

Agonist Gating and Isoflurane Potentiation in the Human γ -Aminobutyric Acid Type A Receptor Determined by the Volume of a Second Transmembrane Domain Residue

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Received June 3, 1999; accepted August 12, 1999

This paper is available online at <http://www.molpharm.org>

ABSTRACT

γ -Aminobutyric acid type A (GABA_A) receptors are targets for allosteric modulation by general anesthetics. Mutation of Ser270 within the second transmembrane domain of the GABA_A receptor α subunit can ablate the modulation of the receptor by the anesthetic ether isoflurane. To investigate further the function of this critical amino acid residue, we made multiple amino acid substitutions at Ser270 and analyzed the concentration-dependent gating by GABA and regulation by isoflurane in each mutant receptor. There is a strong negative correlation between the EC₅₀ for GABA and the molecular volume of the amino acid residue at position 270. Replacement of Ser by large residues such as His and Trp produced a shift of the GABA concentration-response curve to the left, whereas

replacement of Ser with Gly had the opposite effect. There also was a strong negative association between the molecular volume of the amino acid residue at 270 and the degree of enhancement of submaximal GABA responses by isoflurane. These results indicate the significance of the amino acid at position α 270 in gating of the GABA_A receptor. In addition, the data on isoflurane are consistent with the existence of a cavity of finite size in the region of α 270 that may be filled by the anesthetic molecule or by the side chain of a larger residue at α 270. The introduction of isoflurane, or of a large residue, into this cavity may stabilize the open state of the GABA_A receptor relative to the closed state.

The major family of receptors for γ -aminobutyric acid (GABA), the GABA_A receptors, are members of the "gene superfamily" of "Cys-loop" ligand-gated ion channels (Ortells and Lunt, 1995). The GABA_A receptor is a pentameric complex of protein subunits surrounding a central Cl⁻-permeable pore (Bormann et al., 1987). Native GABA_A receptors usually contain α , β , and γ subunits (McKernan and Whiting, 1996) in a 2:2:1 stoichiometry (Chang et al., 1996; Tretter et al., 1997). The existence of six α subunit isoforms enables considerable anatomical and functional diversity of GABA_A receptors (Fritschy and Mohler, 1995; Sieghart, 1995; Nusser et al., 1996). In particular, the α subunit isoform may influence agonist potency (Levitan et al., 1988), agonist efficacy (Ebert et al., 1994), regulation by benzodiazepines (Wafford et al., 1992), and channel

kinetics (Tia et al., 1996; Lavoie et al., 1997). Many general anesthetics are allosteric modulators of the GABA_A receptor (Franks and Lieb, 1994; Harris et al., 1995), and mutation of a critical Ser residue within the second transmembrane domain (TM2) of the GABA_A receptor α subunit can ablate or mask the modulation of the receptor by the anesthetic ethers enflurane (Mihic et al., 1997) and isoflurane (Krasowski et al., 1998). Results obtained with the GABA_A receptor α 2 S270I (Mihic et al., 1997) and S270H mutants (Krasowski et al., 1998) strongly suggested an important role for α Ser270 in the regulation of GABA_A receptor function by these anesthetics. Because the side chains of Ile and His are both physically larger and Ile is considerably more hydrophobic than is Ser, we sought to determine the effects of other amino acid substitutions at this position. The multiple point mutants were then used to investigate whether size, hydrophilicity, or some other physical parameter of the residue at this position was relevant to the gating behavior and anesthetic modulation of the GABA_A receptor.

Materials and Methods

Site-Directed Mutagenesis. To create the mutant series at GABA_A receptor α 2 Ser270, mutations were introduced into the

This research was supported by National Institutes of Health Grants GM 45129 and GM 56850, and Research Career Development Award GM 00623 to N.L.H., and by institutional postdoctoral training Grant DA 07255 (University of Chicago) to V.V.K.

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ABBREVIATIONS: GABA, γ -aminobutyric acid; Glu, glutamate; HEK, human embryonic kidney; α 2(S270X) β 1, receptor harboring a mutation in the α subunit at Ser270; AChR, nicotinic acetylcholine receptor; TM1, -2, -3, first, second, third transmembrane domain.

cDNA encoding the human GABA_A receptor $\alpha 2$ subunit at bases 890 to 892, with simultaneous loss of a *DdeI* restriction site. Oligonucleotides, 24 to 30 bases in length, were obtained from Operon Technologies (Alameda, CA) and 5'-phosphorylated using polynucleotide kinase, and used to create mutations using the unique site-elimination method (Deng and Nickoloff, 1992) (USE kit; Pharmacia Biotechnology Inc., Piscataway, NJ), a two-primer method in which a unique *SspI* site in the expression vector pCIS2 was mutated concurrently to an alternate restriction site (*EcoRV* or *MluI*). *SspI* digestion then was used to select in favor of mutants, and clones were screened for the appearance of the desired mutation by digestion with *DdeI*. A few additional mutations were created, at Thr268, Leu269, and Ile271 in GABA_A receptor $\beta 1$, and at Ser265 in GABA_A receptor $\beta 1$, using a *Pfu* polymerase/*DpnI* selection method (QuikChange; Stratagene, La Jolla, CA). All restriction enzymes and polynucleotide kinase were obtained from New England Biolabs (Beverly, MA). The sequences of all cDNA inserts were confirmed throughout by double-stranded sequencing (Sequenase 2.0; U.S. Biochemical Corp., Cleveland, OH), using appropriate oligonucleotide sequencing primers, and are available for inspection on request.

Cell Culture and Transfection. Wild-type or mutant receptor GABA_A receptor cDNAs were expressed via the vector pCIS2, which contains one copy of the strong promoter from cytomegalovirus and a polyadenylation sequence from simian virus 40. These constructs were used to transfect human embryonic kidney (HEK)293 cells (American Type Culture Collection, Rockville, MD), as described previously (Pritchett et al., 1988). HEK293 cells were maintained in culture on glass coverslips; cells were passaged weekly by trypsin treatment up to 15 times before being discarded and replaced with early passage cells. Each coverslip of cells was transfected using the CaPO₄ precipitation technique (Okayama and Chen, 1987). One to five micrograms of each cDNA was used per coverslip; the cDNA was in contact with the cells for 24 h in an atmosphere containing 3% CO₂ before being removed and replaced with fresh culture medium in an atmosphere of 5% CO₂.

Electrophysiology. The coverslips were transferred, between 24 and 72 h after removal of the cDNA, to a large chamber (60 ml) and perfused continuously (20 ml/min) with extracellular medium. Recordings from HEK293 cells were made using the whole-cell patch-clamp technique, as described previously (Koltchine et al., 1996). Patch pipettes contained: 145 mM *N*-methyl-D-glucamine hydrochloride, 5 mM dipotassium ATP, 1.1 mM EGTA, 2 mM MgCl₂, 5 mM HEPES/KOH, 0.1 mM CaCl₂ (pH 7.2). Pipette resistance was 4 to 5 M Ω . The extracellular medium contained: 145 mM NaCl, 3 mM KCl, 1.5 mM CaCl₂, 1 mM MgCl₂, 6 mM D-glucose, 10 mM HEPES/NaOH (pH 7.4). HEK293 cells were voltage-clamped at -60 mV. In addition to the continuous slow bath perfusion, drugs and solutions were

applied rapidly to the cell by local perfusion using a motor-driven solution exchange device (Bio Logic Rapid Solution Changer RSC-100; Molecular Kinetics, Pullman, WA). Laminar flow was achieved by driving all solutions at identical flow rates via a multichannel infusion pump (Stoelting; Wood Dale, IL). Loss of the anesthetic isoflurane using this perfusion device has been measured using gas chromatography and represents only 5 to 10% of the total applied drug concentration (M. D. Krasowski, unpublished observations). The solution changer was driven by protocols in the acquisition program pCLAMP5 (Axon Instruments, Foster City, CA), as described previously (Koltchine et al., 1996). Responses were digitized (TL-1-125 interface; Axon Instruments) using pCLAMP5 (Axon Instruments). Numerical data are presented throughout as mean \pm S.E. ATP was obtained from Calbiochem and isoflurane from Ohmmeda (Madison, WI); all other chemicals were obtained from Sigma (St. Louis, MO).

Data Analysis, Curve Fitting, and Determination of Parameters of Dose-Response Curves. Control GABA concentration-response data were expressed as a fraction of the maximal response

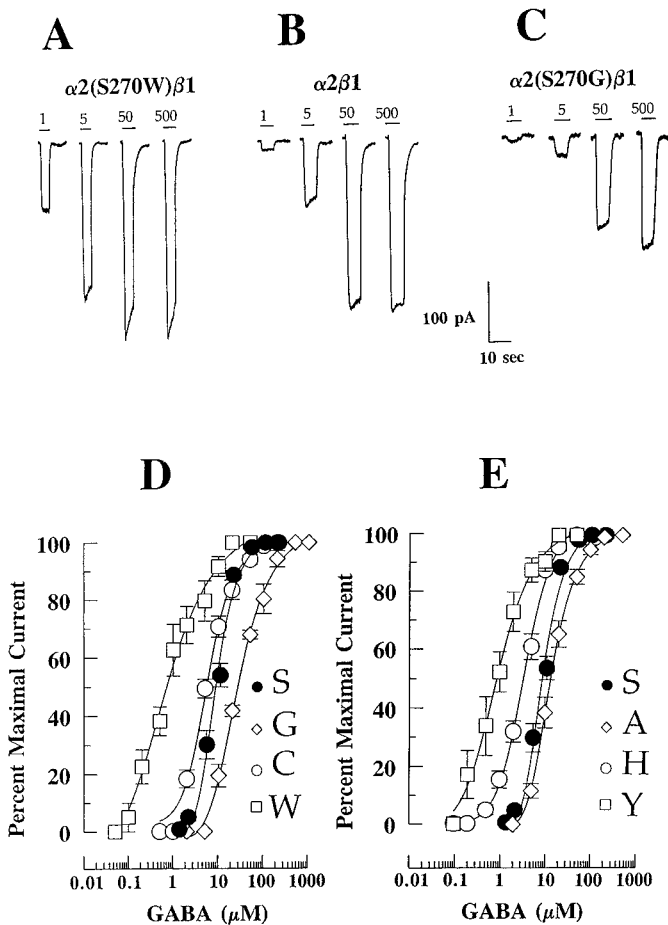


Fig. 1. HEK293 cells coexpressing mutant $\alpha 2$ (S270X) and wild-type $\beta 1$ GABA_A receptor subunits form functional GABA-activated Cl⁻ channels. A–C, representative currents elicited by 2-s applications of 1, 5, 50, and 500 μ M GABA recorded from cells expressing receptors made up of $\alpha 2$ (S270W) $\beta 1$ (A), wild-type $\alpha 2\beta 1$ (B), and $\alpha 2$ (S270G) $\beta 1$ subunits (C). Notice the modest current activated by 5 μ M GABA when $\alpha 2$ Ser270 is mutated to Gly, whereas the same concentration of GABA activates near-maximal current in receptors in which Ser270 is mutated to Trp. The bars above the current traces indicate the period of GABA application and are labeled with the GABA concentration in μ M. D, concentration-response curves for GABA in wild-type (S), and $\alpha 2$ (S270G) $\beta 1$, $\alpha 2$ (S270C) $\beta 1$, and $\alpha 2$ (S270W) $\beta 1$ mutant GABA_A receptors. E, concentration-response curves for GABA in wild-type (S), and $\alpha 2$ (S270H) $\beta 1$, $\alpha 2$ (S270Y) $\beta 1$ mutant GABA_A receptors.

TABLE 1

A summary of the characteristics of GABA responses in the $\alpha 2$ (S270X) $\beta 1$ series of GABA_A receptors. EC₅₀ concentration, Hill coefficient (n_H), and I_{max} are given for each receptor as mean \pm S.E. for N cells determined, using the methods described. Statistical significance was assessed using a Student's *t* test.

GABA _A -R	EC ₅₀ (μ M)	N	n_H	I_{max} (pA)
$\alpha 2\beta 1$ WT	8.6 \pm 0.8	9	1.9 \pm 0.2	455 \pm 76
$\alpha 2$ (S270A) $\beta 1$	15.5 \pm 2.2*	4	1.6 \pm 0.2	168 \pm 36
$\alpha 2$ (S270C) $\beta 1$	4.8 \pm 0.4*	5	1.4 \pm 0.2	168 \pm 23
$\alpha 2$ (S270E) $\beta 1$	3.0 \pm 0.3**	7	1.5 \pm 0.1	197 \pm 28
$\alpha 2$ (S270F) $\beta 1$	1.3 \pm 0.3**	7	1.6 \pm 0.1	219 \pm 20
$\alpha 2$ (S270G) $\beta 1$	27.3 \pm 1.9**	4	1.3 \pm 0.2*	146 \pm 16
$\alpha 2$ (S270H) $\beta 1$	2.4 \pm 0.5**	9	1.5 \pm 0.1	322 \pm 40
$\alpha 2$ (S270I) $\beta 1$	1.3 \pm 0.2**	6	2.0 \pm 0.4	289 \pm 49
$\alpha 2$ (S270R) $\beta 1$	1.1 \pm 0.2**	5	1.9 \pm 0.4	352 \pm 60
$\alpha 2$ (S270T) $\beta 1$	7.2 \pm 1.5	6	1.5 \pm 0.1	442 \pm 62
$\alpha 2$ (S270W) $\beta 1$	0.9 \pm 0.3**	5	1.0 \pm 0.2*	347 \pm 85
$\alpha 2$ (S270Y) $\beta 1$	0.9 \pm 0.2**	4	1.2 \pm 0.1*	332 \pm 86

* *p* < .01 compared with the control group.

** *p* < .001 compared with the control group.

to GABA in each cell, allowing normalized data from different cells to be combined. Pooled data were fitted, using a weighted sum of least-squares method, to a Hill equation of the form:

$$\frac{I}{I_{\max}} = 100 \times \frac{[\text{GABA}]^n}{[\text{GABA}]^n + \text{EC}_{50}^n} \quad (1)$$

where I is the whole-cell current amplitude expressed as a percentage of the current maximal peak current (I_{\max}), $[\text{GABA}]$ is the GABA concentration, EC_{50} is the GABA concentration eliciting a current equal to half of I_{\max} , and n is the Hill coefficient. Percentage potentiation of a submaximal GABA response by the anesthetic isoflurane was then calculated as the percentage increase above the control (EC_{20}) response to GABA in the presence of anesthetic. Statistical comparisons were made, and significance was assessed using Student's t test.

Results

Eleven mutant GABA_A receptors harboring a mutation in the α subunit at Ser270 [$\alpha 2(\text{S270X})\beta 1$] were studied by whole-cell voltage clamp, after transient expression in HEK-293 cells. First, reproducible whole-cell Cl^- currents activated by 50 nM to 1 mM GABA were recorded in the absence of other drugs. In all mutant receptors, the maximal response amplitude was between 30 and 100% of that in the wild-type GABA_A receptor (Table 1). Figure 1A shows that in the wild-type receptor, 5 μM GABA recruited a current that was ~30% of the maximal response activated by 500 μM GABA. When Ser270 was mutated to Trp, the same concentration of GABA elicited a near-maximal response; conversely, when Ser270 was mutated to Ala, only 2% of the maximum current was obtained at 5 μM GABA.

Full concentration-response curves for GABA were determined in cells expressing the wild-type GABA_A receptor and the $\alpha 2(\text{S270X})\beta 1$ receptor mutants. The currents activated by at least seven concentrations of GABA were expressed as a fraction of the maximal GABA response, and these normalized data were fitted by a Hill equation (see *Methods*, equation 1). Mutation of Ser270 to smaller amino acid residues (Ala and Gly) produced a rightward shift in the GABA concentration-response curve; conversely, mutating Ser270 to larger amino acid residues such as His and Tyr caused a leftward shift in the curves (Fig. 1B). Concentration-response curves also were constructed for wild-type and mutant $\alpha 2\beta 1$

and $\alpha 2\beta 1\gamma 2$ s GABA_A receptors (Table 2). As described previously (Draguhn et al., 1990; Smart et al., 1991; Horenstein and Akabas, 1998), the coexpression of the $\gamma 2$ s subunit along with the $\alpha\beta$ subunits was detected by, and associated with, changes in zinc sensitivity of the resulting GABA_A receptor. The inclusion of the $\gamma 2$ s subunit had little or no effect on the GABA EC_{50} in receptors containing either wild-type or mutant $\alpha 2$ subunits (Fig. 2). Therefore, we suggest that the data from $\alpha 2(\text{S270X})\beta 1$ GABA_A receptors also apply to $\alpha 2(\text{S270X})\beta 1\gamma 2$ GABA_A receptors. The isoflurane experiments described below were not repeated in the presence of the $\gamma 2$ subunit, because this subunit is not required for modulation by isoflurane (Harrison et al., 1993; Krasowski et al., 1998).

The effects of Trp mutations at positions adjacent to $\alpha 2$ Ser270 and at the $\beta 1$ homolog Ser265 also were determined. The $\alpha 2(\text{T268W})$ mutant expressed poorly or not at all (typically <50 pA GABA current). The $\alpha 2(\text{I271W})$ and $\alpha 2(\text{L269W})$ mutations had little effect on the GABA concentration-response relationship. Mutation of Ser265 to Trp in the $\beta 1$ subunit reduced the GABA EC_{50} , but less so than for the $\alpha 2(\text{S270W})$ mutant (Table 2). Coexpressing $\alpha 2(\text{S270W})$ and $\beta 1(\text{S265W})$ mutant subunits produced a receptor with a similar GABA EC_{50} , but weak expression.

Clinically relevant concentrations of anesthetics such as isoflurane (0.2–0.7 mM) enhance submaximal responses in neuronal GABA_A receptors (Jones et al., 1992). This enhancement is associated with a parallel leftward shift of the GABA concentration-response curve for the wild-type GABA_A receptor (Fig. 3A), consistent with an increase in the apparent affinity of GABA in the presence of the anesthetic. This leftward shift in the GABA concentration-response curve is strikingly similar to that observed on mutagenesis of Ser270 to Trp (Fig. 3B). Potentiation of receptor function by isoflurane was assessed by using an EC_{20} concentration of GABA appropriate for the receptor under study. Figure 3C shows the modulation by isoflurane of responses to a submaximal (EC_{20}) concentration of GABA in cells expressing wild-type $\alpha 2\beta 1$, mutant $\alpha 2(\text{S270A})\beta 1$, and mutant $\alpha 2(\text{S270W})\beta 1$ GABA_A receptors. In the $\alpha 2(\text{S270A})$ receptor mutant, the magnitude of potentiation by isoflurane is similar to that seen in the wild-type GABA_A receptor, whereas in the $\alpha 2(\text{S270Y})$ mutant, isoflurane does not enhance GABA currents. Table 3 shows the percentage modulation by 0.5 and 1 mM isoflurane of GABA-activated currents in the 11

TABLE 2

A summary of GABA response data for the $\alpha 2(\text{S270X})\beta 1\gamma 2$ series of GABA_A receptors and for mutant GABA_A receptors of the form $\alpha 2^*\beta 1$, in which mutations are made in residues neighboring Ser270

EC_{50} concentration, Hill coefficient (n_H), and I_{\max} are given for each receptor as mean \pm S.E. for N cells determined, using the methods described. Statistical significance was assessed using Student's t test.

GABA _A -R	EC_{50} (μM)	N	n_H	I_{\max} (pA)
$\alpha 2\beta 1$ WT	8.6 \pm 0.8	9	1.9 \pm 0.2	455 \pm 76
$\alpha 2(\text{S270A})\beta 1$	15.5 \pm 2.2*	4	1.6 \pm 0.2	168 \pm 36
$\alpha 2(\text{S270W})\beta 1$	0.9 \pm 0.3**	5	1.0 \pm 0.2*	347 \pm 85
$\alpha 2\beta 1\gamma 2$ WT	12.0 \pm 1.3	5	1.7 \pm 0.2	779 \pm 453
$\alpha 2(\text{S270A})\beta 1\gamma 2$	19.0 \pm 2.7*	4	1.9 \pm 0.1	360 \pm 99
$\alpha 2(\text{S270W})\beta 1\gamma 2$	1.7 \pm 0.9**	4	1.2 \pm 0.3	214 \pm 28
$\alpha 2\beta 1$ WT	8.6 \pm 0.8	9	1.9 \pm 0.2	455 \pm 76
$\alpha 2(\text{L269W})\beta 1$	9.3 \pm 1.0	5	1.3 \pm 0.1*	216 \pm 27
$\alpha 2(\text{I271W})\beta 1$	8.9 \pm 0.9	5	1.5 \pm 0.2	163 \pm 17
$\alpha 2\beta 1(\text{S265W})$	2.4 \pm 0.7**	5	1.2 \pm 0.1*	348 \pm 13
$\alpha 2(\text{S270W})\beta 1(\text{S265W})$	3.5 \pm 0.5**	5	1.5 \pm 0.3	137 \pm 13

* $p < .01$ compared with the control group.

** $p < .001$ compared with the control group.

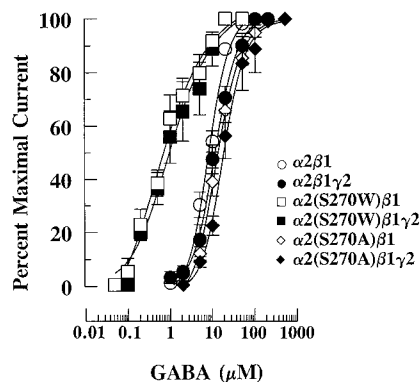


Fig. 2. Inclusion of the γ subunit does not alter significantly the GABA concentration-response curve in GABA_A receptors consisting of $\alpha 2(\text{S270X})\beta 1$.

$\alpha 2$ (S270X) $\beta 1$ mutant receptors. The largest potentiation was observed in the wild-type; $\alpha 2$ (S270A) $\beta 1$ showed identical potentiation. Mutation of Ser270 to Gly, Cys, or Thr resulted in modest anesthetic potentiation; Phe, Ile, His, and larger substitutions rendered the receptor insensitive to clinically relevant concentrations of isoflurane. An extensive study of the concentration-effect curve for GABA potentiation by isoflurane was made in three mutant receptors: $\alpha 2$ (S270C) $\beta 1$, $\alpha 2$ (S270Y) $\beta 1$, and $\alpha 2$ (S270W) $\beta 1$, and compared with the results obtained in the wild-type receptor (Fig. 3D). These data suggest that the effects of Cys and Thr mutations result from a decrease in efficacy for potentiation rather than from a change in the affinity of the receptor for isoflurane. The

mutant receptors $\alpha 2$ (L269W) $\beta 1$ and $\alpha 2$ (I271W) $\beta 1$ showed near-normal potentiation by isoflurane (data not shown).

Discussion

Gating of Receptor Mutants by GABA. We conclude from our data that substitution at $\alpha 2$ Ser270 did not compromise ion channel function, consistent with the notion that these point mutations do not induce large changes in secondary structure, at least in the region of the pore. No mutation at Ser270 completely abolished gating by GABA, consistent with the idea that the structure of the agonist binding site also was not disrupted dramatically. The mutations

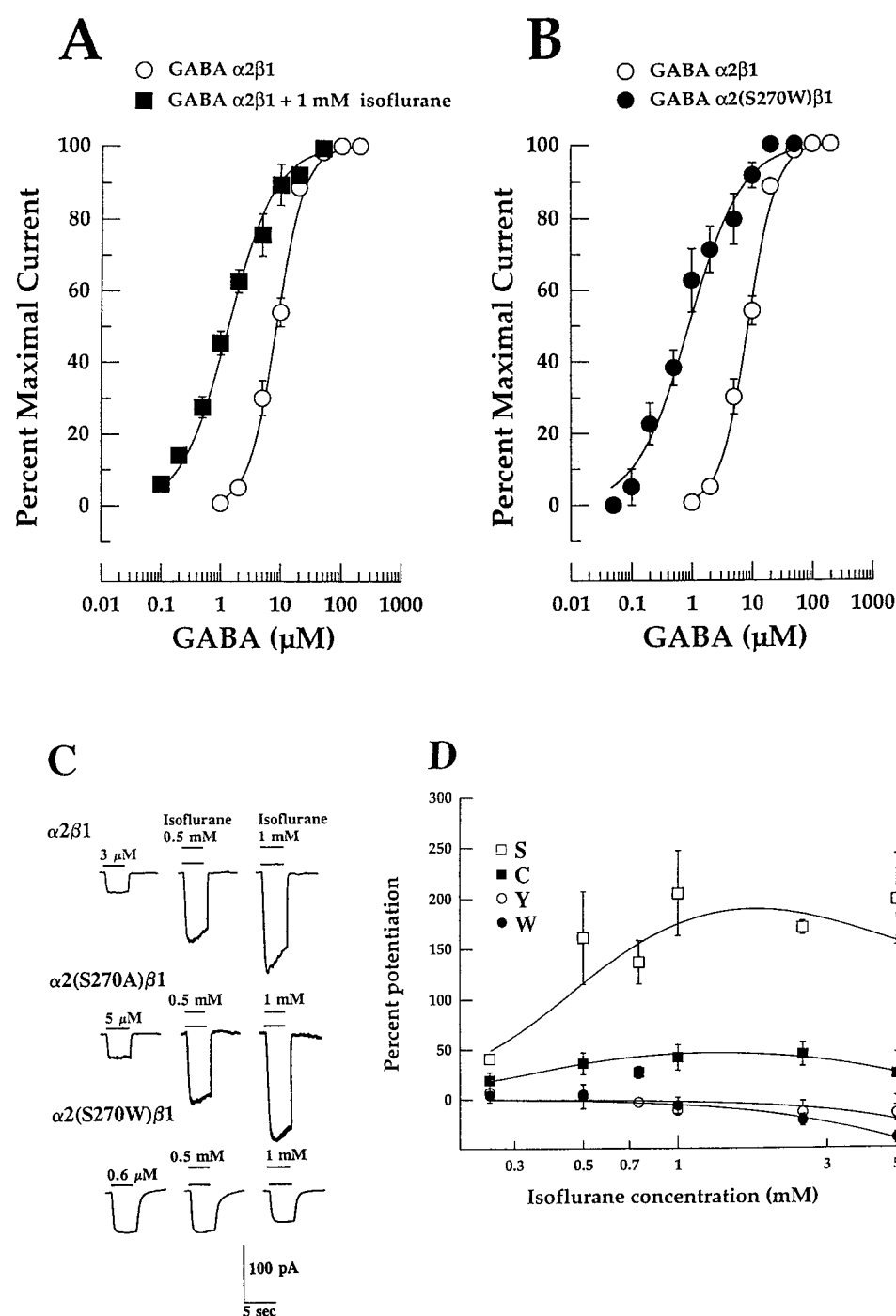


Fig. 3. Trp mutagenesis at α Ser270 mimics the effect of isoflurane on GABA_A receptor function. **A**, leftward shift of the GABA concentration-response curve for the wild-type $\alpha 2\beta 1$ GABA_A receptor in the presence of 1 mM isoflurane. **B**, leftward shift of the GABA concentration-response curve for the $\alpha 2$ (S270W) $\beta 1$ GABA_A receptor relative to the wild-type $\alpha 2\beta 1$ GABA_A receptor. **C**, allosteric potentiation of submaximal (EC_{20}) GABA responses occurs in the $\alpha 2$ (S270X) $\beta 1$ series of GABA_A receptors when the $\alpha 270$ substituent is small (Ser, Ala), but not when it is larger (Tyr). **D**, concentration-response curves for isoflurane potentiation of an EC_{20} concentration of GABA in wild-type (S), and mutant $\alpha 2$ (S270C) $\beta 1$, $\alpha 2$ (S270Y) $\beta 1$, and $\alpha 2$ (S270W) $\beta 1$ mutant GABA_A receptors.

$\alpha 2$ (L269W) and $\alpha 2$ (I271W) had little effect on receptor function, suggesting again no large changes in secondary structure in this region. These results highlight the significance of the α Ser270 residue. In studies of mutations in the highly homologous and presumably structurally related glycine receptor, it appears that mutations in the nearby TM2 to TM3 linker region alter the transduction mechanism between agonist binding and channel gating, but do not affect ligand binding per se (Lynch et al., 1997).

The data shown in Fig. 2 and Table 1 clearly show the

TABLE 3

A summary of the effects of 0.5 and 1 mM isoflurane on the $\alpha 2$ (S270X) $\beta 1$ series of GABA_A receptors

Percent potentiation of EC₂₀ GABA responses by 0.5 and 1.0 mM isoflurane are given for each receptor as mean \pm S.E. for N cells determined, using the methods described. Statistical significance was assessed using a Student's *t* test.

GABA _A -R	Percent potentiation by isoflurane			
	0.5 mM	N	1.0 mM	N
$\alpha 2\beta 1$ WT	161 \pm 46	6	205 \pm 42	6
$\alpha 2$ (S270A) $\beta 1$	162 \pm 20	4	236 \pm 31	4
$\alpha 2$ (S270C) $\beta 1$	36 \pm 11*	6	42 \pm 13*	6
$\alpha 2$ (S270E) $\beta 1$	11 \pm 11*	7	17 \pm 9*	7
$\alpha 2$ (S270F) $\beta 1$	-0.4 \pm 0.6*	6	-13 \pm 5*	6
$\alpha 2$ (S270G) $\beta 1$	14 \pm 8*	6	45 \pm 11*	7
$\alpha 2$ (S270H) $\beta 1$	-8 \pm 2*	4	-5 \pm 2*	4
$\alpha 2$ (S270I) $\beta 1$	2 \pm 6*	8	2 \pm 5*	6
$\alpha 2$ (S270R) $\beta 1$	-5 \pm 14*	6	-12 \pm 18*	5
$\alpha 2$ (S270T) $\beta 1$	47 \pm 6*	4	67 \pm 15*	4
$\alpha 2$ (S270W) $\beta 1$	2 \pm 16*	4	-24 \pm 21*	4
$\alpha 2$ (S270Y) $\beta 1$	3 \pm 12*	5	-11 \pm 5*	5

* *p* < .01 compared with the control group.

apparent affinity for GABA of these mutant GABA_A receptors to be dependent on the specific amino acid residue at position 270 on the $\alpha 2$ subunit. To determine whether this was attributable to a specific physical property of each amino acid, we plotted the GABA EC₅₀ against the volume of the amino acid side chain (Fig. 4A), amino acid polarity (Fig. 4B), hydrophobicity (Fig. 4C), or hydrophilicity (Fig. 4D). A strong negative correlation (*r* = -0.94) was observed between the volume of the amino acid residue/side chain present at $\alpha 270$ and the GABA EC₅₀ value (Fig. 4A). However, no statistically significant correlation was found between GABA EC₅₀ and amino acid polarity, hydrophobicity, or hydrophilicity. The striking association shown in Fig. 4A might reflect an increase in the stability of the open state, relative to the closed state, of the GABA-operated ion channel as the size of the side chain at $\alpha 270$ increases. A similar phenomenon with respect to side chain volume was noted in the nicotinic acetylcholine receptor (nAChR) with restricted series of mutations of a cysteine residue in TM1 of the γ subunit (Lo et al., 1991). In mutational studies of the GABA_A receptor $\alpha 1$ Leu264 residue (Chang et al., 1996), a leftward shift in the GABA concentration-response curve was produced by substitution of Leu with smaller residues such as Ser. This also was ascribed to an effect on channel gating, rather than to alterations in the affinity of agonist binding. In any case, this specific hypothesis can be evaluated in the future with single-channel recordings in selected receptor mutants. A fine example of this is the recent analysis of mutants involving

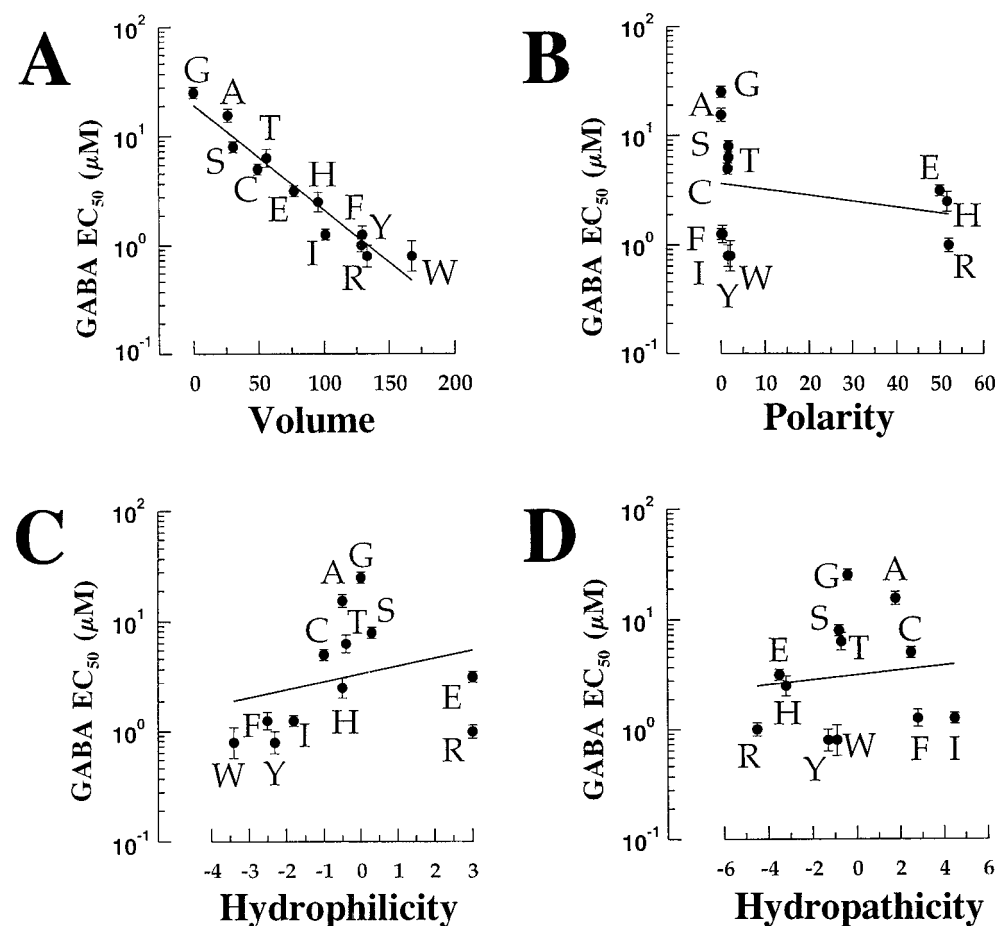


Fig. 4. The EC₅₀ for GABA within the series of $\alpha 2$ (S270X) $\beta 1$ mutant GABA_A receptors is correlated inversely with the molecular volume of the amino acid at position 270 on the GABA_A-R $\alpha 2$ subunit. The correlation of the physical properties of the amino acid at position 270 with GABA EC₅₀ values obtained from Hill equation fits to GABA concentration-response data (see *Materials and Methods*, Fig. 3, and Table 1) showed (A) a strong negative correlation with molecular volume (*T* = 9.25, *p* < .0005, *r* = -0.95), whereas no significant correlations were found with (B) side-chain polarity (*T* = 0.78, *p* > .22, *r* = -0.24), (C) hydrophilicity (*T* = 0.91, *p* > .18, *r* = 0.28), or (D) hydropathicity (*T* = 0.37, *p* > .36, *r* = 0.11). Physical parameters are from Harpaz et al. (1994), Hopp and Woods (1981), Kyte and Doolittle (1982), and Zimmerman et al. (1968).

substitution of a Val residue in TM3 of the nAChR $\alpha 1$ subunit (Wang et al., 1999).

Regulation of Receptor Mutants by Isoflurane. When the GABA_A receptor $\alpha 2$ Ser270 mutants were tested for modulation by isoflurane, we noted that there appeared to be a limiting volume for the side chains, such that amino acid residues with small side chains, such as Ser or Ala, permitted isoflurane modulation, whereas larger side chains such as Cys or Thr allowed only weak modulatory effects of isoflurane (Fig. 5). Many potential explanations exist for the data for the $\alpha 2$ Ser270 mutants and the effects of isoflurane on the wild-type and mutant GABA_A receptors. Without structural information on this part of the receptor molecule, such ideas necessarily must remain speculative. One possibility is that residue $\alpha 2$ Ser270 is involved in structural rearrangements that accompany gating, and that isoflurane, like GABA, binds elsewhere on the receptor molecule to influence the transduction of agonist binding into channel opening. We prefer at present to speculate that the wild-type receptor, with Ser present at $\alpha 270$, contains one or more cavities of finite size within the GABA_A receptor protein, possibly contained entirely within a single α subunit. Mutation of $\alpha 2$ Ser270 to very large residues, such as Phe, Tyr, or Trp (side chain volumes 130, 133, or 168 Å³, respectively; Harpaz et al., 1994), may stabilize the open state of the channel relative to the closed state by occlusion of this cavity. Similarly, the cavity may be filled partially by an isoflurane molecule (molecular volume 140 Å³; J. Trudell, personal communication), stabilizing the open state in similar manner. The existence, although not the location, of such cavities in ion channel proteins has been inferred from studies of the "cutoff" in activity in the *N*-alcohol series as chain length increases. Not only do different ligand-gated ion channels show different alcohol cutoffs (Li et al., 1994; Peoples and Weight, 1995; Mihic and Harris, 1996), suggesting cavities of discrete size in each receptor molecule, but the alcohol cutoff actually can be manipulated by mutagenesis within TM2 and TM3 (Wick et al., 1998).

The concept of a binding cavity occupied by isoflurane is supported further by the observation that the GABA concentration-response curves for the isoflurane-insensitive $\alpha 2$ (S270Y), $\alpha 2$ (S270F), and $\alpha 2$ (S270W) mutants (Figs. 2, 4B) closely resemble the concentration-response curve for the wild-type GABA_A receptor in the presence of 1 mM isoflurane (Fig. 4A). It also would explain why isoflurane does not potentiate GABA in the $\alpha 2$ (S270Y), $\alpha 2$ (S270F), and $\alpha 2$ (S270W) mutants. When the cavity is partially filled by a small side group from $\alpha 270$, as in $\alpha 2$ (S270C) ($\Delta = \pm 49$ Å³), there is a small leftward shift of the GABA concentration-response curve relative to the wild-type, consistent with a modest stabilization of the open state of the channel. However, isoflurane (molecular volume of 140 Å³) still can be accommodated within the remainder of the cavity, resulting in additional potentiation of receptor function; when the side chain volume is increased, for example, in $\alpha 2$ (S270E) (77 Å³) or $\alpha 2$ (S270R) (129 Å³), the combined volume of the isoflurane molecule together with the bulkier side chain is now 217 or 269 Å³. Therefore, we estimate the volume of the hypothetical cavity as between 189 and 217 Å³. By analogy with NMR studies of cavities in soluble proteins such as lysozyme (Eriksson et al., 1992), the rather small free energy of stabilization associated with the presence of a small molecule such

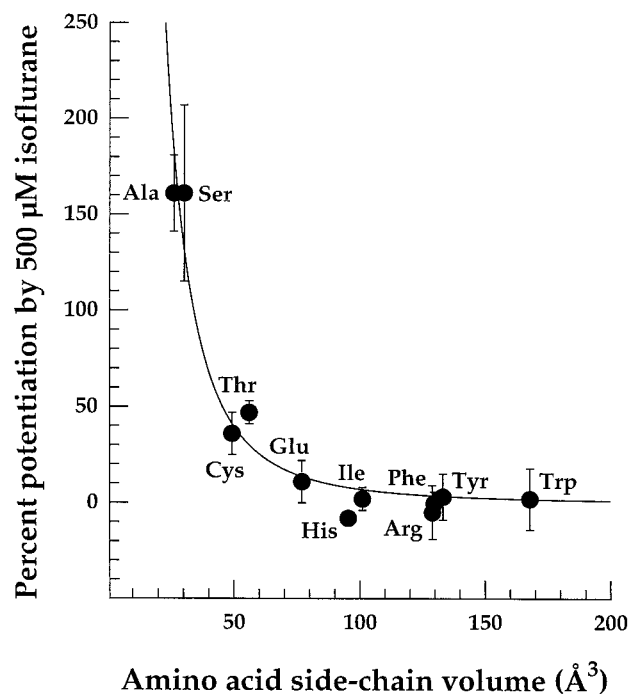


Fig. 5. Potentiation of submaximal GABA responses by isoflurane within the series of $\alpha 2$ (S270X) $\beta 1$ mutant GABA_A receptors declines with increasing molecular volume of the amino acid at position $\alpha 270$. Each amino acid is represented by the usual three-letter abbreviation. The line represents a best fit to the data but has no theoretical significance.

as isoflurane, or of a bulky side chain, might result in part from hydrophobic interactions with the cavity lining, and/or partly from an entropic component caused by displacement of bound water molecules from within the cavity. Clearly, structural studies ultimately will be required to determine the involvement of α Ser270 in cavity formation and anesthetic binding. In this regard, it is worth noting that anesthetic (bromoform) binding within a protein cavity recently has been described in the 2.2 Å resolution X-ray structure of the firefly luciferase molecule (Franks et al., 1998).

Conclusion. Whatever the physical mechanisms involved in GABA_A receptor modulation by anesthetics such as isoflurane, $\alpha 270$ certainly influences the behavior of the GABA_A receptor ion channel. Although it is unlikely to participate directly in permeation, given an α -helical structure for TM2 (Xu and Akabas, 1996), Ser270 probably lies physically close to the ion channel and may play an important role in channel gating. Furthermore, this residue clearly determines the modulation of the GABA_A receptor by isoflurane and may represent one determinant of an anesthetic binding cavity.

Acknowledgments

We are indebted to the late Dolan Pritchett, who supplied cDNAs used in this study. We also thank S. John Mihic and Oliver Gallay for helpful discussions; Jim Trudell for a very valuable comment on the packing of isoflurane molecules; Ted Eger, Caroline Rick, and Lily Wong for critical reading of the manuscript; and Sharon Bouie, Steve Lopez, and Amiinah Kung for technical assistance.

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