

Differential Expression of Peroxisome Proliferator-Activated Receptor- α , - β , and - γ during Rat Embryonic Development*

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ABSTRACT

The expression patterns of the three different peroxisome proliferator-activated receptor (PPAR) isotypes have been determined during rat embryonic development by *in situ* hybridization. The expression of PPAR α starts late in development, with increasing levels in organs such as liver, kidney, intestine, and pancreas, in which it will also be present later in adulthood to regulate its specific target genes. PPAR α is also transiently expressed in the embryonic epidermis and

central nervous system. PPAR γ presents a very restricted pattern of expression, being strongly expressed in brown adipose tissue, in which differentiation it has been shown to participate. Like PPAR α , it is also expressed transiently in the central nervous system. Interestingly, PPAR α , - β and - γ are coexpressed at high levels in brown adipose tissue. Finally, the high and ubiquitous expression of PPAR β suggests some fundamental role(s) that this receptor might play throughout development. (*Endocrinology* **139**: 2748–2754, 1998)

PEROXISOME proliferator-activated receptors (PPARs) are lipid-activatable transcription factors that belong to the nuclear hormone receptor superfamily (see Ref. 1 for a review). To date, three isotypes of PPARs have been described in amphibians, rodents, and humans: PPAR α , PPAR β (also called δ , NUC-1, or FAAR), and PPAR γ (2–10). PPARs were shown to be activated by substances that induce peroxisome proliferation (2, 3) as well as by natural fatty acids (4, 11). It is only recently that fatty acids, some eicosanoids, and some hypolipidemic and antidiabetic drugs have been shown to directly bind to PPARs (12–18; see Ref. 19 for a review).

PPAR target genes encode enzymes involved in peroxisomal and mitochondrial β -oxidation, ketone body synthesis, and microsomal ω -hydroxylation, as well as the production of fatty acid binding proteins, apolipoproteins, lipoprotein lipase, malic enzyme, phosphoenolpyruvate carboxykinase, and the brown adipose tissue (BAT) uncoupling protein (see Refs. 1, 20, and 21 for reviews; 22). Thus, PPARs play key roles in different aspects of lipid metabolism and homeostasis. Consistent with the different pathways they regulate, PPARs were shown to be expressed in a wide range of tissues of the adult organism (3, 7, 23–25). We have shown recently, using *in situ* hybridization, that in the adult rat, PPAR α is expressed in cells with high catabolic rates of fatty acids and high peroxisome-dependent activities (hepatocytes, cardiomyocytes, proximal tubules of kidney, intestinal mucosa). PPAR β is expressed ubiquitously and is abundant

in most tissues, whereas PPAR γ is restricted mainly to adipose tissue, with some expression also in parts of the immune system, the retina, and other organs in trace amounts (25). The localization of PPAR α and PPAR γ gene transcripts and proteins and the nature of their target genes indicates that they play roles in fatty acid catabolism for PPAR α , on the one hand, and adipogenesis and lipid storage for PPAR γ , on the other hand (see Ref. 1 for a review). In contrast, however, the role of the ubiquitously expressed PPAR β remains elusive.

As the ubiquitous expression of PPAR β in the adult rat did not provide clear information as to its roles, developmental expression of this isotype was analyzed, with the goal of unraveling differential patterns of expression that would implicate PPAR β in specific events. Developmental patterns of expression of PPAR α and PPAR γ were also investigated to further understand their roles in the embryo. Previous reports of Northern blot analyses in *Xenopus* and mice showed that PPAR β is expressed early and throughout development, whereas PPAR α and PPAR γ appear only later in relatively high amounts (3, 7). However, these studies did provide only limited information, as the distribution within the embryo could not be resolved by the approach used. It is precisely to answer this question that analysis of the differential tissular expression of PPARs during embryonic development of the rat was undertaken by *in situ* hybridization. Rat embryos were studied using specific probes for rat PPAR α , PPAR β , and PPAR γ (25). Embryonic days (E) E8.5, E11.5, E13.5, E15.5, and E18.5 were chosen to cover the most important periods of development: E8.5 for the beginning of organization of the embryo in three layers; E11.5–E15.5 because of the intense differentiation processes that occur in most tissues, particularly in the central nervous system (CNS); and E18.5 because it represents a stage at which many tissues are already expressing specific functions that can be compared with those found in adulthood. Our results show that PPAR α and PPAR γ start to be expressed only late in

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development (E13.5), mainly in the tissues where they will be found postnatally and in the adult. In addition, both PPAR α and PPAR γ present transient expression in the CNS around E13.5. In contrast to the specific distribution of PPAR α and PPAR γ , PPAR β is expressed ubiquitously and very early during embryogenesis, with a peak of expression in the developing nervous system on E13.5. During late development (E18.5), PPAR β decreases to levels that will be found later ubiquitously in adult tissues. This strikingly high expression of PPAR β during development points to potential new directions of investigation to analyze the to date elusive role of this PPAR isotype.

Materials and Methods

Complementary DNAs (cDNAs) and probes used for in situ hybridization

A cDNA comprising part of the D and E domains of the rat PPAR α (nucleotides 1377–1766) (4) was obtained (25, 26). cDNAs comprising part of the A/B domain of the rat PPAR β (nucleotides 264–398) (8) and part of the A/B and C domains of the rat PPAR γ (403 nucleotides long, 96% homologous to the mouse PPAR γ) (23) were obtained (25). The three rat PPAR (α , β , and γ) cDNAs were subcloned in pBluescript KS⁺ and SK⁺ vectors (Stratagene, Heidelberg, Germany) and used to synthesize *in vitro* transcribed antisense and sense riboprobes (25, 27). Antisense and sense riboprobes were labeled with digoxigenin (Boehringer Mannheim, Mannheim, Germany).

Embryo preparation and in situ hybridization analysis

The age of Sprague-Dawley rat embryos (BRL, Basel, Switzerland) was determined from the appearance of a vaginal plug in pregnant females, and uteruses were dissected out. E8.5 embryos were let *in utero*, whereas E11.5, E13.5, E15.5, and E18.5 embryos were removed from the uterus and separated from the placenta. Uteruses (E8.5) and embryos (E11.5, E13.5, E15.5, and E18.5) were then quickly washed in diethylpyrocarbonate (Fluka, Buchs, Switzerland)-treated PBS and fixed 15 h in 4% paraformaldehyde-PBS at room temperature. Embryos were cryoprotected at 4°C in 12% sucrose-PBS and 18% sucrose-PBS for 6 and 12 h, respectively, and then embedded in tissue-freezing medium (Jung, Nussloch, Germany) and frozen in isopentane and dry ice. Embryos were kept at –80°C until used, and then cut and analyzed by *in situ* hybridization as previously described (25, 27). Briefly, cryosections 12 μ m thick were prepared, and hybridization with digoxigenin-labeled antisense and sense riboprobes for rat PPAR α , β , and γ was carried out at 60°C in 5 \times SSC (standard saline citrate) and 50% formamide for 40 h. Washes (30 min in 2 \times SSC at room temperature, 1 h in 2 \times SSC at 65°C, 1 h in 0.1 \times SSC at 65°C) and alkaline phosphatase staining were performed as previously described (25, 27). After staining, sections were dehydrated and mounted (Eukitt, O. Kindler Co., Freiburg, Germany). The specificity of hybridization was ascertained by the use of sense probes for the PPAR genes with the same length, GC content, and specificity as the corresponding antisense probes.

Histological analysis

In situ hybridization slides were observed and photographed on an Axiophot microscope (Carl Zeiss, Zurich, Switzerland).

Results

In a previous *in situ* hybridization study, we showed that the PPAR riboprobes we used were specific for each PPAR isotype (25). Moreover, we showed that the nonradioactive *in situ* hybridization protocol we used was sensitive enough to allow the detection of as few as 25 transcripts/cell (27).

PPAR α

Transcripts of the PPAR α gene were first detected at stage E13.5, where they were found at relatively high levels in the CNS (brain and spinal cord), tongue, and digestive tract (Fig. 1C). Lower levels were also detected in vertebrae, liver, and heart. On E15.5, PPAR α expression decreased in the CNS, heart, digestive tract, and vertebrae (Fig. 2A), whereas it remained unchanged in the liver and was first detected in the epidermis, the cortex of the kidney, striated muscles, and the lung (Fig. 2C and Table 1). On E18.5, the PPAR α gene was highly expressed in the liver (Fig. 3A and Table 1), the mucosa of the digestive tract (Fig. 3B and Table 1), BAT (Fig. 3C and Table 1), and epidermis (Fig. 3A and Table 1). PPAR α transcripts were also well detected in the kidney cortex and pancreas (Fig. 3B and Table 1), but were barely detectable in muscle (Fig. 3, A and C) and CNS (not shown and Table 1). The staining of sections with a sense control probe for PPAR α was negative at the different stages tested (Figs. 1D and 3D).

PPAR β

The PPAR β gene was expressed as early as E8.5 in the embryonic ectoderm, the visceral endoderm (Fig. 1E and Table 1), and the parietal endoderm (Fig. 1E and Table 1). On E11.5, PPAR β transcripts were present in the CNS (brain and spinal cord), the first branchial arch, and the bud of the digestive tract (Fig. 1F and Table 1). On E13.5, E15.5, and E18.5, PPAR β expression was ubiquitous, with relative levels of transcripts varying from one tissue to another (Figs. 1G; 2, D–F; and 3, E–I; and Table 1). An impressive peak of expression was observed between E13.5–E15.5 (Figs. 1F and 2D and Table 1), followed by a decrease on E18.5 (Fig. 3, E–I) to reach the levels of ubiquitous expression found in the adult rat (25). The peak of PPAR β transcripts was particularly high on E13.5 in the CNS (whole brain and spinal cord), the spinal ganglia, the tongue, the vertebrae, the liver, and the digestive tract. It was also clearly observed in the heart and epidermis, but at lower levels (Fig. 1G and Table 1). On E15.5, PPAR β was still very highly expressed in the CNS (whole brain and spinal cord), particularly in the forebrain (telencephalic cortex; Fig. 2, D and E, and Table 1). The liver, lung, digestive tract, and vertebrae also presented high levels of PPAR β messenger RNAs (mRNAs), whereas it was found at lower levels in epidermis, heart, pancreas, and skeletal muscle on E15.5 (Fig. 2, D and F, and Table 1). On E18.5, very high amounts of PPAR β transcripts were detected in the epidermis and BAT (Fig. 3, G and I, and Table 1), as well as in the follicles of vibrissae, primordia of teeth, and olfactory epithelium (Fig. 3I). It was also well expressed in the mucosa of the digestive tract, the cortex of the kidney, and the pancreas (Fig. 3F), as well as in skeletal muscle, heart, and lung (Table 1 and not shown). Interestingly at this stage, PPAR β expression was decreased in the liver (Fig. 3F and Table 1) and the CNS (Fig. 3E and Table 1). The staining of sections with a sense control probe for PPAR β was negative in the different stages tested (Figs. 1H, 2I, and 3H).

PPAR γ

The expression of the PPAR γ gene was first detected on E13.5, when relatively high transient levels of transcripts

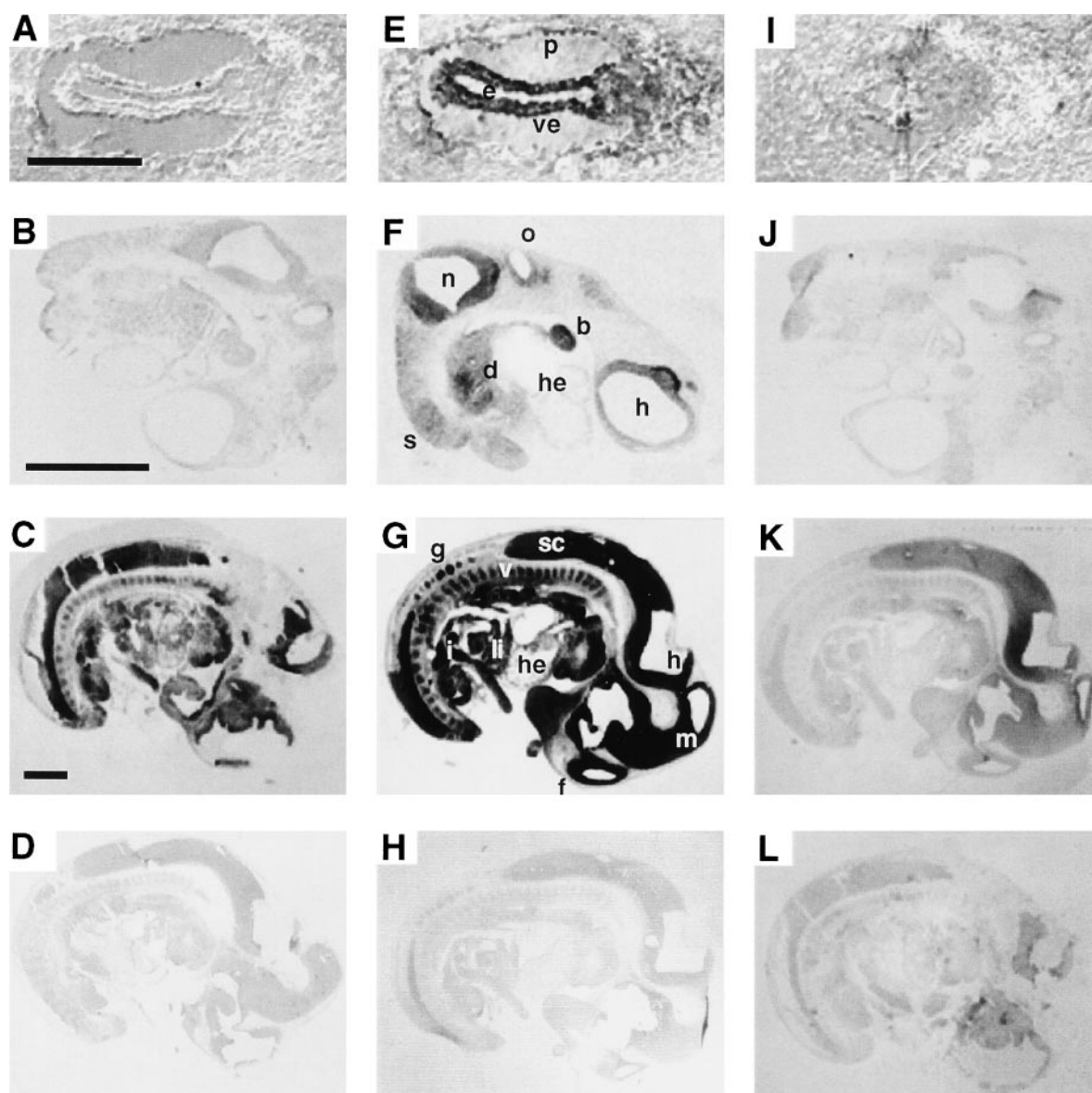


FIG. 1. Expression of PPAR α , PPAR β , and PPAR γ on E8.5, E11.5, and E13.5 in the developing rat embryo. *In situ* hybridization was performed with antisense probes for PPAR α (A–C), PPAR β (E–G), and PPAR γ (I–K), and sense probes for PPAR α (D), PPAR β (H), and PPAR γ (L). Whole embryos of E8.5 (A, E, and I), E11.5 (B, F, and J; sagittal), and E13.5 (C, D, G, H, K, and L; sagittal) were used. b, First branchial arch; d, digestive bud; e, embryonic ectoderm; f, forebrain; g, spinal ganglia; h, hindbrain; he, heart; i, intestine; li, liver; m, midbrain; n, neural tube; o, otic vesicle; p, parietal endoderm; s, somites; sc, spinal cord; v, vertebrae; ve, visceral endoderm. Bars = 200 μ m (A, E, and I) and 1 mm (B–D, F–H, and J–L).

were observed in the CNS only, particularly in the hindbrain (Fig. 1K). On E15.5, the expression of PPAR γ in the CNS was already reduced, and no other tissue was found expressing it (Fig. 2G and Table 1). On E18.5, PPAR γ mRNAs were only detected in BAT, at very high levels (Fig. 3K and Table 1). The staining of sections with a sense control probe for PPAR γ was negative at each stage tested (Figs. 1L, 2H, and 3L).

Discussion

This study establishes that the three PPAR isotypes are expressed differentially in numerous tissues originating from all three embryonic layers during rat development. PPAR α and PPAR γ appear late in development in the tissues

where they will continue to be expressed in adulthood (25, 28), with the exception of a transient expression in the CNS (α and γ) and the epidermis (α). In contrast, PPAR β is already expressed ubiquitously at the earliest stage tested, with a marked peak on E13.5–E15.5, then declining to levels characteristic of adulthood (25).

Late expression of PPAR α in embryogenesis

The late onset of PPAR α expression (E13.5) in liver, cortex of kidney, intestinal mucosa, pancreas, and heart (this work and Ref. 29) correlates with the progressive differentiation of these organs (30), including the maturation of specific metabolic pathways in which PPAR α has been found to be in-

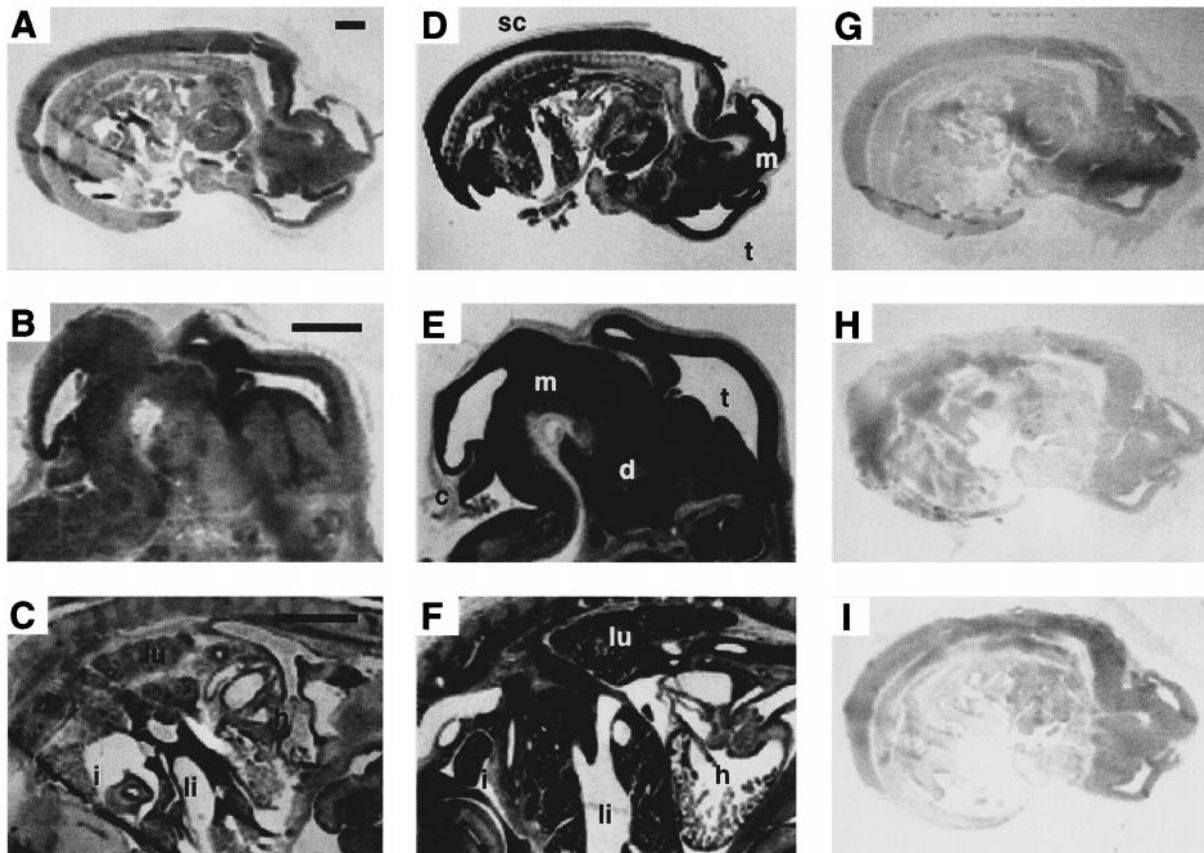


FIG. 2. Expression of PPAR α , PPAR β , and PPAR γ on E15.5 in the developing rat embryo. *In situ* hybridization was performed with antisense probes for PPAR α (A–C), PPAR β (D–F), and PPAR γ (G), and sense probes for PPAR β (I) and PPAR γ (H). Whole embryos of E15.5 (A, D, and G–I; sagittal), and an enlargement of E15.5 brain (B and E; sagittal) and abdominal region (C and F; sagittal) are shown. c, Cerebellum primordium; d, diencephalon; h, heart; i, intestine; li, liver; lu, lung; m, mesencephalon; sc, spinal cord; t, telencephalon. Bars = 1 mm.

volved (see Ref. 1 for a review). Particularly, the expression of PPAR α in the developing liver, kidney, and intestinal mucosa at the starting point of their differentiation makes it possible to regulate, early in histogenesis, the peroxisomal β -oxidation-encoding genes that are expressed in the primordials of these tissues before they differentiate (31). The expression of PPAR α in rat fetal pancreas (E18.5) may indicate its involvement in insulin-secreting β -cells just before they change their metabolism from high fatty acid oxidation toward high glucose oxidation on E19.5 (32). PPAR α knock-out mice develop normally and are fertile, without observable gross defects (33). Thus, either the role(s) of PPAR α in metabolic pathways must be very subtle during embryogenesis, or compensatory events, *e.g.* by the other PPAR isotypes, are responsible for the apparently normal development of PPAR α knock-out mice. PPARs could not be detected in the adult epidermal keratinocytes by the technique used herein (25). In contrast, we show in this study that PPAR α and PPAR β are expressed in the rat embryonic epidermis. In the mouse embryo, PPAR α and PPAR β mRNAs appear even earlier, together with PPAR γ , which we did not observe in the rat (Michalik, L., and W. Wahli, personal communication). The earlier onset of PPAR α and PPAR β in the mouse probably reflects the 2-day advance shift of mouse development compared with that in the rat (30), whereas the difference in PPAR γ expression in embryonic epidermis as well as

liver is illustrative either of differences between species or of the sensitivity of the methods used. However, it indicates that PPARs might be involved in the establishment of the skin lipid barrier, as suggested previously (34), based on a study using a mouse expressing a dominant negative retinoic acid receptor.

Transient expression of PPAR α and PPAR γ in the developing CNS

Interestingly, a transient peak of expression of PPAR α is observed in the whole developing CNS, around the E13.5 stage. The same phenomenon is true for PPAR γ , but is restricted to hindbrain. E13.5 corresponds to the onset of differentiation and apoptosis events in CNS, which would suggest a role for PPAR α and PPAR γ during these processes, but remains to be proven.

Coexpression of PPAR α , - β , and - γ in BAT

White adipose tissue is specialized to store triglycerides and releases fatty acids upon demand, whereas BAT has the additional unique faculty to produce heat. This heat dissipation is made possible by the expression of a specific BAT protein, UCP, which uncouples the fatty acid oxidation from the synthesis of ATP (35, 36). Transgenic mice lacking BAT develop obesity (37), providing evidence for

TABLE 1. Differential expression of PPAR α , PPAR β , and PPAR γ during embryonic development of the rat

	E8.5	E11.5	E13.5	E15.5	E18.5
PPAR α					
Embryonic ectoderm	–				
Visceral endoderm	–				
Parietal endoderm	–				
Forebrain		–	++	+	+/-
Midbrain		–	++	+	+/-
Hindbrain		–	++	+	+/-
Spinal cord		–	++	+	+/-
Spinal ganglia			++	ND	+/-
Epidermis		–	–	+	++
Kidney			ND	+	+
Liver		–	+	+	+++
Pancreas				+/-	+
Heart		–	+	+	–
Vertebrae			+	+/-	–
Squeletic muscle				+	+/-
Brown adipose tissue					++
Lung			ND	+	–
Intestine		–	++	++	++
PPAR β					
Embryonic ectoderm	++				
Visceral endoderm	++				
Parietal endoderm	+				
Forebrain		+	++++	++++	++
Midbrain		+	++++	+++	++
Hindbrain		+	++++	+++	++
Spinal cord		+	++++	+++	++
Spinal ganglia			++++	+++	++
Epidermis		–	+	+	+++
Kidney			ND	++	++
Liver		–	++	+++	+
Pancreas				++	++
Heart		–	+	++	++
Vertebrae			+++	+++	++
Squeletic muscle				++	++
Brown adipose tissue					++++
Lung			ND	+++	+++
Intestine		+	++	+++	+++
PPAR γ					
Embryonic ectoderm	–				
Visceral endoderm	–				
Parietal endoderm	–				
Forebrain		–	+	+/-	–
Midbrain		–	++	+/-	–
Hindbrain		–	+++	+/-	–
Spinal cord		–	++	+/-	–
Spinal ganglia			–	–	–
Epidermis		–	–	–	–
Kidney			ND	–	–
Liver		–	–	–	–
Pancreas				–	–
Heart		–	–	–	–
Vertebrae			–	–	–
Squeletic muscle				–	–
Brown adipose tissue					++++
Lung			ND	–	–
Intestine		–	–	–	–

– or + signs indicate differences in signal intensities observed by optical microscopy and reflect levels of PPAR expression. The number of + signs does not represent a strict linear measure of mRNA levels. –, Absent; +/-, barely detectable; +, weak expression; ++, moderate expression; +++, high expression; +++++, very high expression. ND, Not determined.

an important role of BAT in fatty acid catabolism. Furthermore, the specific expression of UCP in BAT is regulated by PPAR γ (22), which also promotes BAT differen-

tiation at the end of fetal life (28). Our results on PPAR γ expression in embryonic rat BAT underscore and add to these data. Furthermore, we show that the two other iso-types, PPAR α and PPAR β , are concomitantly expressed at high levels with PPAR γ (this work and Ref. 29). This raises the question of the specific role(s) for each of the three receptors for BAT differentiation and functions. Can they all achieve the PPAR γ function in this developing tissue as previously reported (28), or do PPAR α and PPAR β have different specific roles? One would predict that as in adult-hood, PPAR γ is involved primarily in BAT differentiation and fatty acid uptake and storage, whereas PPAR α would regulate BAT fatty acid catabolism. Finally, PPAR β would have a role in basal cellular metabolism, in line with its ubiquitous expression.

Potential roles of PPAR β

PPAR β is expressed ubiquitously, at higher levels dur-ing embryogenesis than in adulthood (this study and Ref. 25). It has been proposed as a repressor of other PPAR isotype activities (38), but its expression levels and pattern during development, compared with those of the α and γ iso-types, argue for a different function. Its ubiquitous expression suggests a specific role in each cell type, from the early embryo to adulthood, possibly under the control of specific ligands. One possibility could be a function in membrane lipid synthesis and turnover. Such a role is compatible with PPAR β expression in giant neurons of the adult brain (25), as these cells are characterized by huge dendritic trees and axons that need high amounts of mem-brane lipids and an efficient rate of membrane turnover both to maintain these structures and to remodel synaptic connections. Another possibility would be a function of PPAR β at the onset of differentiation processes. Indeed, we show that the peak of ubiquitous expression of PPAR β during embryogenesis correlates with that of the period of greatest cell differentiation activity (30), particularly in the CNS (39, 40). One hypothesis would view PPAR β as a sensor for a specific ligand that would induce cell differ-entiation, whereas the absence of ligand would direct the cell toward apoptosis by default, as previously suggested (36). This would be consistent with the PPAR β expression pattern in the adult, where it is found at high levels in tissues with a high rate of cell renewal and differentiation (25).

Conclusion

We have described the expression patterns of the three PPAR isotypes during embryonic development of the rat. PPAR α and PPAR γ appear late in development, in cells where they will be expressed later in adulthood, e.g. liver, intestine, kidney, and pancreas for α , and adipose tissue for γ . Furthermore, an interesting transient peak of expres-sion of α and γ has been noticed in the CNS. The intriguing high coexpression of the three iso-types in the developing BAT and CNS provides opportunities to define their respec-tive roles in these differentiating structures. Furthermore, the very strong ubiquitous PPAR β expression throughout de-velopment argues for a role of this isotype in basic cellular

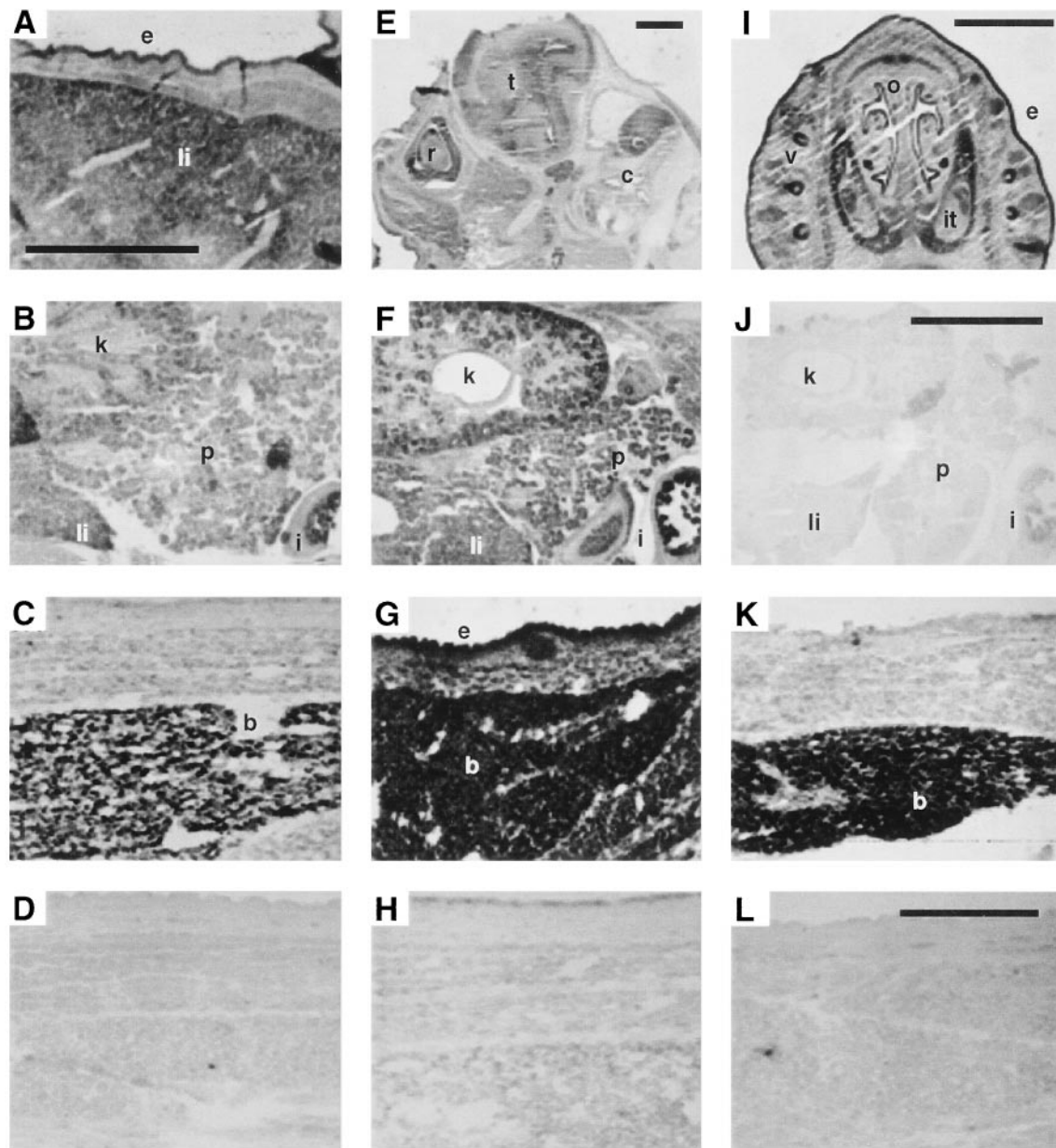


FIG. 3. Expression of PPAR α , PPAR β , and PPAR γ on E18.5 of the developing rat embryo. *In situ* hybridization was performed with antisense probes for PPAR α (A–C), PPAR β (E–G and I), and PPAR γ (J–K), and sense probes for PPAR α (D), PPAR β (H), and PPAR γ (L). Enlargements of E18.5 liver (A and B; sagittal), head (E; sagittal), abdominal region (F and J; sagittal), upper jaw (I; coronal), and BAT (C, D, G, H, K, and L; sagittal) are shown. b, Deposit of BAT; c, cochlea and semicircular canals; e, epidermis; i, intestine; it, primordium of upper incisor tooth; k, kidney; l, liver; o, olfactory epithelium; p, pancreas; r, retina; t, telencephalon; v, follicles of vibrissae. Bars = 1 mm (A, B, E, F, I, and J) and 200 μ m (C, D, G, H, K, and L).

metabolic pathways, such as those involved in membrane synthesis and turnover, and possibly in cell cycle control.

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