

# Differential regulation of peroxisome proliferator-activated receptor (PPAR)-alpha1 and truncated PPARalpha2 as an adaptive response to fasting in the control of hepatic peroxisomal fatty acid beta-oxidation in the hibernating mammal.

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Differential regulation of peroxisome proliferator-activated receptor (PPAR)- $\alpha$ 1 and truncated PPAR $\alpha$ 2 as an adaptive response to fasting in the control of hepatic peroxisomal fatty acid  $\beta$ -oxidation in the hibernating mammal

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**Key words** Acyl-CoA oxidase 1, fasting, hibernation, jerboa, peroxisomal β-oxidation, PGC-1 $\alpha$ , PPAR $\alpha$ ,

**Abbreviations** ACOX1, Acyl-CoA oxidase 1, CPT1, carnitine palmitoyltransferase 1, MCAD, medium chain acyl-CoA dehydrogenase, PBE, peroxisomal bifunctional enzyme, PGC-1 $\alpha$ , peroxisome proliferator-activated receptor gamma co-actovator-1  $\alpha$  PMP70, peroxisomal membrane protein 70kDa, PPAR $\alpha$ , peroxisome proliferator-activated receptor  $\alpha$ , PPAR $\alpha$ 1 wild type, PPAR $\alpha$ 2 truncated.

### **Abstract:**

Seasonal obesity and fasting-associated hibernation are the 2 major metabolic events governing hepatic lipid metabolism in hibernating mammals. In this process, however, the role of the nuclear receptor known as peroxisome proliferator-activated receptor  $\alpha$  (PPAR $\alpha$ ) has not been elucidated yet. Here we show, as in human, that jerboa (*Jaculus orientalis*) liver expresses both active wild type PPAR $\alpha$  (PPAR $\alpha$ 1wt) and truncated PPAR $\alpha$  (PPAR $\alpha$ 2tr) forms, and that the PPAR $\alpha$ 1wt/PPAR $\alpha$ 2tr ratio, which indicates the availability of active PPAR $\alpha$ 1wt, is differentially regulated during fasting-associated hibernation. Functional activation of hepatic jerboa PPAR $\alpha$ , during prehibernating and hibernating states, was demonstrated by the induction of its target genes—which encode peroxisomal proteins such as ACOX1, PMP70, and catalase—accompanied by a concomitant induction of PPAR $\alpha$  thermogenic coactivator PGC-1 $\alpha$ .

Interestingly, sustained activation of PPAR $\alpha$  by its hypolipidemic ligand, ciprofibrate, abrogates the adaptive fasting response of PPAR $\alpha$  during prehibernation and overinduces its target genes, disrupting the prehibernation fattening process. In striking contrast, during fasting-associated hibernation, jerboas exhibit preferential upregulation of hepatic peroxisomal fatty acid oxidation instead of the mitochondrial pathway, which is downregulated. Taken together, our results strongly suggest that PPAR $\alpha$  is subject to a hibernation-dependent splicing regulation in response to feeding-fasting conditions, which defines the activity of PPAR $\alpha$  and the activation of its target genes during hibernation bouts of jerboas.

### **Introduction:**

Numerous data have shown that efficient hepatic fatty acid oxidation depends largely on the transcriptional control of peroxisome proliferator-activated receptor (PPAR)- $\alpha$  (1-5). In fasting PPAR $\alpha$ -null mice, impairment of hepatic mitochondrial or peroxisomal fatty acid oxidation is associated with a dramatic phenotype, characterized by hypoglycemia, hypoketonemia, hypothermia, and hepatic steatosis, (6-8) resembling the fatal clinical phenotype of human inborn errors in mitochondrial fatty acid oxidation (9). The critical fasting regulatory functions of PPAR $\alpha$  are dependent on the availability of coactivator proteins such as the PPAR $\gamma$  coactivator-1 (PGC-1) family (10). Indeed, PGC-1 $\alpha$ , a coldinducible transcriptional coactivator, plays a key role in the regulation of adaptive thermogenesis, mitochondrial biogenesis, and fatty acid metabolism (10, 11).

Jerboa is a rat-sized rodent, family dipodidea, from the subdesert highlands (1500 m) of North Africa; it is mainly a nocturnal and saltatorial herbivore, which can undergo hibernation when is faced in its biotope with critical food shortage and sub-freezing air temperature. Hibernation process is characterized by confinment of jerboa at 9-10°C in the underground plugged burrows at a depth of 30-45 cm (12). Hibernation of jerboa can be induced in the laboratory when its cooled artificially (13). After hibernation induced by food deprivation, animals are characterized by the crouched position and alternate breathing pattern of deep respiration and apnea (13).

As a model of a deep hibernator, jerboas (*Jaculus orientalis*) oscillate from seasonal obesity (due to programmed excess food uptake) to prolonged hibernation-associated fasting to food scarcity of temperate-zone winters (12, 13). Recent large transcript-profiling of the liver of hibernating golden-mantled ground squirrels, *Spermophilus lateralis*, has revealed that metabolic fasting adaptation in this hibernating species is accompanied by increased expression of peroxisomal  $\beta$ -oxidation-encoding genes (14). Fasting-triggered influx of free fatty acids from adipose tissue stimulates a switch to liver fatty acid oxidation and ketone bodies for energy production (15, 16). Despite the large influx of fatty acids in hibernating animals in response to this caloric restriction, no signs of fatty liver or hepatic injury have been observed (17).

Elsewhere, PPAR $\alpha$  is mainly expressed in tissues with high levels of lipid catabolism, such as heart and liver (2). Nevertheless, in addition to the active wild type PPAR $\alpha$ 1 form (PPAR $\alpha$ 1wt) in human and in swine, the liver expresses a truncated PPAR $\alpha$ 2 isoform (PPAR $\alpha$ 2tr). PPAR $\alpha$ 2tr lacks the ligand-binding domain, which results from a

posttranscriptional exon-skipping mechanism (18, 19), and harbors dominant-negative transcriptional repressive activity on PPARα1wt (18).

In liver, PPAR $\alpha$  governs, at the transcriptional level, the expression of genes involved in fatty acid oxidation, which encode mitochondrial, peroxisomal, and some cytochrome P450 enzymes (1-3, 5, 20). In mice, fasting-associated hepatic induction of both mitochondrial and peroxisomal fatty acids oxidation is dependent on PPAR $\alpha$  activation. Such as the peroxisomal membrane protein 70 (PMP70) and the acyl-CoA oxidase 1 (ACOX1), involved respectively in peroxisomal transport and  $\beta$ -oxidation of fatty acids (1, 3, 4, 6-8). However, the mechanisms underlying the induction of hepatic fatty acid oxidation and the involvement of PPAR $\alpha$  during seasonal obesity and fasting-associated hibernation in mammals has not been explored.

In this study, we investigated the expression of PPAR $\alpha$  and its target genes during stepwise deep hibernation of jerboas. We also examined the influence of the sustained activation of PPAR $\alpha$  by its hypolipidemic ligand, ciprofibrate, on fatty acid oxidation during the prehibernation fattening period. Our results show the presence of 2 hepatic PPAR $\alpha$  forms, wild type PPAR $\alpha$ 1 and truncated PPAR $\alpha$ 2, and their season-dependent differential regulation. Prehibernation and hibernation periods are primarily dependent on the upregulation of peroxisomal fatty acid oxidation, which is accompanied by the induction of PGC-1 $\alpha$ . Forced activation of PPAR $\alpha$  with ciprofibrate abrogates the differential regulation of PPAR $\alpha$  forms and overinduces its target genes, disrupting the prehibernation fattening process.

# **Materials and Methods**

### Animals and treatments

Young adult jerboa (*Jaculus orientalis*) between 4 and 6 months old (110–140 g body weight) were captured in the area of Engil Aït Lahcen (Boulemane region in sub-desert of eastern Morocco highland, approximate altitude 1565 meters). Animal studies were conducted in accordance with the ethic committee on Animal Use and Care of the university of Bourgogne. They were pre-acclimatized in the laboratory for 3 weeks at  $22 \pm 2$  °C with food (salad and rat chow), and water *ad libitum* (Table 1). In comparison with euthermic active animals (A), pre-hibernating and hibernating animals, were kept with food in a cold room (6 °C) for 3 weeks. This group was called the pre-hibernator group (Ph). A second group was kept under the same

conditions as Ph, except that the food contained ciprofibrate at an amount of 3 mg/kg body weight/day, and was called the ciprofibrate-treated prehibernator group (PhC). The third group was housed as Ph, and at the end of 3 weeks of the pre-hibernation period, the food was removed leading after 24–36 h to hibernation (group H) (Table 1). These animals were scarified on the fourth day of hibernation. In summary, the physiological characteristics of the hibernation were as follow: after 3 weeks of cold acclimatization  $\pm$  6 °C (12, 13), the rectal temperature of jerboa was not significantly different from control (36  $\pm$  1.5 °C). After hibernation induced by food deprivation, animals were characterized by the crouched position and alternate breathing pattern of deep respiration and apnea (12, 13). The rectal temperature dropped to 9.8  $\pm$  0.7 °C and the mean heart frequency stabilized to 9.3  $\pm$  1.5 beats/min, compared to active animals with 37 °C rectal body temperature and 300 beats/min (12, 13).

# Preparation of tissue homogenates

For activity and immunoblotting of ACOX1, PBE and catalase: 50 to 200 mg of frozen liver tissue were homogenized in 250 mM sucrose, 2 mM EDTA, 20mM Tris-HCl buffer pH 7.5 at a ratio of 3ml/100mg of tissue. The resulting homogenate was centrifuged ( $600 \times g$ , 5 min at  $+4^{\circ}C$ ) and the supernatant (post-nuclear fraction) considered as the crude extract.

For PPAR immunoblotting: Samples were homogenized in 25 mM (1xPBS, 1% Nonidet P-40 or Igepal CA-630, 0.5% sodium deoxycholate, 0.1 % SDS) and a cocktail of protease inhibitors (Complete; Roche, Mannheim, Germany). The homogenates were centrifuged at 15,000g for 30 min at 4°C and the supernatant used for immunoblotting experiments. Protein content was estimated with the Bio-Rad assay using bovine serum albumin (BSA) as standard.

### Enzymatic activities measurements:

Palmitoyl-CoA oxidase activity was measured with the fluorimetric method described by Vamecq (1990). Briefly, the reaction mixture contained: 50 mM Tris buffer, PH 8.3, 0.75mM homovanillic acid, 4400U Peroxydase (25 U), 0.025% Triton X-100 (1.5 mg/ml BSA, 12,5 mM Aminotriazole and  $50\mu$ M Palmitoyl-CoA. *Catalase activity* was measured according to Hildebrand et al., (21). Activity was monitored at 240nm for 2 min at the room temperature. Enzymatic activity was initiated by adding crude extract into the reaction mixture containing  $500\mu$ l of 0.1M potassium phosphate buffer pH 7.4,  $200\mu$ l of 75mM hydrogen peroxide in

final volume of 1 ml. The catalase specific activity was calculated using  $\epsilon$  of 43.6 M<sup>-1</sup>.cm<sup>-1</sup> for hydrogen peroxide at 240nm.

Medium chain Acyl-CoA Dehydrogenase (MCAD) was measured according to Flatmark et al., (22). The reaction medium contains: 20mM Phosphate buffer pH 7.6, dichlorophenolindolphenol (DCIP) 0.005% (w/v), 100 μM de FAD, 25 to 50 μg of crude extract. The reaction is started by  $50\mu$ M palmitoyl-CoA. Carnitine Palmitoyl Transfesrase 1 (CPT1) was measured according to Bieber et al., (1972). The CPT1 activity was monitored at 412nm at 25°C. The reaction medium contains: 116 mM Tris-HCl pH8.0; 1,1 mMtNaEDTA; 35 μM Palimtoyl CoA; 0,12 mM 5,5'-dithiobis(2-nitrobenzoic acid and 1,1 mM L(-) Carnitine. The CPT1 specific activity was calculated using ε of 13600 M<sup>-1</sup>.cm<sup>-1</sup>.

### *Immunoblotting*

Crude extract proteins prepared as indicated above were separated by SDS-PAGE. Electrotransfer and immunostaining were performed as described by Towbin et al. (1979). Detection was performed using alkaline phosphatase conjugated anti rabbit IgG from goat as recommended by the supplier (Santa Cruz Biotechnology). Antibodies used were polyclonal antibody raised against respectively: rat ACOX, rat catalase, rat PBE or rat PMP70, and monoclonal antibody raised against N-terminal peptide (amino acids 4–96) of human PPARα (R&D Systems).

# RNA analysis

Total RNAs were obtained from tissues, previously frozen in liquid nitrogen and stored at –80 °C, using Trizol Reagent according to the supplier protocol (Invitrogen). Two μg of total RNA were reverse-transcribed into cDNA with 200 units of Moloney Murine Leukemia Virus Transcriptase (Promega) and 1 μg of oligodT in a reaction mixture containing 50 mM Tris-HCl buffer pH 8.3, 75 mM KCl, 3 mM MgCl<sub>2</sub>, 10 mM dithiothreitol and 20 pmol each of sense and anti-sense primers. Reverse-transcription reaction was incubated at 48 °C for 45 min and 94 °C for 2 min for 22 to 30 cycles. Primers used in PCR reactions were designed, from two different exonic regions with the highest nucleotides identity, after alignment of mRNA sequences of genes of interst from human, mouse and rat species. Sequences of primers and nucleotides position used to amplify ACOX1, PGC-1α, PMP70, PPARα or β-actin fragments were respectively: for ACOX1 (human, NM\_007292) sense 5'295ACCCGGACCTGCGC<sub>308</sub>3' and anti-sense 5'2272CAGAGCTTGGACTGCAGTG<sub>2254</sub>3';

for PGC-1 $\alpha$  (mouse, NM\_008904) sense 5' $_{110}$ AGCCAAGACTCTGTATGGA $_{128}$ 3' and antisense 5' $_{377}$ TGTCCAGTGTCTCTGTGA $_{360}$ 3'; for PMP70 (human, NM\_002858) sense 5' $_{92}$ TCTGCCTGCTCCACAAGC $_{109}$ 3 ' and antisense 6' $_{711}$ GCCCTGAGCTCCAATTGCAC $_{692}$ 3'; for PPAR $\alpha$  (human, NM\_001001928) sense 5' $_{704}$ ACGAATGCCAAGATCTGAGAAAGC $_{727}$ 3' (Exon 6) and antisense 5' $_{1050}$ ATTCCGTGAGCTCCGTGACG $_{1031}$ 3' (Exon 7) and for  $\beta$ -actin (mouse, NM\_007393) sense 5' $_{535}$ TCAGGTCATCACTATCGGCAA $_{555}$ 3' and antisense 5' $_{815}$ CAGGTCATCACTATTGGCAA $_{834}$ 3'.

# Densitometry and statistical analysis

Quantifications and standardization were obtained using the housekeeping genes as control. GAPDH and  $\beta$ -actin proteins were used for Western blotting and  $\beta$ -actin gene for RT-PCR. Densitometry scanning was realized using the AlphaImager<sup>TM</sup> 1220 (Alphainnotech, VWR International, Fontenay-Sous-Bois, France). Data were expressed as arbitrary units, as mean  $\pm$  standard deviations, meaning the fold activation relative to control active animals. Statistical analysis were performed using t-test and one-factor ANOVA P values were calculated by Student's t test using Statistica software. The level of significance accepted was  $P \le 0.05$ .

# **Results:**

# Expression of PPARα and PGC-1α during the hibernation process

Due to its important role in liver lipid metabolism, we explored the regulation of PPAR $\alpha$ , its coactivator PGC1 $\alpha$ , and their target genes during hibernation bouts. Prehibernation conditions to which jerboa are exposed in the wild were mimicked by housing jerboas for 3 weeks in a cold room at 6°C with access to food *ad libitum*. Two bands were detected by RT-PCR but only the upper one varied during the hibernation-time course; the presence of several PPAR $\alpha$  mRNA variants derived from alternative splicing has already been reported for different species, (18, 19, 23) and 2 spliced mRNA forms in liver have been identified in human, rabbit, rat, and mouse (23). Figure 1 shows that both PPAR $\alpha$ 1wt and PPAR $\alpha$ 2tr transcripts are expressed (lane 1 arrows), similar to the euthermic jerboa liver. Cold exposure of jerboas during the prehibernating period provoked a small but insignificant decrease (0.7-fold) of PPAR $\alpha$ 1wt mRNA, and almost no change of PPAR $\alpha$ 2tr mRNA.

In the same period, mRNA expression of the thermogenic PPAR $\alpha$  coactivator, PGC1 $\alpha$ , was induced 2.9-fold (Figure 1, lanes 1 and 2). This induction was accompanied by an increase in ACOX1 mRNA (2.7-fold) and, to a lesser extent, PMP70 mRNA (1.4-fold); both ACOX1 and PMP70, involved in the peroxisomal fatty acids oxydation pathway, are PPAR $\alpha$  target genes.

Food deprivation of prehibernating jerboas induced hibernation of animals 24 hours later, 4 days after which jerboas were sacrificed. During hibernation, fasting provoked a marked increase in PPAR $\alpha$ 1 mRNA levels by 3.4-fold and a strong decrease (0.3-fold) of PPAR $\alpha$ 2tr mRNA levels. In addition to PGC1 $\alpha$  mRNA levels, which were also strongly induced (4.5-fold), ACOX1 and PMP70 mRNA levels increased by 3.3- and 3.5-fold, respectively, during hibernation (Figure 1, compare lanes and 1 and 3). Thus, transcriptional induction of both ACOX1 and PMP70 mRNA seems to be independent from PPAR $\alpha$ 1 mRNA induction during prehibernation period. While PGC1 $\alpha$ , a key activator of fatty acid oxidation, shows a mRNA increase at the same level as ACOX1 and PMP70 mRNA during prehibernation state.

Hepatic synthesis of jerboa PPARα2 truncated protein is regulated during hibernation

It has been demonstrated in several species, including human, that in addition to the active form of PPAR $\alpha$ 1wt (52-55 kDa), there is an additional inactive truncated form (29-31 kDa) derived from PPAR $\alpha$ 2tr mRNA translation (18, 23), which we designate PPAR $\alpha$ 2tr. Using a monoclonal antibody against an N-terminal polypeptide of human PPAR $\alpha$ , we observed that both PPAR $\alpha$ 1wt and PPAR $\alpha$ 2tr proteins are expressed in jerboa liver (Figure 2A). Truncated PPAR $\alpha$ 2 was expressed at lower levels in jerboa kidneys and absent in jerboa heart. Brain and muscle tissues expressed other PPAR $\alpha$  forms (around 45 kDa) (Figure 2A), which are probably other splice variants that have been described in other species (23).

In figure 2B, densitometric analysis of at least 3 samples from different animals allowed the calculation of both PPARα1wt/GAPDH and PPARα1wt/ GAPDH ratios for each hibernation state. Values were standardized to the ratios of active jerboas (Figure 2B). During prehibernation, the level of the 52 kDa hepatic PPARα1wt protein increased 1.87-fold (Figure 2B), compared with active jerboas. This was concomitant with a modest increase in the PPARα1wt/PPARα2tr ratio, as indicated by a 1.36-fold activation in prehibernating jerboa liver (Figure 2). During hibernation, the level of active PPARα1wt protein did not vary significantly (1.15-fold increase) (Figure 2B). Western blotting, however, revealed a nearly complete absence of truncated PPARα2 (0.06-fold), resulting in a 3.74-fold activation of the

PPAR $\alpha$ 1wt/ PPAR $\alpha$ 2tr ratio, compared with active jerboa (Figure 2B). This change indicates that the transition from the prehibernation period to the hibernation state involves a nearly 3.74-fold increase in the availability of hepatic PPAR $\alpha$ 1wt protein.

Effect of PPAR $\alpha$  ligand ciprofibrate, a hypolipidemic agent, on the expression of PPAR $\alpha$ , its coactivator PGC1 $\alpha$ , and its target genes ACOX1 and PMP70

In the liver of prehibernating jerboas, ciprofibrate treatment increased PPAR $\alpha$ 1wt mRNA levels by 2.8-fold, accompanied by a similar increase (3.1-fold) in PPAR $\alpha$ 2tr mRNA (Figure 1, lane 4). This PPAR $\alpha$  ligand induced PGC-1 $\alpha$  mRNA 1.8-fold, compared with euthermic jerboas. Ciprofibrate treatment also increased ACOX1 and PMP70 mRNA expression 20.6-and 4.8-fold, respectively (Figure 1, lane 4). At the protein level, immunoblotting revealed a slight increase of PPAR $\alpha$ 1wt and PPAR $\alpha$ 2tr (Figure 2B). The calculated PPAR $\alpha$ 1wt/PPAR $\alpha$ 2tr ratio, however, was decreased by ciprofibrate to 0.69-fold, compared with a 1.36-fold activation observed in prehibernating control animals, suggesting that the livers of prehibernating ciprofibrate-treated jerboas possess an increased amount of truncated PPAR $\alpha$ 2 and 69% less available PPAR $\alpha$ 1wt protein.

Peroxisomal β-oxidation system enzymes, PPARα target genes in hibernating jerboa

Peroxisomal acyl-CoA  $\beta$ -oxidation begins with ACOX1, the starting enzyme, and PBE as the second enzyme of this pathway. ACOX1 releases enoyl-CoA and also  $H_2O_2$  as a byproduct, which is a highly oxidant molecule that is degraded rapidly by catalase, a peroxisomal antioxidant protein. PMP70 is involved in the metabolic transport of fatty acids into peroxisomes (24). The expression of these 4 peroxisomal enzymes has been shown previously to be dependant on PPAR $\alpha$  (1, 5). In addition, the 72 kDa ACOX1 protein (polypetide A) undergoes a unique posttranslational proteolytic cleavage responsible for the appearance of 2 additional bands of 50 and 20.8 kDa, respectively, called polypeptides B and C.

Cold exposure during the prehibernation period slightly increased the level of peroxisomal proteins involved in β-oxidation—ACOX1, PBE, and PMP70—above 1.4-fold, whereas only catalase protein was induced 1.9-fold (Figure 3, lane Ph). This increase in peroxisomal proteins was accompanied by both a 40% increase (1.4-fold) in peroxisomal palmitoyl-CoA oxidation and a 100% increase in catalase activity (2.1-fold) (Figure 4A, lane Ph).

The hibernation period was characterized by a strong induction of peroxisomal proteins: ACOX1, 3-fold; PBE, 4.2-fold; and catalase, 3.5-fold. Only PMP70 showed a modest

variation of 1.2-fold (Figure 3, lane H). In addition, peroxisomal palmitoyl-CoA oxidation increased by 180% (2.8-fold), and catalase activity increased by 50% (1.5-fold) (figure 4A). This underline that the peroxysomal fatty acid oxidation pathway is differentially regulated during respectively prehibernation and hibernation periods.

# Hibernation-dependent depression of mitochondrial fatty acid $\beta$ -oxidation

The level of mitochondrial fatty acid oxidation is controlled by carnitine palmitoyl-CoA transferase (CPT1) activity, which is the rate-limiting enzyme responsible for the entry of long-chain fatty acids into the mitochondria (25). During prehibernation, liver CPT1 activity was significantly decreased by 26% (0.74-fold) (Figure 4B, lane Ph), accompanied by a 43% decrease (0.57-fold) of the activity of mitochondrial medium chain acyl-CoA dehydrogenase (MCAD) (Figure 4B, lane Ph). Starvation-induced hibernation was also associated with a 30% depression of CPT1 activity (0.70-fold) (Figure 4B, lane H), compared with that of active euthermic jerboas. But with regard to the prehibernation period, mitochondrial MCAD activity increased greater than 30% (0.57-fold during prehibernation and 0.86-fold during hibernation) (Figure 4B, lane Ph and H). By contrast to peroxisomes mitochondria which exhibits a higher capacity of fatty acid oxidation, seems to be negatively regulated during the hibernation bouts.

Effect of ciprofibrate on mitochondrial and peroxisomal  $\beta$ -oxidation, and peroxisome proliferation

In rodents, induction of peroxisomal  $\beta$ -oxidation by ciprofibrate has been shown to be a PPAR $\alpha$ -dependent phenomenon, which is accompanied by peroxisome proliferation (i.e., an increase in the number and size of peroxisomes) (1, 5, 26). ACOX1, PBE, or PMP70 are typical PPAR $\alpha$ -inducible biomarkers of both peroxisomal  $\beta$ -oxidation and peroxisome proliferation (5). In the preceding section (Figure 1, lane PhC), we demonstrated a strong increase of hepatic ACOX1 mRNA in prehibernating ciprofibrate-treated jerboas. As shown in figure 4, lane PhC, immunoblotting revealed a remarkable induction of peroxisomal  $\beta$ -oxidation enzymes: ACOX1, 6.2-fold; PBE, 5.6-fold; and catalase, 5.6-fold. PMP70 was not strongly induced (1.2-fold). Such inductions were accompanied by a strong increase in palmitoyl-CoA oxidase activity of ACOX1 by 8.2-fold and catalase activity by 2.9-fold (Figure 4A).

In contrast to peroxisomal fatty acid β-oxidation, mitochondrial CPT1 activity was slightly decreased (0.82-fold), compared with the activity in euthermic jerboas; comparison with prehibernating untreated jerboas, however, revealed no significant effect of ciprofibrate (Figure 4B, lane PhC). MCAD activity decreased by 25% (0.75-fold), and compared with prehibernating control jerboas (0.57-fold), MCAD activity increased by 18% (0.75-fold) in the liver of prehibernating jerboas treated with ciprofibrate (Figure 4B, lane PhC). Thus, the overinduction of peroxisomal fatty acids oxidation during the prehibernation period by hypolidemic drug, such as ciprofibrate, prevents fat accumulation in the prehibernating jerboas required for the energy supply during hibernation period.

### **Discussion:**

Seasonal obesity is an evolutionary strategy adopted by hibernators to anticipate food scarcity in inhospitable environments and to control energy consumption in a strict manner. Here, we report a stepwise deep hibernation of jerboas under laboratory conditions mimicking those in the wild (12). Before entering hibernation, jerboas need 3 weeks of cold acclimatization (prehibernation period) with food provided *ad libitum*. Starvation-induced hibernation in jerboas is characterized by a dramatically lowered heartbeat rate, as well as hypothermia to 9°C. During prehibernation, these parameters, particularly body temperature, remain similar to those of active animals, despite the lower ambient temperature (6°C).

During autumn, corresponding to the prehibernation period, jerboas have to manage 2 apparent contradictory demands: (1) fat storage in the adipose tissue as energetic fuel for the hibernation period, and (2) immediate energy supply in a cold prehibernation environment, necessary for thermogenic acclimatization and maintenance of a body temperature of 37°C.

Our previous studies have shown that prehibernation of jerboas is associated with hypotriglyceridemia and hypoketonemia, which result from a high rate of fatty acid and triacylglycerol uptake concomitant with depressed mitochondrial and peroxisomal fatty acid oxidation in adipose tissues (27, 28). We have also reported the participation of jerboa PPAR isotypes  $\beta/\delta$  and  $\gamma$  in brown fat non-shivering thermogenesis and in white fat adipogenesis during hibernation bouts, respectively (28). As in other hibernators, carbohydrates are the main source of energy in prehibernating jerboas, which exhibit the same normal circulating glucose levels as euthermic animals (28). Carbohydrate use helps animals preserve optimal energetic fat storage for their hibernation period (15, 29).

Here, we show that the expression of PPARα in prehibernating jerboa liver is regulated at different levels. Two alternatively-spliced transcripts of PPARα and 2 forms, PPARα1wt (52 kDa) and PPARα2tr (29 kDa), are primarily expressed in the jerboa liver and, to a lesser extent, in kidney. Such a tissue-specific expression profile in jerboas is similar to the human expression pattern of PPARα isoforms (18). The truncated PPARα2 protein lacks the ligand-binding domain (18). PPARα1 mRNA expression is not changed significantly during prehibernation, while at the protein level, the PPARα1wt/PPARα2tr ratio is slightly increased. This seems to be sufficient for the induction of PPARα target genes implicated in peroxisomal fatty acid oxidation (i.e. ACOX1 and PBE) and the recruitment of the coactivator PGC1α, which is clearly upregulated during prehibernation in the jerboa liver.

Concomitant induction of ACOX1, PBE, and PGC1 $\alpha$  is consistent with the known key role of PGC1 $\alpha$  in cold-induced fatty acid oxidation and PPAR $\alpha$  coactivation (30). Transcriptional activation of the ACOX1 and PBE genes throughout PGC1 $\alpha$  coactivation by other nuclear receptors (e.g. hepatic nuclear factor-4 or FOXO1) is not excluded; hepatic nuclear factor-4 has a shared ability with PPAR $\alpha$  to bind PPAR $\alpha$  response elements of the ACOX1 and PBE genes (31, 32), and FOXO1 expression has been shown to be upregulated in the hibernating ground squirrel (*Spemophilus tridecemlineatus*) (33).

The substantial increase in PPAR $\alpha$  target genes (i.e. ACOX1, PBE, PMP70, and catalase) during the prehibernation fattening period is surprising. But, we have to consider that ACOX1, an oxidoreductase, also catalyzes the ultimate anabolic step of docosahexanoic acid synthesis, an important polyunsaturated fatty acid for normal brain function (34, 35). Thus, PPAR $\alpha$ -dependent induction of the peroxisomal  $\beta$ -oxidation pathway may anticipate the selective retention of essential polyunsaturated fatty acids during the hibernation process (36). Furthermore, that the limited hepatic peroxisomal degradation of fatty acids is induced during the fattening prehibernation period may prevent the jerboa from developing a hepatic steatosis (37). Indeed, ACOX1-/- knockout mice develop hepatic steatosis accompanied by sustained activation of hepatic PPAR $\alpha$  and its target genes (7), which underscores the metabolic crosstalk between the nuclear receptor PPAR $\alpha$  and its target gene, ACOX1 (5). In prehibernating conditions, jerboa ACOX1 plays an additional role as a PPAR $\alpha$  sensor, most likely by metabolizing the PPAR $\alpha$  acyl-CoA-ligand.

Long chain fatty acids are proposed to regulate CPT1, a rate-limiting enzyme of mitochondrial fatty acid oxidation, in a PPARα-independent manner (38). Thus, decreased CPT1 activity in jerboa liver during prehibernation is probably due to the lipogenesis-associated increase in liver malonyl-CoA concentrations, which in turn block fatty acid transport across the mitochondrial membrane. This is a consequence of the malonyl-CoA allosteric inhibition of CPT1 (25). Consequently, mitochondrial MCAD fatty acid oxidation, as we reveal in this study, is also decreased in the liver of prehibernating jerboas. Thus, the decrease in mitochondrial fatty acid oxidation is required during this fattening period of prehibernation.

Here, we report that the hibernation-associated fasting period in jerboa liver is characterized by a differential induction of PPAR $\alpha$ 1wt transcripts with a near absence of PPAR $\alpha$ 2tr mRNA. Numerous data from several groups using PPAR $\alpha$ -null mice have demonstrated the crucial role of PPAR $\alpha$  in the adaptive response to fasting and the regulation of liver fatty acid

oxidation rates (4, 8, 39, 40). But the physiological significance of the expression of PPAR $\alpha$  isoforms in liver, particularly PPAR $\alpha$ 2tr, has not been elucidated yet.

In the present study, we show for the first time the physiological link between hibernation-associated fasting in the jerboa liver and the upregulation of the ratio of active PPAR $\alpha$ 1wt to truncated PPAR $\alpha$ 2 isoforms as a response to this metabolic challenge. Posttranscriptional regulation by alternative splicing is a general mechanism that has been described for other nuclear receptors, such as the glucocorticoid receptor (41). A strong diminution of the expression of the dominant-negative PPAR $\alpha$ 2tr in the hibernating jerboa liver has an immediate consequence on the availability of active PPAR $\alpha$ 1wt. Through endogenous activation of PPAR $\alpha$ 1wt, this triggers the upregulation of peroxisomal  $\beta$ -oxidation enzymencoding genes—such as ACOX1 and L-PBE, which are PPAR $\alpha$  target genes (42, 43). Such induction of PPAR $\alpha$ -dependent fatty acid oxidation is accompanied by the induction of the thermogenic PPAR $\alpha$  coactivator, PGC-1 $\alpha$ . In addition, recent studies have reported the increase in PGC-1 $\alpha$  levels in the liver of hibernating bats (*Myotis lucifugus*) (44) and in heart and muscle tissue of hibernating ground squirrels (*Spermophilus tridecemlineatus*) (45).

The relative preference of the induction of peroxisomal fatty acid  $\beta$ -oxidation instead of the mitochondrial pathway can be interpreted in several ways. During hibernation, jerboa body temperature is above 10°C, which is associated with a slow metabolic rate concomitant with the inhibition of carbohydrate oxidation and the induction of a specific pancreatic lipase that releases fatty acids from triglycerides at temperatures as low as 0°C (29, 46). In this context, the 180% increase of peroxisomal  $\beta$ -oxidation has to be considered, in the absence of coupling to oxidative phosphorylation, as a thermogenic source for jerboa liver. On the other hand, induction of peroxisomal fatty acid oxidation, through PPAR $\alpha$ 1wt activation, may underlie the anabolic side of peroxisomes in the synthesis of polyunsaturated fatty acids, which has been well documented (47, 48).

Furthermore, specific lipids, as essential fatty acids and their degree of insaturation, play a determinant role in the frequency of interbouts, in which animals arouse from hibernation during winter (49). Deficiency of such essential fatty acids implicates an increase in the frequency of arousing and rewarming. Consequently, this increase in energy expenditure impairs the ability of hibernators to survive through long winter seasons. Surprisingly, the increase in PPAR $\alpha$ 1 mRNA is not accompanied by an expected augmentation in PPAR $\alpha$ 1 wt protein. This may be explained by the regulated shutdown of cellular protein synthesis throughout the phosphorylation of elongation factor-2 during hibernation (50). Due to its key

role in fatty acid oxidation, such high levels of PPARα1wt mRNA may promote synthesis of the active PPARα1wt form during arousal. Indeed, throughout the winter period, jerboas arouse periodically (51), and 90% of the estimated energetic expenditure throughout winter is used during arousal (52).

In previous studies, we have shown ciprofibrate-dependent peroxisome proliferation and induction of peroxisomal fatty acid oxidation in euthermic active jerboa liver (13, 26). In addition, another fibrate molecule, clofibrate, has been shown to induce PPAR $\alpha$  in euthermic jerboa tissue (53).

Because of its properties as a hypolipidemic drug and a well-known PPAR $\alpha$  ligand, ciprofibrate was administrated to a group of prehibernating jerboas. We observed the absence of fat accumulation in treated jerboas, compared with prehibernating untreated animals (28). In jerboa liver, the induction of both PPAR $\alpha$  mRNA splice variants,  $\alpha 1$  and  $\alpha 2$ , was accompanied by a strong increase of PPAR $\alpha$  target genes—ACOX1, L-PBE, PMP70, and catalase—leading to high fatty acid degradation and less fat storage in adipose tissue.

At the protein level, increases in the hepatic PPAR $\alpha$ 2tr form may have consequences on the transcriptional activity of other nuclear receptors in jerboas. Indeed, it has been shown that human PPAR $\alpha$ 2tr exerts transcriptional repressive activity as a dominant negative receptor on PPAR $\alpha$ 1wt, PPAR $\gamma$ , hepatic nuclear factor-4, and glucocorticoid receptor by titration of a shared common coactivator, CREB-binding protein/p300 (18). Disturbance of lipid metabolism in jerboas by a hypolipidemic drug resulted in the death of all animals within 24 h after the induction of hibernation by food withdrawal. Thus, during jerboa prehibernation, induction of both PPAR  $\alpha$ 1wt and  $\alpha$ 2tr forms in the liver by ciprofibrate effects fatal consequences by enhancing unexpected fatty acid oxidation and by disrupting the nuclear receptor–coactivator crosstalk required for transition to the hibernating state.

Regarding the lipid homeostasis regulation, alternative splicing and has been described for other transcription factors such as sterol regulatory element-binding proteins (SERBPs). SERBP-1a isoform is a potent activator of both cholesterol and fatty acid biosynthetic pathways, while SERBP-1c isoform derived from the same gene is mainly specific for the fatty acid biosynthesis (54). On the other hand, the overexpression of PPARγ1 splice isoform is sufficient to induce adipocyte-specific genes in mouse liver (55). In addition, in human, the caloric restriction-associated regulation of uncoupling protein-3, a mitochondrial thermogenic protein, is dependent on the alternative splicing mechanism in skeletal muscle (56). In this context, our results on the differential expression of the wild type (PPARα1wt) and the

truncated (PPAR $\alpha$ 2tr) isoforms reveal that the alternative transcription regulation is part of a general mechanism which impacts in hibernating jerboa the adaptive response to fasting in the control of hepatic peroxisomal fatty acid  $\beta$ -oxidation.

In conclusion, the data presented here, using an original model of a small, true-hibernating rodent (jerboa), revealed that differential expression of PPAR isoforms  $\alpha 1$ wt and  $\alpha 2$ tr participates in the control of hepatic fatty acid oxidation during hibernation of jerboas as an adaptive response to fasting. Therefore, we proposed a model of the metabolic regulation of PPAR $\alpha$  target genes. In such model, the activity of the liver pool of PPAR $\alpha$  depends largely on the balance of the ratio between the wild type PPAR $\alpha 1$ wt and the dominant negative truncated PPAR o2tr forms during hibernation bouts (Figure 5). A preferential upregulation of peroxisomal fatty acid oxidation is essential for jerboas during both prehibernating and hibernating periods, which are accompanied by the induction of hepatic PGC-1 $\alpha$ . Taken together, our results strongly suggest that PPAR $\alpha$  is subject to regulation of hibernation-dependent splicing in response to fasting conditions, which define the activity of PPAR $\alpha$  and subsequently the activation of its target genes during hibernation bouts of jerboas.

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Table 1: jerboa treatment conditions

group	A	Ph	PhC	Н
n =	10	10	10	10
3 weeks with	$22 \pm 2$ °C	$22 \pm 2$ °C	22 ± 2 °C	22 ± 2 °C
food ad libitum				
3 weeks with	$22 \pm 2$ °C	6 ± 2 °C	$6 \pm 2$ °C	$6 \pm 2$ °C
food ad libitum				
food withdrawal	sacrified	sacrified	sacrified	$6 \pm 2$ °C
				$6 \pm 2$ °C
				4 days
				hibernation
				sacrified

# **Figure Legends:**

Figure 1: Fasting-associated hibernation induction of hepatic PPAR $\alpha$  and PGC-1 $\alpha$  and their target genes ACOX1 and PMP70. (Left panel) Representative RNA analysis performed by RT-PCR of RNA from active (A), prehibernating (P), hibernating (H), and prehibernating ciprofibrate-treated (PhC) jerboas. The signal of  $\beta$ -actin is shown as a housekeeping control gene. (Right panel) Bars represent mean of fold-activation compared with the values of active jerboas, based on densitometric analysis. All values are normalized to  $\beta$ -actin. Letters a, b, c, d, e, and f correspond to a statistical significance of higher mean signal intensity, (p<0.01 for a and d, p<0.02 for b and c, p<0.05 for f), compared with the active control jerboas (a and b) or with the prehibernating jerboas (d, e and f). The values are based on 3 independent experiments. A.U.: arbitrary units.

Figure 2: A. Tissue expression analysis of 52 kDa wild type PPAR $\alpha$  (PPAR $\alpha$ 1wt) and 29 kDa truncated PPAR $\alpha$  (PPAR $\alpha$ 2tr) forms performed by Western blotting (50  $\mu$ g proteins) from liver, kidney, heart, muscle, and brain of euthermic active jerboas (A) using a monoclonal antibody against the N-terminal peptide of human PPAR $\alpha$ .

B. Fasting-associated hibernation regulation of wild type PPAR $\alpha$  (PPAR $\alpha$ 1wt) and truncated PPAR $\alpha$  (PPAR $\alpha$ 2tr) proteins analyzed by Western blotting (lower panel) (50  $\mu$ g proteins) from active (A), prehibernating (P), hibernating (H), or prehibernating ciprofibrate-treated (PhC) jerboas. The signal of GAPDH is shown as a housekeeping control gene. (Upper panel) Bars represent mean of log fold-activation of the ratio compared with active animals. Black bars represent the ratio of PPAR $\alpha$ 1wt to GAPDH values, and white bars represent the ratio of PPAR $\alpha$ 1wt to GAPDH values. All values are normalized to GAPDH based on densitometric analysis. \* denotes a significantly (P < 0.05) higher mean signal intensity compared with active jerboas.

Figure 3: Fasting-associated hibernation has a strong effect on the expression of ACOX1, catalase, L-PBE, and PMP70 proteins encoded by PPAR $\alpha$ -target genes. Western blotting analysis of protein (50  $\mu$ g) homogenates from euthermic active (A), prehibernating (Ph), hibernating (H), and prehibernating ciprofibrate-treated (PhC) Jerboas. The molecular weights in kDa of the 2 ACOX1 polypeptides (72 and 52 kDa) are indicated. The signal of  $\beta$ -actin is shown as a housekeeping control gene.

Figure 4: Hibernation-dependent regulation and ciprofibrate effect on peroxisomal and mitochondrial fatty acid oxidation. A. Fold-activation of peroxisomal ACOX1 (left) and catalase (right) activities. B. Fold-activation of mitochondrial CPT1 (white bars) and MCAD (dark bars) activities. Bars represent mean values  $\pm$  standard deviations of percent fold-activation compared with the active animals of at least 3 different animals. The specific activities were measured in crude liver extracts of euthermic active (A), prehibernating (Ph) hibernating (H), or prehibernating ciprofibrate-treated (PhC) jerboas as described in the Material and Methods. Letters a, b, c, d and e correspond to a statistical significance of higher mean signal intensity, (p<0.01 for a and d, p<0.02 for b and e, p<0.05 for c), compared with the active control jerboas (a, b and c) or with the prehibernating jerboas (d and e). Values ( $\pm$  standard deviations) of the specific enzymatic activities of active jerboas are: ACOX 182  $\pm$  14 pmol/min/mg, catalase 51.5  $\pm$  8.9  $\mu$ mol/min/mg, MCAD 37.7  $\pm$  6.1 nmol/min/mg, and CPT1 19.8  $\pm$  1.5 nmol/min/mg.

Figure 5: Model of the hibernation-dependent splicing of primary PPAR $\alpha$  transcript in response to fasting conditions of jerboas. The expression of PPAR $\alpha$ 2tr isoform, during prehibernation, prevents the full activation of PPAR $\alpha$  target genes involved in the peroxisomal fatty acids oxidation. The absence of the expression of PPAR $\alpha$ 2tr, during hibernation, increases the availability of PPAR $\alpha$ 1wt active isoform, which, in the presence of PGC1 $\alpha$  coactivator, strongly induces the oxidation of fatty acids in the peroxisomal compartment.

Figure1: MS#EN-07-0913

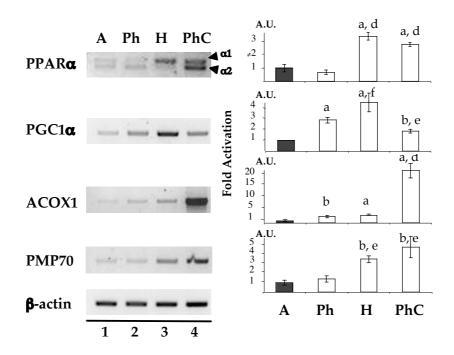


Figure 2: MS#EN-07-0913

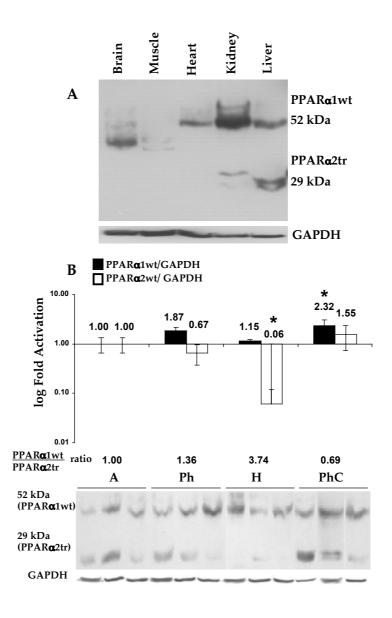


Figure 3: MS#EN-07-0913

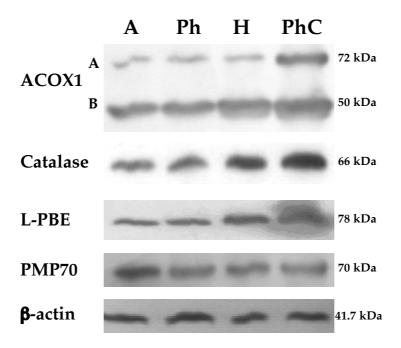
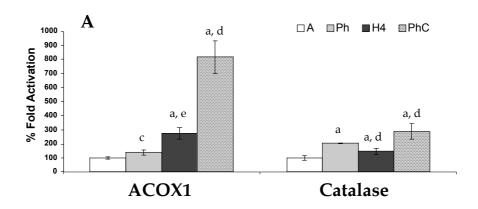


Figure 4: MS#EN-07-0913



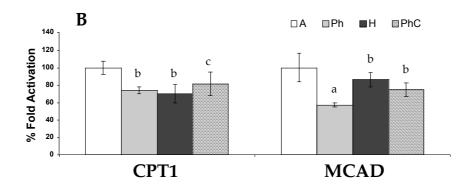
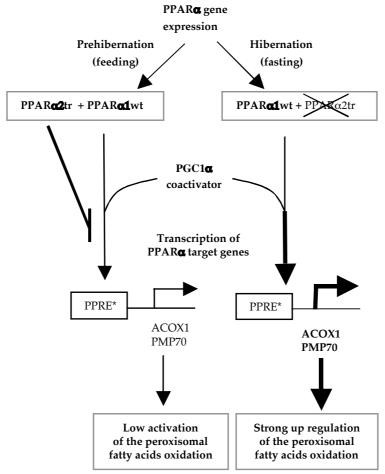


Figure 5: MS#EN-07-0913



(\*PPRE = PPAR Response Element)