

Molecular cloning of the cDNAs coding for the two subunits of soluble guanylyl cyclase from human brain

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Received 16 April 1992

Complementary DNA clones corresponding to the 70 and 82 kDa subunits of soluble guanylyl cyclase from human adult brain have been isolated and sequenced. Their respective open reading frames correspond to 619 amino acids (*M*, 70,469) and 717 amino acids (*M*, 81,324). Southern blots of human genomic DNA using these clones as probes give patterns which might be compatible with the presence of more than one copy per gene, or pseudogenes, for each subunit in the human genome. Comparison of the protein sequence of the large subunit from adult brain with the subunit cloned from human fetal brain (Harteneck, C., Wedel, B., Koesling, D., Malekewitz, J., Böhme, E. and Schultz, G. (1991) *FEBS Lett.* 292, 217–222) revealed only 34% homology. This result demonstrates the existence of a novel large subunit isoform for soluble guanylyl cyclase in human tissues.

Soluble guanylate cyclase; Human brain; cDNA library

1. INTRODUCTION

Cyclic GMP is formed from GTP by guanylyl cyclases which exist in both membrane-bound and soluble forms (GC-S) [1]. The membranous form is a single protein which is the receptor for a family of natriuretic peptides. The GC-S is composed of a large (α) and a small (β) subunit and contains a heme binding site. This soluble form can be activated by nitric oxide (NO) [2], some porphyrins [3], fatty acid hydroperoxides [4], prostaglandin endoperoxides [5] and dehydroascorbate [6].

The β -subunit has been cloned from rat [7] and bovine [8] lung, and an other isoform has been isolated from rat kidney [9]. In human only the partial sequence for two β -subunits of lung GC-S has been published [10]. These two β -subunits result from alternative splicing and are related to the isoforms isolated from rat and bovine lung. The α -subunit has also been cloned from bovine [11] and rat [12] lung; more recently another isoform has been isolated from human fetal brain [13].

In this article, we report the isolation and nucleotide sequence of two cDNA clones coding for the 70 and 82 kDa subunits of GC-S from human adult brain. This is the first characterization of a complete β -subunit of human GC-S, as well as the identification of a novel human GC-S α related to the α -subunits, isolated from bovine and rat lung [11,12].

2. MATERIALS AND METHODS

2.1. cDNA construction and screening

A λ -gt 10 cDNA library (containing 3×10^6 unique recombinants), derived from mRNA purified from the human frontal lobe, was kindly provided by Dr. Yves Le Bouc (INSERM U142, Paris) with the approval of Transgene SA. The library was analyzed as already described [14] using the coding region of the cDNAs corresponding to the 70 and 82 kDa subunit of rat lung GC-S [7] as probes. The inserts of the positive clones, selected under stringent conditions, were subcloned into PGEM 7Zf(+).

2.2. DNA sequencing

DNA sequencing was done on the longest clones corresponding to the β - and the α -subunits of GC-S. The nucleotide sequence of the cDNA clone corresponding to the β -subunit was determined by Genset (Paris). The cDNA clone corresponding to the α -subunit was submitted to a series of progressive unidirectional deletions according to Henikoff [15] using the Erase-a-Base System (Promega). Both strands of the different constructs were sequenced manually by the Sanger's method modified for double stranded DNA [16] by using Sequenase (US Biochem. Corp.) [17].

2.3. Southern blot

High molecular weight DNA was extracted as previously described [18]. Aliquots (40 μ g) were digested overnight at 37°C with *Eco*RI, *Bam*HI and *Kpn*I restriction enzymes (4–12 U/ μ g) (Promega) and blotted as reported [20]. The blots were prehybridized, and hybridized with the insert of clones GC-S β , and GC-S α , according to [20]. Blots were washed for 15 min at room temperature in 0.2 $\times$ SSC, 0.1% SDS, followed by two 45 min washes at 68°C in the same solution. The membranes were exposed to hyperfilm MP (Amersham) at –80°C for 3 days with two intensifying screens.

3. RESULTS

3.1. Cloning of the cDNAs corresponding to the 70 and 82 kDa subunits of GC-S

The human brain cDNA library was screened using the coding region of the 70 and 82 kDa subunit of rat

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ccccccccgcgcgtgcgcgcctctgcctgggtcccttcgggcgtaacctctgcgtgggggtgcctccccgggtcccggtgcagacacc																												-1	
M	Y	G	F	V	N	H	A	L	E	L	L	V	I	R	N	Y	G	P	E	V	W	E	D	I	K	K	E	28	
ATG	TAC	GGA	TTT	GTG	AAT	CAC	GCC	CTG	GAG	TTG	CTG	GTG	ATC	CGC	AAT	TAC	GGC	CCC	GAG	GTG	TGG	GAA	GAC	ATC	AAA	AAA	GAC	34	
A	Q	L	D	E	E	G	Q	F	L	V	R	I	I	Y	D	D	S	K	T	Y	D	L	V	A	A	A	S	56	
GCA	CAG	TTA	GAT	GAA	GAA	GGA	CAG	TTT	CTT	GTC	AGA	ATA	ATA	TAT	GAT	GAC	TCC	AAA	ACT	TAT	GAT	TTG	GTT	GCT	GCT	GCA	AGC	168	
K	V	L	N	L	C	N	A	G	E	I	L	Q	M	F	G	K	M	F	F	V	F	C	Q	E	S	G	Y	D	84
AAA	GTC	CTC	AAT	CTC	AAT	GCT	GGA	GAA	ATC	CTC	CAA	ATG	TTT	GGG	AAG	ATG	TTT	TTC	GTC	TTT	TGC	CAA	GAA	TCT	GGT	TAT	GAT	252	
T	I	L	R	V	L	G	S	N	V	R	E	F	L	Q	N	L	D	A	L	H	D	H	L	A	T	I	Y	112	
ACA	ATC	TTG	CGT	GTC	CTG	GGC	TCT	AAT	GTC	AGA	GAA	TTT	CTA	CAG	AAC	CTT	GAT	GCT	CTG	CAC	GAC	CAC	CTT	GCT	ACC	ATC	TAC	336	
P	G	M	R	A	P	S	F	R	C	T	D	A	E	K	G	K	G	L	I	L	H	Y	Y	S	E	R	E	140	
CCA	GGA	ATG	CGT	GCA	CCT	TCC	TTT	AGG	TGC	ACT	GAT	GCA	GAA	AAG	GGC	AAA	GGA	CTC	ATT	TTG	CAC	TAC	TAC	TCA	GAG	AGA	GAA	420	
G	L	Q	D	I	V	I	G	I	I	K	T	V	A	Q	Q	I	H	G	T	E	I	D	M	K	V	I	Q	168	
GGG	CTT	CAG	GAT	ATT	GTC	ATT	GGA	ATC	ATC	AAA	ACA	GTG	GCA	CAA	CAA	ATC	CAT	GGC	ACT	GAA	ATA	GAC	ATG	AAG	GTT	ATT	CAG	504	
Q	R	N	E	E	C	D	H	T	Q	F	L	I	E	E	K	E	S	K	E	E	D	F	Y	E	D	L	D	196	
CAA	AGA	AAT	GAA	GAA	TGT	GAT	CAT	ACT	CAA	TTT	TTA	ATT	GAA	GAA	AAA	GAG	TCA	AAA	GAA	GAG	GAT	TTT	TAT	GAA	GAT	CTT	GAC	588	
R	F	E	E	N	G	T	Q	E	S	R	I	S	P	Y	T	F	C	K	A	F	P	F	H	I	I	F	D	224	
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R	D	L	V	V	T	Q	C	G	N	A	I	Y	R	V	L	P	Q	L	Q	P	G	N	C	S	L	L	S	252	
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K	E	G	L	L	D	V	E	K	L	E	C	E	D	E	L	T	G	T	E	I	S	C	L	R	L	K	G	308	
AAG	GAA	GGA	TTG	TTG	GAT	GTG	GAG	AAA	TTA	GAA	TGT	GAG	GAT	GAA	CTG	ACT	GGG	ACT	GAG	ATC	AGC	TGC	TTA	CGT	CTC	AAG	GGT	924	
Q	M	I	Y	L	P	E	A	D	S	I	L	F	L	C	S	P	S	V	M	N	L	D	D	L	T	R	R	336	
CAA	ATG	ATC	TAC	TTA	CCT	GAA	GCA	GAT	AGC	ATA	CTT	TTT	CTA	TGT	TCA	CCA	AGT	GTC	ATG	AAC	CTG	GAC	GAT	TTG	ACA	AGG	AGA	1008	
G	L	Y	L	S	D	I	P	L	H	D	A	T	R	D	L	V	L	L	G	E	Q	F	R	E	E	Y	K	364	
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GAA	ATT	GCT	GGC	CAG	GTT	CAA	GTA	GAT	GGT	GAA	TCT	GTT	CAG	ATA	ACA	ATA	GGG	ATA	CAC	ACT	GGA	GAG	GTA	GTT	ACA	GGT	GTC	1596	
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CCA	GTG	TCC	ATG	AAG	GGC	AAA	AAA	GAA	CCA	ATG	CAA	GTT	TGG	TTT	CTA	TCC	AGA	AAA	AAT	ACA	GGA	ACA	GAG	GAA	ACA	AAG	CAG	1848	
D	D	D																										619	
GAT	GAT	GAC	tgaatcttggattatgggggtgaagaggagtacagactaggttccagttttctcttaacacgtgccaaagcccaggagcagttcttccctatgggatacaga																									1956	
ttttcttttggctctgtccattacccaagactttctctctagatatatctctcactatccgtttatccaaccttagctctgctttctattacttttaggctttagtatatta																												2068	
tctaaagtttggcttttgatgtggatgatgtgagcttcattgtgtcttaaatactactacaagcattacctaacatgggtgatcttgcaagtagtaggcacccaataaataatttg																												2180	
ttgaatttagttaaatgaaactgaacagtggtttggccatgtgtatatttatatcatgtttaccacaaatctgttttagtggttccacatatatgtatatgtatatatttaaatgacta																												2292	
taatgtaataaagtttatatcatgttgtgtgtatatcatatagaaatcattttctaaaggagt																												2355	

Fig. 1. Nucleotide sequence and corresponding protein sequence of GC-S β_3 .

lung GC-S [7]. After repeated screening, one positive clone for each subunit, which encoded the entire protein, was isolated. They were designated GC-S β_3 and GC-S α_3 , respectively, according to the nomenclature suggested by Yuen et al. [9]. The nucleotide sequences

of the cDNAs, and the deduced amino-acid sequences for the 70 and 82 kDa subunits, are shown in Fig. 1 and Fig. 2, respectively. The open reading frame of GC-S β_3 (1,857 bp) encodes 619 amino acids. The calculated molecular weight of the protein is 70,469 Da. For GC-S α_3

Fig. 2. Nucleotide sequence and corresponding protein sequence of GC-Sx.

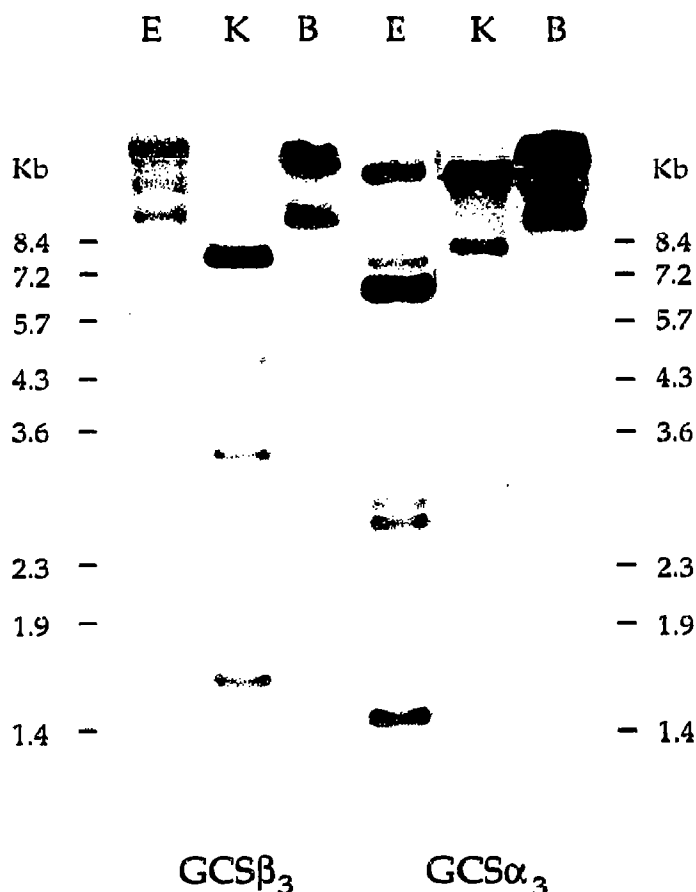


Fig. 3. Southern blot of human genomic DNA. Genomic DNA was digested with restriction enzymes *EcoRI* (E), *KpnI* (K) and *BamHI* (B) and the blots prepared as described in section 2. The blots were hybridized with either GC-S β_3 or GC-S α_3 as probes. The position and the size of the markers run in parallel are indicated on both sides of the figure.

the open reading frame (2,151 bp) codes for 717 amino acids. The calculated molecular weight is 81,324 Da.

3.2. Southern blot analysis

Southern blot analysis of human genomic DNA, digested with *EcoRI*, *BamHI* and *KpnI* were hybridized with the insert of both clones as probes. This hybridization revealed a number of discrete hybridized bands (Fig. 3) with different patterns for the α_3 - and β_3 -subunits. These results suggest either that the genes coding for these subunits might be present in more than one copy in the human genome, or the presence of pseudogenes.

3.3. Comparison of the α_3 - and β_3 -subunits with the known sequences of soluble guanylyl cyclase subunits

There is a considerable homology (i.e. identical plus similar amino acids) between the predicted amino acid sequences of the 70 and 82 kDa subunits of human adult brain GC-S. The homology, in 548 amino acid residues of both chains, is of 34% and rises to 46% if one considers only the last 300 residues of the C-terminal parts (Fig. 4).

We compared the amino acid sequences of the α_3 - and β_3 -subunits with sequences of other GC-S subunits. The comparison of the sequence of various α subunits (four bottom lines of each block, Fig. 4) reveals that the α_3 was 78.5% homologous to the bovine α_1 -subunit and 81% homologous to the rat α_1 -subunit in a 684 amino acid overlap [11,12]. Interestingly, the comparison of α_3 with α_2 from human fetal brain [13] reveals a very limited degree of homology in the N-terminal region but a 72% homology between the 310 amino acids corresponding to the C-terminal sequence of both subunits. Comparison of the protein sequence of β_3 with those of β_1 -subunits from bovine and rat lung [7,8] exhibits an homology of 99 and 98.5%, respectively, in a 619 amino acid overlap (three upper lines, Fig. 4). The homology between β_3 and β_2 from the rat kidney is less pronounced, with only 39% in a 418 amino acid overlap mainly located in the carboxy terminal region of both subunits. From the analysis of Fig. 4 it is clear that a sequence of 268 amino acids of the C-terminal segments (amino acids 428–696) is highly conserved between the α - and the β -subunits of GC-S from various species.

The comparison of the protein sequence of β_3 with the partial sequences, HSGC-1 and HSGC-2, cloned from human lung [10] reveals a 99.5% homology between amino acid 1–209 of β_3 and amino acids 337–545 of HSGC-1, and a 98.3% homology between amino acids 425–545 of β_3 and amino acids 56–176 of HSGC-2 (data not shown). The remaining sequences of HSGC-1 and HSGC-2 are not available.

4. DISCUSSION

Recently, Harteneck et al. described the cloning and expression of a new α_2 -subunit of GC-S isolated from a human fetal brain cDNA library [13]. The comparison of the deduced amino acid sequence of GC-S α_3 with those of this α_2 -subunit reveals only a 34% homology predominantly in the C-terminal segment. It is highly

Fig. 4. Comparison of the protein sequence of the large and small subunits of various GC-S's. The protein sequences of GC-S for the small subunits from human brain (β_3 -hum), bovine lung (β_1 -bov), rat lung (β_1 -rat), and large subunits from human fetal brain (α_2 -hum), human adult brain (α_3 -hum), bovine lung (α_1 -bov) and rat lung (α_1 -rat), were compared on VAX computer [21] using the clustal alignment method [22]. Similar groups of amino acids were defined as follows: {A,G,S,T} {N,D,Q,E,B,Z} {R,K} {I,L,M,Y} {F,W,Y} {C} {X} {H} {P}. Identical and similar residues are boxed using the program Boxshade [21].

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1 MYGFVNHALELLVI-RNY-GPEV-W-EDIKKEAQLDEEGQFLVRIIYDDSKTYDLVAAASKVLNIN β3-HUM
1 MYGFVNHALELLVI-RNY-GPEV-W-EDIKKEAQLDEEGQFLVRIIYDDSKTYDLVAAASKVLNIN β1-BOV
1 MYGFVNHALELLVI-RNY-GPEV-W-EDIKKEAQLDEEGQFLVRIIYDDSKTYDLVAAASKVLNIN β1-RAT
1 M-----GECPLSRLCWNNGSRSEFGPILEPSPAAAAAATAAPATPAASAAAAAATAG-ARRVQRR β2-RAT
1 MSRRRTSSSEFSSLSGSDYLETSPEEGECPLSRLCWNNGSRSEFGPILEPSPAAAAAATAAPATPAASAAAAAATAG-ARRVQRR α2-HUM
1 MECTKLKDKIT-----GECPLSRLCWNNGSRSEFGPILEPSPAAAAAATAAPATPAASAAAAAATAG-ARRVQRR α3-HUM
1 MFCARLKDLOIT-----GDCPFSLL-APGQVPEPTEIEEVAGVSESCQATPPT-CQEFABE-NAEGSHPOKRTSR α1-BOV
1 MFCARLKDLOIT-----GDCPFSLL-APGQVPEPTEIEEVAGVSESCQATPPT-CQEFABE-NAEGSHPOKRTSR α1-RAT

63 AGEILQMFQKMEFFVFCQESGYDTILRVLGSNVREFLONLDALHDHLATIIYPMGRAPSFRCCTDAEKKGKGLILHYYSEREGLQDI β3-HUM
63 AGEILQMFQKMEFFVFCQESGYDTILRVLGSNVREFLONLDALHDHLATIIYPMGRAPSFRCCTDAEKKGKGLILHYYSEREGLQDI β1-BOV
63 AGEILQMFQKMEFFVFCQESGYDTILRVLGSNVREFLONLDALHDHLATIIYPMGRAPSFRCCTDAEKKGKGLILHYYSEREGLQDI β1-RAT
2 -EAILKLEGEYFFKCKMMSGYDRMLRTLGCGNLTEFIENLDALHSYLALSQYQEMNAPSERVEEGADG-AMLLHYYSERHGLCHL β2-RAT
83 RRVNLDLSIGESISRL-TAPSPOTIQTTLKRTLOYEHOVIGYRDA-EKNFHNISN---RCSYADHNSKEETEDVSGILQCTAN α2-HUM
67 SRVYLHTLAESICKL-IFPEFERNLALORTLA-KHKIKENRKS-----LEREDFEKTIABEQAQVQ α3-HUM
68 SRVYLHTLAESICKL-IFPEFERNLALORTLA-KHKIKENRKS-----LEREDFEKIVVDQAIATA α1-BOV
66 RRVYLHTLAESIGKL-IFPEFERNLALORTLA-KHKIKENRKS-----SEKEDLERITABEATAAA α1-RAT

146 VIGIIKTVAQQIHGTEIDMKVIOQRNE---ECDHTOFLI-----E EKES-----KEEDFYB----- β3-HUM
146 VIGIIKTVAQQIHGTEIDMKVIOQRNE---ECDHTOFLI-----E EKES-----KEEDFYB----- β1-BOV
146 VIGIIKTVAQQIHGTEIDMKVIOQRSE---ECDHTOFLI-----E EKES-----KEEDFYB----- β1-RAT
83 VPGIIEAVAKDFDFTDVAMSILDMNEEVSTGKKEHVFLVVO---KAHQIRGAKASRPQGSSEDSQA---DQALQG--- β2-RAT
161 ILGLKFEETIKRFGCEFFFNCFHNERVLRVAVGGTLQDEFN-GFDALLEHIRT--FGKQATIESPSFLCKELPEGCTIMHYFF α2-HUM
126 --S-PVELSKNLLVKRFLKYTRKMKTSLGWLEAPLKIEKQLOYESETEOPLP--RSRKGQLEDA SILCLDKKEDDFLHVYF α3-HUM
127 --GVPVEIKESLGEELFKICYEEDYILGVVGGLTKDFLN-SFSTLLKQSSHCQAEKKGRFEDASILCLDKKDPVLYVYF α1-BOV
125 --GVPVEVLKDSLGEELFKICYEEDYILGVVGGLTKDFLN-SFSTLLKQSSHCQAEKKGRFEDASILCLDKKDPVLYVYF α1-RAT

194 -----DLDR-----FEENGTOESRISPYT----- β3-HUM
194 -----DLDR-----FEENGTOESRISPYT----- β1-BOV
194 -----DLDR-----FEENGTOESRISPYT----- β1-RAT
155 -----TLRMKERYL---NIPV---CPGEKSHST-----AVRASVLEGGKGLRDTFPQVPERVWVEEE β2-RAT
241 HPHHIVGFAMLCMIKAAGKIVRLDVEVEQVAN---EKLCSDVSNPGNCSCLTFLIKECENTNIMKNLPQGTQVPAADLRISIN α2-HUM
204 FPKRTTSLILPGIIAAAHLYETEVEVSLMPPCFHNDCESEFVNO---PYLLYSV---HMKSTKPSLSPSKPO---SSLVIPTS α3-HUM
207 FPKRTTSLILPGIIAAAHLYETEVEVSLMPPCFHNDCESEFVNO---PYLLYSV---HMKSTKPSLSPSKPO---SSLVIPTS α1-BOV
205 FPKRTTALLLPGIIAAAHLYESHEVSLMPPCFHNDCESEFVNO---PYLLYSV---HMKSTKPSLSPSKPO---SSLVIPTS α1-RAT

213 -FCKAPFFHIIFDRDLVVTCGNAIYRVLPQLQ-PGNCSSLSVSLVRPHIDISFHGILSHINTVEVLSRKEGLLDVEKLECE β3-HUM
213 -FCKAPFFHIIFDRDLVVTCGNAIYRVLPQLQ-PGNCSSLSVSLVRPHIDISFHGILSHINTVEVLSRKEGLLDVEKSECE β1-BOV
213 -FCKAPFFHIIFDRDLVVTCGNAIYRVLPQLQ-PGKCSLSVSLVRPHIDISFHGILSHINTVEVLSRKEGLLDVEKLECE β1-RAT
208 VECDAFFPHIVFDEALRVKQAGVNIQKYVPGIL-TOKFALDEYFSIIHPQVTFNIISSICKFINSQFVLKTRKEMMPKAR--- β2-RAT
322 TFCRAFFPHLMFDPMSVLQGEGLRKLQ-RCOTHKVLKPEDCFEIVSPKVNATFERVILRLSTPEVIRTQ---E α2-HUM
279 LECKTFPPFHMFMDKMTILOFGNGIRRLMNRDFOGKPNFE-YFEILTPKINOTFSGIMTMLNMQFVIRVRR---W α3-HUM
282 LECKTFPPFHMLDRDMSILOFGNGIRRLMNRDFOGKPNFE-YFEILTPKINOTFSGIMTMLNMQFVIRVRR---W α1-BOV
280 LECKTFPPFHMLDRDLAILQFGNGIRRLVNRDFOGKPNFE-YFEILTPKINOTFSGIMTMLNMQFVIRVRR---W α1-RAT

294 DELTGTEISCLRLKGOMIYLPEADSILFLCSPSVMNLDLTLRGLYLSDIPLHDATRDVLVLLGEQFREYKLTQBLEILTDRL β3-HUM
294 DELTGTEISCLRLKGOMIYLPEADSILFLCSPSVMNLDLTLRGLYLSDIPLHDATRDVLVLLGEQFREYKLTQBLEILTDRL β1-BOV
294 DELTGTEISCLRLKGOMIYLPEADSILFLCSPSVMNLDLTLRGLYLSDIPLHDATRDVLVLLGEQFREYKLTQBLEILTDRL β1-RAT
286 -----KSPMLKLRGOMIYFESLRCMIFMCSPNVDSLQELSEKMHLSDIAPHDTTRDLILLNQORLAEMELSCOLEKKKEEL β2-RAT
394 ASGSENKDKVMEVKGOMIYFESNLSILFGLSPCVDRLEDFTGRGLYLSDIPIHNAIRDVVVLIGEQAQADGLKKRLGKLLKATL α2-HUM
351 DNSVKKSSSRVMDLKGOMIYFESSAILFLGSPCVDRLEDFTGRGLYLSDIPIHNAIRDVVVLIGEQAQADGLKKRLGKLLKATL α3-HUM
355 DNSMKKSSSRVMDLKGOMIYFESSAILFLGSPCVDRLEDFTGRGLYLSDIPIHNAIRDVVVLIGEQAQADGLKKRLGKLLKATL α1-BOV
353 DNSVKKSSSRVMDLKGOMIYFESSAILFLGSPCVDRLEDFTGRGLYLSDIPIHNAIRDVVVLIGEQAQADGLKKRLGKLLKATL α1-RAT

377 QLTLRALDEKKKTD TLLYSVLPPSVANELRHKRVPVPAKRYDNVTILFSIGVGFNAFCSKHASGEGAMKIVNLLNDLYTRFDT β3-HUM
377 QLTLRALDEKKKTD TLLYSVLPPSVANELRHKRVPVPAKRYDNVTILFSIGVGFNAFCSKHASGEGAMKIVNLLNDLYTRFDT β1-BOV
377 QLTLRALDEKKKTD TLLYSVLPPSVANELRHKRVPVPAKRYDNVTILFSIGVGFNAFCSKHASGEGAMKIVNLLNDLYTRFDT β1-RAT
364 RVLNHLALIEKKKTE TLLYAMLPEHVNQLEKGRVVAEGEFCTILFSDVVTFTNICAACEP-----IQIVNMLNSMYSKFDR α2-RAT
477 ERTHQALEEEKKKTV DLLYSIFPGDVAQQLWQGGQVQARKFDDVTMLFSDIVGFTAIQAQCTP-----MQVISMLNELYTRFDH α2-HUM
434 EAHQALEEEKKKTV DLLCSIFPSEVAQQLWQGGQVQAKKFENVTMLFSDIVGFTAIQSQCSP-----LOVITMLNLYTRFDQ α3-HUM
438 EAHQALEEEKKKTV DLLCSIFPSEVAQQLWQGGQVQAKKFENVTMLFSDIVGFTAIQSQCSP-----LOVITMLNLYTRFDQ α1-BOV
436 EAHQALEEEKKKTV DLLCSIFPSEVAQQLWQGGQVQAKKFENVTMLFSDIVGFTAIQSQCSP-----LOVITMLNLYTRFDQ α1-RAT

460 LTDSRKNPFFVYKVTGVGDKYMTVSGLPEPCIHARSICHLALDMMEIAGQV---QVDGESVOITIGIHTGEVVTGVIGORMPRY β3-HUM
460 LTDSRKNPFFVYKVTGVGDKYMTVSGLPEPCIHARSICHLALDMMEIAGQV---QVDGESVOITIGIHTGEVVTGVIGORMPRY β1-BOV
460 LTDSRKNPFFVYKVTGVGDKYMTVSGLPEPCIHARSICHLALDMMEIAGQV---QVDGESVOITIGIHTGEVVTGVIGORMPRY β1-RAT
443 LTVSDH---VYKVTIGDAYMVVGGVPPVESHQORVANFALGMRISAKEVMNPTGEPIQIRVIGITGPVLGAVGDKMPRY β2-RAT
556 QCGFLD---IYKVTIGDAYCVAGGLHRSKSLCHAKPIALMALKMMELSEEVLTTP-DGRPIQMRIGIHSGSVLGAVGVGMPRY α2-HUM
513 QCGELD---VYKVTIAMPIVWLGGLHKSDDTHAVQIALMALKMMELSEVMSPP-HGEPIMRIGLHSGSVFAGVVGVMKPRY α3-HUM
517 QCGELD---VYKVTIGDAYCVAGGLHRESDDTHAVQIALMALKMMELSEVMSPP-HGEPIMRIGLHSGSVFAGVVGVMKPRY α1-BOV
515 QCGELD---VYKVTIGDAYCVAGGLHRESDDTHAVQIALMALKMMELSEVMSPP-HGEPIMRIGLHSGSVFAGVVGVMKPRY α1-RAT

541 CLFGNTVNLTSRTETTGEKGINVSEYTYRCLMSPENSDDQFHLHRCGPVSMKG---KKEPMQVWFLSRKNTGTBE----- β3-HUM
541 CLFGNTVNLTSRTETTGEKGINVSEYTYRCLMTPENSDDQFHLHRCGPVSMKG---KKEPMQVWFLSRKNTGTBE----- β1-BOV
541 CLFGNTVNLTSRTETTGEKGINVSEYTYRCLMSPENSDDQFHLHRCGPVSMKG---KKEPMQVWFLSRKNTGTBE----- β1-RAT
523 CLFGDVTNTASRMESHGLPSKVHLSPTAHRAL---NKGEFIVRRGEIEVKG---K-GKMTTYELIQNLNATEEDIEIMGRP β2-RAT
635 CLFGNNVTTLASKFESCSHPRKINVSPTTYRLLKDC---ESFTEIPRSREELPDPNFPKEIPGICYFLEV-RTGPKPEKPSLS- α2-HUM
592 CLFGNNVTTLANKFESCSVPRKINVSPTTYRLLKDC---PGFVETPRRSREELPDPNFPSEIPGICHFLDAYQ-QGTNSKPCFOK α3-HUM
596 CLFGNNVTTLANKFESCSVPRKINVSPTTYRLLKDC---PGFVETPRRSREELPDPNFPSEIPGICHFLDAYQ-QGTNSKPCFOK α1-BOV
594 CLFGNNVTTLANKFESCSVPRKINVSPTTYRLLKDC---PGFVETPRRSREELPDPNFPSEIPGICHFLDAYQ-QGTNSKPCFOK α1-RAT

614 -----TKQDDD----- β3-HUM
614 -----TEQDEN----- β1-BOV
614 -----TNQDEN----- β1-RAT
597 SAPADGKEVCTPGNQVRKSPAVPRNTDHOQOQVYKGD PADASNEVTLAGSPVAGRNSTDAVNNQPSPDETKTSVVASGPVLSAF β2-RAT
712 -----SSRIKKVSY-----N-----ETSL----- α2-HUM
670 KDVEDASQFFRQSIKNNRLATYIP-----IYKS-----LGFDLSL-----KMCRASESTLGIVDG α3-HUM
674 KDVEEANANF-----LG-----KASGI-----D----- α1-BOV
673 KDAEDGNANF-----LG-----KASGV-----D----- α1-RAT

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probable that such a difference reflects the expression of two different genes for these two human GC-S α -subunits. The possible expression of two GC-S α -subunit isoforms at different stages of development of the human brain raises the interesting possibility of specific regulation of GC-S expression during ontogeny. The GC-S might also be expressed in a tissue-specific manner. It has been shown by Yuen et al. [9] that two different small subunits of GC-S were present in kidney and liver cells, apparently encoded by two different genes. Recently, Chhajlani et al. [10] reported the heterogeneity of two human GC-S clones isolated from a human lung cDNA library, and which seem to be generated by alternative splicing. Altogether, these results might argue for a tissue-specific expression of GC-S isoforms.

The two GC-S subunits that we have cloned exhibit strong homologies with other known GC-S subunits. This might reflect the existence of a common ancestor for all these proteins, but also the pressure of selection for the maintenance of the active site. Using transfection experiments it has been shown that both subunits are indispensable for the expression of the catalytic activity [13]. The putative catalytic domain has been localized in the C-terminal part of both subunits and corresponds to the region where all subunits exhibit the highest homology.

From the diversity within the GC-S enzyme family one might expect, in a near future, new interesting observations on the expression and regulation of guanylyl cyclase, leading to a better understanding of the role of cyclic GMP in the cells and, more precisely, in nervous tissue.

Acknowledgments: This work was funded by the Mutuelle Générale de l'Éducation Nationale and by the Institut National de la Santé et de la Recherche Médicale. We thank Dr M. Nakane (Tokyo Metropolitan Institute for Neurosciences) for providing us with the rat soluble guanylate cyclase cDNAs, Dr Y. Le Bouc for the human brain cDNA library and Dr. Isao Matsuoka for critical reading of the manuscript. U.S. was a recipient of an INSERM post-doctoral fellowship. We are also very grateful to E. Grandvilliers and L. Rosario for their skilful secretarial assistance.

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