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Sequence and expression of human $GABA_A$ receptor $\alpha 1$ and $\beta 1$ subunits

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The deduced amino acid sequences of cDNA clones encoding human $GABA_A$ receptor $\alpha 1$ and $\beta 1$ subunits are presented. The human subunits display very high levels of sequence identity with the corresponding bovine receptor subunits. The cloned human $GABA_A$ receptor subunits induce the formation of GABA-gated chloride channels when expressed in mammalian cells.

γ-Aminobutyric acid A receptor; Ligand-gated ion channel; Electrophysiology; cDNA cloning; (Human brain)

1. INTRODUCTION

Receptors for the major inhibitory neurotransmitter GABA (γ-aminobutyric acid) are present on the majority of neurons in the mammalian brain. The $GABA_A$ receptor contains an intrinsic chloride ion channel which is opened (gated) by the neurotransmitter, thus stabilizing the neuron's resting potential [1]. Channel activity can be allosterically modulated by therapeutically useful drugs e.g. barbiturates and benzodiazepines [1]. The primary structure of the cloned bovine α and β subunits has shown the existence of a ligand-gated ion channel receptor superfamily [2]. Coexpression of these subunits in *Xenopus* oocytes produces receptors with many functional characteristics of native $GABA_A$ receptors [2]. The clinical importance of drugs that act at this ubiquitous brain receptor makes it desirable to characterize the structure of the human receptor subtypes. To this end we have cloned and sequenced the human $GABA_A$ receptor $\alpha 1$ and $\beta 1$ subunits and expressed them in mammalian cells.

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2. MATERIALS AND METHODS

Full-length $GABA_A$ receptor $\alpha 1$ and $\beta 1$ subunit cDNAs were isolated from a human fetal brain cDNA library, constructed in λgt10 by standard methods. 2×10^6 pfu of this library were screened with subunit-specific radiolabelled oligonucleotides based on the bovine cDNA sequences: $\alpha 1$ subunit, 5′-ACCCTGGCCAGATTAGGTGTGTAGCTGGTTGCTGTTGGA-3′; $\beta 1$ subunit, 5′-TCCCACGCCCGTGAGCACTTCAGAGGCCGCTCGTCTCGTTCCTGATCTCCGGGTACTGAGGAGAATGTTGCCGTG-3′. Three $\alpha 1$ subunit cDNA clones were analyzed and the largest (in λhGRα28), 4.25 kb in size, was sequenced across the coding, and into the 3′-untranslated region. Eight cloned $\beta 1$ subunit cDNAs were obtained and rescreened with specific 5′- and 3′-oligonucleotides based on the known bovine $\beta 1$ cDNA sequence. One (λhGRβ19) which hybridized to both probes was sequenced. Two $\beta 1$ cDNAs positive only to the 3′-probes (λhGRβ18) contained an additional T at position 1220, unlike λhGRβ19. This missing nucleotide was added to the sequence derived from λhGRβ19 by site-directed mutagenesis, using the oligonucleotide 5′-ATGTACTCCTATGACGAGCG-3′, thus restoring the reading frame to complete alignment with the bovine $\beta 1$ subunit cDNA. DNA sequences were obtained using the chain-termination method [4] and M13 vectors.

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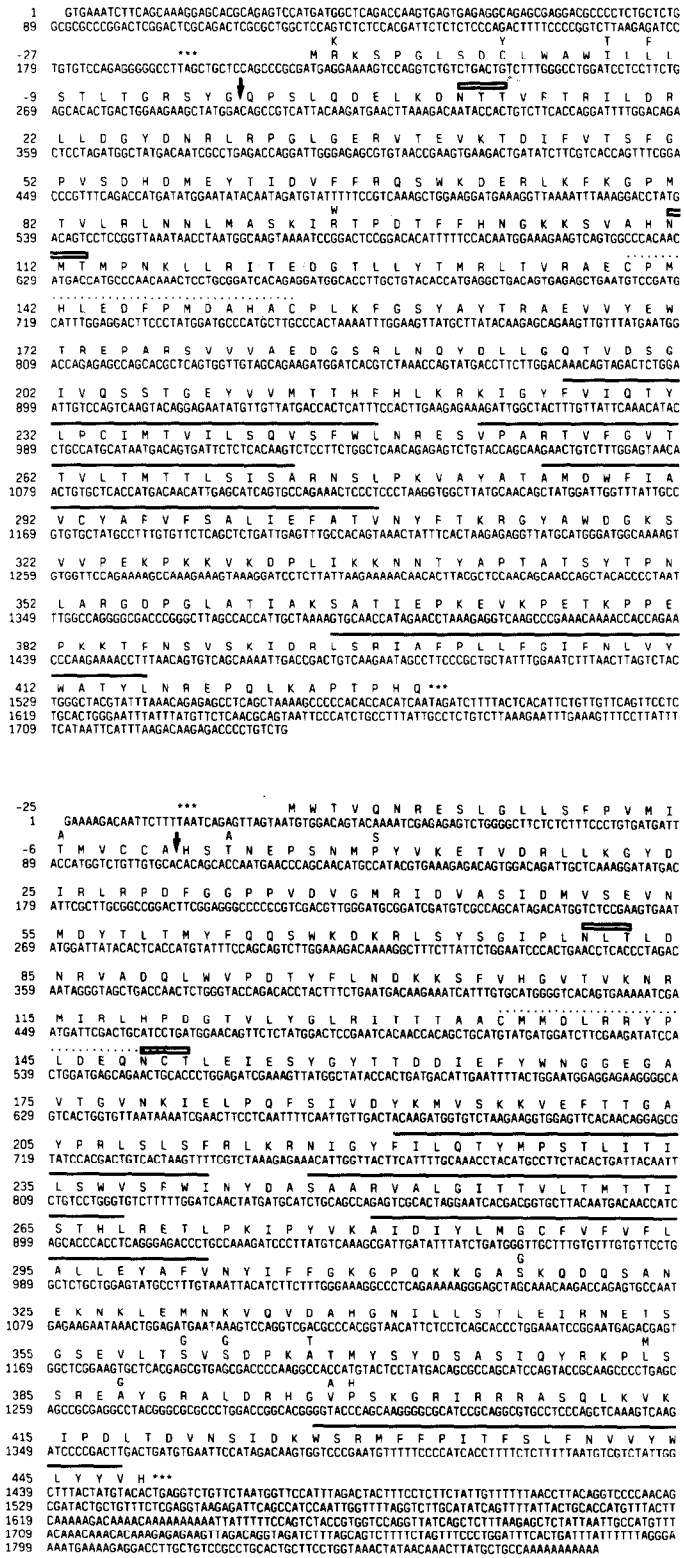

Fig.1. DNA and predicted amino acid sequence of the human $GABA_A$ receptor $\alpha 1$ (a) and $\beta 1$ (b) subunit cDNAs. Amino acid numbering starts at the proposed mature N-terminal residues. The putative signal sequence cleavage site is indicated by an arrow and the signal sequence is shown in negative numbering. The proposed membrane-spanning hydrophobic sequences are highlighted by overscoring, the disulfide-bonded loop region is indicated by a dotted line and the putative extracellularly located *N*-glycosylation sites are boxed. Asterisks denote both 3'-terminal stop codon and the first upstream in-frame stop codon in the 5'-untranslated sequence. Amino acids that differ from the bovine sequences are indicated above the human polypeptide sequence.

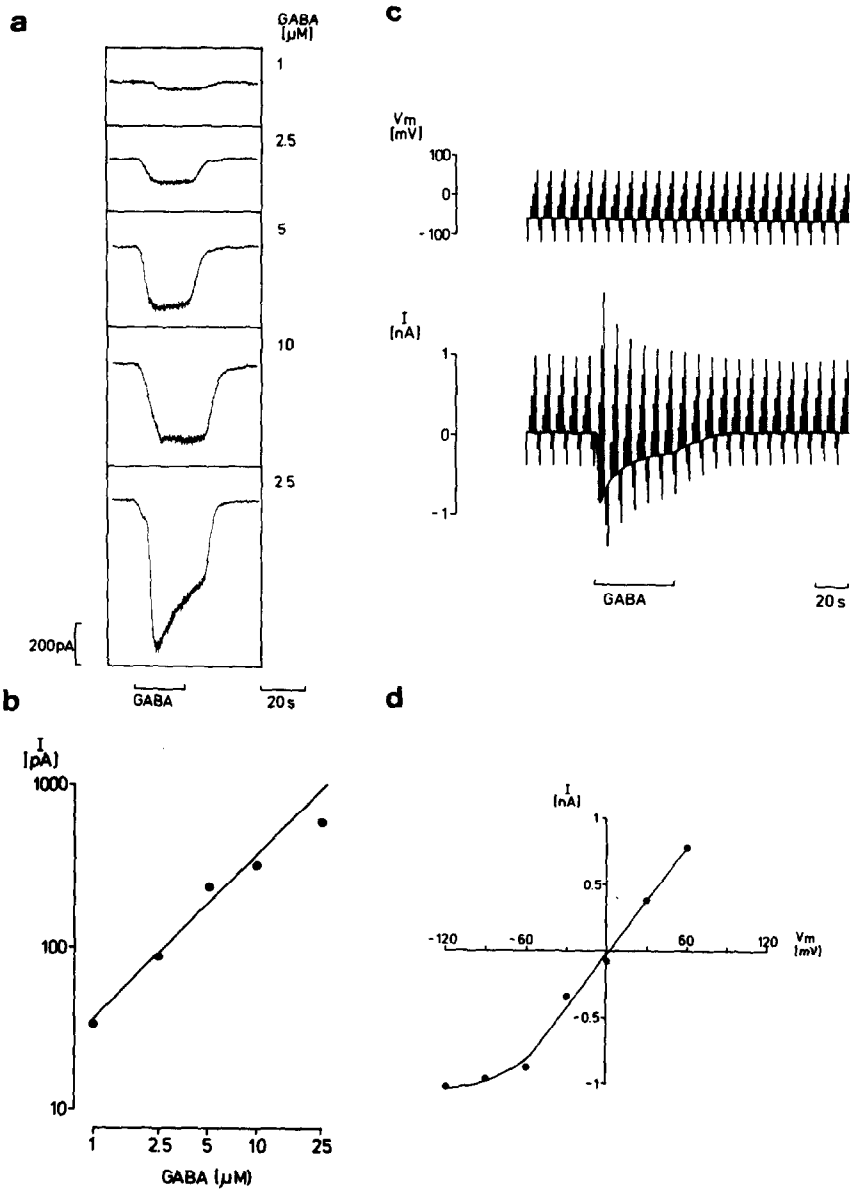

Fig.2. Dependence of the GABA-induced current on ligand concentration. (a) The membrane current at the resting potential (−60 mV) was recorded from a cell transfected with the $\alpha 1 + \beta 1$ subunits using the patch-clamp technique in the whole cell configuration. GABA was applied as indicated by the bar at the given concentrations. A dose-dependent inward current was observed. (b) Dose-response curve of GABA-induced currents (I) for the experiment shown in a, log-log scale (Hill plot). The slope of the curve at low GABA concentrations is approx. 1, suggesting a single-binding site for the ligand. (c) The membrane current was measured while briefly clamping membrane potential (V_m) from the resting value (−60 mV) to 120, −90, −30, 0, 30 and 60 mV for a period of 200 ms with 1 s intervals. This series of voltage jumps was continuously applied. GABA was added as indicated by the bar at a concentration of 10^{-4} M. (d) Currents (I) before application of GABA were subtracted from currents in the presence of GABA for the experiments shown in c and plotted as a function of membrane potential (V_m). $V_m Cl^- = 0$ mV, $V_m K^+ = -84$ mV and $V_m Na^+ \geq 80$ mV.

The α1- and β1-subunit cDNAs were expressed and analysed in mammalian tissue culture cells as previously described [3]. Membrane currents were recorded, using the patch-clamp technique in the whole cell configuration.

3. RESULTS AND DISCUSSION

Using oligonucleotide probes, cloned human $GABA_A$ receptor α1 and β1 subunit cDNAs were isolated from a human fetal brain cDNA library. One of three α1 cDNAs was sequenced and found to be full-length. Rescreening of eight β1 cDNA clones with 5′- and 3′-sequence-specific oligonucleotide probes identified a single full-length cDNA encoding this subunit. The DNA and predicted polypeptide sequence of the α1 and β1 cDNAs (fig.1) reveal a very high degree of conservation with the corresponding bovine sequences [2]. The 456 amino acid α1 subunit which contains a 27 residue signal peptide displays 99% sequence identity (five amino acid differences) with the bovine α1 subunit. However, of these, four are located within the signal sequence. The only difference in this mature protein sequence occurs in the extracellular domain and is a non-conservative replacement. The human sequence contains Trp 95 while this residue is an Arg in the bovine sequence. The 474 amino acid β1 subunit displays 98% sequence identity (11 amino acid differences). In this case, only one of the differences is located within the 25 residue signal peptide. Of the remainder, two non-conservative replacements are found at the extreme N-terminus and the other 8 are located within the intracellular loop located between transmembrane domains 3 and 4. Of these, only two are conservative in nature. The concentration of sequence differences within the intracellular loop is consistent with this region of all members of this receptor superfamily being the most divergent. The results obtained suggest that the $GABA_A$ receptor subunits are very highly conserved among the mammalian species.

The cloned human α1 and β1 subunit cDNAs have recently been expressed in mammalian cells [3]. Using this technique, we transfected human cells as described and obtained electrophysiological recordings 48 h after transfection. $GABA_A$ receptors expressed in mammalian cells have many of the properties of the native receptors [3]. They conduct chloride ions, are specifically inhibited by picrotoxin and the competitive $GABA_A$ receptor antagonist bicuculline and are potentiated by barbiturates. They do not display benzodiazepine responsiveness [3,5]. Single cell dose-response curves of GABA-induced currents (fig.2) had an average slope of 1 (SD = 0.1, N = 5), indicating that binding of only one GABA molecule per receptor caused a channel opening. This is at variance with the observed cooperativity of neurotransmitter gating of $GABA_A$ receptor channels [6–8], but in agreement with results obtained by coexpression of α- and β-subunits in *Xenopus* oocytes [2,5].

Our results suggest a more complex composition of neuronal $GABA_A$ receptors. Other hitherto unknown subunits may coassemble with α1 and β1 subunits to generate a full display of all known receptor properties. The recent isolation in our laboratory of cDNAs which encode proteins with partial sequence identity to the α- and β-subunits should facilitate the experimental evaluation of the design of this important neurotransmitter receptor.

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