reverse 5'-TGTCGTGGGAGGAGCATAGTG-3'; Gapdh forward primer 5'-TTCTCAAGCTTCTTTCTGCTGATG-3' and reverse primer 5'-GATAGGGCCCTTCTTGCTTCTCA-3'. PCR was maintained at 4°C for 10 min, followed by 40 cycles of 10 s at 95°C, 30 s at 60°C, and 2 s at 72°C, followed by a holding at 40°C. For miRNAs, U6 and Sno202 were used as normalizers for miRNA quantification. For U6 we used forward primer 5'-ATTGGAACGATACAGAATTTGG-3' and reverse primer 5'-GGGACGCCATTCCAGATTTGG-3'; Sno202 forward primer 5'-CAGATCTTTGTACCAGTTCCAGATTTGG-3'; reverse primer 5'-GGGACGCCATTCCAGATTTGG-3'; scmir-384-3p forward primer 5'-CATGAATATTCCGTGGTTAAT6FAM for 3'-FAM for mir-384-3p; 5'-AGATTCTCAACCTTGAATTTGCTTCTATTT-3'-FAM for mir-384-3p; 5'-AAACACCTCAACATAGACCTTT-3'-FAM for mir-488-3p; 5'-AGATTCTCAACCTTGAATTTGCTTCTATTT-3'-FAM for mir-384-3p; 5'-AAACACCTCAACATAGACCTTT-3'-FAM for mir-488. Scrambled probes were used for negative control for each experiment. The scramble sequences were 5'-TTCCGACAATCGACTTATGTC-3'-FAM for scramble (sc) mir-383, 5'-CATGAATATTCCACGTTAATCATT-3'-FAM for scmir-384-3p and 5'-AGATTCTCAACCTTTGCTTCTATTT-3'-FAM for scmir-488. Slides were washed with 2× SSC for 15 min at 37°C. High-stringency tetramethyl ammonium chloride (TMAC, Acros Organics, NJ, USA) washes were performed 2 times for 5 min at 54°C and 1 time for 10 min at 54°C then rinsed in PBS-DEPC with 0.1% Triton X-100 (PBT) for 10 min. Slides were incubated in PBT with 20% horse serum for 1 h for blocking. Rabbit polyclonal antibody anti-fluorescein (1:500, Gen Tex, TX, USA) and mouse monoclonal anti-GFP (1:500, Abcam, MA, USA) antibodies in PBT with 20% horse serum were added to sections and incubated for overnight at 4°C. Slides were washed three times in PBT for 10 min. Alexa 488 fluor-conjugated goat anti-mouse and Alexa 594 fluor-conjugated goat anti-rabbit were added to slides and incubated for 30 min.
fluor-conjugated donkey anti-rabbit (1:500, Life Technologies, France) with PBS 3% horse serum and 0.3% Triton X-100 were added sequentially to slides for 1.5 h at room temperature and sections were washed three times with PBS.

Sections were finally Coverslipped with mounting medium for fluorescence microscopy preparation. Sections were observed using a Zeiss LSM 700 confocal microscope (Zeiss, France) associated to ZEN 2012 software and a DDM 1200 Camera (Nikon, France) coupled to ACT-1 software. For quantitative analysis, cells were counted manually using the Image J analysis system (National Institutes of Health, USA). For sections stained for both eGFP and miRNA probes, the double labeled cells were examined at multiple focal levels and at appropriate magnifications to ensure that single cells were indeed immunoreactive for both eGFP and miRNA probes. Because POMC neurons constitute a heterogeneous population in relation to their sensitivity to regulatory factors (Mounien et al., 2006a,b; Williams et al., 2010), the average number of cells counted bilaterally in 8 sections at the anterior and posterior levels of the arcuate nucleus in each animal (n = 4) was used for statistical comparisons.

Statistical Analysis
All data are expressed as mean ± SEM. Statistical analysis was performed by an unpaired 2-tailed Mann-Whitney test. P < 0.05 was considered significant.

Results
Identification and Localization of miRNAs of Interest in the Hypothalamus
We used common prediction programs (http://www.targetscan.org and http://www.microrna.org) to search for potential miRNAs target sites on the 3′ UTR of POMC mRNA. In one hand, we identified three conserved miRNAs (mir-383, mir-384-3p, and mir-488) with targetscan.org. In the other hand, the conserved miRNAs with a good mirSVR scores identified with microrna.org are mir-384-3p, mir-371-3p, and mir-488 (Figure 1A). The distributions of these miRNAs of interest in the mouse CNS were investigated by means of quantitative PCR.

The expression profiles of mir-383, mir-384-3p, and mir-488 miRNAs presented many similarities, but also major differences. Thus, in the CNS, the hypothalamus, brainstem, and cortex were the three regions that contained the highest densities of mir-383 miRNAs (Figure 1B). In other CNS structures such as the cerebellum, hippocampus, and olfactory bulb, much lower concentrations of mir-383 miRNA were recorded (Figure 1B). The highest amounts of mir-384-3p miRNAs were found in the brainstem, cerebellum, and olfactory bulb (Figure 1B). Lower levels of mir-384-3p miRNAs were detected in the hypothalamus, hippocampus, and cortex (Figure 1B). The mir-488 miRNAs were widely expressed throughout the CNS with the same intensity (Figure 1B). It should be noted that mir-471-3p miRNA expression was undetectable whatever the brain region studied (Figure 1B). Considering these expression patterns, we focused our work on mir-383, mir-384-3p as mir-488 which are expressed in the hypothalamus.

The miRNAs of Interest are Expressed in the POMC Neurons of the Arcuate Nucleus
In POMC-Tau-Topaz GFP mice model, double-staining of brain sections with the fluorescein-labeled mir-383 probe and the antibody against GFP showed that a large proportion of neurons in the arcuate nucleus contained simultaneously GFP and mir-383 miRNAs (Figure 2A). Several GFP neurons did not contain mir-383 miRNAs and, reciprocally, several mir-383 miRNAs-expressing neurons did not contain GFP protein (Figure 2A). Similarly, double staining of brain sections with the GFP antibody and mir-384-3p or mir-488 probes showed that a large proportion of GFP neurons expressed mir-384-3p or mir-488 miRNAs (Figures 2B,C). Quantitative analysis of double-labeled neurons showed that, in the whole arcuate nucleus, 80.7 ± 3.4% of the GFP-positive neurons expressed mir-383 miRNAs, 39.8 ± 2.5% of the GFP-positive cells expressed mir-384-3p miRNAs and 64.9 ± 3.2% of the GFP-immunoreactive cells contained mir-488 miRNAs (Figures 2D–F). The proportion of GFP neurons that exhibited mir-383, mir-384-3p, or mir-488 miRNAs were not
different in the anterior and posterior subdivisions of the arcuate nucleus (Figures 2D,F). The control scrambled probes did not produce any labeling (Supplementary Figure 3).

**The miRNA of Interest are Up-regulated in the Hypothalamus of ob/ob and db/db Mice Models**

To evaluate whether leptin signaling in hypothalamus is essential for the expression of mir-383, mir-384-3p, or mir-488 miRNAs, we analyzed the expression of these miRNAs among groups of leptin-deficient (ob/ob) mice and C57BL/6 controls. The levels of mir-383, mir-384-3p, and mir-488 miRNAs in the hypothalamus of 16-week-old ob/ob and C57BL/6 mice were determined by qRT-PCR. Absence of leptin resulted in a significant increase in mir-383, mir-384-3p, and mir-488 miRNAs (+400%, +101%; P < 0.05 and +605%; P < 0.001, respectively) (Figure 3A).
Because the lack of circulating leptin was associated with a significant increase in the miRNAs of interest, we measured the expression of mir-383, mir-384-3p, and mir-488 miRNAs in the hypothalamus of db/db mice, a model that exhibits a non-functional leptin receptor leading to impaired leptin signaling. As shown in Figure 3B, the mir-383, mir-384-3p, and mir-488 miRNAs levels were over-expressed in 16-week-old db/db mice compared to C57BL/6 animals (+25, +32 and +110%, respectively; P < 0.001).

The Expression of Selected miRNAs are Restored in the Hypothalamus of ob/ob Mice after Peripheral Leptin Administration

The above data suggest that leptin may be involved in the regulation of the expression of mir-383, mir-384-3p, and mir-488 miRNAs in the hypothalamus. To directly test this hypothesis, ob/ob mice were i.p. injected with leptin at dose of 5 mg/kg and the hypothalamic expression of mir-383, mir-384-3p, and mir-488 miRNAs was evaluated by qRT-PCR 4 h later. We observed an up-regulation of mir-383, mir-384-3p, and mir-488 miRNAs in 12-week-old ob/ob animals treated with vehicle compared to C57BL/6 control mice (+42, +32%; P < 0.05 and +137%; P < 0.01, respectively) (Figure 4). As expected, leptin treatment significantly reduced hypothalamic expression of mir-383, mir-384-3p, and mir-488 miRNAs in 12-week-old ob/ob animals treated with leptin compared to vehicle-treated ob/ob mice (−25, −21%; P < 0.05 and −58%; P < 0.01, respectively) (Figure 4).

The Expression of mir-488 is Decreased in the Hypothalamus of C57BL/6 Mice after Central Leptin Administration

Because leptin exhibits a large range of effect at peripheral level (Margetic et al., 2002), we next investigated the effect of a daily i.c.v leptin administration (5 µg/mice) during 4 days on hypothalamic expression of mir-383, mir-384-3p, and mir-488 miRNAs. The sub-chronic i.c.v leptin administration significantly reduced food consumption and body weight gain in C57BL/6 mice when compared with the control animals (Figures 5A,B). The i.c.v administration of leptin significantly increased POMC mRNA level in the hypothalamus of leptin-treated group compared with the vehicle-treated animals (+62%; P < 0.05) (Figure 5C). Concurrently, the effects of leptin on miRNAs levels were evaluated. Chronic i.c.v administration of leptin had no effect on mir-383 and mir-384-3p miRNAs levels (Figure 5D). In contrast, leptin significantly decreased mir-488 miRNA contents in the hypothalamus after treatment (−60%; P < 0.01) (Figure 5D).

Discussion

The relevance of miRNAs in the function of melanocortin pathways has been recently highlighted by the deletion of Dicer in POMC-expressing cells which lead to a postnatal ablation of POMC neurons resulting in obesity (Schneeberger et al., 2012; Greenman et al., 2013). In this models, the absence of Dicer in POMC-positive neurons led to hyperphagia (Schneeberger et al., 2012) and a decrease of energy expenditure without any increase in food intake (Greenman et al., 2013). Taken together, the data
suggests that miRNAs are essential for the integrity of POMC neuron activity.

Firstly, we studied the pattern of expression of miRNAs, i.e., mir-383, mir-384-3p, and mir-488, in the CNS. It is already established that these miRNAs are highly expressed in the brain (Chiang et al., 2010). In agreement with this data, we have found by using qRT-PCR that the highest concentrations of mir-383 occurred in the hypothalamus, brainstem, and cortex. The highest amounts of mir-384-3p miRNAs were found in the brainstem, cerebellum, and olfactory bulb while mir-488 miRNAs were widely expressed throughout the structures studied. In many brain regions, mir-383, mir-384-3p, and mir-488 miRNAs distribution patterns did not match each other suggesting that the three miRNAs also exert specific roles. For the first time, we found that the miRNAs encoding the mir-383, mir-384-3p, and mir-488 miRNAs are abundant in the arcuate nucleus. This indicates that a large proportion of the different cell types present in the nucleus are equipped with these miRNAs of interest. The double-staining of POMC-Tau-Topaz GFP mice brain sections with the fluorescein-labeled probes and an antibody against GFP revealed that a high proportion of POMC neurons express mir-383, mir-384-3p, and mir-488, suggesting that these miRNAs target the expression of protein-coding genes that are distributed in this neuronal population. Although mir-383, mir-384-3p, and mir-488 miRNAs were evenly distributed along the rostro-caudal axis of the arcuate nucleus, the proportion of double labeled GFP/mir-383, GFP/mir-384-3p, and GFP/mir-488 neurons did not reflect each other in terms of the proportion of their distribution. These observations are consistent with previous reports demonstrating that POMC neurons constitute an heterogeneous population in relation to their sensitivity to regulatory factors (Mounien et al., 2006a,b; Williams et al., 2010).

In the present context, of special interest is the fact that the POMC neurons are essential for the integration of peripheral signals such as hormones (leptin and insulin) and/or nutrients (glucose) (Morton et al., 2006). For instance, it has been shown recently that leptin directly acts through POMC neurons to stimulate energy expenditure (Berglund et al., 2012). One important goal of current research is to clarify the molecular mechanism involved in the integration of these multiple peripheral metabolic signals such as leptin. One path to reach this goal is to identify the intracellular mediators that allow these POMC neurons to respond to energy status modifications. Interestingly, we observed that the miRNAs targeting POMC miRNAs are up-regulated in ob/ob and db/db mice models. This data provides the first evidence that the expressions of mir-383,
mir-384-3p, and mir-488 are associated with an impaired leptin signaling pathway. However, the miRNAs that target POMC 3′UTR may modulate the melanocortin system at other levels notably by regulating the expression and/or activity of the prohormone convertases PC1 and PC2 which are required for the processing of POMC and the formation of α-melanocyte-stimulating hormone (Smith and Funder, 1988). In accordance with this hypothesis, we observed in the databases that mir-488 can also target PC1 3′UTR. In accordance with this hypothesis, PC1 gene expression is different in the arcuate nucleus of leptin-treated obese ob/ob mice (Nilaweera et al., 2003). It is also conceivable that miRNAs may control the biosynthesis of agouti-related protein; the endogenous antagonist of melanocortin receptors MC3R and MC4R (Ollmann et al., 1997).

Several miRNAs have been reported to be differentially expressed in the hypothalamus of ob/ob and db/db mice, but their precise role in the regulation of the hypothalamus function remains to be determined. Recently, it has been shown that mir-200a, mir-200b, and mir-429 are up-regulated in the hypothalamus of ob/ob and db/db mice (Crépin et al., 2014). The same group showed that daily injection of a pegylated leptin antagonist predisposed rats to obesity, promoted leptin resistance and modified the hypothalamic miRNA expression profile (Benoit et al., 2013). In our study, we identified the presence of new miRNAs that are expressed differently in the hypothalamus of ob/ob and db/db animals compared to control mice. Additional studies will be necessary to understand the regulation of these different miRNAs in the hypothalamus during the progressive onset of the obese phenotype and to determine their complex role in the regulation of feeding behavior.

We observed that the fold change modification of the selected miRNAs in the ob/ob mice increased in an age dependent way. These results suggest that age positively regulates miRNAs expression in ob/ob mice. In accordance with this hypothesis, it has been also shown that mir-184 is differentially expressed in the pancreatic islets of ob/ob mice from age 4–16 weeks (Tattikota et al., 2014). The present study shows that leptin peripheral treatment rescues the expression of mir-383, mir-384-3p, and mir-488 in ob/ob mice. Thus, together with the altered expression of these miRNAs in ob/ob and db/db mice, these results support the idea that leptin plays an important role in the expression of the miRNAs that target POMC mRNA in the hypothalamus. However, leptin exhibits a wide range of effects at peripheral level (Margetic et al., 2002) and its effect on miRNAs expression in the hypothalamus could thus be indirect. In order to test the effect at central level, we then performed chronic i.c.v infusion of leptin. Surprisingly, i.c.v administration of leptin in mice only decreased the expression of mir-488 in the hypothalamus suggesting that the expression of mir-488 is under the control of leptin. The absence of effect by central infusion of leptin on the hypothalamic expression of mir-383 and mir-384-3p can be explained by the peripheral effect of leptin. For instance, it has been shown that leptin increases insulin secretion which in turn modulates the POMC neurons activity and may modulate miRNA expression (Ceddia et al., 1999; Hill et al., 2010).

Interestingly, bioinformatics prediction analysis indicates that the miRNAs targeting POMC can also target genes involved in the leptin signaling pathways such as STAT3 as well as the leptin receptor. For instance, mir-488 could modulate the expression of STAT3. These observations suggest that, mir-383, mir-384-3p, and mir-488 in the arcuate nucleus are involved in a complex network controlling the sensitivity of POMC neurons to peripheral signals. Additional in vitro experiments could clarify this last point. Recently, numerous studies identified several miRNAs as important for the hypothalamic regulation of energy homeostasis. Herz et al. identified mir-7a as a hypothalamic-enriched miRNA with a high expression in Neuropeptide Y/Agouti-related orexigenic peptide neurons (Herz et al., 2012). Interestingly, two extreme conditions of nutritional stress, i.e., caloric restriction and high fat diet-induced obesity, modified the hypothalamic pattern of expression of a set of miRNAs including let7a, mir-9*, mir-30e, mir-132, mir-145, mir-200a, and mir-218 (Sangiao-Alvarellos et al., 2014). Taken altogether, these different studies point to the importance of miRNAs as regulators and sensors of central energy homeostasis.

In conclusion, we observed that the impairment of leptin synthesis or signaling, induced a defect in the hypothalamic expression of a subset of miRNAs that target POMC 3′UTR. It was observed that mir-383, mir-384-3p, and mir-488 were up-regulated in ob/ob and db/db mice and mir-488 was down-regulated in leptin-treated mice. This indicates that the miRNAs that target POMC important mediators of leptin action in the hypothalamus. New miRNAs modulated by leptin could open important therapeutic perspectives for controlling metabolic disorders.

**Author Contributions**

LM planned the project. AD, MD, CA, CP, MD, VT, and CT performed experiments. LM wrote the manuscript. JT, BB, and JT helped with data evaluation, interpretation, and manuscript preparation.

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**Supplementary Material**

The Supplementary Material for this article can be found online at: http://journal.frontiersin.org/article/10.3389/fncel.2015.00172/abstract
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Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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