Cloning and Characterization of χ -1: A Developmentally Regulated Member of a Novel Class of the Ionotropic Glutamate Receptor Family

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lonotropic glutamate receptors are composed of homomeric or heteromeric configurations of glutamate receptor subunits. We have cloned a member of a novel class of the rat ionotropic glutamate receptor family, termed χ -1. This subunit exhibits an average identity of 27% to NMDA subunits and 23% to non-NMDA subunits. Regional transcript levels of χ -1 are elevated just prior to and during the first postnatal week, with the highest levels present in the spinal cord, brainstem, hypothalamus, thalamus, CA1 field of the hippocampus, and amygdala. The spatial distribution of χ -1 expression is similar from postnatal day 1 (P1) to adulthood. However, transcript levels decline sharply between P7 and P14 and remain attenuated into adulthood. Functional expression studies in Xenopus oocytes injected with in vitro transcribed x-1 RNA did not demonstrate agonist-activated currents. Pairwise expression of χ -1 with members of the AMPA, KA, or δ class of glutamate receptor subunits either failed to generate agonist-activated currents or failed to alter the underlying current generated by the coexpressed subunit. However, coexpression of χ -1 with subunits forming otherwise functional NMDA receptors resulted in an inhibition of current responses. Since χ -1 did not alter the currents generated by non-NMDA subunits, this suggests that χ -1 may specifically interact with NMDA receptor subunits. Further characterization will be required to establish the precise role of this glutamate receptor subunit in neuronal signaling.

[Key words: glutamate, receptor, cloning, NMDA, ionotropic, subunit]

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The majority of rapid excitatory transmission in the nervous system is mediated by glutamate-activated ion channels. Ionotropic glutamate receptors have been subdivided pharmacologically into (α-amino-3-hydroxy-5-methyl-4-isoxazole propionic acid), KA (kainate), and NMDA subtypes (Monaghan et al., 1989). These receptors have been implicated in a number of physiological and pathological processes. During development, glutamate receptors are involved in neuronal differentiation, migration, and activity-dependent synapse formation (Balazs et al., 1989; Brewer, 1989; Komoru and Rakic, 1993). In mature neurons, long-term potentiation and long-term depression require ionotropic glutamate receptors (Collingridge and Lester, 1989; McDonald and Johnston, 1990; Bliss and Collingridge, 1993; Malenka, 1994). Glutamate-gated ion channels also play a central role in mediating the excitotoxic effects of glutamate (Olney, 1990). Pathophysiological processes thought to involve glutamate excitotoxicity and neurodegeneration include epilepsy, stroke, Parkinson's disease, Alzheimer's disease, Huntington's disease, and amyotrophic lateral sclerosis (Choi, 1988; Monaghan et al., 1989).

Molecular cloning efforts have identified 16 rat ionotropic glutamate receptor subunits (see Seeburg, 1993; Hollman and Heinemann, 1994). These subunits are divided into six classes, including the AMPA subunits, the high and low affinity KA subunits, the NMDAR1 and NMDAR2 subunits, and the pharmacologically undefined δ class. These subunits are thought to form oligomeric glycoprotein complexes whose precise stoichiometry is unknown (Blackstone et al., 1992; Wenthold et al., 1992; Brose et al., 1993; Chazot et al., 1994).

Functional homomeric NMDA receptors can be formed from the NMDAR1 subunit (Moriyoshi et al., 1991; Nakanishi et al., 1992; Yamazaki et al., 1992). However, coexpression of NMDAR1 with a member of the NMDAR2A-D class greatly enhances the agonist-gated currents. Each NMDAR2 subunit confers unique properties to the resulting heteromeric NMDA receptor (Ikeda et al., 1992; Kutsuwada et al., 1992; Meguro et al., 1992; Monyer et al., 1992; Ishii et al., 1993).

Discrepancies between the properties of heteromeric NMDA receptors formed from cloned subunits and *in vivo* NMDA receptors have suggested that some native NMDA receptors may contain additional uncharacterized subunits. Photoaffinity ligand studies on heteromeric receptors expressed in HEK-293 cells do not adequately describe the patterns of labeling seen *in vivo* (Marti et al., 1993). In addition, glycine affinities for expressed heteromeric NMDA receptors are 10-fold lower than those ob-

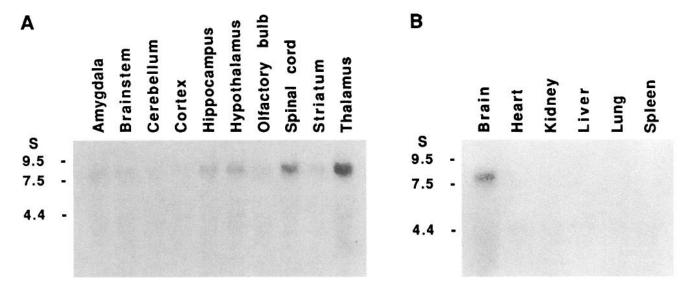


Figure 1. Northern blot analysis of χ -1 transcript expression in brain regions (A) and peripheral tissues (B) of the adult rat. Fifteen micrograms of total RNA were run on a 1% agarose-formaldehyde gel, transferred to a nylon membrane, and probed with a 342 bp ³²P-labeled fragment of the χ -1 subunit. The blot was exposed to film for 4 d with a screen. S, RNA molecular weight standards in kilobases.

served *in vivo*, with the exception of NMDAR1/2C receptors (Laurie and Seeburg, 1994).

We have identified a putative member of a new class of the ionotropic glutamate receptor family, termed χ -1. In the following study, we present the sequence of χ -1, examine its structural features and expression properties, and characterize its mRNA distribution within the developing and adult rat brain.

Materials and Methods

Degenerate polymerase chain reaction. Two degenerate primers, G1 [5'-TGGAA(C,T)GG(C,A,G)ATG(A,G)T(G,A,T)GGNGA-3'] which spans the residues WNGMVGEL upstream of transmembrane region I (TM 1), and G2 [5'-AA(A,G)GC(A,T,G)GCCA(A,G)(A,G)TT(A,T,G)GCIG-T(A,G)T-3'] which spans the residues YTANLAAF in TM III, were designed based on the sequences of GluR1-7, KA-1, KA-2, and NMDAR1. These primers were similar to those used by Monyer et al. (1992). Rat brain mRNA was prepared from total RNA using the PolyATtract system (Promega) and subsequently converted to cDNA using Superscript RNaseH- reverse transcriptase (GIBCO-BRL) as directed by the manufacturer. PCR reactions were performed in 50 µl reactions containing 10 mm Tris-HCl, pH 8.3, 50 mm KCl, 1.5 mm MgCl₂, 0.01% gelatin, 0.2 mm each of dATP, dGTP, dCTP, and dTTP, 80 pmol of each primer, 5 ng of rat brain cDNA, and 1.25 U AmpliTaq DNA polymerase (Perkin-Elmer). Thirty-five cycles of amplification were performed at 95°C, 1 min; 48°C, 1 min; and 71°C, 1 min in a thermocycler (MJ Research). The amplified DNA was fractionated on low-melting agarose, and the products of approximately 450 bp were isolated from the gel, blunt-ended with Klenow enzyme, and ligated into pBluescript (Stratagene) using standard laboratory procedures (Sambrook et al., 1989).

cDNA cloning and genomic fragment isolation. Individual PCR products produced by the degenerate PCR amplification were identified by endonuclease digestion of isolated subclones with the enzymes PleI and NdeII. Unique PCR products were sequenced by the Sanger chain termination method (Sanger et al., 1977) using Sequenase 2.0 (USB). Two specific primers, S1 [5'-TCAGCATCAATACCGCAC-3'] and S2 [5'-TCAGAAACCTTCCAGTCCAG-3'], were used to amplify a 342 bp fragment from the novel subunit sequence identified, which was random prime-labeled with α³²P-dCTP and used to screen 2 × 10° plaques from a Stratagene brainstem/spinal cord library. Filters were hybridized in 50% formamide, 2 × saline–sodium citrate (SSC), 1% sodium dodecyl sulfate (SDS), 10% dextran sulfate, 1 × Denhardt's, and 300 μg/ml salmon sperm DNA at 42°C overnight, and then washed under high stringency conditions (0.1 × SSC at 55°C). The filters were exposed to Kodak XAR film overnight at −70°C with

an intensifying screen. Two clones, which possessed an overlap of 2 kilobases and together spanned the entire open reading frame, were fully sequenced on both strands and ligated together into pBluescript using a unique NcoI site.

A genomic fragment encoding the "TM II" region of χ -1 was obtained by PCR amplification of rat liver DNA with the specific primers S1 and S2 in several separate reactions. TM II has been placed in quotations to denote that recent evidence indicates that it does not traverse the membrane (Hollmann et al., 1994; Wo and Oswald, 1994; Bennett and Dingledine, 1995). Subclones from each of these reactions were independently sequenced.

Northern blot analysis. Total RNA was extracted from rat brain and peripheral tissues using RNAzol B (CINNA/BIOTECX), based on the method of Chomczynski and Sacchi (1987). Total RNA (20 μ g) was separated on 1% agarose-formaldehyde gels and transferred to Biotrans(+) nylon membranes (ICN). Membranes were hybridized overnight at 42°C with the same α^{32} P-dCTP-labeled fragment used for the library screening. Blots were washed under high stringency and exposed to Kodak XAR film with an intensifying screen. Signals were quantitated on an LKB densitometer (Pharmacia).

 3 H-Kainic acid and 3 H-CGP 39653 binding assays. The entire open reading frame of χ -1 was subcloned into the BamHI and EcoRV sites in the polylinker of the eukaryotic expression vector pcDNAI/Neo (Invitrogen). Human embryonic kidney 293 cells (HEK-293 cells, ATCC CRL 1573) were grown in Earle's minimal essential media containing 10% fetal bovine sera (GIBCO) and transfected by the calcium phosphate method as per Chen and Okayama (1987), using 20 μ g of plasmid per 10 cm plate, with transfection efficiencies of 15–20%. Forty-eight hours after transfection, cell membranes were harvested and 3 H-kainic acid binding assays were performed as in Werner et al. (1991). For 3 H-CGP 39653 binding assays, HEK-293 cells were transfected as above, and cell membranes were prepared as per Sills et al. (1991).

Expression studies in Xenopus oocytes. χ-1 cDNA was cloned into the BamHI and HindIII sites of pGEMHE (Liman et al., 1992), a high expression vector containing a T7 promoter and the 5' and 3' untranslated regions of a *Xenopus* β-globin gene. The construct was linearized with SphI prior to transcription with T7 RNA polymerase (Message Machine, Ambion). *Xenopus* oocytes were prepared as described in Hollmann et al. (1993). The methods for electrophysiology were as in Sullivan et al. (1994), except that calcium was used as the divalent cation in the recording solution. A maximum of 20 ng of cRNA was nijected per oocyte. Recordings were performed 2–5 d after injection. Responses to 200 μM NMDA were recorded in the presence of 10 μM glycine. Mutagenesis of the arginine (AGA codon) residue to a glutamine (CAA codon) residue in the "TM II" region of χ-1 was performed

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ATG Het	AGG Arg	λGλ λrg	CTG Leu	AGT Ser	TTG	TGG	TGG	CTG Leu	CTG	AGC	AGG	GTC Val	TGT	CTG	CTG Leu	CTG Leu	CCG	CCG Pro	ccc Pro	TGC Cys	GCA	CTG Leu	GTG Val	CTG Leu	GCC	GGG	GTG Val	CCC	AGC	TCC	TCC	TCG Ser	CAC	CCG Pro	105 35
CAA Gln	ccc Pro	TGC Cys	CAG Gln	ATC Ile	CTC Leu	AAG Lys	cgc	ATC	GCA	CAC	GCG	GTG Val	AGG Arg	GTG Val	GGC Gly	GCG Ala	GTG Val	CAC	TTG Leu	CAA Gln	CCC Pro	TGG Trp	ACC Thr	ACG Thr	GCC Ala	CCA Pro	cgc Arg	GCA Ala	GCC Ala	AGT Ser	ege Arg	GCT Ala	CAG	GAA Glu	210 70
GGC Gly	GGC Gly	AGG Arg	GCG Ala	GGT Gly	GCC Ala	CAG	λGG λrg	GAT	GAT	CCA	GAG Glu	TCC	GGG Gly	ACG Thr	TGG Trp	CGG Arg	CCA Pro	CCG Pro	GCG Ala	ccc	TCG Ser	CAA Gln	GGC Gly	GCA Ala	cgc Arg	TGG Trp	TTG Leu	GGG Gly	AGC Ser	GCC Ala	CTG Leu	CAT	GGC	CGG Arg	315 105
GGT	CCA Pro	ccc Pro	GGC Gly	TOC Ser	CGA Arg	AAG Lys	CTC	GGG	GAG Glu	GGC G1y	GCG Ala	GGG Gly	GCC Ala	GAG Glu	ACC Thr	CTG Leu	TGG Trp	ccg Pro	CGG Arg	GAT Asp	GCC Ala	CTA Leu	CTG Leu	TTC Phe	GCT Ala	GTG Val	GAA Glu	AAC Asn	TTG Leu	AAC Asn	CGT Arg	GTG Val	GAA Glu	GGG Gly	420 140
CTC Leu	CTA Leu	ccc	TAC Tyr	AAC Asn	Leu	TCT Ser	TTG Leu	GAA	GTA Val	GTG Val	ATG Met	GCC Ala	ATT Ile	GAG Glu	GCG Ala	GGC Gly	CTG Leu	GGC Gly	GAT Asp	CTG Leu	CCG Pro	CTT Leu	ATG Net	ccc	TTC Phe	TCT Ser	TCC Ser	CCA Pro	AGC Ser	TCA Ser	ccc Pro	TGG Trp	AGC Ser	AGT Ser	525 175
gac Asp	CCT Pro	TTC Phe	TCC Ser	TTT Phe	CTG Leu	CAG Gln	AGC Ser	GTG Val	TGC	CAC	ACC Thr	GTA Val	GTG Val	GTA Val	CAA Gln	GGG Gly	GTG Val	TCG Ser	GCG Ala	CTG Leu	CTG Leu	GCC Ala	TTC Phe	ccc Pro	CAG Gln	AGC Ser	CAG Gln	GGC Gly	GAA Glu	ATG Net	ATG Het	GAG Glu	CTG Leu	GAC Asp	630 210
TTG Leu	GTC Val	AGC Ser	TCT Ser	GTC Val	CTG Leu	CAC	ATC Ile	CCA Pro	GTG Val	CTC Leu	AGC Ser	ATA Ile	GTG Val	CGC Arg	CAC His	GAG Glu	TTT Phe	ccg Pro	CGG Arg	GAG Glu	AGT Ser	CAG Gln	AAT Asn	ccc Pro	CTG Leu	CAC	CTA Leu	CAG Gln	CTG Leu	AGT Ser	TTA Leu	GAA Glu	AAC	TCA Ser	735 245
CTA .	AGT Ser	TCT Ser	GAT Asp	GCT Ala	GAT Asp	GTC Val	ACT Thr	GTC Val	TCA Ser	ATC Ile	CTG Leu	ACC Thr	ATG Het	AAC Asn	AAC Asn	TGG Trp	TAC Tyr	AAT Asn	TTT Phe	AGC Ser	TTG Leu	TTG Leu	CTC Leu	TGC Cys	CAG Gln	GAA Glu	GAC Asp	TGG Trp	AAT Asn	ATC Ile	ACG Thr	GAC Asp	TTC Phe	CTC Leu	840 290
CTC (CTT Leu	ACG Thr	GAG Glu	AAT Asn	AAC Asn	TCC	AAG Lys	TTC Fhe	CAC	CTC Leu	GAG Glu	7CT Ser	GTT Val	ATC Ile	AAC Asn	ATC Ile	ACT Thr	GCT Ala	AAT Asn	CTG Leu	TCC Ser	TCC Ser	ACA Thr	AAG Lys	GAC	CTT Leu	CTA Leu	AGT Ser	TTC Phe	CTG Leu	CAG Gln	GTC Val	CAG Gln	ATG Met	945 315
GAC A	AAC Asn	ATT Ile	AGG Arg	AAC Asn	AGC Ser	ACA Thr	ccc	ACA Thr	ATG Het	GTG Val	ATG Het	TTT Phe	GGC Gly	TGT Cys	GAC Asp	ATG Het	GAC Asp	AGT Ser	ATC Ile	CGG Arg	CAG Gln	ATA Ile	TTT Phe	GAA Glu	ATG Net	TCC Ser	ACA Thr	CAG Gln	TTT Phe	GGG Gly	CTA Leu	TCA Ser	CCT Pro	CCT Pro	1050 350
GAA (CTT	CAC His	TGG Trp	GTT Val	TTA Leu	GGA Gly	GAC Asp	TCC	CAG Gln	AAT Asn	GTG Val	GAG Glu	GAA Glu	CTG Leu	AGG Arg	ACA Thr	GAA Glu	GGC Gly	CTG Leu	CCC Pro	TTA Leu	GGG Gly	CTC Leu	ATT Ile	GCT Ala	CAT	GGA Gly	AAA Lys	ACC Thr	ACA Thr	CAA Gln	TCT Ser	GTC Val	TTT	1155 385
GAG 1	TAC Tyr	TAC Tyr	GTT Val	CAG Gln	gat Asp	GCC Ala	ATG Het	GAG Glu	TTG Leu	GTT Val	GCA Ala	AGA Arg	GCT Ala	GTA Val	GCC Ala	ACA Thr	GCC Ala	ACC Thr	ATG Het	ATC Ile	CAG Gln	CCA Pro	GAG Glu	CTT Leu	GCT Ala	CTC Leu	CTT Leu	ccc	AGC Ser	ACA Thr	ATG Het	AAC Asn	TGC Cys	ATG Het	1260 420
GAT (GTG Val	λλλ Lys	ACC Thr	ACA Thr	AAT Asn	CTC Leu	ACT Thr	TCT Ser	GGA Gly	CAG Gln	TAT Tyr	TTA Leu	TCA Ser	AGG Arg	TTT Phe	TTA Leu	GCC Ala	AAC Asn	ACC Thr	ACT Thr	TTC Phe	AGA Arg	GGT Gly	CTC Leu	AGT Ser	GGT Gly	TCC Ser	ATC Ile	AAA Lys	GTA Val	AAG Lys	GGC Gly	TCC Ser	ACC Thr	1365 455
ATC I	ATC Ile	AGC Ser	TCA Ser	GAG Glu	AAC Asn	AAC Asn	TTT Phe	TTC Phe	ATC Ile	TGG Trp	AAC Asn	TTG Leu	CAG Gln	CAC His	GAC Asp	CCT Pro	ATG Mec	GGA Gly	AAG Lys	CCA Pro	ATG Net	TGG Trp	ACT Thr	CGC Arg	CTG Leu	GGC Gly	AGC Ser	TGG Trp	CAA Gln	GGA Gly	GGA Gly	AGG Arg	ATA Ile	GTC Val	1470 490
ATG (GAC Asp	TCT Ser	GGA Gly	ATA Ile	TGG Trp	CCA Pro	GAG Glu	CAG Gln	GCC Ala	CAG Gln	AGG Arg	CAC His	AAA Lys	ACC	CAC His	TTC Phe	CAG Gln	CAC His	CCA Pro	AAC Asn	AAG Lys	TTA Leu	CAC His	TTG Leu	AGA Arg	GTG Val	GTG Val	ACA Thr	TTG Leu	ATT	GAA Glu	CAC His	CCA Pro	TTT Phe	1575 525
GTT T	TTC Phe	ACG Thr	AGA Arg	GAA Glu	GTA Val	GAC	GAT Asp	GAA Glu	GGC Gly	TTA Leu	TGC Cys	CCT Pro	GCT Ala	GGA Gly	CAG Gln	CTC Leu	TGT Cys	CTA Leu	GAC Asp	CCT Pro	ATG Het	ACT Thr	AAC Asn	GAC Asp	TCT Ser	TCC	ATG Het	CTG Leu	GAT Asp	CGT Arg	CTG Leu	TTT Phe	AGC Ser	AGC Ser	1680 560
CTG (CAT	AGC Ser	AGT Ser	AAT Asn	GAC Asp	ACA Thr	GTG Val	CCA Pro	ATC Ile	AAG Lys	TTC Phe	AAG Lys	AAG Lys	TGC Cys	TGT Cys	TAT Tyr	GGG Gly	TAC Tyr	TGC Cys	ATC Ile	GAT Asp	CTC Leu	CTG Leu	GAG Glu	CAG Gln	CTA Leu	GCA Ala	GAA Glu	GAC Asp	ATG Ket	AAC Asn	TTT Phe	GAC Asp	TTT Phe	1785 595
GAC (CTC Leu	TAC Tyr	ATT Ile	GTA Val	GGG Gly	GAT Asp	GGA Gly	AAG Lys	TAC Tyr	GGA Gly	GCT Ala	TGG Trp	AAA Lys	AAT Asn	GGT Gly	CAC His	TGG Trp	ACT Thr	GGG Gly	CTG Leu	GTT Val	GGT Gly	GAT Asp	CTC Leu	CTG Leu	AGT Ser	GGG Gly	ACA Thr	GCC Ala	AAC Asn	ATG Het	GCG Ala	GTC Val	ACT Thr	1890 630
TCT 1	Phe	AGC Ser	ATC Ile	AAT Asn	ACC Thr	GCA Ala	CGA Arg	AGC Ser	CAG Gln	GTG Val	ATA Ile	GAT Asp	TTC Phe	ACC Thr	AGC Ser	CCT Pro	TTC Phe	TTC Phe	TCA Ser	ACC Thr	AGT Ser	TTG Leu	GGG Gly	ATC Ile	TTA Leu	GTG Val	AGG Arg	ACT Thr	CGA Arg	GAC Asp	ACA Thr	GCA Ala	GCT Ala	CCA Pro	1995 665
ATT O	GGA Gly	GCC Ala	TTC Phe	ATG Met	TGG Trp	CCA Pro	CTC Leu	CAC His	TGG Trp	ACC Thr	ATG Het	TGG Trp	CTG Leu	GGA Gly	ATT Ile	TTC Phe	GTG Val	GCT Ala	CTC Leu	CAT His	ATC	ACT Thr	GCC Ala	ATT Ile	TTT Phe	CTC Leu	ACT Thr	CTG Leu	TAT Tyr	GAA Glu	TGG Trp	AAG Lys	AGC Ser	CCC Pro	2100 700
TTT C	GT	λTG	ACC	сст	AAG	GGG	AGG	AAC	AGA	AAC	AAA	GTC	TTC	TCC	TTC	TCC	TCA	GCT	TTG	AAT		TGC			CTT	CTG	TTT	GGC	AGA	ACA	GCA	GCC	ATC	AAA	2205
Phe C	Sly	Het	Thr	Pro	Lys	Gly	Arg	Asn	Arg	Asn	Lys	Val	Phe	Ser		ser M I		Ala	Leu	Asn	Val	Cys	Tyr	Ala	Leu	Leu	Phe	Gly	Arg	Thr	Ala	Ala	Ile	Lys	735
CCC C	Pro	AAA Lys	TGC Cy's	TGG Trp	ACT	GGA Gly	AGG Arg	TTT	CTG Leu	ATG Het	AAT Asn	CTT Leu	TGG Trp	GCC Ala	ATT	TTC	TGT	ATG Het	TTT Phe	TGC Cys	CTT Leu	TCT Ser	ACA Thr	TAC Tyr	ACA Thr	GCG Ala	AAC Asn	TTG Leu	GCT Ala	GCT Ala	GTC Val	ATG Het	GTA Val	GGT	2310 770
GAG A	Lys	ATC Ile	TAT Tyr	GAA Glu	GAG Glu	CTT Leu	TCT Ser	GGA Gly	ATT	CAT His	GAC Asp	CCT Pro	AAG Lys	CTT Leu	CAT	CAT His	CCT Pro	TCT Ser	CAA Gln	GGC Gly	TTC Phe	CGC Arg	TTT Phe	GGA Gly	ACT	GTC Val	CGG Arg	GAA Glu	AGC Ser	AGT	GCT Ala	GAA Glu	GAC Asp	TAT Tyr	2415 805
GTG C	ogc Arg	CAG Gln	AGC Ser	TTC Phe	CCA Pro	GAG Glu	ATG Het	CAT His	GAG Glu	TAC Tyr	ATG Het	AGA Arg	AGG Arg	TAC Tyr	AAC Asn	GTG Val	CCA Pro	GCC Ala	ACC Thr	CCT Pro	GAT Asp	GGA Gly	GTG Val	CAG Gln	TAT Tyr	CTG Leu	AAG Lys	AAT Asn	GAT Asp	CCA Pro	GAG Glu	AAA Lys	CTA Leu	GAC Asp	2520 840
GCC T	Phe	ATC Ile	ATG Net	GAC Asp	AAA Lys	GCC Ala	CTT Leu	CTG Leu	GAT Asp	TAT Tyr	GAA Glu	GTG Val	TCA Ser	ATA Ile	GAT Asp	GCT Ala	GAC Asp	TGC Cys	AAG Lys	CTT Leu	CTG Leu	ACC Thr	GTA Val	GGA Gly	AAG Lys	CCA Pro	TTT Phe	GCC Ala	ATC Ile	GAA Glu	GGA Gly	TAT Tyr	GGC Gly	ATT Ile	2625 875
GGT G	erc Leu	CCT Pro	CCA Pro	AAC Asn	TCT Ser	CCA Pro	TTG Leu	ACC Thr	TCT Ser	AAT Asn	ATA Ile	TCT Ser	GAG Glu	CTC Leu	ATC Ile	AGT Ser	CAG Gln	TAC Tyr	AAG Lys	TCT Ser	CAC His	GGG Gly	TTT Phe	ATG Ket	GAT Asp	GTG Val	CTC Leu	CAT				TAC Tyr	AAG Lys	GTG Val	2730 910
GTT C	ecc Pro	TGC Cys	GGA Gly	AAG Lys	AGA Arg	AGC Ser	TTT Phe	GCC Ala	GTC Val	ACT Thr	GAG Glu	ACT Thr	TTG Leu	CAA Gln	ATG Het	GGC Gly	ATC Ile	λλG Lys	CAC His	TTC Phe	TCT Ser	GGA Gly	CTC Leu	TTC Phe	GTG Val	CTG Leu	TTG Leu	TGC Cys		GGA Gly		GGT Gly	CTC Leu	TCC Ser	2835 945
ATC C	TG .eu	ACC Thr	ACC Thr	ATT Ile	GGT Gly	GAA Glu	CAC His	λΤλ Ile	GTG Val	CAC His	AGA Arg	CTG Leu	CTG Leu	TTA Leu	CCA Pro	CGC Arg	ATC Ile	λλλ Lys	AAC Asn	AAA Lys	TCC Ser	AAG Lys	CTG Leu	CAG Gln	TAC Tyr	TGG Trp	CTG Leu	CAC His	ACG Thr	AGT Ser	CAG Gln	AGG Arg	TTT Phe	CAC His	2940 980
AGA G	ica lla	TTA Leu	AAC Asn	ACG Thr	TCA Ser	TTC Phe	GTA Val	GAA Glu	GAA Glu	λλG Lys	CAG Gln	CCA Pro	CGT Arg	TCC Ser	AAG Lys	ACA Thr	AAA Lys	CGT Arg	GTG Val	GAG Glu	AAG Lys	AGG Arg	TCC Ser	AAC Asn	CTG Leu	GGA Gly	ccc Pro	CAG Gln	CAG Gln	CTC Leu	ATG Het	GTA Val	TGG Trp	AAT Asn	3045 1015
ACT T	oc Ser	AAT Asn	CTG Leu	AGT Ser	CAT	GAC Asp	AAC Asn	CAA Gln	CGA Arg	AAA Lys	TAC Tyr	ATC Ile	TTT Phe	AAT Asn	GAC Asp	GAG Glu	GAA Glu	GGA Gly	CAA Gln	AAC Asn	CAG Gln	CTG Leu	GGT Gly	ACC Thr	CAG Gln	GCC Ala	CAC His	CAG Gln	GAC Asp	ATC Ile	CCT Pro	CTC Leu	CCT Pro	CAG Gln	3150 1050
AGG A	IGA Lrg	AGA Arg	GAG Glu	CTC Leu	CCT Pro	GCC Ala	TCA Ser	CTG Leu	ACC Thr	ACC Thr	AAT Asn	GGG Gly	AAA Lys	GCA Ala	GAC Asp	TCC Ser	CTC Leu	AAT Asn	GTA Val	ACT Thr	CGG Arg	AGC Ser	TCC Ser	GTG Val	ATT Ile	CAG Gln	GAA Glu	CTC Leu	TCT Ser	GAG Glu	TTG Leu	GAG Glu	AAG Lys	CAG Gln	3255 1085
									mmo			100	200	110	lC1	210	~~~								~~~	NOT	***	CAL	TCC Ser	T10					3945 1115

as described in Ho et al. (1989). The subcloned insert containing the mutation was confirmed by sequencing.

In situ hybridization. In situ hybridization was performed as described in Hockfield et al. (1993). Brains or whole embryos were obtained from Sprague-Dawley rats, frozen on dry ice in O.C.T. (Fisher), and stored at -80°C until sectioning. Twelve micrometer sections of tissue were cut in a Reichert-Jung cryostat, thaw-mounted onto Probe-On slides (Fisher), and fixed immediately with 4% paraformaldehyde in phosphate-buffered saline (PBS) for 10 min. Slides were then washed in PBS, dehydrated, and stored at -80° C until use. On the day of use, sections were thawed, treated with 0.25% acetic anhydride in 0.1 M triethanolamine, pH 8.0, and prehybridized for 1 hr at 55°C in 50% formamide, 1 × Denhardt's, 0.6 M NaCl, 10 mm Tris-HCl pH 7.5, 1 mm EDTA, 10 mm dithiothreitol, 500 µg/ml salmon sperm DNA, 500 μ g/ml yeast total RNA, and 50 μ g/ml yeast tRNA. α -33P-UTP-labeled cRNA probes were used in these studies because they generated a lower background than α -35S-CTP-labeled probes, and the enhanced sensitivity of 33P-labeled probes was required to delineate the lower level of χ -1 expression in the adult rat brain. Sense and antisense cRNA probes were generated to the regions corresponding to amino acids 671-739, 775-846, and 971-1028 using T3 and T7 RNA polymerases. The second probe (amino acids 775-846) produced the least background and was used to generate the figures shown. Hybridizations were performed for 6-8 hr at 55°C in prehybridization buffer containing 100 μg/ml salmon sperm DNA, 10% dextran sulfate, and 1 × 106 cpm of probe/2 cm² of section. Following hybridization, sections were treated with 20 µg/ml RNAse A at 37°C and then washed twice at 50°C in 2 × SSC for 15 min. Sections were then washed twice at a final stringency of $0.1 \times SSC$ containing 0.1% β -mercaptoethanol at 65°C for 15 min. Following dehydration, sections were exposed to Kodax Biomax film for 4-25 d. Sections were stained with cresyl violet and anatomical landmarks were identified using the atlases of Paxinos and Watson (1986) and Paxinos et al. (1991). To analyze the signal at higher resolution, slides were dipped in NTB-2 emulsion (Kodak). After 6 weeks the slides were developed, stained with cresyl violet, and examined under bright-field microscopy. All three antisense probes detected a single 8 kb transcript on Northern blot analysis and generated identical in situ patterns of expression. Sense probes produced blank autoradiograms at equivalent exposure times. Pretreatment with RNase A or incubation with a 20-fold molar excess of unlabeled competitor cRNA completely abolished the detected signal, while incubation with unlabeled noncompetitor cRNA had little or no effect.

In vitro *translation*. Two micrograms of sense cRNA transcribed with T7 RNA polymerase from the pGEMHE construct were used in a reaction containing 2 mCi/ml ³⁵S-L-methionine (ICN) and 60% rabbit reticulocyte lysate according to the manufacturer's instructions (Amersham). The *in vitro* translation products were separated on a 6% SDS-PAGE gel and examined by autoradiography.

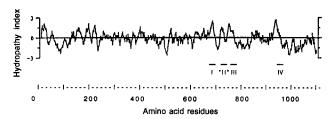


Figure 3. Hydrophobicity profile of χ -1. The algorithm of Kyte and Doolittle (1982) was used with a window setting of 12. The calculations were performed using the PEPPLOT program within the University of Wisconsin sequence analysis software (Devereux et al., 1984). Putative transmembrane regions are indicated.

Results

Identification of a novel glutamate receptor subunit

Two degenerate oligonucleotide primers designed to recognize conserved sequences of GluR1-7, KA-1, KA-2, and NMDAR1 were used to PCR amplify cDNA synthesized from rat brain mRNA. Restriction digestion of 24 cloned PCR products identified 8 independent restriction patterns. Of these 8 PCR clones, all but one was identified by nucleic acid sequencing as a known glutamate receptor subunit. The deduced amino acid sequence of the novel fragment was 29–36% identical to other glutamate receptor subunits. Furthermore, the hydrophobicity profile of the novel fragment was very similar to the profiles of the corresponding region of other glutamate receptor subunits, suggesting that this PCR clone might be a fragment of a novel glutamate receptor subunit.

Northern blot analysis using an internal fragment of the isolated PCR product as a probe revealed a single 8 kb message. Within the adult rat brain, the mRNA was expressed in all regions examined, though at low levels (Fig. 1A). The message was enriched in the thalamus and spinal cord. No message was detected in any of the peripheral tissues examined (Fig. 1B).

In order to obtain the full coding region of the receptor, we screened a $\lambda ZAPII$ rat brainstem/spinal cord library. Multiple clones spanning the entire open reading frame were obtained and overlapping clones verified the full coding sequence. The

Table 1. The average percentage amino acid sequence identity between classes of the glutamate receptor gene family

	GluR1-4	GluR5-7	KA-1,2	NMDAR1	NMDAR2A-D	δ1,2
GluR5-7	40					
KA-1,2	37	44				
NMDAR1	26	28	27			
NMDAR2A-D	25	24	24	27		
δ-1,2	29	30	27	26	23	
χ-1	23	24	23	27	28	22

The average percentage identity between two classes was determined by averaging the identities among all pairwise combinations of subunits between two classes. The percentage identity between any given pair of subunits was computed using the GAP program of the University of Wisconsin sequence analysis software (Devereux et al., 1984).

(

Figure 2. The deduced amino acid sequence of the rat χ -1 glutamate receptor subunit. Twelve potential glycosylation sites in the predicted extracellular region (*), and one potential site for Ca²⁺/calmodulin-dependent protein kinase type II (\Diamond) in the predicted intracellular region are indicated. Black bars indicate the signal peptide (SP) and the three transmembrane regions in glutamate receptor subunits. Recent evidence suggests that "TM II" does not traverse the membrane as previously thought (Hollmann et al., 1994; Wo and Oswald, 1994; Bennett and Dingledine, 1995). The cleavage site of the signal peptide is predicted by the method of von Heijne (1983). The nucleic acid sequence data will appear in Genbank under the accession number L34938.

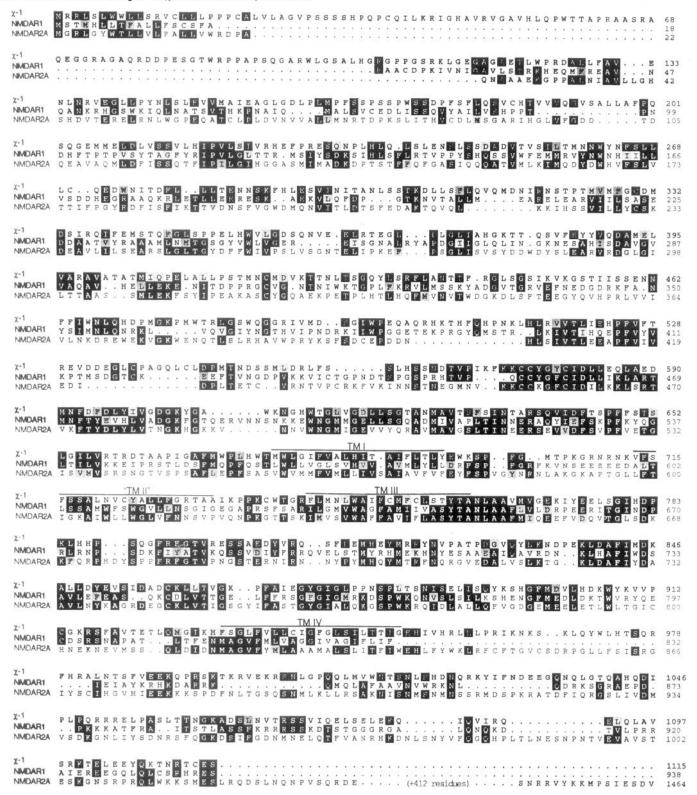


Figure 4. Alignment of the amino acid sequences of χ -1, NMDAR1 (Moriyoshi et al., 1991), and NMDAR2A (Ishii et al., 1993). The putative transmembrane regions are indicated. Identical residues are enclosed in *solid boxes*, while conservatively related residues are in *shaded boxes*. The alignment was generated with the PRETTYBOX program within the University of Wisconsin sequence analysis software (Devereux et al., 1984).

translational start site was assigned to the first methionine in the large open reading frame. Since no single clone contained the entire coding region, two clones, which overlapped over an interval of 2 kilobases, were used to construct the full open reading frame for expression studies.

Structural features of χ -1

The open reading frame of χ -1 encodes a protein of 1115 amino acids (Fig. 2) with a calculated molecular weight of 125 kDa. The sequence of χ -1 has an average homology of 27% to NMDA receptor subunits and 23% to non-NMDA subunits (Ta-

ble 1). The percent identity between χ -1 and other glutamate receptor subunits (21-29%) is similar to the percent identity between other classes of the glutamate receptor family (23–44%), and therefore would support the placement of this subunit in a new class within the glutamate receptor family. χ-1 is intermediate in size between the smaller NMDAR1 subunit (938 amino acids) (Moriyoshi et al., 1991) and the larger NMDAR2A-D subunits (1464, 1482, 1250, and 1356 amino acids, respectively) (Ishii et al., 1993).

The amino acid sequence of x-1 possesses features common to members of the glutamate receptor family, including an N-terminal hydrophobic region encoding a putative signal peptide, and a large N-terminal extracellular domain containing multiple potential sites for glycosylation (Fig. 2). Eleven of the 12 potential glycosylation sites are located in the N-terminal extracellular domain. The x-1 subunit possesses one potential phosphorylation site for the Ca2+/calmodulin-dependent protein kinase type II (Pearson et al., 1985). Several potential protein kinase C sites (Woodgett et al., 1986) are also present in the putative intracellular regions of χ -1. The hydrophobicity profile of χ -1 is similar to the profiles reported for other glutamate receptor subunits (Fig. 3).

An additional feature common to all ionotropic glutamate receptors, including χ -1, is homology of the region upstream of TM I (amino acids 513-661) to the periplasmic glutamine binding protein of E. coli, which is thought to encode the glutamate binding domain (Nakanishi et al., 1990; Stern-Bach et al., 1994). In non-NMDA subunits this region is approximately 115 amino acids, but in all NMDA subunits and in χ -1, this region is approximately 145 amino acids, indicating that χ -1 may be more structurally related to the NMDA class of subunits. Further supporting this possibility, the C-terminus of χ -1 (ELEEYQKTN-RTCES) shares homology with the C-terminus of NMDAR1 (EREEGOLOLCSRHRES). C-terminal homology between functionally related glutamate subunits is seen NMDAR2A-D (Ishii et al., 1993), GluR2 and GluR3 (Boulter et al., 1990; Keinanen et al., 1990; Nakanishi et al., 1990; Sakimura et al., 1990), and GluR5 and GluR6 (Bettler et al., 1990; Egebjerg et al., 1991; Sommer et al., 1992). An alignment of χ-1, NMDAR1, and NMDAR2A is shown in Figure 4.

The "TM II" segment (see Fig. 2 caption) of glutamate-gated channels is thought to control ion selectivity of the channel (Betz, 1990). The "TM II" regions of GluR2, GluR5, and GluR6 contain a site termed the glutamine(Q)/arginine(R) site, which influences the ion permeability of these subunits (Hume et al., 1991; Sommer et al., 1991). The genomic sequence of all three subunits contains a glutamine codon in the Q/R site. However, mRNA transcripts encoding an arginine codon in the Q/R site can be generated by RNA editing (Sommer et al., 1991). The most striking feature of the "TM II" region of χ -1 is the presence of an arginine residue. Analysis of the genomic sequence encoding the "TM II" region of χ -1 revealed that the arginine residue is encoded by the genomic sequence, and therefore is not a result of RNA editing. Accordingly, χ -1 is the first glutamate subunit to possess an unedited arginine residue in the "TM II" region.

Distribution of χ -1 mRNA during development

Parasagittal sections of rat embryos ages E15 and E19, and horizontal sections of brains from postnatal day 1 (P1), P7, P14, and adult rats were examined by in situ hybridization using antisense riboprobes specific for the coding sequence of the χ -1

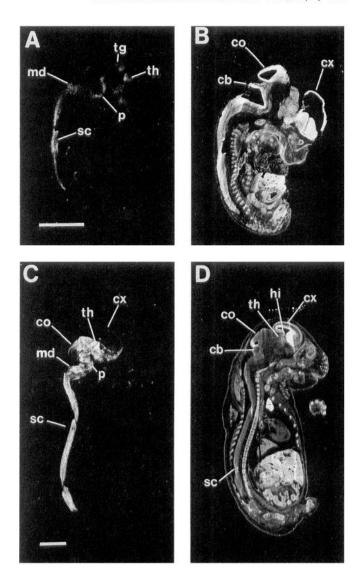


Figure 5. The distribution of χ -1 mRNA in E15 and E19 rat embryos. Sagittal sections of E15 (A) and E19 (C) embryos were hybridized to a 33P-labeled antisense RNA probe. Nissl (cresyl violet) stained sections of E15 (B) and E19 (D) embryos are shown for comparison. Abbreviations: cb, cerebellum; co, fetal colliculi; sc, spinal cord; cx, cortical neuroepithelium; hi, fetal hippocampus; md, medulla; p, pons; tg, tegmentum; th, thalamus. Scale bars, 3 mm.

transcript. x-1 transcripts were detected at E15, the earliest developmental stage examined (Fig. 5). In E15 embryos, χ-1 transcripts were detected in the spinal cord, medulla, pons, tegmentum, thalamus, and hypothalamus. x-1 transcripts were also detected in peripheral ganglia. Transcripts were not detected in the hippocampus, cortical neuroepithelium, or cerebellar neuroepithelium.

In E19 embryos, χ -1 signal intensity increased and displayed a similar but expanded spatial distribution compared to E15 embryos (Fig. 5). Transcripts were detected throughout the spinal cord, brainstem, hypothalamus, and thalamus. χ-1 transcripts were now also detected at lower levels in the hippocampus and the outer layer of the cortical neuroepithelium. Transcripts were not detected in the striatum or cerebellum.

χ-1 transcript levels remained elevated during the first postnatal week (Figs. 6, 7). In horizontal sections of P1 brains, χ-1 transcripts are abundant in several thalamic nuclei, the CA1 field

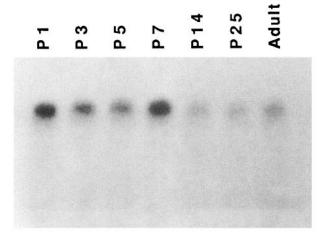


Figure 6. χ-1 mRNA expression during postnatal development. Fifteen micrograms of total RNA extracted from whole brain on postnatal day 1, 3, 5, 7, 14, 25, and adult brain were run on a formaldehydeagarose gel and transferred to nylon membranes. Following hybridization with a ³²P-labeled probe and exposing to film for 2 d with a screen, the signal was quantitated by densitometry.

of the hippocampus, the colliculi, entorhinal cortex, central gray, and inner and outer layers of the cortex. The spatial distribution of χ -1 remains similar from P1 to the adult brain. Sections from P7 brains revealed a similar, equally intense pattern of distribution compared to P1 brains.

Examination of emulsion-dipped slides from P7 brains revealed that the pyramidal cell layer of CA1, but not CA3, is strongly labeled (Fig. 8A). In the thalamus, labeling of large cells, presumably neurons, is heterogeneous with a subpopulation of cells being strongly labeled (Fig. 8B). Layers II–VI of the cortex also possess a subpopulation of cells which are strongly labeled (data not shown).

There is a sharp decline in χ -1 transcript levels by P14, and levels remain attenuated into adulthood (Figs. 6, 7). Quantitation of χ -1 transcript levels from the Northern blot analysis revealed that χ -1 transcripts are fourfold more abundant in P1 brain than in adult brain.

Distribution of χ -1 mRNA in the adult rat brain

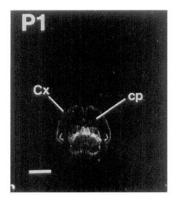
In general, regions expressing χ -1 subunit mRNA during development exhibit lower but detectable levels of χ -1 transcripts in

the adult rat brain. The highest density of χ -1 mRNA expression in the adult rat brain is in the thalamus and amygdala (Fig. 9). Within the thalamus, the central medial, intermediodorsal, and paraventricular thalamic nuclei possess the highest levels of x-1 mRNA. x-1 transcripts are also detected in several other thalamic nuclei including the reticular thalamus. Within the amygdala, the posteroventral medial amygdaloid nucleus and the posterolateral cortical amygdaloid nucleus show the highest transcript levels. In the adult, deep cortical layers exhibit higher transcript levels than superficial layers. The hypothalamus, central gray, colliculi, and pontine nuclei also express χ-1 transcripts. In contrast to the high signal intensity observed in the CA1 field of the hippocampus during the early postnatal period, the adult CA1 region possesses a very low level of χ -1 transcripts. Within the adult rat spinal cord, χ -1 transcripts were detected throughout the gray matter with a predominance in laminae 2 and 3 of the dorsal horn (Fig. 10).

Functional expression and ligand binding studies

Functional expression studies with x-1 mRNA injected into Xenopus oocytes did not demonstrate agonist-activated currents when 50-1000 μM glutamate, 300 μM kainate, or 200 μM NMDA was administered. In addition, no responses were obtained using 200 µm of the neurotransmitter candidate L-homocysteic acid. Many glutamate receptor subunits, including GluR5(R), GluR7, KA-1, KA-2, NMDAR2A-D, δ-1, and δ-2, fail to produce currents when expressed in a homomeric fashion. Therefore, we tested pairwise combinations of χ -1 and a member from every other class of glutamate receptor subunits. Pairwise expression of χ -1 with NMDAR2B, NMDAR2D, GluR1, GluR6, KA-1, and δ-1 either failed to generate agonist-activated currents or failed to increase the underlying current generated by the coexpressed subunit. However, χ-1 markedly diminished heteromeric NMDAR1/2B and NMDAR1/2D receptor channel currents (Table 2). To specifically examine the interaction of x-1 with NMDAR1, we coexpressed χ -1 with NMDAR1 alone. χ -1 significantly diminished NMDAR1 channel currents activated by NMDA (Table 2) or glutamate (data not shown). In contrast, χ -1 did not affect kainate or glutamate-gated currents through homomeric GluR1 or GluR6 channels (Table 2).

Since the edited forms of GluR2 and GluR5, which contain an arginine in the "TM II" region, display little or no current when expressed in a homomeric configuration (Hume et al., 1991; Sommer et al., 1992), we constructed a mutant of χ -1,



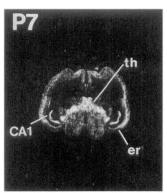






Figure 7. χ -1 expression in the brains of P1, P7, P14, and the adult rat as revealed by *in situ* hybridization. Horizontal sections were hybridized to a ³³P-labeled antisense RNA probe. Each section was exposed for 6 d. Abbreviations: *CA1*, CA1 field of the hippocampus; *cp*, caudate-putamen; *Cx*, cerebral cortex; *er*, entorhinal cortex; *th*, thalamus. Scale bar, 3 mm.

Figure 8. High resolution bright-field microscopy of emulsion-dipped sections from P7 brain stained with cresyl violet. A, Expression of χ -1 transcripts in the CA1 and CA3 hippocampal pyramidal cell layer. The *arrow* indicates the approximate boundary between the larger, more loosely packed CA3 pyramidal cell layer and the smaller, more densely packed CA1 cell layer. B, Expression of χ -1 in the thalamus illustrating the heterogeneity of cellular signal intensity. Arrows indicate examples of strongly labeled cells.

converting the arginine to a glutamine with the aim of enhancing the homomeric channel current. However, the mutated χ -1 did not form glutamate-activated homomeric channels.

The ligand binding of χ -1 was investigated using HEK-293 cells transiently transfected with a eukaryotic expression vector containing the coding sequence of χ -1. Binding of ³H-kainate or the NMDA receptor ligand 3H-CGP 39653 (Sills, 1991) to membranes from χ-1 expressing cells was not detected. Recently, binding of ³H-CGP 39653 has been demonstrated to heteromeric NMDAR1/NMDAR2A receptors, but not other homomeric or heteromeric NMDA receptors (Laurie and Seeburg, 1994). We further examined 3H-CGP 39653 binding in HEK-293 cells cotransfected with NMDAR1 and χ-1, but no binding was detected. Northern blot analysis revealed that levels of the χ -1 transcript in the transiently transfected HEK-293 cells were as high as or higher than levels of a GluR6 clone that were sufficient to demonstrate 3H-kainate binding (data not shown). To determine if the cloned cDNA could be properly translated, in vitro transcribed cRNA was translated in a reticulocyte lysate system. The χ-1 cRNA generated a protein of approximately 125 kDa, the predicted molecular weight of the mature protein (data not shown).

Discussion

We have identified a novel member of the ionotropic glutamate receptor family which we have designated χ -1. The χ -1 subunit possesses structural features common to members of the glutamate receptor family. The lack of high homology to previously identified subunits places χ -1 in a new class. Transcripts of the χ -1 subunit in the rat brain are detected at E15, the earliest stage examined. The spatial distribution of χ -1 subunit expression is similar from P1 to adulthood and includes the spinal cord, brainstem, thalamus, hypothalamus, amygdala, CA1 field of the hippocampus, and the cortex. During late embryonic development, χ -1 transcript levels increase and remain elevated until the second postnatal week, when levels sharply decline. The observed

decline in χ -1 transcript levels could be due to either a decrease in cellular expression levels of χ -1 or a decrease in the number of cells expressing the subunit. The majority of neurogenesis in the rat brain takes place from E13–E16 in the thalamus (Altman and Bayer, 1979), from E11–E16 in the spinal cord (Nornes and Das, 1974), and from E16–E19 in the hippocampus (Bayer, 1980). The high levels of the χ -1 transcript during and shortly after neurogenesis in these regions may indicate a role for the χ -1 subunit in early neuronal differentiation, migration, and synapse formation. χ -1 may play a lesser role in mature synapse formation since transcript levels decline before many mature synapses form. For instance, in the cortex, χ -1 transcript levels decrease sharply before a large increase in the synaptic density takes place from P14–P26 (Aghajanian and Bloom, 1967).

Functional expression studies in Xenopus oocytes demonstrated that the x-1 subunit specifically attenuates currents generated by homomeric and heteromeric NMDA receptors, but not non-NMDA receptors. The mechanism of the observed inhibition of NMDA currents by χ -1 is unknown. It is possible that χ -1 interferes with the translation or assembly of functional NMDA receptor subunits rather than by altering channel properties by coassembly with NMDA subunits. We were unable to directly detect by Western blot analysis NMDAR1 protein from oocytes injected with NMDAR1 RNA, presumably because of low NMDAR1 protein levels. However, immunoprecipitation of a larger quantity of oocyte protein with an NMDAR1 antibody (Pharmingen), allowed the detection of NMDAR1 protein. No difference in NMDAR1 protein levels was observed between oocytes injected with NMDAR1 or NMDAR1/χ-1 (data not shown). Therefore, a reduction in the translation of NMDAR1 protein does not appear to be mediated by χ -1 RNA coinjection.

If incorporated into the NMDA receptor complex, the apparent inhibitory effect of χ -1 on NMDA-mediated current may be due to a change in channel properties resulting in more rapid desensitization kinetics, lower open probability, or lower conductance of the channel. It is possible that a specific combination

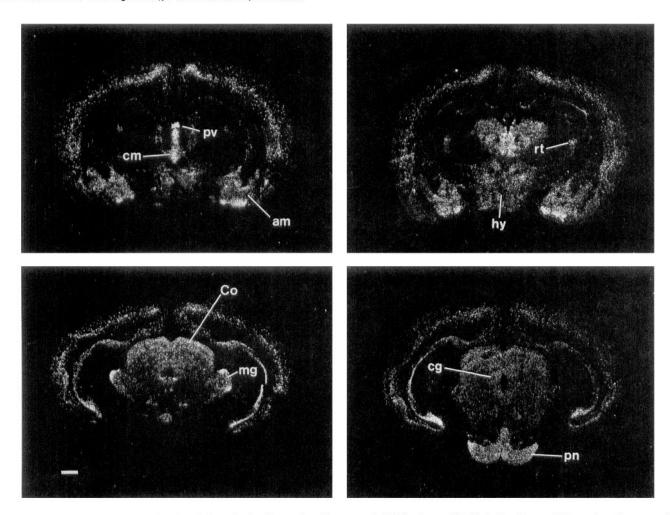
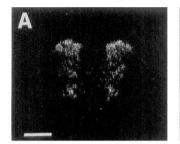


Figure 9. The expression of χ -1 in the adult rat brain. Coronal sections were hybridized to a ³³P-labeled antisense RNA probe. Exposure times were approximately four times as long as those in Figure 7. Abbreviations: am, amygdala; CA1, CA1 field of the hippocampus; cm, centromedial thalamic nucleus; hy, hypothalamus; Co, superior colliculus; mg, medial geniculate nucleus; pn, pontine nucleus; pv, paraventricular thalamic nucleus; rt, reticular thalamus. Scale bar, 1 mm.

of subunits, or a yet unidentified subunit, may be necessary for reproducing other properties that the χ -1 subunit may possess. Furthermore, the observed channel properties of χ -1 could be dependent on the expression system. For instance, the particular phosphorylation state of χ -1 in the *Xenopus* oocyte system may cause x-1 to diminish currents through NMDA receptors. Investigation of the properties of χ -1 homomeric and heteromeric channels in other expression systems may reveal other functional properties.



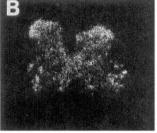


Figure 10. The expression of χ -1 in the adult rat spinal cord. Transverse sections were hybridized to a 33P-labeled antisense RNA probe. Cervical (A) and lumbar (B) levels are shown. Scale bar, 1 mm.

An unusual feature of the χ -1 subunit is that it is the first glutamate receptor to possess a genomically encoded arginine residue in the "TM II" region. Based on studies of the other members of the glutamate receptor family, we would expect heteromeric receptors containing χ -1 to possess a low permeability to calcium. AMPA channels formed with the edited GluR2(R) subunit have a low calcium permeability (Hume et al., 1991; Verdoorn et al., 1991). Similarly, an NMDAR1 subunit mutant,

Table 2. Inhibition of NMDA currents by χ -1 in Xenopus oocytes

Receptor injected	Mean current (nA ± SD)	Mean current with χ -1 co-injected ^a (nA \pm SD)
NMDAR1 ^b	$71 \pm 14, n = 6$	$12 \pm 6, n = 6$
NMDAR1 ^c /NMDAR2B	$367 \pm 46, n = 8$	$77 \pm 20, n = 7$
NMDAR1º/NMDAR2D	$53 \pm 40, n = 12$	0.2 ± 0.4 , $n = 6$
GluR1	$197 \pm 37, n = 6$	$203 \pm 25, n = 6$
GluR6	$213 \pm 114, n = 5$	$323 \pm 85, n = 6$

^a 2 ng of χ-1 cRNA injected.

^b 0.5 ng of NMDAR1 cRNA injected.

^{0.05-0.25} ng of NMDAR1 cRNA injected.

containing an arginine instead of an asparagine in the Q/R site of "TM II," displays a markedly reduced calcium permeability (Sakurada et al., 1993). In addition, GluR6(R) channels exhibit a decreased calcium permeability compared to GluR6(Q) channels expressed in *Xenopus* oocytes (Egebjerg and Heinemann, 1993).

Recently, NMDA receptors have been classified into four pharmacological classes whose distributions correlate with the distributions of the four NMDAR2 subunits (Buller et al., 1994). Although binding of χ -1 to 3 H-CGP 39653 was not detected, 3 H-CGP 39653 binding has only been demonstrated for heteromeric NMDAR1/2A receptors (Laurie and Seeburg, 1994). Therefore, it is possible that NMDA receptor ligands specific for other NMDA pharmacological classes may prove useful in defining the binding characteristics of χ -1.

We have presented the sequence and characterized the structural features and mRNA distribution of a novel member of the glutamate receptor family which may interact with NMDA receptor subunits. The temporal expression of this subunit indicates that it may play a role in early neuronal differentiation, migration, and synapse formation. Additional biochemical and electrophysiological studies will be needed to elucidate further the role of this subunit in glutamate neurotransmission.

Note added in proof

During the course of this work we learned that a clone identical to χ -1 had been obtained independently and named NMDAR-L by Sucher et al. (1995). The two groups generated data largely in accord, communicated their results freely with one another, and now publish the work as contiguous articles.

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