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Acetoacetyl-CoA synthetase gene is abundant in rat adipose, and related with fatty acid synthesis in mature adipocytes

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Abstract

Acetoacetyl-CoA synthetase (AACS, acetoacetate-CoA ligase, EC 6.2.1.16) is a novel cytosolic ketone body (acetoacetate)-specific ligase, the physiological role of which remains to be elucidated. We examined the expression profiles of AACS mRNA in adult rat tissues, finding that it was particularly abundant in male subcutaneous white adipose tissue after weaning. In white adipose tissue, AACS mRNA was preferentially detected in mature adipocytes but not in preadipocytes. The AACS mRNA expression in primary preadipocytes increased during the adipocyte differentiation. These expression profiles were similar to that of acetyl-CoA carboxylase-1, but not like to that of 3-hydroxy-3-methylglutaryl-CoA reductase. These results suggest that AACS in adipose tissue plays an important role in utilizing ketone body for the fatty acid-synthesis during adipose tissue development.

Keywords: Acetoacetyl-CoA synthetase; Ketone body; Tissue distribution; Sex difference; Adipose tissue; Adipogenesis; Cell differentiation; mRNA expression

In the mitochondria, ketone bodies, D(−)-β-hydroxybutyrate and acetoacetate are important energy source, and succinyl-CoA:3-ketoacid CoA transferase (SCOT; EC 2.8.3.5) has been regards as for the ketone body utilization in the mitochondria [1]. On the other hand, in the cytosol, ketone body is known to be activated and incorporated into cholesterol and fatty acids by acetoacetyl-CoA synthetase (AACS, acetoacetate-CoA ligase, EC 6.2.1.16), which we purified for the first time from bacterium, Zoogloea ramigera I-16-M [2], and rat liver cytosol [3]. This enzyme is the strictly acetoacetate-specific ligase [4,5]. Endemann et al. [6] have proposed that main function of AACS is direct supply of acetyl-CoA from acetoacetate in the cytosol for the synthesis of the lipidic substances and that such cytosolic activation could bypass the pathway involving ATP-dependent supply of acetyl-units from mitochondria to cytosol.

Previously, we showed that the AACS activity in the liver of rats remarkably increased and then decreased during the animal's development [5] and increased upon the administration of hypocholesterolemic compounds, cholestyramine and/or pravastatin, to rats [7]. We have also demonstrated that hepatic AACS activity markedly decreased in streptozotocin-induced diabetic rats as in the case of 3-hydroxy-3-methylglutaryl-CoA reductase (HMGCR) or acetyl-CoA carboxylase [8]. Furthermore, we found that AACS mRNA in the cerebellum was restricted to glial cells, while in the cerebral cortex, it was restricted to neural cells [9]. These results suggest that direct activation of acetoacetate by AACS in the cytosolic compartment of the cells is an important step for the regulation of ketone body utilization on cholesterol and/or fatty acids biosynthesis.

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In order to clarify a physiological role of AACS in the lipogenesis, we examined expression levels of AACS mRNA in a variety of rat lipogenic tissues. The present manuscript describes the remarkable expression of AACS mRNA in male subcutaneous white adipose tissue among the lipogenic tissues, its preferential expression in mature adipocytes, and the alteration of its level during the adipocyte-differentiation.

Materials and methods

Preparation of RNA. RNA was prepared from rat tissues using a QuickPrep total RNA extraction kit (Amersham Biosciences), and from primary adipocytes using a RNeasy mini kit (Qiagen).

Northern blotting analysis. Aliquots of RNAs (10 μg each) were dissolved on a denaturing agarose gel (1%) containing formaldehyde and transferred to a nylon membrane in 20× SSC (1× SSC = 0.15 M NaCl/0.015 M sodium citrate) overnight. The membrane was prehybridized at 42 °C for 4 h in a hybridization solution (10% dextran sulfate, 50% formamide, 2% SDS, 5× SSPE, 5× Denhardt's solution, and 100 μg/ml heat-denatured salmon sperm DNA), followed by hybridization at 42 °C for 18 h in the hybridization solution containing a ^{32}P-labeled probe labeled by Ready-To-Go DNA Labeling Beads (Amersham Biosciences) with cytidine 5′-[α-^{32}P]dCTP (~30 TBq/mmol, Amersham Biosciences). The membrane was then washed at room temperature three times for 5 min each time in 2× SSC/0.1% SDS, and at 65 °C twice for 30 min each time in 0.25× SSC/0.1% SDS. The washed membrane was analyzed with a radioimaging analyzer (BAS2000, Fuji Photo Film, Japan).

PT-PCR for PPARγ. Aliquot of RNAs (4 μg) was incubated for 60 min at 37 °C in the reaction mixture (20 μl) containing 300 U of moloney murine leukemia virus reverse transcriptase (Gibco-BRL, USA), 15 U of human placenta RNase inhibitor (WAKO), and 0.5 μg of random hexadeoxynucleotide primer (Takara). To amplify the human AACS cDNA fragment, PCR was performed for 30 cycles in the reaction mixture containing an aliquot of the above cDNA solution, 0.05 U/μl EX *Taq* DNA polymerase (Takara) and 4 pmol/μl each of sense (gagatgccattctggcccaccaacttcgg) and antisense (tatcataaataagcttcaatcggatggttc) primers of rat PPARγ (Accession No.: AF156666) [10].

Preparation of probes. The cDNA fragments of AACS, SCOT, HMGCR, and ACC1 were amplified from rat liver cDNA. The oligonucleotide primers used for amplification were: forward (atgtccaagctggcacggct) and reverse (ttcagaagtcctgcagctca) for rat AACS (GenBank Accession No. AB026291) [7]; forward (atgacnccncarggnacntt) and reverse (gtccgtgtctgaagacaact) for human SCOT (GenBank Accession No. P55809) [11]; forward (acggtgacacttactatctg) and reverse (accatgtgacttctgacaag) for rat HMGCR (GenBank Accession No. NM013134); forward (gtccgtgtctgaagacaact) and reverse (tcctaactgttccagagct) for rat ACC1 (GenBank Accession No. J03808) [12]. The cDNA fragment of leptin was amplified from rat epididymal adipose tissue. The oligonucleotide primers used for amplification were: forward (tgctccagcagctgcaaggt) and reverse (gaagaatgtcctgcagagag) for rat leptin (GenBank Accession No. NM013076) [13]. The fragments were cloned into the pGEM-T vector (Promega).

Preparation of mature adipocytes and stromal–vascular cells. Mature adipocytes and stromal–vascular cells were prepared from rat subcutaneous white adipose tissue essentially according to the method of Ogawa et al. [13].

Primary culture of preadipocytes. Primary preadipocytes were cultured and differentiated according to Mitchell et al. [14]. The stromal–vascular cells were suspended in Dulbecco's modified Eagle's medium (DMEM; Sigma) supplemented penicillin (100 U/ml; Gibco-BRL) and streptomycin (100 μg/ml; Gibco-BRL), and re-filtered. The cells were adjusted to a density of 4.0×10^5 cells/ml in DMEM with 10% fetal bovine serum (FBS; Gibco-BRL). Two milliliters volumes of these cells was plated onto 35 mm dishes. After 1 day in culture at 37 °C in an atmosphere of 5% CO_2, differentiation was induced by the addition of medium supplemented with isobutylmethylxanthine (IBMX; 0.5 mM; Sigma), dexamethasone (DEX; 0.25 μM; Nacalai tesque), and insulin (10 μg/ml; Sigma). After 48 h, the induction medium was removed and replaced by DMEM containing 10% FBS supplemented with insulin (10 μg/ml) alone [15]. This medium was changed every 2 days.

Results and discussion

Expression of AACS mRNA in rat lipogenic tissues

Fig. 1 shows the expression levels of AACS mRNA in male and female rat lipogenic tissues: brain, liver, white adipose tissue, and brown adipose tissue. The white adipose tissue was prepared from the subcutaneous region, and the brown adipose tissue from the interscapular region. The integrity of RNAs was confirmed by electrophoresis on a denaturing agarose gel containing formaldehyde (lower lane). The labeled probe hybridized to an mRNA of about 4.7 kb in all tissues examined. AACS mRNA was particularly abundant in male white adipose tissue. But in other lipogenic tissues, such remarkable sex difference of AACS expression level was not observed. SCOT, that is known as a key mitochondrial enzyme in the energy production from ketone bodies in various tissues except liver [16], was equally expressed in all tissues examined except for the liver. 3-Hydroxy-3-methylglutaryl-coenzyme A reductase (HMGCR; EC 1.1.1.34), the rate-limiting enzyme of

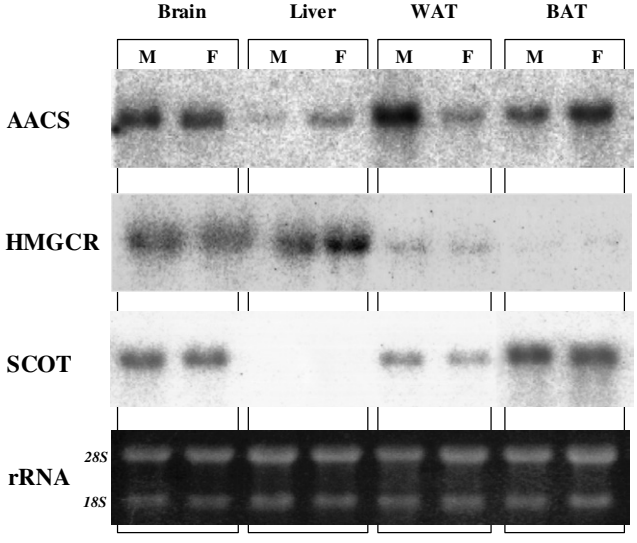

Fig. 1. Gene expression of acetoacetyl-CoA synthetase mRNA in rat lipogenic tissues. Total RNAs were isolated from brain, liver, white adipose tissue (WAT), and brown adipose tissue (BAT) of male and female rats (8-week old). Aliquots of RNAs (10 μg) were subjected to Northern blotting analysis of AACS, SCOT, and HMGCR cDNA probes. M and F indicate male and female, respectively. The lower panel shows EtBr staining of ribosomal RNAs (2 μg/lane).

cholesterol-synthesis [17], was highly expressed in the brain and liver, but apparently absent in the white adipose tissues.

Preferential expression of AACS mRNA in subcutaneous white adipose tissue

Adipose tissue is involved in the pathogenesis of diabetes, which causes to increase the blood concentration of ketone body. Of the two types of adipose tissues, white adipose tissue provides the primary site of energy storage and also serves as an important endocrine organ through secretion of hormones such as leptin, adiponectin, resistin, and other cytokines [18]. Brown adipose tissue is major site of energy expenditure through expression of uncoupling protein 1 and its role in thermogenesis [19].

Since male white adipose tissue contained significant levels of AACS mRNA, we examined the mRNA expression of AACS and other enzymes in a variety of adipose tissues including subcutaneous, perigonadal and mesenteric white adipose tissues, and interscapular brown adipose tissue (Fig. 2). SCOT mRNA expression was weaker in subcutaneous white adipose tissues than in other regions. HMGCR mRNA was apparently absent in any adipose tissue examined. Whereas, AACS mRNA expression was high especially in the male subcutaneous white adipose tissue. These data suggest that among the enzymes examined, only AACS mRNA has the sex difference in the expression level in adipose tissue.

Expression of AACS mRNA was increased in male white adipose tissue during postnatal development

Rat white adipose tissue cannot be detected macroscopically during embryonic stage and at birth, and its growth is greatly stimulated during postnatal development. The sucking–weaning transition is a physiological situation during which marked nutritional changes occur spontaneously [20]. Cell-size and cell-number of white adipose tissue is changed very little during the sucking, but increased markedly after weaning. So, we examined the expression profile of AACS mRNA in male and female subcutaneous adipose tissues at sucking (2 week) and after weaning (4, 6, 8, and 10 week). AACS expression was detected at low level at sucking, then increased after weaning (Fig. 3). Interestingly, in male subcutaneous adipose, AACS mRNA was greatly increased after 6 week of age. On the other hand, HMGCR and SCOT mRNA expression was not significantly changed during all ages examined. These data indicate that AACS may play some important roles during postnatal adipose development, especially after sexual maturation.

AACS mRNA was expressed in mature adipocytes

White adipose tissue is composed of mature adipocytes and stromal–vascular cells [21]. To determine the cellular localization of AACS mRNA expression in

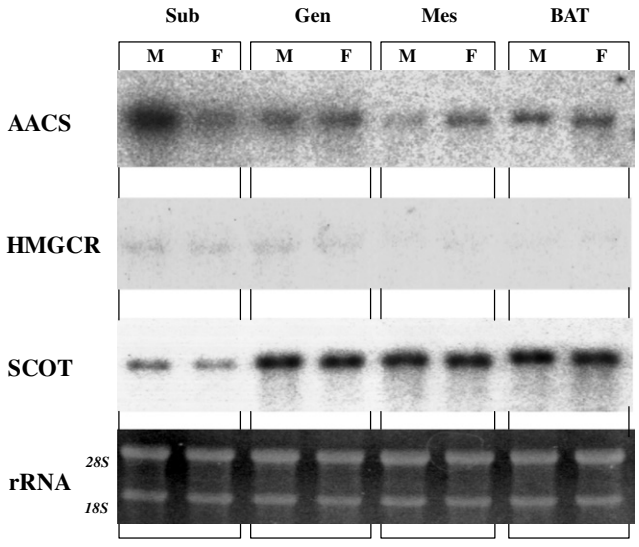

Fig. 2. Gene expression of acetoacetyl-CoA synthetase mRNA in rat adipose tissues. Total RNAs were isolated from various adipose tissues of male and female rats (8-week old). Aliquots of RNAs (10 μg) were subjected to Northern blotting analysis of AACS, SCOT, and HMGCR cDNA probes. Sub, gen, mes, and BAT indicate a subcutaneous, paragenitalium, mesenterium, and brown adipose tissue, respectively. M and F indicate male and female, respectively. The lower panel shows EtBr staining of ribosomal RNAs (2 μg/lane).

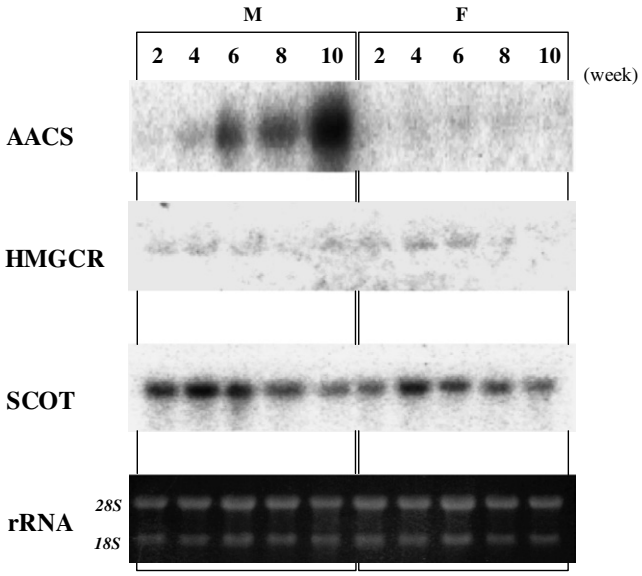

Fig. 3. The developmental profile of AACS mRNA expression in subcutaneous white adipose tissue. Total RNAs were isolated from subcutaneous adipose tissues of male and female rats (2-, 4-, 6-, 8-, and 10-week old). Aliquots of RNAs (10 μg) were subjected to Northern blotting analysis of AACS, SCOT, and HMGCR cDNA probes. M and F indicate male and female, respectively. The lower panel shows EtBr staining of ribosomal RNAs (2 μg/lane).

white adipose tissue, we prepared mature adipocytes and stromal–vascular cells from subcutaneous adipose tissue. Leptin mRNA, which produces a hormone inducing satiety and increasing energy expenditure, is known to preferentially be expressed in mature adipocytes but not in stromal–vascular cells of white adipose tissue [13]. On our preparations, leptin mRNA was preferentially detected in mature adipocytes but not stromal–vascular cells (Fig. 4), indicating that the mature adipocytes and stromal–vascular cells were properly prepared. Similarly as leptin mRNA, AACS mRNA was preferentially detected in mature adipocytes but not in stromal–vascular cells. These results suggest that AACS has a characteristic role in mature adipocytes.

Expression profiles of AACS mRNA in adipocyte during adipogenesis

Mature adipocytes are differentiated from preadipocytes included in stromal–vascular cells. During the differentiation, a large number of genes have to be regulated in a selective and coordinated manner, and cell morphology as well as gene expression undergo significant changes [22]. Therefore, we examined the temporal expression of AACS, HMGCR, ACC-1, and PPARγ during the differentiation of rat primary preadipocytes. PPARγ is a transcription factor that plays a pivotal role in adipocyte differentiation [23,24], so we used it as the adipocyte-differentiation marker gene. Primary preadipocytes prepared from rat epididymal white adipose tissue can undergo the differentiation to mature adipocytes in the presence of mixture of adipogenic inducers, DEX,

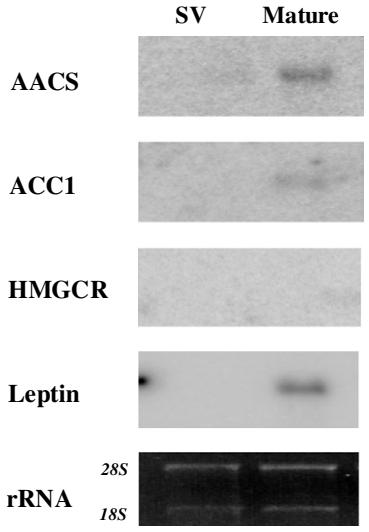

Fig. 4. AACS mRNA expression in pre-adipocytes and mature adipocytes Mature and preadipose cells were prepared by the collagenase-digestion method described under Materials and methods. Total RNAs (8 μg/lane) were isolated from these cells, and subjected to the Northern analysis of AACS, ACC-1, HMGCR, and leptin cDNA probes. SV indicates stromal–vascular cells. The lower panel shows EtBr staining of ribosomal RNAs (1 μg/lane).

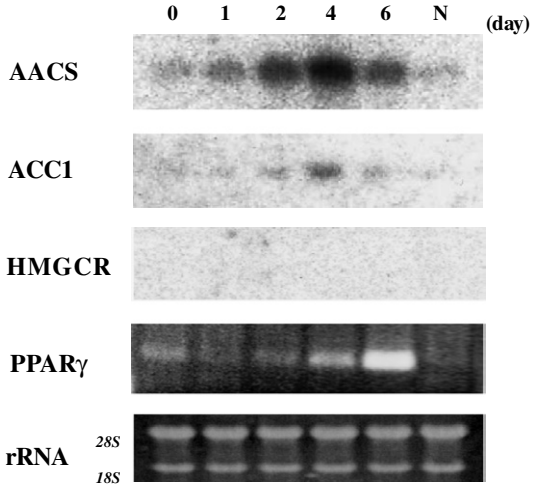

Fig. 5. Time course of the AACS mRNA expression during adipocyte differentiation in rat primary culture Total RNA from cultured cells at the indicated time points of day 0, day 1, day 2, day 4, and day 6 were prepared. Four micrograms of extracted RNAs was subjected to RT-PCR analysis of PPARγ, and 8 μg of extracted RNAs was subjected to the Northern blot analysis of AACS, ACC-1, and HMGCR cDNA probes. N indicates the lane of non-induced cells on day 6. The lower panel shows EtBr staining of ribosomal RNAs (2 μg/lane).

IBMX, and insulin, for 48 h. Northern blots (AACS, HMGCR, and ACC-1) and RT-PCR products (PPARγ) are shown in Fig. 5. PPARγ mRNA was increased around days 1–4, and reached the maximum level on day 6. HMGCR mRNA was hardly detected during differentiation. ACC-1 mRNA expression was increased and transiently peaked on day 4. AACS mRNA expression was detected in predifferentiated state (day 0) and increased around days 1–4, and transiently peaked on day 4. This alteration in the gene expression during the adipocytes differentiation was similar to that of ACC-1.

AACS is regarded as the enzyme that supplies acetyl units directly from acetoacetate in the cytosolic compartment for cholesterol and/or fatty acids biosynthesis [6]. In adipose tissues, HMGCR, the rate-limiting enzyme of cholesterol-synthesis, was weakly expressed (Figs. 1 and 2), and hardly detected in preadipocytes and mature adipocytes (Fig. 5). On the other hand, expression pattern of ACC-1, the key enzyme of fatty acid-synthesis, was quite similar to that of AACS during preadipocytes-differentiation. These results indicate that AACS supply acetyl units from acetoacetate for fatty acid-synthesis in adipocytes.

Moreover, AACS and ACC-1 were peaked on the same differentiation period when PPARγ was up-regulated. PPARγ is the transcription factor that has important effects on lipid deposit via regulation of the expression of genes involved in lipid metabolism, such as lipoprotein lipase, fatty acid translocase/CD36, fatty acid-binding protein aP2, acyl-CoA synthetase, and phosphoenolpyruvate carboxylase [25]. Indeed, we observed multi lipid droplets after day 5. These results

indicate that AACS gene expression is closely related to the initiation of depositing lipid droplets.

In summary, our study showed that AACS was highly expressed in rat adipose tissues, especially in adipocytes on initiation-period of the lipid deposit. These results suggest that AACS gene expression is closely related with adipogenesis, especially with fatty acid-synthesis. Moreover, AACS mRNA expression is strongly dependent upon the site of adipose deposit and sexual maturation of the rats. Regional adipose distribution differs between men and women, and is thus considered as a secondary sex character [26]. Such sex differences in white adipose tissue metabolism were reported previously for gene expression of mitochondrial 3-hydroxy-3-methyl-glutaryl-CoA synthase (mtHMGCS) [27]. This enzyme, the rate-limiting enzyme of ketogenesis [28], is highly expressed in the male subcutaneous white adipose tissue. Since these two enzymes related to ketone body-metabolism were highly expressed in the same region of adipose deposit, ketone body, and its utilizing enzymes could play an important role on lipogenesis of the male subcutaneous white adipose tissue.

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References

[1] G.A. Mitchell, S. Kassovska-Bratinova, Y. Boukaftane, M-F. Robert, S.P. Wang, L. Ashmarina, M. Lambert, P. Lapierre, E. Potier, Medical aspects of ketone body metabolism, Clin. Invest. Med. 18 (1995) 193–216.

[2] T. Fukui, M. Ito, K. Tomita, Purification and characterization of acetoacetyl-CoA synthetase from Zoogloea ramigera I-16-M, Eur. J. Biochem. 127 (1982) 423–428.

[3] M. Ito, T. Fukui, M. Kamokari, T. Saito, K. Tomita, Purification and characterization of acetoacetyl-CoA synthetase from rat liver, Biochim. Biophys. Acta 794 (1984) 183–193.

[4] G.Q. Cai, B.T. Driscoll, T.C. Charles, Requirement for the enzymes acetoacetyl coenzyme A synthetase and poly-3-hydroxybutyrate (PHB) synthase for growth of Sinorhizobium meliloti on PHB cycle intermediates, J. Bacteriol. 182 (2000) 2113–2118.

[5] M. Nakamoto, N. Takahashi, A. Iwahori, H. Sato, T. Fukui, Effects of development on acetoacetyl-CoA synthetase biosynthesis in rat liver, Biol. Pharm. Bull. 22 (1999) 981–983.

[6] G. Endemann, P.G. Goetz, J. Edmond, H. Brunengraber, Lipogenesis from ketone bodies in the isolated perfused rat liver. Evidence for the cytosolic activation of acetoacetate, J. Biol. Chem. 257 (1982) 3434–3440.

[7] A. Iwahori, N. Takahashi, M. Nakamoto, M. Iwama, T. Fukui, cDNA-derived amino acid sequence of acetoacetyl-CoA synthetase from rat liver, FEBS Lett. 466 (2000) 239–243.

[8] H. Sato, N. Takahashi, M. Nakamoto, M. Ohgami, M. Yamazaki, T. Fukui, Effects of streptozotocin-induced diabetes on acetoacetyl-CoA synthetase activity in rats, Biochem. Pharmacol. 63 (2002) 1851–1855.

[9] M. Ohnuki, N. Takahashi, M. Yamasaki, T. Fukui, Different localization of mRNA of acetoacetyl-CoA synthetase, a novel cytosolic ketone body-utilizing enzyme, from that of succinyl-CoA:3-oxoacid CoA-transferase in rat brain. Biochim. Biophys. Acta 1729 (2005) 147–153.

[10] H.M. Guardiola-Diaz, S. Rehnmark, N. Usuda, T. Albrektsen, D. Feltkamp, J.A. Gustafsson, S.E. Alexson, Rat peroxisome proliferator-activated receptors and brown adipose tissue function during cold acclimatization, J. Biol. Chem. 274 (1999) 23368–23377.

[11] S. Kassovska-Bratinova, T. Fukao, X.Q. Song, A.M. Duncan, H.S. Chen, M.F. Robert, C. Perez-Cerda, M. Ugarte, C. Chartrand, S. Vobecky, N. Kondo, G.A. Mitchell, Succinyl CoA: 3-oxoacid CoA transferase (SCOT): human cDNA cloning, human chromosomal mapping to 5p13, and mutation detection in a SCOT-deficient patient, Am. J. Hum. Genet. 59 (1996) 519–528.

[12] F. Lopez-Casillas, D.H. Bai, X.C. Luo, I.S. Kong, M.A. Hermodson, K.H. Kim, Structure of the coding sequence and primary amino acid sequence of acetyl-coenzyme A carboxylase, Proc. Natl. Acad. Sci. USA 85 (1988) 5784–5788.

[13] Y. Ogawa, H. Masuzaki, N. Isse, K. Okazaki, K. Mori, M. Shigemoto, N. Satoh, N. Tamura, K. Hosoda, Y. Yoshimasa, H. Jingami, T. Kawada, K. Nakao, Molecular cloning of rat obese cDNA and augmented gene expression in genetically obese Zucker fatty (fa/fa) rats, J. Clin. Invest. 96 (1995) 1647–1652.

[14] S.E. Mitchell, W.D. Rees, L.J. Hardie, N. Hoggard, M. Tadayyon, J.R. Arch, P. Trayhurn, ob gene expression and secretion of leptin following differentiation of rat preadipocytes to adipocytes in primary culture, Biochem. Biophys. Res. Commun. 230 (1997) 360–364.

[15] A.K. Student, R.Y. Hsu, M.D. Lane, Induction of fatty acid synthetase synthesis in differentiating 3T3-L1 preadipocytes, J. Biol. Chem. 255 (1980) 4745–4750.

[16] J.T. Tildon, D.A. Sevdalian, CoA transferase in the brain and other mammalian tissues, Arch. Biochem. Biophys. 148 (1972) 382–390.

[17] J.L. Goldstein, M.S. Brown, Regulation of the mevalonate pathway, Nature 343 (1990) 425–430.

[18] A.R. Saltiel, You are what you secrete, Nat. Med. 7 (2001) 887–888.

[19] B.B. Lowell, B.M. Spiegelman, Towards a molecular understanding of adaptive thermogenesis, Nature 404 (2000) 652–660.

[20] J. Girard, P. Ferre, J.P. Pegorier, P.H. Duee, Adaptations of glucose and fatty acid metabolism during perinatal period and suckling–weaning transition, Physiol. Rev. 72 (1992) 507–562.

[21] G. Ailhaud, P. Grimaldi, R. Negrel, Cellular and molecular aspects of adipose tissue development, Annu. Rev. Nutr. 12 (1992) 207–233.

[22] D. Rosen, B.M. Spiegelman, Molecular regulation of adipogenesis, Annu. Rev. Cell Dev. Biol. 16 (2000) 145–171.

[23] B.M. Spiegelman, Peroxisome proliferator-activated receptor gamma: a key regulator of adipogenesis and systemic insulin sensitivity, Eur. J. Med. Res. 2 (1997) 457–464.

[24] S. Mandrup, M.D. Lane, Regulating adipogenesis, J. Biol. Chem. 272 (1997) 5367–5370.

[25] P. Escher, W. Wahli, Peroxisome proliferator-activated receptors: insight into multiple cellular functions, Mutat. Res. 448 (2000) 121–138.

[26] P. Bjorntorp, Adipose tissue distribution and function, Int. J. Obes. 15 (1991) 67–81.

[27] S. Thumelin, C. Kohl, J. Girard, J.P. Pegorier, Atypical expression of mitochondrial 3-hydroxy-3-methylglutaryl-CoA synthase in subcutaneous adipose tissue of male rats, J. Lipid Res. 40 (1999) 1071–1077.

[28] A.M. Robinson, D.H. Williamson, Physiological role of ketone bodies as substrates and signals in mammalian tissues, Physiol. Rev. 60 (1980) 143–187.