Properties of Triheteromeric N-Methyl-D-Aspartate Receptors Containing Two Distinct GluN1 Isoforms

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ABSTRACT

N-Methyl-D-aspartate (NMDA)–type glutamate receptors mediate excitatory synaptic transmission in the central nervous system and play critical roles in many neuronal processes. The physiologic roles of NMDA receptors are shaped by their functional properties, which are highly dependent on subunit composition. Most NMDA receptors are assembled from two GluN1 and two GluN2 subunits, but diversity in subunit composition is made possible by eight GluN1 splice variants (i.e., isoforms) and four distinct GluN2 subunits (GluN2A-D). We demonstrate using Förster resonance energy transfer and fluorescence lifetime imaging that GluN1-1a and GluN1-1b isoforms, which include or lack residues encoded by exon 5, form triheteromeric GluN1-1a/GluN1-1b/GluN2A (1a/1b/2A) and GluN1-1a/GluN1-1b/GluN2B (1a/1b/2B) receptors. We describe the selective expression of NMDA receptors containing two different GluN1 isoforms, and show that triheteromeric 1a/1b/2A and 1a/1b/2B receptors exhibit intermediate deactivation kinetics and pharmacological properties compared with the respective diheteromeric GluN1-1a/GluN1-1a/GluN2 and GluN1-1b/GluN1-1b/GluN2 receptors. These results highlight the intriguing possibility that neurons can finely tune NMDA receptor signaling by shifting the ratio of expressed GluN1-1a and GluN1-1b isoforms. Furthermore, we evaluate the contribution of channel pore residues to magnesium block and calcium permeability. These data point to the asymmetric contribution of pore residues in GluN1 and GluN2 to magnesium block, and reveal that a single copy of pore residues from GluN3 subunits strongly attenuates magnesium block and calcium permeability of NMDA receptors. Thus, the selective expression of NMDA receptors containing two distinct GluN1 isoforms provides new opportunities to study functional properties relevant to neuronal receptors.

Introduction

N-Methyl-D-aspartate (NMDA) receptors are ionotropic glutamate receptors that play critical roles in synaptic plasticity and neuronal development, but aberrant NMDA receptor signaling is implicated in a plethora of neurological and psychological diseases (Traynelis et al., 2010; Paoletti et al., 2013). The majority of NMDA receptors in the central nervous system (CNS) are tetrameric assemblies of two glycine/D-serine-binding GluN1 and two glutamate-binding GluN2 subunits (Traynelis et al., 2010; Paoletti et al., 2013). Four different GluN2 subunits have been identified (GluN2A-D) that display pronounced variation in regional and developmental expression levels, and each GluN2 subunit endows NMDA receptors with distinct functional and pharmacological properties (Monyer et al., 1992, 1994; Ishii et al., 1993; Akazawa et al., 1994; Vicini et al., 1998; Gielen et al., 2009; Yuan et al., 2009). The GluN2 subunits are therefore principle mediators of functional diversity among NMDA receptor subtypes and dictate their psychological roles in the CNS. The GluN1 subunit, which is obligatory in all NMDA receptor subtypes, is expressed from a single gene, but has eight different isoforms that arise from alternative splicing of three exons (Durand et al., 1992; Nakanishi et al., 1992; Sugihara et al., 1992; Hollmann et al., 1993). Exon 5 encodes the N1 cassette of 21 highly charged amino acids in the extracellular GluN1 amino-terminal domain, while exons 21 and 22 encode C1 and C2 cassettes in the intracellular C-terminal domain (CTD). Alternative splicing of exons 21 and 22 has no discernible effects on the functional and pharmacological properties of NMDA receptors, but rather alter interactions with intracellular proteins that can influence the subcellular distribution of NMDA receptors (Scott et al., 2001; Mu et al., 2003). By contrast, GluN1 subunits that contain the N1 cassette (e.g., GluN1-1b), encoded by exon 5, reduce agonist potency of NMDA receptors and decrease sensitivity to inhibition by extracellular zinc and protons compared with GluN1 subunits lacking the N1 cassette (e.g., GluN1-1a) (Traynelis et al., 1995, 1998). The presence of the N1 cassette also accelerates deactivation of glutamate-activated NMDA receptor responses and shortens the time course of excitatory postsynaptic currents.

ABBREVIATIONS: CFP, cyan fluorescent protein; CNS, central nervous system; CTD, C-terminal domain; EGFP, enhanced green fluorescent protein; ER, endoplasmic reticulum; FLIM, fluorescence lifetime imaging; FRET, Förster resonance energy transfer; GR, glycine-arginine; NMDA, N-methyl-D-aspartate; ORF, open reading frame; YFP, yellow fluorescent protein.
We developed a specialized DNA construct for expression of GluN1 in HEK293 cells, in which cDNA encoding enhanced green fluorescent protein (EGFP) was inserted between the CMV promoter in pC1-neo and the ORF of GluN1 (i.e., EGFP and GluN1 were not expressed as a fusion protein). This DNA construct resulted in high expression of EGFP and low expression of GluN1, while maintaining a linear relationship between EGFP and GluN1 expression. The ribosome scans the 5′-untranslated region of the mRNA for AUG initiation codons and the first AUG in the ORF will initiate translation of the ORF for EGFP. However, the ribosome will frequently skip this first AUG and instead initiate translation from downstream AUG codons, in which this construct encodes GluN1. The placement of 0–3 AUGs between EGFP and GluN1, which initiate short upstream ORFs (Meijer and Thomas, 2002; Barbosa et al., 2013) encoding 42–58 amino acids, results in a gradual reduction of GluN1 expression, while maintaining high expression of EGFP.

Amino acids are numbered according to the full-length protein, including the signal peptide. Site-directed mutagenesis was performed using the QuikChange method (Agilent Technologies, Santa Clara, CA) and verified by DNA sequencing. For expression in Xenopus oocytes, DNA constructs were linearized by restriction enzymes to produce the template for in vitro cRNA synthesis (mMessage mMachine; Thermo Fisher Scientific, Waltham, MA). Ifenprodil and spermine were purchased from Hello Bio (Princeton, NJ), and all other ligands were purchased from Sigma-Aldrich (St. Louis, MO).

Confocal Imaging and Fluorescence Lifetime Measurements. HEK293 cells were seeded in 12-well culture plates approximately 24 hr before transfection in this culture. Cells will initiate translation of the ORF for EGFP. However, the ribosome will frequently skip this first AUG and instead initiate translation from downstream AUG codons, in which this construct encodes GluN1. The placement of 0–3 AUGs between EGFP and GluN1, which initiate short upstream ORFs (Meijer and Thomas, 2002; Barbosa et al., 2013) encoding 42–58 amino acids, results in a gradual reduction of GluN1 expression, while maintaining high expression of EGFP.

Fluorescence lifetime measurements of CFP were conducted on live HEK293 cells approximately 48 hours following transfection. The cells were replated to 33 mm poly-D-lysine-coated (0.1 mg/ml) coverslips in DMEM (GIBCO; Thermo Fisher Scientific) supplemented with GlutaMax-I and sodium pyruvate (GIBCO; Thermo Fisher Scientific) supplemented with 10% dialyzed bovine serum (GIBCO; Thermo Fisher Scientific), 10 U/ml penicillin, and 10 μg/ml streptomycin (GIBCO; Thermo Fisher Scientific). Cells were transfected using TransIT Transfection Reagent (Mirus Bio, Madison, WI) with plasmid cDNAs encoding CFP-GluN1, YFP-GluN1, and GluN2A at a ratio of 1:1:1 or CFP-GluN1 and GluN2A at a ratio of 1:1. To prevent NMDA receptor-mediated cytotoxicity, the antagonists D-2-amino-5-phosphonovalerate (200 μM), 7-chlorokynurenic acid (200 μM), and MK-801 (10 μM) were added to the culture medium.

Fluorescence lifetime measurements of CFP were conducted on live HEK293 cells approximately 48 hours following transfection. The cells were replated to 33 mm poly-D-lysine-coated (0.1 mg/ml) coverslips in culture medium 1 to 2 hours before measurements. Hanks' balanced salt solution without divalent cations (GIBCO; Thermo Fisher Scientific) was used to detect cells (i.e., trypsin was not used) and the cells were allowed to recover in culture medium. Immediately before imaging, the cells were transferred to Hanks' balanced salt solution with CaCl2 and MgCl2 (GIBCO; Thermo Fisher Scientific) was used to detach cells (i.e., trypsin was not used) and the cells were allowed to recover in culture medium. Immediately before imaging, the cells were transferred to Hanks' balanced salt solution with CaCl2 and MgCl2 (GIBCO; Thermo Fisher Scientific). Confocal images were acquired using a Zeiss 880 confocal microscope (Carl Zeiss, Oberkochen, Germany) with a 63 × 1.4 Oil DIC M27 objective and an argon laser. CFP/YFP-tagged receptors were visualized using a 458-nm laser at 20% input power for CFP excitation and 514-nm laser at 15% input power for YFP excitation. CFP emission was collected between 463 and 492 nm and YFP emission was collected between 500 and 530 nm. For FRET-FLIM measurements, the cells were excited by an LDH-P-C-440 diode laser at 440 nm with a 458-nm laser at 20% input power for CFP excitation and the cells were allowed to recover in culture medium. Immediately before imaging, the cells were transferred to Hanks' balanced salt solution with CaCl2 and MgCl2 (GIBCO; Thermo Fisher Scientific). Confocal images were acquired using a Zeiss 880 confocal microscope (Carl Zeiss, Oberkochen, Germany) with a 63 × 1.4 Oil DIC M27 objective and an argon laser. CFP/YFP-tagged receptors were visualized using a 458-nm laser at 20% input power for CFP excitation and 514-nm laser at 15% input power for YFP excitation. CFP emission was collected between 463 and 492 nm and YFP emission was collected between 500 and 530 nm. For FRET-FLIM measurements, the cells were excited by an LDH-P-C-440 diode laser at 440 nm controlled by a PDL 828 Sepia II Driver (PicoQuant, West Springfield, MA). Excitation light was pulsed at a 20 MHz repetition rate through a 2T442 dichroic beam combiner (PicoQuant). Emission light was controlled by a PDL 828 Sepia II Driver (PicoQuant, West Springfield, MA). Excitation light was pulsed at a 20 MHz repetition rate through a 2T442 dichroic beam combiner (PicoQuant). Emission light was collected between 500 and 530 nm.
interest to a monoeponential function for cells expressing CFP only and a two-exponential function for cells expressing both CFP and YFP.

**Two-Electrode Voltage-Clamp Recordings.** Injection of cRNA and maintenance of *Xenopus* oocytes (purchased from Rob Weymouth at Xenopus 1, Dexter, MI) was performed as previously described (Hansen et al., 2013). For experiments with triheteromeric NMDA receptors that contain distinct GluN1 isoforms, the cRNAs encoding C1- and C2-tagged GluN1 as well as GluN2 were injected at a 1:1:1 ratio at a total volume of 50 nl, and the cRNA was diluted with RNase-free water to yield 2.5·3 ng total injected cRNA. For experiments with triheteromeric NMDA receptors that contain distinct GluN2 subunits, the cRNAs encoding GluN1 as well as C1- and C2-tagged GluN2 were injected at a 1:1:1 ratio at a total volume of 50 nl, and the cRNA was diluted with RNase-free water to yield 6 to 7 ng total injected cRNA. The injected *Xenopus* oocytes were incubated at 17°C for expression of diheteromeric NMDA receptors, but required incubation at 19°C for expression of triheteromeric NMDA receptors (Yi et al., 2017). Two-electrode voltage-clamp recordings (OC-725; Warner Instruments, Hamden, CT) were performed 2–4 days after injection at room temperature (20°C). Except for experiments involving extracellular Zn²⁺, the extracellular recording solution contained 90 mM NaCl, 1 mM KCl, 10 mM HEPES, 0.5 mM BaCl₂, and 0.01 mM EDTA (pH 7.4 with NaOH). For the Zn²⁺ experiments, the pH of the extracellular solution was 7.4 and EDTA was replaced with 10 mM tricine to buffer extracellular Zn²⁺. The pH of the extracellular solution was 7.4 and EDTA was replaced with 10 mM tricine to buffer extracellular Zn²⁺ as previously described (Traynelis et al., 1998). Recording electrodes were filled with 3.0 M KCl, and recordings were performed using a holding potential at −40 mV, unless otherwise stated and except for experiments with Zn²⁺ and spermine, in which the holding potential was −20 mV to minimize voltage-dependent channel block. For experiments with triheteromeric receptors, the fraction of current response from escaped receptors compared with the total current response was always determined on the day of the experiment, and experiments were only performed if the escape current response was <10% of the total current response.

**Whole-Cell Voltage-Clamp Recordings.** HEK293 cells were plated onto poly-D-lysine-coated (0.1 mg/ml) glass coverslips approximately 48 hours before experiments and cultured in Dulbecco's modified Eagle's medium with GlutaMax-I and sodium pyruvate (GIBCO; Thermo Fisher Scientific) supplemented with 10% dialyzed horse serum (GIBCO; Thermo Fisher Scientific), 10 U/ml penicillin, and 100 μg/ml streptomycin (GIBCO; Thermo Fisher Scientific). Cells were transfected using the calcium phosphate precipitation method with plasmid cDNAs encoding GluN1 (together with EGFP in the PC1-neo vector) and GluN2 subunits at a ratio of 1:1. For experiments with triheteromeric NMDA receptors, plasmid cDNAs encoding the two distinct GluN1 isoforms and the GluN2 subunit were transfected at 1:1:5 (1ac5/1bc2/2A) or 1:1:2 (1ac5/1bc2/2B) ratios and plasmid cDNAs encoding GluN1 and the two distinct GluN2 isoforms were transfected at a 1:2:2 ratio. To prevent NMDA receptor-mediated cytotoxicity, the antagonists D,L-2-amino-5-phosphonovalerate (200 μM) and 7-chlorokynurenic acid (200 μM) were added to the culture medium, and experiments were performed approximately 24 hours following transfection.

Whole-cell voltage-clamp recordings (Axopatch 200B; Molecular Devices, Sunnyvale, CA) were performed at room temperature (20°C) at a holding potential of −60 mV (unless otherwise stated). Recording electrodes with open-tip resistance of 2–4 MΩ were made from thin-wall glass micropipettes (TW150F-4; World Precision Instruments, Sarasota, FL) pulled using a horizontal puller (P-1000; Sutter Instruments, Novato, CA). The electrodes were filled with internal solution containing 110 mM D-glutamic acid, 130 mM CsCl, 30 mM NaCl, 5 mM HEPES, 4 mM NaCl, 0.5 mM CaCl₂, 2 mM MgCl₂, 5 mM 1,2-bis(2-aminophenoxy)ethane-N,N,N',N'-tetraacetic acid, 2 mM NaATP, and 0.3 mM NaGTP (pH 7.35 with CsOH). The extracellular recording solution was composed of 150 mM NaCl, 10 mM HEPES, 3 mM KCl, 0.5 mM CaCl₂, and 0.01 mM EDTA (pH 7.4 with NaOH). Holding potentials were not corrected for the liquid junction potential, which was measured to be ±10.1 ± 0.6 mV ($n = 4$). Rapid solution exchange was achieved on lifted cells with a two-barrel theta-glass pipette controlled by a piezoelectric translator (MXPZT-300; Siskiyou Corporation, Grants Pass, OR) and the 10%–90% open-tip solution exchange times were 0.6–0.8 ms. Only cells with current responses of less than 1000 pA and series resistance of less than 10 MΩ were used for data analyses.

**Data Analysis.** Concentration-response data were analyzed with GraphPad Prism (GraphPad Software, La Jolla, CA). Agonist concentration-response data for individual oocytes were fitted to the following Hill equation:

$$I = I_{\text{max}} \left( \frac{1 + 10^\frac{\log EC_{50} - \log (A) \cdot H}{nH}}{1 + 10^\frac{\log IC_{50} - \log (A) \cdot H}{nH}} \right)$$

where $I_{\text{max}}$ is the maximum current in response to the agonist, $A$ is the Hill slope, $(A)$ is the agonist concentration, and $EC_{50}$ is the agonist concentration that produces half-maximum response. Antagonist concentration-response data were fitted to the following equation:

$$I = I_{\text{min}} + \left( I_{\text{max}} - I_{\text{min}} \right) \left( \frac{1 + 10^\frac{\log IC_{50} - \log (A) \cdot H}{nH}}{1 + 10^\frac{\log IC_{50} - \log (A) \cdot H}{nH}} \right)^n$$

where $I_{\text{min}}$ is the minimum current in response to the agonist plus a saturating concentration of antagonist. For graphical presentation, data points from individual oocytes were normalized to the maximum current response to glutamate plus glycine in the same recording and averaged.

Whole-cell voltage-clamp recordings using HEK293 cells were analyzed using Axograph (www.axograph.com). The deactivation time courses of current responses (each averaged from at least five sweeps) were fitted using: $I_{\text{total}} = I_{\text{fast exp}}(−t/τ_{\text{fast}}) + I_{\text{slow exp}}(−t/τ_{\text{slow}})$, where $τ_{\text{fast}}$ and $τ_{\text{slow}}$ are the deactivation time constants for the fast and slow components, respectively, and $I_{\text{max}}$ and $I_{\text{min}}$ are the current amplitudes of the fast and slow components, respectively. Weighted deactivation time constants were calculated using: $τ_{\text{weighted}} = τ_{\text{fast}} \cdot I_{\text{fast}} + τ_{\text{slow}} \cdot I_{\text{slow}} / (I_{\text{fast}} + I_{\text{slow}})$. In FRET-FLIM experiments, the fluorescence decay of photon counts in the region of interest was analyzed essentially as the deactivation time course of current amplitudes using either monoeponential or two-exponential functions, and the weighted decay constants were also calculated using the aforementioned function. Data are provided as mean ± S.E.M. unless otherwise stated.

**Results.**

**Assembly of NMDA Receptors with Two Distinct GluN1 Isoforms.** To determine if GluN1-1a and GluN1-1b isoforms coassemble in NMDA receptors, we fused CFP or YFP to their extracellular amino-terminal domains. Upon coexpression with GluN2A, we identified NMDA receptors containing both CFP- and YFP-tagged subunits in the region corresponding to the surface membrane of live HEK293 (Fig. 1A). The localization of CFP- and YFP-tagged GluN1 subunits at the cell surface indicates that they are assembled with GluN2A (Monyer et al., 1992). To determine whether CFP- and YFP-tagged GluN1 subunits were assembled in the same receptor we used FLIM to quantify FRET. FRET only occurs when the donor (CFP) and acceptor (YFP) pair of fluorescent proteins are in close proximity (i.e., <10 nm) and the fluorescence lifetime of the donor is accelerated by energy transfer. The lifetime of CFP fluorescence in the absence of FRET (i.e., donor-only $τ_D$) was determined from cells coexpressing CFP-tagged GluN1-1a (CFP1a) and GluN2A using a monoeponential fit, revealing a donor-only $τ_D$ of 3.62 ns (Fig. 1; Table 1). Coexpression of CFP1a and YFP1b subunits together with GluN2A can, in theory, result in three
receptor populations, namely donor-only (τD) CFP1a/2A donor/acceptor (τDA) CFP1a/YFP1b/2A receptors, and YFP1b/2A with no CFP fluorescence. The CFP lifetime in the membrane of CFP1a/YFP1b/2A-expressing cells was analyzed using a two-exponential fit and the amplitude-weighted average lifetime (τweighted) was 3.13 ns with τD of 3.63 ns and τDA of 1.24 ns (Fig. 1; Table 1). The significant decrease in τweighted for CFP1a/YFP1b/2A-expressing cells compared with CFP1a/GluN2A-expressing cells indicates that FRET occurs as a result of coassembly of CFP1a and YFP1b subunits into CFP1a/YFP1b/2A receptors. Importantly, the amplitude of the donor/acceptor component was 21% of the donor-only component (Table 1), suggesting that a robust fraction of the NMDA receptors contained both CFP- and YFP-tagged GluN1 subunits. Similar results were obtained for cells expressing different combinations of CFP- and YFP-tagged GluN1-1a and GluN1-1b isoforms, expressing cells indicates that FRET occurs as a result of coassembly of CFP1a and YFP1b subunits into CFP1a/YFP1b/2A receptors. Importantly, the amplitude of the donor/acceptor component was 21% of the donor-only component (Table 1), suggesting that a robust fraction of the NMDA receptors contained both CFP- and YFP-tagged GluN1 subunits. Similar results were obtained for cells expressing different combinations of CFP- and YFP-tagged GluN1-1a and GluN1-1b isoforms,

**Table 1**

Detection of triheteromeric NMDA receptors using FRET-FLIM

Fluorescence lifetime of CFP in HEK293 cells expressing CFP- and YFP-tagged GluN1-1a and GluN1-1b isoforms together with GluN2A. Regions corresponding to the cell surface were selected and CFP lifetimes were analyzed with monoexponential fits for cells expressing CFP-tagged GluN1 (i.e., donor only) or two-exponential fits for cells expressing both CFP- and YFP-tagged GluN1 (i.e., donor/acceptor). The τD and τDA values represent the lifetimes for donor only and donor/acceptor, respectively; % DA is the amplitude of the donor/acceptor component relative to the donor-only component; τweighted is the weighted time constant calculated as described in Materials and Methods. FRET efficiencies (E) are calculated as 1 − (τDA/τD). Dashes indicate data not available. Data are presented as mean ± S.E.M., and n is the number of cells used to generate the data.

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<th>τD</th>
<th>τDA</th>
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<tr>
<td>CFP1a/2A</td>
<td>3.62 ± 0.01</td>
<td>—</td>
<td>—</td>
<td>3.62 ± 0.01</td>
<td>14</td>
<td>—</td>
</tr>
<tr>
<td>CFP1b/2A</td>
<td>3.60 ± 0.01</td>
<td>—</td>
<td>—</td>
<td>3.60 ± 0.01</td>
<td>9</td>
<td>—</td>
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<tr>
<td>CFP1a/YFP1b/2A</td>
<td>3.72 ± 0.02</td>
<td>1.26 ± 0.03</td>
<td>17 ± 1</td>
<td>3.29 ± 0.02*</td>
<td>16</td>
<td>0.66</td>
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<tr>
<td>CFP1b/YFP1b/2A</td>
<td>3.63 ± 0.03</td>
<td>1.24 ± 0.06</td>
<td>21 ± 1</td>
<td>3.13 ± 0.03*</td>
<td>10</td>
<td>0.66</td>
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<tr>
<td>YFP1a/CFP1b/2A</td>
<td>3.67 ± 0.02</td>
<td>1.18 ± 0.07</td>
<td>22 ± 1</td>
<td>3.10 ± 0.03*</td>
<td>10</td>
<td>0.66</td>
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<tr>
<td>YFP1b/CFP1b/2A</td>
<td>3.66 ± 0.01</td>
<td>1.24 ± 0.03</td>
<td>19 ± 1</td>
<td>3.19 ± 0.01*</td>
<td>12</td>
<td>0.66</td>
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<tr>
<td>CFP1a/2A + YFP</td>
<td>3.63 ± 0.02</td>
<td>—</td>
<td>—</td>
<td>3.63 ± 0.01</td>
<td>10</td>
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*indicates significantly different from τweighted for CFP1a/2A (P < 0.05; one-way analysis of variance with Tukey’s post hoc test). Only τweighted values were compared.

Fig. 1. Detection of triheteromeric GluN1-1a/GluN1-1b/GluN2A NMDA receptors using FRET-FLIM. (A) Images of CFP fluorescence lifetime (FLIM images) for HEK293 cells expressing combinations of GluN2A with GluN1 isoforms tagged with CFP or YFP at the amino-terminal domain. The corresponding images of fluorescence intensities for CFP and YFP emission are shown below. The pixel color corresponds to the measured CFP lifetime as indicated by the color scale. The cells were replated approximately 1 to 2 hours before measurements using Hank’s balanced salt solution without divalent cations to detach the cells. (B) Representative decays of CFP fluorescence at the cell surface of cells expressing donor and acceptor (CFP1a/YFP1b/2A) and donor only (CFP1a/2A). The decay of CFP1a/2A follows a monoexponential time course, whereas the decay of CFP1a/YFP1b/2A follows a two-exponential time course consistent with the assembly of a population of triheteromeric 1a/1b/2A receptors and FRET occurring between CFP1a and YFP1b subunits. The insets illustrate the region of interest (i.e., the cell surface membrane) used for the fluorescence lifetime measurements. (C) Summary of the weighted CFP lifetimes (i.e., weighted time constants of fluorescence decay) with the black bars indicating the CFP lifetime of donor only in CFP1a/2A and CFP1b/2A. Coassembly of CFP- and YFP-tagged GluN1 subunits is demonstrated by reduced CFP lifetimes compared with donor only. *indicates significantly different from CFP1a/2A (P < 0.05; one-way analysis of variance with Tukey’s post hoc test). Data are mean ± S.D. from 9 to 16 cells and decay time constants are shown in Table 1.
thereby demonstrating that GluN1-1a and GluN1-1b isoforms readily coassemble in GluN2A-containing NMDA receptors (Fig. 1C; Table 1). Independent on the coexpressed GluN1-1a and GluN1-1b isoforms, the fraction of donor/acceptor component relative to the donor-only component was 17%–22% and the FRET efficiency calculated from $r_D$ and $r_{DA}$ was 66%–68% (Table 1). The consistent results among the different conditions indicates a lack of preference for assembly of GluN1-1a and GluN1-1b isoforms into either 1a/1a, 1a/1b, or 1b/1b pairs, and that FRET is specific to intrareceptor interactions and unaffected by relative expression levels. To provide additional control for intrareceptor versus inter-receptor FRET, we coexpressed CFP1a/2A with YFP to fused the amino-terminal domain of the GluA2 AMPA receptor subunit (YFPGluA2). Coexpression of CFP1a/2A and YFPGluA2 did not change the lifetime of CFP fluorescence compared with cells expressing CFP1a/2A alone, consistent with a lack of inter-receptor FRET (Table 1). In summary, the FRET-FLIM experiments demonstrate that GluN1-1a and GluN1-1b isoforms readily coassemble into NMDA receptors expressed at the cell surface, albeit the functional properties of these receptors are yet to be characterized.

Selective Cell-Surface Expression of NMDA Receptors with Two Distinct GluN1 Isoforms. For expression of triheteromeric NMDA receptors containing two distinct GluN1 isoforms without accompanying coexpression of diheteromeric NMDA receptors, we adapted a method previously described for expression of triheteromeric NMDA receptors containing two distinct GluN2 subunits (Hansen et al., 2014). This method relies on engineered C-terminal peptide tags that prevent trafficking of diheteromeric NMDA receptors to the cell surface, while allowing cell-surface expression of triheteromeric NMDA receptors with a defined subunit composition. The engineered C-terminal peptide tags are composed of a peptide linker (L4) and the leucine zipper motifs from GABAB receptor subunits (LZ1 and LZ2), followed by dilyosine (KKXX) endoplasmic reticulum (ER) retention/retrieval motifs that prevent trafficking to the cell surface unless masked by heterodimeric coiled-coil formation between LZ1 and LZ2 (Hansen et al., 2014) (Fig. 2, A and B). In this study, the engineered C-terminal peptide tags (C1 and C2) are fused to the C-terminus of GluN1 isoforms, thereby enabling expression of triheteromeric NMDA receptors with a defined composition of GluN1 subunits.

To evaluate the efficiency by which the C1 and C2 tags control GluN1 subunit composition, GluN1-1aC2 (1aC2), GluN1-1bC1 (1bC1), and GluN2 subunits were initially coexpressed in Xenopus oocytes. In theory, the presence of C1 and C2 in the same receptor would mask the retention signals and exclusively allow cell-surface expression of 1aC2/1bC1/2 receptors (Fig. 2B). However, some 1aC2/1aC2/2 and 1bC1/1bC1/2 receptors may escape ER retention. To determine the functional contribution of these escaped receptors to the overall NMDA receptor-mediated currents, we generated 1aC2 and 1bC1 subunits with two mutations in the agonist binding pocket that abolish glycine binding (F484A + T518L in GluN1-1a and F505A + T539L in GluN1-1b, hereinafter denoted as FATL) and render any receptor containing these subunits nonfunctional (Kvist et al., 2013). Coexpression of 1aC2, 1bC1-FATL, and GluN2 only generates functional receptors that are escaped 1aC2/1aC2/2 receptors, while coexpression of 1aC2-FATL, 1bC1, and GluN2 only generates functional receptors that are escaped 1bC1/1bC1/2 receptors (Fig. 2C). Thus, the efficiency of selective expression of triheteromeric NMDA receptors can be assessed by determining the functional contribution of escaped receptors using the FATL mutations (Fig. 2, C–E). We determined the maximal response to saturating concentrations of glutamate + glycine from oocytes coexpressing 1aC2 + 1bC1 + GluN2 (total current), 1aC2 + 1bC1-FATL + GluN2 (escape current), and 1aC2-FATL + 1bC1 + GluN2 (escape current). On days 2–4 after cRNA injection, the fractional escape current, calculated as the sum of escape currents divided by the total current, were typically smaller than 10% (Fig. 2, D and E). This result could be reproduced using distinct GluN1 isoforms in combination with either GluN2A or GluN2B, demonstrating the efficiency of the method for expression of triheteromeric 1aC2/1bC1/2A and 1aC2/1bC1/2B NMDA receptors in Xenopus oocytes (Fig. 2E). The FATL controls would detect if C1 and C2 tags interact between receptors, rather than within one receptor as intended. For example, if 1aC2/1aC2/2 and 1bC1/1bC1/2 receptors interact via the C1 and C2 tags to enable surface expression, then this would manifest in current responses for cells coexpressing 1aC2 + 1bC1-FATL + GluN2 or 1aC2-FATL + 1bC1 + GluN2. The results also suggest that the inclusion of one copy of GluN1 with FATL mutations in the NMDA receptor is sufficient to render this receptor nonfunctional, consistent with the requirement of simultaneous agonist binding to all GluN1 and GluN2 subunits for NMDA receptor activation (Benveniste and Mayer, 1991; Clements and Westbrook, 1991).

Activation and Deactivation of Triheteromeric 1a/1b/2A and 1a/1b/2B Receptors. NMDA receptors that contain two GluN1-1a isoforms (1a/1a/2) have increased agonist potency and display slower deactivation of glutamate-activated responses compared with receptors that contain two GluN1-1b isoforms (1b/1b/2) (Przyborski et al., 2000; Rumbaugh et al., 2000; Vance et al., 2012; Swanger et al., 2015). GluN1-1b isoforms have been shown to shorten the time course of excitatory postsynaptic currents, thereby creating the possibility that neurons can tune NMDA receptor signaling by shifting the ratio of expressed GluN1-1a and GluN1-1b isoforms in a spatiotemporal manner (Przyborski et al., 2000; Rumbaugh et al., 2000; Swanger et al., 2015). However, the agonist potencies and deactivation kinetics for NMDA receptors that contain one GluN1-1a and one GluN1-1b isoform (1a/1b/2) are unresolved.

We determined glutamate and glycine potencies at 1a/1b/2A and 1a/1b/2B receptors as well as the respective diheteromeric 1a/2 and 1b/2 receptors expressed in Xenopus oocytes using two-electrode voltage-clamp recordings (Fig. 3, A and B; Table 2). Glutamate potencies were intermediate at 1aC2/1bC1/2A and 1aC2/1bC1/2B receptors compared with the respective 1a/2 and 1b/2 receptors. The same trend was observed for glycine potencies, albeit the differences between 1a/2 and 1b/2 receptors were less pronounced for glycine compared with glutamate activation (Fig. 3, E and F; Table 2). Importantly, the presence of the C1 and C2 tags did not change glutamate potencies in 1aC1/1aC2/2 and 1bC1/1bC2/2 compared with wild-type 1a/2 and 1b/2, respectively (Table 2).

To evaluate the deactivation time course of triheteromeric 1aC2/1bC1/2A and 1aC2/1bC1/2B receptors, we adapted the method for expression in HEK293 cells to enable rapid-perfusion
whole-cell patch-clamp recordings. The key requirement for fidelity of the method in HEK293 cells is to maintain a relatively low NMDA receptor expression, presumably to minimize crowding of the ER and Golgi compartments with receptors containing unmasked ER retention/retrieval signals. To achieve this, we developed DNA constructs for simultaneous low GluN1 expression and high expression of EGFP (see Materials and Methods). These constructs are useful for patch-clamp electrophysiological experiments that require low NMDA receptor expression but high EGFP expression for identification of transfected cells. We compared the deactivation time courses of 1aCX/1bC2/2A and 1aC1/1bCX/2B receptors as well as the respective diheteromeric 1a/2 and 1b/2 receptors. The weighted deactivation time constant (τw) following brief (3–5 ms) activation by 1 mM glutamate in the continuous presence of 100 μM glycine was intermediate for 1aC2/1bC1/2A (41 ms) compared with 1a/2A (49 ms) and 1b/2A (32 ms) (Fig. 3C, Table 3). The intermediate τw was also observed for glutamate deactivation of 1aC2/1bC1/2B (279 ms) compared with 1a/2B (511 ms) and 1b/2B (151 ms) (Fig. 3D; Table 3). The deactivation time course following brief (3–5 ms) activation by 100 μM glycine in the continuous presence of 1 mM glutamate was also evaluated. The τw for glycine deactivation was intermediate for 1aC2/1bC1/2A (190 ms) compared with 1a/2B (223 ms) and 1b/2A (159 ms) as well as for 1aC2/1bC1/2B (563 ms) compared with 1a/2B (748 ms) and 1b/2B (457 ms) (Fig. 3, G and H; Table 3).

In summary, these data corroborate the previously described accelerated deactivation of diheteromeric 1b/2 receptors compared with 1a/2 receptors (Rumbaugh et al., 2000; Vance et al., 2012; Swanger et al., 2015). Furthermore, the results establish that the inclusion of one copy of GluN1-1b, which includes residues encoded by exon 5, is sufficient to decrease agonist potency and to accelerate the deactivation time course, resulting in functional properties that are intermediate to those of 1a/2 and 1b/2 receptors.

1aC2/1aC2/2A and 1bC1/1bC1/2A receptors are prevented from trafficking to the cell surface due the presence of unmasked dilysine (KKXX) ER retention signals in the CTD, whereas heterodimeric coiled-coil formation between C1 and C2 tags in triheteromeric 1aC2/1bC1/2A receptors masks the ER retention signals and enable trafficking to the cell surface. Coexpression of 1aC2 and 1bC1 (as well as GluN2A or GluN2B) produced robust current responses on days 2–4 after cRNA injection, whereas current responses from 1aC2/1aC2/2 and 1bC1/1bC1/2 receptors that may have escaped ER retention remained small compared with the total currents. Data are mean ± S.D., and each bar is from six oocytes. (E) The efficiency of selective expression of NMDA receptors containing two distinct GluN1 isoforms can be assessed by determining the fractional escape current, calculated as the sum of escape currents divided by the total current, on days 2–4 after cRNA injection, whereas current responses from 1aC1/1aC2/2 and 1bC1/1bC1/2 receptors that may have escaped ER retention remained small compared with the total currents. Data are mean ± S.D., and each bar is from six oocytes. (E) The efficiency of selective expression of NMDA receptors containing two distinct GluN1 isoforms can be assessed by determining the fractional contribution of escaped receptors using the FATL mutations. The fractional escape current, calculated as the sum of escape currents divided by the total current, were always smaller than 10% on days 2–4 after cRNA injection for GluN1 isoforms in combination with either GluN2A or GluN2B. Data are mean ± S.D.
Proton Inhibition of Triheteromeric 1a/1b/2A and 1a/1b/2B Receptors. Neuronal NMDA receptors are inhibited by extracellular protons with a proton IC₅₀ near physiological pH (7.2–7.4), and can therefore respond to small changes in extracellular pH under physiological conditions (Giffard et al., 1990; Traynelis and Cull-Candy, 1990, 1991; Vyklický et al., 1990). Residues encoded by exon 5 in the GluN1 subunit attenuate proton inhibition since proton sensitivity is diminished for NMDA receptors with two copies of the GluN1-1b isoform (Traynelis et al., 1995, 1998). We examined proton inhibition of triheteromeric 1a/1b/2A and 1a/1b/2B receptors expressed in Xenopus oocytes using two-electrode voltage-clamp recordings. Proton pIC₅₀ (i.e., pH that produce 50% inhibition) was 6.70 for 1aC2/1bC1/2A, which is significantly different from both 1a/2A (6.74) and 1b/2A (6.47), and proton pIC₅₀ was intermediate for 1aC2/1bC1/2B (7.19) compared with 1a/2B (7.49) and 1b/2B (6.71) (Fig. 4, A–C; Table 4). Thus, the inclusion of one copy of GluN1-1b reduces proton inhibition, albeit this reduction is less pronounced for GluN2A-containing receptors compared with GluN2B-containing NMDA receptors.

Allosteric Inhibition of Triheteromeric 1a/1b/2A and 1a/1b/2B Receptors. Extracellular Zn²⁺ is a GluN2A-selective negative allosteric modulator with a high-affinity binding site located in the amino-terminal domain of the GluN2A subunit (Romero-Hernandez et al., 2016). Similarly, ifenprodil is a GluN2B-selective allosteric modulator, albeit this non-competitive antagonist binds with high affinity to a site located at the interface between the amino-terminal domains of the GluN1 and GluN2B subunits (Karacas et al., 2011). High-affinity inhibition by extracellular Zn²⁺ and ifenprodil appears to be mediated by a mechanism in which binding of these ligands enhances proton inhibition and thereby reduces receptor function (Pahk and Williams, 1997; Mott et al., 1998; Traynelis et al., 1998; Choi and Lipton, 1999; Erreger and Traynelis, 2008; Bhatt et al., 2013). Since residues encoded by exon 5 in the GluN1 subunit are
key determinants of proton inhibition, we evaluated inhibition of triheteromeric NMDA receptors by Zn\(^{2+}\) and ifenprodil at physiological pH 7.4. Extracellular Zn\(^{2+}\) inhibited diheteromeric 1aC2/1bC1/2A with greater potency and efficacy compared with diheteromeric 1bC1/1bC2/2A, whereas triheteromeric 1aC2/1bC1/2A was inhibited with intermediate potency and efficacy (Fig. 4D; Table 4). Extracellular Zn\(^{2+}\) up to 300 nM only minimally affected responses from GluN2B-containing NMDA receptors (Fig. 4E), consistent with the absence of a high-affinity binding site in the GluN2B amino-terminal domain (Rachline et al., 2005; Karakas et al., 2009). Ifenprodil potency was intermediate for 1aC2/1bC1/2B (143 nM) compared with 1aC2/1aC1/2B (94 nM) and 1bC2/1bC1/2B (225 nM), but maximal inhibition was unaffected by residues encoded by exon 5 in GluN1 (Fig. 4F; Table 4). These results suggest that one copy of GluN1-1b reduces inhibition of 1a/1b/2 receptors by both extracellular Zn\(^{2+}\) and ifenprodil. Intermediate inhibition of 1a/1b/2 receptors would be consistent with a mechanism of action in which proton inhibition is enhanced by extracellular Zn\(^{2+}\) and ifenprodil since 1a/1b/2 receptors display intermediate proton sensitivity (Fig. 4, A–C; Table 4).

Potentiation of Triheteromeric 1a/1b/2 Receptors by Extracellular Polyamines. Binding of extracellular polyamines, such as spermine, to GluN2B-containing NMDA receptors have been proposed to enhance receptor function by relieving proton inhibition (Traynelis et al., 1995; Kashiwagi et al., 1996, 1997; Gallagher et al., 1997). Spermine potentiation is therefore strongly influenced by residues encoded by exon 5 in GluN1, and 1a/2B receptors, which are highly sensitive to proton inhibition, are strongly potentiated by

### Table 3

<table>
<thead>
<tr>
<th>Glutamate Activation</th>
<th>EC(_{50}) (µM)</th>
<th>Hill Slope</th>
<th>n</th>
<th>EC(_{50}) (µM)</th>
<th>Hill Slope</th>
<th>n</th>
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<td>1a/2A</td>
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<td>1.86 ± 0.03#</td>
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<td>1.07 ± 0.02+</td>
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<td>1a/2B</td>
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<td>6</td>
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<tr>
<td>1aC2/1bC1/2B</td>
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<td>1.63</td>
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<td>0.29 ± 0.01</td>
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<tr>
<td>1aC2/1aC1/2B</td>
<td>1.32 ± 0.06+</td>
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<td>6</td>
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<td>1bC2/1bC1/2B</td>
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<td>1bC2/1bC1/2B</td>
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<td>1.58</td>
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<tr>
<td>1b/2B</td>
<td>2.93 ± 0.17+</td>
<td>1.52</td>
<td>6</td>
<td>0.29 ± 0.01</td>
<td>1.57</td>
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</table>

*indicates significantly different from 1a/2 and # indicates significantly different from 1b/2 (P < 0.05; one-way ANOVA with Tukey’s post hoc test).
spermine compared with 1b/2B receptors (Rumbaugh et al., 2000). We evaluated potentiation of GluN2B-containing NMDA receptors by spermine at physiological pH 7.4 and acidic pH 6.8 using two-electrode voltage-clamp recordings at a holding potential of $-20 \text{ mV}$ to minimize voltage-dependent channel block by spermine. Spermine (100 $\mu$M) potentiated responses from 1a/2B by 2.6- and 6.9-fold at pH 7.4 and 6.8, respectively (Fig. 5, A–C). Responses from 1aC2/1bC1/2B were more modestly enhanced by spermine (1.3-fold potentiation at pH 7.4 and 2.8-fold at pH 6.8), and the strong potentiation by spermine was markedly reduced at 1b/2B (0.9-fold potentiation at pH 7.4 and 1.2-fold at pH 6.8) (Fig. 5, A–C).

Concentration-response data showed that 100 $\mu$M spermine produces maximal enhancement of 1a/2B at physiological pH 7.4, whereas channel block by spermine counteracts the potentiating effect at higher concentrations (Fig. 5, D–F).

These results suggest that 1a/1b/2B receptors are potentiated by extracellular spermine despite the presence of one copy of residues encoded by exon 5 in GluN1-1b.

**Contribution of Channel Pore Residues at the N Site to Block by Extracellular Mg$^{2+}$.** We have previously described an approach to manipulate a single GluN2 subunit in NMDA receptors (Hansen et al., 2014), which has provided insight into interactions between subunits and their influence on receptor function (Sun et al., 2017). The method to manipulate only one of the two GluN1 subunits in the NMDA

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**TABLE 4**

<table>
<thead>
<tr>
<th>Proton Inhibition</th>
<th>IC$_{50}$</th>
<th>Inhibition</th>
<th>Hill Slope</th>
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<tr>
<td>pH</td>
<td>nM</td>
<td>%</td>
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<tr>
<td><strong>Zn$^{2+}$ inhibition</strong></td>
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<tr>
<td>1a/2A</td>
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<td>1b/2A</td>
<td>6.70 ± 0.01+*</td>
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<td>1bC2/1bC1/2A</td>
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<td>1.6</td>
<td>6</td>
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<tr>
<td>1b/2A</td>
<td>6.47 ± 0.01+*</td>
<td>1.7</td>
<td>4</td>
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<td><strong>Ifenprodil inhibition</strong></td>
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<tr>
<td>1a/2B</td>
<td>7.49 ± 0.01+*</td>
<td>1.5</td>
<td>4</td>
</tr>
<tr>
<td>1aC2/1aC1/2B</td>
<td>7.54 ± 0.01+*</td>
<td>1.4</td>
<td>4</td>
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<td>1bC2/1bC1/2B</td>
<td>6.83 ± 0.01+*</td>
<td>1.2</td>
<td>4</td>
</tr>
<tr>
<td>1b/2B</td>
<td>6.71 ± 0.03+*</td>
<td>1.2</td>
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*Indicates significantly different from 1a/2 and # indicates significantly different from 1b/2 ($P < 0.05$; one-way ANOVA with Tukey’s post hoc test).
receptor creates additional possibilities for experimental design in studies of receptor structure and function. To explore this idea, we evaluated the contribution of residues in the ion channel pore of GluN1 and GluN2A subunits to Ca\textsuperscript{2+} permeability and voltage-dependent block by extracellular Mg\textsuperscript{2+}.

Key determinants of channel block by Mg\textsuperscript{2+} residue at a narrow constriction of the channel pore formed by residues in the membrane reentrant loop M2 (i.e., the N site) (Burnashev et al., 1992; Wollmuth et al., 1996, 1998; Sobolevsky et al., 2002) (Fig. 6). The residue at the position of the N site is an asparagine (N) in both GluN1 and GluN2 subunits (Fig. 6C). However, the narrow constriction in GluN1/2 receptors is formed by the N site asparagine in GluN1 and the asparagine residue adjacent to the N site (i.e., N\textsubscript{+1} site) in GluN2.

We evaluated Mg\textsuperscript{2+} block of NMDA receptors with a glycine residue at the N site in either one GluN1 (N616G) or one GluN2A (N614G) subunit (1a/1aG/2A or 1a/2A/2AG receptors). Mg\textsuperscript{2+} block of these triheteromeric receptors were compared with wild-type 1a/2A and receptors with glycine residues at both N sites in either GluN1 or GluN2 subunits (1a/2A or 2A/2AG receptors).

![Fig. 5. Potentiation of triheteromeric NMDA receptors by spermine.](image)

(A and B) Representative two-electrode voltage-clamp recordings showing potentiation of GluN2B-containing NMDA receptors by extracellular spermine at pH 7.4 and 6.8. Responses were activated by 100 μM glutamate in the continuous presence of 100 μM glycine. Oocytes were voltage-clamped at −20 mV to minimize voltage-dependent channel block by spermine. (C) Summary of potentiation of GluN2B-containing NMDA receptors by 100 μM spermine at pH 7.4 and 6.8. Data are normalized to control in the absence of spermine (100%) and are shown as mean ± S.D. from six to eight oocytes. *indicates significantly different from 1a/2B at the same pH (P < 0.05; one-way analysis of variance with Tukey’s post hoc test). (D) Representative two-electrode voltage-clamp recordings showing the concentration dependence of potentiation by spermine for GluN2B-containing NMDA receptors at pH 6.8. Responses were activated by 100 μM glutamate in the continuous presence of 100 μM glycine. (E and F) Spermine concentration-response data for responses from GluN2B-containing NMDA receptors at pH 7.4 and 6.8. Data are mean ± S.D. from five to six oocytes.

![Fig. 6. Key determinants of channel permeation and block in NMDA receptor subunits.](image)

(A) Crystal structure of the GluN1/2B NMDA receptor (PDB ID 4TLM) (Lee et al., 2014). The intracellular CTD is omitted from the structure. (B) Isolated views of the M2 membrane reentrant loops from the crystal structure with residues at the N and N + 1 sites highlighted as spheres. (C) Sequence alignment of residues in the M2 membrane reentrant loops of rat, mouse, and human GluN1-1a, GluN2A, GluN2B, and GluN3A subunits with residues at the N and N + 1 sites highlighted.
The current-voltage relationship of NMDA receptor responses was determined in the absence and presence of 0.1 mM Mg$^{2+}$ using two-electrode voltage-clamp recordings (Fig. 7), and IC$_{50}$ values for Mg$^{2+}$ block were determined at holding potentials from −100 to −20 mV (Fig. 8). One copy of glycine at the N site in GluN1 diminished Mg$^{2+}$ block and significantly increased Mg$^{2+}$ IC$_{50}$ at −60 mV by 2.2-fold from 34 ± 2 μM (n = 12) at wild-type 1a/2A to 75 ± 3 μM (n = 12) at 1a/1a$^{G}$/2A (Figs. 7C and 8A; see Supplemental Table 1 for statistical tests). This effect was increased for 1a$^{G}$/2A receptors, which contain two copies of glycine at the N site; the current-voltage relationship of 1a$^{G}$/2A revealed some inward rectification under these experimental conditions, and the Mg$^{2+}$ IC$_{50}$ at −60 mV was significantly increased by 5.3-fold to 177 ± 19 μM (n = 6) at 1a$^{G}$/2A compared with wild-type 1a/2A (Figs. 7C and 8A; Supplemental Table 1). By contrast, one or two copies of glycine at the N site in GluN2A (i.e., 1a/2A/2AG and 1a2AG) were less effective at reducing Mg$^{2+}$ block; the Mg$^{2+}$ IC$_{50}$ at −60 mV was unaffected for 1a/2A/2AG (25 ± 3 μM; n = 12).
To determine the influence of pore residues at the N and N + 1 sites in GluN3 on permeation and block in GluN1/2 receptors, we evaluated Mg$^{2+}$ block of NMDA receptors with glycine-arginine (GR) residues at the N and N + 1 sites in either one GluN1 (N616G + S617R) or one GluN2A (N614G + N615R) subunit (1a/1aGR/2A or 1a/2A/2AGR receptors). These 1a/1aGR/2A or 1a/2A/2AGR receptors were designed to mimic the narrow constriction of the channel pore in triheteromeric GluN1/2/3 receptors, in which one GluN3 subunit replace either one GluN1 or one GluN2 subunit. Mg$^{2+}$ block of these triheteromeric receptors was compared with wild-type 1a/2A and receptors with substitutions in either two GluN1 or two GluN2A subunits (1aGR/2A or 1a/2AGR receptors). One copy of GR residues in GluN1 strongly diminished Mg$^{2+}$ block and significantly increased Mg$^{2+}$ IC$_{50}$ at $-60$ mV by 39-fold from 1300 ± 60 $\mu$M (n = 6) at 1aGR/2A compared with wild-type 1a/2A (Figs. 7D and 8A; Supplemental Table 1). This effect was not changed for receptors with two copies of GR residues in GluN1, since the Mg$^{2+}$ IC$_{50}$ at $-60$ mV was similarly increased by 41-fold from 1370 ± 100 $\mu$M (n = 6) at 1a/2A/2AGR compared with wild-type 1a/2A (Figs. 7D and 8A; Supplemental Table 1). One or two copies of GR residues in GluN2A (i.e., 1a/2A/2AGR and 1a/2AG) also resulted in strong reduction of Mg$^{2+}$ block; the Mg$^{2+}$ IC$_{50}$ at $-60$ mV was significantly increased by 36-fold for 1a/2A/2A/2GR (1200 ± 80 $\mu$M; n = 11) and by 700-fold for 1a/2A/2GR (23.4 ± 7.1 mV; n = 6) compared with wild-type 1a/2A (Figs. 7F and 8B; Supplemental Table 1). One copy of GR residues in GluN1 therefore reduces Mg$^{2+}$ block to virtually the same extent as two copies, whereas one copy of GR residues in GluN2A produces a lower reduction of Mg$^{2+}$ block compared with two copies. Thus, these results further highlight the asymmetric contribution of pore residues in GluN1 and GluN2A to channel block. In addition, these results demonstrate that a single copy of pore residues from GluN3 subunits strongly attenuates Mg$^{2+}$ block of NMDA receptors, independently of whether the residues are introduced to one GluN1 or one GluN2 subunit.

**Contribution of Channel Pore Residues to Ca$^{2+}$ Permeability.** We also determined the impact of G and GR mutations at the N and N + 1 sites on Ca$^{2+}$ permeability of NMDA receptors expressed in HEK293 cells using whole-cell patch-clamp recordings. We determined the current-voltage relationships of responses activated by 100 $\mu$M glutamate plus 100 $\mu$M glycine in the presence of 0.5 or 10 mM external Ca$^{2+}$, since the change in reversal potential ($\Delta$E$_{rev}$) is dependent on Ca$^{2+}$ permeability (Fig. 9, A and B). The reversal potential increases by 7.5 ± 0.8 mV (n = 6) for wild-type 1a/2A receptors when external Ca$^{2+}$ is increased from 0.5 to 10 mM, consistent with high Ca$^{2+}$ permeability (Fig. 9, C and D). However, the response amplitude of wild-type 1a/2A is inhibited in high external Ca$^{2+}$ (Fig. 9, A and B), consistent previous observations from single-channel recordings of a Ca$^{2+}$-dependent decrease in channel conductance (PREM, 1996; WYLIE, et al., 1996; PREMKUMAR, et al., 1997; DRAVID, et al., 2008). Glycine at the N site in GluN1 has no effects on $\Delta$E$_{rev}$ for 1a/1a/2A (7.5 ± 0.8 mV; n = 10) and 1a/2AG (7.6 ± 0.6 mV; n = 10) compared with wild-type 1a/2A, suggesting that Ca$^{2+}$ permeability is unchanged. Glycine at the N site in GluN2A increases $\Delta$E$_{rev}$ for 1a/1a/2AG (9.9 ± 1.1 mV; n = 5) and 1a/2AG (9.0 ± 0.5 mV; n = 6), suggesting that the Ca$^{2+}$ permeability is increased (Fig. 9D). By contrast, GR residues in GluN1 results
GluN2A appear to result in a stronger reduction in Ca\(^{2+}\) permeability compared with one copy. Similar to the effects in Mg\(^{2+}\) block, a single copy of pore residues from GluN3 virtually abolishes Ca\(^{2+}\) permeability of NMDA receptors, independently of whether the residues are introduced to one GluN1 or one GluN2 subunit.

**Discussion**

We demonstrate that GluN1-1a and GluN1-1b isoforms can form functional triheteromeric 1a/1b/2A and 1a/1b/2B receptors and describe a method for selective expression of recombinant NMDA receptors containing two different GluN1 isoforms in *Xenopus* oocytes and HEK293 cells. We reveal intermediate deactivation kinetics and pharmacological properties of 1a/1b/2A and 1a/1b/2B receptors compared with the respective diheteromeric NMDA receptor subtypes. The intermediate properties of triheteromeric NMDA receptors with two distinct GluN1 isoforms contrast the dominant effect of GluN2A on the function of triheteromeric GluN1/2A/2B receptors (Tovar et al., 2013; Hansen et al., 2014; Sun et al., 2017), which account for a large portion of NMDA receptors in the adult cortex and hippocampus (Sheng et al., 1994; Luo et al., 1997; Rauner and Köhr, 2011). During development of the CNS, the prevalence of diheteromeric GluN1/2B receptors with slow deactivation kinetics is decreased due to increased expression of GluN2A and increased assembly of triheteromeric GluN1/2A/2B receptors with faster deactivation kinetics. This developmental shift in subunit composition from GluN1/2B to GluN2A-containing receptors therefore accelerates NMDA receptor-mediated synaptic currents. Triheteromeric NMDA receptors containing other combinations of GluN2 subunits, such as GluN1/2A/2C and GluN1/2B/2D, are also widely expressed in the CNS (Chazot et al., 1994; Cathala et al., 2000; Piña-Crespo and Gibb, 2002; Brickley et al., 2003; Jones and Gibb, 2005; Brothwell et al., 2008; Swanger et al., 2015; Perszyk et al., 2016). The intermediate properties of triheteromeric NMDA receptors containing two different GluN1 isoforms create the possibility that neurons can also tune NMDA receptor signaling by shifting the ratio of expressed GluN1-1a and GluN1-1b isoforms.

In addition to enabling functional evaluation of triheteromeric NMDA receptor subtypes, the method to control subunit composition also provides the ability to introduce mutations in a single subunit. To demonstrate this, we evaluated the contribution of channel pore residues to Mg\(^{2+}\) block and Ca\(^{2+}\) permeability. We introduced a glycine substitution at the N site of one GluN1-1a (a \(1^a\)) or one GluN2A (2A\(^G\)) subunit in triheteromeric 1a/1a\(^G\)/2A and 1a/2A/2A\(^G\) receptors and compared the properties of these receptors to those of wild-type 1a/2A and receptors with substitutions in both GluN1 (1a/1b/2A) or both GluN2A (1a/2A/2A\(^G\)) subunits. This approach to control the mutation copy number (or mutation dosage) clearly exposed the previously described asymmetric contribution of N site residues in GluN1 and GluN2 to Mg\(^{2+}\) block (Burnashev et al., 1992; Wollmuth et al., 1996, 1998; Sobolevsky et al., 2002). This asymmetric contribution would have been less discernable if only diheteromeric 1a/1b/2A and 1a/2A\(^G\) receptors were compared with wild-type 1a/2A receptors. In addition, we demonstrate that a single copy of pore residues from GluN3 subunits provides strong relief of Mg\(^{2+}\) block and abolishes Ca\(^{2+}\) permeability, independent of whether the GluN3...
and discussions.

at University of Montana for the use of equipment, critical comments, distance and the staff in the BioSpectroscopy Core Research Laboratory

residues are introduced into one GluN1 or one GluN2 subunit in the GluN1/2 receptor. There is currently a lack of published evidence to show whether GluN3 substitutes one GluN1 or one GluN2 subunit to form triheteromeric GluN1/2/3 receptors and these findings do not distinguish between the two potential subunit stoichiometries. However, the findings provide, for the first time, important clues to permeation and block of putative triheteromeric GluN1/2/3 receptors, which have not yet been functionally characterized as a homogenous receptor population in heterologous or native expression systems. Thus, examination of functional receptor properties and mutation copy number (0, 1, or 2 mutations) can reveal important new insights to structure-function relationships of NMDA receptors.

The approach to control the mutation copy number provides a powerful tool to determine the functional impact of disease-related de novo mutations identified in NMDA receptor subunits of patients with neurological conditions (reviewed in Burnashev and Szepetowski, 2015; Yuan et al., 2015; Hu et al., 2016). These patients are heterozygous for the disease-related de novo mutation and only a fraction of their NMDA receptors will possess two copies of the mutation, whereas a larger fraction presumably will have only one copy of the mutation. Here, we provide an approach to evaluate the relationship between NMDA receptor function and the copy number of GluN1 mutations. Understanding such relationships could be useful to rationalize the link between de novo GluN1 mutations and symptoms in various neurological conditions.

In summary, we reveal additional complexity in NMDA receptor signaling created from diversity in subunit composition by demonstrating that coexpression of GluN1-1a and GluN1-1b results in the formation of functional triheteromeric receptors with properties intermediate to those of the respective diheteromeric NMDA receptors. This new insight suggests a mechanism by which neurons could tune NMDA receptor signaling by shifting the ratio of expressed GluN1-1a and GluN1-1b isoforms, although evidence for expression of NMDA receptors containing two distinct GluN1 isoforms in vivo is currently lacking. We describe a method to selectively express triheteromeric NMDA receptors containing two distinct GluN1 isoforms in heterologous expression systems, which can enable new studies on receptor structure and function, mechanisms of allosteric modulation, and functional consequences of GluN1 mutations. This work expands the repertoire of innovative approaches to study NMDA receptors, thereby facilitating new discoveries related to NMDA receptor signaling in key brain functions as well as in CNS disorders.

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Authorship Contributions

Participated in research design: Yi, Zachariassen, Dorsett, Hansen. Conducted experiments: Yi, Zachariassen, Dorsett, Hansen. Performed data analysis: Yi, Zachariassen, Dorsett, Hansen. Wrote or contributed to the writing of the manuscript: Yi, Zachariassen, Dorsett, Hansen.

References


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Kvist T, Greenwood JR, Hansen KB, Traynelis SF, and Bräuner-Osborne H (2013) Characterization and comparison of the NR3B subunit of the NMDA receptor in recombinant systems and primary cortical neu-


Properties of triheteromeric NMDA receptors containing two distinct GluN1 isoforms

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MOLECULAR PHARMACOLOGY
SUPPLEMENTAL DATA
Supplemental Table 1. Concentration-inhibition data for extracellular Mg\textsuperscript{2+} at wild type and mutant GluN1-1a/2A NMDA receptors.

<table>
<thead>
<tr>
<th></th>
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<tr>
<td></td>
<td>IC\textsubscript{50} (µM)</td>
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<td>IC\textsubscript{50} (µM)</td>
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<td>1a/2A</td>
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<tr>
<td>1a/1a\textsuperscript{G}/2A</td>
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<td>12</td>
<td>0.043 ± 0.001*</td>
<td>12</td>
<td>0.075 ± 0.002*</td>
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<td>0.217 ± 0.009</td>
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<td>1a\textsuperscript{G}/2A</td>
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<td>6</td>
<td>0.159 ± 0.023*#</td>
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<td>0.177 ± 0.019*#</td>
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<td>0.397 ± 0.061*</td>
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<tr>
<td>1a/1a\textsuperscript{G}/2A</td>
<td>0.285 ± 0.013*</td>
<td>6</td>
<td>0.611 ± 0.029*</td>
<td>6</td>
<td>1.30 ± 0.06*</td>
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<td>2.19 ± 0.09*</td>
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<td>1a\textsuperscript{G}/2A</td>
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<td>1.37 ± 0.10*</td>
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<td>1.97 ± 0.19*</td>
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<tr>
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<td>1.20 ± 0.08*</td>
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<td>2.87 ± 0.27*</td>
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<tr>
<td>1a/2A\textsuperscript{G}</td>
<td>5.44 ± 0.36*#</td>
<td>6</td>
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<td>23.37 ± 7.12*#</td>
<td>6</td>
<td>25.6 ± 11.3*#</td>
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Data were measured using two-electrode voltage-clamp recordings of responses from recombinant NMDA receptors expressed in *Xenopus* oocytes. Responses were activated by 100 µM glutamate plus 100 µM glycine and inhibited by increasing concentrations of extracellular Mg\textsuperscript{2+} at the indicated holding potentials (-100 to -20 mV). Data are mean ± SEM, and n is the number of oocytes. * indicates significantly different from wild type 1a/2A at the same holding potential, and # indicates that two copies a mutation (e.g. 1a\textsuperscript{G}/2A) is significantly different from one copy of the same mutation (e.g. 1a/1a\textsuperscript{G}/2A) at the same holding potential (P < 0.05; one-way ANOVA with Tukey’s post hoc test). Statistical tests were performed using logIC\textsubscript{50} values. ND indicates not determined.