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An mRNA Encoding a Putative GABA-Gated Chloride Channel Is Expressed in the Human Cardiac Conduction System

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Abstract: GABA-gated chloride channels are the main inhibitory neurotransmitter receptors in the CNS. Conserved domains among members of previously described GABA_A receptor subunits were used to design degenerate sense and antisense oligonucleotides. A PCR product from this amplification was used to isolate a full-length cDNA. The predicted protein has many of the features shared by other members of the ligand-gated ion channel family. This channel subunit has significant amino acid identity (25–40%) with members of GABA_A and GABA_C receptor subunits and thus may represent a new subfamily of the GABA receptor channel. Although we cannot rule out that this clone encodes a receptor for an unidentified ligand, it was termed GABA_χ. This gene is mainly expressed in placenta and in heart; however, placenta appears to express only an unspliced mRNA. In situ hybridization reveals that the GABA_χ subunit mRNA is present in the electrical conduction system of the human heart. Our results suggest that novel GABA receptors expressed outside of the CNS may regulate cardiac function. **Key Words:** GABA receptors—Conduction system—Heart—Reverse transcriptase—PCR—In situ hybridization. *J. Neurochem.* **68**, 1382–1389 (1997).

The ligand-gated ion channels that are activated by GABA, acetylcholine, glycine, and serotonin share several features (Noda et al., 1982; Grenningloh et al., 1987; Schofield et al., 1987; Maricq et al., 1991): A large NH₂-terminal extracellular domain containing a signature consensus sequence, the Cys–Cys loop, four hydrophobic transmembrane domains (M1–M4), and a long cytoplasmic loop connecting M3 and M4. The ligand-gated channels are pentameric membrane proteins comprised of homologous subunits (Langosch et al., 1988; Cooper et al., 1991). By analogy, it is assumed that the GABA-gated chloride channels are also pentameric (Nayem et al., 1994). Single subunits from some members of this family can form functional homomeric receptors, but they typically lack properties

of the native multisubunit receptor (Schofield et al., 1987).

GABA is the major inhibitory neurotransmitter in the CNS. However, GABA is also present in peripheral tissues where it acts on GABA receptors identical to those found in the CNS (Rorsman et al., 1988; Boué-Grabot et al., 1995). Different subtypes of GABA-gated chloride channels are generated by coassembly of subunits $\alpha 1$ –6, $\beta 1$ –3, $\gamma 1$ –3, δ (GABA_A), and $\rho 1$ –3 (GABA_C) (for review, see Sieghart, 1995). Subunits are grouped according to the degree of sequence identity. For example, the six α subunits are ~70% identical, but only 25–30% identical to β subunits (DeLorey and Olsen, 1992). Glycine receptors also form chloride channels, and their subunits are similar to those of the GABA receptors (Grenningloh et al., 1987). These similarities are mainly found in the transmembrane domains believed to form the Cl[−] channel. We set out to clone new chloride channels; consensus sequences for the transmembrane domains of GABA/glycine receptor subunits were used to design degenerate oligonucleotides, which were then used as primers in the PCR.

We report here the cDNA sequence of an mRNA, expressed in human heart, encoding a protein that contains the hallmarks of ligand-gated channel subunits. The predicted protein displays strong similarities to GABA_A and GABA_C receptor subunits and was termed GABA_χ. It is highly expressed in the electrical conduction system of the heart.

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Abbreviations used: ORF, open reading frame; RT, reverse transcription.

MATERIALS AND METHODS

PCR amplification

Primers for the PCR were selected from the second (M2) and third (M3) transmembrane domains, which are highly conserved among the GABA_A and glycine receptor subunits.

Mixed oligonucleotide primers M2: 5' TCGAATTC ACNATGACNAC were derived from amino acid sequence TMTT. Mixed primers M3: 5' CAAAGCTT (A,G) AA (G,T,C) AC (A,G) AA were derived from amino acid sequence FVF. In the oligonucleotide sequences, N stands for G+A+T+C and underlined nucleotides indicate 5'-extensions that include the *Eco*RI restriction enzyme site for M2 and the *Hind*III site for M3. PCR amplification was performed in a final volume of 50 μ l containing 1 U of Taq polymerase (Cetus) in the buffer supplied by the manufacturer, with 1 μ l cDNA obtained from T84 RNA, 1 μ M concentration of each primer, and 0.2 mM concentration of each deoxyribonucleotide. Amplification was performed according to the following schedule: first, three cycles of denaturation 60 s at 95°C, annealing 30 s at 29°C, and an extension for 30 s at 72°C, followed by 30 cycles of 30 s at 95°C, 30 s at 50°C, and 30 s at 72°C. The amplified products were then separated on a 6% acrylamide gel. A gel slice containing the band size ranging from 90 to 130 bp was cut out and incubated in 20 μ l of water; 5 μ l of the eluate was used for PCR amplification as described above, except that the first three cycles were omitted. The amplified cDNA was ethanol-precipitated, digested with *Eco*RI and *Hind*III restriction enzymes, and ligated into pBluescript (Stratagene). The recombinant DNA was transfected into *E. coli* and individual clones were analyzed by enzymatic sequencing (Sanger et al., 1977).

PCR analysis of RNA expression

Total RNA from the sinus node of a 20-week-old human fetus was isolated by the method of Chomczynski and Sacchi (1987). cDNAs were synthesized in 20 μ l of reverse transcription mixture using superscript reverse transcriptase (GibcoBRL). Subsequently, 1 μ l of sinus node cDNA was amplified by PCR; 1 μ l of a λ gt10 human fetal heart library (Clontech) was likewise amplified. The primers used for the GABA χ PCR were (5'-3') C3 (reverse): AGATGATGT-CAATGGTGTTATCCATG and C4 (forward): TCCCGT-GATGTTGTCTATGGC. PCR products were generated by 1 U of Taq DNA Polymerase (Appligene, Illkirch, France) in the manufacturer's buffer. Reactions were performed for 35 cycles: 94°C, 30 s; 60°C, 30 s; and 72°C, 30 s in a tri-thermoblock apparatus (BIOMETRA, Göttingen, Germany). The primers used for the human tryptophanyl-tRNA (Frolova et al., 1991) synthetase were HWS1: GTGAAA-GAGTTCATGACTC, HWS2: ACCTACTGGCTGACAGGAG, and HWS3: AGGGCAGAGTGCTCCAGAGGA. Reactions were performed for 35 cycles: 94°C, 30 s; 56°C, 30 s; and 72°C, 90 s with primers HWS1 and HWS2. Then 1 μ l of this reaction was used for a nested PCR with primers HWS1 and HWS3 as above; 5 μ l of the 50- μ l PCR reactions was used for separation of the DNA products on a 2% agarose gel in TAE (Tris-acetate-EDTA) buffer.

Screening of a T84 cell line library

RNA was isolated from T84 cells by guanidinium thiocyanate dissolution followed by centrifugation in cesium chloride solutions; poly(A)⁺ RNA was isolated on an oligo(dT)

cellulose column (Sambrook et al., 1989). A cDNA library was constructed using the pSPORT-cDNA cloning kit (GibcoBRL). The library was screened under high-stringency conditions. The nucleotide sequence of the cDNA insert of positive clones was determined on both strands by the dideoxy chain termination method (Sanger et al., 1977). The 5'Ampli FINDER RACE kit (Clontech) with poly(A)⁺ RNA from adult human heart (Clontech) was used to clone the remaining portion of the coding region. Specific primers from the T84A clone and from the λ gt10 cloning vector sequences were also used to screen a fetal heart library (Clontech) by PCR. The full-length cDNA insert was constructed from pieces of the PCR products and pSPORT-T84 cDNA clone and subcloned into the pCDNA3 vector (Invitrogen). To verify the final construct, the pCDNA3 insert was sequenced.

Northern blot and in situ hybridization

Poly(A)⁺ RNA from T84 cells was electrophoresed in a 1.2% agarose gel containing 2.2 M formaldehyde and transferred to Hybond-N membrane (Amersham). A multiple tissue northern blot containing human mRNAs (Clontech) was also used. The hybridization was performed at 42°C for 20 h in a standard solution containing 50% formamide (Sambrook et al., 1989).

A human fetal heart was obtained at autopsy after spontaneous abortion at the Centre Hospitalier Regional de Bordeaux (France) in accordance with guidelines and recommendations of the Comité National d'Éthique. The heart was fixed by immersion for 24 h in 1% paraformaldehyde, then stored at -80°C until sectioning. The *Eco*RI-*Kpn*I fragment (nucleotides 526-1,573, see Fig. 3) was subcloned into pBluescript. Radiolabeled antisense and sense cRNA probes were prepared by in vitro transcription of the pBluescript subclone with [³³P]UTP (Amersham). Probes were hydrolyzed to ~250 bases length and used at 20 \times 10⁶ cpm/ml. Sections (10 μ m thick) were cut on a cryostat, collected on gelatin-coated slides, and fixed in 4% paraformaldehyde. Hybridization was performed as described (Brana et al., 1995) with 1 month of exposure time before development.

RESULTS

PCR amplification of a GABA receptor-related cDNA

T84 cells, derived from a colon tumor, are known to contain Cl⁻ channels (Schoumacher et al., 1990) and were used in reverse transcription-PCR (RT-PCR) experiments. T84 first-strand cDNA was amplified with the two degenerate oligonucleotides M2 and M3 derived from the ligand-gated chloride channel subunit transmembrane domains M2 and M3. These domains, believed to form the chloride channel pore, are conserved among the GABA/glycine receptor subunits. The PCR amplification product was cloned and the DNA sequenced. Analysis of the inferred amino acid sequence showed significant similarities with those of GABA_A and glycine receptor subunits. Screening 3 \times 10⁵ clones from a T84 cDNA library with this cDNA yielded 11 positively hybridizing clones. Four clones were isolated and sequenced. Two clones, T84A (2.2 kb) and T84I (3.5 kb), contained an open reading

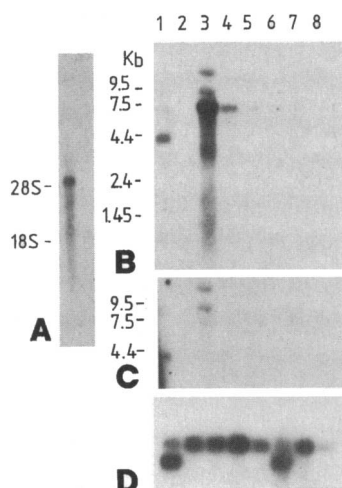


FIG. 1. Northern blot analysis of T84A GABA_A-like mRNA expression. Poly(A)⁺ RNA (2 μ g) was extracted from T84 cells (**A**) and from human tissues (**B**, **C**, and **D**). **B**: Heart (lane 1), brain (lane 2), placenta (lane 3), lung (lane 4), liver (lane 5), skeletal muscle (lane 6), kidney (lane 7), and pancreas (lane 8). RNAs were loaded on the gel, electrophoresed, transferred, and subjected to RNA hybridization analysis. **A** and **B**: Hybridization with the random-labeled T84A probe. **C**: The RNA blot shown in **B** was hybridized with the labeled 5'-end of the T84A clone insert. **D**: The RNA blot shown in **B** and **C** was hybridized with a β -actin probe to control for variation in sample loading. Molecular weights were determined using ribosomal RNA (**A**) or an RNA ladder (**B**, **C**).

frame (ORF) predicted to encode a protein of 242 amino acids. The other two clones, T84K and T84H, were quite similar to the T84A and T84I clones but contained an 11-bp insert (not shown) that introduced an in-frame stop codon. It is noteworthy that this insert is found at a position corresponding to a conserved intron between exons 8 and 9 of GABA and glycine receptor genes (Sommer et al., 1990). The stop codon reduced the size of the predicted protein from 242 to 116 amino acids. T84A and T84I clones were identical in their 3'-part, containing the 242 amino acids ORF; however, their 5'-part contained different sequences. The predicted 242-amino acid long protein showed significant identities with the four-transmembrane domains of GABA and glycine receptors.

To examine the tissue distribution of this mRNA, northern blots with poly(A)⁺ RNA from T84 cells and human tissues were hybridized with a probe derived from the T84A cDNA insert (Fig. 1). T84 RNA provided a major band at 6.5 kb (Fig. 1A), migrating at the level of the 28S ribosomal RNA used as size marker. Placental RNA provided a strong signal, with a major band at 6.5 kb and minor bands at 8 and 11 kb (Fig. 1B). Hybridization was also observed with lung, liver and kidney (6.5-kb band), and heart (4-, 6.5-, and 8-kb bands) RNAs. No signal was detectable with brain, skeletal muscle, and pancreas RNAs.

Northern blots using the 5'-end of the T84A insert mainly showed hybridization to heart (4-kb band) and placenta (8- and 11-kb bands) RNAs (Fig. 1C).

Identification of a novel GABA receptor-like subunit

Several independent RT-PCR amplifications were performed with human heart RNA to obtain the remaining 5'-region. A RACE-PCR procedure (Tessier et al., 1986) was used with poly(A)⁺ RNA from adult human heart and specific primers derived from the T84A clone cDNA sequence. A fetal heart library in the λ gt10 vector was also screened by PCR with specific primers from the T84A clone and from the λ gt10 vector sequences. In this way, we identified a DNA sequence containing an ORF encoding a predicted protein of 505 amino acids (Fig. 2); the RT-PCR cloned part of the sequence comprises nucleotides 1–834. The cDNA contains a consensus polyadenylation signal followed by a poly(A) tail. An initiation codon was assigned based on the match to the consensus sequence for translation initiation (Kozak, 1991). Sequence analysis of the predicted protein indicates several features common to members of the GABA-gated chloride channel family. These features include an 18-residue signal peptide, a large N-terminal extracellular domain containing potential sites for glycosylation, potential transmembrane regions, and a potential protein kinase C site in the putative large intracellular region. In addition, the protein is predicted to contain a neurotransmitter-gated ion-channel signature, the Cys–Cys loop in which two cysteines separated by 13 residues are thought to participate in the formation of a disulfide bond (Sieghart, 1995) (Fig. 2).

Alignment with multiple members of GABA_A and glycine receptor subunits (Pritchett et al., 1989; Ymer et al., 1989; Kuhse et al., 1990; Harvey et al., 1993; McLean et al., 1995) is shown (Fig. 3). The most conserved regions are (1) the N-terminal half, postulated to form the ligand binding domain, and (2) the transmembrane region. Pairwise alignment between the predicted protein and GABA_A, GABA_C, and glycine receptor subunits shows that this clone is most closely related to chicken GABA γ 4 subunit (46% identity). The amino acid identity with mammalian subunits ranges from 40% (GABA γ 2) to 25% (GABA ρ 1 and glycine receptor subunits).

GABA χ mRNA expression

The regional pattern of expression of the mRNA was examined by in situ hybridization in human heart (embryonic week 20). Sections were hybridized with radiolabeled antisense cRNA specific for the coding sequence of GABA χ transcript. The mRNA is expressed exclusively and throughout the specialized electrical conduction system. Labeling is evident in the atrioventricular node, in the conduction bundle, and in the Purkinje fibers (Fig. 4). The atrioventricular node

FIG. 2. Nucleotide and predicted amino acid (one-letter code) sequence of cloned cDNA indicate several features common to ligand-gated channels. The potential signal sequence cleavage site is indicated (arrow). Potential *N*-glycosylation sites are boxed; a potential protein kinase C phosphorylation site is indicated by an asterisk. The four-transmembrane segments are underlined and the ligand-gated disulfide-loop domain (amino acids 195–209) is overlined. The polyadenylation signal is boxed. The first methionine residue of the ORF encoded by T84 cDNA library clones is circled. The left column numbers refer to the first nucleotide in each line; the right column numbers refer to the last amino acid in each line. For convenience of presentation, part of the nucleotide sequence in the 3'-untranslated region corresponding to positions 1,659–3,093 was omitted. The complete cDNA sequence is available from EMBL and NCBI nucleotide sequence databases under accession number Y07637.

	AGAGCGTGAGCGCGACCTCCGCGCAGGTGGTGGCGCGGCTCTCCGCGGAA																								
1	M	L	S	K	V	L	P	V	L	C	L	G	I	L	L	I	L	Q	17						
51	ATG	TTG	TCC	AAA	GTT	CTT	CTA	GTC	CTC	CTA	GGC	ATC	TTA	TTG	ATC	CTC	CAG								
	S	T	R	V	E	G	P	Q	T	E	S	K	N	E	A	S	R	34							
103	TCG	AGG	GTC	GAG	GGA	CCT	CAG	ACT	GAA	TCA	AAG	AAT	GAA	GCC	TCT	TCC	CGT								
	D	V	V	Y	G	P	Q	P	Q	P	L	E	N	Q	L	L	S	51							
154	GAT	GTT	GTC	TAT	GGC	CCC	CAG	CCC	CAG	CCT	CTG	GAA	AAT	CAG	CTC	CTC	TCT								
	E	E	T	K	S	T	E	T	E	T	G	S	R	V	G	K	L	68							
205	GAG	GAA	ACA	AAG	TCA	ACT	GAG	ACT	GAG	ACT	GGG	AGC	AGA	GTT	GGC	AAA	CTG								
	P	E	A	S	R	I	L	N	T	I	L	S	N	Y	D	H	K	85							
256	CCA	GAA	GCC	TCT	CGC	ATC	CTG	AAC	ACT	ATC	CTG	AGT	AAT	TAT	GAC	ACA	AAA								
	L	R	P	G	I	G	E	K	P	T	V	V	T	V	E	I	A	102							
307	CTG	CGC	CCT	GGC	ATT	GGA	GAG	AAG	CCC	ACT	GTG	GTC	ACT	GTT	GAG	ATC	GCC								
	V	N	S	L	G	P	L	S	I	L	C	D	M	G	Y	T	I	119							
358	GTC	AAC	AGC	CTT	GGT	CCT	CTC	TCT	ATC	CTA	GAC	ATG	GAA	TAC	ACC	ATT	GAC								
	I	I	F	S	Q	T	W	Y	D	E	R	L	C	Y	N	D	T	136							
409	ATC	ATC	TTT	TCC	CAG	ACC	TGG	TAC	GAC	GAA	CGC	CTC	TGT	TAC	AAC	GAC	ACC								
	F	E	S	L	V	L	N	G	N	V	V	S	Q	L	W	I	P	153							
460	TTT	GAG	TCT	CTT	GTT	CTG	AAT	GGC	AAT	GTG	GTG	AGC	CAG	CTA	TGG	ATC	CCG								
	D	T	F	F	R	N	S	K	R	T	H	E	H	E	I	T	M	170							
511	GAC	ACC	TTT	TTT	AGG	AAT	TCT	AAG	AGG	ACT	CAC	GAG	CAT	GAG	ATC	ACC	ATG								
	P	N	Q	M	V	R	I	Y	K	G	K	V	L	Y	T	I		187							
562	CCC	AAC	CAG	ATG	GTC	CGC	ACT	TAC	AAG	DAT	GGC	AAG	GTG	TTC	TAC	ACA	ATT								
	R	M	T	I	D	A	G	C	S	L	H	M	L	R	F	P	M	204							
613	AGG	ATG	ACC	ATT	GAT	GCC	GGA	TGC	TCA	CTC	CAC	ATG	CTC	AGA	TTT	CCA	ATG								
	D	S	H	S	C	P	L	S	F	S	S	F	S	Y	P	E	N	221							
664	GAT	TCT	CAC	TCT	TGC	CCT	CTA	TCT	TTC	TCT	AGC	TTT	TCC	TAT	CCT	GAG	AAT								
	E	M	I	Y	K	W	E	N	F	K	L	E	I	N	E	K	N	238							
715	GAG	ATG	ATC	TAC	AAG	TGG	GAA	AAT	TTC	AAG	CTT	GAA	ATC	AAT	GAG	AAG	AAC								
	S	W	K	L	F	Q	F	D	F	T	G	V	S	N	K	T	E	255							
766	TCC	TGG	AAG	CTC	TTC	CAG	TTT	GAT	TTT	ACA	GGG	GTG	AGC	AAC	AAA	ACT	GAA								
	I	T	T	P	G	D	F	M	V	M	T	I	F	F	N	V		272							
817	ATA	ATC	ACA	ACC	CCA	GGT	GAC	TTC	ATG	GTC	ATG	ACG	ATT	TTC	TTC	AAT	GTG								
	S	R	R	F	G	Y	V	A	F	Q	N	Y	V	P	S	S	V	289							
868	AGQ	AGG	CGG	TTT	GGC	TAT	GTT	GCC	TTT	CAA	AAC	TAT	GTC	CCT	TCT	TCC	GTG								
	T	T	M	L	S	W	V	S	F	W	I	K	T	E	S	A	P	306							
919																									

at the junction of the interatrial and interventricular septa (Fig. 4C) was labeled (Fig. 4A). Accumulation of silver grains was visible in the node cells (Fig. 4E). A Purkinje strand recognizable as a band of lighter staining cells under a papillary muscle and in the immediate subendocardial area (Fig. 4D) was also labeled (Fig. 4B). Accumulation of silver grains was visible in the cells underneath the endocardial cells (Fig. 4F). For each section, an adjacent section was

hybridized with sense probe. As an example, Fig. 4G and H show a Purkinje strand hybridized with antisense (Fig. 4G) and sense (Fig. 4H) probes.

The sinoatrial node was not present in the heart used in these *in situ* hybridization experiments. This tissue was obtained after dissection of another fetal heart; total RNA was extracted and RT-PCR with GABA χ -specific primers (corresponding to nucleotide positions 148–168 and 390–415, Fig. 2) was performed. The

glycine	VLYSIRLTTLTSCFMDLKNFPMVDVQCTMQLESFGYTMNDLIFEW-LSDG-PVQVAEGLT--L	218
alpha4	ILYTMRLTISAECPMRLVDFFPDGHACPLKFGSYAYPKSEMIYTWTKGPEKSVEVPKESS-SL	222
beta2	VLYGLRITTTAAECMMDLRRYPLDEQNCTLEIESYGYTTDDIEFYW-RGDDNAVTVGVTKE--L	207
gamma2	VLYSLRLTIDAECQLQHNFPMDHSCPLFSSSYGYPREEIVYQWKR---SSVEVGDRSRWRL	237
gamma4	VLYTLRLTIEAECLLQNFPMDDTHSCPLVFSSSYGYPREEIVYRWR---YSIEVSDQRTWRL	220
gaba χ	VLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSSYYPENEMIYKWN---FKLEINEKNSWKL	242
glycine	PQFILKEEKELGYCTKH--YNTGKFTCIEVKFHLERQMGYYLIQMYIPSLILVILSWVSFWIN	279
alpha4	VQYDLIGQTVSSETIKSI---TGEYIVMTVYFHLRRKMGYFMIQTYIPCIMTVILSQVSFWIN	282
beta2	PQFSIVDYKLI---TKKVVFSTGSYPRLSLKFLLKRNIGYFILQTYMPSILITILSWVSFWIN	267
gamma2	YQFSFVGLRNTTEVVKT---SGDYVVMVSFVFDLSRRMGYFTIQTYPCTLIVVLSWVSFWIN	297
gamma4	YQFDFGTGLRNTSEVLRTG---AGEYVMTVSFDFLSRRMGYFAIQTYIPCILTIVVLSWVSFWIK	280
gaba χ	FQFDFGTGVSNKTEII--TT---PGDFVMTIFFNVSRRFVYAFQNYVPSVTTMLSWVSFWIK	301
glycine	MDAAPARVALGITTVLTMTTQSSGSRASLPKVSIVKAIIDWMAVCLLFVFAALLEYAAVNFS	342
alpha4	KESVPARTVFGITTVLTMTTSLISARHSLPKVSYLTAMDWFIACFAVVFSALEFAAVNYFT	345
beta2	YDASAARVALGITTVLTMTTINTHLRETLPKIPYVKAIDMYLMGCFVVFMALEALVNYIF	330
gamma2	KDAVPARTSLGITTVLTMTTSLTIARSLPKVSYVTAMDLFVSVCFIFVFSALVEYGLTHYFV	360
gamma4	RDSTPARTSLGITTVLTMTTSLTISRKHLPRVSYITAMDLFVSVCFIFVFAALMEYATLNLYV	343
gaba χ	TESAPARTSLGITSVLTMTTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFI	364

FIG. 3. Comparison of predicted amino acid sequence of cloned GABA χ cDNA with human $\alpha 4$ (alpha4), $\beta 2$ (beta2), $\gamma 2$ (gamma2), and chicken $\gamma 4$ (gamma4) GABA_A receptor subunit and rat $\alpha 3$ glycine receptor subunit (glycine) sequences. Only the Cys–Cys loop and M1–M3 regions are shown; amino acid numbers start with the first methionine. Identical residues in all subunits are indicated by a dot. The proposed transmembrane domains are indicated by an underbar and the consensus Cys–Cys sequence by an overbar.

expected PCR product was identified in cDNA from the sinus node and with a fetal heart cDNA library (Fig. 5). PCR amplification with specific primers for the human tryptophanyl-tRNA synthetase (Frolova et al., 1991), a ubiquitous enzyme, showed that the amount of target DNA in the two samples was comparable. We conclude that the GABA χ mRNA is also present in the sinus node.

DISCUSSION

Several types of GABA-gated Cl[−] channel subunits have been characterized. These subunits can be classified into the α , β , γ , δ , and ρ subfamilies according to their amino acid sequence. Members of the same class exhibit 70–80% amino acid sequence identity, compared with 30–40% identity between different classes. The newly found subunit reported here shares 45–25% amino acid sequence identity with the GABA_A and GABA_C receptor subunits and may therefore represent a novel subfamily of the GABA-gated Cl[−] channels. We propose to name this clone and putative subfamily GABA χ .

We have introduced The GABA χ clone into CHO cells, COS cells, and *Xenopus* oocytes (M. Garrett, unpublished data). However, GABA and glycine failed to activate whole-cell currents in transfected cells. Two GABA binding domains have been identified by mutagenesis on GABA $\beta 2$ receptor subunit (Amin and Weiss, 1993; amino acids 181–184 and 226–229, Fig. 3). The GABA χ -predicted polypeptide does not contain the same sequence at these positions (amino acids 216–219 and 260–263, Fig. 3). This difference may explain the insensitivity of the GABA χ -transfected cells to GABA. However, previous studies of single GABA_A receptor subunits expressed by cell transfection either did not detect any current or noted small currents activated only by high concentrations of GABA (Schofield et al., 1987). Ro-

bust GABA-gated Cl[−] currents are found only after coexpression of different types of GABA receptor subunits. The GABA χ subunit may also be part of a heteromultimeric receptor. Coexpression of this clone with other members of the GABA_A receptor subunit family or analysis of the GABA χ polypeptide with antibodies may answer this question. However, it is also possible that this clone encodes a receptor for an unidentified ligand.

The DNA sequence of clones obtained from the T84 cDNA library and the northern blot experiments indicate that an unspliced form of GABA χ mRNA is present in some human tissues. The presence of an unspliced intron in $\alpha 3$ GABA_A receptor subunit mRNA has been reported (Levitan et al., 1988). Incompletely or aberrantly spliced mRNAs have also been noted for the GABA_C $\rho 2$ subunit in human retina (Cutting et al., 1992). For some GABA_A receptor subunits, northern blot experiments with RNA extracted from several brain regions revealed the presence of multiple bands, suggesting alternative splicing of these subunits (Khrestchatsky et al., 1991; O'Hara et al., 1995). Moreover, the gene that encodes the GABA $\beta 3$ subunit contains two alternative 5'-untranslated sequences and a strong promoter (Kirkness and Fraser, 1993). RNase protection showed that mRNA for this subunit is widely expressed, including immortalized cell lines such as human kidney 293 cells (Kirkness and Fraser, 1993). It would be interesting if mRNA for this $\beta 3$ subunit (or others) is also expressed, spliced or not, in tissues outside the CNS.

Recent evidence indicates that GABA may have diverse functions other than neurotransmission in peripheral tissues such as the gut, urinary bladder, lung, ovary, heart, and pancreas (for review, see Erdö and Wolff, 1990). GABA-gated chloride channels are present in pancreatic and pituitary cells (Anderson and Mitchell, 1986; von Blankenfeld et al., 1995) where

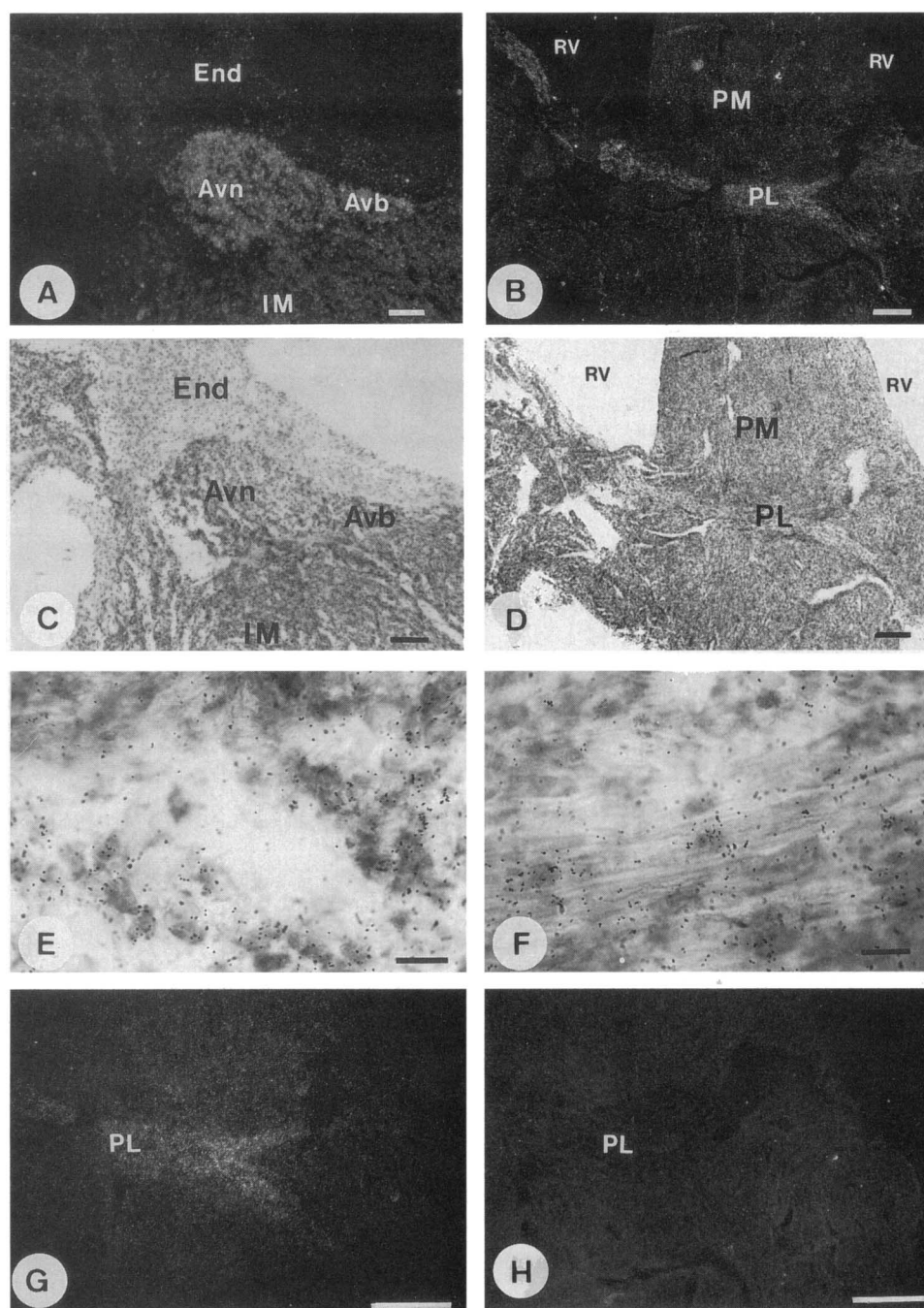


FIG. 4. Regional expression of GABA χ subunit in a horizontal section of fetal human heart. Avn, atrioventricular node; Avb, atrioventricular bundle; IM, interventricular myocardium; End, endocardium; RV, right ventricle; PM, papillary muscle; PL, Purkinje layer. **A** and **B**: Dark-field photomicrographs of sections hybridized with a ^{33}P -labeled probe. **C** and **D**: Bright-field photomicrographs of Coomassie Blue-stained sections are shown for comparison. **E** and **F**: High-resolution bright-field microscopy of Coomassie Blue-stained sections showing silver grains (black dots) indicative of probe hybridization. **G** and **H**: Dark-field photomicrographs of adjacent sections hybridized with antisense (**G**) and sense (**H**) probes. The scale bars represent 200 μm (**A**, **B**, **C**, **D**, **G**, and **H**) and 10 μm (**E** and **F**).

they regulate hormone secretion. These channels appear to be identical to those found in the CNS (Boué-Grabot et al., 1995). If the sequence reported here does indeed encode a GABA-gated chloride channel,

this would be the first case of such a subunit specifically expressed outside of the CNS.

The peripheral and central GABAergic systems affect the regulation of cardiovascular function (Matsu-

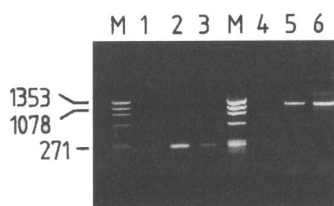


FIG. 5. Expression of GABA χ mRNA in sinus node. This figure shows ethidium bromide-stained products of PCR amplifications resolved by electrophoresis in 2% agarose gel. Oligonucleotide primers specific for GABA χ subunit (lanes 1–3) and for the ubiquitous tryptophanyl-tRNA synthetase (lanes 4–6) were used. PCRs were performed on cDNA obtained from fetal sinus node (lanes 2 and 5) or on adult heart cDNA library (lanes 3 and 6). Control experiments were run with water instead of DNA (lanes 1 and 4). Standard molecular weight markers (M) are *Hae*III cut Φ X174. The positions of 1,353, 1,078, and 271–281 nucleotide bands are indicated to the left of the gel.

yama et al., 1991). Among various regions of the guinea pig heart, it has been shown that the amount of GABA is highest in the sinus node, where it may act through a GABA $_A$ receptor located on cell bodies of the postganglionic cholinergic neurons (Matsuyama et al., 1993). Our finding opens the possibility that GABA acts directly on cardiac function through GABA receptors located within the electrical conduction system cells. The cardiac conduction system is responsible for the initiation and the propagation of the heartbeat and expresses both muscle- and neuron-specific genes. Both myogenic and neural origins have been suggested for this specialized tissue (Gorza et al., 1988; Gourdie et al., 1995). The expression of an mRNA encoding a protein similar to a neurotransmitter receptor is consistent with the neuronal properties for these cardiac cells (Gorza et al., 1988). Our northern blot, PCR, and in situ hybridization experiments on adult and fetal heart suggest that GABA χ mRNA is expressed at all stages of development. This may be relevant to function and dysfunction of this system.

Note added in proof: While this article was in press, the same mRNA was found expressed in the brain subthalamic nucleus. This subunit named ϵ can form a GABA-gated chloride channel when coexpressed in the presence of both an α and a β GABA $_A$ receptor subunit [Davies P. A., Hanna M. C., Hales T. G., and Kirkness E. F. (1997) Insensitivity to anaesthetic agents conferred by a class of GABA $_A$ receptor subunits. *Nature* **385**, 820–823].

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REFERENCES

Amin J. and Weiss D. S. (1993) GABA $_A$ receptor needs two homologous domains of the beta-subunit for activation by GABA but not by pentobarbital. *Nature* **366**, 565–569.

- Anderson R. and Mitchell R. (1986) Biphasic effect of GABA $_A$ receptor agonists on prolactin secretion: evidence for two types of GABA $_A$ receptor complex on lactotropes. *Eur. J. Pharmacol.* **124**, 1–9.
- Boué-Grabot E., Dufy B., and Garret M. (1995) Molecular diversity of GABA-gated chloride channels in the rat anterior pituitary. *Brain Res.* **704**, 125–129.
- Brana C., Charron G., Aubert I., Carles D., Martin-Negrier M. L., Trouette H., Fournier M. C., Vital C., and Bloch B. (1995) Ontogeny of the striatal neurons expressing neuropeptide genes in the human fetus and neonate. *J. Comp. Neurol.* **360**, 488–505.
- Chomczynski P. and Sacchi N. (1987) Single step method of RNA isolation by acid guanidinium thiocyanate-phenol-chloroform extraction. *Anal. Biochem.* **162**, 156–159.
- Cooper E., Couturier S., and Ballivet M. (1991) Pentameric structure and subunit stoichiometry of a neuronal nicotinic acetylcholine receptor. *Nature* **350**, 235–238.
- Cutting G. R., Currstin S., Zoghbi H., O'Hara B., Seldin M. F., and Uhl G. R. (1992) Identification of a putative γ -aminobutyric acid (GABA) receptor subunit rho2 cDNA and colocalization of the genes encoding rho2 (GABRR2) and rho1 (GABRR1) to human chromosome 6q14-q21 and mouse chromosome 4. *Genomics* **12**, 801–806.
- DeLorey T. M. and Olsen R. W. (1992) γ -Aminobutyric acid $_A$ receptor structure and function. *J. Biol. Chem.* **267**, 16747–16750.
- Erdő S. L. and Wolff J. R. (1990) γ -Aminobutyric acid outside the mammalian brain. *J. Neurochem.* **54**, 363–372.
- Frolova L. Y., Sudomoina M. A., Grigorieva A. Y., Zinovieva O. L., and Kisselev L. L. (1991) Cloning and nucleotide sequence of the structural gene encoding for human tryptophanyl-tRNA synthetase. *Gene* **109**, 291–296.
- Gorza L., Schiaffino S., and Vitadello M. (1988) Heart conduction system: a neural crest derivative? *Brain Res.* **457**, 360–366.
- Gourdie R. G., Mima T., Thompson R. P., and Mikawa T. (1995) Terminal diversification of the myocyte lineage generates Purkinje fibers of the cardiac conduction system. *Development* **121**, 1423–1431.
- Grenningloh G., Rienitz A., Schmitt B., Methfessel C., Zensen M., Beyreuther K., Gundelfinger E. D., and Betz H. (1987) The strychnine-binding subunit of the glycine receptor shows homology with nicotinic acetylcholine receptors. *Nature* **328**, 215–220.
- Harvey R. J., Kim H. C., and Darlison M. G. (1993) Molecular cloning reveals the existence of a fourth gamma subunit of the vertebrate brain GABA $_A$ receptor. *FEBS Lett.* **331**, 211–216.
- Khrestchatsky M., MacLennan A. J., Tillakaratne N. J., Chiang M.-Y., and Tobin A. J. (1991) Sequence and regional distribution of the mRNA encoding the α_2 polypeptide of rat γ -aminobutyric acid $_A$ receptors. *J. Neurochem.* **56**, 1717–1722.
- Kirkness E. F. and Fraser C. M. (1993) A strong promoter element is located between alternative exons of a gene encoding the human GABA-type A receptor $\beta 3$ subunit. *J. Biol. Chem.* **268**, 4420–4428.
- Kozak M. (1991) Structural features in eukaryotic mRNAs that modulate the initiation of translation. *J. Biol. Chem.* **266**, 19867–19870.
- Kuhse J., Schmieden V., and Betz H. (1990) Identification and functional expression of a novel ligand binding subunit of the inhibitory glycine receptor. *J. Biol. Chem.* **265**, 22317–22320.
- Langosch D., Thomas L., and Betz H. (1988) Conserved quaternary structure of ligand-gated ion channels: the postsynaptic glycine receptor is a pentamer. *Proc. Natl. Acad. Sci. USA* **85**, 7394–7398.
- Levitan E. S., Schofield P. R., Burt D. R., Rhee L. M., Wisden W., Kohler M., Fujita N., Rodriguez H. F., Stephenson A., Darlison M. G., Barnard E. A., and Seeburg P. H. (1988) Structural and functional basis for GABA $_A$ receptor heterogeneity. *Nature* **335**, 76–79.
- Maricq A. V., Peterson A. S., Brake A. J., Myers R. M., and Julius

- D. (1991) Primary structure and functional expression of the 5HT₃ receptor, a serotonin-gated ion channel. *Science* **254**, 432–437.
- Matsuyama S., Saito N., Taniyama K., and Tanaka C. (1991) GABA is a neuromodulator in sinus node of guinea pig heart. *Am. J. Physiol.* **261**, H1437–H1442.
- Matsuyama S., Saito N., Shuntoh S., Taniyama K., and Tanaka C. (1993) GABA modulates neurotransmission in sinus node via stimulation of GABAA receptors. *Am. J. Physiol.* **264**, H1057–H1061.
- McLean P. J., Farb D. H., and Russek S. J. (1995) Mapping of the alpha 4 subunit gene (GABRA4) to human chromosome 4 defines an alpha 2-alpha 4-beta 1-gamma 1 gene cluster: further evidence that modern GABAA receptor gene clusters are derived from an ancestral cluster. *Genomics* **26**, 580–586.
- Nayeem N., Green T. P., Martin I. L., and Barnard E. A. (1994) Quaternary structure of the native GABA_A receptor determined by electron microscopic image analysis. *J. Neurochem.* **62**, 815–818.
- Noda M., Takahashi H., Tanabe T., Toyosato M., Furutani Y., Hirose T., Asai M., Inayama S., Miyata T., and Numa S. (1982) Primary structure of alpha-subunit precursor of *Torpedo californica* acetylcholine receptor deduced from cDNA sequence. *Nature* **299**, 793–797.
- O'Hara B. F., Andretic R., Heller H. C., Carter D. B., and Kilduff T. S. (1995) GABAA, GABAC, and NMDA receptor subunit expression in the suprachiasmatic nucleus and other brain regions. *Mol. Brain Res.* **28**, 239–250.
- Pritchett D. B., Sontheimer H., Shivers B. D., Ymer S., Kettenmann H., Schofield P. R., and Seeburg P. H. (1989) Importance of a novel GABAA receptor subunit for benzodiazepine pharmacology. *Nature* **338**, 582–585.
- Rorsman P., Berggren P. O., Bokvist K., Ericson H., Möhler H., Östenson C. G., and Smith P. A. (1988) Glucose-inhibition of glucagon secretion involves activation of GABAA-receptor chloride channels. *Nature* **341**, 233–236.
- Sambrook J., Fritsch E. F., and Maniatis T. (1989) *Molecular Cloning: A Laboratory Manual*. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York.
- Sanger F., Miklen S., and Coulson A. R. (1977) DNA sequencing with chain-termination inhibitors. *Proc. Natl. Acad. Sci. USA* **74**, 5463–5467.
- Schofield P. R., Darlison M. G., Fujita N., Burt D. R., Stephenson F. A., Rodriguez H., Rhee L. M., Ramachandran J., Reale V., Glencorse T. A., Seeburg P. H., and Barnard E. A. (1987) Sequence and functional expression of the GABA_A receptor show a ligand-gated receptor super-family. *Nature* **328**, 221–227.
- Schoumacher R. A., Ram J., Iannuzzi M. C., Bradbury N. A., Wallace R. D., Tom Hon C., Kelly D. R., Schmid S. M., Gelder F. B., Rado T. A., and Frizzell R. A. (1990) A cystic fibrosis pancreatic adenocarcinoma cell line. *Proc. Natl. Acad. Sci. USA* **87**, 4012–4016.
- Sieghart W. (1995) Structure and pharmacology of γ -aminobutyric acid A receptor subtypes. *Pharmacol. Rev.* **47**, 181–234.
- Sommer B., Poustka A., Spurr N. K., and Seeburg P. H. (1990) The murine GABAA receptor delta-subunit gene: structure and assignment to human chromosome 1. *DNA Cell Biol.* **9**, 561–568.
- Tessier D. C., Brouseau R., and Vernet T. (1986) Ligation of single-stranded oligodeoxyribonucleotides by T4 RNA ligase. *Anal. Biochem.* **158**, 171–178.
- von Blankenfeld G., Turner J., Ahnert-Hilger G., John M., Enkvist M. O., Stephenson F., Kettenmann H., and Wiedenmann B. (1995) Expression of functional GABAA receptors in neuroendocrine gastropancreatic cells. *Pflugers Arch.* **430**, 381–388.
- Ymer S., Schofield P. R., Draguhn A., Werner P., Kohler M., and Seeburg P. H. (1989) GABAA receptor beta subunit heterogeneity: functional expression of cloned cDNAs. *EMBO J.* **8**, 1665–1670.