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1997年度日中医学協力事業助成報告書

-在留中国人研究者研究助成-

98年3月24日

財団法人 日中医学協会

理事長 中島章殿

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II. 過去の研究歴

1992.4-1996.3 名古屋大学医学研究科 大学院 卒業

1996.4-1997.3 国立小児病院小児医療研究センター HS研究員

III. 過去の研究実績

1). Hang Li, et al. "Intranuclear localization of a multifunctional protein, collagenase inhibitor in proliferating human fibroblasts in culture" Acta Anat Nippon. Vol.69, No.4, 508.1994.

2). Hang Li, et al. "Cell cycle-dependent localization of tissue inhibitor of metalloproteinases-1 immunoreactivity in cultured human gingival fibroblasts" Nagoya Journal of Medical Science. Vol.58, No.3, 1995.

3) Hang Li "Depletion of Gelatinolytic Activity in Dental Pulp in Response to the Administration of Lead in Mice" Aichi-Gakuin Dent Sci. No.9, 1-4.1996.

IV. 本年度の研究業績

(1) 学会、研究会等における口頭発表 (学会名・内容)

第71回日本薬理学会年会

Characterization of the genomic regions regulating expression of mouse aldose reductase gene.

第41回日本糖尿病学会年会

マウスアルドース還元酵素の遺伝子構造と遺伝子発現調節領域の解析 (予定)

(2) 学会誌等に発表した論文 無 ・ (有) (雑誌名・論文名)

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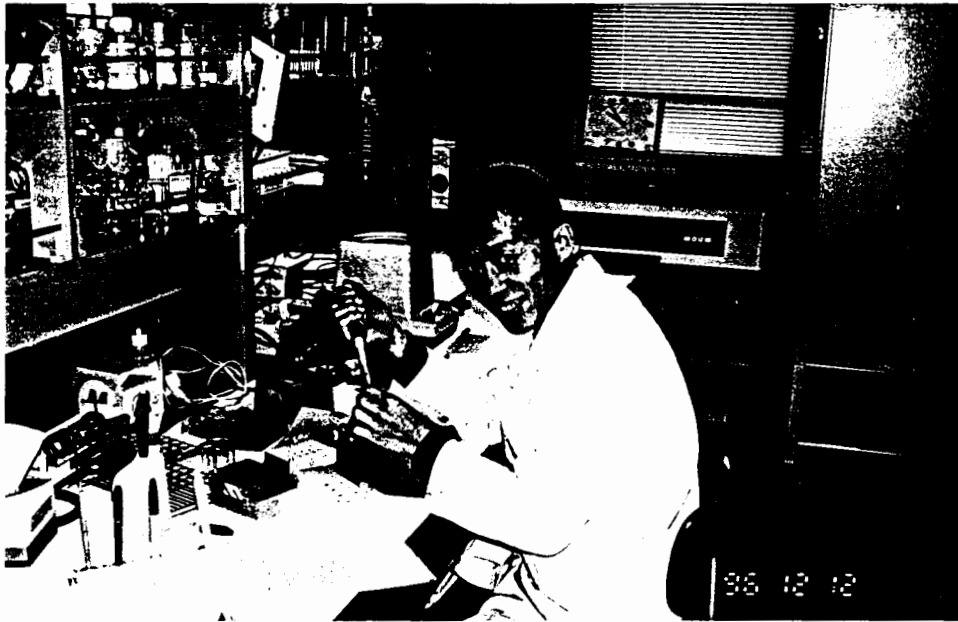
Characterization of the genomic regions regulating expression of mouse aldose reductase gene.

V. 今後の研究計画及び希望

なるべく早くこの研究テーマ(マウスアルドース還元酵素の遺伝子構造と遺伝子発現調節領域の解析)を完成する。

VI. 研 究 報 告 (日本語、又は英語で書いて下さい。4,000字以上で記載して下さい。別紙可)

別紙



VII. 指導教官の意見

李博士は貴財団の助成のもとに15 Kb にわたるマウス Aldose Reductase 遺伝子の構造と遺伝子上流領域の塩基配列を決定し、さらに最新の分子生物学的・細胞生物的手法を用いて本酵素の発現調節領域の解析に着手することが出来ました。

彼は次々と新しい実験技術を習得し、きわめて勤勉に実験を進め、今年度の教室の研究の発展に大きく貢献してくれました。この1年間、貴財団からの助成を受けて李博士が研究に専念できたことを指導教官として深く感謝している次第です。

矢部 千尋

## マウスアルドース還元酵素の遺伝子構造と遺伝子発現調節領域の解析

アルドース還元酵素は NADPH を補酵素とするアルド・ケト還元酵素の一員であり、グルコースをソルビトールに変換する酵素である。この酵素はソルビトールをフルクトースに変換するソルビトール脱水素酵素とともにグルコース代謝の副経路であるポリオールを形成している。

糖尿病合併症の発症に関わるアルドース還元酵素は、高浸透圧負荷により遺伝子上流領域に位置する osmotic response element を介して発現上昇をきたし、腎髄質の浸透圧調節物質の一つであるソルビトールを産生すると考えられている。しかし腎以外の組織における Aldose Reductase の生理的意義は未だ明らかではなく、長期の Aldose Reductase 阻害剤投与による副作用は予測出来ない。そこで我々は遺伝子改変マウスを用いて本酵素の生理的役割の全貌を解明するべく、今回はマウスアルドースリダクターゼの遺伝子構造とその生理的条件下での発現調節領域について解析を進めた。

まず Mouse Aldose Reductase の cDNA を probe としてラムダファージマウスゲノムライブラリーをスクリーニングし、3個のオーバーラップしたクローンを得た。制限酵素地図並びにエクソン-イントロン構造とその接合部の塩基配列を決定した。続いて Aldose Reductase の遺伝子上流領域約 3.4 kb をルシフェラーゼレポータープラスミドに挿入し、プロモーター領域の serial deletion mutant を作製すると同時に遺伝子上流領域の塩基配列を決定した。これらのキメラプラスミドを NIH3T3、CV1、CHO の各細胞株にリン酸カルシウム法にて遺伝子導入後、ルシフェラーゼ活性を測定することにより転写活性に重要な領域を同定した。

Aldose Reductase の発現量はマウスの各組織間において、また各種の培養細胞株において大きく異なることがわかった。即ち Aldose Reductase はほとんどすべての組織(座骨神経、網膜、水晶体、卵巣、睾丸輸精管、脳、腎臓、肝、骨格筋)に発現していたが、その発現量は各組織において大きく異なっていた。また異なった組織由来の培養細胞株 NIH3T3, Y1, NG108, L6, CHO, Hela, MG63, NEC8, CV1) での発現量にも大きな違いがあることがわかった。Mouse Aldose Reductase 遺伝子は全長約 15 Kb で、10コの Exon よりなり、Exon 1 と Exon 2 の間は約 4.3 Kb であったが、Exon 2 から Exon 8 までは 3.6 Kb の間に局在していた。また Mouse Aldose Reductase プロモーターは、TATA box と二つの CCAAT box を持つことが確認され、上流約 1.1Kb に Osmotic Response Element と呼ばれる領域と AP1 結合コンセンサス配列があった。

トランスフェクションアッセイの結果、NIH3T3 細胞において転写活性が大きく変わる二つの領域を認めた。一つは上流約 -1.1 kb から -0.85 Kb の領域で、この領域には、これまでに報告された TonE という Osmotic Response Element が存在し、もう一つは -0.6 Kb から -0.24 Kb の領域で、この領域をけずることにより転写活性は 2.0 倍低下することが分

かった。一方 CHO 細胞においては、-0.6 Kb から-0.24 Kb の領域を除くと NIH3T3 細胞同様に、転写活性は 3.5 倍低下したが、-1.1 kb から -0.85 Kb の領域をけずってもプロモーター活性に大きな違いは認められなかった。

本年度得られた結果をまとめると、

1. Mouse Aldose Reductase 遺伝子は全長約 15 Kb の大きさと、10コの Exon よりなる。
2. Mouse Aldose Reductase の発現量は各組織間において、また各種の培養細胞間において大きく異なる。
3. Mouse Aldose Reductase のプロモーター領域には TATA box と二つの CCAAT box が存在し、Aldose Reductase プロモーター活性は転写開始点より上流約 1.1 kb を含むフラグメントでほぼ最大活性を示す。
4. NIH3T3 細胞において転写活性が大きく変わる二つの領域がある。一つは上流約 -1.1 kb から -0.85 Kb の領域で、この領域には、Aldose Reductase 発現の浸透圧調節にかかわる Osmotic Response Element が存在する。もう一つは -0.6 Kb から -0.24 Kb の領域で、この領域をけずることにより転写活性は 2.0 倍低下する。
5. CHO 細胞においては、-0.6 Kb から -0.24 Kb の領域を除くと NIH3T3 細胞同様に、転写活性は 3.5 倍低下するが、-1.1 kb から -0.85 Kb の領域をけずってもプロモーター活性に大きな違いは認められない。-1.1 kb から -0.85 Kb の領域が、各組織あるいは培養細胞間における Aldose Reductase の発現量の違いにどのような役割を果たしているかについて、今後更に検討する予定である。

以上、貴財団の奨学金により私の研究を一年間ご援助頂きまして、心より感謝致します。

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1997年度日中医学協力事業助成報告書

- 在留中国人研究者研究助成 -

10年3月12日

財団法人 日中医学協会

理事長 中島章殿

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II. 過去の研究歴  
肝線維症と関係ある遺伝子の解析  
C型肝炎に関する母子感染及び治療診断

III. 過去の研究実績  
肝線維症で遺伝子発現の上昇するものとして転写因子と翻訳調節因子の両者からクローニングされたものを解析して Grb1R と TAF112 を解析してやる。

IV. 本年度の研究業績  
 (1) 学会、研究会等における口頭発表 (学会名・内容)  
 ① 日本神経科学学会 赤松第一ラット胎期におけるミオサイト-ルトランスポーターの遺伝子発現  
 ② 日本解剖学会 口演: ラット結腸におけるミオサイト-ルトランスポーター (SM2P) の高浸透圧負荷による発現変化。 ③ 口演: 浸透圧応答性の新規 RNA helicase の cDNA の単離と高浸透圧

(2) 学会誌等に発表した論文 無 (有) (雑誌名・論文名) 発荷時の発現調節機構の解析  
MOLECULAR BRAIN RESEARCH  
Developmental regulation of Na<sup>+</sup>/myo-inositol cotransporter gene expression

V. 今後の研究計画及び希望  
新規 RNA helicase の機能解析を継続して研究 (cDNA) と関係する。

VI. 研 究 報 告 (日本語、又は英語で書いて下さい。 4,000字以上で記載して下さい。別紙可)

別紙



VII. 指導教官の意見

郭薇氏は短期間で留学生という言語や生活体系の違いも克服し、多くの難しい実験手法を習得し、さらに自主的な考えで研究を発展させ、それらの研究成果を、国際誌や学会を通して発表し、教室に多大な貢献をしてくれました。現在も我々の研究室の主要な研究プロジェクトの中心人物として研究を引っ張っております。申請者の研究に対する厳しい姿勢と最後までやり抜く態度には、常々感心しております。また一方では、性格は温厚で明るく、素直で、後輩の面倒見も良く、研究室の皆に慕われております。

袁山正彌 (印)

論文:

1. **Guo, W.**, Shimada, S., Tajiri, H., Yamauchi, A., Yamashita, T., Okada, S., Tohyama, M. Developmental regulation of Na<sup>+</sup>/myo-inositol cotransporter gene expression  
Mol Brain Res 51(1997) 91-96
2. Yamashita, T., Shimada, S., Yamaguchi, A., **Guo, W.**, Kohmura, E., Hayakawa, T., and Tohyama, M. Induction of Na<sup>+</sup>/myo-inositol cotransporter mRNA after rat cryogenic injury.  
Mol Brain Res 56(1997) 128-134
3. Yamashita, T., Shimada, S., **Guo, W.**, Kohmura, E., Hayakawa, T., Takagi, T. and Tohyama, M. Cloning and functional expression of a brain peptide/histidine transporter.  
J Biol Chem 272, 10205-10211, 1997.
4. Tada, K., Tajiri, H., Kozaiwa, K., Sawada, A., **Guo, W.**, and Okada, S. Role of screen for hepatitis C virus in children with malignant disease and who undergo bone marrow transplantation  
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5. Etani, Y., **Guo, W.**, Tajiri, H., Okada, S., Shimada, S., Tohyama, M. Analysis of glucose transporter gene in a case of fructose malabsorption with chronic Diarrhea  
Digestion & Absorption 1995, 18, 40-4( Japanese)
6. Tada, K., Tajiri, H., Sawada, A., **Guo, W.**, Etani, Y., Kozaiwa, K., Ozaki, Y., Okada, S. HCV Infection in Children with Primary Malignant Diseases  
The Journal of the Japan Pediatric Society (Japanese)
7. **Guo, W.**, Shimada, S., Mushiage, S., Tajiri, H., Yamauchi, A., Yamashita, T., Okada, S., Tohyama, M.  
Differential localization and induction of Na<sup>+</sup>/myo-inositol cotransporter mRNA in the large intestine.  
投稿中
8. **Guo, W.**, Shimada, S., Yamashita, T., Yamauchi, A., Okada, S., Tohyama, M.  
Purification and Characterization of a new member of DEAD box of RNA helicase  
投稿中

## 研究報告書

私は小児の消化器系の疾患に興味を持ち、最初に、肝線維症で同一患者の正常な肝組織と線維症の起こっている肝組織の間で differential display 法を用いることにより、プロトオンコジーンのRETと結合するGrb10と、RNA結合蛋白であるiron-responsive element-binding protein (IRE-BP)が肝線維症で遺伝子発現が上昇していることを明らかにした。肝線維症で遺伝子発現の上昇するものとして転写調節因子と翻訳調節因子の両者がクローニングされたのは興味深い。この二つの遺伝子については症例を増やし、肝線維症との関係を検討中である。このようなヒトの剖検組織を用いた疾患関連遺伝子の検索を進める一方、基礎的な研究として、消化管での浸透圧変化に対する細胞保護機構を解析している。グリセロール注腸動物や脱水モデル動物を用いて、大腸の吸収上皮細胞や杯細胞でミオイノシトールトランスポーターのmRNAが管腔内の浸透圧が上昇した際や、血清浸透圧が上昇した際に顕著に上昇することを明らかにし、大腸の上皮細胞が細胞外の浸透圧変化から細胞を保護するためにミオイノシトールの取り込みを増加させていることを示した。さらに、ミオイノシトールトランスポーターの発達段階での遺伝子発現及び蛋白発現の変化を解析し、中枢神経系で胎生期に一過性の非常に強い発現が神経系に認められることを明かとした。最近、Differential Display法により浸透圧調整に関係する新規のRNAhelicaseのcDNAを単離して、現在その機能解析を行っています。

消化管は管腔内に様々な摂取物、水分、分泌液が存在し、これらの濃度や量が吸収や分泌によって複雑に調整されている。このことは消化管上皮が絶えず浸透圧の変化に曝されていることを意味する。さらに大腸上皮では浸透圧勾配を利用し、水分の吸収を行うために、この部位の細胞には極端に高い浸透圧負荷が、常時かかっている。またこれらの浸透圧変化及び調節に異常を来すと下痢等の様々な消化器症状を来す。細胞外の浸透圧変化は細胞内の体積や電解質組成に、大きな影響を与えるため、浸透圧変化から細胞を保護する機構が存在すると考えられる。このような浸透圧変化からの細胞保護機構の研究は主に腎臓で行われてきた。浸透圧物質（オスモライト）のトラ



ンスポーターは細胞外の高浸透圧に対抗して、オスモライトを細胞内に蓄積することによって、細胞内外の浸透圧バランスを保つという有効浸透圧作用と、同時に細胞内の蛋白質や核酸の高次構造が高浸透圧により変化するのを防ぐ細胞機能保護作用を示すと考えられている。私どものグループはオスモライトトランスポーターの発現調節について、多くの解析を進めてきた。しかし、浸透圧の変化する刺激からオスモライトトランスポーターの発現誘導までの経路はほとんど明らかにされていない。そこで本研究では大腸上皮由来のCaco-2細胞を用いて、Differential Display法によって、浸透圧負荷時に必要となる新規の遺伝子を解析する。

消化器系において高浸透圧刺激からオスモライトのトランスポーターの遺伝子発現誘導がおこるまでの経路に関与している遺伝子を検討するため、CACO-2培養細胞を、高張、等張、低張の培養液下で、培養しmRNA抽出後、differential display法を用いて浸透圧負荷時に新たに発現する遺伝子を同定する。これらのin vitro系を用いてdifferential display法で得られた浸透圧応答候補遺伝子を、ノーザンプロット解析により実際にCACO-2培養細胞で浸透圧負荷時に、発現誘導がかかるかどうかスクリーニングする。浸透圧負荷時に発現が上昇する遺伝子については、蛍光プライマー法を用いて塩基配列を決定する。その中で新規遺伝子についてはそのcDNAの全長を獲得するために、高浸透圧下で培養したCACO-2細胞から、cDNAライブラリーを作製し、スクリーニングする。このスクリーニングでも全長が得られない場合は、5'や3'race法を用いてcDNAを延長する。

これらの浸透圧応答遺伝子は、その相同性から機能が推測できるものに関しては、cDNAを適切な発現ベクターに組み替えて、HEK細胞発現系やアフリカツメガエル卵母細胞発現系を用いて適切な解析を行い、浸透圧変化時におけるこの遺伝子の役割を検討する。また大腸菌の発現系を用いて、浸透圧応答遺伝子の蛋白を単離し、抗体を作製し、結合蛋白を作製しました。

これらの機能解析により浸透圧応答遺伝子の特性を明らかにするとともに、in

vivoでの浸透圧負荷モデル、虚血、浮腫等の動物モデルを用いてその発現調節を解析する。さらにCACO-2細胞を用いて、antisense法により、浸透圧負荷時にこれらの浸透圧遺伝子の発現が抑制されると°Cのような細胞傷害が起こるか検討する。

最近、私はこの実験計画をスタートし、Differential Display法の系から、浸透圧負荷により遺伝子発現が上昇するRNAhelicase遺伝子ファミリーに属する新しい遺伝子を単離しました。現在大腸菌BL21細胞を用いて、融合蛋白を合成し、2本鎖のDNAやRNAのhelicase活性があるかどうか検討中です。

郭 敬

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# MOLECULAR BRAIN RESEARCH

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Molecular Brain Research 51 (1997) 91–96

Research report

## Developmental regulation of Na<sup>+</sup>/*myo*-inositol cotransporter gene expression

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# BRAIN RESEARCH

## SCOPE AND PURPOSE

**MOLECULAR BRAIN RESEARCH** is a special section of **Brain Research** which provides a medium for prompt publication of studies on molecular mechanisms of neuronal, synaptic and related processes that underlie the structure and function of the brain. Emphasis is placed on the molecular biology of fundamental neural operations relevant to the integrative of the nervous system.

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Research report

## Developmental regulation of Na<sup>+</sup>/*myo*-inositol cotransporter gene expression

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### Abstract

*myo*-Inositol plays a role in many important aspects of cellular regulation including membrane structure, signal transduction and osmoregulation. It is taken up into the cells by the Na<sup>+</sup>/*myo*-inositol cotransporter (SMIT). We investigated developmental changes in the expression of SMIT mRNA and protein in the rat. In the fetal rat brain, SMIT mRNA was abundantly and diffusely expressed throughout the whole brain and the spinal cord. Positive signals were expressed in neuronal and non-neuronal cells in these regions. SMIT is gradually down-regulated nearer birth, but intense signals were still detected in the brain at postnatal day one. In the adult rat brain, very weak hybridization signals were detected throughout whole brain except for the choroid plexus where SMIT mRNA expression remained high. In contrast, the pattern of developmental regulation of SMIT gene expression in the kidney was opposite to that seen in the brain. Signals in the kidney were very weak during embryonic stages, whereas SMIT expression increased significantly after birth. These results suggest that *myo*-inositol and its transporter play an important role in the CNS developmental stage. © 1997 Elsevier Science B.V.

**Keywords:** Osmolyte; Blood-brain barrier; Na<sup>+</sup>/*myo*-inositol cotransporter

### 1. Introduction

*myo*-Inositol and its various biochemical derivatives are widely distributed in mammalian tissues and cells [10]. The levels of *myo*-inositol in most mammalian cells or tissues are much higher than those in plasma and interstitial fluids [5,13]. Plasma concentrations in adult mammals have been reported to be 10–200 μM [10], whereas tissue *myo*-inositol levels are usually greater than 1 mM. Sodium-dependent *myo*-inositol transporter (SMIT) appears to be responsible for the maintenance of these concentration gradients. Interestingly, *myo*-inositol concentrations in fetal mammalian serum may be elevated with levels which are sometimes greater than 1 mM, depending on the time of gestation [4,9]. Similarly, while the range of

*myo*-inositol in adult cerebrospinal fluid (CSF) is 100–500 μM [20,22], the concentration in fetal CSF may reach 3 mM [1].

The reasons for the elevated *myo*-inositol levels in fetuses are unknown. Fruen and Lester have shown more recently that sodium-dependent *myo*-inositol uptake in fetal brain cells in vitro is also increased when compared to adult cells [6]. They postulated that disruption of *myo*-inositol homeostasis in Down syndrome (trisomy 21) may affect the developing brain and thus contribute to the pathogenesis of mental retardation, the most consistent and debilitating feature of the syndrome. There is some supportive evidence for their hypothesis. When polyol species were examined in CSF, a significant increase in the level of *myo*-inositol alone was observed in Down syndrome compared with controls [21]. Furthermore, recent mapping of a human SMIT gene onto the long arm of chromosome 21 [3] suggested that the altered *myo*-inositol homeostasis

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involving the CSF may result from increased transport. Despite these studies, no information is available about expression of SMIT during fetal development.

To gain insight into the expression of SMIT during time of gestation, we determined regional distributions of SMIT mRNA in rat fetuses using *in situ* hybridization. The results obtained demonstrated that SMIT is highly expressed in the fetal brain and spinal cord, whereas there were only weak signals in the kidney. The significance of SMIT in development of the CNS will be discussed.

## 2. Materials and methods

### 2.1. *In situ* hybridization

Pregnant Wistar rats were anesthetized with pentobarbital (65 mg/kg intraperitoneally) and fetuses were removed at embryonic day (E) 14, E16, and E18. Animals were also examined at postnatal day (P) 1 ( $n = 5$  for each age). Fetuses and P1 rats were sacrificed by decapitation and their whole bodies were immediately frozen at  $-80^{\circ}\text{C}$ . Adult rats (postnatal week 3,  $n = 5$ ) were treated in the same manner and their brains and kidneys were removed. Serial coronal sections (5  $\mu\text{m}$  thick) were obtained from the frozen tissues and the whole bodies with a cryostat and stored in a tightly closed case at  $-80^{\circ}\text{C}$ . The antisense probe for SMIT was synthesized from a 490 bp rat SMIT cDNA (bases 808–1297) insert cloned into the Novagen T-vector. The sense probe for SMIT was synthesized from a 490 bp rat SMIT cDNA insert cloned in the vector pSPORT 1. To synthesize hybridization riboprobes by *in vitro* transcription, this sequence was first linearized by digestion with restriction endonucleases of *EcoRI* for both antisense and sense RNA synthesis. The linearized cDNA was then incubated at  $37^{\circ}\text{C}$  for 60 min with a mixture of reagents. This mixture consisted of 2  $\mu\text{l}$  of transcription buffer ( $\times 5$ ), 0.5  $\mu\text{l}$  of 100 mM dithiothreitol, 0.5  $\mu\text{l}$  of RNase inhibitor, 0.5  $\mu\text{l}$  of 10 mM ATP, CTP and GTP, 5  $\mu\text{l}$  of [ $^{35}\text{S}$ ]UTP (NEG-039H, New England Nuclear), 0.5  $\mu\text{l}$  of DNA template (1 mg/ml) with 1  $\mu\text{l}$  of appropriate RNA polymerase (T7 RNA polymerase for antisense; SP6 RNA polymerase for sense probe). DNA was digested by addition of 2  $\mu\text{l}$  of DNase (1 U/ $\mu\text{l}$ ) and incubation at  $37^{\circ}\text{C}$  for 10 min. Efficacy of labeling was estimated by counting radioactivity of the synthesized probes.

*In situ* hybridization techniques for SMIT mRNA (RNA probe) were based on those of Wilkinson et al. [23] with some modifications. Briefly, sections were fixed in 4% paraformaldehyde in 0.1 M phosphate buffer (PB) for 20 min. After washing with PBS, the sections were treated with 10 mg/ml of proteinase K in 50 mM Tris-HCl and 5 mM EDTA (pH 8.0) for 5 min at room temperature. They were fixed again in the same fixative, then acetylated with acetic anhydride in 0.1 M triethanolamine, rinsed with

PBS, dehydrated and air-dried. The  $^{35}\text{S}$ -labeled RNA probes (sense and antisense) were diluted in hybridization buffer, applied to the sections and covered with siliconized coverslips. Hybridization was performed overnight in a humid chamber at  $55^{\circ}\text{C}$ . The hybridization buffer consisted of 50% deionized formamide, 0.3 M NaCl, 20 mM Tris-HCl, 5 mM EDTA, 10 mM PB, 10% dextran sulfate,  $1 \times$  Denhardt's solution, 0.2% sarcosyl, 500 mg/ml yeast tRNA, and 200 mg/ml herring sperm DNA (pH 8.0). The probe concentration was  $5 \times 10^5$  cpm/150  $\mu\text{l}$  per slide. After hybridization, the slides were soaked in  $5 \times$  SSC at  $55^{\circ}\text{C}$ , and the coverslips were allowed to slough off. The sections were then incubated at  $65^{\circ}\text{C}$  in 50% deionized formamide with  $2 \times$  SSC for 30 min. After rinsing with RNase buffer (0.5 M NaCl, 10 mM Tris-HCl, 5 mM EDTA (pH 8.0)) four times for 10 min each time at  $37^{\circ}\text{C}$ , the sections were treated with 1 mg/ml of RNase A in RNase buffer for 30 min at  $37^{\circ}\text{C}$ . After an additional washing in RNase buffer, the slides were incubated in 50% formamide with  $2 \times$  SSC for 30 min at  $65^{\circ}\text{C}$ , rinsed with  $2 \times$  SSC and  $0.1 \times$  SSC for 10 min each at room temperature, dehydrated through an ascending alcohol series and air-dried.

X-ray film was placed on uncoated sections for 3 days. The slides were then coated with Ilford K-5 emulsion diluted in distilled water containing 2% glycerine (1:1). The slides were exposed for 3 weeks in a tightly sealed dark box at  $4^{\circ}\text{C}$ , developed in Kodak D-19, fixed with photographic fixer, stained with thionine and coverslipped. The tissue sections were examined under a light microscope. For quantitative assessment of SMIT mRNA expression on the macroautoradiograms, an optical density of a target region was measured, and optical density ratio (ODR) was calculated in comparison with the film background density. Statistical analysis was performed using non-parametric analysis of the Mann-Whitney *U*-test with two-tailed probability.

### 2.2. Western blotting

Anti-SMIT antibody was raised against a synthetic peptide, CTPPTKEQ, corresponding to amino acids 533–540 of SMIT [12]. The peptide was coupled with KLH and used to immunize rabbits.

Extracts were prepared from E16, E18 and P1 and P21 rat brain. Aliquots of 20  $\mu\text{g}$  of protein were electrophoresed in 10% SDS-polyacrylamide gels. Proteins were transferred from the gels onto nitrocellulose membranes in a modified Towbin transfer buffer (25 mM Tris, 192 mM glycine, pH 8.4, containing 0.05% 2-mercaptoethanol). The nitrocellulose was blocked with blot buffer (20 mM Tris (pH 7.6), 150 mM NaCl, 0.05% Tween-20, 0.05%  $\text{NaN}_3$ ) containing 3% BSA for 1 day at  $4^{\circ}\text{C}$ . The filters were probed at room temperature for 2 h with anti-SMIT rabbit antiserum diluted in blot buffer, washed

with blot buffer, and then incubated for 2 h with anti-rabbit IgG HRP antibody diluted 1:500 in blot buffer containing 1% BSA. After washing with blot buffer, immunoreactivity was visualized using the ECL system (Amersham, Braunschweig, Germany).

### 3. Results

Throughout the present study, adjacent sections were hybridized with both sense and antisense probes to confirm the specificity of SMIT mRNA hybridization signals. Signals were observed only in sections hybridized with the antisense probes. Fig. 1 and Fig. 2 show developmental changes in the expression of SMIT mRNA; since signifi-

cant expression was observed in the fetal brain and the kidney after birth, we focused on these two organs.

#### 3.1. SMIT mRNA expression in the brain

The most intense SMIT mRNA hybridization signals were constantly found in the choroid plexus of the lateral ventricle and fourth ventricle constantly from E14 to P21. In contrast, other regions of the brain showed intense hybridization signals until P1, while these hybridization signals were markedly decreased and reached low levels at P21.

Detailed observations revealed low to moderate levels of SMIT mRNA in the neocortical neuroepithelium, septum, rhinencephalon, pallidal subventricular zone, pal-

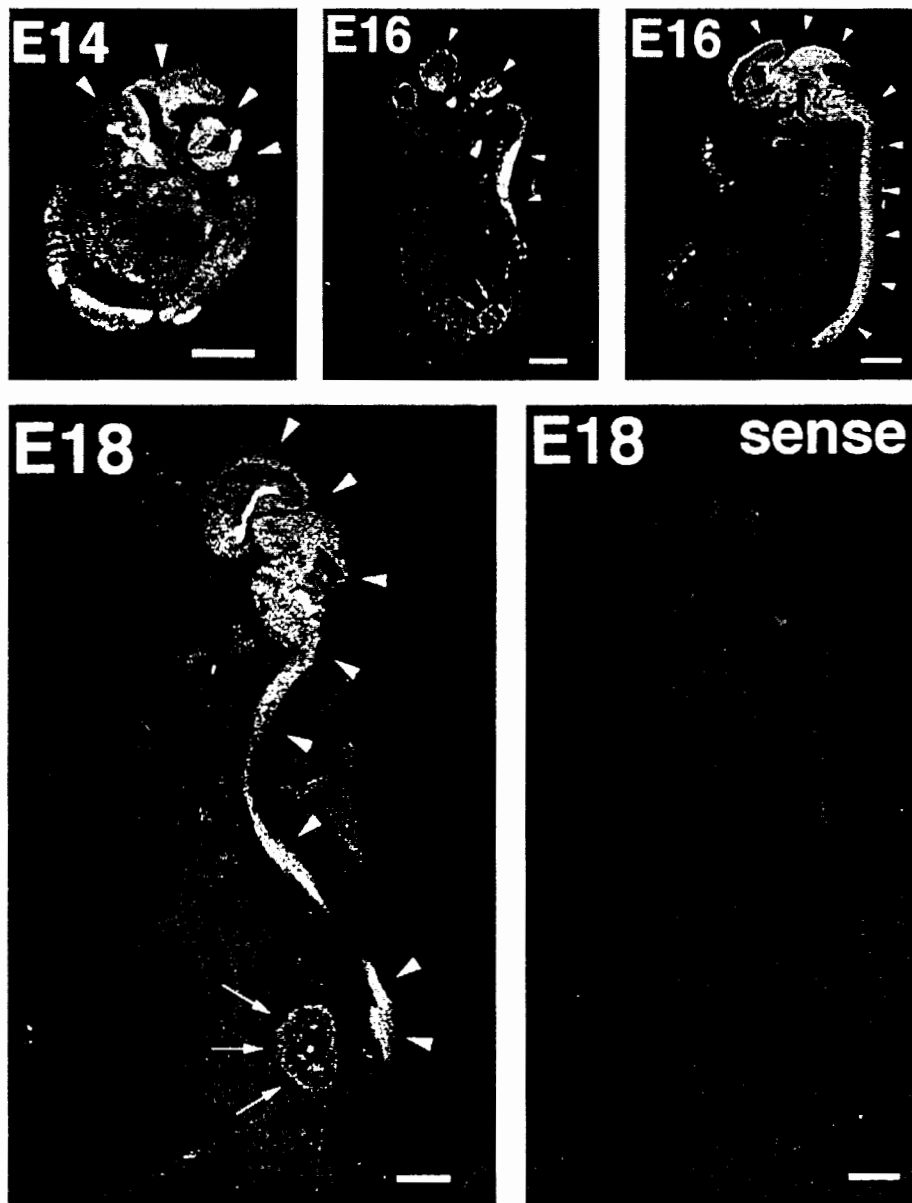


Fig. 1. SMIT mRNA hybridization signals were widely distributed throughout the fetal brain (E14, E16, E18) with the most intense signals in the choroid plexus. In contrast, SMIT mRNA levels were low in the fetal kidney. No specific hybridization signals were found using a sense SMIT probe. Scale bar = 2 mm.

lidum and thalamus at E14, while intense hybridization signals were seen in the hypothalamus, pretectum, tegmentum, anterior pons, posterior pons, medulla and spinal cord. At E16, intense hybridization signals were observed in the cortical plate and neocortical neuroepithelium, whereas weak signals were detected in the intermediate zone in the cerebral cortex. Most of the other areas in the brain showed moderate to intense hybridization signals with less intense signals in the pallidal subventricular zone. Moderate to intense hybridization signals were also seen in the neural layer of the retina at E16. At E18, almost all the regions in the brain and neural layer of the retina showed moderate to intense SMIT mRNA signals with less intense signals in the intermediate zone in the cerebral cortex, striatal subventricular zone and pallidal subventricular zone. At P1, moderate to intense hybridization signals were found throughout whole brain. Particularly high expression of SMIT mRNA was detected in the subiculum, CA1–3 fields in the hippocampus, hypothalamus and amygdaloid complex. At P21, very low signals were widely distributed throughout the whole brain with slightly higher

intensity in the olfactory bulb, hippocampus and cerebellum. No signals were found with the sense probe.

### 3.2. SMIT mRNA expression in the kidney

In contrast, SMIT mRNA levels were low in the kidney during fetal stages, whereas the hybridization signals were markedly increased after birth.

Detailed observation revealed weak SMIT mRNA signals in the nephrogenic zone, and low-level signals were scattered in the medulla at E16. Moderate hybridization signals were sporadically spread over cortical and medullary regions with higher levels in the nephrogenic zone at E18. At P1, intense hybridization signals were concentrated in the medulla, whereas weak signals were scattered in the cortex. At P21, SMIT mRNA was intensely expressed in the outer medulla. SMIT mRNA signals showed a gradient of concentration along the corticomedullary axis from the inner medulla to the papillary tip, with the most abundant transcript levels in the papillary tip. These signals in the papillary tip were as intense

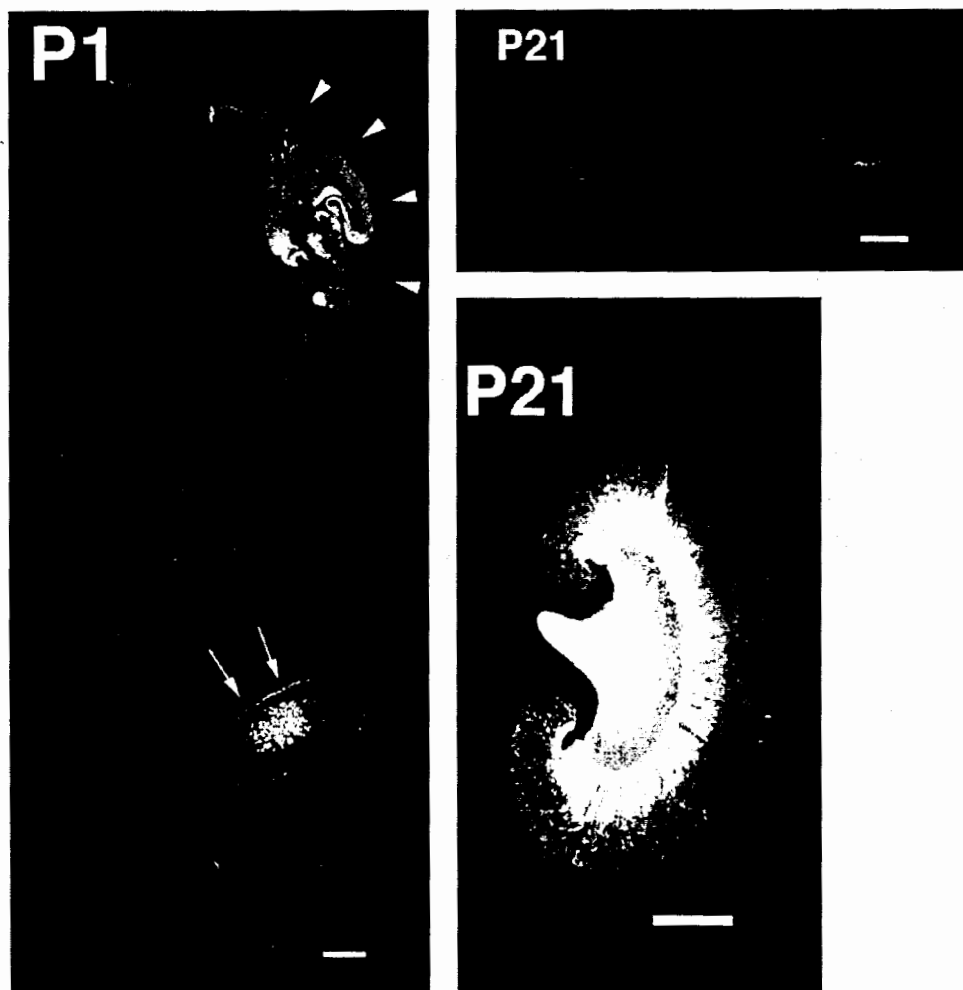


Fig. 2. Postnatal day 1 (P1) rat, and the brain and kidney of postnatal day 21 (P21) adult rat. The brain showed intense hybridization signals at P1, while these hybridization signals were markedly decreased and reached low levels at P21. In contrast, the hybridization signals in the kidney were markedly increased after birth, especially in the medulla.



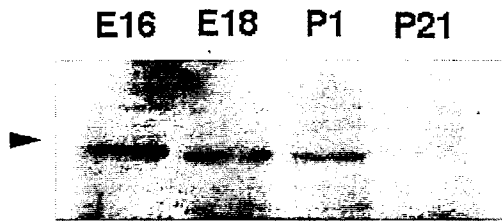


Fig. 3. On Western blotting analysis, polyclonal antiserum against SMIT recognized a single protein with  $M_r$  of 80000. The levels of SMIT protein in the brain were decreased from embryonic day 16 (E16) to postnatal day 21 (P21). Arrowhead indicates 83 kDa marker.

as those in the outer medulla. Moderate hybridization signals were scattered in the cortex.

### 3.3. Western blotting analysis

We also analyzed levels of SMIT protein in the rat brain at E16, E18, P1 and P21 by immunoblotting. As shown in Fig. 3, SMIT was expressed as a single component with an  $M_r$  of 80000. The protein levels of SMIT throughout developmental stages showed a pattern similar to that observed for SMIT mRNA. The brain SMIT protein levels were high during embryonic stages and decreased with development.

## 4. Discussion

Our results indicated that SMIT mRNA and SMIT protein are highly expressed in the fetal CNS and decrease with development. This result is consistent with *in vitro* study using cultured brain cells from fetal mice [6] in which  $\text{Na}^+$ -dependent *myo*-inositol uptake in fetal brain cells was significantly higher than that in adult brain cells. Their results together with our observations suggest that the development of the brain from the fetal to the adult stage is associated with a significant decrease in SMIT activity as well as in its mRNA and protein levels. A similar decrease in SMIT activity accompanies differentiation of neuroblastoma cells in culture [19]. Changes in brain SMIT with development may be related to the high ambient concentration of *myo*-inositol. Considering the marked elevation of its concentration in fetal plasma [4,9] and CSF [1], one would expect that intracellular concentration would be extremely high. Since *myo*-inositol levels in most mammalian tissues are 10–100-fold higher than those in plasma [5,13], its concentration in the fetal CNS might be more than 10 mM. This raises the question why the fetal CNS need such a large amount of *myo*-inositol. The rate of synthesis of phosphatidylinositol would not be markedly affected because it is already saturated at much lower concentrations [2]. Low levels of ambient *myo*-inositol seem to be adequate to maintain normal cellular phosphatidylinositol production. Thus, it is possible that *myo*-inositol plays another role in the fetal brain that is

distinct from that of a simple substrate for phospholipid biosynthesis.

In addition to its role in membrane structure and signal transduction, *myo*-inositol functions as an osmolyte in the kidney and the brain [7,8]. It is accumulated under hypertonic conditions by increasing SMIT activity [17]. The abundance of SMIT mRNA and the transcription rate of the SMIT gene increased when the cultured kidney cells were cultured in hypertonic medium, suggesting that transcription is the primary step in regulation of *myo*-inositol transport by hypertonicity [12,25]. Similar results were obtained from brain glial cells [18] and lens epithelial cells [26]. We have recently reported the localization and regulation of SMIT mRNA in kidney [24], brain [11,14], eye [16] and ear [15]. These results strongly suggest an important role of SMIT in the CNS regarding cell volume regulation. Although we found intense expression of SMIT in the fetal CNS, it is unknown whether the transporter is also under osmoregulatory control. Berry et al. [2] suggested that *myo*-inositol may be an osmolyte in fetal endothelial cells since they have a high-affinity transport system for *myo*-inositol and accumulate more *myo*-inositol with fetal bovine serum than with adult bovine serum. It is possible that *myo*-inositol functions as an osmolyte in the fetal CNS. We speculate that the intense expression of SMIT might be related to the immature blood–brain barrier in the fetus, which is much more permeable to a variety of solutes than that in adults.

Our results thus suggest that SMIT plays an important role in the fetal CNS but not in the kidney. The hypothesis proposed by Fruen et al. [6] regarding the relationship between Down syndrome and SMIT gene is consistent with our results. In patients with Down syndrome, mental retardation and neurological abnormalities are always present but the kidney is usually normal. Further studies are necessary to clarify the significance of *myo*-inositol and its transporter in this syndrome.

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