**GRIN2A mutation and early-onset epileptic encephalopathy: personalized therapy with memantine**

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**Introduction**

Genomic research has identified an increasing number of human developmental and seizure disorders that are associated with mutations of subunits of the N-methyl-D-aspartate receptors (NMDARs).1-8 For example, mutations in the GluN2A subunit of the NMDARs have been associated with several childhood-onset epilepsy syndromes. One such condition is early-onset epileptic encephalopathy (EAE), which is characterized by seizures and developmental delay in infancy. The identification of the causative mutation in a patient with EAE can provide insights into the pathophysiology of the disease and help guide personalized therapeutic approaches.

The objective of this study was to identify a novel mutation in the GRIN2A gene and determine its potential as a target for therapy. The study utilized modern translational medicine tools, including high-throughput sequencing, in vitro expression and electrophysiology assays, and screening of existing drug libraries to identify potential therapeutic compounds.

**Objective**

Early-onset epileptic encephalopathies have been associated with de novo mutations of numerous ion channel genes. We employed techniques of modern translational medicine to identify a disease-causing mutation, analyze its altered behavior, and screen for therapeutic compounds to treat the proband.

**Methods**

Three modern translational medicine tools were utilized: (1) high-throughput sequencing technology to identify a novel de novo mutation; (2) in vitro expression and electrophysiology assays to confirm the variant protein’s dysfunction; and (3) screening of existing drug libraries to identify potential therapeutic compounds.

**Results**

A de novo GRIN2A missense mutation (c.2434C>A; p.L812M) increased the charge transfer mediated by N-methyl-D-aspartate receptors (NMDAs) containing the mutant GluN2A-L812M subunit. In vitro analysis with NMDA receptor blockers indicated that GLuN2A-L812M-containing NMDARs retained their sensitivity to the use-dependent channel blocker memantine; while screening of a previously reported GRIN2A mutation (N615K) with these compounds produced contrasting results. Consistent with these data, adjunct memantine therapy reduced our proband’s seizure burden.

**Interpretation**

This case exemplifies the potential for personalized genomics and therapeutics to be utilized for the early diagnosis and treatment of infantile-onset neurological disease.
syndromes within the epilepsy-aphasia spectrum. These syndromes include benign epilepsy with centrotemporal spikes (BECTS), Landau-Kleffner syndrome (LKS), and epileptic encephalopathy with continuous-spike-and-waves-during-slow-wave-sleep (CSWSS). In contrast, other GluN2A mutations extend the range of phenotypes beyond disorders in the epilepsy-aphasia spectrum to include early-onset epileptic encephalopathy, which is characterized by severe infantile-onset epilepsy and lack of development.

The NMDARs are ligand-gated ion channels that mediate a slow component of synaptic transmission in the central nervous system. The GluN1 and GluN2 subunits of NMDARs bind glutamate and glycine, respectively, leading to the opening of a cation-selective pore. This action results in a current flux with subsequent depolarization and increase intracellular Ca²⁺, which can lead to changes in synaptic strength. Currently, four GluN2 subtypes (A–D) have been identified. The four known GluN2 subtypes (A–D) have varying temporal and spatial expression patterns throughout the nervous system, and control key functional and pharmacological properties of synaptic NMDARs. The GluN2A mutations identified to date cause either haploinsufficiency of the GluN2A subunit or altered activity of the mutant-GluN2A-containing NMDAR complexes.

Based on the observation of altered activity of mutant-GluN2A-containing NMDAR complexes, we hypothesized that understanding the alteration in activity and identification of a targeted therapy improves outcome. Hence, we report the clinical characteristics and genome-based therapy of a child with an early-onset epileptic encephalopathy due to a novel GluN2A missense mutation (NP_000824.1:p.L812M).

**Materials and Methods**

**Patients and DNA samples**

The NHGRI IRB reviewed and approved all clinical and laboratory protocols. Patients and family members who were enrolled in the clinical protocol gave written informed consent. Seizures were logged by parents and school teachers on a daily basis. Genomic DNA was extracted from peripheral whole blood using the Gentra Puregene Blood kit (Qiagen, Valencia, CA) per manufacturer’s standards. The proband’s examination and diagnostic evaluation included EEGs, electromyography/nerve conduction studies (EMG/NCV), magnetic resonance imaging (MRI) of the brain, buffy coat analysis, and skin and muscle biopsies.

**Genotyping**

Illumina (San Diego, CA) HumanOmni1-Quad genotyping arrays were run for the affected child, unaffected sister, and parents. Analyses, including homozygosity mapping, were carried out using Illumina GenomeStudio Software. SNP chip data were also used to verify exome sample IDs and parental identity for quality control purposes and to calculate sensitivity and specificity for genotype calling in exome sequence data.

**Exome sequencing**

Exome sequencing for this case was previously described.

**Neurophysiology and GRIN2A-L812M functional validation**

For two-electrode voltage-clamp (TEVC) recordings, the cDNA for wild type human NMDA subunit GluN1-1a (hereafter GluN1) and GluN2A in pCI-neo were described previously (GenBank: NP_000824.1:p.L812M). When studied in heterologous expression systems, this GluN2A-L812M subunit had increased NMDAR activity that was inhibited by several channel blockers including memantine. A previously reported GRIN2A mutation was also evaluated in vitro using NMDA blockers with contrasting responses. Treatment of our proband with memantine improved his electroencephalogram (EEG) and reduced his seizure burden.

**Screening of FDA-approved NMDA receptor antagonists**

FDA-approved drugs that might act as NMDA receptor open channel blockers were screened using TEVC recordings from *Xenopus laevis* oocytes were performed as previously described. The recording solution contained (in mmol/L) 90 NaCl, 1 KCl, 10 HEPES, 0.5 BaCl₂, 0.01 EDTA (pH 7.4). The membrane potential was held at -40 mV in all oocyte experiments unless otherwise stated. EC₅₀ values were obtained by fitting the concentration–response curve with

\[
\text{Response} = 100\%/(1 + (\text{EC}_{50}/[\text{agonist}])^N)
\]

where N is the Hill slope.
Response(%) = [(100 − minimum) / (1 − ([concentration]/IC50)^N)] + minimum

where IC50 is the concentration of drug that produces a half-maximal effect, N is the Hill slope, and minimum is the degree of residual inhibition at a saturating concentration of drug.

**Results**

**Clinical summary**

The proband (UDP1130; Fig. 1A) presented to the NIH Undiagnosed Diseases Program (UDP)\(^{16–18}\) at 6.5 years of age with a history of early-onset epileptic encephalopathy associated with profound cognitive impairment, absent motor development, and intractable seizures. An older sister was unaffected. His asymptomatic parents were non-consanguineous and of European and Hispanic descent. There was no family history of a similar condition.

The proband was the full-term product of an uncomplicated pregnancy. He never visually tracked or made any purposeful movements. At 6 weeks of age, he had poor head control, axial hypotonia, and appendicular hypertonia. Parents noted frequent eye blinking movements and myoclonic jerks (not in clusters), which were sometimes associated with external stimuli. Neurological consultation at 7 months of age noted the above features and trace deep tendon reflexes. Brain MRI at the time reportedly showed enlarged frontal extra-axial spaces. At 2.5 years of age, the proband developed “near-constant flinging movements of his extremities”. His responses to stimuli included behavioral arrest, agitation, or laughter.

Figure 1. Proband and neuroimaging. (A) The proband was nondysmorphic. (B–D) MRI of the brain at 9 years of age (B-Axial T1, C-Sagittal T1, D-Axial FLAIR) showed progressive cerebral atrophy and a thin corpus callosum associated with subtle abnormalities of the white matter including hypomyelination of the terminal zones and the temporal lobes.
Development was static at a neonatal level without further progression or regression. The proband’s epilepsy followed an intractable course. His first suspected seizure occurred at ~2 months of age and was characterized as tonic extension of all extremities that lasted less than a minute. Between 2 and 18 months of age there were no documented seizures, but in retrospect, his parents feel that he was having frequent unrecognized episodes. His second definite seizure occurred at around 18 months of age and was described as having an initiating myoclonic jerk followed by tonic extension of all extremities, which evolved to slow rhythmic movements of the right arm and leg lasting for 5 min. The child was subsequently started on leviteracetam without efficacy. Prior to this time, the proband had frequent myoclonic jerks that were not treated. Seizures evolved to involve tonic flexion or extension of all extremities lasting minutes, with the myoclonic jerks continuing to occur alone or in association with these larger seizures. Over time, both types of episodes increased in frequency from monthly to a nearly daily frequency and were not responsive to numerous antiepileptic drug (AED) regimens (see Supplementary Materials).

The evolution of the proband’s EEG features paralleled his clinical course. An EEG at 2 months of age was reportedly normal. Another at 13 months of age identified a potential epileptic focus in the right cerebral hemisphere, as well as a single polyspike-like complex that correlated with a nocturnal episode of a whole body jerk with prominent trunk flexion. Therapy was not initiated because the treating physician was unsure that the episode was ictal. Over time, EEGs were reported to possess a diffusely slow and disorganized background with irregularly generalized or lateralized runs of spike and slow wave discharges (see Supplementary Materials). These EEGs were noted to only have very mild activation of the right-sided discharge during sleep and were without any features of electrical status epilepticus of sleep (ESES).

Upon initial examination at the NIH Clinical Center at 6.5 years of age, the patient did not visually track or exhibit any purposeful interaction with his environment. He was nondysmorphic and had axial hypotonia, appendicular hypertonia, and diffuse hyporeflexia. The child exhibited frequent random multifocal myoclonic movements of his extremities. Ophthalmological examination was normal. The patient was having near-daily seizures and was being treated with valproic acid. Over the next 2 years, rufinamide and lacosamide were added to his AED regimen with little improvement in seizure frequency.

Neuroimaging revealed widespread cerebral parenchymal volume loss, a thin corpus callosum, and abnormal myelination of the terminal zones and temporal lobes bilaterally. The cerebellum and brainstem were relatively spared (Fig. 1B–D). These findings reflected progression compared to previous studies.

The proband’s EEG was abnormal with slow activity of 3.5–4.5 hertz and 1–3 hertz delta and disorganized activity with intermittent frontally predominant irregular high amplitude 2.5-hertz spike-wave discharges that were greater on the right than left. The frequency of 2.5 hertz spike-wave discharges did not increase with sleep. More detailed information regarding the proband’s phenotype and evaluation can be found in the Supplementary Materials.

Exome sequencing identifies a variant encoding the GluN2A p.L812M mutation

As previously reported,13 exome sequencing identified a novel de novo variant (NM_000833.3:c.2434C>T) in exon 13 of GRIN2A, which encodes the NMDA subunit GluN2A (Fig. 2A). This mutation resulted in a leucine to methionine substitution (NP_000824.1:p.L812M) in the linker region connecting the ligand-binding domain to the pore-forming transmembrane region of GluN2A (Fig. 2B–C).19 This leucine is highly conserved across vertebrate species (Fig. 2B).

Functional analysis of mutant NMDA receptors

The pharmacological properties of this mutant receptor, GluN2A-L812M, were compared with wild-type GluN2A receptors using the Xenopus leavis oocyte expression system and TEVC recordings. We determined the concentrations of glutamate and glycine that can produce a half-maximal current response (EC50). Receptors containing GluN2A-L812M showed an eightfold reduction in EC50 (i.e., increased potency) for glutamate (0.42 μmol/L vs. 3.4 μmol/L of wild type) as well as glycine (0.14 μmol/L vs. 1.1 μmol/L of wild type), consistent with a previous study describing function of this residue in recombinant receptors at the single channel (Fig. 3; Table 1) (Yuan et al. in press). These data support the idea that GluN2A-L812M-containing NMDARs are overactive due to the increased activation at low concentrations of agonists. The resulting enhanced excitatory drive is consistent with the production of an epileptic phenotype. More extensive mechanistic studies of GluN2A-L812M-containing NMDARs are described elsewhere13.

We compared the above results with those for another GRIN2A mutation (p.N615K), previously associated with early-onset epileptic encephalopathy in a young girl.2 The GluN2A-N615K mutation resides near the apex of the pore-lining reentrant loop in the receptor subunit, a site known to strongly influence Mg2+ block.20 Interestingly, GluN2A-N615K had EC50 values that were unchanged.
when compared to wild-type receptors (Fig. 3; Table 1),
but the mutation had dramatic effects on Mg2+ inhibition
of NMDAR activity.2 Although, the L812M mutation
caused a significant but incomplete reduction in Mg2+
sensitivity, the GluN2A-N615K mutation was reported to
eliminate Mg2+ block at all physiologically relevant con-
centrations.2

**Figure 2.** Genetic and protein changes of GRIN2A and GluN2A. (A) Family pedigree and genotypes reveal a de novo mutation (affected proband is indicated by arrow; parentage was confirmed by SNP array; data not shown). (B) Schematic representation of GluN2A subunit (asterisk notes the position of the L812M mutation). The L812 residue is highly conserved across vertebrate species. (C) A homology model of GluN2A subunit28 built from the GluA2 crystallographic data29 and shown as space fill. The red asterisk in the cartoon depicting the domain arrangement of an individual subunit shows the position of L812M in the linker region between the ligand-binding domain (S2, LBD) and the transmembrane domain (M4).

**Figure 3.** Functional analysis of GluN1/GluN2A receptors, GluN1/GluN2A-N615K receptors, and GluN1/GluN2A-L812M receptors. (A) The composite glutamate (in the presence of 100 μmol/L glycine) and (B) glycine (in the presence of 100 μmol/L glutamate) concentration-response curves indicate an increased agonist potency in GluN1/GluN2A-L812M compared to wild-type and GluN1/GluN2A-N615K NMDA receptors. Fitted EC50 values are given in μmol/L in the symbol legend.

**Screening of FDA-approved NMDA-antagonists**
Since conventional anticonvulsant medications did not provide adequate control of the proband’s seizures, a number of FDA-approved NMDAR antagonists were evaluated for their ability to inhibit receptors containing...
Targeted therapy with memantine altered EEG appearance, decreased seizure frequency and allowed for tapering of conventional AEDs

On the basis of these findings, memantine had been shown to exert anticonvulsant effects in a wide range of animal models of epilepsy, and had been used in children without toxicity. In vitro analysis revealed that memantine inhibited GluN2A-L812M-containing NMDARs with an IC\textsubscript{50} of 12 \( \mu \)mol/L compared with 4.6 \( \mu \)mol/L for the wild type (at a holding potential of \(-40\) mV) indicating that this compound can effectively reduce GluN2A-L812M-related NMDAR hyperactivity (Fig. 4A; Table 2). We also evaluated the inhibition of FDA-approved NMDAR channel blockers on currents arising from GluN2A-N615K-containing NMDARs. Interestingly, both dextromethorphan and its metabolite dextrorphan showed enhanced potency on N615K-containing NMDARs in comparison to wild-type NMDARs (twofold and 5.6-fold, respectively; Table 2). These values are in stark contrast to the potency of these blockers at L812M (Table 2), which is lower than that observed in WT receptors.

Discussion

The diagnosis and treatment of our patient’s early-onset epileptic encephalopathy highlights three tools currently available for translational medicine: (1) the identification of a pathogenic mutation using high-throughput sequencing technology; (2) confirmation of the variant protein’s dysfunction using in vitro expression and electrophysiology assays; and (3) identification of a potential therapeu-
tic compound through screening of existing drug libraries. Specifically, we identified a de novo GRIN2A mutation that characterized the increased activity of NMDARs with which it was incorporated, and showed that memantine inhibited this hyperactivity in vitro. Completing this illustration of personalized medicine, we showed that initiation of memantine as an adjunct antiepileptic medication reduced seizure frequency and allowed for a reduction in the number of antiepileptic medications.

GRIN2A-associated early-onset epileptic encephalopathy is a rare disorder, with only a few patients reported to date. Mutant NMDARs associated with this disorder underwent electrophysiological analysis to provide insight into their pathological mechanisms. Our proband’s GRIN2A mutation (L812M) possessed increased intrinsic activity in response to agonists and decreased response to negative modulators, which translated into a charge transfer that was enhanced by over an order of magnitude. In contrast, another child’s early-onset epileptic encephalopathy was the result of a different GRIN2A mutation (N615K) acting via a different mechanism, the relief of Mg²⁺ blockade. Both of these cases of early-onset epileptic encephalopathy were the result of greatly increased current flow through mutant-GluN2A-containing NMDARs, leading to excessive excitatory drive, thereby inducing seizure activity and/or excitotoxicity. In our proband, this likely led to neuronal loss, motor dysfunction, cognitive impairment, and the other neurological...
features. Whether other cases of GRIN2A-associated early-onset epileptic encephalopathy (e.g., Pro522Arg mutation\(^5\)) share these features requires further investigation.

The next step in our analysis involved screening these mutations with known inhibitors of NMDAR function to reduce activity. Interestingly, memantine was shown to antagonize L812M-associated hyperactivity, and consistent with this result, memantine treatment of our proband resulted in the substantial reduction in his seizure burden. Although this change may have had other causes (e.g., the placebo effect or the loss of the potentially seizure-provoking effects of rufinamide and lacosamide), our proband’s persistent response (loss of lifelong myoclonic jerks and a reduction in seizure frequency) to over a year of treatment implies a memantine effect is the more likely possibility. Whether higher memantine dosages may further reduce his seizure burden needs to be determined; however, at this time, the pediatric safety guidelines of memantine dosing have limited our ability to test this hypothesis.

Our results show that other NMDAR antagonists (dextromethorphan and dextrophorphan) possess enhanced potency at a different GluN2A mutation (N615K),\(^2\) and raise the possibility that treatment with either dextromethorphan or dextrophorphan may have some efficacy in treating patients possessing the GluN2A-N615K or other mutations within the channel pore. The differential response of GluN2A-N615K and GluN2A-L812M-containing NMDARs to NMDAR antagonists is consistent with a previous report that dextromethorphan engages different structural determinants at its binding site in the pore than do other channel blockers.\(^{27}\) Together, these results indicate a need for specific electrophysiological evaluation of each mutant GRIN2A to evaluate its response to NMDAR antagonists.

These cases, with their infantile-onset and their dramatic effect on development, differ from GRIN2A-associated epilepsy-aphasia syndromes, such as BECTS, LKS or CSWSS.\(^6\)–\(^8\) These disorders have periods of normal development prior to the development of epilepsy, and their associated encephalopathy is typically less severe. Interestingly, several families with these epilepsy-aphasia disorders were shown to possess GRIN2A missense mutations. Further electrophysiological characterization of these missense mutations may provide more insight into GRIN2A phenotype–genotype correlations, as well as additional therapeutic options for these disorders.

Finally, it is important to note that future evaluation of GRIN2A in patients with undiagnosed epileptic disorders, including early-onset epileptic encephalopathies, may expand the clinical phenotype associated with GRIN2A defects. High-throughput sequencing may be employed for genomic screening with subsequent electrophysiological studies and similar therapeutic screening strategies performed on mutated proteins. These strategies, especially in the context of early-onset encephalopathies, may dramatically improve a patient’s overall development if instituted early. Eventually, patient-derived induced pluripotent stem cells could also serve as models for investigation (especially in GRIN2A-related cases due to haploinsufficiency\(^6\)–\(^8\)), and therapies identified in vitro can be applied in vivo, as described in this report.

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**Conflict of Interest**

None declared.

**References**


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Supporting Information

Additional Supporting Information may be found in the online version of this article:

Data S1. Clinical data.
Figure S1. Ultrastructural analysis of (A) Buffy Coat and (B) Skin biopsies. Lysosomal storage is present in lymphocytes and skin cells (please note differences in scale).