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Deficient RNA editing of GluR2 and neuronal death in amyotrophic lateral sclerosis

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Abstract One plausible hypothesis for selective neuronal death in sporadic amyotrophic lateral sclerosis (ALS) is excitotoxicity mediated by α -amino-3-hydroxy-5-methyl-4-isoxazolepropionate (AMPA) receptors, which are a subtype of ionotropic glutamate receptors. The Ca^{2+} con-

ductance of AMPA receptors differs markedly depending on whether the GluR2 (or GluR-B) subunit is a component of the receptor. The properties of GluR2 are generated posttranscriptionally by RNA editing at the Q/R site in the putative second membrane domain (M2), during which the glutamine (Q) codon is substituted by an arginine (R) codon. AMPA receptors containing the unedited form of GluR2Q have high Ca^{2+} permeability in contrast to the low Ca^{2+} conductance of those containing the edited form of GluR2R. The role of Ca^{2+} -permeable AMPA receptors, particularly GluR2 Q/R site RNA editing status, in neuronal death has been clearly demonstrated both in mice deficient in editing at the GluR2 Q/R site and in mice transgenic for an artificial Ca^{2+} -permeable GluR2 subunit. We analyzed the expression level of mRNA of each AMPA receptor subunit in individual motor neurons, as well as the editing efficiency of GluR2 mRNA at the Q/R site in the single neuron level in control subjects and ALS cases. There was no significant difference as to the expression profile of AMPA receptor subunits or the proportion of GluR2 mRNA to total GluRs mRNA between normal subjects and ALS cases. By contrast, the editing efficiency varied greatly, from 0% to 100%, among the motor neurons of each individual with ALS, and was not complete in 44 of them (56%), whereas it remained 100% in normal controls. In addition, GluR2 editing efficiency was more than 99% in the cerebellar Purkinje cells of ALS, spinocerebellar degeneration and normal control groups. Thus, GluR2 underediting occurs in a disease specific and region selective manner. GluR2 modification by RNA editing is a biologically crucial event for neuronal survival, and its deficiency is a direct cause of neuronal death. Therefore, marked reduction of RNA editing in ALS motor neurons may be a direct cause of the selective motor neuron death seen in ALS. It is likely that the molecular mechanism underlying the deficiency in RNA editing is a reduction in the activity of ADAR2, a double-strand RNA specific deaminase. The restoration of this enzyme activity in ALS motor neurons may open the novel strategy for specific ALS therapy.



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Abbreviations *ADAR*: Adenosine deaminases acting on RNA · *ALS*: Amyotrophic lateral sclerosis · *AMPA*: α -Amino-3-hydroxy-5-methyl-4-isoxazolepropionate · *PCR*: Polymerase chain reaction

ALS: history

The most common motor neuron disease, amyotrophic lateral sclerosis (ALS), is characterized by a selective loss of upper and lower motor neurons that initiates in mid-life by a progressive paralysis with muscle wasting. ALS has a uniform worldwide prevalence (0.8–7.3 cases per 100,000 individuals), with risk of disease increasing in an age-dependent manner after the sixth decade of life, and only approximately 5–10% of all ALS cases are familial. Although three causal genes have been so far identified in individuals affected with familial ALS (*SOD1*, *ALS2*, *senataxin*) [1–4], the mechanism underlying motor neuron death or familial ALS pathology has not been elucidated. With regard to the non-hereditary form of ALS (sporadic ALS), which accounts for most cases of ALS, virtually no clues to the causal mechanism have been gleaned since the establishment of the disease entity by Jean-M. Charcot in 1874.

ALS etiology: the AMPA receptor-mediated neuronal death hypothesis

Several hypotheses have been proposed to explain the etiology of sporadic ALS, including genetic and/or non-genetic abnormalities of cytoskeletal and axonal transporting proteins [5, 6], vascular endothelial growth factor (VEGF) [7, 8], and viruses [9, 10], among others. Of these, one plausible hypothesis for selective neuronal death in sporadic ALS is excitotoxicity mediated by α -amino-3-hydroxy-5-methyl-4-isoxazolepropionate (AMPA) receptors, which are a subtype of ionotropic glutamate receptors. Because the pyramidal tract that projects to the motor neurons in the spinal cord uses glutamate as the excitatory neurotransmitter, motor neurons express abundant glutamate receptors and hence are vulnerable to exaggerated receptor activation by glutamate. The first act of the excitotoxicity story opened by selective loss of glutamate uptake due to loss of a glutamate transporter in the ALS motor cortex [11, 12], which was later proved to be not disease selective [13]. Including the neuronal death induced by glutamate transporter blockade, it has been repeatedly shown that motor neurons are differentially more vulnerable to AMPA receptor-mediated slow neuronal death than are other neuronal subsets in rat and mouse spinal cord cultures [14–16] and in the adult rat spinal cord [17, 18]. An increased influx of Ca^{2+} through activated

AMPA receptor-coupled channels appears to play a key role in this type of neuronal death [19, 20].

Functional AMPA receptors are homo- or heterooligomeric assemblies that are composed of four subunits, GluR1, GluR2, GluR3, and GluR4, in various combinations. The Ca^{2+} conductance of AMPA receptors differs markedly depending on whether the GluR2 subunit is a component of the receptor. AMPA receptors that contain at least one GluR2 subunit have low Ca^{2+} conductance, whereas those lacking a GluR2 subunit are Ca^{2+} permeable (Fig. 1A) [21–24]. These properties of GluR2 are generated posttranscriptionally by RNA editing at the Q/R site in the putative second membrane domain (M2; Fig. 1B), during which the glutamine (Q) codon is substituted by an arginine (R) codon [22, 23, 25]. Analyses of adult rat, mouse, and human brain RNA have demonstrated that almost all GluR2 mRNA *in vivo* is edited

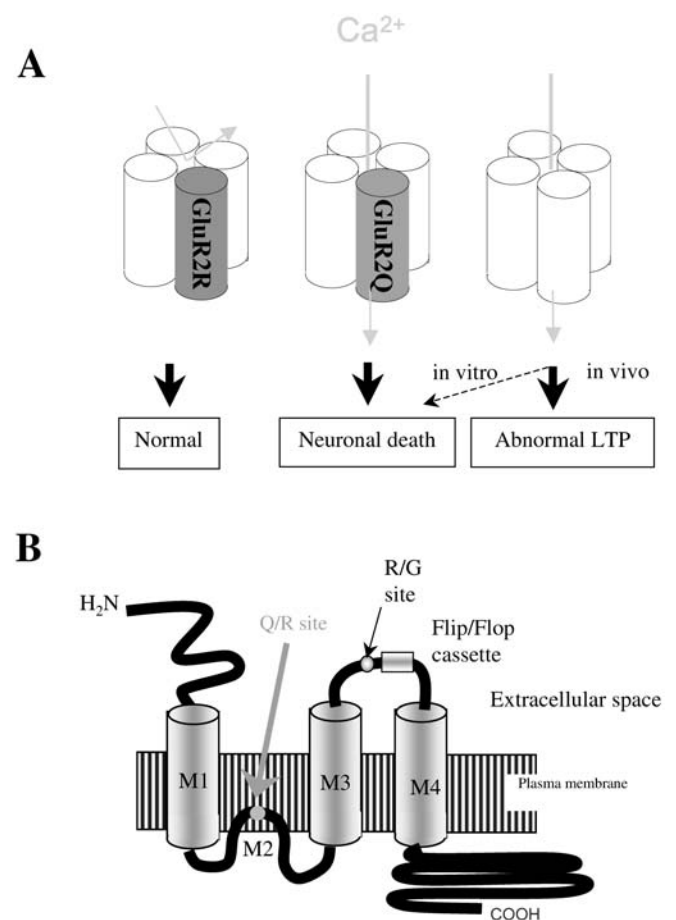


Fig. 1 Ca^{2+} permeability of AMPA receptors and the GluR2 subunit. **A** Functional AMPA receptors are homo- or heterooligomeric assemblies that comprise the four subunits GluR1, GluR2, GluR3, and GluR4 in various combinations. The Ca^{2+} conductance of AMPA receptors differs markedly depending on whether they contain the GluR2 subunit. AMPA receptors that contain at least one edited GluR2 subunit have low Ca^{2+} conductance (*left*), whereas those lacking a GluR2 subunit (*right*) and those containing unedited GluR2Q (*middle*) have high Ca^{2+} conductance. Neuronal death is induced when RNA editing at the GluR2 Q/R site is deficient. **B** Structure of GluR2: the Q/R site is located in the putative second membrane domain (M2)

(i.e., R is found at the Q/R site), whereas Q remains at this critical position in the GluR1, GluR3, and GluR4 subunits. AMPA receptors containing the unedited form of GluR2Q have high Ca^{2+} permeability in contrast to the low Ca^{2+} conductance of those containing the edited form of GluR2R (Fig. 1A) [26, 27].

The role of Ca^{2+} -permeable AMPA receptors in neuronal cell death has been demonstrated in animal models. Although low expression of GluR2 was found to influence AMPA receptor-mediated neuronal death in cultured hippocampal neurons from GluR2-null mice [28], low GluR2 expressed caused abnormal long-term potentiation (LTP) but not neuronal death *in vivo* [29]. By contrast, the effects of the GluR2 Q/R site RNA editing status on neuronal death have been clearly demonstrated both in mice deficient in editing at the GluR2 Q/R site [30] and in mice transgenic for an artificial Ca^{2+} -permeable GluR2 subunit [31]. Total Ca^{2+} influx depends on relative Ca^{2+} permeability, and on the number of open channels, as determined by the other factors including the proportion of flip/flop splice variants in AMPA receptor subunits and on the cellular density of AMPA receptors, although these factors rarely induce neuronal death.

Accordingly, two mechanisms have been proposed for the AMPA receptor-mediated neuronal death observed in ALS spinal motor neurons. The first is a selective reduction in GluR2 expression, which results in a decrease in the proportion of GluR2-containing, and therefore Ca^{2+} -impermeable, AMPA receptors owing to a low relative abundance of GluR2 among the four subunits. The second is a reduction in GluR2 RNA editing, which results in the number of GluR2Q-containing, Ca^{2+} -impermeable AMPA receptors increasing to a non-negligible amount.

AMPA receptor subunits in normal human CNS neurons

To our surprise, only inconsistent evidence had been available concerning the expression profile of AMPA receptor subunits in human brain. Therefore, we first quantified the expression level of each subunit in various neural subsets including spinal motor neurons. Notwithstanding studies reporting the expression of GluR2 [32, 33], some studies based on *in situ* hybridization or immunocytochemistry had claimed that GluR2 is not expressed in the spinal motor neurons of control human subjects [34, 35], and there was no evidence concerning whether or not

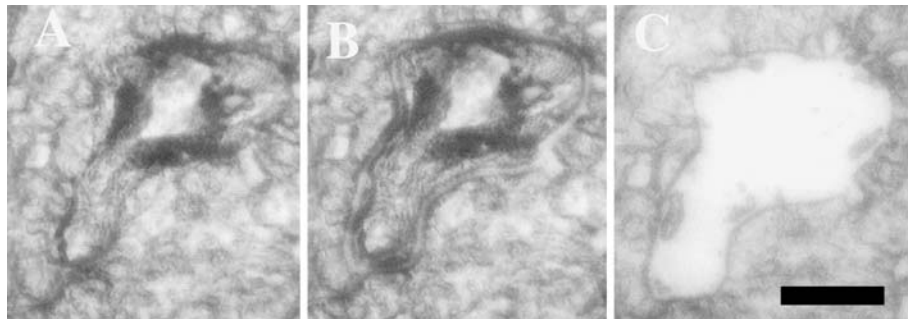
GluR2 is present in ALS motor neurons. By means of a laser microdissector (Fig. 2) and real-time quantitative RT-PCR, we measured the relative abundance of GluR2 mRNA *in situ* in human spinal motor neurons and other neuronal tissues from control subjects. We found a stronger relative abundance of GluR2 mRNA, representing 77.8–95.5% of the total AMPA receptor subunits, as compared to other AMPA receptor subunit mRNAs throughout the neuronal subsets examined [36]. However, the motor neurons of control subjects expressed significantly lower levels of GluR2 ($77.8 \pm 2.0\%$), as compared to other neuronal subsets ($89.8 \pm 1.2\%$ in Purkinje cells, $95.5 \pm 0.5\%$ in cerebellar granule cells; Fig. 3) [36].

In rat spinal cords, the mRNA of all four AMPA receptor subunits has been detected in spinal motor neurons by *in situ* hybridization [37–40], and quantification of the relative abundance of GluR2 mRNA by single-cell RT-PCR has demonstrated a weaker predominance of GluR2 (from 2.1 to 63%) in cultured spinal motor neurons than what we found in human motor neurons [16, 41, 42]. The AMPA receptor subunit composition did not differ between motor neurons and dorsal horn neurons in immature rat dissociated spinal cord cultures [16], but significantly lower expression of GluR2 mRNA has been demonstrated in adult rat motor neurons than in dorsal horn neurons that are dissected with a laser microdissector (unpublished observation), which probably reflects age-dependent alterations of the AMPA receptor expression profile.

With regard to the other AMPA receptor subunits, the expression profiles differed among neuronal subsets, but were consistent between the same neuronal subsets analyzed from human and rat brains [36]. Low expression of GluR1 mRNA has been repeatedly shown in human and rat spinal motor neurons [36–38]. Rapid progress in the field of AMPA receptor trafficking has demonstrated the elaborate machinery that controls the activity-dependent trafficking of GluR1/GluR2 subunits differentially from the constitutive replacement of GluR2/GluR3 subunits [43, 44]. Thus, the different expression profiles of AMPA receptor subunits among neuronal subsets may reflect a subset-specific balance between activity-dependent and constitutive AMPA receptor regulatory mechanisms, rather than a species-specific difference.

Although the proportion of GluR2 varies relative to the other subunits, it is likely that GluR2 mRNA accounts for the major proportion of AMPA receptor subunits in neu-

Fig. 2 Dissection of single motor neurons with a laser microdissector. **A** Before dissection; **B** demargination with a narrow laser beam; **C** after capturing the neuronal tissue. *Bar* = 40 μm



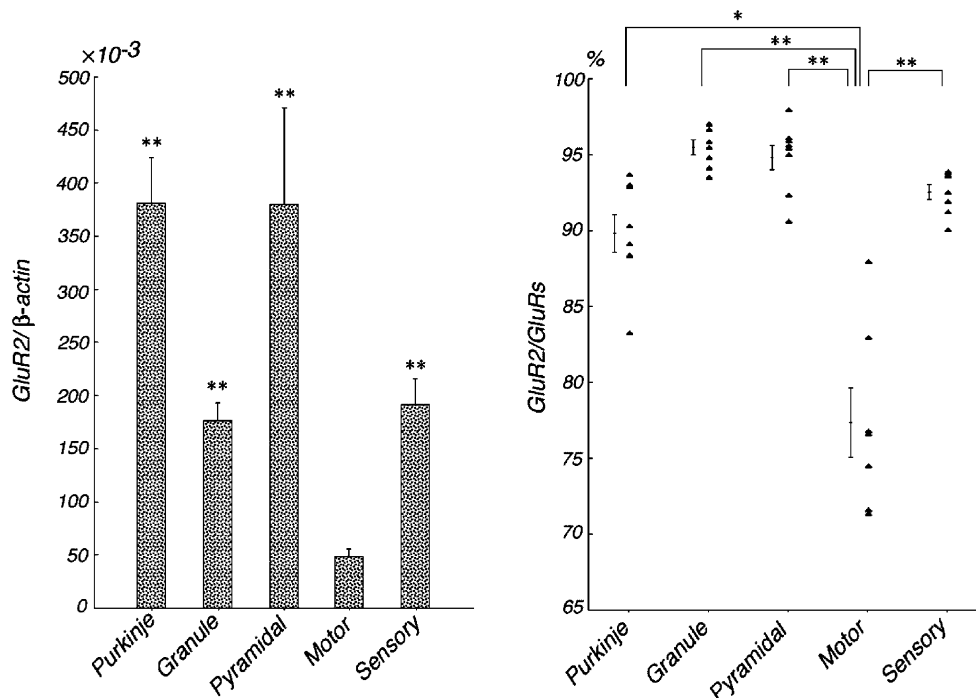


Fig. 3 Expression profile of AMPA subunit mRNA in single neuronal subsets of normal subjects. *Left:* The copy number of GluR2 mRNA has been normalized to the β -actin control (mean \pm SEM; $n=8$). Samples significantly different from spinal motor neurons (*Motor*) are indicated (Mann-Whitney U test, $^{**}P<0.001$). *Right:* Each symbol represents the GluR2 mRNA copy number relative to the sum of the copy numbers of all GluR mRNAs (*GluRs*)

in one subject. For each group, the mean \pm SEM ($n=8$) is also displayed. The magnitude of GluR2 mRNA predominance is significantly lower in spinal motor neurons (*Motor*) than in other neuronal subsets (Mann-Whitney U test, $^{*}P<0.01$, $^{**}P<0.001$). *Purkinje*, Purkinje cells; *Granule*, cerebellar granule cells; *Pyramidal*, cortical pyramidal neurons; *Sensory*, spinal dorsal horn neurons in substantia gelatinosa. (Modified from [36] with permission)

rons, including motor neurons of the spinal cords of humans as well as other mammals, and that the expression level of GluR2 mRNA is significantly lower in motor neurons than in other neuronal subsets in adult brains.

RNA editing

RNA editing has been defined as a posttranscriptional modification of the base sequence of mRNA and is recognized as a genetic mechanism for changing gene-specified codons and thus protein structure and function [45, 46]. In mammals, the main types of RNA editing are the base conversion of adenosine (A) to inosine (I) and that of cytidine (C) to uracil (U), which has been demonstrated to occur only in apolipoprotein B (ApoB) [47, 48] and neurofibromatosis type 1 (NF1) [49].

The conversion of A-to-I is most active in the central nervous system and has been found to occur predominantly in receptors and ion channels, including ionotropic glutamate receptor subunits [50–52], the serotonin $5HT_{2C}R$ [53], the voltage-dependent potassium channel Kv1.1 [54], and the RNA editing enzyme ADAR2 [55]. Among these, the biological effects of RNA editing have been most clearly demonstrated in ionotropic glutamate receptors, where editing positions have been identified in the subunits of AMPA receptors and kainate

receptors, which, like AMPA receptors, are tetrameric assemblies comprising different combinations of the homologous subunits GluR5–GluR7, KA1, and KA2. Editing positions have been named after the amino acids that can occupy them, including the Q/R site in GluR2, GluR5, and GluR6 [50], the R/G site in GluR2, GluR3, and GluR4 [52], and the I/V and Y/C sites in GluR6 [51]. The change in amino acid residue caused by RNA editing, particularly at the Q/R site of GluR2, results in alterations in channel properties, including Ca^{2+} permeability [21, 22, 26, 27, 51, 56–59] and kinetic aspects of channel gating [52] in AMPA receptors.

AMPA receptors in ALS

As mentioned above, AMPA receptor-mediated neuronal death occurs after an increase in Ca^{2+} influx through AMPA receptor-coupled ion channels, and either a decrease in GluR2 expression or insufficient RNA editing at the GluR2 Q/R site is the causative molecular change. A decrease in GluR2 mRNA has been demonstrated after ischemia [60], but insufficient RNA editing had not been shown in any human neurological disease [61–63] or animal models under conditions inducing neuronal death after cerebral hypoxia [64] or kindling [65]. Owing to the lack of evidence on ALS motor neurons, we investi-

gated, both quantitatively and qualitatively, these molecular changes in AMPA receptors in motor neuron tissues of ALS patients, as compared to disease control and normal control subjects.

Quantitative analysis (RNA expression)

On the basis of the AMPA receptor mRNA expression profile in normal human neurons, we investigated whether the composition of AMPA receptor subunits is altered in ALS motor neurons. Quantitative analyses for AMPA receptor mRNA on both 100 motor neurons and single motor neurons showed that ALS motor neurons expressed almost the same amount of GluR2 mRNA relative to the β -actin baseline as control motor neurons (Fig. 4) [36]. Neither the ratio of β -actin mRNA-positive neurons to total dissected neurons (83.5% vs. 82.7%) nor the ratio of GluR2 mRNA-positive neurons to β -actin mRNA-positive neurons (57.9% vs. 53.7%) differed between the ALS and control groups, indicating that GluR2 mRNA expression is not altered in individual motor neurons of ALS [36]. Thus, selective reduction in GluR2 does not occur, and, therefore, an increase in the proportion of Ca^{2+} -permeable AMPA receptors owing to a reduced proportion of GluR2-containing AMPA receptors cannot be the mechanism underlying AMPA receptor-mediated neuronal death in ALS.

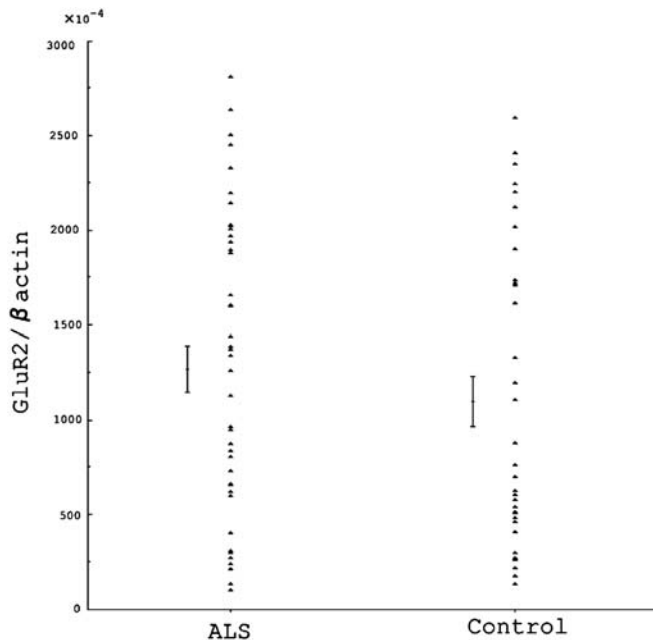


Fig. 4 Expression level of GluR2 mRNA in single motor neurons of ALS and control subjects. Each symbol represents the copy number of GluR2 mRNA normalized to the β -actin control in a single motor neuron. The expression levels in 44 motor neurons from three subjects with ALS and 36 motor neurons from three control subjects is shown. There is no significant difference between motor neurons from the ALS group and those from the control group (Mann-Whitney U test, $P > 0.01$). For each group, the mean \pm SEM is also displayed. (Adapted from [36] with permission.)

Qualitative analysis (RNA editing)

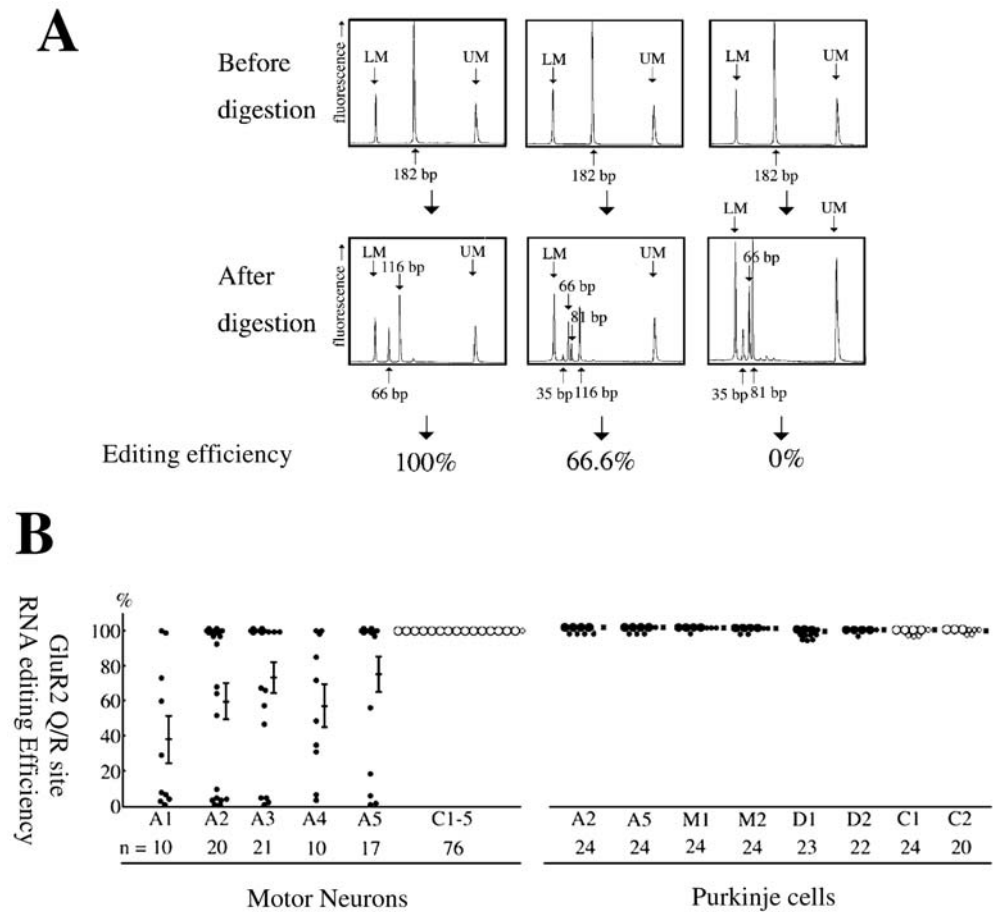
The alternative explanation for the AMPA receptor-mediated selective motor neuronal death in ALS is a deficiency in GluR2 Q/R site editing, which we have observed in the ventral gray matter of the ALS spinal cord [66]. In order to analyze neuron-selective tissue, we extracted RNA from single motor neurons isolated with a laser microdissector [36] from five individuals with ALS and five normal control subjects [67]. The editing efficiency was calculated by measuring differences in the digestion patterns of nested RT-PCR products of GluR2 mRNA obtained with the restriction enzyme *BbvI*, whose cutting site depends on the occurrence of editing (Fig. 5A) [66–68]. The editing efficiency in GluR2 in cerebellar Purkinje cells was also quantified in individuals with ALS, dentatorubral-pallidoluysian atrophy (DRPLA), and multiple system atrophy (MSA) and compared with that in normal subjects.

The frequency of GluR2 mRNA positivity did not differ significantly between the ALS and the control groups (two-sample test for equality of proportions, $P > 0.05$). The editing efficiency varied greatly, from 0% to 100%, among the motor neurons of each individual with ALS, and was not complete in 44 of them (56%); this was in marked contrast to the control motor neurons, of which all 76 examined showed 100% editing efficiency. The editing efficiency in Purkinje cells was virtually complete in the ALS, DRPLA, MSA, and normal groups (Fig. 5B) [67]. We confirmed that laser-captured neuronal tissue was not contaminated with tissues derived from glial cells or other cells, by PCR for microtubulus associate protein 2 (MAP2) and glial fibrillary acidic protein (GFAP) on neural tissue and PCR for GluR2 on tissues from neuropil.

Albeit at a tissue level, GluR2 Q/R site editing has been reported to be preserved in the severely pathological brain areas of other neurodegenerative diseases including the striatum of Huntington disease, the neocortex and hippocampus of Alzheimer and Pick diseases, and the cerebellum of diseases of spinocerebellar degeneration [61–63, 69]. In addition, GluR2 editing was found to be virtually complete in Purkinje cells (Fig. 5B) [67] and the motor cortex [66] of ALS patients, indicating that the defect in GluR2 editing at the Q/R site is disease specific to ALS and site-selective to spinal motor neurons.

In accordance with our results, mice transgenic for an artificial Ca^{2+} -permeable GluR2 develop motor neuron disease late in life [31], indicating that motor neurons are specifically vulnerable to a deficiency in RNA editing. The proportion of the artificial Ca^{2+} -permeable GluR2 out of total GluR2 mRNA was only about 25% in that study, which raises questions about the type of molecular mechanism that could result in a small proportion of unedited GluR2Q altering the channel conductance of AMPA receptors to an extent sufficient to induce neuronal death. It has been reported that a GluR2Q subunit is more readily incorporated into functional AMPA receptors than is an edited GluR2R at the stage of tetramer (dimer of dimers) formation [70], as well as during receptor trafficking from

Fig. 5 A Analysis of RNA editing efficiency: When all of the RT-PCR products are derived from edited GluR2 mRNA, two bands (66 and 116 bp) are detected; by contrast, when all of the RT-PCR products are derived from unedited GluR2, three bands (35, 66, and 81 bp) are detected. When both edited and unedited GluR2 subunits coexist, four bands (35, 66, 81, and 116 bp) are detected. **B** Editing efficiency at the GluR2 Q/R site in single neurons of ALS, disease control and normal control subjects (modified from Fig. 1 in [67]). The editing efficiency varied greatly, from 0% to 100% (mean: 38.1–75.3%), among the motor neurons of each individual with ALS (A1–A5), and was not complete in 44 of them (56%); this was in marked contrast to the control motor neurons (C1–5), of which all 76 examined showed 100% editing efficiency. The editing efficiency in Purkinje cells was virtually complete (greater than 99.8%) in the ALS, disease control (dentatorubral-pallidoluysian atrophyDRPLA (D), multiple system atrophyMSA (M)) and the normal control groups (C)



the endoplasmic reticulum (ER) to the cell surface [71]. Therefore, if the RNA editing were deficient, even in a small proportion, then GluR2Q-containing receptors would be formed preferentially in the endoplasmic reticulumER, and receptors containing GluR2Q and GluR1 or GluR3 would be readily transported to the membrane, resulting in the preferential expression of Ca^{2+} -permeable functional AMPA receptors in the postsynaptic membrane. The effects of GluR2 RNA editing deficiency may be more conspicuous in spinal motor neurons, where the expression level of GluR2 is relatively low compared with that in other neuronal subsets [36]. According to this scheme, a small increase in GluR2Q with deficient GluR2 RNA editing will greatly increase the proportion of GluR2Q-containing, and therefore Ca^{2+} -permeable, functional AMPA receptors, thereby promoting excitotoxicity in ALS motor neurons [47, 48, 50–52].

Editing enzymes and RNA editing of GluR

Enzymes responsible for the A-to-I conversion have been termed “adenosine deaminases acting on RNA” (ADARs), and three structurally related ADARs (ADAR1 to ADAR3) have been identified in mammals [72–77]. ADAR1 and ADAR2 are expressed in most tissues [72, 74, 78, 79] and recognize the adenosine residue to be edited through the

structure of the duplex that is formed between the editing site and its editing site complementary sequence (ECS), which is located in a downstream intron of the precursor (pre-) mRNA (Fig. 6) [80–82]. ADAR2 predominantly catalyzes RNA editing at the Q/R site of GluR2 both in vivo and in vitro, whereas both ADAR1 and ADAR2 catalyze the Q/R sites of GluR5 and GluR6, which are subunits of kainate receptors [83, 84]. ADAR3 is expressed

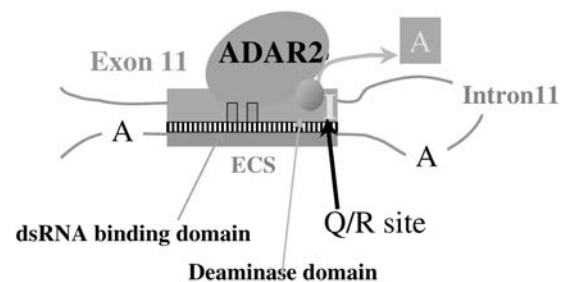


Fig. 6 ADAR2 and RNA editing. ADAR2 has two double-stranded RNA-binding domains (square) and one catalytic domain (cube), and it recognizes the adenosine residue (A) to be edited through the structure of the duplex that is formed between the editing site (e.g., the Q/R site in exon 11 of GluR2 pre-mRNA) and its editing site complementary sequence (ECS), which is located in a downstream sequence (e.g., in intron 11 of GluR2 pre-mRNA). Adenosine in the edited site is substituted to inosine (I), but adenosine that is not located in the editing site or the ECS remains unedited

exclusively in the brain, but is catalytically inactive on both extended double-stranded RNA and known pre-mRNA editing substrates [75, 77].

In mammalian and human brains, the editing efficiency at each editing position of GluRs is developmentally and regionally regulated [52, 56, 62, 85, 86], and the Q/R sites of GluR5 and GluR6 have been reported to be edited less in white matter than in gray matter [58, 68, 86–91]. By contrast, the GluR2 Q/R site is almost completely edited in various brain regions, including white matter in neonatal and adult rodent brains [56, 87, 92, 93]. GluR2 mRNA in human brains including white matter is, however, not always completely edited at the Q/R site [61, 62, 65, 66, 68, 91, 94, 95]. We have demonstrated an editing efficiency of virtually 100% in single neuron tissues from various neuronal subsets, but a significantly low editing efficiency in adult, but not in immature, human white matter [68, 91]. It seems likely that, in contrast to neurons, human glial cells physiologically express Ca^{2+} -permeable AMPA receptors: oligodendrocytes express those containing unedited GluR2 subunits, and astrocytes and Bergmann's glial cells express those lacking edited GluR2 subunits [23, 96, 97]. Therefore, the regional, and thus presumably cell-specific, regulation of GluR2 Q/R editing might occur in the human central nervous system.

ADAR2

It has been shown that the mRNA expression of ADAR2, the most efficient double-stranded RNA deaminase for editing GluRs, is regulated in a cell-specific manner throughout development and in rodent brain, is first detected by in situ hybridization in the thalamic nuclei formation at embryonic day 19 (E19), with more extensive and widespread distribution by the third postnatal week when the expression is highest in the thalamic nuclei and very low in white matter [98]. Editing efficiency at the editing sites of GluRs have been found to parallel the expression levels of ADAR2 mRNA in developmental rat [86, 87, 99–101] and human [91] brains, in a cultured human teratocarcinoma cell line [102], and in surgically

excised hippocampus from patients affected with refractory epilepsy [103].

An association between the level of ADAR2 expression and editing efficiency at the GluR2 Q/R site has been also demonstrated by the observation that an RNA editing efficiency of less than 100% occurred only when the ratio of ADAR2 mRNA to total AMPA receptor subunit (GluR1-GluR4) mRNA was below 20×10^{-3} in human white matter (Fig. 7B) [68]. No such correlation was observed between the editing efficiency at GluR2 mRNA and the ratio of ADAR1 mRNA to total GluR mRNA, or between the editing efficiency at GluR5 or GluR6 mRNA and the ratio of either ADAR1 or ADAR2 mRNA to total GluR mRNA (Fig. 7A) [68]. Our results on human brain are in agreement with in vivo and in vitro evidence obtained in animal brains, indicating that ADAR2 predominantly catalyzes RNA editing at the Q/R site of GluR2 [55, 74, 78, 83, 104, 105], whereas the Q/R sites of GluR5 and GluR6 are edited not only by ADAR2 but also by ADAR1 [74, 75, 78, 81, 83, 84].

Taken together, the expression level of ADAR2 mRNA is one factor determining the editing efficiency of GluR2 at the Q/R site, although the nonlinear correlation suggests that another factor or factors may be also involved in the regulation of editing activity. Indeed, inhibitors of ADARs have been identified as sequence-nonspecific double-stranded RNA-binding proteins in *Xenopus oocytes* [106].

Significance of GluR2 underediting

GluR2 Q/R site editing in neurons occurs with virtually 100% efficiency throughout life from an embryonic stage, and the early demise of mice deficient in GluR2 RNA editing caused by neuronal death [30] can be rescued by restoring RNA editing [84], indicating that GluR2 modification by RNA editing is a biologically crucial event for neuronal survival and its deficiency is a direct cause of neuronal death. Thus, marked reduction of RNA editing in ALS motor neurons [67] may be a direct cause of the selective motor neuron death seen in ALS.

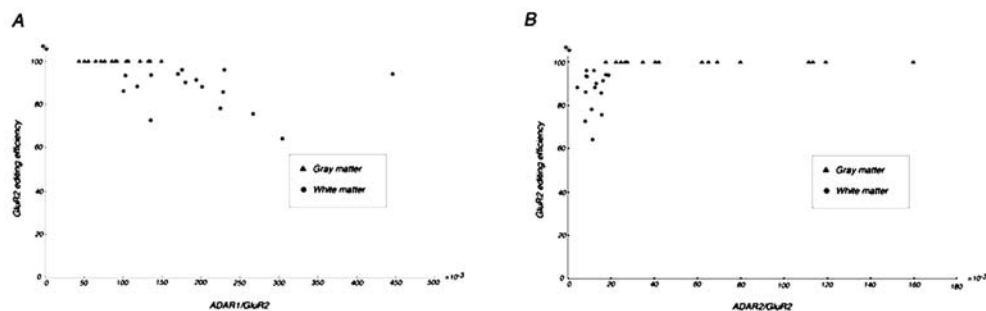


Fig. 7 Relationship between editing efficiency at the Q/R site of GluR2 and the abundance of ADAR1 mRNA (A) or ADAR2 mRNA (B) relative to GluR2 mRNA. A No relationship is found between GluR2 editing and the expression of ADAR1 mRNA relative to GluR2 mRNA. B In samples where the abundance of

ADAR2 mRNA relative to GluR2 mRNA is less than 20×10^{-3} , GluR2 is not completely edited. By contrast, when the relative abundance is greater than 20×10^{-3} , GluR2 is completely edited. *Cbl*, Cerebellum; *BW*, cerebellar white matter; *Cx*, cerebral cortex; *CW*, cerebral white matter. (Adapted from Fig.7 in [68] with permission)

As mentioned above, AMPA receptors in glial cells seem to be more Ca^{2+} permeable than those in neurons, and a deficiency in RNA editing at the GluR2 Q/R site seems to cause significant cell death only when it occurs in neurons. Therefore, the recent finding of a reduction in GluR2 Q/R editing in malignant gliomas [94] may have different biological significance in comparison to the editing deficiency that occurs in neuronal tissue in ALS [67]. Indeed, the magnitude of the editing efficiency that was observed in malignant gliomas (69–88%) was within the range that we detected in normal white matter (64–99%) [68].

It is likely that the molecular mechanism underlying the deficiency in RNA editing is a reduction in ADAR2 deaminase activity. Our results suggest that the expression level of ADAR2 mRNA is a determining factor in this reduced activity; thus, restoring ADAR2 activity selectively in motor neurons, for example, by transfection of an ADAR2 cDNA construct using a motor neuron-specific vehicle for enhancing ADAR2 mRNA levels may be a specific therapeutic strategy for ALS. With this more focused research target, it is our sincere hope that a specific therapy for ALS will be developed in the near future.

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