The mouse 5HT5 receptor reveals a remarkable heterogeneity within the 5HT1D receptor family

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Serotonin (5-HT) is a neuromodulator that mediates a wide range of physiological functions by activating multiple receptors. Using a strategy based on amino acid sequence homology between 5-HT receptors that interact with G proteins, we have isolated a cDNA encoding a new serotonin receptor from a mouse brain library. Amino acid sequence comparisons revealed that this receptor was a distant relative of all previously identified 5-HT receptors; we therefore named it 5HT5. When expressed in Cos-7 cells and NIH-3T3 cells, the 5HT5 receptor displayed a high affinity for the serotonergic radioligand ^{[125}I]LSD. Surprisingly, its pharmacological profile resembled that of the 5HT1D receptor, which is a 5-HT receptor subtype which has been shown to inhibit adenylate cyclase and which is predominantly expressed in basal ganglia. However, unlike 5HT1D receptors, the 5HT5 receptor did not inhibit adenylate cyclase and its mRNA was not found in basal ganglia. On the contrary, in situ hybridization experiments revealed that the 5HT5 mRNA was expressed predominantly in cerebral cortex, hippocampus, habenula, olfactory bulb and granular layer of the cerebellum. Our results therefore demonstrate that the 5HT1D receptors constitute a heterogeneous family of receptors with distinct intracellular signalling properties and expression patterns.

Key words: cerebral cortex/G protein-coupled receptor/ hippocampus/5HT1D receptor/LSD serotonin

Introduction

Serotonin is a neuromodulator that elicits and modulates a wide range of behaviours such as sleep, appetite, locomotion, sexual activity and vascular contraction (Wilkinson and Dourish, 1991). Both pharmacological studies and molecular cloning of 5-HT receptors have revealed a multiplicity of receptor subtypes. The receptors that have been cloned so far belong to either the ligand-gated ion channel family (5HT3 receptor) or to the large family of receptors that interact with G proteins and share a putative seven transmembrane domains structure (Julius, 1991). Amino acid sequence comparisons have revealed that the G proteincoupled 5-HT receptors can be subdivided into two distinct groups: the 5HT1 group, which contains the mammalian

5HT1A, 1B and 1D subtypes as well as three Drosophila 5-HT receptors, and the 5HT2 group, which contains the 5HT2 and 5HT1C subtypes. These receptors differ in their affinity for serotonin, their intracellular signalling properties, their pattern of expression and their subcellular localization (for a review see Hen, 1992).

Pharmacological studies have revealed the existence of additional receptor subtypes such as the 5HT4 receptor as well as a number of '5HT1D-like' receptors (for a review see Peroutka, 1991b). In order to isolate some of these subtypes, we used a strategy based on nucleotide sequence homology between transmembrane domains III and VI of 5-HT receptors. A mouse brain cDNA library was screened and one of the resulting clones was shown to encode a functional 5-HT receptor. Sequence comparisons have revealed that this receptor is a new member of the G proteincoupled receptor family that does not belong to either 5HT1 or 5HT2 groups. We therefore named it 5HT5. The pharmacological profile of the 5HT5 receptor is similar to that of the 5HT1D receptor and suggests that this receptor may correspond to previously described rat 5HT1D binding sites (Herrick-Davis and Titeler, 1988). Furthermore, the 5HT5 receptor is expressed in the cerebral cortex, hippocampus and cerebellum, which are structures that were shown to contain 5HT1D sites in the rat (Herrick-Davis and Titeler, 1988), as well as 5HT1D-like sites in various mammalian species including human (for a review see Peroutka, 1991b).

Our results demonstrate that the 5HT5 receptor is a novel serotonin receptor whose sequence is not closely related to that of any known serotonin receptor, but whose pharmacological profile resembles that of the 5HT1D receptor. These data therefore confirm previous pharmacological studies suggesting that the 5HT1D receptors are a heterogeneous family of receptors.

Results

Isolation of a mouse cDNA clone encoding a new member of the G protein-coupled receptor family: the 5HT5 receptor

Sequence comparisons of serotonin receptors have revealed a striking amino acid sequence conservation particularly in certain putative transmembrane domains such as domains III and VI (Hen, 1992). We therefore decided to use degenerate oligonucleotides corresponding to these two regions to perform a series of PCR experiments on mouse brain RNA. The resulting fragments were subcloned and sequenced. One of these fragments was used to screen a mouse brain cDNA library. We obtained one phage recombinant that contained a 4 kbp long cDNA insert. Sequence analysis revealed one long open reading frame (357 amino acids) and a poly A tail (Figure 1). The hydropathy analysis of this predicted protein revealed seven hydrophobic domains (numbered I-VII in Figure 1), a feature shared

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158	CCAC	CCTC	3CAC'	rggg	CGGGG	GCCGI	ACCC	AAGG	ATGC:	ICTC	CTGCI	AGGC	GACCI	GAC	AACAG	STCTO	CCCC	CTAG	GTGA	GGAA	CAGCI	AGGG	CATG	FGAT	AGCA	AAAG	GCGG	GCCC	IGGC	TTCT	
277	AGA	TCAC	SCCC	CTTG	AGTCO	CGCT	FTCC/	ATATO	CTCT	VVCC	ATACO	CTGGG	SCTG	GCTO	SCTTO	STAGO	CCA	GCAC	CTC	CTCT	CTGCI	raca/	ATTTO	CCTC	CGGA	CTCTO	GACTO	GGGT	GGAG	ACTG	
396	AGG	CAG	STTC	rtgg(CTCT	FAGCI	AAAA	TCCT	CTCCI	ATTG	GCCA	rcgg1	ICGCI	AACA	ATCT	GAT	IGACI	FTCA	JICC	SCTC	GTG	GCAA	CACAC	STCT	AAAC	ACAG	STGTO	CCTG	GGAC	AGCA	
515	ATG	GAT	CTG	CCT	GTA	AAC	TTG	ACC	TCC	TTT	TCT	CTC	TCT	ACT	ccc	TCC	TCT	TTG	GAA	CCT	AAC	CGC	AGC	TTG	GAC	ACG	GAA	GTC	CTG	CGC	
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	v	L	A	т	I	L	к	v	R	т	F	н	R	v	P	н	N	L	v	A	S	M	A	I	S	D	v	L	v	A	90
785	GTG	CTG	GTT	ATG	CCA	CTG	AGC	CTG	GTA	CAT	GAG	CTG	TCT	GGG	CGC	CGC	TGG	CAG	CTG	GGC	CGG	CGT	CTA	TCC	CAG	CTG	TGG	ATC	GCA	TGT	
	v	L	V	M	P	L	S	L	V	н	Е	L	s	G	R	R	W	Q	L	G	R	R	L	С	Q	L	W	I	Α	С	120
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965	CTC L	CGT R	ACC	CGC R	AAG K	CGT R	GTC V	TCC	AAT N	GTG V	ATG M	ATC I	CTG L	CTC L	ACC T	TGG W	GCA A	CTC L	s	ACT T	V V	ATC I	TCT S	L	GCT A	CCA P	CTG L	CTA L	TTT F	GGC	180
965	CTC L	CGT R	ACC T	CGC R	AAG K	CGT R	GTC V	TCC S	AAT N	GTG V	ATG M	ATC I	CTG L	CTC L	ACC T	TGG W	GCA A	CTC L	s	ACT T	V	I	TCT S	L	GCT A	CCA P	CTG L	CTA L	TTT F	GGC	180
965 1055	CTC L TGG	CGT R GGA	ACC T GAG	CGC R ACT	AAG K TAT	CGT R TCT	GTC V GAG	TCC S CCC	AAT N AGT	GTG V GAG	ATG M GAA	ATC I TGC	CTG L CAA	CTC L GTC	ACC T AGT	TGG W CGC	GCA A GAG	CTC L CCT	TCC S TCC	TACT T	V ACC	I	TCT S TTC	L TCC	A ACC	CCA P GTG	CTG L GGT	CTA L V GCC	TTT F TTC	GGC G TAC	180
965 1055	CTC L TGG W	CGT R GGA G	ACC T GAG E	CGC R ACT T	AAG K TAT Y	CGT R TCT S	GTC V GAG E	TCC S CCC P	AAT N AGT S	GTG V GAG E	ATG M GAA E	ATC I TGC C	CTG L CAA Q	CTC L GTC V	ACC T AGT S	TGG W CGC R	GCA A GAG E	CTC L CCT P	TCC S TCC S	TACT TAC	V ACC T	I GTG V	TCT S TTC F	CIG L TCC	GCT A ACC T	CCA P GTG V	CTG L GGT G	CTA L GCC A	TTT F TTC F	GGC G TAC Y	180 210
965 1055	CTC L TGG W	CGT R GGA G	ACC T GAG E	CGC R ACT T	AAG K TAT Y	CGT R TCT S	GTC V GAG E	TCC S CCC P	AAT N AGT S	GTG V GAG E	ATG M GAA E	ATC I TGC C	CTG L CAA Q	CTC L GTC V	ACC T AGT S	TGG W CGC R	GCA A GAG E	CTC L CCT P	TCC S TCC S	TACT TAC	V ACC T	I GTG V	TCT S TTC F	TCC S	GCT A ACC T	CCA P GTG V	CTG L GGT G	CTA L GCC A	TTT F TTC F	GGC G TAC Y	180 210
965 1055 1145	CTC L TGG W CTG	CGT R GGA G CCG	ACC T GAG E CTG	CGC R ACT T	AAG K TAT Y GTG	CGT R TCT S GTG	GTC V GAG E CTC	TCC S CCC P TTT	AAT N AGT S GTG	GTG V GAG E TAC	ATG M GAA E TGG	ATC I TGC C AAA	CTG L CAA Q ATT	GTC V TAC	ACC T AGT S AGG	TGG W CGC R GCG	GCA A GAG E GCG	CTC L CCT P	TCC S TCC S TTC	TAC TAC Y CGC	ACC T ATG	I GTG V GGC	TCT S TTC F TCC	TCC S AGG	ACC A ACC T AAG	CCA P GTG V ACT	CTG L GGT G AAC	CTA L GCC A AGC	TTT F TTC F GTC	GGC G TAC Y TCC	180 210
965 1055 1145	CTC L TGG W CTG L	CGT R GGA G CCG P	ACC T GAG E CTG L	CGC R ACT T TGC C	AAG K TAT Y GTG	CGT R TCT S GTG V	GTC V GAG E CTC L	TCC S CCC P TTT F	AAT N AGT S GTG V	GTG V GAG E TAC Y	ATG M GAA E TGG W	ATC I TGC C AAA K	CTG L CAA Q ATT I	CTC L GTC V TAC Y	ACC T AGT S AGG R	TGG W CGC R GCG A	GCA A GAG E GCG A	CTC L CCT P AAA K	TCC S TCC S TTC F	TAC T TAC Y CGC R	ACC T ATG M	ATC I GTG V GGC G	TTC S TTC F TCC S	TCC S AGG R	ACC ACC T AAG K	CCA P GTG V ACT T	CTG L GGT G AAC N	CTA L GCC A AGC S	TTT F TTC F GTC V	GGC G TAC Y TCC S	180 210 240
965 1055 1145	CTC L TGG W CTG L	CGT R GGA G CCCG P	ACC T GAG E CTG L	CGC R ACT T TGC C	AAG K TAT Y GTG V	CGT R TCT S GTG V	GTC V GAG E CTC L	TCC S CCC P TTT F	AAT N AGT S GTG V	GTG V GAG E TAC Y	ATG M GAA E TGG W	ATC I TGC C AAA K	CTG L CAA Q ATT I	CTC L GTC V TAC Y	ACC T AGT S AGG R	TGG W CGC R GCG A	GCA A GAG E GCG A	CTC L CCT P AAA K	TCC S TCC S TTC F	TAC T TAC Y CGC R	ACC T ATG M	GTG V GGC G	TTC F TCC S	TCC S AGG R	ACC A ACC T AAG K	CCA P GTG V ACT T	CTG L GGT G AAC N	CTA L GCC A AGC S	TTT F TTC F GTC V	G G TAC Y TCC S	180 210 240
965 1055 1145 1235	CTC L TGG W CTG L CCC	CGT R GGA G CCCG P GTA	ACC T GAG E CTG L CCC	CGC R ACT T TGC C GAA	AAG K TAT Y GTG V GCT	CGT R TCT S GTG V GTG	GTC V GAG E CTC L GAG	TCC S CCC P TTT F GTG	AAT N AGT S GTG V AAG	GTG V GAG E TAC Y AAT	ATG M GAA E TGG W GCT	ATC I TGC C AAA K ACA	CTG L CAA Q ATT I CAA	CTC L GTC V TAC Y CAT	ACC T AGT S AGG R CCC	TGG W CGC R GCG A CAG	GCA A GAG E GCG A ATG	CTC L CCT P AAA K GTG	TCC S TCC S TTC F TTC	TAC TAC Y CGC R ACG	ACC T ATG M GTC	I GTG V GGC G CGC	TTC F TCC S CAT	TCC S AGG R GCC	ACC AAG K ACC	CCA P GTG V ACT T GTC	CTG L GGT G AAC N ACC	CTA L GCC A AGC S TTC	TTT F TTC F GTC V CAG	G G TAC Y TCC S ACA	180 210 240
965 1055 1145 1235	CTC L TGG W CTG L CCC P	CGT R GGA G CCG P GTA V	ACC T GAG E CTG L CCC P	CGC R ACT T TGC C GAA E	AAG K TAT Y GTG V GCT A	CGT R TCT S GTG V GTG V	GTC V GAG E CTC L GAG E	TCC S CCC P TTT F GTG V	AAT N AGT S GTG V AAG K	GTG V GAG E TAC Y AAT N	ATG M GAA E TGG W GCT A	ATC I TGC C AAA K ACA T	CTG L CAA Q ATT I CAA Q	CTC L GTC V TAC Y CAT H	ACC T AGT S AGG R CCC P	TGG W CGC R GCG A CAG Q	GCA A GAG E GCG A ATG M	CTC L CCT P AAA K GTG V	TCC S TTC F TTC F	TAC TAC Y CGC R ACG T	ACC T ATG M GTC V	ATC I GTG V GGC G CGC R	TTC F TCC F CAT H	TCC S AGG R GCC A	ACC AAAG K ACC T	CCA P GTG V ACT T GTC V	CTG L GGT G AAC N ACC T	CTA L GCC A AGC S TTC F	TTT F TTC F GTC V CAG Q	G G TAC Y TCC S ACA T	180 210 240 270
965 1055 1145 1235	CTC L TGG W CTG L CCC P	CGT R GGA G CCCG P GTA V	ACC T GAG E CTG L CCC P	CGC R ACT T TGC C GAA E	AAG K TAT Y GTG V GCT A	CGT R TCT S GTG V GTG V	GTC V GAG E CTC L GAG E	TCC S CCC P TTT F GTG V	AAT N AGT S GTG V AAG K	GTG V GAG E TAC Y AAT N	ATG M GAA E TGG W GCT A	ATC I TGC C AAA K ACA T	CTG L CAA Q ATT I CAA Q	CTC L GTC V TAC Y CAT H	ACC T AGT S AGG R CCC P	TGG W CGC R GCG A CAG Q	GCA A GAG E GCG A ATG M	CTC L CCT P AAA K GTG V	TCC S TTC F TTC F	TAC TAC Y CGC R ACG T	ACC T ATG M GTC V	GTG V GGC G CGC R	TTC F TCC S CAT H	TCC S AGG R GCC A	ACC AAAG K ACC T	CCA P GTG V ACT T GTC V	CTG L GGT G AAC N ACC T	CTA L GCC A AGC S TTC F	TTT F TTC F GTC V CAG Q	G G TAC Y TCC S ACA T	180 210 240 270
965 1055 1145 1235 1325	CTC L TGG W CTG L CCC P GAA	CGT R GGA G CCG P GTA V GGG	ACC T GAG E CTG L CCC P GAT	CGC R ACT T TGC C GAA E ACG	AAG K TAT Y GTG V GCT A TGG	CGT R TCT S GTG V GTG V AGG	GTC V GAG E CTC L GAG E GAG	TCC S CCC P TTT F GTG GTG V CAG	AAT N AGT S GTG V AAG K AAG	GTG V GAG E TAC Y AAT N GAG	ATG M GAA E TGG W GCT A CAA	ATC I TGC C AAA K ACA T AGG	CTG L CAA Q ATT I CAA Q GCA	CTC L GTC V TAC Y CAT H	ACC T AGT S AGG R CCC P CTC	TGG W CGC R GCG A CAG Q ATG	GCA A GAG E GCG A ATG M GTG	CTC L CCT P AAA K GTG V GGC	TCC S TTC F TTC F ATC	TAC TAC Y CGC R ACG T OTC	ACC T ATG M GTC V ATC	ATC I GTG V GGC G CGC R GGA	TTC F TCC S CAT H V GTG	TCC S AGG R GCC A I TTT	ACC AAG K ACC T AAG K ACC T	CCA P GTG V ACT T GTC V CTC	CTG L GGT G AAC N ACC T TGC	CTA L GCC A AGC S TTC F	TTT F TTC F GTC V CAG Q TTC	GGC G TAC Y TCC S ACA T	180 210 240 270
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965 1055 1145 1235 1325 1415	CTC L TGG W CTG L CCC P GAA E TTC F	CGT R GGA G CCCG P GTA V GGG G TTC F	ACC T GAG E CTG L CCC P GAT D GTC V	CGC R ACT T TGC C GAA E ACG T ACA T	AAG K TAT Y GTG V GCT A TGG W GAG E	CGT R TCT S GTG V GTG V GTG CTC L	GTC V GAG E CTC L GAG E GAG E ATC I	TCC S CCC P TTT F GTG V CAG Q AGT S	AAT N AGT S GTG V AAG K AAG K CCC P	GTG V GAG E TAC Y AAT N GAG E CTG L	ATG M GAA E TGG W GCT A CAA Q TGT C	ATC I TGC C AAAA K ACA T AGG R TCC S	CTG L CAA Q ATT I CAA Q GCA A TGG W	CTC L GTC V TAC Y CAT H GCC A GAC D	ACC T AGT S AGG R CCC P CTC L GTC V	TGG W CGC R GCG A CAG Q ATG M CCT P	GCA A GAG E GCG A ATG M GTG V GCC A	CTC L CCT P AAAA K GTG G G G G C G ATC I	TCC S TTC F TTC F ATC I TGG W	ACT T TAC Y CGC R ACG T CTC L AAG K	ACC T ATG M GTC V ATC I AGC S	ATC I GTG V GGC G CGC R GGA G GGA G ATC I	TCT S TTC F TCC S CAT H V GTG V TTC F	TCC S AGG R GCC A I TTT F CTG L	ACC T AAG K ACC T GTG V TGG W	CCA P GTG V ACT T GTC V CTC L TTG L	CTG L GGT G AAC N ACC T TGC C GGC G	CTA L GCC A AGC S TTC F TGG W TAT Y	TTT F TTC F GTC V CAG Q TTC F TCT S	G G TAC Y TCC S ACA T CCT P AAT N	180 210 240 270 300 330
965 1055 1145 1235 1325 1415	CTC L TGG W CTG L CCC P GAA E TTC F	CGT R GGA G CCG P GTA V GGG G TTC F	ACC T GAG E CTG L CCC P GAT D GTC V	CGC R ACT T TGC C GAA E ACG T ACA T	AAG K TAT Y GTG C C C C C A TGG W GAG E	CGT R TCT S GTG V GTG V AGG R CTC L VI	GTC V GAG E CTC L GAG E GAG E ATC I I	TCC S CCC P TTT F GTG V CAG Q AGT S	AAT N AGT S GTG V AAG K AAG K AAG K CCC P	GAG E TAC Y AAT N GAG E CTG L	ATG M GAA E TGG W GCT A CAA Q TGT C	ATC I TGC C AAAA K ACA T AGG R TCC S	CTG L CAA Q ATT I CAA Q GCA A TGG W	CTC L GTC V TAC Y CAT H GCC A GAC D	ACC T AGT S AGG R CCC P CTC L GTC V	TGG W CGC R GCG A CAG Q ATG M CCT P	GCA A GAG E GCG A ATG M GTG V GCC A	CTC L CCT P AAA K GTG G GGC G ATC I	TCC S TTC F TTC F ATC I TGG W	ACT T TAC Y CGC R ACG T CTC L AAG K	ACC T ATG M GTC V ATC I AGC S	ATC I GTG V GGC G CGC R GGA G ATC I	TCCT TTCC F TCCC S CAT H V GTG V TTCC F	L TCC S AGG R GCC A I TTT F CTG L	GCT A ACC T AAG K ACC T GTG V TGG W	CCA P GTG V ACT T GTC V CTC L TTG L	CTG L GGT G AAC N ACC T TGC C GGC G	CTA L V GCC A AGC S TTC F TGG W TAT Y	TTT F TTC F GTC V CAG Q TTC F TCT S	G G TAC Y TCC S ACA T CCT P AAT N	180 210 240 270 300 330
965 1055 1145 1235 1325 1415 1505	CTC L TGG W CTG L CTG L CCC P GAA E TTC F	CGT R GGA G CCG P GTA V GGG G TTC F TTC	ACC T GAG E CTG L CCC P GAT D GTC V	CGC R ACT T TGC C GAA E ACG T ACA T AAC	AAG K TAT Y GTG V GCT A GCT A GCT A GCT A CCA	CGT R TCT S GTG V GTG V AGG R CTC L VI CTC	GTC V GAG E CTC L GAG E GAG E ATC I I ATC	TCC S CCC P TTTT F GTG V CAG Q AGT S TAC	AAT N AGT S GTG V AAAG K AAAG K CCC P ACA	GAG E TAC Y AAT N GAG E CTG L GCA	ATG M GAA E TGG W GCT A CAA Q TGT C	ATC I TGC C AAAA K ACA T AGG R TCC S AAC	CTG L CAA Q ATT I CAA Q GCA A TGG W AGG	CTC L GTC V TAC Y CAT H GCC A GAC D AGC	ACC T AGT S AGG R CCC P CTC L GTC V TAC	TGG W CGC R GCG A CAG Q ATG M CCT P AGC	GCA A GAG E GCG A ATG M GTG V GCC A AGT	CTC L CCT P AAAA K GTG G G G G G G C C I G CT I G CT	TCC S TTC F TTC F ATC I TGG W TTC	ACT T TAC Y CGC R ACG T CTC L AAG K AAG	ACC T ATG M GTC V ATC I AGC S GTC	ATC I GTG V GGC G G G G G G G ATC I TTC	TCCT TTCC F TCCC S CAT H V GTG V TTCC F TTCC F TTCC	L TCC S AGG R GCC A I TTT F CTG L TCC	GCT A ACC T AAG K ACC T GTG V TGG W AAG	CCA P GTG V ACT T GTC V CTC L TTG L CAA	CTG L GGT G AAC N ACC T TGC C GGC G CAA	CTA L V GCC A AGC S TTC F TGG W TTAT Y TGA	TTT F TTC F GTC V CAG Q TTC F TCT S GAG	GCC G TAC Y TCC S ACA T CCCT P AACA N AACA	180 210 240 270 300 330
965 1055 1145 1235 1325 1415 1505	CTC L TGG W CTG L CCC P GAA E TTC F TCC S	CGT R GGA G CCG P CCG P GTA V GGG G TTC F TTC F	ACC T GAG E CTG L CCC P GAT D GTC V TTC F	CGC R ACT T TGC C GAA E ACG T ACA T AACA N	AAG K TAT Y GCTG V GCT A TGG W GAG E CCA P	CGT R TCT S GTG V GTG V AGG R CTC L VI CTC L	GTC V GAG E CTC L GAG E GAG E ATC I I ATC I	TCC S CCC P TTTT F GTG V CAG Q AGT S TAC Y	AAT N AGT S GTG V AAG K AAG K CCC P ACA T	GAG E TAC Y AAT N GAG E CTG L GCA A	ATG M GAA E TGG W GCT A CAA Q TGT C TTCC F	ATC I TGC C AAAA K ACA T AGG R TCC S AACC N	CTG L CAA Q ATT I CAA Q CAA Q GCA A TGG W AGG R	CTC L GTC V TAC Y CAT H GCC A GAC D AGC S	ACC T AGT S AGG R CCC P CTC L GTC V TAC Y	TGG W CGC R GCG A CAG Q ATG M CCT P AGC S	GCA A GAG E GCG A ATG M GTG V GCC A AGT S	CTC L CCT P AAAA K GTG V GGC G ATC I GCT A	TCC S TTC F TTC F ATC I TGG W TTC F	TAC T TAC Y CGC R ACG T CTC L AAG K AAG K	ACC T ATG M GTC V ATC I AGC S GTC V	ATC I GTG V GGC G CGC R GGA G ATC I TTC F	TTCT TTCC F TTCC S CAT H V CAT H V TTCC F TTCC F TTCC F	TCC S AGG R GCC A I TTT F CTG L TCC S	GCT A ACC T AAG K ACC T GTG V TGG W AAG K	CCA P GTG V ACT T GTC V CTC L CTC L CAA Q	CTG L GGT G AAC N ACC T TGC C GGC G CAA Q	CTA L V GCC A A AGC S TTC F TGG W TTAT Y TGA *	TTT F TTC F GTC V CAG Q TTC F TTC F GAG	GCC G TAC Y TCC S ACA T CCT P AAT N ACCA	180 210 240 270 300 330 330

1596 CATGGGAGTGCCTTCTTCCCATAGCTTGTAGCTCAGTGGGTTATATTGTCCCATGAACCTTTGCAGGCTGCCCAGCTGTCTTTGAGGACAAGATCC

Fig. 1. Nucleotide sequence of the 5HT5 cDNA. The 4 kbp long EcoRI - XhoI cDNA fragment was sequenced on both strands from the EcoRI site to position 1691. The remaining 2300 nucleotides were not sequenced except the 3' end, which contained a poly A tail. The seven putative transmembrane domains are boxed and numbered (I-VII). Arrows indicate sites of potential N-linked glycosylation. Circles and triangles correspond to consensus sites for phosphorylation by protein kinases C and A, respectively. An in frame stop codon upstream of the ATG is underlined. The asterisk indicates the terminal stop codon.

by all other cloned members of the G protein-coupled receptor family. The amino-terminal end displayed two putative sites for N-linked glycosylation and the presumed cytoplasmic domains contained consensus sites for phosphorylation by protein kinases C and A (Figure 1), features that are also found in most members of that family.

Amino acid sequence comparisons revealed homologies with G protein-coupled receptors in the putative transmembrane domains and short connecting loops, but not in the amino- and carboxy-terminal ends or in the third cytoplasmic loop, which are very variable in sequence and in length within this gene family. Percentages of homology were therefore calculated over the conserved regions (Figure 2A) and used to establish a dendrogram (Figure 2B). The percentages of homology with known receptors are low, the best score being 37% with a *Drosophila* serotonin receptor 5HT-dro2A (Saudou *et al.*, 1992). The dendrogram clearly shows that the 5HT5 receptor does not belong to a subfamily of serotonin receptors such as for example the 5HT1B/1D family or the 5HT2/5HT1C family.

Pharmacological profile of the 5HT5 receptor

To determine whether the 5HT5 cDNA clone encoded a functional receptor, we introduced it into a eukaryotic expression vector and transfected Cos-7 cells with the

[¹²⁵I]LSD displayed a single saturable binding site: $K_d =$ 340 pM and $B_{max} =$ 1.6 pmol/mg of membrane protein (Figure 3). In a control experiment, [¹²⁵I]LSD did not bind to mock-transfected Cos-7 cells. To determine the pharmacological profile of the 5HT5 receptor, bound [¹²⁵I]LSD was displaced with various serotonergic drugs (Table I). These compounds displayed the following rank order of potencies: 2-bromo LSD > ergotamine > 5-CT > methysergide > 5-HT = RU24969>bufotenine = yohimbine = 8-OH-DPAT (Table I). Ketanserin, (-) pindolol, sumatriptan, dopamine and (-) norepinephrine were inactive. In some experiments, the competition curves obtained with 5-HT were slightly biphasic and indicated that 5-10% of the [¹²⁵I]LSD binding sites may have a high affinity for

5-HT were slightly biphasic and indicated that 5-10% of the [¹²⁵I]LSD binding sites may have a high affinity for 5-HT. This observation suggested that in the transient Cos-7 expression system, most of the 5HT5 receptor may be in a low affinity state, possibly because of its overexpression in this system. A similar observation had been previously made after expressing the *Drosophila* 5-HT receptors in Cos-7 cells (Saudou *et al.*, 1992). Therefore it was decided

resulting recombinant. Membranes of transfected cells were

then assayed for their ability to bind a number of serotonergic radioligands. While [¹²⁵I]cyanopindolol, [³H]8-OH-DPAT

and [³H]spiperone did not bind to these membranes,



Fig. 2. A. Percentages of amino acid homologies between the 5HT5 receptor and other members of the G protein-coupled receptor family. These percentages of homology were calculated over the sequences that are conserved in this gene family: the transmembrane domains and short connecting loops (Hen, 1992). B. Dendrogram. The sequences of the mouse $5HT1B\beta$ (Maroteaux *et al.*, 1992), human $5HT1D\alpha$ (Hamblin and Metcalf, 1991), human 5HT1A (Fargin *et al.*, 1988), *Drosophila* 5HT-dro1 and 5HT-dro2A (Saudou *et al.*, 1992), human α 2A adrenergic (Kobilka *et al.*, 1987), rat D2 dopaminergic (Bunzow *et al.*, 1988), human β 1 adrenergic (Frielle *et al.*, 1987), human D1 dopaminergic (Dearry *et al.*, 1990), human H2 histaminergic (Gantz *et al.*, 1991), rat 5HT1C (Julius *et al.*, 1988) and rat 5HT2 (Pritchett *et al.*, 1988) receptors were compared and clustered with the program 'clustal' (Higgins and Sharp, 1988). The lengths of the horizontal lines are inversely proportional to the percentages of homology (A).

to introduce the 5HT5 receptor in a more physiological environment by generating stable cell lines expressing variable levels of this receptor. NIH-3T3 cells were chosen because they do not express any endogenous serotonin receptor and because they have been used to characterize various 5-HT receptors. The 5HT5 expression vector was introduced in these cells together with the Neo gene encoding resistance to G418. G418-resistant cell lines were isolated and a Northern analysis was performed with RNA from these cells. We selected two cell lines, NS1 and NS4, expressing high and low levels of 5HT5 mRNA, respectively. Membranes prepared from these cells displayed high affinity ^{[125}I]LSD binding sites, indicating that both cell lines expressed the 5HT5 receptor (Figure 4). The Scatchard analysis revealed that [125]LSD had about the same affinity for both cell lines as for Cos-7 cells: $K_d = 240$ pM in the case of NS1 cells and $K_d = 280$ pM in the case of NS4 cells. As expected from the RNA analysis, NS1 cells expressed more 5HT5 receptor as NS4 cells: B_{max} (NS1) = 350 fmol of receptor/mg of membrane protein, while B_{max} (NS4) = 105 fmol/mg. In a control experiment, membranes from wild type 3T3 cells did not bind [125I]LSD. Displacement studies were performed with various compounds (Figure 5). In the case of 5-HT, 5-CT, sumatriptan and 8-OH-DPAT, the resulting competition curves were biphasic. A computer-generated two-site analysis of these data revealed both a high affinity and a low affinity binding site (Table I). In the case of NS1 cells, ~10% of the $[^{125}I]$ LSD sites displayed a high affinity for 5-HT while in the case of NS4 cells, which express lower levels of 5HT5 mRNA, 25% of the sites had a high affinity for 5-HT. These high affinity sites may correspond to receptors coupled with G proteins. Such G proteins may be present in limiting amounts and therefore, when the 5HT5 receptor is expressed at high levels, like in Cos-7, only a small fraction of the receptors may couple with G proteins. To test the hypothesis that the high affinity sites correspond to G protein-coupled receptors, the same competition studies were performed in the presence of GTP, which has been shown to uncouple various receptors (De Lean et al., 1982). The resulting curves were shifted to the right and revealed only a low affinity component, suggesting that the high affinity sites have been converted in low affinity sites due to the uncoupling effect of GTP (Figure 6).

The NS1 and NS4 cells were also used to investigate a possible effect of the 5HT5 receptor on second messenger levels. In a series of preliminary experiments we have not been able to detect any changes in the levels of cAMP or inositol phosphates in response to serotonin, in these cells. In the same conditions, the 5HT1B β receptor induced a



Fig. 3. Saturation isotherm of $[^{125}I]$ LSD binding to membranes of Cos-7 cells expressing the SHT5 receptor. Membranes were incubated with concentrations of $[^{125}I]$ LSD ranging from 50 pM to 1.25 nM \pm 10 μ M 5-HT. Specific binding is represented. Inset, Scatchard analysis of $[^{125}I]$ LSD binding: $K_d = 340$ pM, $B_{max} = 1.6$ pmol receptor/mg of membrane protein. Data are representative of two independent experiments with each point performed in triplicate.

Table I. Pharmacological profile of the 5HT5 receptor

decrease in cAMP levels (Saudou *et al.*, 1992). Our negative results therefore suggest that the 5HT5 receptor has different intracellular signalling properties than the 5HT1B β receptor.

The 5HT5 receptor is expressed in the central nervous system

Expression of 5HT5 transcripts was analysed by Northern, quantitative PCR and by *in situ* hybridization experiments. The Northern analysis revealed three transcripts in brain and cerebellum (5.8, 5 and 4.5 kb); no transcripts were detected in kidney or liver (Figure 7A). These three transcripts could derive either from a single gene or from several genes that are very homologous to one another.

We used also a more sensitive technique, 'quantitative PCR', to analyse 5HT5 RNA levels in a wider range of tissues. Specific PCR fragments could be amplified from spinal cord and brain RNAs, but not from RNAs prepared from spleen, liver, kidney, lung or heart (Figure 7B). To analyse further the pattern of expression of this receptor, we performed in situ hybridization experiments on adult mouse brain sections (Figures 8 and 9). The main sites of expression were the cerebral cortex, the hippocampus, the granular layer of the cerebellum, the habenula and the olfactory bulb. In a control experiment performed in the same conditions with a 'sense' RNA probe, no hybridization was observed. Bright-field observation of the emulsion coated slides revealed that the 5HT5 mRNA was expressed in the granule cells of the cerebellum and of the dentate gyrus and in pyramidal cells of the layers CA1, CA2 and CA3 of the hippocampus. A large number of neurons were stained in all areas of the cerebral cortex. In the olfactory bulb the

	pK _i values									
	SHT5	5HT5 (NIH-31	'3 cells)	5HT1D	5HTID					
	(Cos-7 cells)	Low	High	(rat cortex)	(Call caudate)					
5-HT	6.6 (7)	6.6 (6)	8.1 (6)	8.7	8.4					
5-CT	7.8 (3)	7.9 (3)	9.5 (3)	8.6	8.6					
RU 24969	6.5 (2)				7.3					
TFMPP	5.6 (2)			6.6	6.2					
8-OHDPAT	5.9 (2)	5.8 (2)	7.0 (2)	6.6	5.9					
Sumatriptan	4.8 (2)	4.7 (5)	6.8 (5)		7.5					
Bufotenine	6.0 (2)		.,		8.1					
Methysergide	7.2 (5)	7.1	(2)	7.3	8.4					
Ergotamine	8.4 (2)	8.2	(2)		7.8					
2-Bromo LSD	8.7 (2)									
Methiothepin	7.0 (2)	6.9	(2)		6.3					
Yohimbine	6.0 (2)	6.2	(2)		7.1					
(-)Pindolol	4.7 (2)			< 5	5.2					
(-)Propranolol	4.9 (2)				5.5					
Ketanserin	4.8 (2)			< 5	5.7					
Spiperone	5.6 (2)				5.3					
Dopamine	4.1 (2)									
(-)Norepin	2.8 (2)									

Data correspond to competition for $[^{125}I]$ LSD binding to membranes of either Cos-7 cells expressing transiently the 5HT5 receptor (first column) or NS4 cells which derive from NIH-3T3 cells and stably express the 5HT5 receptor (second column). IC₅₀ values required to displace 50% of $[^{125}I]$ LSD were determined experimentally and converted to pK_i values according to the equation $K_i = IC_{50}/(1 + C/K_d)$ where C is the $[^{125}I]$ LSD concentration (150 pM) and K_d is the equilibrium dissociation constant of $[^{125}I]$ LSD. The data obtained with 5-HT, 5-CT, sumatriptan and 8-OH-DPAT in NS4 cells were best fit by a computer-generated two-site analysis. In these cases both the low affinity and the high affinity pK_i values are indicated. Numbers in parentheses correspond to the number of independent experiments each point being performed in triplicate. Individual pK_i values differed by <20%. The pK_i values for the 5HT1D receptor in rat cortex correspond to the high affinity binding components (Herrick-Davis *et al.*, 1988). In the case of the calf caudate 5HT1D receptor, pK_i values are taken from Waeber *et al.* (1990).

strongest staining was observed in the tufted cells (arrows in Figure 9A and B).

Discussion

Our data indicate that we have isolated a functional serotonin receptor that is expressed predominantly in the central nervous system. The sequence of this receptor reveals that it is a new member of the G protein-coupled receptor family. Although its closest relatives are serotonin receptors, this new receptor does not exhibit a strong homology to any of the already cloned serotonin receptors. Therefore it does not belong to existing subfamilies of serotonin receptors such as the 5HT1B/1D family or the 5HT1C/5HT2 family. Since the numbers 3 and 4 have been already used to designate different subtypes of 5-HT receptors, it was decided to name this receptor 5HT5.



Fig. 4. [¹²⁵I]LSD binding to membranes of NS1 and NS4 cells. NS1 and NS4 cells are NIH-3T3 derivatives that stably express the 5HT5 receptor (Materials and methods). Saturation isotherms were performed as described in legend to Figure 3. The Scatchard analysis is represented. Open circles correspond to NS4 cells: $K_d = 280$ pM, $B_{max} = 105$ fmol/mg of membrane protein; closed circles correspond to NS1 cells: $K_d = 240$ pM, $B_{max} = 350$ fmol/mg. Data are representative of two independent experiments with each determination performed in triplicate.



Fig. 5. Competition displacement of $[^{125}I]LSD$ from membranes of NS4 cells. Membranes of NS4 cells were incubated with 150 pM of $[^{125}I]LSD$ and various concentration of the following drugs: 5-CT (open circles), 5-HT (closed triangles), methysergide (open triangles) and sumatriptan (open squares). The displacement curves obtained with 5-CT, 5-HT and sumatriptan were best fit by a computer-generated two-site analysis. 20-25% of the binding sites had a high affinity for these compounds; the high and low affinity pKi values are indicated in Table I. Data are representative of five independent experiments with each determination performed in triplicate.

The pharmacological profile of the 5HT5 receptor, transiently expressed in Cos-7 cells, was unusual and did not correspond to the profile of any of the previously characterized serotonin receptors. However, these studies were performed in cells where the 5HT5 receptor was overexpressed. Therefore the low affinity pK_i values obtained with agonists such as 5-HT may correspond to receptors that were not coupled to G proteins. In support of this hypothesis is the fact that when the 5HT5 receptor was expressed at lower levels, such as in the stable cell line NS4, it displayed two affinities for 5-HT, a high affinity and a low affinity, which was similar to the low affinity observed in Cos-7 cells (Table I). Furthermore, the high affinity sites were converted into low affinity sites by GTP suggesting that they correspond to receptors coupled to G proteins. If one considers the high affinity pK_i values of the 5HT5 receptor obtained in NS4 cells, then the pharmacological



Fig. 6. Effect of GTP on [¹²⁵I]LSD binding to NS4 cells. Membranes of NS4 cells were incubated with 150 pM of [¹²⁵I]LSD and various concentrations of 5-HT in the presence or in the absence of 100 μ M GTP. The displacement curve obtained in the absence of GTP was best fit by a computer-generated two-site analysis (pKi values are shown in Table I). In the presence of GTP the displacement was monophasic: pK_i = 6.6. Data are representative of three independent experiments with each determination performed in triplicate.



Fig. 7. Distribution of 5HT5 transcripts. A. Northern blot analysis of $poly(A)^+$ RNA (5 μg) from various organs. Three transcripts were detected in cerebellum and brain, but not in liver or kidney. The probe used is the ³²P-labelled *EcoRI*-*XhoI* cDNA fragment. B. Quantitative PCR analysis performed with 1 μg of total RNA from various organs. A 404 bp specific PCR product (arrow) is detected in spinal cord, hindbrain and forebrain, but not in all other organs tested.



Fig. 8. In situ hybridization. The RNA probe was prepared as described in Materials and methods. In the experiment presented (panels a-c), the probe corresponds to the full-length cDNA plasmid (Figure 1). The same results were obtained with a shorter probe corresponding to the coding region (see Materials and methods). **a.** Dark field microscopy of the emulsion autoradiograph of an horizontal section through an adult mouse brain (8 mm wide). **b** and **c**. 2-fold magnifications of the hippocampal and cerebellar regions seen in panel a. Abbreviations: Cx, cerebral cortex; OB, olfactory bulb; H, Hippocampus; Cb, Cerebellum; CA 1–3, CA1, CA2 and CA3 hippocampal areas; DG, dentate gyrus; G, granular layer of the cerebellum.

profile of this receptor becomes similar to that of the 5HT1D receptor (Table I).

Until recently there was little evidence of heterogeneity within the 5HT1B/1D receptor family. Most authors believed that the 5HT1B and 5HT1D receptors were species variants of a same receptor subtype, the 5HT1B receptor being present in mice and rats and the 5HT1D receptor in all other mammals. Recently, however, indications of heterogeneity came from both pharmacological studies and molecular cloning studies. 5HT1D sites were found in rat brain in addition to 5HT1B sites (Herrick-Davis and Titeler, 1988; Weisberg and Teitler, 1992). Furthermore, the biphasic competition curves obtained with compounds such as 5-CT, sumatriptan, RU24969 and TFMPP on brain membranes from various mammalian species including human, have suggested that 5HT1D and 5HT1B sites may be heterogeneous (Asarch et al., 1985; Heuring et al., 1986; Leonhardt et al., 1989; Sumner and Humphrey, 1989; Mahle et al., 1991a; Peroutka, 1991a; Beer et al., 1992). In addition, molecular cloning studies identified two 5HT1B/1D receptor subtypes, α and β , in mice (Maroteaux et al., 1992), rats (Voigt et al., 1991) and human (Weinshank et al., 1992). The RNA corresponding to the α subtype is expressed in very low amounts in the mouse

SHT1B pharmacological profile. The $5HT1B\beta$ receptor therefore most probably corresponds to the 5HT1B sites that have been characterized in the substantia nigra of mice and rats (Schoeffter and Hoyer, 1989; Bouhelal *et al.*, 1988). The human counterpart of this receptor is the $5HT1D\beta$ receptor (Adham *et al.*, 1992). The mouse and rat $5HT1B\beta$ receptors, which have a 5HT1B pharmacological profile, cannot account for the 5HT1D sites that have been reported in rats, because these sites were detected in conditions where the 5HT1B sites were blocked (Herrick-Davis and Titeler, 1988). Because of its very low abundance, the rat $5HT1D\alpha$ is also an unlikely

candidate for these 5HT1D sites that are relatively abundant in most brain areas (Herrick-Davis and Titeler, 1988). We therefore believe that the 5HT5 receptor may correspond to the 5HT1D sites observed in the rat brain, or to a fraction of these sites. In keeping with this hypothesis, is the fact

brain (our unpublished observation); this receptor, which has a 5HT1D-like pharmacological profile (Voigt *et al.*, 1991),

may therefore be very rare and has probably not been

detected by classical pharmacological techniques. In contrast,

the 5HT1B β subtype is abundant, it is expressed

predominantly in striatal neurons projecting to the substantia

nigra (Hen, 1992; Maroteaux et al., 1992) and it has a



Fig. 9. In situ hybridization. The same probe as in Figure 8 was hybridized to adult mouse brain horizontal sections. Panels A-B correspond to the glomerular layer of the olfactory bulb (100 μ m wide). Panels C-D represent a region containing the habenula and the dorsal third ventricule (1 mm wide). A and C. Bright-field microscopy of emulsion autoradiographs counterstained with toluidine blue to reveal cell bodies. Autoradiographic grains are most abundant over tufted cells (arrows in panel A). B and D. Dark-field photomicrographs of the same emulsion-coated slides as in panels A and C, respectively. The lowest arrow in panels C and D indicates a group of cell bodies that may correspond to the subcommissural organ and that does not express the SHT5 RNA. Abbreviations: Gl, olfactory glomerulus; MH, median habenula.

that the 5HT5 receptor is expressed in cortex, hippocampus and cerebellum, brain regions where the rat 5HT1D sites were also found.

The 5HT5 receptor may also correspond to some of the 5HT1D-like sites that have been reported in the brain of various mammalian species and that could have slightly different pharmacological profiles due to species differences. However, the high affinity of 5-CT and ergotamine for the 5HT5 receptor, indicates that this receptor does not probably correspond to the 5HT1E sites that have a low affinity for 5-CT and ergotamine and have been found in human brain (Leonhardt *et al.*, 1989) and possibly in rat brain (Weisberg and Titeler, 1992).

It is also interesting to notice that unlike the 5HT1B and 5HT1D receptors, the 5HT5 receptor does not inhibit adenylate cyclase in NIH-3T3 cells. No effect on phospholipase C could be detected either. *In vivo*, this receptor may therefore interact with a different signalling system such as ion channels. Consistent with this hypothesis is the fact that, while 5HT1D receptors have been shown to inhibit adenylate cyclase in substantia nigra, no such coupling could be detected in other brain regions where 5HT1D receptors are also found, such as cortex and striatum (Waeber *et al.*, 1990). These authors actually postulated on that basis, a possible heterogeneity of 5HT1D receptors. Because of its expression in cerebral cortex, the 5HT5 receptor may correspond to some of the previously reported cortical 5HT1D sites.

Concerning a possible function of the 5HT5 receptor, due to the similarity between this receptor and the 5HT1D receptor, it is conceivable that some of the effects attributed to the 5HT1D receptors such as their involvement in motor control, feeding, anxiety and depression (Wilkinson and Dourish, 1991), may actually be mediated by the 5HT5 receptor. The 5HT5 receptor may also be involved in some of the physiological effects evoked by 5HT1D-like receptors. In the cerebellum for example, a 5HT1D-like receptor has been shown to inhibit the release of glutamate from granule cell nerve endings (Raiteri et al., 1986). In the hippocampus, a number of effects mediated by 5HT1D-like receptors have also been reported, such as a stimulation of phosphoinositide turnover (Conn and Sanders-Bush, 1985) and a modulation of K-conductances (Colino and Halliwell, 1987; Yakel et al., 1988).

Our results confirm previous pharmacological studies indicating that the 'non-5HT1A, -1B, -1C and -2' receptors constitute a heterogeneous family of receptors. Some of these 5HT1D receptors are close relatives such as the 5HT1D α and 5HT1D β receptors. Others, like the 5HT5 receptor, are very different not only in their amino acid sequence, but also in their expression pattern and in their intracellular signalling properties. The availability of the genes encoding the various 5HT1D receptors should allow us, via gene targeting techniques, to dissect the individual roles of each of these receptor subtypes in the mouse.

Materials and methods

Isolation and sequence of the 5HT5 cDNA

A nested PCR experiment was performed with the following oligonucleotides: (i) AGAACTAGTGGATCCAA(A/G)AA(A/G/C/T)GG(A/G/C/T)A(A/G)-CCA(A/G)CA; (ii) CTTGATATCGAATTCGA(T/C)(A/G)T(A/G/C/T)CT-(A/G/C/T)TG(C/T)TG(C/T)AC; (iii) GGTATCGATAAGCTTAT(C/T/A)-GC(C/T)CT(A/G/C/T)GA(C/T)(C/A)G(A/G/C/T)TA. 5 µg of adult mouse brain RNA were reverse transcribed in the presence of 500 ng of oligo (i) and 200 units of MMLV reverse transcriptase (BRL). Half of that reaction was then amplified for 30 cycles in the presence of 5 units of Taq polymerase (Cetus) and 1 μ g of oligonucleotides (i) and (ii). One-twentieth of that reaction was amplified for 30 more cycles with oligonucleotides (i) and (iii). The resulting products were digested with BamHI and HindIII, inserted in the Bluescript plasmid and sequenced. One of resulting fragments that exhibited homology with 5-HT receptors, was labelled by random priming and used to screen a mouse brain cDNA library constructed in the Uni-Zap phage (Stratagene). Positive phages were isolated, the cDNA inserts were recovered in the Bluescript plasmid and sequenced on both strands by the dideoxynucleotide technique using successive synthetic oligonucleotides.

Expression of the 5HT5 receptor in cultured cells

The *Eco*RI–*Xho*I cDNA fragment (Figure 1) was inserted between the *Eco*RI and *Xho*I sites of expression vector p513, which is a derivative of pSG5 (Green *et al.*, 1988) containing a multiple cloning site. The resulting recombinant was introduced into mouse NIH-3T3 cells by calcium phosphate-mediated transfection together with the recombinant pRSVneo, which encodes resistance to G418 (20 μ g of 5HT5 recombinant and 1 μ g of pRSVneo per 10 cm dish). Transformed clones were selected in the presence of 0.5 mg of G418/ml. Isolated foci were amplified and total RNA was prepared and analysed for expression of 5HT5 RNA. Two clonal cell lines were selected (NSI and NS4) that expressed variable levels of 5HT5 RNA as determined by Northern blot analysis.

For transient expression of the 5HT5 receptor, Cos-7 cells were transfected

by the calcium phosphate technique with the 5HT5 recombinant alone (20 μg per 10 cm dish) and harvested 48 h after transfection.

Radioligand binding assay

Membranes were prepared as described in Amlaiky and Caron (1985). [¹²⁵I]LSD saturation and competition binding experiments were performed with $10-20 \mu g$ protein per sample in a final volume of 250 μ l in 50 mM Tris-HCI (pH 7.4) at 37°C for 10 min. Reactions were terminated by filtration under vacuum over Whatman GF/C glass fibre filters and rinsed four times with 4 ml of 50 mM Tris-HCl (pH 7.4). Non-specific binding was defined with 10 µM 5-HT. Radioactivity was determined in a gamma counter.

Northern and quantitative PCR analysis

Poly(A)⁺ RNA was prepared, fractionated on a 1% agarose-formaldehyde gel and transferred to a nitrocellulose filter. The probe was the EcoRI-XhoI cDNA fragment that was ³²P-labelled by random priming and hybridized to the filter at high stringency (42°C, 50% formamide, 5×SSC, 1×Denhardt's, 20 mM sodium phosphate buffer pH 6.5, 0.1% SDS and 100 μ g/ml tRNA). Washes were performed at high stringency (60°C, 0.1×SSC and 0.1% SDS).

For the quantitative PCR analysis we used the following oligonucleotides: (i) CTTCTGCTCCCTCCACGTATC and (ii) CGCCACCTGGAGTAC-ACACTC corresponding to positions 1351 and 947, respectively (Figure 1). 1 µg of total RNA was reverse transcribed with 200 units of MMLV reverse transcriptase and 300 ng of oligonucleotide (i) for 1 h at 37°C. Half of that reaction was amplified in the presence of 5 units of Taq polymerase (Cetus) and 500 ng of oligonucleotides (i) and (ii) for 20 cycles. These PCR products were transferred to filters and hybridized as described above.

In situ hybridization

In situ hybridizations were performed on cryostat sections of adult mouse brains (~8 weeks old) as described by Hafen et al. (1983). The probe used was a single stranded RNA probe produced in the presence of [⁵SICTP and as a template, either the full-length cDNA plasmid (Figure 1) or a plasmid containing a PCR fragment corresponding to most of the 5HT5 coding region (from positions 375-1351 in Figure 1). The antisense probe was produced in the presence of T7 polymerase and a template linearized by EcoRI, while for the sense probe, we used T3 polymerase and a template linearized by XhoI.

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