Expression of Steroid Sulfatase during Embryogenesis*

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ABSTRACT

Neurosteroids are steroids that are synthesized *de novo* in the brain from cholesterol and, in general, mediate their effects through ion-gated channel receptors such as γ -aminobutyric acid_A (GABA_A) and *N*-methyl-D-aspartate receptors rather than through classical nuclear steroid hormone receptors. Steroid hormones are known to exist not only as free compounds, but also as sulfated derivatives. Pharmacological studies indicate that unconjugated and sulfated steroids, such as pregnenolone and pregnenolone sulfate, may have opposite effects on GABA_A receptors. Thus, pregnenolone acts as a potent positive allosteric modulator of γ -aminobutyric acid action at GABA_A receptors, whereas pregnenolone sulfate acts as a potent negative modulator. Recent experiments also suggest that dehydro-

 \mathbf{C} TEROID sulfatase (STS) is an important enzyme in steroid metabolism because its activity increases the pool of precursors that can be metabolized by other steroidogenic enzymes to produce biologically active sex steroids (1, 2). The human STS gene has been cloned and mapped to Xp22.3 chromosome, proximal to the pseudoautosomal region (PAR), and the genetic aspect of this enzyme has been widely documented (3). A deficiency of STS activity results in severe ichthyosis caused by accumulation of steroid sulfates in the stratum corneum of the skin (4, 5). The main secretory product of the human fetal adrenal is dehydroepiandrosterone (DHEA) sulfate (DHEAS) (6). This steroid is not a substrate for the enzyme 3B-hydroxysteroid dehydrogenase in the adrenal and, therefore, is not metabolized further in the adrenal. DHEAS can be converted to 16α -hydroxy-DHEAS in the liver and other tissues, but it must undergo the sulfatase reaction in the placenta to be metabolized to estriol, the main estrogen of the placenta. Diminished or absent placental sulfatase activity reduces the pool of free DHEA available for placental conversion to estrogen, resulting in prolonged gestation and failure of induction of labor.

Previous studies have demonstrated STS activity in a variety of tissues other than the placenta, including the brain (7), and in virtually all tissues of the rhesus monkey (8), mouse macrophages (9), serum (10), human leukocytes (11), epiandrosterone and dehydroepiandrosterone sulfate may have distinct effects on growth of neurites from embryonic neocortical neurons *in vitro*. Thus, regulation of steroid sulfation may have profound behavioral and morphological effects on the nervous system. We, therefore, studied the developmental expression of the enzyme steroid sulfatase (STS), which converts sulfated steroids to free steroids. By *in situ* hybridization, STS messenger RNA was expressed in the embryonic mouse cortex, hindbrain, and thalamus during the last third of gestation. The sites of expression of STS were similar to those of P450c17, suggesting that these two enzymes may have concerted actions in similar functional processes. (*Endocrinology* **138:** 4768– 4773, 1997)

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and testes (12). In general, high levels of STS activity have been found in tissues in which the biological activity of DHEA or its metabolites regulates cellular function.

We demonstrated that P450c17, the enzyme necessary for the synthesis of DHEA from pregnenolone, is transiently expressed in the neocortical subplate during embryogenesis (13). Furthermore, we recently demonstrated that DHEA and DHEAS affect the development of embryonic neocortical neurons in vitro (14). We further showed that these two steroids have different biological effects. Thus, regulation of the interconversion of these two steroids may play an important role in the development of the nervous system in vivo. We, therefore, studied the expression of STS in the developing rodent to characterize the distribution of this enzyme and thus determine the areas in the brain where sulfate hydrolysis may regulate neurosteroid activity. The rat and mouse STS have recently been cloned (15, 16), and we generated riboprobes from the mouse STS complementary DNA (cDNA) to study the expression of this enzyme by in situ hybridization. This report shows distribution of mouse STS during late embryogenesis. Our results show that the cortex, the hindbrain, and, interestingly, the thalamus, which is involved in supporting cortical differentiation during development (17), are sites in the central nervous system where STS is expressed during the last third of gestation. The sites of expression of STS are similar to those of P450c17, suggesting that these two enzymes may have concerted actions in similar functional processes.

Materials and Methods

Animals

Fresh frozen mouse embryos were obtained from BALB/c mice. The mating day (positive plug test) was referred to as embryonic day 0.5

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(E0.5). Embryos were removed from the mother's uterus under anesthesia, dissected from the implantation site when possible (from E11.5), and quickly frozen in dry ice/2-methylbutane (isopentane). Frozen 8- μ m sections were made on a cryostat.

Ribonuclease (RNase) protection assays

Mouse steroid sulfohydrolase (mSTS) cDNA fragments were subcloned into pSKII⁺ (Stratagene, La Jolla, CA) for the synthesis of RNA probes. A 447-bp HindIII/BamHI fragment of mouse STS cDNA (nucleotides 1289–1736) was used to prepare a 507-base mSTS probe. RNA was extracted from tissues using a Trizol messenger RNA (mRNA) extraction kit (Life Technologies, Grand Island, NY), and analyzed by RNase protection assays. Total RNA was analyzed from the following sources: E18.5 central nervous system tissues and E18.5 intestine (200 μ g), E18.5 lung (150 μ g), E18.5 skin (60 μ g), and adult mouse cortex (160 μ g). RNA was combined with 0.5 \times 10⁶ cpm ³²P-labeled riboprobe; precipitated with ethanol; resuspended in 80% formamide, 400 mM piperazine-N-N'-bis[ethanesulfonic acid] (pH 6.4), and 1 mм EDTA; boiled for 5 min; and incubated overnight at 42 C. Samples were diluted 10-fold with 10 mм Tris-HCl (pH 7.9), 300 mм NaCl, and 5 mм EDTA; treated with RNase A (30 μ g/ml); incubated for 30 min at 37 C; treated with 0.25 μ g/ml proteinase K and 0.5% SDS for an additional 15 min at 37 C; extracted once with phenol/chloroform; and precipitated with ethanol. Protected ³²P-labeled fragments were separated by electrophoresis on 6% polyacrylamide-7.5 M urea gels.

In situ hybridization

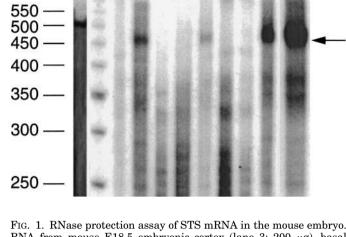
Mouse STS cDNA has 63% nucleotide identity with human STS and 75% nucleotide identity with rat STS (16). Furthermore, mouse STS does not share homology with other sulfatases, such as iduronate sulfate (mouse) and chondroitin sulfate (goat), because these sequences only have 36% nucleotide identity with the mSTS. A 447-bp HindIII-BamHI (nucleotides 1289–1736) cDNA fragment of mSTS cDNA was subcloned into PSKII (Stratagene) for 35 S-labeled sense and antisense RNA probe synthesis. In situ hybridization was performed as previously described (18). Briefly, slides were fixed in 4% paraformaldehyde in PBS for 20 min at room temperature, and sections were treated with $1 \mu g/ml$ proteinase K in 100 mM Tris-HCl, pH 8, containing 50 mM EDTA and acetylated with acetic anhydride in 0.1 M triethanolamine buffer for 10 min at room temperature. Slides were hybridized overnight at 52 C with 106 cpm probe in buffer containing 50% formamide, $5 \times SSC (1 \times SSC = 0.15 \text{ M})$ NaCl and 0.015 M sodium citrate), 10 mM β-mercaptoethanol, 10% dextran sulfate, 2 × Denhardt's solution (0.02% polyvinylpyrrolidone, 0.02% Ficoll, and 0.02% BSA), 250 μ g/ml yeast transfer RNA, and 500 μ g/ml salmon sperm DNA. Nonhybridized probe was washed from the slides with 2 \times SSC containing 10 mM β -mercaptoethanol for 30 min at room temperature. Sections were then treated with 20 μ g/ml RNase A at room temperature for 40 min, followed by two washes for 30 min each time at 55 C in 50% formamide-2 \times SSC containing 1 mM EDTA and 10 mm β -mercaptoethanol and a wash for 2 min at room temperature in $0.2 \times$ SCC. Slides were dipped in Ilford K5 nuclear emulsion (Warrington, PA), dried, and stored at 4 C until developed.

Results

RNase protection assay

STS mRNA was initially assayed using RNase protection assays. Due to the apparent low abundance of this mRNA in the developing embryo, it was necessary to use large quantities of RNA to detect STS mRNA in developing mouse brain regions (Fig. 1). On E18.5, we detected mSTS mRNA expression in the cortex and hindbrain, but we did not detect this mRNA in the basal ganglia or diencephalon of the mouse embryo. Using reverse transcription-PCR, we detected mSTS mRNA in the mouse diencephalon (not shown), suggesting that this mRNA was expressed at extremely low levels in this region.

We also studied the expression of mSTS mRNA in several



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FIG. 1. RNASE protection assay of S1S mRNA in the mouse embryo. RNA from mouse E18.5 embryonic cortex (lane 3; 200 μ g), basal ganglia (lane 4; 200 μ g), diencephalon (lane 5; 200 μ g), hindbrain (lane 6; 200 μ g), intestine (lane 7; 200 μ g), lung (lane 8; 150 μ g), and skin (lane 9; 60 μ g) as well as mouse adult cortex (lane 10; 150 μ g) or transfer RNA alone (lane 2; 200 μ g) was combined with 0.5 × 10⁶ cpm ³²P-labeled mSTS complementary RNA probe (lane P), hybridized overnight, digested with RNase A, and separated on 6% acrylamide-7.5 M urea sequencing gels. Gels were exposed overnight. Lane 10 is from a shorter exposure (4 h) from an adjacent lane on the same gel. Mol wt markers (lane 1) are ³²P-labeled 50-bp DNA ladder fragments (Life Technologies), and their sizes are indicated on the *left* of the autoradiogram.

other tissues reported to have STS activity in the adult rhesus monkey (8). Expression of mSTS mRNA was detected in E18.5 intestine, but was not detected in E18.5 lung. STS mRNA was also not detected in skin.

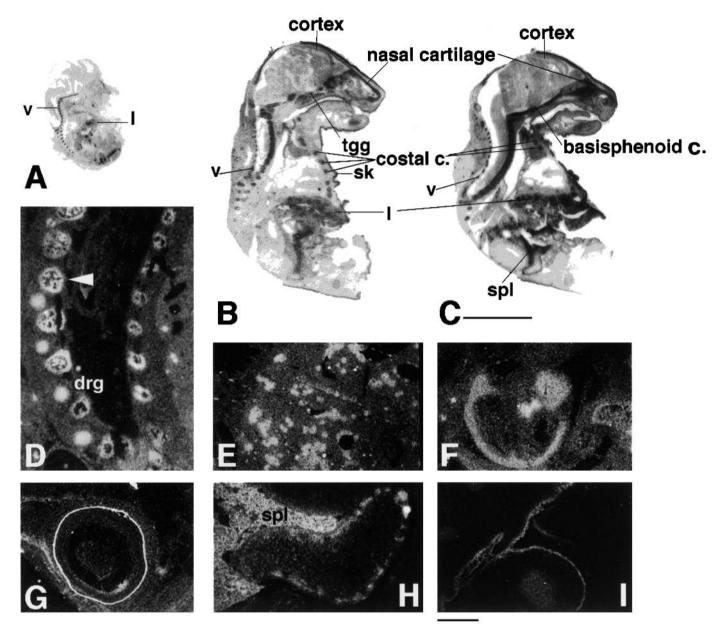
In the adult rat, we detected STS mRNA in the cortex (using 160 μ g total RNA). As the signal in the cortex was robust, we used less RNA from other regions of the adult brain (thalamus, hypothalamus, hindbrain, and cerebellum; 25–90 μ g) and detected no STS mRNA in these regions.

In situ hybridization

We detected STS mRNA in cartilage primordia and in the liver on E14.5 (Fig. 2A). In the liver, STS mRNA was observed in restricted areas (Fig. 2E). In cartilage, expression of mSTS mRNA was first observed at the base of the skull and in the cartilage of the ribs and vertebrae (E14.5). Later in ontogeny (E16.5–E18.5), expression of mSTS mRNA was observed in the cartilage of the temporal and occipital regions of the head as well as in the facial region, the eye, and the ear (Fig. 2, B, C, F, and G). Figure 2D shows a higher magnification of the vertebral cartilage of the rib.

Later in ontogeny (E16.5), the strongest signal was observed in the spleen and the inner epithelial layer of the intestine (Fig. 2H). As expected, mSTS mRNA was strongly expressed in the skin of E16.5 embryos (Fig. 2I).

In the central nervous system, a hybridization signal was first observed on E16.5. At this time, STS mRNA was found in the thalamus (Fig. 3C). By E18.5, STS mRNA was found in the cortex, hippocampus, thalamus, cerebellum, and spinal cord (not shown), and expression in these regions persisted 9 days after birth (Fig. 3B). Expression of STS mRNA in the



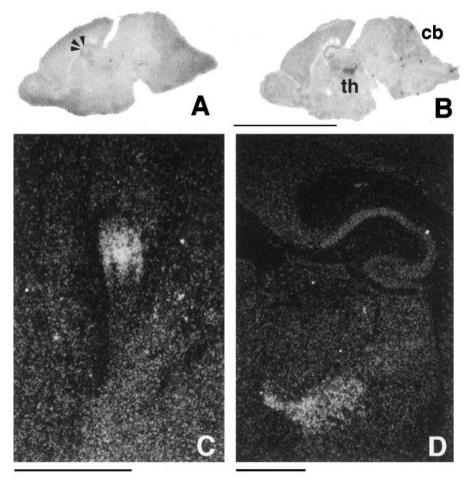
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FIG. 2. In situ hybridization of STS mRNA in the mouse embryo. A–C, Autoradiogram of an *in situ* hybridization for mSTS mRNA in E14.5 mouse embryo (A) and E18.5 mouse embryo (B and C). A, Hybridization signal is observed in cartilage primordium in the skull and vertebrae (v). In the liver (1), a strong hybridization signal is localized in restricted areas. B and C, In E18.5 embryos, the hybridization signal was also observed in vertebrae (v) and liver (1) as well as in the trigeminal ganglia (tgg), skin (sk), spleen (spl), nasal cartilage, basisphenoid cartilage (basisphenoid c.), costal cartilage (costal c.), and cortex. D–I, Darkfield microscopy of E16 embryo sections after *in situ* hybridization for mSTS mRNA. D, Strong staining is observed in vertebral earliage (*arrow*) as well as in dorsal root ganglia (drg). E, In the liver the hybridization signal is not evenly distributed. Note the presence of strong signals around blood vessels. F, Cochlea; staining of the ear cartilage and of the spiral ganglia. G, Signal in the eye cartilage and retina. H, Spleen (spl) and outer membrane of the intestine. I, Skin at the level of the paw. A–C are at the same magnification. The *bar* in C represents 1 cm. D–I are at the same magnification. The *bar* in I represents 1 mm.

cortex and cerebellum was diffuse, suggesting that mSTS mRNA may be expressed in cells not restricted to anatomical nuclei. By contrast, expression of mSTS mRNA in the thalamus was highly selective and was found in a small number of cells whose distribution suggested that its expression was restricted to a particular anatomical domain of the anterior thalamus (Fig. 3D). Hybridization signals for mSTS mRNA persisted in 9-day-old neonatal mouse brains (Fig. 3, B and D) in the (subicular area) CA1 region of the hippocampus and in the anterior thalamus.

From E16.5–E18.5, mSTS mRNA was also expressed in the peripheral nervous system. A signal less intense than that in the thalamus was observed in cranial ganglia (trigeminal ganglia and spiral ganglia; Fig. 2F) and in dorsal root ganglia (Fig. 2D) as well as in the inner neural layer of the retina (Fig. 2G).

FIG. 3. In situ hybridization of STS mRNA in the thalamus. Autoradiogram (A and B) and darkfield microscopy (C and D) of mSTS in situ hybridization in 9-day-old (P9; A, B, and D) and E16.5 (C) thalamus. A, Nonspecific hybridization signal observed after annealing reactions with the sense mSTS probe. Some nonspecific binding is observed in hippocampus (arrowheads). B, Sister section after hybridization with the antisense mSTS probe; a strong signal is observed in the thalamus (th) and the subicular region (CA1) of the hippocampus, and a less intense signal is seen in the cerebellum (cb). In the subicular area of the hippocampus, the density of silver grains with the antisense probe (B) is greater than that with the sense probe (A). C, Hybridization signal in the thalamus is first observed on E16.5. D. Darkfield microscopy and higher magnification of the thalamic staining in the neonate (P9). The signal is mainly located in the anterior thalamus. A and B are at the same magnification; the bar in B represents 7 mm. The bars in C and D represent 1 mm.



To ensure the specificity of the hybridization signal, we performed *in situ* hybridizations on sister sections of postnatal day 9 mice brains using a sense RNA probe (Fig. 3A). The sense probe did not show any hybridization signal in the thalamus. There was a weak signal in the dentate gyrus and in Ammon's horn, which probably represents nonspecific RNA binding, but no signal was observed in the subicular area, suggesting that the hybridization signals observed using the STS antisense RNA probe were specific.

Discussion

Sulfated steroids are ubiquitously distributed compounds with many putative biological functions (reviewed in Ref. 3). Sulfated forms of 3β -hydroxysteroids (such as dehydroepiandrosterone) have been thought to be inert forms of more active hormones that are released by the action of STS. Our results show a restricted expression of STS mRNA during mouse embryonic development. The sites of STS expression provide more precise indications of the target tissues in which active, nonsulfated steroid hormones resulting from STS activity may act during embryogenesis. Our results are also consistent the demonstration of STS activity in various tissues of the adult rhesus monkey that have been suggested to be able to form biologically active androgens and estrogens (8).

In addition to the known roles of STS in the placenta and

skin, our results emphasize other possible roles for STS in the function of other organs during embryogenesis. In the liver the signal is clustered in restricted areas resembling blood islands, suggesting that STS may be active in the hematopoiesis signaling processes. Spleen expression of mSTS is very high, and this strongly suggests a role for mSTS in lymphocyte production. Sulfatase activity, recently found in endothelial cells and monocytes, has been shown to be an important regulator of the inflammatory response, as the efficiency of this response relies on the ability of leukocytes, platelets, and/or endothelial cells to degrade the subendothelial basement membrane, which is considered to be an important barrier to the entry of leukocytes into inflammatory sites (19). Sulfatase activity in endothelial cells, but not in monocytes, could be induced by tumor necrosis factor, interleukin-1, and interleukin-8 (19).

Expression of STS mRNA in the developing cartilage early during embryogenesis coincides with the appearance of ossification centers (E14–E14.5), suggesting that this enzyme may participate in the differentiation of the skeletal system. Consistent with our observation of mSTS mRNA expression in developing ossification centers, STS may continue to play an important role in the maintenance of bones throughout life. The conversion of estrone sulfate to estradiol plays an important role in modulating bone turnover. Estrone sulfatase activity was detected in the MG63 human osteoblast cell line (20), suggesting that development of osteoporosis in postmenopausal women may be due to a reduction in the activity of the enzymes responsible for local estrogen production.

Expression of mSTS mRNA in the skin only appeared on E16.5, concomitant with the formation of the multilayered structure of the epidermis and with a peak in expression of cholesterol sulfatase, another sulfatase involved in epidermal differentiation (21).

In the central and peripheral nervous systems, the expression of mSTS mRNA may be related to the expression of steroidogenic enzymes involved in neurosteroid synthesis. We have previously shown the expression of P450c17 in restricted areas of the developing nervous system (13), particularly in the neocortex, and demonstrated a role for both DHEA and DHEAS in neocortical neuron differentiation. Although DHEA promotes axonal growth, DHEAS promotes dendrite growth and cell clustering (14). The expression of STS in the neocortex, hippocampus, and thalamus may regulate the ratio of DHEA/DHEAS. Furthermore, as the thalamus has been shown to influence the survival of the cortical subplate (17), where we detected P450c17-expressing neurons, the ratio of these two steroids may play crucial roles in controlling axonal vs. dendritic growth of cortico-thalamic fibers during neocortex organization. The afferent and efferent connections of the cerebral neocortex develop simultaneously toward the end of embryogenesis. At this stage, the neocortex comprises two main cell-dense layers: the thicker and more superficial cortical plate (future layers 2-6) and the thinner underlying subplate. Many early thalamocortical projections temporarily innervate the subplate before leaving it to locate their ultimate targets in the overlying cortical plate. The subplate then disappears. In addition, subplate neurons have been shown to prime thalamic connections in the cortex (22, 23). Hence, we propose that thalamic conversion of DHEA to DHEAS in the thalamus may be a regulatory mechanism controlling axonal growth of thalamic fibers during neocortex cytoarchitectural organization. Furthermore, as DHEA has been shown to modulate GABA_A and N-methyl-D-aspartate receptor activities (24–29), STS activity in the thalamus might be considered a regulatory process of the thalamic neurosecretion.

STS expression most likely persists beyond embryonic development into adulthood. In earlier studies assaying STS activity, investigators detected abundant quantities of STS activity in the central nuclei of the thalamus of two adult males, aged 44 and 63 yr, who died of lymphatic leukemia and pulmonary embolus, respectively (30). The thalamus had the greatest amount of STS activity, which was about twice as much activity as any other region per g tissue. The hippocampus and hypothalamus had lesser, but still substantial, amounts of activity. Many other regions of the brain contained less activity. Thus, the thalamus may continue to be a central region for coordinating the relative abundance of sulfated and free steroids in the brain throughout life.

In addition to possible roles in axonal and dendritic growth during embryogenesis, others have proposed a role for DHEAS in memory in adult humans and rodents (31–35). Chemical inhibition of STS activity *in vivo* was associated with changes in memory in adult rats (31, 36). Thus, regu-

lation of STS activity in the thalamus and hippocampus may have implications for learning and/or memory enhancement throughout life.

The distribution of STS mRNA in other regions of the central and peripheral nervous systems is compatible with a concerted action of both STS and P450c17 in similar processes during embryogenesis. The concept of functional regulation of some neurosteroids by their sulfation or sulfate hydrolysis, suggested by our previous data (14) and others (reviewed in Ref. 37) is thus supported by the localization and ontogeny of mSTS mRNA.

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