Action of nicotine and analogs on acetylcholine receptors having mutations of transmitter-binding site residue \(\alpha_{G153}\)

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A primary target for nicotine is the acetylcholine receptor channel (AChR). Some of the ability of nicotine to activate differentially AChR subtypes has been traced to a transmitter-binding site amino acid that is glycine in lower affinity and lysine in higher affinity AChRs. We studied the effects of mutations of this residue (G153) in neuromuscular AChRs activated by nicotine and eight other agonists including nornicotine and anabasine. All of the mutations increased the unliganded gating equilibrium constant. The affinity of the resting receptor \((K_0)\) and the net binding energy from the agonist for gating \((\Delta G_b)\) were estimated by cross-concentration fitting of single-channel currents. In all but one of the agonist/mutant combinations there was a moderate decrease in \(K_0\) and essentially no change in \(\Delta G_b\). The exceptional case was nicotine plus lysine, which showed a large, >8,000-fold decrease in \(K_0\) but no change in \(\Delta G_b\). The extraordinary specificity of this combination leads us to speculate that AChRs with a lysine at position \(\alpha_{G153}\) may be exposed to a nicotine-like compound in vivo.

**INTRODUCTION**

Acetylcholine (Ach) receptor channels (AChRs) are ligand-gated ion channels that regulate the flow of cations across cell membranes. These membrane proteins alternatively adopt two stable shapes having a closed or an open channel (C\(\leftrightarrow\)O). In the periphery, AChRs mediate vertebrate neuromuscular synaptic transmission, and in the central nervous system, they are thought to play roles in cognition, attention, addiction, analgesia, and other behaviors (Gotti et al., 1997; Lindstrom, 1997; Changeux and Edelstein, 2001). Neuronal AChRs are sites of action for nicotine and are potential targets for the treatment of schizophrenia, Alzheimer’s, epilepsy, and other human neurological diseases (Jensen et al., 2005; Gotti et al., 2006).

AChRs spontaneously switch between C and O conformations, but without agonists, the unliganded “gating” equilibrium constant is small and there is hardly any constitutive activity. The rate and probability of adopting the O shape increase substantially when the transmitter-binding sites are occupied by certain ligands, such as the neurotransmitter Ach. In neuromuscular AChRs, many other ligands including nicotine and choline increase the open-channel probability \((P_o)\) but to smaller maximum extents than Ach does.

The neuromuscular AChR (adult-type) has two transmitter-binding sites located in the extracellular domain at the \(\alpha_{\epsilon}\)- and \(\alpha_{\delta}\)-subunit interfaces (Fig. 1 A). A thermodynamic cycle provides a good description of AChR activation (Fig. S1) (Monod et al., 1965; Karlin, 1967; Auerbach, 2012). The unliganded gating equilibrium constant \((E_0\), which sets the minimum \(P_o)\), is determined by the intrinsic energy difference between the O and C conformational ensembles with only water present at the transmitter-binding sites \((\Delta G_0)\). When agonists are present, a low-to-high affinity change at each site generates binding energy \((\Delta G_b)\) that increases the relative stability of O and, hence, \(P_o\). The maximum \(P_o\) is determined by the energy difference between O versus C when agonists are present at both transmitter-binding sites \((\Delta G_2)\). From the cycle, and with equivalent binding sites (Jha and Auerbach, 2010),

\[
\Delta G_2 = 2\Delta G_b - \Delta G_0.
\]

In AChRs, \(\Delta G_0 = +8.4\) kcal/mol \((P_o \text{ min} \sim 10^{-6})\), \(\Delta G_2^{\text{ACh}} = -1.9\) kcal/mol \((P_o \text{ max} \sim 0.96)\), and \(\Delta G_0^{\text{ACh}} = -5.1\) kcal/mol (Nayak et al., 2012).

Three aromatic rings in the \(\alpha\)-subunit side of each binding site provide most of the \(\Delta G_b\) energy for gating with Ach: \(\alpha\)W149 (in loop B), and \(\alpha\)Y190 and \(\alpha\)Y198 (both in loop C; Fig. 1 B) (Purohit et al., 2012). In this paper, we examine in detail the functional properties of \(\alpha\)G153 (also called GlyB2), a loop B residue that is near this “aromatic triad.” We investigated the effects of \(\alpha\)G153 mutations on \(\Delta G_0\), \(\Delta G_b\) (with several agonists), and the lower affinity equilibrium dissociation constant for agonist binding to resting AChRs \((K_0)\).
There are three reasons why we chose to focus our attention on αG153. First, some neuronal AChR subtypes (those with α<sub>2</sub>, α<sub>3</sub>, α<sub>4</sub>, and α<sub>6</sub> subunits) have a lysine at this position. These subtypes have a higher affinity for nicotine than for ACh (Connolly et al., 1992; Chavez-Noriega et al., 1997), and a lysine mutation of αG153 in α<sub>7</sub> or α<sub>1</sub> AChRs increases the resting affinity for nicotine (Corringer et al., 1998; Grutter et al., 2003; Xiu et al., 2009). A search of the sequence database shows that in vertebrate α subunits, the αG153 residue is usually a glycine (61%), sometimes a lysine (38%), and rarely anything else.

Second, whereas almost all mutations of amino acids at the binding sites decrease activation by agonists, in neuromuscular AChRs, those of αG153 increase activation. The αG153 mutations that have been studied so far increase activity by making ΔG<sub>0</sub> less positive and decreasing K<sub>d</sub> for both ACh and its breakdown product choline (Zhou et al., 1999; Purohit and Auerbach, 2011). The αG153S mutation causes a human congenital myasthenic syndrome as a result of these two effects (Sine et al., 1995). We wanted to ascertain the generality of the uniquely positive effect on AChR activation of αG153 mutations.

The third reason we probed αG153 in detail was to explore its role in the agonist-binding structural rearrangement. The targeting of a receptor by a ligand depends on K<sub>d</sub>. Evidence was presented recently suggesting that the binding of ligands to resting AChRs requires both diffusion and a conformational change that involves, in part, a “capping” motion of loop C (Jadey and Auerbach, 2012). This is an interesting development because it offers a novel mechanism for ligands to modulate transmitter occupancy of the binding sites, for example by altering noncompetitively the intrinsic equilibrium constant of the binding conformational change. Other experiments show that the rate constants for association and dissociation of choline to the transmitter-binding sites have a high temperature dependence in the mutant αG153S (Gupta and Auerbach, 2011). This suggests that this residue, which is in loop B, is involved in the binding conformational change.

In this paper, we present binding and gating constants, determined by single-channel kinetic analyses, for nicotine, nornicotine, and anabasine in WT neuromuscular AChRs. We also give the parameters for these and six additional agonists in AChRs having a mutation of αG153 (Fig. 1 C). The results show that all αG153

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Figure 1. Structures. (A) Low resolution cryo-EM image of the unliganded Torpedo AChR (Protein Data Bank accession no. 2bg9) (Unwin, 2005). A transmitter-binding site region is boxed. Lines mark approximately the membrane. (B) Close-up of a ligand-binding site of the Lymnaea ACh–binding protein (Protein Data Bank accession no. 1uw6) (Ruchtooa et al., 2009), a homologue of the AChR transmitter-binding site. Loops A–D are labeled. Cα of αG153 (mouse numbering) is a green sphere, nicotine is green, and the aromatic triad is tan. (C) Structures of the agonists.
mutations increase unliganded gating, and that all agonist/mutant combinations increase resting affinity but have little effect on the affinity ratio. The increase in resting affinity is particularly great in the lysine plus nicotine combination. In the ACh-binding protein (AChBP), a good structural model for the AChR transmitter-binding site (Brejc et al., 2001), the residue corresponding to αG153 is a serine or a glycine. However, no structures of AChBPs with a lysine (or other side chains) at this position have yet been reported.

**MATERIALS AND METHODS**

**Mutagenesis and expression**

The QuikChange Site-Directed Mutagenesis kit (Agilent Technologies) was used to make mutant cDNAs of mouse AChR subunits. All sequences were verified by dideoxy sequencing. Transient transfection of HEK 293 cells was performed using calcium phosphate precipitation. 3.5 µg of subunit cDNA was added in the transfection of HEK 293 cells was performed using calcium phosphate precipitation. The bath solution was (mM): 142 KCl, 5.4 NaCl, 1.8 CaCl2, 1.7 MgCl2, and 1 HEPES, pH 7.4. The pipette solution contained the specified concentration of agonist dissolved in Dulbecco’s phosphate precipitation. Unless noted otherwise, the cell membrane potential (Vm) was +100 mV so that the currents were in the outward direction. For details see Jadey et al. (2011).

**Equilibrium and rate constant estimation**

The equilibrium dissociation constant of resting receptors (Kd = koff/kon) and the diliganded gating equilibrium constant (E2 = f2/b2) were estimated by fitting globally interval durations obtained at several different agonist concentrations by:

\[
\frac{2[A]k_{on}}{2A+C} \rightarrow A+AC \rightarrow A_2C \rightarrow A_2O
\]

\[
f_2 = \frac{k_{on}}{2A+C}, \quad b_2 = \frac{k_{off}}{2A+C}.
\]

(Scheme 1)

where [A] is the agonist concentration, C is a resting (low affinity/closed-channel) AChR, and O is an active (high affinity/open-channel) AChR. The model assumes that the two binding sites are functionally equivalent (Fig. S1). E2 = f2/b2 and ΔG2 = −0.39 ln E2. See the first section of the Results for a discussion of how brief, undetected gating intermediate states do not influence the ΔG2 estimates obtained by using Scheme 1 and Eq. 1.

The equilibrium dissociation constant for channel block by the agonist (Kb) was estimated by fitting the single-channel current amplitudes by (i/bi) = 1/(1 + [A]/Kb), where i is the amplitude at concentration [A], and bi is the current amplitude extrapolated to zero concentration. This equation is an approximation that assumes b2 is much slower in blocked versus unblocked receptors.

**E0 estimation**

For E0 measurements, the αG153 (GlyB2) mutants were coexpressed with a gain-of-function double mutant construct eL269F (in M2) + βT456F (in M4) + δNT, and single-channel currents were recorded without any agonists in the pipette or bath. The effects of the background mutations on ΔG0 were shown experimentally to be approximately independent (Jadey et al., 2011). Individually, each of these mutations increases E0 by an approximately equivalent increase in E0 = εL269F by 179-fold (Jha et al., 2009) and βT456F by 5.2-fold (Mitra et al., 2004). Thus, the double mutant background combination increases E0 (and, hence, E2) by ~950-fold (ΔΔG0 = −4.0 kcal/mol). The observed E0 for each αG153 mutant was therefore corrected as observed E0 corr = observed E0 / 930.

For a few mutants, the spontaneous unliganded open- and closed-interval durations within clusters were well described by a single-exponential component. For these, f0 and b0 were simply the inverse mean lifetimes of the nonconducting and conducting intervals. Most of the αG153 mutants produced unliganded currents exhibiting multiple open/shut components within clusters (Purohit and Auerbach, 2009). For these, the intra-cluster-interval durations were fitted by using a kinetic model having the appropriate number of nonconducting (three) and conducting (two) states. The f0 and b0 were the inverse lifetimes of the predominant shut and open components.

**Dose-response analysis**

The probability of being open within a cluster (P0) was calculated as f2/(f2 + b2). f2 was estimated from the high concentration asymptote of the effective opening rate constant (the inverse of the longest component of intra-cluster closed-interval durations, t*), and b2 was the closing rate constant measured at a low agonist concentration where there was no apparent channel block. This P0 corresponds to a whole-cell current measurement with rapid agonist application (no desensitization). The EC50 was estimated as the concentration producing a half-maximal response. Each symbol is the average P0 from more than three patches.

**E2 measurements**

For E2 measurements, the various side-chain/agonist combinations were made at +100 mV and by using previously characterized background mutations that decreased E0 (made ΔG0 less positive) but had no effect on ΔG0 (Table S8). The change in membrane potential from ~100 to +100 mV, which reverses the direction of current flow, decreases E0 by a factor of 12.5 (ΔΔG0 = +1.5 kcal/mol) but has no effect on ΔG0. The backgrounds were necessary to compensate for the higher E0 (less positive ΔG0) of some of the αG153 mutations. The mutated side chains of the background constructs were shown by experiments to be approximately energetically independent (Jadey et al., 2011), except for αV261F, which was assumed to be independent of the other perturbations. The observed gating rate constants f2 and b2 were corrected for the effects of the background. The reported ΔG2 values were calculated using the background-corrected values of ΔG0 (notation, background in parentheses; αG153 side chain/agonist): (a: eS450W), S/Cho, A/Cho, P/Cho, K/Cho; (b: δ414H + eS450W), S/DMP, S/DMP, S/Nic, S/TMA, S/ChCh, P/DMP, P/DMP, P/Nic, A/DMP, A/DMP, A/Nic, K/DMP, K/DMP; (c: αT422V + δ414H + eS450W), S/ACh; (d: αT422 + δ414A + eS450W), P/TMA, P/ChCh, P/ACh, A/TMA, A/ChCh, A/ACh; (e: αV261F + δ414A + eS450W), K/Nic, K/TMA, K/ChCh; (f: αV261F + δ414A + eS450W + δ1257A), K/ACh (all at +100 mV). The fold changes in f2/b2 (WT/mut) for backgrounds are (notation, background; αG153 side chain/agonist): +200-mV depolarization, 0.7/8.3; a, 1.5/0.12; b, 0.468/1.2; c, 0.015/6.5; d, 0.095/8.2; e, 0.00987/1.54; f, 0.000077/8.0. The corresponding equilibrium values (fold change in E0/ΔΔG0 in kcal/mol) are: +200-mV depolarization, 0.6/8 = 1.5; a, 12.5/+1.5; b, 0.057/+1.7; c, 0.0028/+3.6; d, 0.0116/+2.6; e, 0.00056/+4.4; f, 0.0000996/+68.

**Online supplemental material**

The supplemental material consists of eight supplemental tables that give all of the primary and background-corrected rate and
equilibrium constants. There are two supplemental figures. Fig. S1 shows the thermodynamic cycle of AChR activation. Fig. S2 shows examples of nicotine-activated single-channel currents in various αG153 mutants, and the corresponding shut- and open-interval duration histograms. The online supplemental material is available at http://www.jgp.org/cgi/content/full/jgp.201210896/DC1.

RESULTS

Gating models and protein engineering

The isomerization of an AChR is a huge chemical reaction that involves energy (structure) changes of many elements in the protein–lipid–water complex. It is a priori certain that within the global conformational change the system adopts transiently short-lived (ps-µs) intermediate states in its passage between the stable C and O ground states. In experiments, three such intermediates have been detected indirectly by using rate-equilibrium analyses, and one intermediate has been detected directly by using high resolution kinetic analyses.

Here, we use the word “gating” to describe the complete allosteric transition between the C and O end states, rather than just the microscopic event that regulates ion and water passage across the membrane. The state model for gating can be expanded to incorporate the intermediate states. Assuming that there is a single sequential pathway through the intermediates, \(C \leftrightarrow F_1 \leftrightarrow F_2 \leftrightarrow \ldots \leftrightarrow O\), where each \(F\) represents an intermediate state. In our experiments, the \(F\) states were too brief to be detected; hence, the \(\Delta G_n\) values we obtained by using a two-state gating scheme reflect the sum of the energy changes for all of the steps in the sequence. Although the affinity change appears to occur early in the sequence, the \(\Delta G_n\) measurements we report pertain to the total energy arising from the affinity change, regardless of when it occurs in the gating sequence.

Some agonist/mutant combinations are difficult to study using WT AChRs because the gating rate and equilibrium constants are outside of the range suitable for single-channel cluster analysis, which is approximately \(\Delta G_2 = \pm 2\) kcal/mol (0.03 < \(E_2\) < 30). We addressed this problem by adding voltage and background mutations that increased or decreased \(\Delta G_0\) to known extents. These manipulations placed \(\Delta G_2\) and, hence, the rate and equilibrium constants into a more easily measurable range (Eq. 1). Previous studies showed that none of the background perturbations we used had any effect on \(\Delta G_n\) (Jadey et al., 2011). We corrected the observed \(\Delta G_2\) value by the \(\Delta G_0\) offset provided by the background to estimate gating parameters for our reference condition (−100 mV; WT \(\Delta G_0\)). The magnitudes of the background effects on \(\Delta G_0\) are given at the end of Materials and methods.

We use interchangeably the gating energy and equilibrium constant: \(\Delta G\) (kcal/mol) = −0.59ln\(E\). The error limits on the rate and equilibrium constants are given

![Figure 2](http://www.jgp.org/.../Figure_2.png)

**Figure 2.** Action of nicotine on WT AChRs. (A; top) Low time-resolution view of single-channel current clusters, each reflecting the activity of an individual AChR (open is down). (Bottom left) Higher time-resolution view of clusters. (Bottom right) The current amplitude (i) declines with increasing concentration because nicotine is a fast channel blocker. \(K_{B_{nicotine}}\) is the equilibrium dissociation constant of nicotine for the pore. (B; top) Low time-resolution view of current clusters (open is up). (Bottom) Clusters of openings at increasing [nicotine] and corresponding intra-cluster–interval duration histograms. Solid lines are the global fit by Scheme 1. (C) Single-channel current amplitude at 100 mV is constant at [nicotine] < 10 mM because depolarization reduces channel block. (D) With increasing [nicotine], the effective opening rate (\(f^*\)) reaches a plateau that is the fully liganded opening rate constant (\(\sim 2,400\) s\(^{-1}\)). The highest tested concentration was 8 mM nicotine. The \(E_2\) estimates were not affected by channel block because the transmitter-binding sites are fully saturated at \(\sim 6\) mM. The activation constants for nicotine on WT AChRs (−100 mV) are \(E_2 = 0.87\), \(K_d = 1\) mM, and \(\Delta G_n = -4.1\) kcal/mol (Table S1).
in Table S8. A 20% difference in an equilibrium constant translates to an ~0.1 kcal/mol difference in energy. The error limits on the energy values are approximately ±0.2 kcal/mol.

Nicotine, nornicotine, and anabasine in WT AChRs
Nicotine, one of the drugs in tobacco that is addictive, is consumed daily by more than one billion people worldwide. The action of nicotine on neuromuscular AChRs has been investigated (Akk and Auerbach, 1999), but new technical advances in rate constant estimation motivated us to revisit this agonist. Fig. 2 A shows single-channel currents from adult WT mouse neuromuscular AChRs activated by nicotine at a membrane potential of −100 mV. The top trace is a low time-resolution view showing that openings (down) occurred in clusters. The events within clusters reflect multiple cycles of agonist binding and channel gating in a single AChR, and the intervening silent periods reflect times when all of the AChRs in the patch are in states associated with desensitization. This clustering allows the estimation of binding and gating rate constants for single AChRs. It was not possible to use neuronal AChRs in our experiments because their single-channel openings are not clustered. The higher resolution single-channel traces show that in WT neuromuscular AChRs, millimolar concentrations of nicotine are required to elicit clusters having a moderately high Po.

With increasing concentrations of nicotine, the single-channel current amplitude declined because this agonist is a fast channel blocker (Fig. 2 A, bottom right). From the pattern of decline we estimate that nicotine has an equilibrium dissociation constant for the pore of K[guillemot]nicotine = 0.7 mM. Channel block by nicotine not only limits cellular currents at high concentrations but, because we must fully saturate the binding sites to measure the diliganded gating equilibrium constant E2, also our ability to estimate Kd and E2.

To estimate these quantities, we depolarized the membrane to reduce channel block and reverse the direction of the ionic current. This allowed us to use higher [nicotine] (Fig. 2, B and C; open is up). Under these conditions, outward single-channel currents could be measured using [nicotine] up to ~10 mM, which is sufficiently high to saturate the two AChR transmitter-binding sites (Fig. 2 D). The net effect of +200-mV depolarization (and the current reversal) is to increase AG0 by approximately +1.5 kcal/mol (Nayak et al., 2012). We added a background mutation that canceled the effects of depolarization on gating (that decreased AG0 by approximately −1.5 kcal/mol), so the equilibrium and rate constants we measured at +100 mV pertain to our reference condition, which is WT AChRs at −100 mV (Jadey et al., 2011). From the durations of open and shut intervals within clusters, measured at several different [nicotine], we estimate that at the reference condition K[guillemot]nicotine = 1.0 mM and the diliganded gating equilibrium constant E2[nicotine] = 0.87 (AG2 = −0.08 kcal/mol). This E2 estimate is ~1.7 times greater than the one reported previously (Akk and Auerbach, 1999), presumably because in those experiments channel block prevented the use of saturating [nicotine].

The WT unliganded gating equilibrium constant is E0 = 7 × 10−7 or AG0 = +8.4 kcal/mol (Nayak et al., 2012). The average energy from the affinity change for each nicotine molecule can be calculated by using Eq. 1: 2ΔG[nicotine] = (−0.08–8.4) kcal/mol. We calculate that in adult WT neuromuscular AChRs, each nicotine molecule provides on average ΔG[nicotine] = −4.1 kcal/mol to power channel opening, which is only ~1 kcal/mol more positive than with ACh (ΔG[ACh] = −5.1 kcal/mol) (Jadey et al., 2011). A 1-kcal/mol loss of favorable (more negative) binding energy at each of the two binding sites translates to an ~30-fold reduction in E2 and a reduction in the maximum Po from ~0.97 to ~0.48. Nicotine is a moderately effective partial agonist of neuromuscular AChRs (Table S1).

We also investigated at the single-channel level two related tobacco alkaloids, anabasine and nornicotine (Kem et al., 1997; Papke et al., 2007). Another ligand, methyl-anabasine, blocked the channel so avidly that depolarization to +100 mV was insufficient to allow binding site saturation and rate constant estimation.
As with nicotine, we measured single-channel currents at different agonist concentrations to estimate $E_2$ and calculate $K_d$ from the ratio of the dissociation/association rate constant estimates obtained by cross-concentration fitting. To summarize the results graphically, we also estimated the cluster $P_o$ at each concentration and fit these values to an empirical equation to generate a normalized dose–response curve (Fig. 3 A). The $E_2^{WT}$ values (which depend only on $\Delta G_0$ and determine the maximum $P_o$) for nicotine, nornicotine, and anabasine were, respectively, 0.87, 5.0, and 21 (Fig. 3 B, top, and Table S1). Anabasine provides almost as much binding energy as the neurotransmitter. The order of $K_d$ values for these three agonists was nornicotine (21 µM) < anabasine (250 µM) < nicotine (1,000 µM). The differences in $K_d$ were mainly attributable to changes in the agonist association rate constant. The activation equilibrium constants for all of the ligands shown in Fig. 1 C in adult WT neuromuscular mouse AChRs have been estimated (Table S2) (Jadey et al., 2011).

$\alpha$G153 mutants: Unliganded gating and the affinity ratio

The analysis of $\alpha$G153 mutations on AChR activation starts with describing their effects on the intrinsic, unliganded gating equilibrium constant $E_0$. In many places in the protein, side-chain substitutions alter the relative stability of the O versus C ground states and, hence, $E_0$ and dose–response profiles. The logarithm of the fold change in $E_0$ (relative to the WT) is proportional to the change in the intrinsic energy of the unliganded C↔O gating isomerization ($\Delta G_0$). We first sought to estimate $\Delta G_0$ values for different mutations of $\alpha$G153.

Some example currents (obtained in the absence of any agonists) and $\Delta G_0$ values for 14 different $\alpha$G153 mutations are shown in Fig. 4 A. All of the mutations increased $E_0$ (increased the relative stability of O; $\Delta G_0$ is more negative) (Table S3). The large aromatic substitutions F, Y, W, and H had relatively small effects (less than −2 kcal/mol), but those of C, D, and K substitutions were greater (approximately −3 kcal/mol). We could not discern a clear pattern relating side-chain chemistry with $\Delta G_0$, so perhaps this energy is mainly determined by the disposition of the loop B backbone. Of the mutations we studied, $E_0$ was smallest with glycine and largest with lysine, the two amino acids that are present naturally in AChRs. The higher $E_0$ value of $\alpha$G153K AChRs will cause higher leak currents and stronger cellular responses (lower EC50 and higher maximum $P_o$ values) for all agonists (Table S4) (Zhou et al., 1999).

Next, we determined the effects of $\alpha$G153 mutations on $\Delta G_B$, which is the energy for increasing $P_o$ by agonists arising from the low-to-high affinity change at the binding site. We examined all 9 agonists and 6 side chains (GSAPKER) in 39 different combinations. The results are summarized in Fig. 4 B. The effects of $\alpha$G153 mutations on $\Delta G_B$ were, in all cases, small. The largest increase in the agonist energy was only −0.5 kcal/mol, and the largest decrease was only +0.3 kcal/mol (Table S5). These energies are miniscule compared with the −2-kcal/mol changes in $\Delta G_0$ apparent with some mutations of the aromatic triad (Purohit et al., 2012). For the side-chain/agonist combinations we tested, $\alpha$G153 had little to do with setting the energy from the agonist for gating.

Figure 4. The unliganded gating equilibrium constant and affinity ratio in $\alpha$G153 mutants. (A) Bars show the fold change in $E_0$ relative to the WT value ($7 \times 10^{-7}$) on a log scale ($\Delta G_0$). All mutations increased $E_0$, with lysine having the largest effect (200-fold) (Table S3). (Inset) Example currents obtained in the absence of agonists ($V_m = -100$ mV; open is down; background, $\alpha$L269F + $\beta$T456I). (B) None of the mutations had a large effect on $\Delta G_B$ for any agonist (Table S5). Agonist order for $\alpha$G153K is (left to right): choline, DMP, DMT, TMA, ACh, nicotine (arrow), CCh, anabasine, and nornicotine.

$\alpha$G153 mutants: Dose–response curves and $K_d$

Fig. 5 A shows dose–response curves for six different $\alpha$G153 mutants using nicotine as the agonist. All of the $\alpha$G153 mutations increased the resting affinity (reduced
3.8 kcal/mol. The increase with E, R, P, A, and S substitutions was similar and modest, on average ~20-fold (approximately ~1.8 kcal/mol). In all cases, the decrease in $K_d$ was mainly caused by an increase in the agonist association rate constant.

The effect of the lysine mutation was, however, remarkable. This substitution increased the affinity of the resting binding site for nicotine by 8,130-fold (~5.3 kcal/mol), from ~1 mM to ~120 nM. As a consequence of both this extraordinarily large decrease in $K_d$ and the increase in $E_0$ caused by the lysine substitution, the EC_{50} of the normalized dose–response curve for nicotine shifted from 1.3 mM in the WT to 724 nM in αG153K (Table S4). At [nicotine] generating approximately equivalent cluster $P_o$ values, the single-channel currents in all of the αG153 constructs were similar (Fig. 5 B, bottom).

Because of the unusual effect of the lysine substitution on activation by nicotine, we examined the dose–response properties of other agonists using this mutant (Fig. 6). The resting affinity was highest for nicotine, but those for nornicotine and carbamylecholine (CCh), too, were high ($K_d = 325$ and 700 nM) (Table S7).

Fig. 7 shows the change in the resting affinity relative to the WT for 21 different αG153 mutant/agonist combinations, on a log scale. Most of these combinations behaved similarly, with the side-chain substitution increasing the resting affinity for the agonist by ~25-fold ($-1.9$ kcal/mol) (Table S6). The only extraordinary effect was for the nicotine plus lysine combination, described above. A smaller, but notable, effect was for the CCh plus lysine combination, in which $K_d$ decreased by 580-fold ($-3.8$ kcal/mol).

**DISCUSSION**

Nicotine, nornicotine, and anabasine on WT AChRs

Because so many people consume tobacco, nicotine and nornicotine can be considered to be physiological ligands, along with ACh and its metabolites choline and betaine. It is currently not possible to measure from single channels the binding, gating, and blocking constants (energies) for these agonists in neuronal AChRs. Although there is substantial sequence conservation between AChR subtypes, even a small perturbation in structure (that is perhaps too small to be detected even by high resolution x-ray crystallography) can result in a large difference in energy properties. The constants and energies we have measured pertain only to adult-type mouse neuromuscular AChRs and cannot be extrapolated directly to neuronal subtypes.

Nicotine is a high efficacy agonist of adult WT neuromuscular AChRs. This ligand provides ~80% of the binding energy, as does the natural transmitter. However, nicotine is not effective with regard to causing cell depolarization, for two reasons. First, it has a low affinity for resting receptors. $K_{nictine} = 1$ mM, which is approximately six times higher than for ACh. Second, nicotine is an effective channel blocker. The ratio of the equilibrium dissociation constant for channel block versus binding ($K_b/K_d$) is one index of the ability of an agonist to depolarize cells. This ratio (at ~100 mV) is ~7.2 for ACh but only ~0.7 for nicotine. The equilibrium dissociation constant of nicotine for the AChR pore is about the same as for the transmitter-binding sites, and channel block by nicotine mitigates the cellular response. The amino acids at the transmitter-binding sites and the pore of neuromuscular and neuronal AChRs are similar but not identical. We have not measured $J_{GB}$, $K_b$, $K_d$, and $K_b/K_d$ for nicotine in brain AChRs.

Nornicotine is a minor tobacco alkaloid that is present at a level only ~3% that of nicotine (Jacob et al., 1999). However, the ~50-fold higher affinity and fivefold greater efficacy of nornicotine compared with nicotine suggest that this compound may be more important with regard to its psychoactive properties and smoking than previously considered. Also, $K_d$ nornicotine is only 21 µM, which suggests that its effects, unlike those of nicotine, may not be dulled by channel block.
αG153 mutants

All of the αG153 mutant–agonist combinations we examined increased activation by increasing both unliganded gating and the resting affinity. The increase in activation with αG153 mutations is quite general. The smallest $E_0$ value was with glycine, and the largest was with lysine. It appears that these two amino acids at this position have been selected by nature to provide the minimum and maximum activation by physiological ligands.

None of the α153 mutations had a large effect on the agonist affinity ratio. Although αG153 is near αW149, a member of the aromatic triad, this result suggests that it is not part of the binding site apparatus that increases the open probability by increasing the agonist affinity.

All αG153 mutations decreased $K_d$ for all agonists. A comparison of AChBP structures without and with various ligands at the binding site suggests that an inward displacement of loop C occurs in agonist binding (Celie et al., 2004; Hansen et al., 2005; Brams et al., 2011; Shahsavar et al., 2012). Although in Aplysia AChBPs there is no discernible displacement of the αG153 backbone between the apo- and ligand-bound structures, the results suggest that in AChRs, loop B also participates in the low affinity–binding rearrangement. As for unliganded gating, glycine and lysine also were the amino acids that fostered the highest and lowest equilibrium constants. This is consistent with the idea that the binding conformational change also occurs in the absence of agonists.

The reduction in $K_d$ was similar for all but one of the mutant/agonist combinations that we examined (~20-fold). The exceptional case was for nicotine plus lysine, which showed a much greater reduction in $K_n^{nicotine}$ compared with the other combinations. That one mutation of one amino acid profoundly increases one activation parameter for one agonist is unusual. The association rate constant for nicotine on αG153K AChRs was $\sim 10^{10}$ M$^{-1}$s$^{-1}$ (Table S1). Although the geometry and charge of the AChR-binding sites will influence the maximum possible ligand association rate constant, $k_n^{nicotine}$ may be close to the upper limit set by diffusion (Berg and von Hippel, 1985). The entry of some agonists into the resting transmitter-binding site has recently been shown to require a conformational change of the protein (Jadey and Auerbach, 2012). The fast association of nicotine in αG153K AChRs indicates that with lysine, this binding conformational change is extremely rapid.

Without structural information is it difficult to infer the molecular forces that determine the fast association of nicotine in αG153K AChRs. It has been suggested that the high resting affinity for nicotine in αG153K AChRs arises from interactions between the lysine and the backbone of loop C at αP197 (Grutter et al., 2003). However, the agonist specificity of the high affinity...
phenotype indicates that the ligand, too, is important and is likely involved directly in generating the effect. Our experiments show that methyl pyrrolidine (a fragment of nicotine) and nornicotine do not show the special interaction but that CCh does, to some extent. It has been proposed that the pyridine nitrogen of nicotine makes a cross-subunit hydrogen bond (Blum et al., 2010), so it may be that an interaction of the secondary nitrogen of the agonist is involved in generating fast association in αG153K AChRs.

An experimental association rate is the product of [A] and the association rate constant (k_{on}). It may be that k_{on} nicotine is unusually high in αG153K AChRs, but it is not inconceivable that the lysine induces a rearrangement of the binding site that makes the local [nicot ine] (and to some extent CCh) higher than in the bulk extracellular solution. It may be that the long lysine side chain places its ε-amino group near a cluster of charged residues (αK145 and αD200) that have been implicated in starting the agonist-driven opening isomerization (Lee and Sine, 2004; Purohit and Auerbach, 2007). Further experiments are needed to test these speculations.

The exceptionally high affinity for nicotine in αG153K AChRs raises two interesting possibilities. First, it is reasonable to hypothesize that the ancestral tobacco plant synthesized nicotine to target organisms (other than humans) that have a lysine at this position in AChRs. All insects, however, have a glycine at this position and do not respond significantly to nicotine in the nanomolar range (Matsuda et al., 1998). Nicotine is an insecticide, but it will be interesting to ascertain the αG153 side chain in other tobacco pests.

Second, the high affinity for nicotine of αG153K AChRs raises the possibility that mammalian AChRs that have a lysine at this position are exposed to a nicotine-like compound in normal physiology. Aside from its spectacular effect with regard to the resting affinity for nicotine, the functional effects of the lysine substitution are rather pedestrian, yet this amino acid is conserved in many neuronal AChR subtypes. A further exploration of endogenous nicotinoid compounds (for instance, nicotinamide and its metabolites) on K-type AChRs, having a lysine at position αG153, may be informative.

We thank Mary Teeling, Marlene Shero, and Mary Merritt for technical assistance.

This work is supported by National Institutes of Health (grants NS064969 and NS023513).

Edward N. Pugh Jr. served as editor.

Submitted: 13 September 2012
Accepted: 10 December 2012

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