# Alternative splicing generates two isoforms of the $\alpha 2$ subunit of the inhibitory glycine receptor

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The inhibitory glycine receptor (GlyR) is a ligand-gated chloride channel protein which displays developmental heterogeneity in the mammalian central nervous system. Here we describe 2 novel cDNA variants of the rat GlyR 22 subunit and demonstrate that alternative splicing generates these 2 isoforms. The deduced protein sequences (22A and 22B) exhibit 99% identity with the previously characterized human 22 subunit. In situ hybridization revealed expression of both 22A and 22B mRNAs in the prenatal rat brain, suggesting that these variant proteins may have a role in synaptogenesis. Heterologous expression in *Xenopus* oocytes showed that the more abundantly expressed 22A subunit forms strychnine-sensitive ion channels which resemble human 22 subunit GlyRs in their electrophysiological properties.

Glycine receptor; Alternative splicing: Receptor heterogeneity; Brain development

## 1. INTRODUCTION

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The inhibitory glycine receptor (GlyR) is a ligandgated chloride channel which antagonizes depolarization of the postsynaptic membrane in spinal cord and other regions of the vertebrate central nervous system [1]. Sedimentation and crosslinking experiments have revealed a pentameric structure of this membrane protein which is assembled from ligand binding  $\alpha$  subunits of 48 kDa and homologous  $\beta$  polypeptides of 58 kDa [2-6]. The ensemble of these subunits forms an anion selective membrane channel which opens upon binding of the agonistic amino acids glycine, taurine or  $\beta$ alanine [7].

Immunological and molecular cloning data have disclosed heterogeneity of GlyR  $\alpha$  subunits during development [8-10]. In spinal cord of adult rats,  $\alpha 1$  and  $\alpha 3$  subunit genes are expressed [5,9] whereas  $\alpha 2^*$ mRNA is predominantly found in newborn animals [10]. In addition to this heterogeneity resulting from different GlyR  $\alpha$  subunit genes, a splice variant of the  $\alpha 1$  subunit has been described which originates from alternative splice acceptor site selection, thus producing

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a novel potential phosphorylation site within the predicted cytoplasmic loop region of this protein [11]. Here we report the characterization of 2 rat  $\alpha$  subunit cDNAs which are highly homologous to the previously described human  $\alpha 2$  [12] and rat  $\alpha 2^*$  [10] sequences. These  $\alpha 2$  variants are generated by alternative splicing of 2 homologous exons, and differ in the primary structure of their extracellular domains. In situ hybridization with radiolabelled probes specific for  $\alpha 2A$  and  $\alpha 2B$ showed that these 2 isoforms are expressed during early brain development.

#### 2. MATERIALS AND METHODS

#### 2.1. RNA isolation

RNA was isolated from rat spinal cord and cortex using the method of Cathala [13]. Poly(A)<sup>+</sup> RNA was enriched by chromatography on oligo(dT) cellulose.

#### 2.2. Construction and screening of cDNA libraries

Two cDNA libraries were constructed from mRNA isolated from brain and spinal cord of newborn (P0) rats. The brain library was obtained by cloning size-fractionated cDNA into the lambda phage vector lambda gt10 while cDNA synthesized from spinal cord poly(A)<sup>+</sup> RNA was directionally cloned into lambda ZAP II according to the protocols supplied with cDNA cloning systems from Pharmacia and Stratagene. Size fractionation of cDNAs was achieved either by gel filtration on a Sepharose CL 4B column (brain cDNA), or by separating the cDNA in an agarose gel followed by electroelution (spinal cord cDNA). From the spinal cord cDNA, 3 independent sublibraries were constructed which contained insert sizes of 6–10 kb (I), 2–6 kb (II) and 0.5–2 kb (III), respectively.

#### 2.3. Isolation and sequencing of GlyR cDNAs

A <sup>32</sup>P-labelled XhoI fragment (1794 bp) of the rat GlyR  $\alpha 2^*$  cDNA [12] was used to screen about  $2 \times 10^5$  plaque forming units each, of the

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lambda gt10 P0 rat brain cDNA library, the spinal cord P0 library II, and an adult rat brain library [14]. Screening was performed using stringent conditions for hybridization (50% formamide, 5×SET, 42°C) and washing (0.2 × SSC, 0.1% (w/v) SDS, 60°C) of screening filters [9]. After exposure to Kodak X-Omat films we identified one positive clone in the P0 brain library (clone a2A-1), 2 in the spinal cord library (clones a2A11 and a2A111), and one in the adult brain library (clone a2B). After plaque purification, the EcoRI fragments of these clones were recloned into a Bluescript vector (Stratagene) or exclsed from the lambda vector ZAPII using helper phage functions, resulting in clones pGRa21, II, III and pGRa2B. The nucleotide sequences of these clones were determined for both strands with the chain termination method [15] using specific primers.

#### 2.4. Isolation and characterization of genomic fragments of the er2 gene from mouse

A mouse genomic library in lambda EMBL3 (a kind gift from Dr K. Chowdhury, Max-Planck-II with the radiolabelled 830 bp which contains most of the region of the human GlyR a2 in 5×SSPE at 60°C, and filt 5×SSPE at 60°C. From a num by hybridization with a <sup>32</sup>P-lab ding to positions 788-807 of several subcloned DNA fragm ment of 2 kb was identified, w specific for  $\alpha 2A$  and  $\alpha 2B$ . U primer, about 550 bp of the D was determined.

#### 2.5. In situ hybridization

Preparation of sections fro procedures were as described [ used were for a2A: 5'-GTG TOTTGATAAAAATATTGC CTGCTATTGACCCAAAGC

### 3. RESULTS

To further investig regional heterogeneity of structed and screened cD brain of newborn and ad be. This approach led overlapping cDNAs enco GlyR subunit. Three of EcoRI fragments spanni This sequence codes for amino acids (Fig. 1) wh acid sequence identity w and differs from the pre [10] at only a single an

Fig. 1. Nucleotide and deduc  $\alpha$ 2A and  $\alpha$ 2B subunit variant shown for  $\alpha 2A$ , and only the d spans nucleotides 662-2235 residues are indicated in the single letter of quences. The putative signal peptidase cleavage site is marked by an arrow. Proposed transmembrane spanning regions M1 to M4 are underlined, and putative extracellular N-glycosylation sites are boxed. An asterisk denotes the 3'-terminal stop codon. Numbering of nucleotides is indicated on the left and of amino acid residues on the right side of the figure.

Institut, Göttingen, FRG) was screened Pvull fragment of clone huBI [12], coding sequence for the extracellular subunit. Hybridization was performed lers were washed twice for 20 min in the of positive clones, one was selected belled oligonucleotide probe correspon- the rat $\alpha$ 2A cDNA sequences. Within ents, a HindIII-EcoRI restriction frag- which hybridized with oligonucleotides	841 901 941 1021	1 F 1   ΤΑΤΤΤΑΤΟ 1 F 1   ΤΤΟΤΛΛΩΑ F L 1   ΤΤΟΠΑΝΤΤΤΟ L D L   ΛΟΛΑΛΟΘΑ E K G   ΑΤΟΘΟΛΑΛΟΘΑ E K G
Ising these oligonucleotides and a T7 NA sequence of this genomic fragment	) 083	N G R AGAACTTT R N F
	1141	M N D
m rat brain and in situ hybridization 16]. Specific antisense oligonucleotides	1201	CCCTGCCT T L P
AA-3' and for $\alpha$ 2B: 5'-GTAGTTT-	1561	NCACTOOC
IGTIOATAAATATOTTOCAU-3 .	1321	ATTTCATC Y L I
	1301	GGATAAAC W I N
ate the developmental and of $GlyR \alpha$ subunits, we con-	1441	TGACTACO
NA libraries of spinal cord and ult rats with an $\alpha^{2*}$ cDNA pro-	1 501	TTGACATO
to the isolation of several	1561	CAGTGAAC
the clones isolated contained $\alpha^2$	1621	GGCAGAAT R Q N
ng a sequence of about 3.2 kb.	1601	TGGGTCAC
ich displays about 99% amino	1741	TTCCGCAN L P Q
with the human $\alpha^2$ subunit [12] eviously identified $\alpha^2$ * subunit	1800	GAATCGAC R I D
nino acid position (pos. 167).	1861	ACTGGATC Y W I
	1921	TTATATTC
	2041	TCTGGCAC
	2101	AGAGGACI
ed amino acid sequences of the GlyR	2221	TGGTTTG/
s from rat. The complete sequence is	2341	CTACCAU
ivergent region for $\alpha 2B$ (the $\alpha 2B$ cDNA	2401	CAAGCOTO
of clone $\alpha$ 2A). Deduced amino acid	2461	GACTAAG
ple letter code below the nucleotide se-	05.01	00000000

(ATTAAATCACETETECETETETETETAGECETEATTECAGEACACEACEACEATCTCAGEATT 181 341 ALAAFTETAADA TUTATETETETETETAADA TAATA TUTATETAADA TUTATE 341 TAACAAATTAATTITEAADA TAAATTAAATTETTITETAADAAAATTAAATTAA 311 AATAAATTITEAATTITEAADAAAAATAAATTETTAETAADAATTAATTITEAAAAATAA 341 TAAAAAATTITEATTITEAADAATTATTITETTETTAATTITEAAAAATAA HHRQLVNILTALPAPP 141 TAGGACAMACCACTTCAGARAAGEATTETCCAAAGACCATGACTECEAGGTCTCGAAAAG GTNHPAEAPCANDHDSNSG HPSQTLEP S O F L D K L H G K 781 GATATGATGAAAATCAGGCCAAAFTTTAAAGGTCCCCGGTAAACGTTACTTGCAATA G T B A R I R P R P K G P P V R V T C R осстестотька тогоська .....P P W V T C 761 TTTTTATCAACAGTTTTUGATCOUTCAUAUAAACCACCATUGACTACCGAGTGAACATT N APGSVTETTHOYAV алелестттосотеллтлослолллстаслато..... F G S I A E T T HILLINGSTRATIONS CAGCAGTOGAACGATTCACGGCTGGCATACAGTGAGTACCCAGATGATTCCC Q Q W H D S R L A Y S R Y P D D S KATCCATCCATCCTCCATTCCATTCCACACACACACACTCCTTCCCCAATC GECANTTTCCATGATGTCACCACTCATAACAAGTTCCCCCCCATTTCCAAAA N H P H D V T T D H R L L B I S R NOTICETETACAGEATTAGACEACCETCACETTATECETUTECCATOGACETCA V L Y S I H L T L T L S C P H D L CCAATGGATGTCCAGACCTGTACAATGCAGCCTGCAGAGTTTTGGGTACACCA CTUATATTTOACTOGTTAAUTUATGGTCCAGTACAAGTTGCTGAAGGACTCA 1. 1 8 EWLSDGPVQVAEGL CAGTTTATTTGAAAGAAGAAGAAGGAACTTGGCTATTGCACAAAGCATTAC Q F I L K E E K E L G Y C T K H Y 209 ANGTITACCTOCATTONOGTCANGTTTCACCTGGAACGCCAGATGGGGCTATT FTCIEVKFHLER<u>OHGY</u> 229 CAGATGTATATCCCCAGCCTGCTGATAGTCATTTTGTCCTGGGTCTCCTTT 249 P S L L CATGGATGCAGCTCCTGCCAGGGTTGCCCTTGGCATCACAACCGTCCTGACAA 269 <u>M D A A P A R <u>V A E G I T T V</u></u> CAGAGTTCAGGTTCCAGGGCATCTCTGCCAAAGGTCTCATATGTGAAAGCAA <u>OSSGS</u>RASLPKVSYVK<u>A</u> 289 TGGATGGCAGTGTCCCTTCTGTTTGTGTTGCTGCCTTACTGGAATATGCAG <u>M M A V C L L F V F A A L L E Y A</u> 309 TTTGTCTCCAGGCAACACAAGGAGTTCCTTCGTCTCCGGAGACGACAGAAGA SRQHKEFLRLRRQK 329 AAGGAAGAAGATGTTACTCGTGAAAGCCGTTTTAACTTCAGCGGTTATGGGA K E E D V T R E S R F N F S G Y G 349 TGCCTCCAAGTGAAAGATGGTACAGCTGTCAAGGCTACACCTGCCAACCCAC

CLQVKDGTAVKATPANP 369 CCCCCANAAGATGCAGATGCTATCAAGAAGAAGTTTGTGGATCGGGCAAAAA PPKDADAIKKKFVDRAK 389 ACCATATCTCGAGCTGCCTTCCCACTGGCCTTCCTCATTTTCAACATCTTTT TISRAAFPLAFL 409 T FN ACATACAAGATCATTCGGCATGAAGATGTCCACAAGAAATAGATGTATCCTA YKIIRHEDVHKK 425 GGGACCTTCTTTGCCTAAGTGTTGTGCTTGTAAATACACAGTAATAGTGTCT CTTTGACAGAGAACATTGAGGGTGGGGGGGGGGGAAAATCATGAGGGTGGGGTT

CITACTEGACANAGEACEGGTTCTATEGGGAAGAAAACTGCACAAATT TGCAGAATCACANAGEACEGGTTCTATEGGGAAGAAGAAACTGCACAAATT TGCAGAATCACATGAGAATAACTCCCATCCATAGTCTTATAGCATTGTTCTTTC ACATCACTCAGACATGATATGCAAGGTCAAGTTCTTGAGGGCTGGTTATCTTA TAGTAAATTGAGGACCAAACTTTTTCAGGAAAATGCTGCCTCATTTTTTAAAA CCTGAGGTATGATATTTACAATGTCTGTAATTAGTGTTTCACCCAAGAAATCC 5GTTGTAAATTCTTTCTACAAATCCAGGAAACAA CAACAAGATAAACACAAAA AGCAGATTTCTACTCTGCTGTGTGTGTGTGTGCACTTTGATATTTTTCTT 2641 2701 TGCCACAGTATTTATGGAGAGCGGGGTGTGTGTGTGTGGGGTATCTGAGGGGGGCGAAACT TCCCATTTCTGCCCTCATTGTAGCTGTAACTACTAGTCGTAATGTGACTGGACCGGACCTGTAA TTTGTACTTTCAATCCAAGTGAATATCGTTTTAAATATCCCTTGATTAACTGAAAAAATT 2761 2821 2881 2941 3001 AACCTGTAAAGTTATATGGAAATAATTACATTTTACATGTGCTGTAAAAGGGATTATTTT 3061 3121 AAAAAAGCATTTGTTCAGTTTCAATAAAGGTAAGTGTGCC

Moreover, this cDNA contained a 5'-nontranslated region of 551 bp and a 3'-nontranslated region of 1250 bp. At positions 3143-3148, a putative polyadenylation signal AATAAA was found, indicating that this cDNA ( $\alpha$ 2A) might be almost complete at its 3'end.

Another hybridization-positive clone ( $\alpha$ 2B) was isolated from a rat brain cDNA library [14] whose sequence proved to be identical to the above-mentioned clones with the exception of a continuous short sequence region, where identity dropped to about 79%. Out of 22 amino acid positions encoded by this diverging part of the DNA sequence of  $\alpha$ 2B, only 2 residues were different between both variants. In  $\alpha$ 2B, an isoleucine is found at position 58 and an alanine at position 59, instead of valine and threonine residues, respectively, in the rat  $\alpha$ 2A and  $\alpha$ 2\* [10] and human  $\alpha$ 2 [13] proteins. Interestingly, the same isoleucine and alanine residues are conserved at the corresponding positions of the rat  $\alpha$ 1 [6] and  $\alpha$ 3 [9] subunits.

To investigate whether the difference between the sequenced cDNAs originates from an alternative splicing event, we isolated the corresponding region from the mouse genome. An 2 kb *Eco*RI-*Hin*dIII fragment subcloned from a recombinant lambda phage was



Fig. 2. (A) Schematic diagram of the position of exon 3 encoded amino acid residues in the primary structure of the GlyR polypeptide. Residues encoded by exons 3A or 3B are indicated by a black box; M1 to M4 shows positions of putative transmembrane regions of the GlyR. The signal peptide sequence is indicated by hatches. (B) Nucleotide sequence of the two exon 3 variants of the mouse  $\alpha 2$  gene. Exonic regions are indicated by the encoded amino acid sequences, and intronic sequences are underlined.

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found to contain 2 variants of the putative exon 3 (Y. Maulet and B. Matzenbach, unpublished data) or the  $\alpha$ 2 gene, which were identical to the sequences found in the rat cDNA clones  $\alpha$ 2A and  $\alpha$ 2B (Fig. 2). These variant exons are separated by a short intervening sequence of 91 bp, and both are surrounded by proper splice acceptor and donor sequences (Fig. 2).

Two 45 bp antisense oligonucleotide probes specific for exons 3A and 3B were used to perform in situ hybridization experiments. Rat brain sections of different developmental stages were incubated with the radiolabelled oligonucleotides, and hybridizing RNA sequences located by autoradiography. These experiments demonstrated the expression of the a2A sequence in various higher brain regions during pre- and postnatal development (Fig. 3). Unexpectedly,  $\alpha 2A$ mRNA was strongly expressed in cortex, thalamus and hippocampus at embryonic day 19 (E19) and at birth (P0). Expression of  $\alpha$ 2B transcripts was also mainly seen at prenatal day E19. At this stage, the regional distribution of both sequences appeared to be quite similar, although hybridization signals were significantly lower for the  $\alpha$ 2B mRNA. At later postnatal stages,  $\alpha 2A$  expression was clearly decreasing and  $\alpha 2B$ transcripts were barely detectable, although a low basal level of expression may still persist (Fig. 3). To investigate the pharmacological properties of the rat GlyR  $\alpha 2$  polypeptide, in vitro synthesized  $\alpha 2A$  RNA was injected into Xenopus oocytes. After 2-5 days, the cells were analyzed for glycine responses by electrophysiology in the voltage clamp mode. Membrane currents were seen at glycine concentrations  $< 100 \,\mu M_{\odot}$ with half-maximal responses being obtained at about 250 µM, a value similar to those required for gating human  $\alpha 2$  and mutated rat  $\alpha 2^*$  GlyR proteins (data not shown; see refs [10,12]. Strychnine blocks the opening of channels formed by the rat and human  $\alpha$  1 and the human  $\alpha 2$  subunits at concentrations of 20-100 nM [10,12,17]. A similar inhibition of chloride currents was observed here upon expression of  $\alpha 2A$  mRNA in the oocyte system indicating that the  $\alpha 2A$  polypeptide forms strychnine-sensitive GlyR channels (data not shown).

## 4. DISCUSSION

The identification of 2 variants of the GlyR  $\alpha 2$ subunit resulting from alternative exon selection corroborates alternative splicing as an important mechanism to generate GlyR heterogeneity. The conservation of splicing pathways in mouse and rat demonstrated in this paper suggests a crucial role of minor sequence variations in GlyR function. Interestingly, the novel exon 3B of the  $\alpha 2$  gene identified here codes for amino acid residues which are conserved in rat  $\alpha 1$  [5] and  $\alpha 3$  [9] subunits at identical positions, thus supporting further the evolutionary conservation

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P20

of this subunit domain. Comparison of our data with alternative splicing events reported for other ligand gated ion channel proteins [18-21] raises the question whether similar exon variations might exist in GlyR  $\alpha$ I and  $\alpha$ 3 subunit genes. Indeed, alternative splicing cassettes have recently been shown to be conserved in the kainate/AMPA class of glutamate receptors and found to determine the functional properties of the resulting channels [22]. If so, alternative exon usage may constitute a general mechanism to provide plasticity of synaptic connections, a function which probably evolved before subunit diversification via gene duplication.

In a previous report, we have analyzed a GlyR subunit sequence termed  $\alpha 2^*$  which is highly expressed in the spinal cord of newborn, but not adult, rats [10]. As shown above,  $\alpha 2^*$  and  $\alpha 2A$  cDNA sequences are identical except for an A to G substitution at position 1132, which results in a glycine residue at position 167 in the  $\alpha 2A$  protein instead of a glutamate in the  $\alpha 2^*$ polypeptide. Besides, a further nucleotide exchange was found in the 5' nontranslated region (pos. 371 G/C). Thus, the PCR amplification experiments in our earlier studies [10] did not distinguish between  $\alpha$ 2A,  $\alpha$ 2B and  $\alpha^{2*}$  subunits, and all these  $\alpha^{2}$  sequences might indeed be expressed at early stages of spinal cord development. This assumption is supported by in situ hybridization experiments with  $\alpha 2A$  and  $\alpha 2B$  specific oligonucleotides on spinal cord sections which produced clear hybridisation signals for both probes at early postnatal stages (M.L. Malosio, unpublished data). As demonstrated previously by site-directed mutagenesis, the glutamate residue at position 167 of the  $\alpha 2^*$  subunit causes a loss of a strychnine sensitivity of the receptor upon expression in Xenopus oocytes [10]. We therefore had proposed that the  $\alpha 2^*$  sequence might correspond to the ligand-binding subunit of the biochemically characterized neonatal GlyR, which displays only low affinity binding of the antagonist strychnine [8]. As the sequences of the  $\alpha 2A$  and  $\alpha 2^*$  cDNAs are identical besides 2 nucleotide substitutions in the 5' nontranslated and the coding regions, it seems unlikely that 2 genes of nearly identical sequence exist in the rat genome. We therefore speculate that  $\alpha 2^*$  and  $\alpha 2$ mRNAs may represent allelic variations of the same  $\alpha^2$ subunit gene. This would be one possible explanation for the isolation of  $\alpha 2^*$  and  $\alpha 2A$  cDNAs, which now is under investigation in our laboratory.

The in situ hybridization experiments with brain sections from pre- and postnatal rats performed here

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Fig. 3. In situ hybridization of GlyR subunit mRNAs in horizontal sections of rat brain using antisense oligonucleotide probes specific for  $\alpha$ 2A and  $\alpha$ 2B GlyRs. Hybridizations to sections from a late prenatal (E19) and 3 postnatal (P0, P5 and P20) stages are shown. Cx, cortex; Hi, hippocampus; La, lateral amygdaloid nucleus; Th,

thalamus. Exposure on X-Omat AR film was for 8 weeks.

revealed strong signals in higher brain regions. Cortical layers in forebrain were labelled by both the  $\alpha 2A$  and  $\alpha 2B$  probes already at E19. During further development,  $\alpha 2B$  transcripts appeared to be down-regulated, whereas  $\alpha 2A$  gene expression remained well detectable beyond early postnatal stages and was still seen in the hippocampus and thalamus of P20 rats. Thus, the  $\alpha 2A$ and  $\alpha 2B$  subunit variants may have different roles during synapse formation in the mammalian brain.

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