



Voltage-Dependent Inhibition of Glycine Receptor Channels by Niflumic Acid

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Niflumic acid (NFA) is a member of the fenamate class of nonsteroidal anti-inflammatory drugs. This compound and its derivatives are used worldwide clinically for the relief of chronic and acute pain. NFA is also a commonly used blocker of voltage-gated chloride channels. Here we present evidence that NFA is an efficient blocker of chloride-permeable glycine receptors (GlyRs) with subunit heterogeneity of action. Using the whole-cell configuration of patch-clamp recordings and molecular modeling, we analyzed the action of NFA on homomeric $\alpha 1\Delta$ Ins, $\alpha 2B$, $\alpha 3L$, and heteromeric $\alpha 1\beta$ and $\alpha 2\beta$ GlyRs expressed in CHO cells. NFA inhibited glycine-induced currents in a voltage-dependent manner and its blocking potency in $\alpha 2$ and $\alpha 3$ GlyRs was higher than that in $\alpha 1$ GlyR. The Woodhull analysis suggests that NFA blocks $\alpha 1$ and $\alpha 2$ GlyRs at the fractional electrical distances of 0.16 and 0.65 from the external membrane surface, respectively. Thus, NFA binding site in $\alpha 1$ GlyR is closer to the external part of the membrane, while in $\alpha 2$ GlyR it is significantly deeper in the pore. Mutation G254A at the cytoplasmic part of the $\alpha 1$ GlyR pore-lining TM2 helix (level 2') increased the NFA blocking potency, while incorporation of the β subunit did not have a significant effect. The Hill plot analysis suggests that $\alpha 1$ and $\alpha 2$ GlyRs are preferably blocked by two and one NFA molecules, respectively. Molecular modeling using Monte Carlo energy minimizations provides the structural rationale for the experimental data and proposes more than one interaction site along the pore where NFA can suppress the ion permeation.

Keywords: chloride-permeable channels, patch-clamp recordings, cys-loop receptors, Woodhull analysis, Monte Carlo energy minimizations

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INTRODUCTION

The main inhibitory drive in mammalian CNS is provided by chloride (Cl^-)-permeable GABA_A- and glycine receptors (GlyRs) (Sigel and Steinmann, 2012; Lynagh and Pless, 2014). These transmembrane proteins belong to the superfamily of pentameric Cys-loop ligand-gated channels, which also includes cation-selective nicotinic acetylcholine receptor and serotonin type3 receptor (Betz, 1990; Miller and Smart, 2010). GlyRs are predominantly expressed in the spinal cord

Abbreviations: CNS, central nervous system; cry-EM, cryoelectron microscopy; GlyR, Glycine Receptor; NFA, Niflumic acid, MC, Monte Carlo; MCM, Monte Carlo energy minimization; MP, membrane potential; V_{hold} , holding potential.

(Young and Snyder, 1973), in the brain stem (Frostholm and Rotter, 1985; Probst et al., 1986), cerebellum (Garcia-Alcocer et al., 2008), other higher brain regions (Bristow et al., 1986), and in retina (Haverkamp et al., 2003). Functionally GlyRs participate in the movement control, perception of visual, acoustic and sensory signals and pain sensation (Harvey et al., 2004; Betz and Laube, 2006). Dysfunction of these receptors is associated with hyperekplexia and temporal lobe seizures accompanied by memory deficits (Lynch, 2009; Schaefer et al., 2012; Zuliani et al., 2014). In the nervous system of vertebrates, molecular cloning identified four genes encoding alpha ($\alpha 1$ – $\alpha 4$) subunits and one single gene encoding beta GlyR subunits (Grenningloh et al., 1987, 1990; rev. Dutertre et al., 2012). These subunits assemble to form homopentameric α GlyRs and heteropentameric α/β GlyRs (Lynch, 2004).

Niflumic acid (NFA) (**Figure 1**) is a member of the fenamate class of nonsteroidal anti-inflammatory drugs originally developed for the treatment of rheumatic disorders. This drug and its derivatives are used worldwide clinically for the relief of chronic and acute pain conditions (Vincent et al., 1999; Kang et al., 2008; Cremonesi and Cavalieri, 2015). As a compound with anti-inflammatory, antipyretic, and analgesic therapeutic activity, NFA has been successfully used in clinical trials in adults (Sauvage et al., 1990; Mero et al., 2013) and children (Manach and Ditisheim, 1990; Lantz et al., 1994; Sturkenboom et al., 2005). The primary mechanism of NFA action is the inhibition of enzymes involved in the synthesis of proinflammatory prostaglandins (Smith, 1992; McCarberg and Gibofsky, 2012): cyclooxygenase (prostaglandin synthase) (Barnett et al., 1994;

Johnson et al., 1995) and phospholipase A2 (PLA₂) (Jabeen et al., 2005). The structure of the complex of PLA₂ with NFA has been determined at the 2.5 Å resolution revealing residues in the substrate-binding hydrophobic channel of the enzyme (Jabeen et al., 2005).

NFA is also known as a modulator, mainly inhibitor, of different types of anion-permeable channels. However, mechanism of its action on these proteins remains unclear. NFA blocks voltage-gated chloride channels, CLC-1 (Liantonio et al., 2007), as well as Ca²⁺-activated Cl⁻ channels (CaCCs) (White and Aylwin, 1990; Yang et al., 2008; Huanosta-Gutierrez et al., 2014). The effect of NFA on CaCCs is voltage-independent and it blocks the channels when applied from either outside or inside the cell (Qu and Hartzell, 2001). A recent study demonstrated the voltage-independence of NFA action on TMEM16A-encoded CaCCs but did not determine the site of its action, suggesting the pore-blocking or/and allosteric mechanisms (Ni et al., 2014).

A synthetic peptide corresponding to the TM2 transmembrane helix of GlyR forms functional ion channels in lipid bilayer, which can be blocked by NFA (Reddy et al., 1993). However, electrophysiological analysis on cells and subunit specificity of this interaction were not performed.

The aim of this study was to clarify the molecular mechanism of NFA action on GlyRs. We expressed GlyRs in different subunit combinations in CHO cells and recorded glycine-induced ionic currents under NFA application using the patch-clamp technique. The NFA action at different concentrations and membrane potentials in homomeric GlyRs (formed by $\alpha 1$ – $\alpha 3$ subunits) and heteromeric GlyRs (formed by $\alpha 1\beta$ or $\alpha 2\beta$ subunits) were analyzed. We found that the apparent NFA affinity, the voltage-dependence and the depth of its binding in the membrane strongly depend on the GlyR subunit composition, which possess different TM2 transmembrane helices.

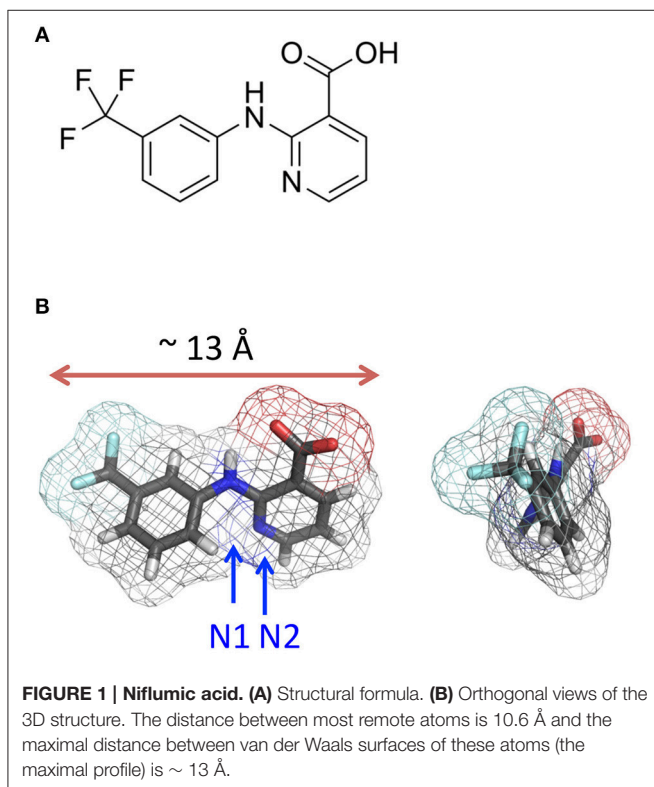
We further used molecular modeling with Monte Carlo energy minimizations to compute energy profile of NFA in the pore of $\alpha 1$ and $\alpha 2$ GlyRs. The calculations suggest that NFA can bind at more than one site within the pore. Based on our experimental data, suggesting that two and one NFA molecules block ion permeation through $\alpha 1$ GlyR and $\alpha 2$ GlyR channels, respectively, we elaborated models of NFA-bound $\alpha 1$ and $\alpha 2$ GlyRs.

MATERIALS AND METHODS

Cell Culture and Transfection

The experiments were carried out on cultured Chinese hamster ovary (CHO) cells obtained from the American Type Tissue Culture Collection (ATCC, Molsheim, France) that were maintained in culture conditions as previously described (Mukhtarov et al., 2013; Maleeva et al., 2015).

For electrophysiological analysis cells were transfected with cDNAs of different subunits of glycine receptor ($\alpha 1\Delta$ Ins, $\alpha 2B$, $\alpha 3L$, $\alpha 1$ -G254A, and β). One day before transfection, cells were plated on the cover slips (12 mm in diameter) and placed inside 35-mm cell culture dishes with 2 ml of medium. Transfection was performed using the Lipofectamine 3000 protocol (Life



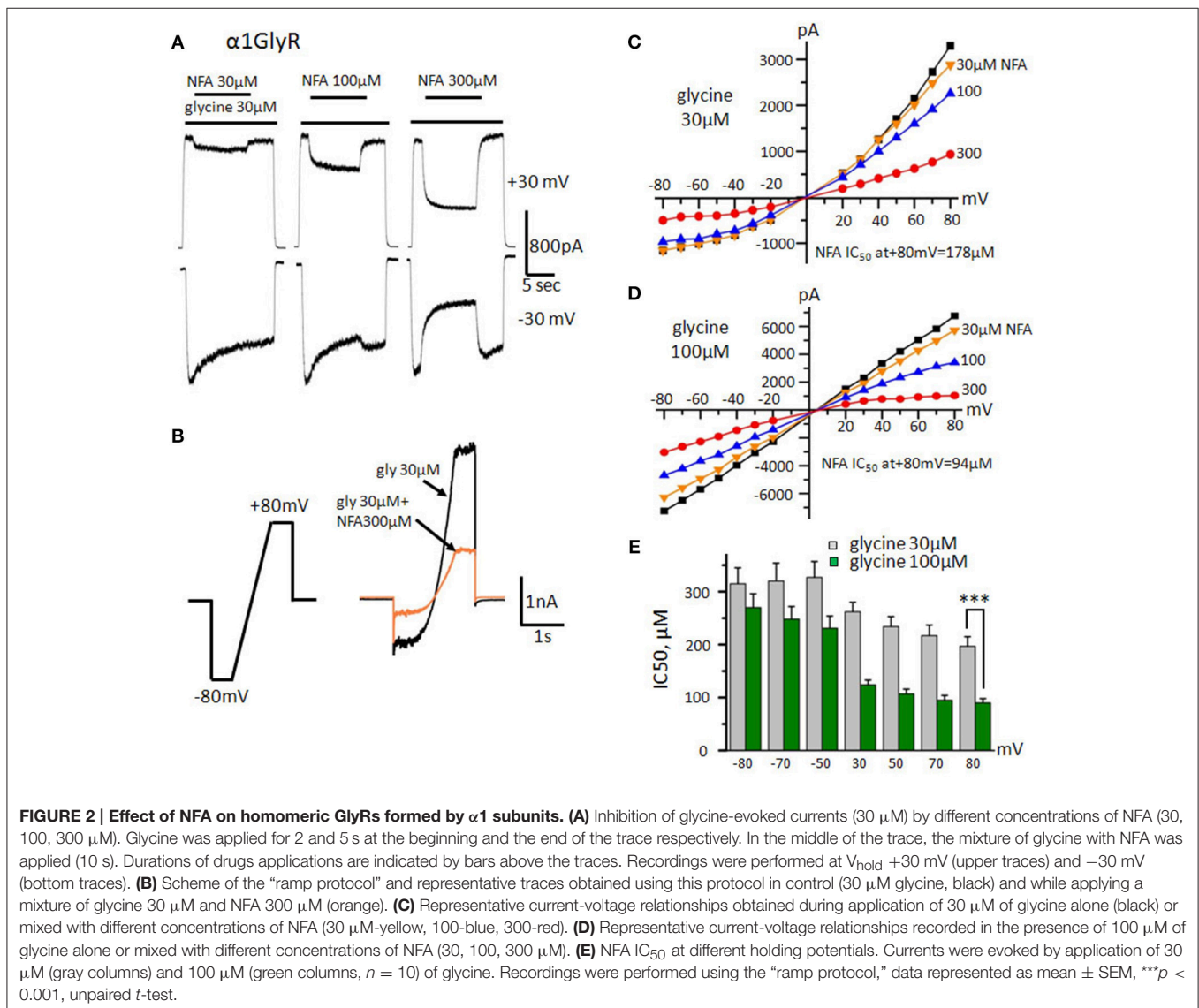
Technology, USA). To facilitate identification of transfected cells a green fluorescent protein (GFP) was added to the transfection mixture. For expression of functional heteromeric receptors, cells were simultaneously transfected with cDNAs of α and β subunits in the ratio 1:10. Three hours after the initial exposure of cells to the cDNAs the culture medium was replaced with that containing strychnine (1 μ M), which prevents spontaneous activation of GlyRs. Electrophysiological recordings were performed in the fluorescent cells 24–72 h after transfection.

Electrophysiological Recordings

Whole-cell and outside-out recordings were performed at room temperature (20–25°C) using an EPC-9 amplifier (HEKA Elektronik, Germany). Cells were continuously superfused with external solution containing (mM): NaCl 140, CaCl₂ 2, KCl 2.8, MgCl₂ 4, HEPES 20, glucose 10; pH 7.4; 320–330 mOsm. Intracellular solution used for filling recording patch pipettes

contained (mM): CsCl 140, CaCl₂ 6, MgCl₂ 2, MgATP 2, NaGTP 0.4, HEPES/CsOH 10, BAPTA (tetrapotassium salt) 2; pH 7.3; 290 mOsm. Two different protocols of solutions application were used in this study. A “long protocol” was designed to obtain recordings of current induced by subsequent application of glycine (2 s)/glycine+NFA (10 s)/glycine (5 s) on the same trace; holding potential (V_{hold}) was fixed at -30 or $+30$ mV. A “ramp protocol” implies the gradual change of V_{hold} alternately from -80 to $+80$ mV and from $+80$ to -80 mV during 1 s, V_{hold} was fixed at -80 or $+80$ mV at the beginning and at the end of the ramp for 500 ms (Figure 2B).

Nonsaturating and subsaturating concentrations of glycine for different subunit combinations of GlyRs were chosen according to the EC₅₀ curves obtained in previous studies. It was shown that for homomeric $\alpha 1$ GlyRs EC₅₀ varies between 25 and 40 μ M (Zhang et al., 2008; Lynagh et al., 2011; Maleeva et al., 2015), thus nonsaturating concentration of the agonist used for



$\alpha 1$ GlyRs was 30 μM , subsaturating – 100 μM . For $\alpha 2$ GlyRs mean value of EC_{50} for glycine was estimated as $42 \pm 2 \mu\text{M}$ (Maleeva et al., 2015), i.e., close to that for $\alpha 1$ GlyRs, so subsaturating concentrations of glycine were the same as for $\alpha 1$ GlyRs. The sensitivity of $\alpha 3$ GlyRs to glycine is significantly lower than of $\alpha 1$ and $\alpha 2$ GlyRs, comprising 80–150 μM (Zhang et al., 2008; Maleeva et al., 2015; Sánchez et al., 2015); according to this we used 100 μM of glycine as nonsaturating concentration of the agonist. Sensitivity of $\alpha 1\beta$ GlyRs is close to that of homomeric $\alpha 1$ GlyRs, i.e., between 25 and 50 μM (Rundstrom et al., 1994; Shan et al., 2001; Islam and Lynch, 2012); EC_{50} of $\alpha 2\beta$ GlyRs varies between 50 and 85 μM (Pribilla et al., 1992; Miller et al., 2005; Zhang et al., 2008). It was demonstrated previously (Shan et al., 2001; Islam and Lynch, 2012) and confirmed by our experiments that mutation G254A does not change sensitivity of $\alpha 1$ GlyRs to glycine.

Recording pipettes were pulled from borosilicate glass capillaries (Harvard Apparatus Ltd, USA) and had resistances of 5–10 M Ω . For the rapid replacement of the solutions, the fast application system was used. Three parallel rectangular tubes (100 \times 100 μm) were positioned 40–50 μm above the recorded cell. The movement of the tubes was controlled by a computer-driven fast exchange system (SF 77A Perfusion Fast-Step, Warner, USA) allowing a 10–90% solution exchange in 3–5 ms, as measured by open electrode controls (1/10 external solution/water). Cells with low input resistance (<150 M Ω) and a rapid run-down (>30% with repetitive application) were excluded from analysis.

Drugs

All the drugs were obtained from Tocris or Sigma–Aldrich (France). NFA (100 mM) and picrotoxin (50 mM) were first dissolved in DMSO and then diluted with the extracellular solution to the final concentrations. In the test experiments, DMSO itself had no effect on the glycine-induced current (data not shown; see also Mascia et al., 1996; Hall et al., 2004). A stock solution of glycine (1M) was prepared using MilliQ water.

Data Analysis and Statistics

Electrophysiological recordings were performed using PatchMaster (HEKA Electronic, Germany) software. To plot concentration-response curves, responses to different concentrations of glycine and NFA were fitted using a nonlinear fitting routine of the Origin 7.5 software (OriginLabs, USA) with the Hill equation:

$$\text{For glycine: } I = I_{\text{max}} / (1 + (\text{EC}_{50} / [\text{A}])^{n_H})$$

$$\text{For NFA: } I = I_{\text{max}} / (1 + ([\text{inh}] / \text{IC}_{50})^{n_H})$$

where I is the normalized current amplitude induced by the agonist at concentration $[\text{A}]$, $[\text{inh}]$ – concentration of NFA, I_{max} is a maximal current induced at given cell, n_H is the Hill coefficient and EC_{50} or IC_{50} are the concentrations at which a half-maximum response was induced.

The fractional electrical distance from the external side of the membrane (δ) at which bound NFA blocked the current was

calculated using the Woodhull equation:

$$\text{IC}_{50}(V) = \text{IC}_{50}(0) \exp(-\delta FV/RT),$$

where $\text{IC}_{50}(V)$ is IC_{50} at the given membrane potential, $\text{IC}_{50}(0)$ – at 0 mV, V – membrane potential and F , R , T have their usual meanings. δ was determined from a plot of IC_{50} values against membrane potential.

For statistical analysis paired and unpaired t -tests were used. Data are represented as means \pm SEM.

Molecular Modeling

General Features of the Model

The cryo-EM structure of the open state $\alpha 1$ GlyR (Du et al., 2015) (PDB code 3JAE) was used to create models of transmembrane parts of $\alpha 1$ and $\alpha 2$ GlyR channels and explore interactions of NFA with these models. We removed the extracellular region and focused on the central pore region, which is lined by five M2 helices. In the $\alpha 2$ GlyR model, five Gly254 residues at level 2' were replaced with alanines. Each model also included 10 M1 and M3 helices. The 15-helix bundles of $\alpha 1$ and $\alpha 2$ GlyRs were optimized using the ZMM program (<http://www.zmmsoft.com>) and the Monte Carlo energy-minimization (MCM) protocol (Li and Scheraga, 1987) as described elsewhere (Bruhova et al., 2008; Garden and Zhorov, 2010). Molecular images were created using the PyMol Molecular Graphics System, Version 0.99rc6 (Schrödinger, LLC, New York, NY).

Niflumic Acid Geometry

In the X-ray structures of free NFA (Murthy and Vijayan, 1978) the molecule is virtually planar. In the available X-ray structures of proteins with NFA (Jabeen et al., 2005) (PDB codes 1TD7 and 2WM3) it is also nearly planar. We have built the ligand using a 2-fold torsional potential for the Ph-COO bond (benzoic acid) with the barrier height of 3 kcal/mol and minima at 90 and -90° (Lautenschlager and Brickmann, 1991). NFA adopted a nearly planar conformation with the intramolecular H-bond NH—O (Figure 1).

Pulling NFA through the Pore

The interaction energy of NFA with the channel was computed as in Bruhova and Zhorov (2010). We pulled NFA from the cytoplasmic side to the extracellular side of the pore starting from the level below $-2'$ (Pro250) to level $20'$ (Ala/Gly272) with the step of 0.5 Å. At each step, the nitrogen atom located between two rings of NFA (N1) was constrained to the plane, which is normal to the pore axis and crosses the axis at this level. To prevent “escape” of NFA from the pore, another constraint was used that allowed atom N1 to deviate up to 6 Å from the pore axis and imposed an energy penalty for larger deviations. At each level of the pore, the energy was MC-minimized until 100 consecutive energy minimizations did not decrease the best energy found at this level. To preclude large deviations of the model backbones from the X-ray templates and thus preserve the channel folding during docking of flexible ligand to the flexible protein, a set of distance constraints (pins), was imposed between matching alpha carbons in the X-ray structure and in the model. A pin constraint is a flat-bottom parabolic energy function that allows

an atom (in this study, an alpha carbon) to deviate penalty-free up to 1 Å from the template and imposes a penalty of 10 kcal mol⁻¹ Å⁻¹ for larger deviations. The MC-minimization protocol optimized the system energy that included the penalty energy. In every MC-minimized structure, the energy of constraints was close to zero indicating that the ligand binding did not affect the protein folding in our models.

RESULTS

Action of Niflumic Acid on $\alpha 1$ GlyRs

The NFA ability to modulate currents in different GlyR subtypes was determined using a whole-cell configuration of patch-clamp technique. GlyRs composed of different subunits were transiently expressed in the CHO cell line. First, we have examined the effect of varying concentrations of NFA on homomeric $\alpha 1$ GlyR at constant holding membrane potentials (V_{hold}) of +30 and -30 mV using a “long” protocol of solutions application. Ionic currents were evoked by 30 μM of glycine alone (near EC_{50} concentration for $\alpha 1$ and $\alpha 2$ GlyRs, Maleeva et al., 2015) or mixed with different NFA concentrations. The inhibition was more pronounced at positive membrane potentials (Figure 2A). Thus, at V_{hold} of -30 mV, concentrations of NFA 30, 100 and 300 μM caused inhibition of $\alpha 1$ GlyR-mediated currents by 3 ± 4 , 16 ± 6 , and $48 \pm 9\%$, respectively ($n = 7$), while at V_{hold} of +30 mV currents were inhibited by 16 ± 7 , 43 ± 11 , and $75 \pm 4\%$, respectively ($n = 7$).

To examine in detail the voltage dependence of GlyR block by NFA we have used a “ramp” protocol that allowed fast changes of the membrane potential from -80 to +80 mV (Figure 2B). Representative current-voltage dependence curves recorded during application of glycine alone or mixed with different concentrations of NFA are shown in Figure 2C. Glycine concentration of 30 μM (near EC_{50}) produced an outwardly rectifying current due to the higher probability of the open-state $\alpha 1$ GlyR at positive potentials (Fucile et al., 1999). While NFA exhibited rather low affinity to $\alpha 1$ GlyR, especially at negative potentials, we have revealed significant ($p < 0.01$) voltage dependence of inhibition. Figure 2E shows that at -80 mV IC_{50} of NFA was $315 \pm 30 \mu\text{M}$, while at +80 mV it was $197 \pm 18 \mu\text{M}$ ($n = 10$). The voltage dependence of inhibition suggests that NFA acts as an open channel blocker of $\alpha 1$ GlyRs.

To test this hypothesis we performed the same experiment with higher, near-saturating concentration of glycine (100 μM) that causes longer mean open time of GlyR channels. The potency of the channel block by NFA increased, particularly at positive potentials ($p < 0.001$). IC_{50} of NFA at -80 mV was $270 \pm 26 \mu\text{M}$, while at +80 mV about 3-fold decrease was observed: $IC_{50} = 90 \pm 8 \mu\text{M}$ ($n = 10$) (Figures 2D,E). These results provide additional support to the suggestion that NFA inhibits $\alpha 1$ GlyR currents as an open channel blocker.

Action of Niflumic Acid on $\alpha 2$ GlyRs

Analysis of NFA action on $\alpha 2$ GlyR revealed two important peculiarities. Firstly, its inhibitory activity was much higher in comparison with that on $\alpha 1$ GlyR. Secondly, the voltage-dependence of inhibition was much more profound. Using a

“long application” protocol we have demonstrated that NFA concentration as small as 10 μM inhibited currents by $\sim 50\%$ at MP of +30 mV (Figure 3A). The voltage dependence of $\alpha 2$ GlyR inhibition by NFA (10 μM) was also prominent: at MP = -80 mV glycine-evoked current comprised $89 \pm 4\%$ from the control, while at +80 mV it was as small as $43 \pm 5\%$ ($n = 5$) (Figure 3B).

To study in detail the voltage dependence of $\alpha 2$ GlyR block by NFA, we have used the same “ramp” protocol as we did for $\alpha 1$ GlyR. Unlike in $\alpha 1$ GlyRs, activation of $\alpha 2$ GlyRs by nonsaturating agonist concentration (30 μM) produced inwardly rectifying currents, suggesting that the open probability of $\alpha 2$ GlyR channel is higher at negative potentials. Another peculiarity of NFA action on $\alpha 2$ GlyRs was the strong voltage dependence of inhibition (Figure 3C). Thus, at -80 mV IC_{50} of NFA was $166 \pm 28 \mu\text{M}$, while at +80 mV it decreased nearly 20 times, to $9 \pm 2 \mu\text{M}$ ($n = 8$). Contrary to $\alpha 1$ GlyRs, the potency of NFA block did not increase further with elevation of glycine concentration (Figure 3D; $p > 0.05$). Currents induced by 100 μM of glycine were inhibited by NFA with IC_{50} of $133 \pm 20 \mu\text{M}$ at -80 mV and $9 \pm 2 \mu\text{M}$ at +80 mV ($n = 7$).

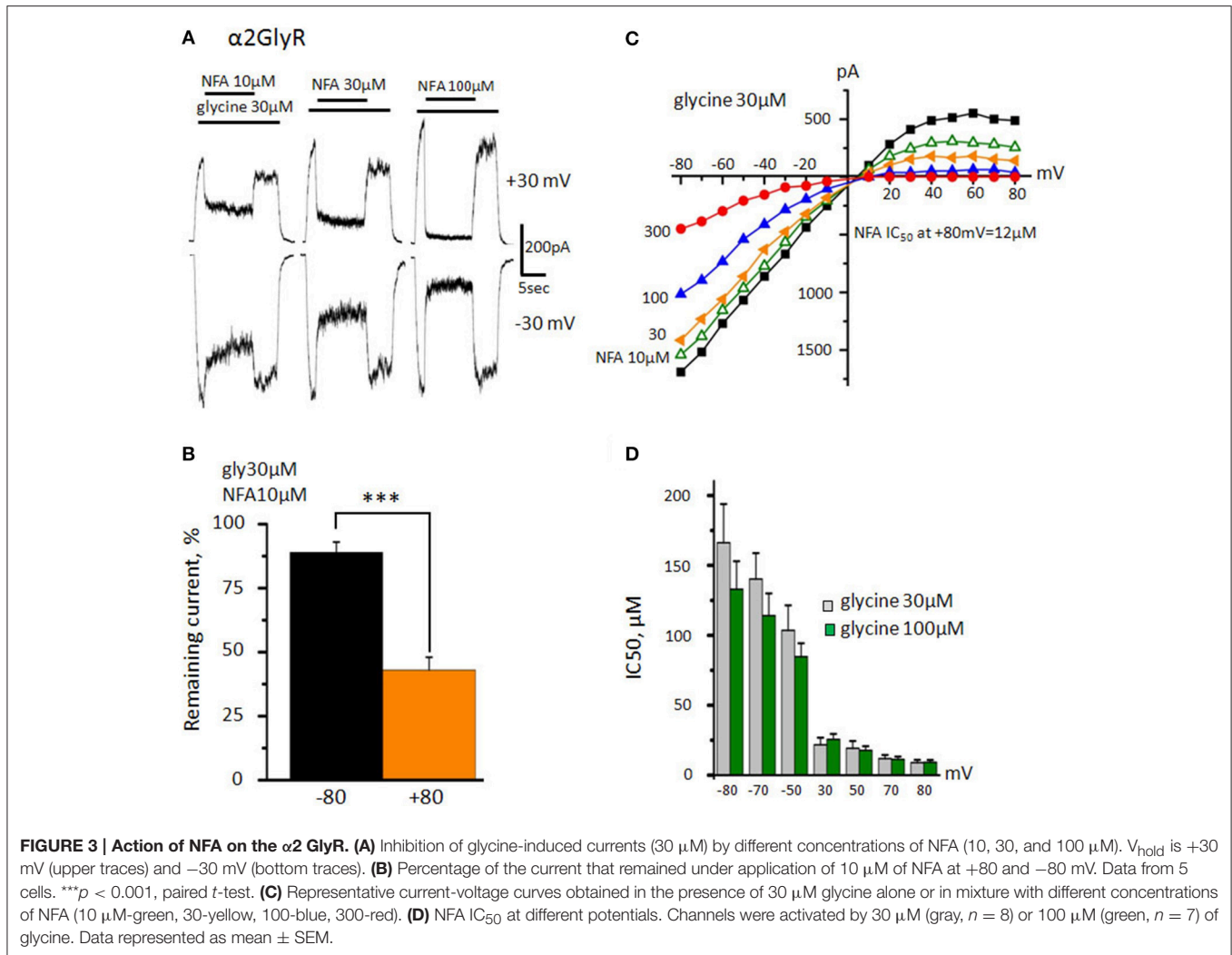
The strong voltage dependence of the block suggests that NFA is an open channel blocker interacting with residues located deeply in the pore.

This suggestion was confirmed by results of single channel recordings performed in outside-out patches from cells expressing $\alpha 2$ GlyRs in the presence of glycine or mixture of glycine with NFA (Supplementary Figure 1). In control conditions, application of 5 μM glycine at V_{hold} -30 mV induced single channel openings (mean amplitude 2,8 pA) with rare short closings (Supplementary Figure 1A). Addition of 30 μM NFA transferred rectangular single channel pulses into bursts with high frequency interburst flickering (Supplementary Figure 1B). The effect became much more profound at elevation of the NFA concentration to 100 μM (Supplementary Figure 1C). This phenomenology is similar to earlier described phenomenology of channel blockers, for instance, action of local anesthetics on single acetylcholine-receptor channels (Neher and Steinbach, 1978) or flickering mode of NMDA receptors channel block by Mg^{++} (Nowak et al., 1984) or amantadine (Blanpied et al., 2005).

Action of Niflumic Acid on $\alpha 3$ GlyRs

Since NFA has shown distinct profiles of interaction with $\alpha 1$ and $\alpha 2$ GlyRs, we decided to explore its action on $\alpha 3$ GlyR with the aim to determine the critical amino acids for the blocker action. Notably, the TM2 helix in $\alpha 3$ GlyR is the same as in $\alpha 2$ GlyR. Both possess alanine in position 2' (Figure 9A) implying that NFA may block $\alpha 3$ GlyR as strongly as $\alpha 2$ GlyR and stronger than $\alpha 1$ GlyR, which has glycine at position 2'.

Indeed, during “long application” protocol, $\alpha 3$ GlyR-mediated currents induced by 100 μM of glycine (near EC_{50} concentration for $\alpha 3$ GlyRs, Maleeva et al., 2015) were blocked by NFA with the higher potency than currents mediated by $\alpha 1$ GlyRs (Figure 4A). 30 μM of NFA inhibited $\alpha 3$ GlyR-mediated currents by $32 \pm 4\%$ at -30 mV and by $62 \pm 5\%$ at +30 mV, while 300 μM NFA at -30 mV inhibited ionic currents by $86 \pm 5\%$ and by $90 \pm 2\%$ at +30 mV ($n = 7$). It is well documented that $\alpha 3$ GlyRs rapidly desensitize (Nikolic et al., 1998) and this complicates



accurate estimation of the NFA blocking potency. Thus, over all the cells percentage of inhibition was measured as the ratio of the current amplitudes at the maximal inhibition (I_1) and after washout of NFA, when the glycine-induced current reaches the quasi-stationary level (I_2 , **Figure 4A**).

Interestingly, the current/voltage dependence recorded during application of 100 μM of glycine demonstrated the outward rectification, similar to that observed for $\alpha 1$ GlyRs. Like for both $\alpha 1$ and $\alpha 2$ GlyRs, the efficiency of $\alpha 3$ GlyRs block by NFA was higher at positive potentials (**Figures 4B,C**). At MP of -80 mV and +80 mV, IC_{50} of NFA was 86 ± 14 and 16 ± 6 μM , respectively ($n = 7$).

Thus, the sensitivity of $\alpha 3$ GlyRs to NFA is higher than that of $\alpha 1$ GlyRs and is rather close to that of $\alpha 2$ GlyRs.

Niflumic Acid Action on the $\alpha 1$ Glycine Receptor Mutant G254A

Taking into account the voltage dependence and presumably pore-blocking mechanism of NFA action, we suggested that amino acids, which are crucial for the interaction of NFA with

GlyRs, are located in the pore-lining helices. The TM2 helices are highly conserved between different α subunits of GlyRs and differ only at position 2' where $\alpha 1$ subunit has glycine, while $\alpha 2$ and $\alpha 3$ subunits have alanine (**Figure 9A**). We suggested that this difference is the main determinant of the distinct profiles of inhibition of different GlyRs by NFA. To test this hypothesis, we performed a point mutation at position 254 of the $\alpha 1$ subunit exchanging glycine for alanine (**Figure 5A**). We expected to convert low NFA sensitivity of the $\alpha 1$ GlyR to high sensitivity, characteristic for $\alpha 2$ and $\alpha 3$ GlyRs.

The dose/response relationships showed that the G254A- $\alpha 1$ GlyR mutant sensitivity to glycine is similar to that of the wild-type $\alpha 1$ GlyR: the EC_{50} was 34 ± 6 μM ($n = 6$, data not shown), which agrees with previous data (Shan et al., 2001). At the "long application" protocol, NFA relatively weakly inhibited G254A- $\alpha 1$ GlyR mediated currents induced by 30 μM glycine, but its potency was higher than that in the wild-type $\alpha 1$ GlyRs (**Figure 5A**). At V_{hold} of -30 mV, 30, 100, and 300 μM of NFA inhibited G254A- $\alpha 1$ GlyR mediated currents by 22 ± 4 , 34 ± 6 , and $52 \pm 11\%$, respectively ($n = 6$), while at V_{hold} of +30 mV, the

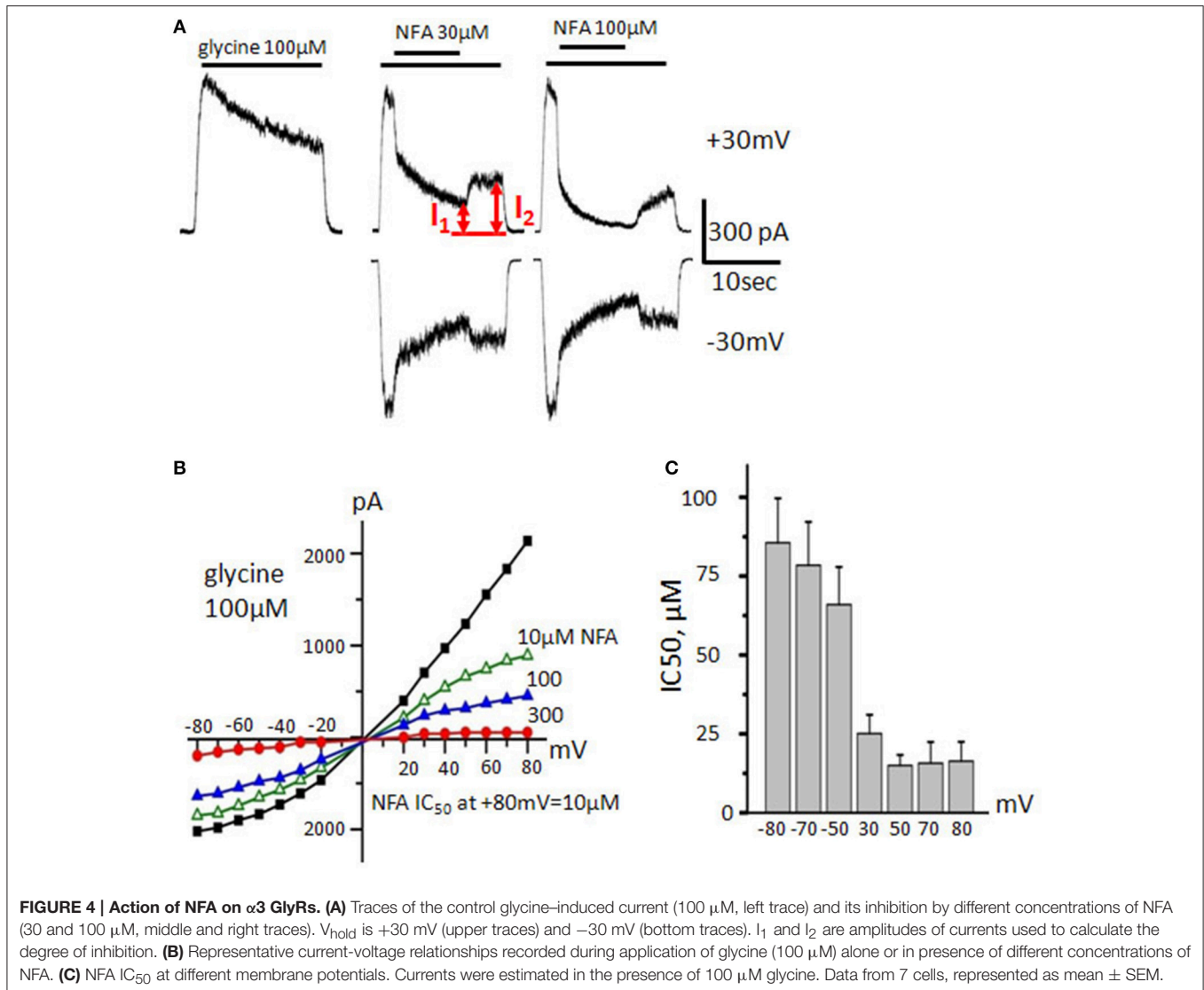


FIGURE 4 | Action of NFA on $\alpha 3$ GlyRs. (A) Traces of the control glycine-induced current (100 μM , left trace) and its inhibition by different concentrations of NFA (30 and 100 μM , middle and right traces). V_{hold} is +30 mV (upper traces) and -30 mV (bottom traces). I_1 and I_2 are amplitudes of currents used to calculate the degree of inhibition. (B) Representative current-voltage relationships recorded during application of glycine (100 μM) alone or in presence of different concentrations of NFA. (C) NFA IC_{50} at different membrane potentials. Currents were estimated in the presence of 100 μM glycine. Data from 7 cells, represented as mean \pm SEM.

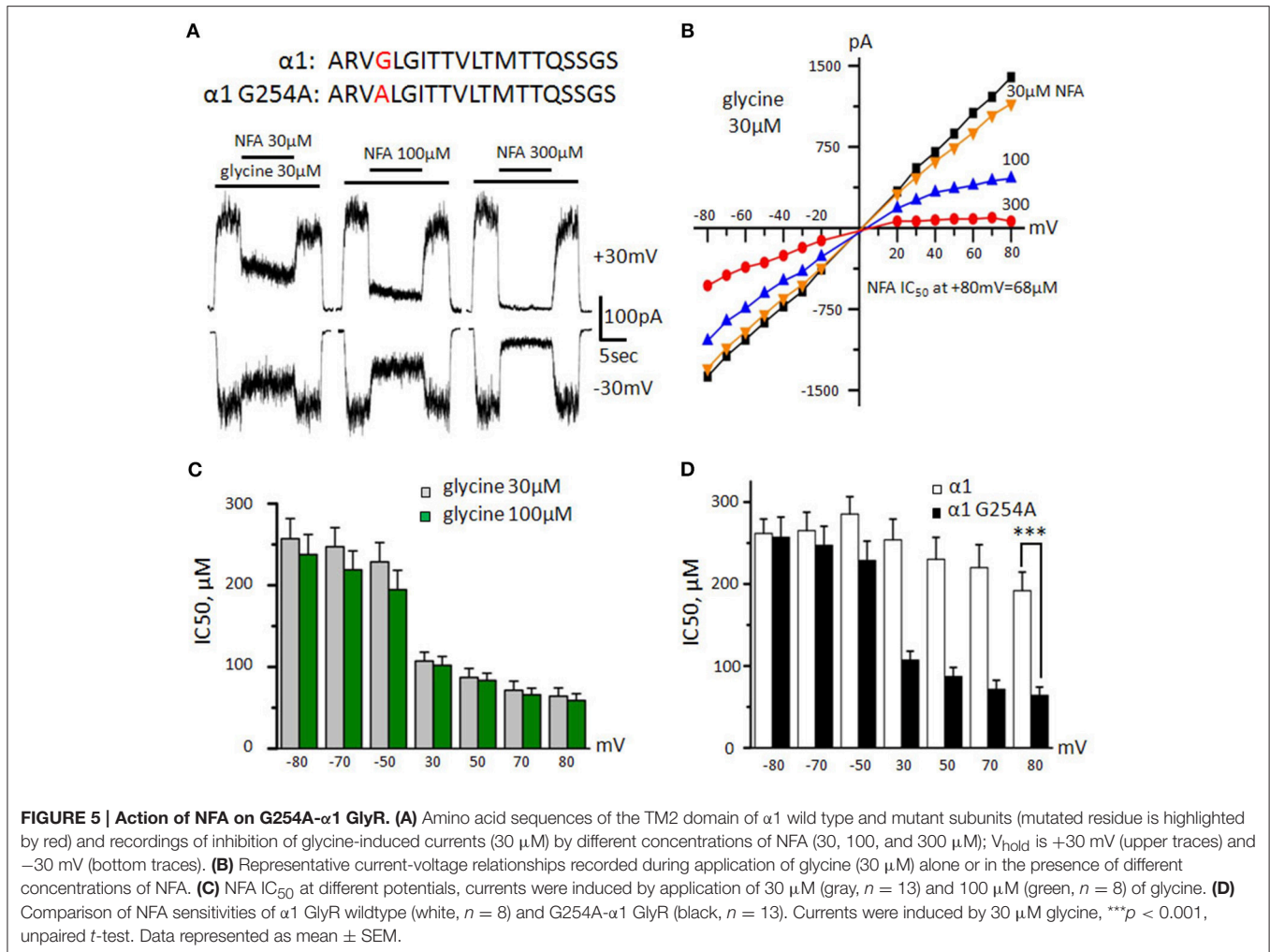
same NFA concentrations inhibited currents by 23 ± 7 , 43 ± 10 , and $76 \pm 4\%$, respectively ($n = 7$).

Using the “ramp” protocol, we found the above effect to be more pronounced at higher potentials (Figure 5B). Notably, at +80 mV currents induced by 30 μM of glycine were inhibited by NFA with IC_{50} of $64 \pm 10 \mu\text{M}$ ($n = 13$; Figure 5D), which was significantly lower ($p < 0.001$) than for the wild-type $\alpha 1$ GlyR ($192 \pm 23 \mu\text{M}$, $n = 8$). However, at negative potentials sensitivity of the G254A- $\alpha 1$ GlyR was close to that of wild type $\alpha 1$ GlyR and comprised $257 \pm 25 \mu\text{M}$ ($n = 13$). With the increase of agonist concentration, the strength of the block did not increase significantly and comprised $58 \pm 8 \mu\text{M}$ ($n = 8$) at MP = +80 mV.

Importantly, the NFA blocking potency for G254A- $\alpha 1$ GlyR was lower than that for $\alpha 2$ and $\alpha 3$ GlyRs. This suggests that amino acids beyond the TM2 helices affect the NFA action, likely by an allosteric mechanism.

Woodhull Analysis of Voltage Dependence of the GlyR Channel Block by NFA

To estimate the fractional depth of the NFA binding sites in the pore with respect to the external membrane surface, we used classical Woodhull analysis developed to describe the hydrogen block of sodium channels (Woodhull, 1973). We have plotted NFA IC_{50} values against membrane potential for $\alpha 1$, $\alpha 2$, and G254A- $\alpha 1$ GlyRs at glycine concentrations of 30 and 100 μM (Figure 6A). The calculated values of δ correspond to the percentage of the transmembrane electric field that is sensed by the bound NFA (Figure 6B). For the NFA block of $\alpha 1$ GlyR, mean δ values at 30 and 100 μM of glycine were 0.16 ± 0.03 ($n = 7$) and 0.26 ± 0.02 ($n = 10$), respectively. The NFA binding site in $\alpha 2$ GlyR was found to be significantly deeper. With 30 and 100 μM of glycine, the sensed electric field (δ) increased to 0.65 ± 0.07 and 0.63 ± 0.07 , respectively ($n = 7$, $p < 0.001$). The NFA binding site in the G254A- $\alpha 1$ GlyR was situated between



the sites in the $\alpha 1$ and $\alpha 2$ GlyRs, at the level of $\sim 30\%$ from the extracellular side at both examined agonist concentrations (Table 1).

Hill Coefficient of NFA/GlyR Interaction

To estimate cooperativity of NFA inhibition of GlyRs, we determined the Hill coefficient (n_H) for $\alpha 1$, $\alpha 2$, and G254A- $\alpha 1$ GlyRs. The amplitude of glycine-evoked currents at different potentials was plotted against the NFA concentration and fitted with the Hill equation. At positive membrane potentials, n_H decreased with the membrane depolarization for the three GlyRs (Table 2 and Figure 6C). For $\alpha 1$ and $\alpha 2$ GlyRs n_H was significantly different at all the tested membrane potentials (-80 mV, -70 mV $p < 0.001$; -50 - +50 mV $p < 0.01$; 70, 80 mV $p < 0.05$), and for the G254A- $\alpha 1$ GlyR n_H values were between those for $\alpha 1$ and $\alpha 2$ GlyRs. Concentration dependencies of NFA action on different GlyR subunits are presented in the Supplementary Figure 2.

These data suggest that the cooperativity of NFA block strongly depends on the GlyR subtype.

Action of Niflumic Acid on $\alpha 1\beta$ and $\alpha 2\beta$ GlyRs

In the adult CNS of vertebrates, the predominant GlyR subtype is heteromeric $\alpha 1\beta$ (Lynch, 2004). Several inhibitors, e.g., picrotoxin (Pribilla et al., 1992; Wang et al., 2006) and ginkgolides (Kondratskaya et al., 2005) have different affinity in heteromeric and homomeric GlyRs. To estimate the NFA sensitivity to heteromeric GlyRs we studied its interaction with $\alpha 1\beta$ and $\alpha 2\beta$ GlyRs. The concentration of the agonist was chosen according to the previous studies, demonstrating that 30 μ M of glycine is below EC₅₀ for $\alpha 1\beta$ and $\alpha 2\beta$ glycine receptors (Rundstrom et al., 1994; Miller et al., 2005).

To prove formation of functional heteromeric GlyRs, we implemented a widely used picrotoxin (PTX) test: PTX blocks $\alpha X\beta$ GlyRs much weaker than homomeric αX GlyRs (Pribilla et al., 1992; Shan et al., 2001). In our preparations, under application of 20 μ M of PTX amplitudes of $\alpha 1$ and $\alpha 2$ GlyR-mediated currents were, respectively, $27 \pm 3\%$ ($n = 12$) and $3 \pm 1\%$ ($n = 9$) of the control. Heteromeric GlyRs were inhibited much weaker: the current in $\alpha 1\beta$ GlyR was $75 \pm 2\%$ ($n = 15$)

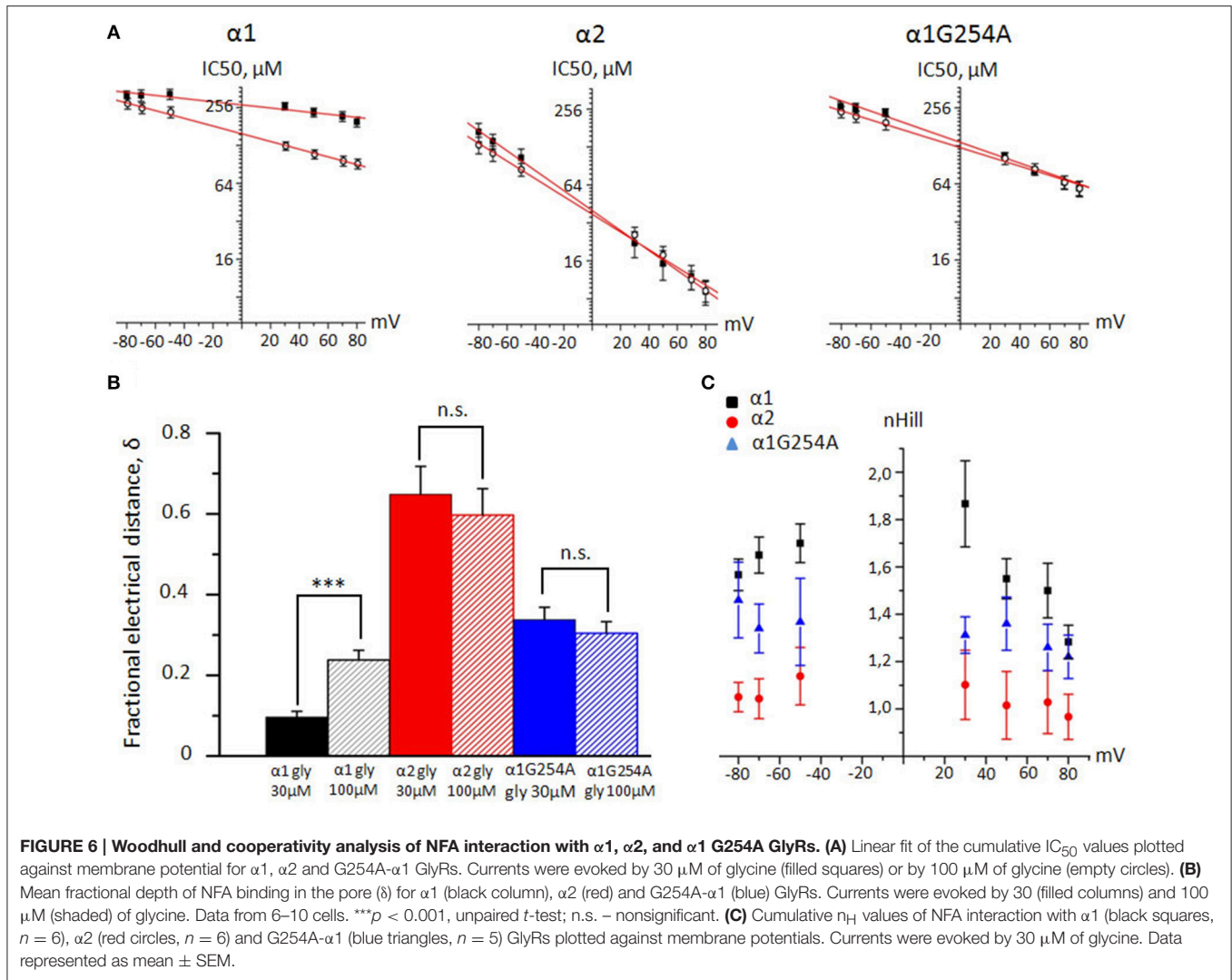


TABLE 1 | Fractional electrical distance (δ) from the extracellular side of the membrane at which NFA blocks the pore in $\alpha 1$, $\alpha 2$ and G254A- $\alpha 1$ GlyRs.

Glycine concentration	$\alpha 1$ GlyR	$\alpha 2$ GlyR	G254A- $\alpha 1$ GlyR
30 μM	0.16 ± 0.03 ($n = 7$)	0.65 ± 0.07 ($n = 7$)	0.37 ± 0.04 ($n = 9$)
100 μM	0.26 ± 0.02 ($n = 10$)	0.63 ± 0.07 ($n = 7$)	0.30 ± 0.04 ($n = 7$)

The data are represented as mean \pm SEM.

and in $\alpha 2\beta$ GlyR it was $41 \pm 4\%$ ($n = 7$) from the control (Figures 7A–C).

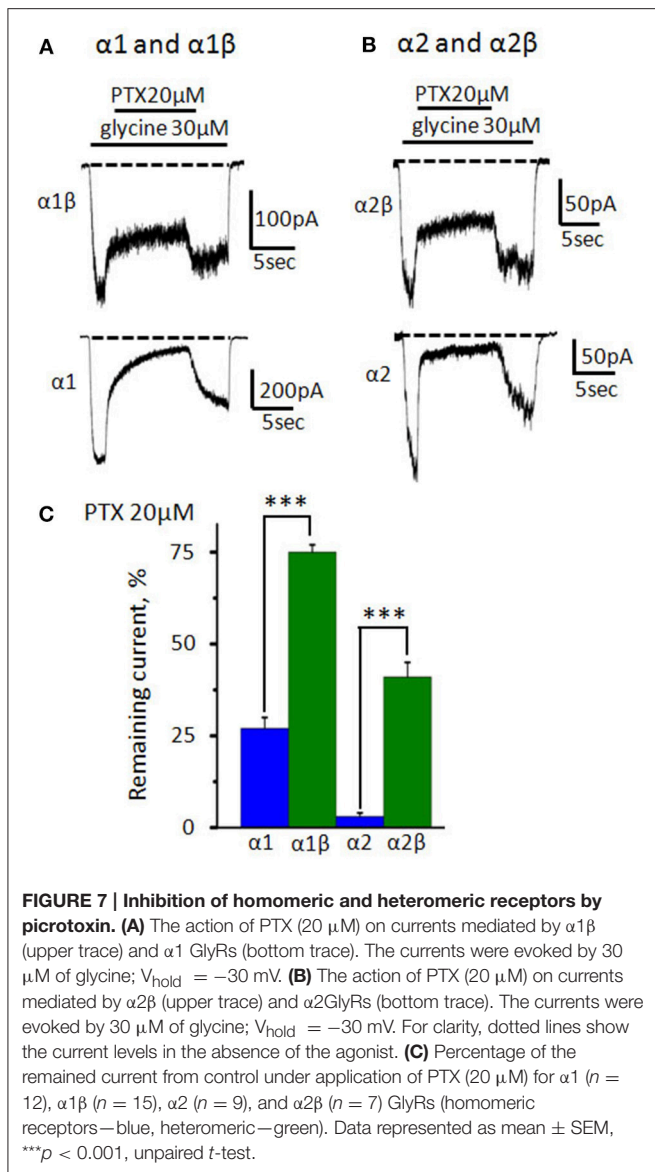
Estimation of NFA IC_{50} at different membrane potentials has shown that incorporation of the β subunit does not change significantly ($p > 0.05$) the sensitivity of $\alpha 1$ GlyR to NFA: at +80 mV IC_{50} of NFA was $150 \pm 14 \mu M$ ($n = 5$) (Figure 8A). Analysis of I/V curves also revealed a similarity to $\alpha 1$ GlyRs: currents mediated by $\alpha 1\beta$ GlyRs (30 μM of glycine) were outwardly rectifying (data not shown).

TABLE 2 | Hill coefficient (n_H) of NFA interaction with $\alpha 1$, $\alpha 2$, and G254A- $\alpha 1$ GlyRs at different membrane potentials.

Membrane potential (mV)	$\alpha 1$ GlyR ($n = 6$)	$\alpha 2$ GlyR ($n = 6$)	G254A- $\alpha 1$ GlyR ($n = 5$)
–80	1.56 ± 0.07	1.05 ± 0.06	1.46 ± 0.16
–70	1.65 ± 0.08	1.04 ± 0.08	1.34 ± 0.1
–50	1.7 ± 0.08	1.14 ± 0.12	1.37 ± 0.18
30	1.87 ± 0.02	1.1 ± 0.14	1.3 ± 0.08
50	1.55 ± 0.08	1 ± 0.14	1.36 ± 0.11
70	1.5 ± 0.11	1 ± 0.13	1.26 ± 0.1
80	1.28 ± 0.07	0.97 ± 0.09	1.22 ± 0.09

Data are represented as mean \pm SEM.

Surprisingly, $\alpha 2\beta$ GlyRs demonstrated the outwardly rectifying currents, contrary to inwardly rectifying $\alpha 2$ GlyRs (Figures 8B,C). In comparison to $\alpha 2$ GlyRs NFA stronger inhibited heteromeric $\alpha 2\beta$ receptors at negative potentials being



less effective at positive ones. This resulted in slightly weaker voltage dependence of the block vs. homomeric GlyRs: at -80 and $+80$ mV, IC_{50} was 107 ± 37 and 20 ± 8 μM , respectively ($n = 5$, **Figure 8D**). In general, the β subunit does not have a strong impact on the interaction of NFA with GlyRs.

Computational Search for Possible NFA Binding Sites in the Pore of GlyRs

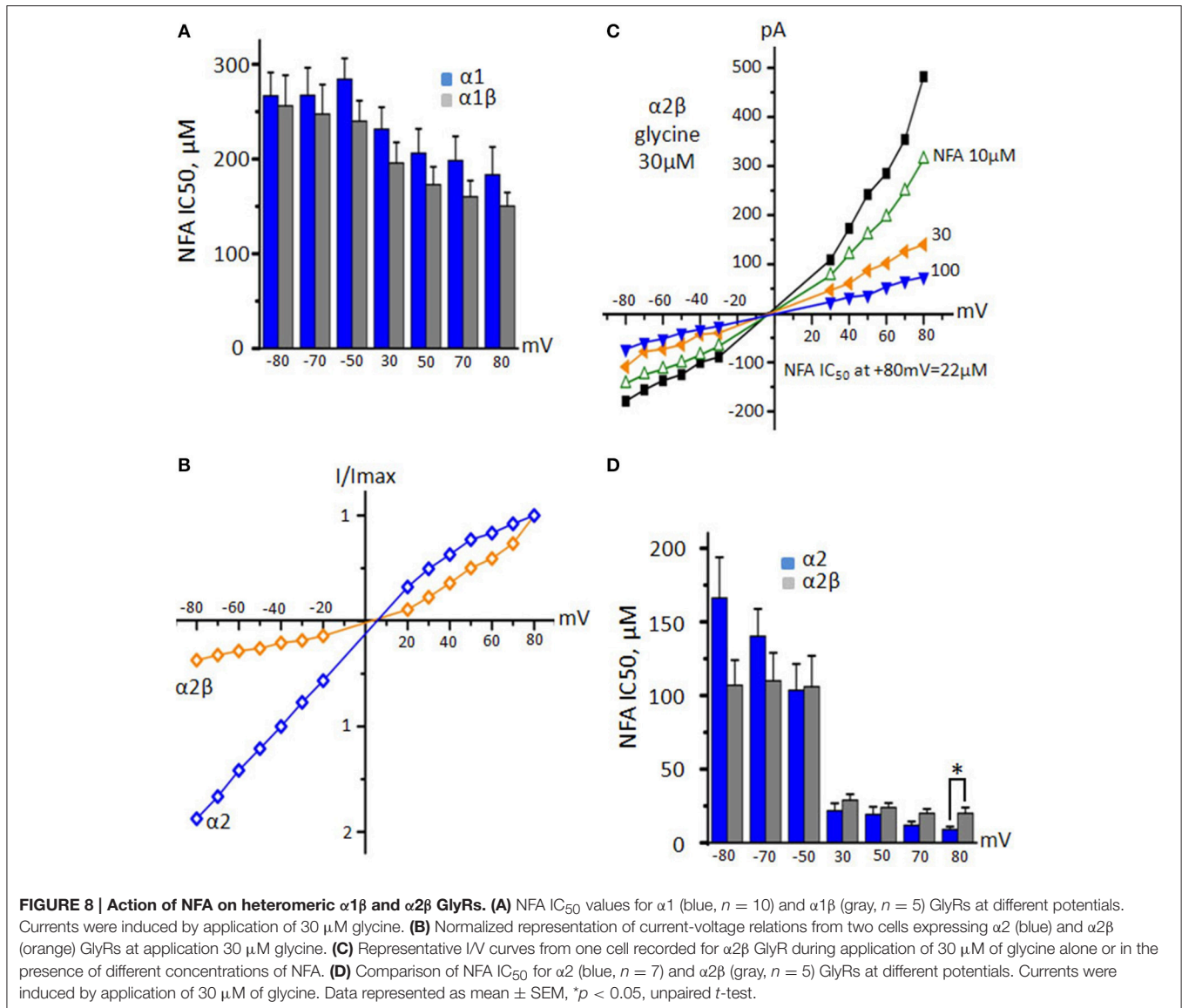
A systematic search for possible binding sites of NFA in different regions of the large GlyR proteins was beyond goals of this study. Here we focused on the pore region where NFA is likely to bind. Several arguments support this proposition. First, the voltage-dependence of the NFA action (**Figures 2–6**) strongly suggests that the compound binds within the membrane. Second, the anionic NFA molecules would enjoy favorable electrostatic interactions within the anion-selective pore. Third, results of

single channels experiments demonstrated dramatic increase of the open state fluctuations caused by NFA application. Fourth, upon the channel activation, the $\alpha 2$ GlyR appears to open for a longer time than $\alpha 1$ GlyR (Takahashi et al., 1992; Morales et al., 1994). The longer openings would give NFA molecules more chances to reach their binding site(s) within the pore. This may explain why $\alpha 2$ GlyR is more sensitive to the NFA block than $\alpha 1$ GlyR.

Figure 9B shows computed energy (kcal/mol) of NFA interaction with $\alpha 1$ and $\alpha 2$ GlyR models and **Figure 10A** shows superposition of 74 snapshots with NFA at different levels of the $\alpha 2$ GlyR pore. The $\alpha 1$ and $\alpha 2$ GlyR models differ only at level 2' where they have, respectively, the rings of Gly254 and Ala254 residues, but the computed energy values are rather different at each level (**Figure 9B**). The cause is the NFA molecule size (~ 13 Å between most remote atoms, see **Figure 1B**), which is bigger than, e.g., the distance of 5.8 Å between C^β atoms of the same TM2 helix at levels 2' and 6'. Since the preferable orientation of NFA in the pore is unknown, the NFA molecule was allowed to rotate during MC-minimizations at each step. As a result, once the energetically favorable orientation was found at some level, the probability to find the energetically better orientation at the same level become small. A bottom line from a large number of independent runs with different seed random numbers might yield smoother trajectories, but such computations, which would require large computational resources, were beyond goals of our study.

The NFA interaction energy with the $\alpha 1$ and $\alpha 2$ GlyR models differs not only around level 2', but also at the levels where the pore-facing residues are identical. At most of the levels, the energy difference between the two models does not exceed 2 kcal/mol, but it reaches 5 kcal/mol at level 6' (Thr258). Despite the differences, the two trajectories have several common features as described below. First, there are rather deep minima at the cytoplasmic side of the pore, which are due to electrostatic interactions between NFA and Arg252 (**Figure 10B**). Second, there are energy minima at level 6', which are due to H-bonds between NFA and Thr258 residues and hydrophobic interactions of NFA with the intracellularly-oriented side of the Leu261 ring. Third, there are energy minima at level 13', which are due to H-bonds between NFA and Thr265 and favorable hydrophobic interactions of NFA with the extracellularly-oriented side of the Leu261 ring. Fourth, there are energy maxima at level 9', which are due to certain repulsion between NFA and Leu261 residues that form the open pore constriction. However, even at this level the NFA-channel energy remains favorable (around -10 kcal/mol), partially because the ligand carboxylic group can accept up to four H-bonds from Thr258, Thr264, and Thr265 (**Figure 10C**). Fifth, relatively large energies at the extracellular part of the pore (levels 17' to 20') are due to two reasons. (i) The pore at these levels is too wide and NFA cannot simultaneously interact with three helices as it does at lower levels. (ii) Levels 13' and 17' are both hydrophilic (**Figure 9A**) and predominantly hydrophobic NFA cannot form multiple favorable contacts with the pore-facing residues.

Based on these results we suggest that there are more than one site along the pore where NFA can bind and block the ion



permeation. The most likely locations of the NFA binding sites are at the opposite sides of the Leu261 ring, which forms the open pore constriction. And the most likely mechanism of the current block is the combination of the hydrophobic and steric block: NFA exposes its hydrophobic groups to the pore lumen, binds above and/or below the Leu261 ring and thus precludes permeation of the hydrated chloride ion. This block may be enforced by the electrostatic repulsion of the negatively charged carboxylate group of NFA and negatively charged chloride ions.

Our data on the Hill coefficient and the fractional electrical distance of the NFA binding site suggest two peculiarities of NFA action on GlyRs. Firstly, two NFA molecules preferably block permeation through the $\alpha 1$ GlyR channel, whereas the $\alpha 2$ GlyR channel is blocked by a single NFA molecule. Secondly, the NFA binding site in the $\alpha 2$ GlyR is located deeper than in the $\alpha 1$ GlyR. These experimental data provide important constraints to further elaborate models of NFA-bound $\alpha 1$ and $\alpha 2$ GlyRs.

The $\alpha 2$ GlyR block by a single NFA molecule bound deeply inside the pore can be illustrated by the binding mode found without constraints (**Figures 10D–F**). In this mode, NFA binds between hydrophobic rings Ala254 and Leu261 and accepts an H-bond from Thr258. This and similar binding modes collected in the MC-minimizations correspond to the energy minima at the left part of the energy profile (**Figure 9B**).

The energy profile of NFA in the $\alpha 1$ GlyR shows that NFA-channel interactions at levels $-2'$ to $6'$ are energetically less preferable than in the $\alpha 2$ GlyR. A reason is the ring of Gly254 residues in $\alpha 1$ GlyR, which does not form as favorable van der Waals and hydrophobic contacts with NFA as the ring of Ala254 residues in $\alpha 2$ GlyR does. In particular, water molecules that hydrate the pore-exposed hydrophilic backbone atoms of Gly254 residues would destabilize binding of the hydrophobic NFA.

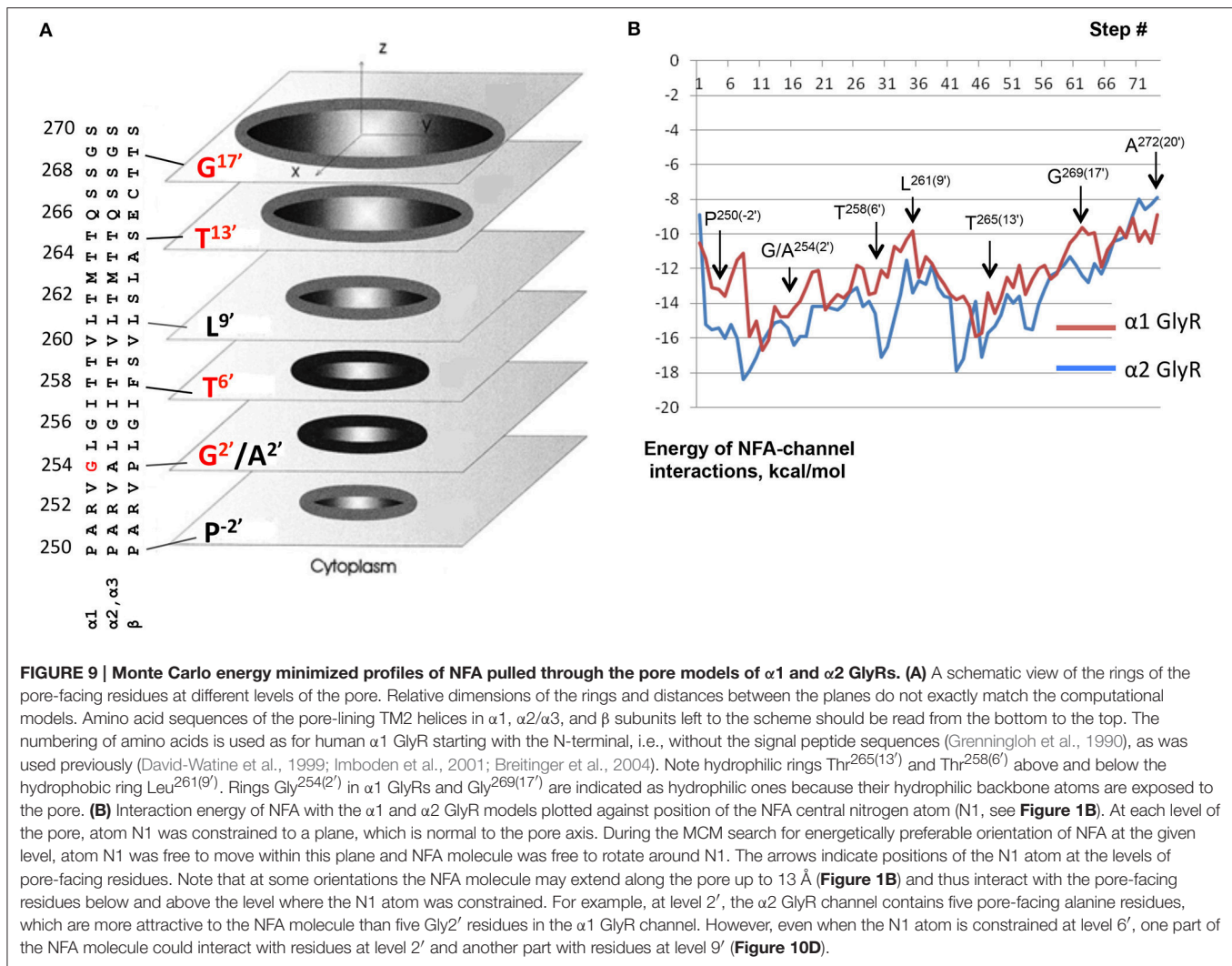


FIGURE 9 | Monte Carlo energy minimized profiles of NFA pulled through the pore models of $\alpha 1$ and $\alpha 2$ GlyRs. (A) A schematic view of the rings of the pore-facing residues at different levels of the pore. Relative dimensions of the rings and distances between the planes do not exactly match the computational models. Amino acid sequences of the pore-lining TM2 helices in $\alpha 1$, $\alpha 2/\alpha 3$, and β subunits left to the scheme should be read from the bottom to the top. The numbering of amino acids is used as for human $\alpha 1$ GlyR starting with the N-terminal, i.e., without the signal peptide sequences (Grenningloh et al., 1990), as was used previously (David-Watine et al., 1999; Imboden et al., 2001; Breiteringer et al., 2004). Note hydrophilic rings Thr²⁶⁵(13') and Thr²⁵⁸(6') above and below the hydrophobic ring Leu²⁶¹(9'). Rings Gly²⁵⁴(2') in $\alpha 1$ GlyRs and Gly²⁶⁹(17') are indicated as hydrophilic ones because their hydrophilic backbone atoms are exposed to the pore. **(B)** Interaction energy of NFA with the $\alpha 1$ and $\alpha 2$ GlyR models plotted against position of the NFA central nitrogen atom (N1, see Figure 1B). At each level of the pore, atom N1 was constrained to a plane, which is normal to the pore axis. During the MCM search for energetically preferable orientation of NFA at the given level, atom N1 was free to move within this plane and NFA molecule was free to rotate around N1. The arrows indicate positions of the N1 atom at the levels of pore-facing residues. Note that at some orientations the NFA molecule may extend along the pore up to 13 Å (Figure 1B) and thus interact with the pore-facing residues below and above the level where the N1 atom was constrained. For example, at level 2', the $\alpha 2$ GlyR channel contains five pore-facing alanine residues, which are more attractive to the NFA molecule than five Gly2' residues in the $\alpha 1$ GlyR channel. However, even when the N1 atom is constrained at level 6', one part of the NFA molecule could interact with residues at level 2' and another part with residues at level 9' (Figure 10D).

A complex $\alpha 1$ GlyR with a single NFA bound above the ring of Leu261 residues, at level 13' (Thr265) corresponds to the wide energy minima (Figure 9B). We docked the second NFA molecules to this complex and MC-minimizing the energy. The pore easily accommodated two NFA molecules at this level and calculations predicted several possible low-energy binding modes of the two ligands. One of these is shown at Figures 10G–I, where two NFA molecules form favorable hydrophobic contacts with each other and the extracellularly-oriented side of the Leu261 ring, thus blocking the ion permeation, whereas their carboxylate groups accept H-bonds from the Thr265 residues.

DISCUSSION

NFA is an anti-inflammatory drug clinically used for the relief of chronic and acute pain (Cremonesi and Cavalieri, 2015). In comparison with other nonsteroidal anti-inflammatory drugs or nonopioid analgesics, it is not associated with side effects, particularly, reactions in children (Sturkenboom et al., 2005). NFA is also widely used for inhibition of some types of

Cl⁻-selective channels, blocking primary voltage-gated CLC-1 channels (Sturkenboom et al., 2005) and Ca²⁺-activated Cl⁻ channels (CaCCs) (White and Aylwin, 1990; Yang et al., 2008; Huanosta-Gutierrez et al., 2014).

It has been shown that a distinct branch of the CLC protein family, CLC-K kidney Cl⁻ channels, which are important for renal and inner ear trans-epithelial Cl⁻ transport (Zifarelli and Pusch, 2007), are modulated by NFA in a biphasic way: it activates CLC-K at low concentrations, but blocks the channels at high concentrations, above ~1 mM (Zifarelli et al., 2010). Guided by the crystal structure of a bacterial CLC homolog and site-directed mutations of CLC-K, authors suggested three amino acids as candidates for the potentiation effect of NFA. A subunit-specific NFA action has been demonstrated on the ligand-gated Cl⁻-permeable GABA_A receptors. Those, formed by $\alpha 1/\beta 2/\gamma 2$ subunits, the main receptor combination in the brain, were potentiated by application of NFA, while $\alpha 6/\beta 2/\gamma 2$ and $\alpha 1/\beta 2$, $\alpha 6/\beta 2$ receptors were inhibited by NFA (Sinkkonen et al., 2003). These observations suggest that NFA regulates the function of different Cl⁻-selective channels via different pathways. However,

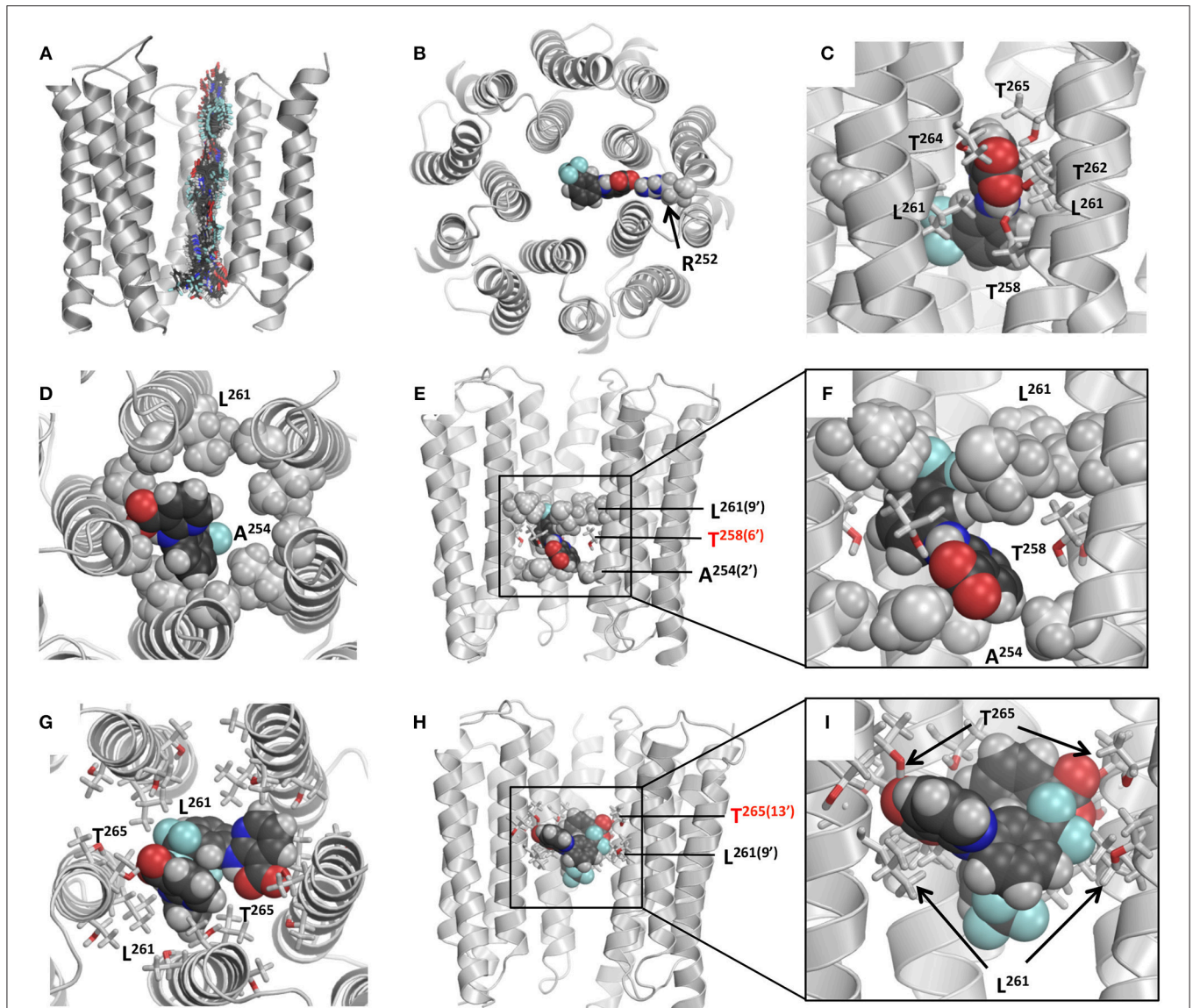


FIGURE 10 | Models of NFA binding in the GlyRs. (A) Superposition of snapshots with NFA at different levels of the $\alpha 2$ GlyR model. Front subunit is removed for clarity. At each level, the energy is MC-minimized as described in Materials and Methods. **(B)** Cytoplasmic view at $\alpha 2$ GlyR with the NFA molecule electrostatically attracted to Arg252. Due to this attraction both $\alpha 1$ GlyR-NFA and $\alpha 2$ GlyR-NFA trajectories have deep minima at level $-2'$. **(C)** Side view of the $\alpha 1$ GlyR model with NFA at level $9'$, which corresponds to the energy maxima in **Figure 9**. At this level NFA squeezes through the pore constriction formed by the Leu $^{261(9')}$ residues, but due to deep penetration of the NFA carboxylic group between two M2 helices, it may accept up to four H-bonds from Thr $^{258(6')}$, Thr 262 , Thr 264 and Thr $^{265(13')}$. **(D–F)** Intracellular, side, and enlarged side views of the $\alpha 2$ GlyR model with atom N1 of NFA bound level $6'$, where a minimum is seen at the energy profile (**Figure 9B**). The front subunit is removed for clarity at **(E,F)**. NFA accepts an H-bond from Thr $^{258(6')}$ and forms hydrophobic contacts with the rings of Ala $^{254(2')}$ and Leu $^{261(9')}$ residues by the trifluoromethyl-aryl and pyridine groups, respectively. **(G–I)** Extracellular, side, and enlarged side views of the $\alpha 1$ GlyR model two NFA molecules bound above the Leu $^{261(9')}$ ring. The front subunit is removed for clarity at **(H,I)**. Both NFA molecules accept H-bonds from Thr $^{265(13')}$, and form hydrophobic contacts with each other and Leu $^{261(9')}$ residues.

molecular mechanisms of its action on Cys-loop receptors are elusive.

Here we used electrophysiological, mutational and molecular modeling analyses to investigate the effects of NFA on Cl⁻-selective GlyR channels of known subunit composition. We have demonstrated that NFA inhibits currents mediated by homomeric $\alpha 1$, $\alpha 2$, and $\alpha 3$ GlyRs with different efficacy: $\alpha 1$

receptors demonstrated the lowest affinity to NFA, while for $\alpha 2$ and $\alpha 3$ GlyRs the NFA affinity was more than ten times higher (**Figures 2, 3**). Inhibition of all three types of GlyRs by NFA was voltage dependent with higher affinity at positive potentials. This effect was especially pronounced for $\alpha 2$ GlyRs. The voltage dependence of NFA action allowed us to suggest that the site(s) of NFA interaction with GlyR are located in the channel pore.

Moreover, the Woodhull analysis suggested that the NFA binding site in $\alpha 1$ GlyR is closer to the external part of the membrane, while for $\alpha 2$ GlyR it is significantly deeper in the pore.

The NFA ability to block $\alpha 1$ GlyRs at positive potentials significantly increased with the concentration of the glycine. In contrast, this effect in $\alpha 2$ GlyRs was not observed. We suggest that this difference is due to the different kinetics of channels' gating. Analysis of single-channel properties demonstrated that the mean open time of $\alpha 2$ GlyR channels exceeds that of $\alpha 1$ channels by almost 100-fold (Takahashi et al., 1992). Presumably, the different NFA potency in blocking the $\alpha 1$ GlyR currents induced by 30 and 100 μM of glycine is due to the different mean open times of the channel. Augmentation of the agonist concentration did not have an impact on the $\alpha 2$ GlyR block by NFA because in this GlyR subtype the mean open time even at low concentration of glycine was long enough for development of the maximum NFA effect.

The ion-conducting pore of GlyRs is lined by TM2 helices of five subunits. The TM2 segments of different alpha subunits differ only at the 2' position: $\alpha 1$ receptors contain Gly, while $\alpha 2$ and 3 subunits have Ala (**Figure 9A**). The pore-blocking mechanism of NFA action suggests that the revealed difference in NFA sensitivity of different GlyRs is due, primarily, to different amino acids in the 2' position.

In order to verify this, we have performed a point mutation in $\alpha 1$ subunit exchanging Gly254 for Ala. The G254A- $\alpha 1$ mutant was more sensitive to NFA than wild-type $\alpha 1$ GlyR and the NFA block in the mutant increased at positive potentials. However, this mutation did not convert completely the profile of $\alpha 1$ GlyR interaction with NFA to the one of $\alpha 2$ GlyR, suggesting that amino acids beyond the TM2 segments also influence the NFA action.

In our study, we have confirmed the importance of 2' residue of TM2 segments in determining the action of pore-blocking molecules on GlyR. Several studies provided evidence of the implication of this amino acid in the interaction of GlyR with ion channel blockers (Pribilla et al., 1992; Rundstrom et al., 1994; Shan et al., 2001). For instance, cyanotryphenilborate (CTB) blocks $\alpha 1$ GlyRs more potently than $\alpha 2$ GlyRs, while mutation G254A in the $\alpha 1$ subunit makes the channel less sensitive to CTB (Rundstrom et al., 1994).

A prominent difference in the voltage dependence of $\alpha 1$ and $\alpha 2$ GlyRs block by NFA motivated us to implement the Woodhull analysis to determine the fractional electrical distance (δ) from the external side of the membrane at which NFA molecules bind to the $\alpha 1$, $\alpha 2$, and G254A- $\alpha 1$ GlyRs. This analysis revealed that the δ value was largely different in different GlyR subtypes. Thus, the currents evoked by 100 μM of glycine were inhibited by NFA with higher potency likely due to the increase of the accessibility of deeper parts of the pore. A similar explanation is possible for the high NFA potency in $\alpha 2$ GlyRs. NFA molecules could penetrate to the pore by more than 60% of its length. The G254A- $\alpha 1$ GlyR mutant, which had a higher NFA sensitivity than the $\alpha 1$ wild-type, also has a more extracellularly located NFA binding site.

Previous studies that considered voltage dependence of currents mediated by GlyRs formed a discrepant picture.

Glycine-evoked currents demonstrated both an outwardly rectifying (Bormann et al., 1987; Schmieden et al., 1989; Morales et al., 1994; Downie et al., 1996; Fucile et al., 1999) and linear behaviors (Bormann et al., 1993; Wang et al., 2006) upon gradually changing V_{hold} . This difference may be resulted from the use of different agonist concentrations and protocols of voltage change. Earlier study presented a clear explanation of these changes in I/V relations (Akaike et al., 1986).

A systematic study of I/V relations for different subunits of GlyRs was undertaken recently, but for desensitized channels, activated by high concentration of glycine (Raltshev et al., 2016). It was shown that currents mediated by $\alpha 2$ and $\alpha 3$ GlyRs in desensitized state are inwardly rectifying, while $\alpha 1$ GlyRs currents are linear. These results are partially overlapping with ours, but they cannot be fairly compared as Raltshev et al. (2016) studied desensitized receptors.

The Hill equation analysis demonstrated the different degree of cooperativity of NFA inhibitory action. It was higher for $\alpha 1$ GlyRs with n_{H} close to 1.5 suggesting at least two molecules of NFA are necessary to block the pore, while for $\alpha 2$ GlyR n_{H} was close to 1. While there is no direct relation between Hill coefficients and stoichiometry of interaction, our observation that n_{H} for $\alpha 1$ receptors is higher than for $\alpha 2$ receptors is in agreement with the proposed binding of two NFA molecules in the pore of alpha GlyR channels and supported by the model analysis.

Heteromeric $\alpha 1\beta$ and $\alpha 2\beta$ receptors were also inhibited by NFA. Incorporation of β subunit did not change significantly sensitivity of $\alpha 1\beta$ GlyR to NFA, while at positive potentials NFA inhibited the $\alpha 2\beta$ GlyR less potently than $\alpha 2$ receptors. The amino acid sequence of β subunit is very different from α subunits (**Figure 9A**). It was shown that Phe258 plays important role in determining the $\alpha 1\beta$ sensitivity to PTX, and its substitution for threonine significantly increases the affinity of heteromeric receptors to PTX (Shan et al., 2001).

Our molecular modeling provided the possible structural rationale for the experimental data. The likely reason for the different strength, depth and stoichiometry of NFA binding in $\alpha 1$ and $\alpha 2$ GlyRs is favorable interactions of the hydrophobic ligand with the hydrophobic 2' alanine ring in $\alpha 2$ GlyR and unfavorable interactions with the hydrated 2' glycine ring in $\alpha 1$ GlyR. Being unable to bind at the 2' glycine ring in $\alpha 1$ GlyR, NFA binds at the upper, wider levels of the pore that can accommodate two ligands. In a simplified way, NFA can be described as a molecule with two hydrophobic ends and a hydrophilic middle part (**Figure 1**). Such a molecule would favorably interact with the channel that has a hydrophilic ring with hydrophobic rings below and above it. The rings of Ala254, Thr258, and Leu261 residues in $\alpha 2$ GlyR do form such a pattern. $\alpha 1$ GlyR lacks such a pattern, and in the absence of the second hydrophobic ring, two NFA molecules enjoy hydrophobic contacts with each other. It should be noted that prediction of NFA binding sites in the big GlyR proteins would be hardly possible in a purely theoretical study. It is the experimental data on the mutational analysis of the pore-lining residue, the Hill coefficients of NFA

action and the depth of the NFA binding sites revealed by the Woodhull analysis that provided strong experimental constraints to elaborate structural models of NFA action in $\alpha 1$ and $\alpha 2$ GlyRs.

In conclusion, several results of our study evidence in favor of the pore-blocking mode of NFA action on glycine receptors: (i) the voltage dependence of the block; (ii) increase of the $\alpha 1$ GlyR blocking efficacy with the increased glycine concentration; (iii) appearance of high frequency interburst flickering upon NFA application revealed by single channel recordings, and (iv) mutation G254A in the TM2 segment of $\alpha 1$ subunit increased the receptors sensitivity to NFA. Molecular modeling provided a possible structural rationale for our experimental observations and suggested several blocking sites of NFA with preferable sites between levels 2' and 9' in $\alpha 2$ GlyR and between levels 9' and 13' in $\alpha 1$ GlyR.

AUTHOR CONTRIBUTIONS

GM and PB designed carried out and analyzed all patch clamp experiments, FP produced mutagenesis of glycine receptor and BZ performed molecular modeling.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: <http://journal.frontiersin.org/article/10.3389/fnmol.2017.00125/full#supplementary-material>

Supplementary Figure 1 | Representative traces of single channel currents from $\alpha 2$ GlyRs recorded in outside-out configuration of patch-clamp technique evoked by 5 μ M of glycine (A), by mixture of 5 μ M glycine+30 μ M of NFA (B) and by glycine 5 μ M+NFA 100 μ M (C); V_{hold} -30 mV.

Supplementary Figure 2 | IC₅₀ curves for NFA at -80, -30, +30, and +80 mV obtained from current-voltage dependencies recorded during application of mixture of glycine with different NFA concentrations. (A) Representative NFA IC₅₀ curves for currents mediated by $\alpha 1$ GlyRs, induced by 30 μ M of glycine; NFA IC₅₀ at -80 mV = 272 μ M, -30 mV = 256 μ M, +30 mV = 218 μ M, +80 mV = 178 μ M. **(B)** Representative NFA IC₅₀ curves for currents mediated by $\alpha 1$ GlyRs, induced by 100 μ M of glycine; NFA IC₅₀ at -80 mV = 209 μ M, -30 mV = 171 μ M, +30 mV = 107 μ M, +80 mV = 94 μ M. **(C)** Representative NFA IC₅₀ curves for currents mediated by $\alpha 1\beta$ GlyRs, induced by 30 μ M of glycine; NFA IC₅₀ at -80 mV = 191 μ M, -30 mV = 200 μ M, +30 mV = 152 μ M, +80 mV = 144 μ M. **(D)** Representative NFA IC₅₀ curves for currents mediated by $\alpha 2$ GlyRs, induced by 30 μ M of glycine; NFA IC₅₀ at -80 mV = 155 μ M, -30 mV = 75 μ M, +30 mV = 17 μ M, +80 mV = 12 μ M. **(E)** Representative NFA IC₅₀ curves for currents mediated by $\alpha 2$ GlyRs, induced by 100 μ M of glycine; NFA IC₅₀ at -80 mV = 100 μ M, -30 mV = 39 μ M, +30 mV = 12 μ M, +80 mV = 7 μ M. **(F)** Representative NFA IC₅₀ curves for currents mediated by $\alpha 2\beta$ GlyRs, induced by 30 μ M of glycine; NFA IC₅₀ at -80 mV = 84 μ M, -30 mV = 47 μ M, +30 mV = 24 μ M, +80 mV = 22 μ M. **(G)** Representative NFA IC₅₀ curves for currents mediated by $\alpha 3$ GlyRs, induced by 100 μ M of glycine; NFA IC₅₀ at -80 mV = 117 μ M, -30 mV = 78 μ M, +30 mV = 23 μ M, +80 mV = 10 μ M. **(H)** Representative NFA IC₅₀ curves for currents mediated by $\alpha 1$ G254A GlyRs, induced by 30 μ M of glycine; NFA IC₅₀ at -80 mV = 230 μ M, -30 mV = 185 μ M, +30 mV = 92 μ M, +80 mV = 68 μ M. **(I)** Representative NFA IC₅₀ curves for currents mediated by $\alpha 1$ G254A GlyRs, induced by 100 μ M of glycine; NFA IC₅₀ at -80 mV = 260 μ M, -30 mV = 190 μ M, +30 mV = 106 μ M, +80 mV = 57 μ M.

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Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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