10F12; T. A. Springer for RR1/1 and TS2/9; M. Hemler for TS2/7 (anti-VLA α_1); V. Woods for 12F1 (anti-VLA α_2); L. Old for J143 (anti-VLA α_3); C. Damsky for BIE5 (anti-VLA α_5); A. Sonnenberg for GOH3 (anti-VLA α_6); G. S. Kansas for 515 (anti-CD44); and A. W. Boyd for W-CAM-1. BRIC 5 was provided from the 4th International Workshop on Leukocyte Differentiation Antigens. We appreciate the assistance of K. Hildebrandt for preparation of the manuscript. Supported by NIH grants CA40216, AR33713, 5T32HL07627-03, PO1 HL36028, and HL07727; PHS grant CA-01105 (to A.S.F.); American Cancer Society grant IM-549 and Texas Advanced Research Program grant 15-071 (to B.W.M.); and the American Heart Association (to J.S.P.).

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Molecular Cloning and Functional Expression of Glutamate Receptor Subunit Genes

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Three closely related genes, GluR1, GluR2, and GluR3, encode receptor subunits for the excitatory neurotransmitter glutamate. The proteins encoded by the individual genes form homomeric ion channels in *Xenopus* oocytes that are sensitive to glutamatergic agonists such as kainate and quisqualate but not to *N*-methyl-D-aspartate, indicating that binding sites for kainate and quisqualate exist on single receptor polypeptides. In addition, kainate-evoked conductances are potentiated in oocytes expressing two or more of the cloned receptor subunits. Electrophysiological responses obtained with certain subunit combinations show agonist profiles and current-voltage relations that are similar to those obtained in vivo. Finally, in situ hybridization histochemistry reveals that these genes are transcribed in shared neuroanatomical loci. Thus, as with γ-aminobutyric acid, glycine, and nicotinic acetylcholine receptors, native kainate-quisqualate–sensitive glutamate receptors form a family of heteromeric proteins.

THE AMINO ACID L-GLUTAMATE ACTS as an excitatory neurotransmitter at many synapses in the mammalian central nervous system. Glutamate is involved in fast excitatory synaptic transmission (*1*), the regulation of neurotransmitter release (*2*), long-term potentiation, learning and memory (*3*), developmental synaptic plasticity (*4*), hypoxic-ischemic damage and neuronal cell death (*5*), epileptiform seizures (*6*), as well as the pathogenesis of several neurodegenerative disorders (*7*). This functional diversity is reflected by complex electrophysiology and pharmacology in which glutamate acts via disparate receptors and conductance mechanisms (*8*). Glutamate receptor classification schemes are based on pharmacological criteria that define five receptor subtypes or classes: receptors gating cation-selective ion channels that are activated by *N*-methyl-D-aspartic acid (NMDA), kainic acid (KA), α-amino-3-hydroxy-5-methyl-isoxazole-4-propionic acid (AMPA) (formerly called the quisqualic acid or QUIS receptor), or 2-amino-4-phosphonobutyric acid (AP4), and the metabotropic receptor activated by 1-amino-cyclopentyl-1,3-dicarboxylic acid (ACPD).

The relation between the KA and AMPA receptor subtypes and the channels they gate is uncertain. It is not known if KA and AMPA activate the same receptor-channel complex with different efficacies or if distinct receptor-channel complexes exist for these agonists (*9*). Since no specific antagonists are available that distinguish KA- from AMPA-evoked responses, the existence of two non-NMDA receptor subtypes has been inferred from the differential potency of specific agonists. Results from [^{3}H]KA and [^{3}H]AMPA binding studies have been cited as evidence both for (*10*) and against (*11*) the hypothesis of distinct KA and AMPA receptor subtypes. However, definitive conclusions are difficult to make because of the uncertain relation between binding sites and the effector sites for depolarization.

To investigate the relation between structure and function of the various glutamate receptor subtypes we have applied molecular biological techniques. As a first step, we used an expression cloning approach to isolate a cDNA clone, GluR1 (*12*), which encodes a 99,800-dalton protein capable of forming a homomeric, KA-gated ion channel in *Xenopus* oocytes (*13*). Our initial results suggested that the KA responses measured in oocytes injected with in vitro synthesized GluR1 RNA or rat brain polyadenylated [poly(A$^+$)] RNA were indistinguishable. We have now tested whether the GluR1 gene is a member of a larger, glutamate receptor subunit gene family and whether the proteins encoded by these related genes function as subunits of glutamate receptors other than the KA subtype.

Complementary DNA clones encoding the GluR2 (λRB14) and GluR3 (λRB312) genes were isolated from an adult rat forebrain library by using a low-stringency hybridization screening protocol and a radiolabeled fragment of the GluR1 cDNA as a probe (*14*) (Fig. 1). The calculated molecular weights of the mature, nonglycosylated forms of GluR2 and GluR3 are 96,400 (862 amino acids) and 98,000 (866 amino acids), respectively. Potential N-linked glycosylation sites occur in the GluR2 protein at Asn^{235}, Asn^{349}, Asn^{385}, Asn^{392}, and Asn^{835} and in the GluR3 protein at Asn^{35}, Asn^{238}, Asn^{352}, Asn^{387}, and Asn^{394}. As for GluR1 (*12*), the hydrophobicity profiles for GluR2 and GluR3 reveal five strongly hydrophobic regions: one such domain is located at the NH_2-terminus of each protein and has characteristics of a signal peptide (*15*), while four additional hydrophobic regions probably form membrane-spanning helices (*16*) (MSR I to IV) (Fig. 1 and below) and are located in the COOH-terminal half of each polypeptide.

Significant sequence identity exists between GluR1 and both GluR2 (70%) and GluR3 (69%) as well as between GluR2 and GluR3 (74%), particularly in the COOH-terminal half of each protein. This region includes the four postulated membrane-spanning regions where, acknowledging five conservative substitutions, there is complete sequence identity. An unexpected finding is the extensive sequence identity (allowing conservative substitutions, 98%) in the segment between MSR III and IV. In other ligand-gated ion channels this region, modeled to be part of a cytoplasmic loop, shows the highest intersubunit variation in both length and sequence.

To test whether the GluR2 and GluR3 proteins function as homomeric, KA-sensitive ion channels, we injected oocytes with RNA transcripts synthesized in vitro from individual cDNA clones (*17*). Both GluR2- and GluR3-injected oocytes depolarized in response to bath application of 100 μM KA (Fig. 2A). However, the amplitudes of the KA responses were not equivalent for the glutamate receptor subunits: with equal amounts of injected RNA (2 ng), responses in GluR3 RNA-injected oocytes were invariably larger than GluR1 responses. KA-

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evoked depolarizations in GluR2-injected oocytes were the smallest and could only be detected in oocytes injected with larger amounts of RNA (10 to 25 ng).

Oocytes injected with GluR1 or GluR3 also respond to QUIS (10 μM), AMPA (50 μM), and glutamate (100 μM) (Fig. 2B). No detectable responses were obtained with NMDA (30 μM plus 10 μM glycine) or AP4 (50 μM, not shown). Responses obtained from oocytes injected with GluR2 RNA were too small for reproducible quantitation and were, therefore, excluded from this analysis. For GluR1-injected oocytes the responses to AMPA and QUIS were 35 to 40% of the response to 100 μM KA (*18*), while for GluR3 they were about 10% of the KA response. Relative to KA, the response of GluR1 to domoic acid (10 μM) was about sixfold greater than that for GluR3. Thus, receptors assembled from GluR1 or GluR3 subunits are pharmacologically distinct. Furthermore, the observation that homomeric GluR1 and GluR3 receptors respond to both QUIS and AMPA provides evidence that KA, QUIS, and AMPA can bind to the same receptor polypeptide.

The pharmacological profile of oocytes injected with individual GluR1 or GluR3 subunit RNAs was significantly different than that seen in oocytes injected with rat brain hippocampal poly(A$^+$) RNA (*19*). It

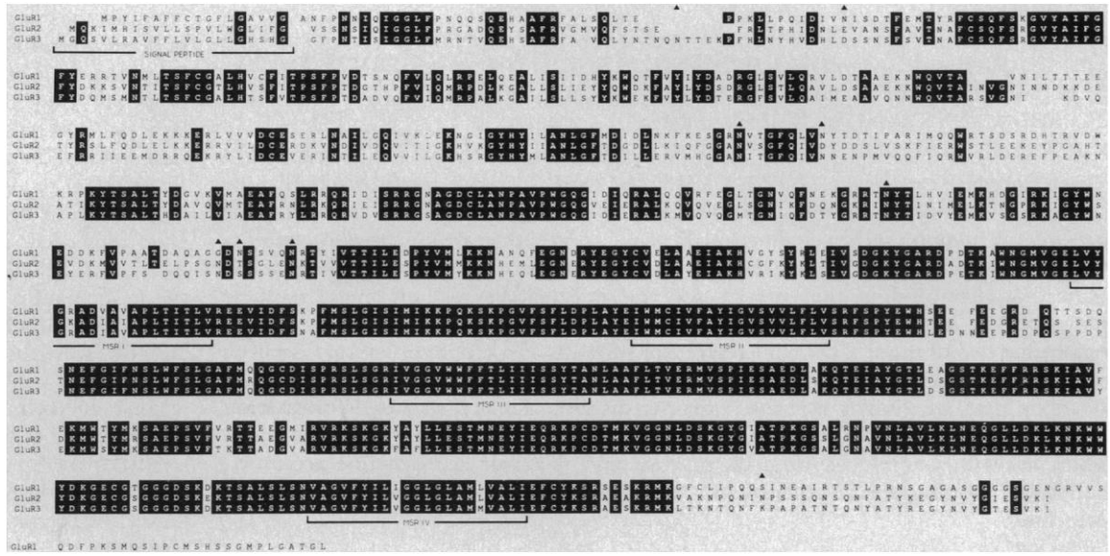

Fig. 1. Alignment of deduced amino acid sequences for the GluR1, GluR2, and GluR3 subunits of the glutamate receptor gene family. Aligned positions with identical amino acids in all compared sequences are boxed against a black background. Predicted signal peptides (*15*) and four potential membrane spanning regions (MSR, I to IV) (*16*) are indicated. ▲, potential N-linked glycosylation site in one or more of the subunits. Sequence analysis was performed with programs from the University of Wisconsin Genetics Computer Group (*29*).

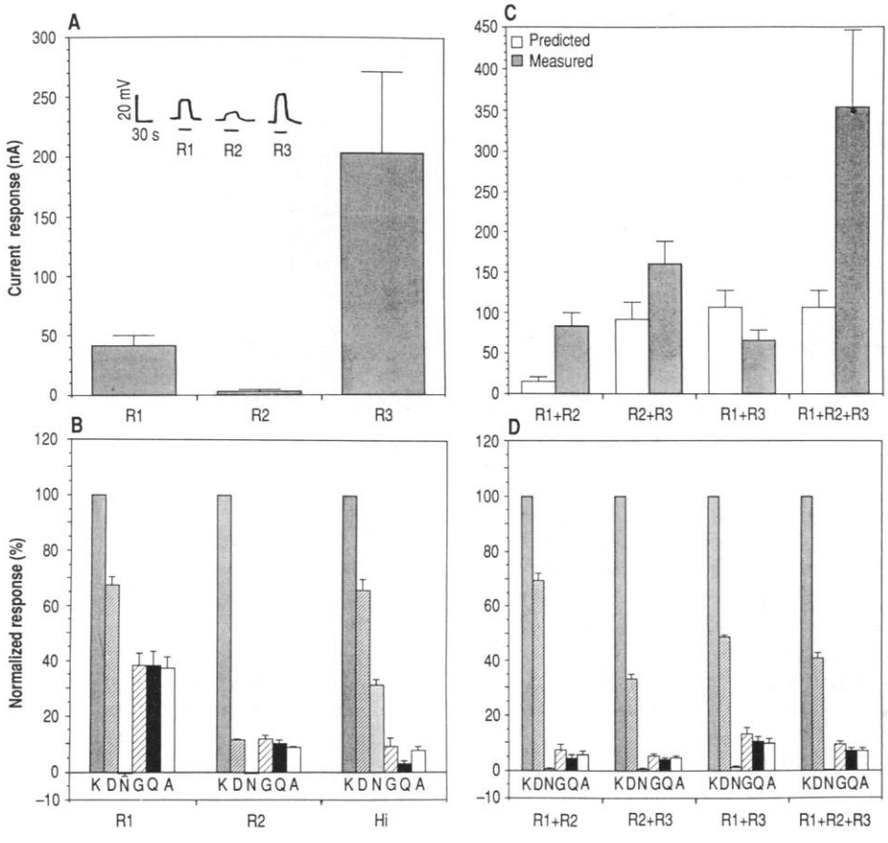

Fig. 2. Comparison of current responses measured in *Xenopus* oocytes injected with individual GluR1, GluR2, and GluR3 subunit RNAs, combinations of subunits, or rat brain hippocampal poly(A$^+$) RNA. (**A**) Responses of oocytes to 100 μM KA measured 3 days after injection of individual GluR1 (2 ng), GluR2 (10 ng), or GluR3 (2 ng) RNA. The inset shows examples of voltage recording traces obtained from such oocytes except that the GluR2 response was obtained 5 days after injection of 25 ng of RNA. (**B**) Responses of oocytes to the indicated agonists measured 3 days after injection with GluR1 (2 ng) or GluR3 (2 ng) RNA or adult rat brain hippocampal poly(A$^+$) RNA (~50 ng). K, kainate; D, domoic acid; N, NMDA; G, glutamate; Q, quisqualate; A, AMPA. (**C**) Responses of oocytes expressing combinations of GluR subunits to 100 μM KA measured 3 days after injection of 2 ng of RNA for each of the indicated GluR subunits. Open columns, the sum of the responses measured in oocytes expressing the individual GluR subunit RNAs (predicted); shaded columns, the measured amplitudes after co-expression of the GluR subunit RNAs in individual oocytes. (**D**) Responses of oocytes expressing combinations of GluR subunits to the indicated agonists measured 3 days after injection of 2 ng of RNA for each of the indicated GluR subunits or 50 ng of rat brain hippocampal poly(A$^+$) RNA. See (B) for agonist identification. All values have been normalized to the response obtained with 100 μM KA and are presented as the mean ± SEM with $n \geq 3$ for all measurements. All oocytes were voltage-clamped to −70 mV and recordings performed as described (*13*).

is possible that the responses seen in oocytes injected with hippocampal RNA are mediated by heteromeric glutamate receptors assembled from various combinations of GluR1, GluR2, and GluR3 subunit polypeptides, especially since all three GluR subunit genes are actively transcribed in the hippocampus (see below). We therefore determined whether the proteins encoded by GluR1, GluR2, and GluR3 could form functional heteromeric receptors.

We compared the KA-activated currents recorded from oocytes injected with mixtures of GluR1, GluR2, and GluR3 subunit RNAs with the summed currents for the individual subunits (Fig. 2C). Kainate-evoked currents were potentiated in oocytes co-expressing GluR1 plus GluR2 subunits (approximately fourfold over the summed responses) or GluR2 plus GluR3 subunits (approximately twofold). Injection of all three subunit RNAs resulted in an average 2.5-fold increase in KA-evoked currents. Thus, in oocytes individual GluR subunit polypeptides interact with each other. Such interaction may result in the generation of heteromeric glutamate receptors with properties distinct from receptors composed of one type of GluR subunits.

For the agonists we tested, there were few substantial differences in the pharmacology of the various receptors (Fig. 2, B and D). However, the responses to QUIS, AMPA, and GLU were, relative to GluR1, significantly reduced in the oocytes expressing the subunit combinations. Except for the NMDA response, the overall agonist profiles for oocytes injected with GluR subunit combinations were more similar to oocytes containing hippocampal poly(A^+) RNA than to those injected with either GluR1 or GluR3 subunit RNA alone.

We examined the current-voltage (*I/V*) relations for KA-evoked responses in oocytes injected with individual GluR subunit RNAs (Fig. 3A), oocytes expressing combinations of subunits (Fig. 3, B and C) and, for purposes of comparison, oocytes expressing hippocampal poly(A^+) RNA (Fig. 3A). As reported (*20*), the KA responses in oocytes injected with brain poly(A^+) RNA show an approximately linear *I/V* relation with a reversal potential of about −10 mV. This result is in contrast to the *I/V* curves for oocytes injected with single GluR1 or GluR3 subunit RNA. The GluR1 and GluR3 *I/V* curves show strong inward rectification and reversal potentials near −40 mV. Therefore, the KA-sensitive receptors in oocytes injected with hippocampal RNA are different from those assembled by oocytes injected with GluR1 or GluR3 subunit RNAs.

The *I/V* curve for the GluR1 plus GluR2 combination was different from that observed for the GluR1 subunit alone (Fig. 3B). Oocytes injected with this pair of RNAs showed a nearly linear *I/V* plot and had a reversal potential of approximately −10 mV. This plot was similar to that of oocytes injected with hippocampal RNA (Fig. 3A). In contrast, the *I/V* curve for the GluR1 plus GluR3 combination was only marginally different from those measured in oocytes expressing the individual subunits. There was some inward rectification in the *I/V* curve for GluR2 plus GluR3, as well as a reversal potential somewhat more negative (−20 mV) than those determined for GluR1 plus GluR2 or hippocampal RNA (−10 mV) (Fig. 3C). When all three subunit RNAs were combined in a single oocyte, the resulting *I/V* curve approximated that seen for the GluR1 plus GluR2 combination in both reversal potential and slope; however, the responses with three subunits showed a pronounced inward rectification not observed with GluR1 plus GluR2.

Our data are consistent with the idea that glutamate receptors can be assembled from either individual GluR1, GluR2, or GluR3 subunits (homomeric) or from combina-

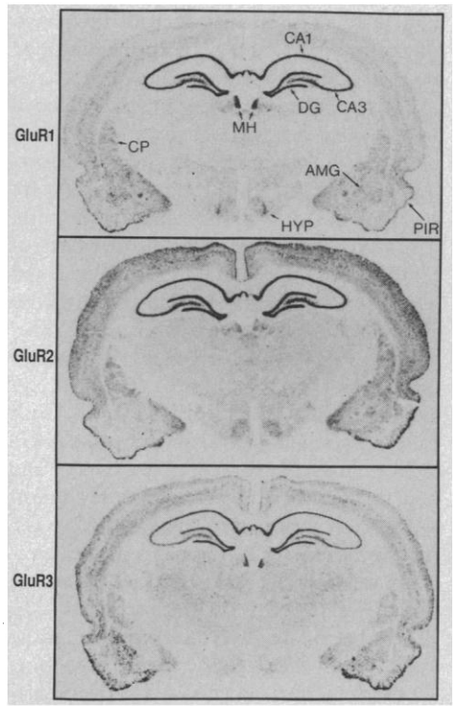

Fig. 4. The localization of GluR1, GluR2, and GluR3 RNA in the adult rat brain with in situ hybridization histochemistry. Coronal sections and [^{35}S]antisense RNA probes were prepared as described (*21*). AMG, amygdala; CA1 and CA3, regions within the hippocampus; CP, caudate-putamen; DG, dentate gyrus; HYP, hypothalamus; MH, medial habenula; PIR, piriform cortex.

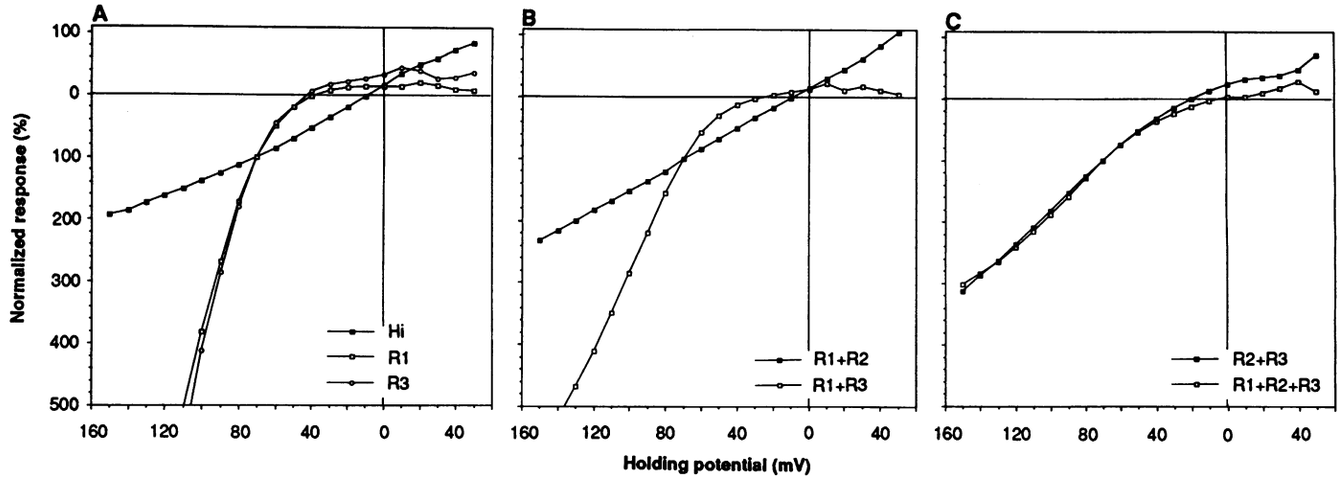

Fig. 3. Current responses to 100 μM KA as a function of membrane potential. (**A**) Data obtained from oocytes injected with rat brain hippocampal poly(A^+) RNA (50 ng) (Hi), GluR1 RNA, or GluR3 RNA, (**B**) GluR1 plus GluR2 RNAs or GluR1 plus GluR3 RNAs, and (**C**) GluR2 plus GluR3 RNAs or all three GluR subunit RNAs. Recordings were made from oocytes 3 days after injection of 2 ng of RNA for each GluR subunit. Voltages were stepped by 10 mV between −150 mV and +50 mV, and all values were normalized to the response measured at −70 mV.

tions of subunit polypeptides (heteromeric). Both types of receptors are sensitive to KA and, to a lesser extent, AMPA, QUIS, and GLU. Electropharmacological responses observed with certain GluR subunit combinations (those containing GluR2) are more like responses elicited from oocytes injected with hippocampal RNA than responses from oocytes injected with an individual subunit. Thus, some KA-AMPA–sensitive glutamate receptors may be made up in vivo of two or more of the polypeptides encoded by the GluR1, GluR2, or GluR3 genes.

The hypothesis that the subunits encoded by the three genes could form heteromeric receptors in vivo can be disproven by showing that the individual subunit genes are transcribed in different neuroanatomical loci. We examined the distribution of GluR1, GluR2, and GluR3 RNAs in the adult rat brain with radiolabeled antisense RNA probes and in situ hybridization histochemistry (*21*). The hybridization patterns obtained with the GluR1, GluR2, and GluR3 probes were nearly identical, with the strongest hybridization seen in the CA1-CA3 regions of the hippocampus and the dentate gyrus (Fig. 4). High-resolution analysis of these areas suggested that the hybridization signal originates in the pyramidal cell layer of regions CA1-CA3 and the granule cell layer of the dentate gyrus (*22*). Somewhat weaker hybridization of all three probes was seen in the piriform cortex, caudate-putamen, amygdala, and hypothalamus. Low levels of hybridization were detected in the thalamus, with little or no signal observed in fiber tracts. Although differential hybridization was seen in the medial habenula and neocortex, the overall patterns of expression for the GluR1, GluR2, and GluR3 subunit genes showed substantial concordance.

In conclusion, there exists a family of related but distinct genes encoding subunits of glutamate receptors. The full complement of genes is, at present, unknown; however, preliminary results suggest the existence of at least two additional, related genes (*23*). The GluR subunit polypeptides do not, either individually or in concert, form detectable NMDA or AP4-sensitive receptors in oocytes. Likewise, it is doubtful that the metabotropic ACPD subtype is assembled from these subunits since QUIS, an ACPD receptor agonist, does not evoke the slow-onset, oscillating waveforms typical of a metabotropic response (*24*). However, oocytes expressing individual GluR subunits or combinations of subunits respond to both KA and AMPA-QUIS. That KA and AMPA-QUIS can bind to and activate the same receptor polypeptide supports the existence of unitary KA-AMPA receptors in the vertebrate central nervous system (*11, 25*). For all combinations of glutamate receptors, the strongest responses were elicited by KA and domoate. Although the basis for this preference is unknown, the observed responses may have been obtained from glutamate receptors that were in desensitized configurations. Finally, our data do not rule out the existence of receptor-ionophore complexes in vivo that are uniquely activated by KA or AMPA or that prefer AMPA.

Since the *I-V* relations of KA-superfused oocytes vary with the GluR subunit or combination of subunit RNAs injected, a variety of structurally and functionally distinct KA-AMPA receptor-channel complexes may exist in vivo. Indeed, whole-cell voltage-clamp recording data from cultured rat hippocampal neurons reveal the presence of two KA responses, which differ in their rectification properties and their permeability to Ca^{2+} (*26*). *I/V* plots from these neurons had reversal potentials near 0 mV; however, in about 70% of the cells the KA responses showed slight outward rectification (type I response), while the remaining 30% were characterized by a marked inward rectification (type II response). Because of differences in the recording conditions, direct comparisons of the type I and type II KA responses with those described here for the GluR subunits is not possible; however, it seems likely that the type I and II responses are mediated by structurally distinct KA receptors since the rectification properties of KA-sensitive ion channels can be influenced by subunit composition (Fig. 4).

Although our results begin to define the molecular basis for glutamate receptor function and diversity, a complete molecular and physiological description of glutamate receptor subtypes will require knowledge of the entire repertoire of receptor subunit genes, the subunit composition and stoichiometry of each receptor subtype, as well as an identification of the cell types that elaborate these combinations of subunits (*27*).

Note added in proof: After we submitted this manuscript, Keinänen *et al.* (*28*) described the isolation and characterization of four rat brain cDNA clones that encode a family of AMPA-selective glutamate receptor subunits. The first of these cDNA clones, designated GluR-A, is identical to GluR1 [previously named GluR-K1 (*12*)] except for amino acid residues 680 (Leu for Arg), 692 (Thr for Ser) and 875 (Ser for Cys). Clones GluR-B and GluR2 are identical, while a third clone, GluR-C, has the same sequence as GluR3 except for amino acid positions 495 (Lys for Asn) and 496 (Pro for Ala).

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13. A generic nomenclature has been adopted for the cloned glutamate receptor subunit genes that reflects their sequence relatedness and their ability to function as glutamate receptor subunits. This seemed prudent given the uncertainty regarding the relations between the proteins encoded by these genes and the pharmacologically defined glutamate receptors in vivo. We have renamed the first glutamate receptor subunit gene isolated, previously called GluR-K1 (*12*), glutamate receptor subunit gene 1 or, more simply, GluR1. Additional glutamate receptor subunit or subunit-related genes have been called GluR2, GluR3, and so forth.
14. The construction of an adult rat forebrain cDNA library in λZAPII has been described (*12*). The library was screened under low-stringency hybridization conditions [J. Boulter and P. D. Gardner, *Methods Neurosci.* **1**, 328 (1990)] with a 1411-bp Bam H1–Xho I restriction endonuclease fragment of GluR1 clone p59/2 (nt 1599–3010) as radiolabeled probe. Of 1×10^6 clones screened, ~600 were positive at low-stringency and ~320 remained positive after high-stringency washes. Clones selected for further study were plaque-purified, rescued as plasmids, and analyzed by restriction endonuclease digestion. Clone λRB14 (GluR2) was isolated by a combination of low-stringency hybridization and expression cloning methods. Both strands of clones λRB14 and λRB312 (GluR3) were sequenced by the dideoxynucleotide chain termination method [F. Sanger, S. Nicklen, A. R. Coulson, *Proc. Natl. Acad. Sci. U.S.A.* **74**, 5463 (1977)].
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19. The hippocampal poly(A$^+$) RNA (Figs. 2 and 3) was extracted from adult rat brain hippocampus and is, therefore, derived from a complex mixture of neuronal and non-neuronal cell types, each of which may express some GluR subunit RNAs and not others. The hippocampal RNA may also contain, in addition to GluR1, GluR2, and GluR3 RNAs, transcripts encoding as yet uncharacterized GluR subunits or proteins that can modulate glutamate receptor responses. Therefore, the data obtained with hippocampal RNA must be considered as a composite response of all expressed, functional glutamate receptors. Furthermore, the bringing together of inappropriate types, numbers, or combinations of GluR subunits in a single oocyte may result in receptors having an uncertain physiological relevance. The precise relationship, then, between bona fide glutamate receptors in neurons and the responses in oocytes injected with hippocampal poly(A$^+$) RNA remains to be established.
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21. In situ hybridization histochemistry was performed as described [E. S. Deneris, J. Boulter, L. W. Swanson, J. Patrick, S. Heinemann, *J. Biol. Chem.* **264**, 6268 (1989)] with [^{35}S]antisense RNA probes and 30-μm-thick paraformaldehyde-fixed coronal sections of adult rat brains. Antisense RNA was prepared from full-length plasmid clones p59/2 (GluR1), pRB14 (GluR2), and pRB312 (GluR3). Sections were exposed to DuPont Cronex film for 10 days. To assess specificity, a second set of hybridizations was performed with short (600 to 900 nt) antisense probes from untranslated regions or from areas of minimal nucleotide sequence homology. The hybridization patterns were identical for both sets of probes.
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Stereoscopic Depth Discrimination in the Visual Cortex: Neurons Ideally Suited as Disparity Detectors

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The possibility has been explored that a subset of physiologically identifiable cells in the visual cortex is especially suited for the processing of stereoscopic depth information. First, characteristics of a disparity detector that would be useful for such processing were outlined. Then, a method was devised by which detailed binocular response data were obtained from cortical cells. In addition, a model of the disparity detector was developed that includes a plausible hierarchical arrangement of cortical cells. Data from the cells compare well with the requirements for the archetypal disparity detector and are in excellent agreement with the predictions of the model. These results demonstrate that a specific type of cortical neuron exhibits the desired characteristics of a disparity detector.

THE NEURAL PROCESS OF STEREOscopic depth discrimination is thought to be initiated in the visual cortex. However, the mechanisms of this neural process are not clear (*1*). One fundamental question concerns the roles of specific cell types in the processing of information concerning stereoscopic depth. The two major subdivisions of cortical cells, as determined physiologically, are "simple" and "complex." Simple cells have receptive fields (RFs) that consist of spatially separate subregions that respond to either onset or offset of a flashed stationary bar of light (ON or OFF responses). Alternatively, a bar stimulus that is brighter or darker than the background may be used to classify a simple cell (Fig. 1A) (*2*). Complex cells, on the other hand, respond to a stimulus anywhere within the RF for both bright and dark bars (Fig. 1B). Complex cells, therefore, are insensitive to contrast polarity, that is, whether the stimulus is darker or brighter than the background, and are only broadly selective to stimulus position. Upon cursory analysis, these monocular characteristics of complex cells appear inappropriate for fine stereoscopic depth discrimination because precise position and contrast information are not available. However, the study of binocular properties of these cells, reported here, demonstrates that a proportion of complex cells is especially suited as fine binocular disparity sensors (*3*). A model of this sensor provides quantitative predictions that may be compared with responses of cells.

What additional binocular properties of complex cells are required in order to create a suitable disparity detector? First, the disparity selectivity of complex cells must be much finer than that predicted by the size of the RFs (*4*). Second, the preferred disparity must be constant for all stimulus positions within the RF. Third, incorrect contrast polarity combinations should be ineffective if presented at the optimal disparity for the matched polarity pair, that is, a combination of a bright bar to one eye and a dark bar to the other should not elicit a response at the preferred disparity of the detector.

The first two requirements are illustrated in Fig. 2. In Fig. 2A, a cross-sectional view is shown of the plane containing the two eyes and the RFs. The RF of a cortical neuron is depicted in image space on left eye and right eye retinas. When extended into object space, the intersections between left and right RF projections define the region that is "viewed" by the cell through both eyes (hatched, diamond-shaped zone). Planes of constant disparities are indicated by horizontal lines for uncrossed (positive) and crossed (negative) disparities. If a neuron simply detects the simultaneous presence of a stimulus within both left eye and right eye RFs, any stimulus that falls within the diamond-shaped zone will excite the cell. Because this region spans a wide range of binocular disparities, the neuron is limited to crude disparity sensitivity. A disparity detector must respond to a much more restricted range of visual space. In this case, the dark shaded oval region around zero disparity represents a suitable zone.

A graphical depiction of this region is shown in Fig. 2B. Stimulus positions along the left eye and right eye RFs are represented on the x_L and x_R axes, respectively. The diagonal slope represents a plane of constant (zero) disparity. As in Fig. 2A, a region of visual space is defined (hatched square) within which left eye and right eye RFs are jointly stimulated. The dark shaded area corresponding to the oval in the upper part of the figure is shown along the diagonal, which represents zero disparity. Again, this latter zone represents the narrow response range of our disparity detector tuned to a

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