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Activation of $\alpha 6$ -containing GABA_A receptors by pentobarbital occurs through a different mechanism than activation by GABA

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Abstract

The GABA_A receptors are ligand-gated chloride channels which are the targets for many clinically used sedatives, including the barbiturates. The barbiturate pentobarbital acts through multiple sites on the GABA_A receptor. At low concentrations (μM), it acts as a positive allosteric modulator while at higher concentrations it can directly activate the receptor. This agonist action is influenced by the subunit composition of the receptor, and pentobarbital is a more effective agonist than GABA only at receptors containing an $\alpha 6$ subunit. The conformational change that translates GABA binding into channel opening is known to involve a lysine residue located in an extracellular domain between the 2nd and 3rd transmembrane domains. Mutations of this residue disrupt activation of the channel by GABA and have been linked to inherited epilepsy. Pentobarbital binds to the receptor at a different agonist site than GABA, but could use a common signal transduction mechanism to gate the channel. To address this question, we compared the effect of a mutating the homologous lysine residue in the $\alpha 1$ or $\alpha 6$ subunits (K278 or K277, respectively) to methionine on direct activation of recombinant GABA_A receptors by GABA or pentobarbital. We found that this mutation reduced GABA sensitivity for both $\alpha 1$ and $\alpha 6$ subunits, but affected pentobarbital sensitivity only for the $\alpha 1$ subunit. This suggests that pentobarbital acts through a distinct signal transduction pathway at the $\alpha 6$ subunit, which may account for its greater efficacy compared to GABA at receptors containing this subunit.

Introduction

Ligand-gated channels such as the GABA_A receptors (GABA_ARs) are complex, multimeric proteins. For the GABA_ARs, the pentameric complex can include subunits from seven different families and sixteen different subtypes (α_{1-6} , β_{1-3} , γ_{1-3} , δ , ϵ , π and θ) [3, 14]. Neurotransmitter binding occurs in the large extracellular domain while the ion channel gate is controlled by transmembrane domains. The structural mechanisms that link the binding event with the channel gating process have been the subject of much investigation. A recent study suggests that electrostatic interactions between negatively charged residues within the extracellular N-terminal domain and a positively charged lysine in the TM2–TM3 extracellular region are important for GABA-mediated channel gating [9]. Mutations of this

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lysine in the α or β subunit reduce GABA sensitivity [8, 15] while an inherited mutation of this lysine to methionine in the $\gamma 2$ subunit has been linked to epilepsy in humans [2].

In addition to GABA, a variety of compounds are known to act as agonists through different binding sites on the GABA_AR. Agonist activity is particularly associated with the i.v. anesthetics, which include the barbiturates. At low concentrations (<10 μ M, within the sedative therapeutic range of 0.5–3 μ g/ml), barbiturates act at a positive allosteric site to increase the response to GABA but at higher concentrations (>100 μ M) they can act as agonists, directly activating the receptor [6, 12, 13]. At most GABA_ARs, pentobarbital is a partial agonist. However, when the receptor contains an $\alpha 6$ subunit, pentobarbital produces larger maximum currents than GABA. [5, 16]. Pentobarbital acts as an agonist through a site distinct from the GABA binding site [16], and mutations within the extracellular N-terminal domain that reduce GABA binding do not typically influence activation by pentobarbital and vice versa [1, 5].

Although pentobarbital and GABA have separate binding sites, they may share a common structural mechanism to translate the binding signal into channel opening. To address this question, we compared the effect of mutating the M2–M3 lysine residue in the $\alpha 1$ and $\alpha 6$ subunits (Figure 1) on the ability of GABA or pentobarbital to activate the receptor. Wild-type or mutated α subunits were transiently transfected into HEK-293T cells along with $\beta 1$ and $\gamma 2L$ subunits. The functional responses of the receptors to GABA or pentobarbital were measured using whole-cell patch clamp recordings.

Materials and Methods

Transfection of mammalian cells

Full-length cDNAs encoding rat GABA_AR subunits in mammalian expression vectors were transiently transfected into the human embryonic kidney cell line HEK-293T. For selection of transfected cells, the plasmid pHookTM-1 (Invitrogen) encoding the surface antibody sFv was also transfected into the cells. Cells were maintained in DMEM supplemented with 10% fetal bovine serum, 100 IU/ml penicillin and 100 μ g/ml streptomycin. The cells were transfected using calcium phosphate precipitation with 2 μ g of each of the GABA_AR subunit cDNAs along with 1 μ g of the pHook plasmid. After a 2–5 hour incubation at 3% CO₂, the cells were treated with a 15% glycerol solution for 30 seconds. Cells were selected for pHook expression 44–52 hours after transfection [4]. Cells were resuspended into supplemented DMEM following a 2 min. incubation with 0.025% trypsin/0.01% EDTA solution in phosphate-buffered saline (10 mM Na₂HPO₄, 150 mM NaCl, pH = 7.3), incubated with antigen-coated magnetic beads ($\sim 6 \times 10^5$ beads), for 30–60 min. and then isolated with a magnetic stand. The isolated cells were plated onto glass coverslips coated with poly-lysine and collagen, and used for recording 20–28 hours later.

Electrophysiological recording of transfected cells

External solution for all recordings consisted of (in mM): 142 NaCl, 8.1 KCl, 6 MgCl₂, 1 CaCl₂ and 10 HEPES (4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid), (295–305 mOsm, pH=7.4). Recording electrodes were pulled from borosilicate glass on a two-stage puller (Narishige, Japan) to a resistance of 5–10 M Ω and filled with an internal solution consisting of (in mM); 153 KCl, 1 MgCl₂, 5 K-EGTA (ethylene glycol-bis (β -aminoethyl ether N,N,N',N'-tetraacetate) and 10 HEPES (295–305 mOsm, pH = 7.4). Drugs were applied to cells using a stepper solution exchanger (SF-77B, Warner Instruments) with a complete exchange time of <50 msec and currents were recorded with an Axon 200B patch clamp amplifier. GABA and pentobarbital were diluted into external solution from stock solutions in water.

Construction of mutations

Single point amino acid mutations were generated using the QuikChange procedure (Agilent Tech.). Oligonucleotide primers were synthesized and sequencing was performed by the University of South Carolina DNA core facility (Columbia, SC).

Data Analysis

Whole-cell currents were analyzed using Clampfit (pClamp 8.2 suite, Axon Instruments, Foster City CA) and Prism v.3.03 (Graphpad, San Diego, CA). Concentration response data were fit with a four-parameter logistic equation ($\text{Current} = [\text{Maximum current} + (\text{Maximum current} - \text{Minimum current}) / (1 + 10^{(\log EC_{50} - \log[GABA]^n)})$ where n represents the Hill number. Fits were made to data normalized to the maximum response for each cell. Because of the onset of inhibition, the response to 1 mM pentobarbital was excluded from the fit for the $\alpha 6\beta 3\gamma 2L$ isoform. To determine statistical significance, unpaired t-tests were performed using the Instat program (Graphpad) with a significance level of $p < 0.05$. The logs of the GABA EC_{50} measurements were used for statistical comparison.

RESULTS

Mutation of a TM2–TM3 lysine residue to methionine in either the $\alpha 1$ or $\alpha 6$ subunit reduces GABA sensitivity

All GABA_AR subunits contain a conserved lysine residue within the TM2–TM3 extracellular domain (Figure 1). Electrostatic interactions between its positively charged sidechain and negatively charged residues within the extracellular N-terminal domain have been suggested to mediate part of the signal transduction pathway from agonist binding to channel opening [9]. This lysine residue was changed to methionine to produce the $\alpha 1_{(K278M)}$ and $\alpha 6_{(K277M)}$ subunits. Each α subunit was co-expressed with wild-type $\beta 1$ and $\gamma 2L$ subunits to form heteromeric receptors. The $\beta 1$ subunit was used because it reduces the agonist activity of pentobarbital compared to the $\beta 3$ subunit and therefore produces a greater differentiation between $\alpha 1$ - and $\alpha 6$ -containing receptors [5, 16].

The mutations in either the $\alpha 1$ or the $\alpha 6$ subunit produced comparable effects on GABA sensitivity (Figure 2). Receptors containing $\alpha 1_{(K278M)}$ had an average GABA EC_{50} of $70.0 \pm 8.4 \mu\text{M}$ ($N=4$), significantly different ($p < 0.05$) from the wild-type $\alpha 1\beta 1\gamma 2L$ receptors ($17.6 \pm 3.7 \mu\text{M}$, $N=5$). Receptors containing the $\alpha 6$ subunit had an increased sensitivity to GABA compared to $\alpha 1$ -containing receptors, but the mutation produced a similar shift in GABA sensitivity, from $2.3 \pm 0.3 \mu\text{M}$ ($N=5$) for the wild-type receptors to $10.7 \pm 1.5 \mu\text{M}$ ($N=5$) for $\alpha 6_{(K277M)}\beta 1\gamma 2L$ ($p < 0.001$ compared to wild-type). Except for the change in GABA sensitivity, the mutations had no obvious effect on other properties of the whole-cell current. Consistent with the change in EC_{50} , currents from receptors with mutated subunits typically showed modestly faster deactivation and slower onset of desensitization. Quantification of these effects would require rapid application recordings from excised patches.

These data suggest that this lysine residue performs a similar role in signal transduction in response to GABA for both the $\alpha 1$ and $\alpha 6$ subunits. Since pentobarbital is a partial agonist at $\alpha 1$ -containing receptors, but is more efficacious than GABA at $\alpha 6$ -containing receptors, we compared the effect of the mutation in each subunit on the agonist activity of pentobarbital.

Mutation of lysine to methionine in the $\alpha 1$, but not the $\alpha 6$ subunit, reduced pentobarbital sensitivity

The mutation in the $\alpha 1$ subunit reduced its sensitivity to direct activation by pentobarbital (Figure 3). Pentobarbital is a relatively poor agonist at $\alpha 1\beta 1\gamma 2L$ receptors, producing a response to 1 mM pentobarbital averaging $66.3 \pm 4.2\%$ of the response to 1 mM GABA (N=7). The mutation significantly reduced the relative response to pentobarbital from the lowest effective concentration (100 μ M) to 1 mM. Inclusion of responses from higher concentrations of pentobarbital is limited by the onset of inhibition, making it difficult to accurately fit the concentration-response relationship for individual cells. Therefore, we were unable to statistically compare EC_{50} values. However, the EC_{50} to the fit of the averaged data (Figure 3B) was increased by the mutation from 630.9 μ M to 1.69 mM. These results are consistent with those reported by Sigel et al., [15], who also found reduced responsiveness to pentobarbital when the homologous lysine in the $\alpha 1$ or $\beta 2$ subunit was mutated to alanine.

In contrast, the K277M mutation in the $\alpha 6$ subunit had no apparent effect on the activation of the receptor by pentobarbital (Figure 3A, 3B). Pentobarbital is more efficacious than GABA at these receptors, and the mutation did not alter the maximum response. 300 μ M pentobarbital produced a current $204.0 \pm 7.4\%$ (wild-type, N=6) or $243.7 \pm 32.5\%$ ($\alpha 6_{(K277M)}$, N=6) of the response to 1 mM GABA ($p > 0.05$). The mutation also had no effect on the sensitivity of the receptor to direct activation by pentobarbital, with EC_{50} 's averaging $125.5 \pm 20.6 \mu$ M (wild-type, N=6) and $139.9 \pm 28.9 \mu$ M ($\alpha 6_{(K277M)}$, N=6) ($p > 0.5$).

Interestingly, the mutation did appear to reduce sensitivity to the inhibitory effects of pentobarbital, normally prominent at mM levels in these receptors (Figure 3B). To further characterize this observation, we tested the response to concentrations up to 10 mM. The mutations did not eliminate the inhibitory effect, as the reduced amplitude and rebound current were apparent for receptors containing all subunits in response to pentobarbital levels of 1 mM and higher (Figure 3C). However, for both α subunits, the mutation caused a slight shift in the concentration dependence of inhibition. For the $\alpha 6_{(K277M)}$ subunit, the amplitude of the current was significantly higher than the wild-type receptor at concentrations that produce inhibition (1–10 mM) although the maximum response still decreased with higher pentobarbital concentrations. For the $\alpha 1_{(K278M)}$ subunit, which shows reduced sensitivity to the agonist action of pentobarbital, the amplitude of the response was similar at 1 and 3 mM, suggesting that it also exhibits a lower sensitivity to inhibition. Therefore, unlike the effect on activation, the reduction in inhibition is observed in both $\alpha 1$ and $\alpha 6$ subunits.

These data suggest that this highly conserved lysine residue in the extracellular M2–M3 domain is important for agonist activity of both GABA and pentobarbital for the $\alpha 1$ subunit, but that it does not play a significant role in activation of $\alpha 6$ -containing receptors by pentobarbital. The ability of pentobarbital to utilize a distinct pathway for channel activation may be responsible for its greater efficacy compared to GABA at these receptors.

Discussion

The goal of this work was to determine whether pentobarbital and GABA rely upon the same structural mechanisms to induce the conformational changes that lead to channel gating. We compared the effect of mutating a conserved lysine residue in the extracellular TM2–TM3 domain of the α subunit on the response to GABA and pentobarbital. This residue is known to interact with negatively charged residues in the extracellular N-terminal domain of the subunit [9]. We found that mutating this residue to methionine in the $\alpha 1$ subunit had similar effects on the sensitivity to activation by either GABA or pentobarbital.

However, when created in the $\alpha 6$ subunit, the mutation reduced only the response to GABA, and not that to pentobarbital. At most GABA_ARs, including the $\alpha 1$ -containing receptors, pentobarbital is a weak partial agonist. However, at GABA_ARs containing the $\alpha 6$ subunit, pentobarbital is a better agonist, producing a maximum current nearly twice that seen in response to GABA. Our results suggest that this greater efficacy may be achieved through a unique signal transduction pathway, accessible by pentobarbital in the $\alpha 6$, but not the $\alpha 1$ subunit. Our finding that mutation of K278 in the $\alpha 1$ subunit reduced sensitivity to the agonist activity of both GABA and pentobarbital are in line with the findings of Hales et al. [8], who found that agonist activity of the anaesthetic propofol was also reduced by this mutation. Together these results suggest that all three of these agonists rely upon a common signal transduction pathway for the $\alpha 1$ subunit.

Our findings also suggest that the inhibitory effect of pentobarbital, apparent as a rapid channel block at mM levels, is also affected by this lysine residue. Unlike the agonist action, however, the mutation in either the $\alpha 1$ or $\alpha 6$ subunit had equivalent effects on the onset of inhibition. In this study we did not examine allosteric modulation by pentobarbital, but it may be of interest to determine if mutations at sites known to alter agonist properties also influence the activity of modulators. An earlier study found that modulation by phenobarbital was enhanced in receptors containing a $\gamma 2$ subunit mutated at the equivalent lysine residue [10]. However, this may have been related to the reduced sensitivity to inhibition that we observed in our study.

A substantial body of evidence suggests that the agonist binding sites for barbiturates and GABA are distinct [1, 5, 16]. Results from structural studies of $\alpha 1$ and $\beta 2$ subunits indicate that the conformational changes induced by these different agonists differ as well [11, 12]. The structural differences may reflect stabilization of distinct open or desensitized states of the channel. Interestingly, single channel studies have shown that for the $\alpha 1\beta 3\delta$ isoform, pentobarbital-gated openings have a longer mean duration than GABA-gated openings [6]. In particular, pentobarbital was able to induce openings to an additional, longer duration, open state that was not observed in response to GABA. Similar studies have not yet been performed with receptors containing the $\alpha 6$ subunit.

While our results indicate that the M2–M3 lysine residue is not critical for pentobarbital activation of $\alpha 6$ -containing receptors, it is not known what other structural interactions might be utilized by barbiturates to gate this channel. Amino acid residues within the N-terminal extracellular domain, the pre-M1 domain, the M2–M3 extracellular domain and the transmembrane domains have all been implicated in the signal transduction process for various members of the cys-loop family of ligand-gated channels (see [7] for review). Comparing the effects of mutations in these regions on activation of $\alpha 6$ -containing receptors by various agonists may provide insight into the multiple mechanisms by which signal transduction can occur at the GABA_ARs.

Acknowledgments

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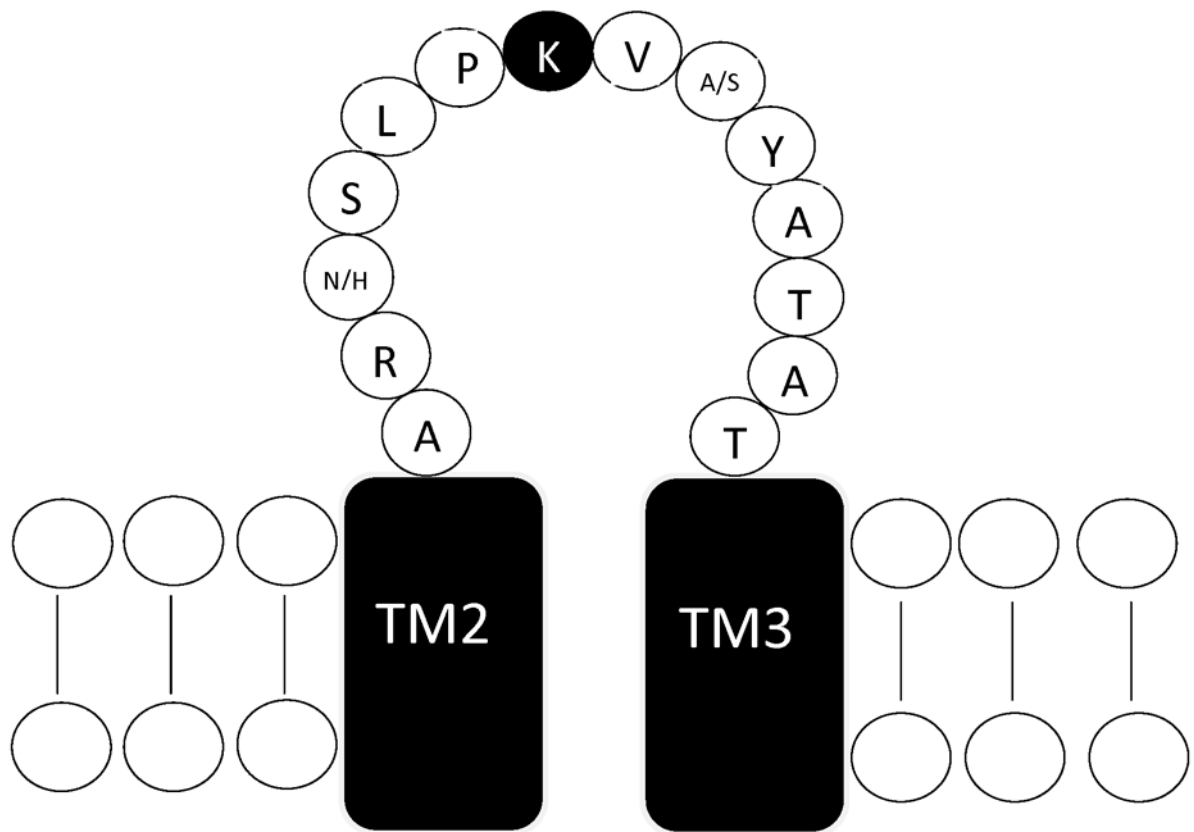


Figure 1. Location of mutation site

Schematic representation of the TM2–TM3 extracellular domain of the GABA_AR subunit. The conserved lysine residue mutated in this study is indicated by the filled circle. The $\alpha 1$ and $\alpha 6$ subunits differ at only two residues within in this domain, shown as $\alpha 1/\alpha 6$. Sequence from [17].

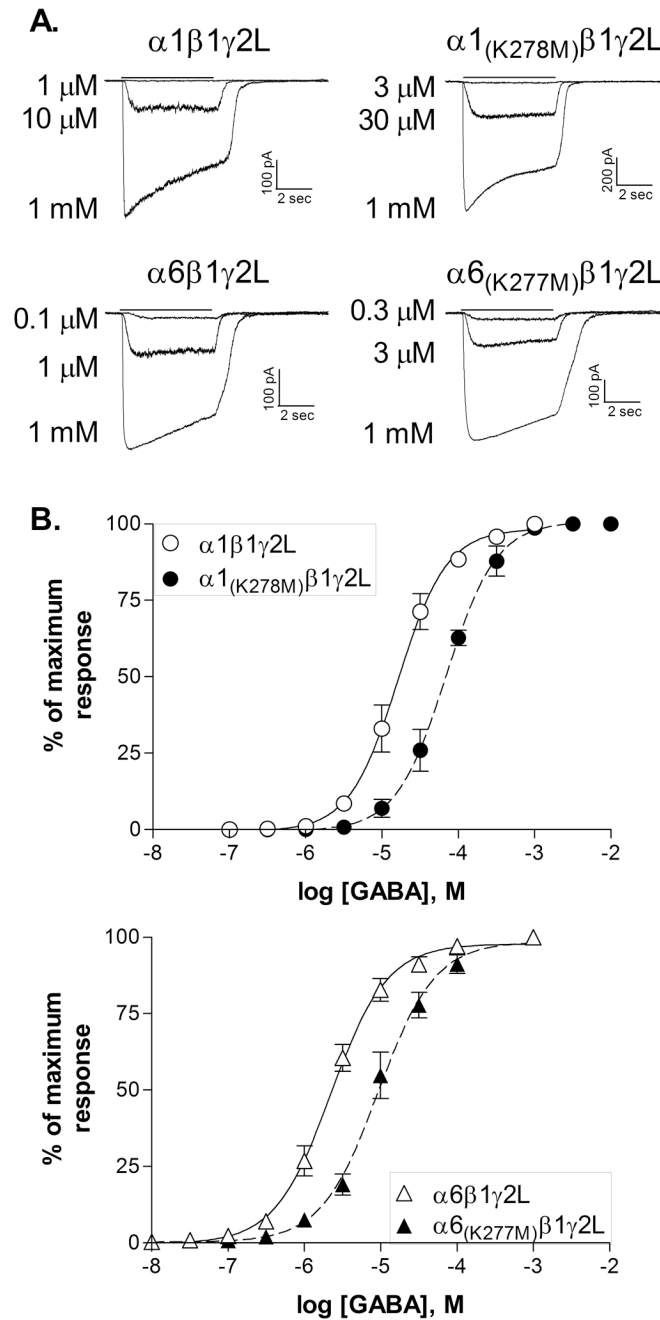


Figure 2. GABA sensitivity is reduced by the mutation of lysine to methionine

A. Representative current traces from receptors containing the subunits indicated in response to 5 sec applications of GABA (solid line). Whole-cell recordings were obtained at a membrane potential of -50 mV.

B. Concentration-response relationships were constructed by normalizing the peak response to each concentration of GABA to the maximum current response for each cell. Points shown are the mean \pm SEM. Averaged data were fit with a four-parameter logistic equation represented by the solid (wild type) or dashed (mutated) line. EC_{50} s for the fits shown are 16.2 μ M ($\alpha 1\beta 1\gamma 2L$, $N=5$), 69.1 μ M ($\alpha 1_{(K278M)}\beta 1\gamma 2L$, $N=4$), 2.2 μ M ($\alpha 6\beta 1\gamma 2L$, $N=5$) and 9.3 μ M ($\alpha 6_{(K277M)}\beta 1\gamma 2L$, $N=5$).

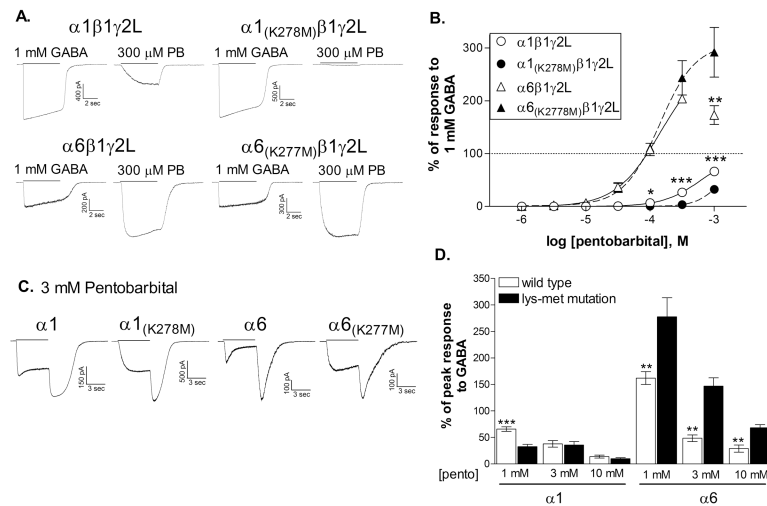


Figure 3. Direct activation by pentobarbital is reduced by the mutation of the $\alpha 1$ subunit but not of the $\alpha 6$ subunit

A. Representative whole-cell traces in response to a 5 sec applications (solid line) of 300 μM pentobarbital or 1 mM GABA at a membrane potential of -50 mV. Traces were obtained from the same cell for each subunit combination.

B. Concentration-response relationships were constructed by dividing the peak response to each concentration of pentobarbital by the response to 1 mM GABA for each cell. The maximum response to GABA (100%) is indicated by the dotted line. Points shown are the mean \pm SEM. Averaged data were fit with a four-parameter logistic equation represented by the solid (wild type) or dashed (mutated) line. Because of the onset of inhibition, the response to 1 mM pentobarbital was not included in the fit for the wild-type $\alpha 6\beta 3\gamma 2L$ isoform. EC_{50} s for the fits shown are 630.9 μM ($\alpha 1\beta 1\gamma 2L$, N=7), 1.69 mM ($\alpha 1(K278M)\beta 1\gamma 2L$, N=6), 143.9 μM ($\alpha 6\beta 1\gamma 2L$, N=6) and 140.2 μM ($\alpha 6(K277M)\beta 1\gamma 2L$, N=6). *(p 0.05) or ***(p 0.001) indicate a significant difference between the wild-type and mutated counterparts (unpaired, 2-tailed t-test).

C. Whole-cell traces in response to a 5 sec applications (solid line) of 3 mM pentobarbital at a membrane potential of -50 mV. Rebound current following the removal of applied drug is characteristic of rapid open channel block.

D. The peak current response during pentobarbital application was measured. Symbols and bars represent the average \pm SEM. Data from 5–10 cells for each concentration *(p 0.01) or ***(p 0.001) indicate a significant difference from the mutated counterpart (unpaired, 2-tailed t-test).