The ladder-shaped polyether toxin gambierol anchors the gating machinery of Kv3.1 channels in the resting state

Ivan Kopljar,1 Alain J. Labro,1 Tessa de Block,1 Jon D. Rainier,2 Jan Tytgat,3 and Dirk J. Snyders1

1Laboratory for Molecular Biophysics, Physiology and Pharmacology, University of Antwerp, 2610 Antwerp, Belgium
2Department of Chemistry, University of Utah, Salt Lake City, UT 84112
3Laboratory for Toxicology, Campus Gasthuisberg, University of Leuven, 3000 Leuven, Belgium

Voltage-gated potassium (Kv) and sodium (Nav) channels are key determinants of cellular excitability and serve as targets of neurotoxins. Most marine ciguatoxins potentiate Nav channels and cause ciguatera seafood poisoning. Several ciguatoxins have also been shown to affect Kv channels, and we showed previously that the ladder-shaped polyether toxin gambierol is a potent Kv channel inhibitor. Most likely, gambierol acts via a lipid-exposed binding site, located outside the K⁺ permeation pathway. However, the mechanism by which gambierol inhibits Kv channels remained unknown. Using gating and ionic current analysis to investigate how gambierol affected S6 gate opening and voltage-sensing domain (VSD) movements, we show that the resting (closed) channel conformation forms the high-affinity state for gambierol. The voltage dependence of activation was shifted by >120 mV in the depolarizing direction, precluding channel opening in the physiological voltage range. The (early) transitions between the resting and the open state were monitored with gating currents, and provided evidence that strong depolarizations allowed VSD movement up to the activated-not-open state. However, for transition to the fully open (ion-conducting) state, the toxin first needed to dissociate. These dissociation kinetics were markedly accelerated in the activated-not-open state, presumably because this state displayed a much lower affinity for gambierol. A tetrameric concanavalin with only one high-affinity binding site still displayed high toxin sensitivity, suggesting that interaction with a single binding site prevented the concerted step required for channel opening. We propose a mechanism whereby gambierol anchors the channel’s gating machinery in the resting state, requiring more work from the VSD to open the channel. This mechanism is quite different from the action of classical gating modifier peptides (e.g., hanatoxin). Therefore, polyether toxins open new opportunities in structure–function relationship studies in Kv channels and in drug design to modulate channel function.

INTRODUCTION

Gambierol is a ladder-shaped polyether toxin from the ciguatoxin-producing dinoflagellate Gambierdiscus toxicus (Satake et al., 1993). Ciguatoxins are well known modulators of voltage-gated sodium (Nav) channels and cause ciguatera food poisoning (Nicholson and Lewis, 2006). These toxins enhance cellular excitability by shifting the threshold for Nav channel opening toward more negative potentials and/or by destabilizing the inactivation process (Catterall et al., 2007). Several ciguatoxins have been identified as potent voltage-dependent potassium (Kv) channel inhibitors as well, suggesting a potential contribution of Kv channel inhibition to ciguatera (Hidalgo et al., 2002; Birinyi-Strachan et al., 2005; Mattei et al., 2010; Schlumberger et al., 2010a,b). Gambierol does not affect Nav channel function (Ghiaroni et al., 2005; Cuypers et al., 2008), but inhibits Kv1 and Kv3 subtypes in the nanomolar range (Cuypers et al., 2008; Kopljar et al., 2009).

Kv channels are tetramers of a subunits, each with a six-transmembrane segment (S1–S6) topology. The S5–S6 segments coassemble with a fourfold symmetry into the central K⁺ permeation pore that is surrounded by four voltage-sensing domains (VSDs) composed of S1–S4 (Long et al., 2005). Opening of Kv channels requires that the VSD of each subunit moves from the resting to the activated state; when all four subunits have reached this activated-not-open state, gate opening proceeds in a “concerted” manner (Bezania et al., 1994; Zagotta et al., 1994b; Schoppa and Sigworth, 1998; Ledwell and Aldrich, 1999). At the molecular level, the outward movement (activation) of the VSD transduces via an electromechanical coupling to the activation gate in the bottom part of the S6 segment (S6 gate; Liu et al., 2002; Long et al., 2005; Blunck and Batulan, 2012; Labro and Snyders, 2012). Conversely, the inward movement of the VSD toward its resting state closes the S6 gate. We showed previously that the molecular determinants for inhibition of Kv3.1 by gambierol are located outside the K⁺ pore and involve lipid-facing residues on...
both the S5 and S6 segment of the α subunits (Kopljar et al., 2009). This high-affinity binding site is accessible in the closed state, and, in contrast to gating modifiers such as hanatoxin (Swartz, 2007), short depolarizations did not overcome the inhibition.

To address the mechanism by which gambierol inhibits Kv channels, we used gating and ionic current analysis to track the VSD movement and the S6 gate opening, respectively. By examining the state-dependent inhibition of Kv3.1 gating and ionic currents, and by controlling the number of high-affinity binding sites using tetrameric concatemers, we show that gambierol binds with high affinity to the resting (closed) state of the channel. When bound, the voltage dependence of activation is shifted by >120 mV toward more depolarized potentials, as if gambierol anchors the gating machinery in the resting state. This condition can be reversed by very strong depolarizations that push the subunits toward the low-affinity activated state from which channel opening proceeds upon gambierol unbinding. These findings represent a novel mechanism of gating modification in Kv channels by a ladder-shaped polyether toxin where the resting state is the high-affinity site and binding of gambierol to a single binding site is sufficient to inhibit ion permeation.

**MATERIALS AND METHODS**

**Molecular biology**

Kv3.1b was cloned in a pEGFP-N1 expression vector. Concatemeric constructs were created using the QuikChange Site-Directed Mutagenesis kit (Agilent Technologies) and mutant primers. Each monomer was tagged with a linker sequence of 60 bp containing a unique restriction-enzyme digest site that was used to link the monomers together. Double strand sequencing using the EZ-Tn5 <TET-1> Insertion kit (Epicentre) confirmed the presence of the desired modifications and the absence of unwanted mutations. Plasmid DNA was amplified in XL2 blue script cells (Agilent Technologies) and isolated using the GenElute HP plasmid maxi-prep kit (Sigma-Aldrich).

**Electrophysiology**

Lf²k cells (mouse fibroblasts, ATCC CLL.1.3) were cultured in Dulbecco’s modified Eagle’s medium with 10% horse serum and 1% penicillin/streptomycin. Cells were transiently transfected with 50–250 ng plasmid DNA for monomer or concatemer constructs using polyethyleneimine (PEI; Sigma-Aldrich); for gating current measurements, 5 µg of plasmid DNA was transfected. 20 h (48 h for gating currents) after transfection, ionic and gating current measurements were done at room temperature (20–23°C) with an Axopatch-200B amplifier, and the recordings were digitized with a Digidata-1200A (Axon Instruments). Command voltages and data storage were controlled with pClamp8 software. Patch pipettes were pulled from 1.2-mm quick-fill borosilicate glass capillaries (World Precision Instruments) with a P-2000 puller (Sutter Instrument Co.) and heat polished after sintering. Pipette solutions were prepared as 20 µM and 300 µM in DMSO and diluted with the external solution to appropriate concentrations. The final DMSO concentration never exceeded 0.5% and toxins were applied using a fast perfusion system (ALA Scientific Instruments).

**Data analysis**

Dose–response curves were obtained by plotting \( y \), the fraction of current remaining, as a function of toxin concentration \( T \) and fitted with the Hill equation \( I / \left( I + (I_{50} / T)^{nH} \right) \), where \( I_{50} \) is the concentration that generates 50% inhibition and \( nH \) is the Hill coefficient. The voltage dependence of activation and inactivation was fitted with a single Boltzmann equation. Time constants were determined by fitting the current recordings with a single exponential function. Charge (Q) measurements were obtained by integrating the \( I_{OFF} \) and/or \( I_{ON} \) currents over sufficient time. The time constants of \( I_{OFF} \) and \( I_{ON} \) decay were determined with a single or double exponential function. Results are expressed as mean ± SEM, with \( n \) being the number of cells analyzed; error bars are shown if larger than symbol size.

To express the shift in the voltage dependence of gating charge activation in terms of free energy difference between the resting and the activated state, we calculated the Gibbs free energy of gating current activation at 0 mV (\( \Delta G_0 \)) for control condition and in the presence of gambierol. Fitting the charge (Q) versus voltage (V) QV curves with a Boltzmann function yielded a midpoint potential \( V_{1/2} \) and a slope factor \( k = RT/2F \), with \( z \) as the equivalent potential. Data analysis was done with the software Origin Scientific Instruments).

**Online supplemental material**

Fig. S1 shows the design of concatemers, their Western Blot analysis, and their biophysical properties. Fig. S2 shows the washout of gambierol for the low-affinity T427V mutant, indicating that any lipid (de)partitioning of gambierol out of the membrane is not the rate-limiting step in the overall process of toxin–channel interaction. Online supplemental material is available at http://www.jgp.org/cgi/content/full/jgp.201210890/DC1.

**RESULTS**

Kv3.1 channels display a state-dependent affinity for gambierol

Previously, we proposed that the ladder-shaped polyether toxin gambierol is a gating modifier that acts at the lipid-exposed surface of the pore domain and stabilizes the closed pore conformation through a yet-unresolved mechanism (Kopljar et al., 2009). Inhibition by gambierol did not require channel opening (Kopljar
et al., 2009), but to explore whether gambierol can also inhibit channels in the open conformation, 100 nM gambierol was applied during a prolonged membrane depolarization to +60 mV (a potential where most channels quickly reach the open conformation). If inhibition would be state-independent, there should be \( \sim 37\% \) reduction in total current 30 s after gambierol application because the time constant of inhibition for 100 nM gambierol was \( \sim 65 \) s (Kopljar et al., 2009). Fig. 1 A shows that after the 30-s test pulse, there was no marked difference in the currents between control conditions and after gambierol application. This indicated that gambierol cannot exert its potent inhibiting effect at depolarized potentials, i.e., on open or inactivated channels. Interestingly, the time constant for induction of subsequent inhibition (monitored by 250-ms steps to +40 mV every 10 s) was \( 36 \pm 3 \) s (\( n = 4 \); Fig. 1 B), which is approximately twice as fast compared with the onset (time constant of 65 s) obtained by monitoring current inhibition upon fast application of gambierol (Kopljar et al., 2009). This difference might reflect the establishment of a steady-state gambierol concentration in the vicinity of the channel’s binding site, i.e., a lipid partitioning step.

If the open state of Kv3.1 channels has a lower affinity for gambierol, then established inhibition in the closed state might be relieved by pushing the bound channels to the open conformation. However, unlike

Characterization of Kv3.1 gating currents
Kv channels can detect changes in the membrane potential by their positively charged VSDs, which rearrange and result in a transient charge displacement detectable as a gating current (Bezanilla, 2008). Because of the fourfold symmetry, each Kv channel possesses four identical VSDs, which all need to move from their resting (inward-facing) “down” state to their active (outward-facing) “up” state before the concerted step can occur that leads to S6 gate opening and ion permeation (Zagotta et al., 1994a; Schoppa and Sigworth, 1998).

The voltage dependence of gating charge movement in Kv3.1 channels was determined using a classical activation voltage protocol (Fig. 2, A and B). Integrating

Figure 1. State-dependent inhibition of Kv3.1. (A) The potential inhibition of the open state for gambierol was tested by applying 100 nM gambierol during a 30-s depolarizing pulse to +60 mV. The corresponding currents are shown in the absence (black) or presence (red) of gambierol. After a control 100-ms prepulse (Ic) to +60 mV, gambierol was added simultaneously with the start of the subsequent 30-s depolarization (arrow). Thereafter, the membrane was clamped to \(-100 \) mV for 2 s to recover all inactivated channels, followed by a step to +60 mV to determine the postpulse amplitude (Ip). The ratio of Ip/Ic was \( 98.5 \pm 0.6\% \) (\( n = 4 \)) in control and \( 98.7 \pm 1.1\% \) (\( n = 4 \)) with gambierol, indicating that there was no gambierol inhibition during the 30-s long depolarization. (B) Subsequent establishment of inhibition at \(-80 \) mV after the 30-s step shown in A. (C) Slow recovery from inhibition by strong depolarizations. After a control 100-ms step to +40 mV (Ic), full inhibition was established with 100 nM gambierol, as confirmed by the lack of current at +40 mV recorded 240 s after gambierol wash-in (asterisk). In the continued presence of gambierol, 5-s depolarizing steps to potentials between +60 and +140 mV were applied. The recovered ionic current was quantified with a postpulse step to +40 mV (Ip). (D) Fractional current recovery (Ip/Ic) as a function of the step potential in C. (E) Time dependence of current recovery at +140 mV from fractional current recovery as a function of the pulse duration. Error bars indicate SEM.
we characterized the slowing in $I_{\text{OFF}}$ decay of Kv3.1 channels using an envelope protocol with steps of different durations to $+60$ mV and $-5$ mV, respectively (Fig. 2 D). Very short depolarizations to $+60$ mV generated an $I_{\text{OFF}}$ that decayed mono-exponentially with a time component $\tau_{\text{OFF,fast}}$ of $0.35 \pm 0.02$ ms ($n = 6$) at $-80$ mV, whereas after prolonged depolarizations $I_{\text{OFF}}$ decayed markedly slower, with a $\tau_{\text{OFF,slow}}$ of $3.44 \pm 0.11$ ms ($n = 6$). Intermediate step durations resulted in bi-exponential $I_{\text{OFF}}$ decays that were a weighted combination of both the fast ($I_{\text{OFF,fast}}$) and the slow ($I_{\text{OFF,slow}}$) component. In contrast, depolarizations to $-5$ mV, which is below the apparent threshold for channel opening, resulted in fast mono-exponential decaying $I_{\text{OFF}}$, with a $\tau_{\text{OFF,fast}}$ of $0.20 \pm 0.02$ ms ($n = 3$), irrespective of the duration of depolarization.

4-Aminopyridine (4-AP) is a universal Kv channel inhibitor (Grissmer et al., 1994) and has been shown to inhibit Shaker Kv channels by preventing the channels from passing the concerted step leading to S6 gate opening has been passed. Therefore,
opening (Loboda and Armstrong, 2001). Application of 3 mM 4-AP, a concentration sufficient to fully inhibit Kv3.1 ionic current, resulted in a disappearance of the slow component of I\textsubscript{gOFF}, whereas the fast kinetics remained unaltered (τ of 0.55 ± 0.02 ms, n = 4) irrespective of step duration (Fig. 2, C and D). This time constant is comparable to the I\textsubscript{gOFF,fast} decay in control conditions. Furthermore, 4-AP resulted in a 14.7 ± 1.0% (n = 5) reduction of the total charge movement, indicating that the amount of charge carried by the final concerted step in the activation pathway is somewhat larger in Kv3.1 than in Shaker, where it was reported to be ~5% (Loboda and Armstrong, 2001).

Gambierol immobilizes the VSD in the resting state
We next investigated the effect of gambierol on the gating charge movement of Kv3.1 channels. Application of 100 nM gambierol resulted in a 96 ± 1% (n = 4) reduction of both I\textsubscript{gON} and I\textsubscript{gOFF} charge movement (Fig. 3, A and B) evoked by depolarizations to +40 mV. This loss in charge movement is substantially more than the 15% of gating charge linked to the final concerted step in channel opening; therefore, gambierol most likely prevents VSD movement between deeper closed states. The time course of reduction in total charge movement (Fig. 3 C) was determined by integrating I\textsubscript{gOFF} and occurred with a time constant of 100 ± 4 s (n = 4), which is clearly slower than the onset of ionic current inhibition. Because the opening of the gate occurs in a concerted manner, requiring all four VSDs being in the active state, then preventing one VSD from reaching its activated state would be sufficient to inhibit channel opening. Indeed, monitoring the kinetic behavior of I\textsubscript{gOFF} showed a clear decrease of I\textsubscript{gOFF,slow} in the overall I\textsubscript{gOFF} decay that developed quicker than the reduction of the total Q\textsubscript{OFF} charge movement. To quantify this, the amplitude of the I\textsubscript{gOFF,slow} was plotted as a function of gambierol application time (Fig. 3 D). I\textsubscript{gOFF,slow} disappeared with a time constant of 68 ± 3 s (n = 4), which was similar to the onset of ionic current inhibition. Furthermore, the decrease in I\textsubscript{gOFF,slow} was accompanied with an initial increase in the amplitude of I\textsubscript{gOFF,fast} (Fig. 3, B and E). This suggests that when one toxin has bound to one of the four binding sites, the concerted step of S6 gate opening cannot occur, precluding gate opening. The further reduction in I\textsubscript{gOFF,fast} amplitude then reflects progressive immobilization of all VSDs. Recovery of I\textsubscript{gOFF,slow} upon washout (Fig. 3 D) was extremely slow and displayed an initial lag phase, similar to the washout of the ionic current (Kopljar et al., 2009).

Determination of the QV curve in the presence of 300 nM gambierol (Fig. 4, A and B) was done by brief 50-ms pulses up to +160 mV, yielding a V\textsubscript{1/2} of 124 ± 6 mV.

Figure 3. Gambierol immobilizes gating charge movement. (A) Gating current recordings in control (black) and after steady-state inhibition with 100 nM gambierol (red). I\textsubscript{gON} were elicited by 125-ms steps to +40 mV from −80 mV holding potential. Subsequently, I\textsubscript{gOFF} were recorded upon repolarizing back to −80 mV. (B) The development of gating current inhibition in A was monitored with steps every 10 s; for clarity, only the gating currents in control (black) and after 60 s (blue), 180 s (gray), and 360 s (red) of gambierol wash-in are shown. (C) Total Q\textsubscript{OFF} charge movement upon gambierol wash-in (red) and washout was obtained by integrating the I\textsubscript{gOFF} currents from B and plotted as a function of time. (D and E) Changes in the amplitude of the slow and fast component of I\textsubscript{gOFF}. In D, the gradual decrease in I\textsubscript{gOFF,slow} was fitted with a mono-exponential function (solid line), yielding a time constant of 76 s. In E, the recovery of I\textsubscript{gOFF,fast} upon washout yielded a time constant of 524 s. Note the transient increase of I\textsubscript{gOFF,fast} (blue arrow) peaks around 60 s (blue tracing in B).
with a $k$ of $21 \pm 2$ mV for $I_{\text{OFF}}$ ($n = 4$). Hence, gambierol acts as a gating modifier that shifts the voltage dependence of charge movement by $\sim 120$ mV toward more depolarized potentials. In control, the decay of $I_{\text{ON}}$ mirrors the rise in ionic current (Fig. 4 C), as has been shown in Shaker (Schoppa et al., 1992; Zagotta et al., 1994b). However, under influence of gambierol, the ionic current does not activate within the time window of $I_{\text{ON}}$ decay. Moreover, the maximal amount of charge moved (determined from the amplitude of the QV curve) was $81 \pm 2\%$ ($n = 4$) of the total charge in control, which is comparable to the amount of charge moved under influence of 4-AP. These data suggest that gambierol-bound channels can move up to the activated-not-open state upon strong depolarizations; however, they cannot pass the concerted step leading to pore opening.

**A single toxin-binding site interaction inhibits ion permeation**

The gating current data suggest that a single toxin-binding site interaction is sufficient to inhibit ion permeation, whereas current recovery requires all binding sites to be toxin-free. To determine the effect of gambierol on a channel containing only a single high-affinity binding site, we created several Kv3.1 concatemers in which four subunits were linked together, resulting in a single polypeptide (Fig. S1 A). The WT concatemer yielded functional channels with biophysical properties and gambierol sensitivity (IC$_{50}$ of $1.2 \pm 0.1$ nM, $n = 3$) similar to WT Kv3.1 channels, assembled from monomers (Figs. 5 A and S1). Mutation of the residue T427 in the S6 segment to a valine drastically reduced the channel’s sensitivity for gambierol (Kopljar et al., 2009). In agreement, the concatemer with four T427V mutant subunits resulted in channels with a $1,000$-fold lower affinity, yielding an IC$_{50}$ of $2.3 \pm 0.3$ µM ($n = 4$), which was comparable to the affinity of tetrodotoxin assembled from T427V monomers. A concatemer that contains one WT and three T427V subunits would yield Kv3.1 channels with only a single high-affinity binding site. Two such concatemers with a different position of the WT subunit were created: WT-mut-mut-mut and mut-mut-WT-mut, which posses the high-affinity binding site in the first and third subunit, respectively. The mut-mut-WT-mut concatemer generated functional channels, with a concentration dependence of gambierol inhibition that could be fitted with a Hill equation yielding an IC$_{50}$ of $23 \pm 3$ nM and a Hill coefficient n$_{H}$ of $0.86 \pm 0.09$ ($n = 5$; Fig. 5, A and B). The WT-mut-mut-WT-mut concatemer had a similar IC$_{50}$ of $20 \pm 2$ nM ($n = 3$), which indicates that the position of the WT subunit within the concatemer did not affect the affinity for gambierol.

The kinetics of gambierol binding and unbinding at a single high-affinity binding site were explored using the mut-mut-WT-mut concatemer (Fig. 5 D). Onset of current inhibition with 100 nM gambierol occurred with a time constant of $110 \pm 8$ s ($n = 3$) or a rate $\lambda$ of $0.009$ s$^{-1}$, yielding an apparent association rate constant $k$ of $0.08 \times 10^6$ M$^{-1}$s$^{-1}$. In contrast to WT Kv3.1 channels, the recovery from current inhibition upon gambierol washout developed mono-exponentially in the mut-mut-WT-mut concatemer with a time constant of $698 \pm 78$ s ($n = 4$) or a dissociation rate constant $l$ of $1.4 \times 10^{-3}$ s$^{-1}$ that was still relatively slow. The initial lag phase in the recovery from current inhibition observed in WT Kv3.1 channels (Fig. 5 C) upon washout of a saturating 100-nM gambierol concentration could be explained by having more than one binding site occupied. To compare the association and dissociation kinetics between the concatemer with a single high-affinity site and WT Kv3.1 channels under nonsaturating conditions, we used 40 nM for the mut-mut-WT-mut concatemer and 10 nM for the WT channel, each yielding $\sim 70\%$ inhibition (Fig. 5, C and D). Under these conditions, the onset of inhibition was similar and the washout displayed a shorter lag phase for WT Kv3.1, followed by a mono-exponential component, equally
slow after exposure with 100 nM (Fig. 5 C). For the concatemer, the recovery after 40 nM followed a mono-exponential time course similar to that after 100 nM. If the toxin acts through the lipid bilayer, the slow dissociation could be caused by the departitioning of gambierol from the plasma membrane. If this would be the rate-limiting step during washout, then the washout in the low-affinity T427V mutant should be similarly slow. However, the T427V mutant displayed a relatively fast washout with a time constant of $21 \pm 2$ s ($n = 3$; Fig. S2), indicating that the slow dissociation kinetics (Fig. 5, C and D) reflect the toxin–channel dissociation rate constants.

**DISCUSSION**

Ladder-shaped polyether toxins (e.g., maitotoxin and yessotoxin) have been proposed to target transmembrane proteins within the lipid bilayer (Murata et al., 2008). Their unique structure, in which the spacing of the ether-oxygens closely matches the pitch of $\alpha$-helices of transmembrane proteins, enables multiple interactions involving hydrogen bonding and/or hydrophobic interactions (Murata et al., 2008; Ujihara et al., 2008, 2010; Torikai et al., 2008). Hence, its amphipathic nature might allow gambierol to modulate Kv channels through the lipid bilayer, where the closed channel conformation represents the high-affinity binding site.

The analysis of the state-dependence of the affinity of Kv3.1 channels for gambierol showed that open channels could not be inhibited in the nanomolar range (Fig. 1 A). However, subsequent induction of current inhibition (Fig. 1 B) occurred with a $\tau$ of 36 s, which is almost twofold faster than the $\tau$ of 65 s determined immediately after gambierol application (Kopljar et al., 2009). If gambierol needs to partition in the membrane to induce channel inhibition, then the kinetics of current inhibition ($\tau$ of 65 s) immediately after gambierol application also include this lipid-partitioning step. In this scenario, the $\tau$ of 36 s most likely reflects the effective onset of channel inhibition for an apparent toxin concentration of 100 nM. Pushing gambierol-bound channels toward the open state (Fig. 1 C) by applying strong membrane depolarizations reverted the inhibition, indicating that activated channels have a much lower affinity than those residing in the resting (closed) state. Furthermore, the reinduction of inhibition developed with a $\tau$ of 39 s, which is similar to the effective onset of channel inhibition, suggesting that current recovery had originated from gambierol dissociation.

The effect of gambierol on gating currents, which reflect the movement of the VSDs, provided further insight into the mechanism of channel inhibition. In control, the $V_{1/2}$ of $Q_{ON}$ and $Q_{OFF}$ was $\sim 15$ mV more...
negative than the $V_{1/2}$ of the voltage dependence of channel opening. Furthermore, with depolarizations >0 mV, there was a clear slowing in the decay of $I_{\text{OFF}}$.

Using envelope protocols, we provided evidence that this slowing in $I_{\text{OFF}}$ is linked to the final concerted step leading to channel gate opening, as it is in other Kv channels (Bezanilla et al., 1994; Chen et al., 1997; Wang et al., 2007). This conclusion was further strengthened by the eliminated slow component in $I_{\text{OFF}}$ by 4-AP, similar to the data for Shaker (Loboda and Armstrong, 2001). However, the fast component was left unaltered, indicating that this charge displacement is linked to VSD movements early in the activation pathway (before the concerted step) when the subunits move between the resting (closed) and the activated-not-open state.

Application of gambierol resulted in a time-dependent reduction of the total charge movement at +40 mV (for both $Q_{\text{ON}}$ and $Q_{\text{OFF}}$; Fig. 3, A and B). During this progressive loss of charge movement, the relative contribution of the fast ($I_{\text{OFF,fast}}$) and slow ($I_{\text{OFF,slow}}$) decaying component in $I_{\text{OFF}}$ changed. The decrease in $I_{\text{OFF,slow}}$ amplitude occurred on the same time scale as the onset of ionic current inhibition (Fig. 3 D), which indicated that inhibition of ion permeation is directly linked to the failure of channels to pass the final concerted opening step. The decrease in $I_{\text{OFF,slow}}$ was initially accompanied by an increase in the amplitude of $I_{\text{OFF,fast}}$ (but not of the total charge integral). Together with the data on the Kv3.1 concatemers that a single high-affinity binding site is sufficient for inhibition of the ionic current (Fig. 5), we interpret this as follows: when a single gambierol molecule binds to one of the four binding sites, this subunit cannot move to the activated state, and the channel cannot open (i.e., pass the concerted step); however, the other subunits, free of gambierol, are still able to move their VSD up to the activated state upon strong depolarizations, but cannot pass the concerted step leading to channel opening as long as gambierol remained bound.

Kv3.1 concatemers with a single WT binding site displayed an IC$_{50}$ of 20 nM, which should represent the intrinsic affinity of a single binding site. Indeed, assuming four equivalent and independent binding sites, this would yield an apparent IC$_{50}$ of 3–4 nM for the WT channel, which is close to the reported IC$_{50}$ of 1.2 nM (Kopljar et al., 2009). Onset of gambierol inhibition was about twofold slower ($\tau = 110$ s) than previously reported for WT (Kopljar et al., 2009). This differs from the fourfold change expected in the case of four independent binding sites per channel. However, the value of $\sim 65$ s for WT may not reflect the true toxin–channel interaction kinetics: as argued before, a value of 35–40 s is more likely. Under nonsaturating conditions, a fourfold higher gambierol concentration was indeed required to obtain a similar time course of inhibition in the mut-mut-WT-mut concatemer compared with WT channels (40 nM compared with 10 nM, respectively; Fig. 5, C and D). The washout in the mut-mut-WT-mut concatemer was mono-exponential ($\tau = 698$ s) and faster compared with WT channels. The association and dissociation rate constants $k$ and $l$ obtained from this concatemer most likely reflect the intrinsic kinetics for the interaction of gambierol with the resting (closed) state. Indeed, in WT channels, the dissociation kinetics are complicated by the fourfold symmetry (Kopljar et al., 2009). Thus, the washout in WT channels displays a more complex time course with an initial lag phase, whereas the washout in the mut-mut-WT-mut concatemer (Fig. 5 D) was mono-exponential and similar to the recovery of $I_{\text{OFF,fast}}$ (Fig. 3 E). These data suggest that a single toxin-binding site interaction is sufficient to inhibit ion permeation, whereas current recovery requires all binding sites to be toxin-free.

Several tarantula and sea anemone toxins (e.g., hanatoxin, BDS-II) are well-known gating modifiers of Kv channels (Swartz, 2007; Wang et al., 2007). Both peptide toxins also stabilize the resting state, but their mechanism differs from the polyether toxin gambierol. Hanatoxin and BDS-II act as a cargo attached to the VSD imposing an energetic penalty for its movement (Phillips et al., 2005; Wang et al., 2007), thus requiring stronger depolarizations to open these toxin-bound channels. In contrast, gambierol acts like an anchor that immobilizes the gating machinery in a more profound manner. Although hanatoxin-bound channels can open, gambierol-bound ones cannot and require dissociation of the toxin to restore permeation.

Based on the experimental data, we propose two mechanisms for channel inhibition by gambierol, both resulting in VSD immobilization. For Shaker-type Kv channels, it has been proposed that the VSD has to
possibility that one gambierol molecule affects multiple (i.e., two) VSDs. However, the time dependence of the reduction of total charge and IgOFF,fast was noticeable different from the reduction of the IgOFF,slow component. This indicates that one gambierol molecule cannot affect all four VSDs simultaneously, because in that case both processes should occur simultaneously. The initial lag in the time course of recovery and the difference in the apparent affinities of WT and mut-mut-WT-mut concatemers is also most easily explained by a model with four independent binding sites. Thus, we provide a novel mechanism for Kv channel inhibition that relies on anchoring the gating machinery in its resting (closed) state. Upon strong depolarizations, the VSD can be pushed toward its activated-not-open state, but as long as gambierol is bound, the channel gate remains closed, similar to the effect of 4-AP or channel mutations that isolate the final concerted step of channel opening. The conformational change associated with this activated-not-open state most likely reduces the affinity for gambierol and presumably enhances the dissociation rate. Consequently, the channel eventually opens when fully freed of toxin (Fig. 6). However, the depolarizations required for activating gambierol-bound channels exceed by far the physiologically relevant voltage range.

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Figure 6. Cartoon of the proposed mechanistic models (S6 gate and VSD anchoring) for Kv channel inhibition. Residue T427 in S6 is shown in red, and for clarity only one VSD is shown. The closed channel conformation with the VSD in the resting state forms the high-affinity state that is stabilized by gambierol (resting-bound). With strong depolarizations (ΔV), the VSDs move to the activated state, which displays a lower affinity for gambierol (activated-bound). Spending sufficient time (Δt) in this low-affinity conformation results in an accelerated unbinding of gambierol, allowing channels to open (open-unbound).


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