

Substitution of a Single Residue in *Stichodactyla helianthus* Peptide, ShK-Dap²², Reveals a Novel Pharmacological Profile

Richard E. Middleton,^{‡,§} Manuel Sanchez,^{‡,§} Ana-Rosa Linde,^{‡,§,||} Randal M. Bugianesi,[‡] Ge Dai,[‡] John P. Felix,[‡] Sam L. Koprak,[‡] Mary Jo Staruch,[‡] Marc Bruguera,[‡] Rachael Cox,[‡] Amrita Ghosh,[‡] Jeremy Hwang,[‡] Simonette Jones,[‡] Martin Kohler,[‡] Robert S. Slaughter,[‡] Owen B. McManus,[‡] Gregory J. Kaczorowski,[‡] and Maria L. Garcia^{*,‡}

Departments of Ion Channels and Immunology Research, Merck Research Laboratories, P.O. Box 2000, Rahway, New Jersey 07065

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ABSTRACT: ShK, a peptide isolated from *Stichodactyla helianthus* venom, blocks the voltage-gated potassium channels, K_v1.1 and K_v1.3, with similar high affinity. ShK-Dap²², a synthetic derivative in which a diaminopropionic acid residue has been substituted at position Lys²², has been reported to be a selective K_v1.3 inhibitor and to block this channel with equivalent potency as ShK [Kalman et al. (1998) *J. Biol. Chem.* 273, 32697–32707]. In this study, a large body of evidence is presented which indicates that the potencies of wild-type ShK peptide for both K_v1.3 and K_v1.1 channels have been previously underestimated. Therefore, the affinity of ShK-Dap²² for both channels appears to be ca. 10²–10⁴-fold weaker than ShK. ShK-Dap²² does display ca. 20-fold selectivity for human K_v1.3 vs K_v1.1 when measured by the whole-cell voltage clamp method but not in equilibrium binding assays. ShK-Dap²² has low affinity for K_v1.2 channels, but heteromultimeric K_v1.1-K_v1.2 channels form a receptor with ca. 200-fold higher affinity for ShK-Dap²² than K_v1.1 homomultimers. In fact, K_v1.1-K_v1.2 channels bind ShK-Dap²² with only ca. 10-fold less potency than ShK and reveal a novel pharmacology not predicted from the homomultimers of K_v1.1 or K_v1.2. The concentrations of ShK-Dap²² needed to inhibit human T cell activation were ca. 10³-fold higher than those of ShK, in good correlation with the relative affinities of these peptides for inhibiting K_v1.3 channels. All of these data, taken together, suggest that ShK-Dap²² will not have the same in vivo immunosuppressant efficacy of other K_v1.3 blockers, such as margatoxin or ShK. Moreover, ShK-Dap²² may have undesired side effects due to its interaction with heteromultimeric K_v1.1-K_v1.2 channels, such as those present in brain and/or peripheral tissues.

Peptides isolated from scorpion, snake, and sea anemone venoms have become invaluable tools for studying the outer pore structure of potassium channels (1). From the sea anemone venoms *Stichodactyla helianthus* and *Bunodosoma granulifera*, two peptides, ShK¹ and BgK, have been purified and characterized (2, 3). ShK and BgK contain 35 and 37 amino acid residues, respectively, and block with different potencies and selectivities a subset of voltage-gated potassium channels of the K_v1.x family. ShK is a high-affinity blocker of K_v1.1 and K_v1.3 channels, whereas BgK blocks with similar potency K_v1.1, K_v1.2, and K_v1.3 channels. The three-dimensional structure of these peptides, containing a

central helix–kink–helix fold, is quite different from that of the K_v1 scorpion channel blocking peptides (4). Despite this fact, all of these pore-blocking peptides appear to use a common functional diad for blocking the channel, consisting of a lysine and a hydrophobic residue, separated by about 7 Å (5). Substitution of the critical lysine²² residue of ShK with the unnatural amino acid, diaminopropionic acid (ShK-Dap²²), has been reported to weaken the resulting peptide's affinity for K_v1.1 ca. 100-fold but to have no significant effect on K_v1.3 channel blocking potency (6). Thus, ShK-Dap²² has been proposed to be a selective K_v1.3 inhibitor. A similar substitution in BgK led to >100-fold decrease in the potency of the resulting peptide for all three BgK-sensitive channels, K_v1.1, K_v1.2, and K_v1.3 (7).

The discovery of selective K_v1.3 inhibitors is of interest, given the critical role that K_v1.3 plays in human T lymphocyte activation. In human T lymphocytes, K_v1.3 sets the resting potential, and its inhibition causes cell depolarization, leading to attenuation in the rise of intracellular calcium levels that occurs upon T cell receptor stimulation, which is necessary for T cell proliferation (8, 9). In addition, K_v1.3 channels appear to be specifically upregulated in activated human effector memory cells, suggesting a role for this channel in autoimmune diseases (10). Peptides and small

* To whom correspondence should be addressed at P.O. Box 2000, RY80N-C31, Rahway, NJ 07065. Tel: 732-594-7564. Fax: 732-594-3925. E-mail: maria_garcia@merck.com.

[‡] Department of Ion Channels, Merck Research Laboratories.

[§] Contributed equally to this work.

^{||} Present address: National School of Public Health, Oswaldo Cruz Foundation, Brazil.

¹ Immunology Research, Merck Research Laboratories.

¹ Abbreviations: K_v, voltage-gated potassium channel; ¹²⁵I-HgTX₁-A19Y/Y37F, monoiodotyrosine-hongotoxin₁-A19Y/Y37F; K_d, equilibrium dissociation constant; K_i, equilibrium inhibition constant; MgTX, margatoxin; ShK, *Stichodactyla helianthus* peptide; ShK-Dap²², *Stichodactyla helianthus* lysine²²-diaminopropionic acid; VIPR, voltage/ion probe reader; PBMC, peripheral blood mononuclear cells.

molecule K_v1.3 blockers have been shown to have immunosuppressant activity in in vivo animal models (11–14).

In this study, evidence is presented which indicates that the potency of ShK-Dap²² for human K_v1.3 is >100-fold weaker than ShK. This was observed in five different cell-based assays. ShK-Dap²² does block current through K_v1.3 about 20-fold more potently than human K_v1.1 channels, but in equilibrium binding studies, it binds to both channels with similar affinity. Although ShK-Dap²² displays low potency for K_v1.2 channels, it binds with relatively high affinity to K_v1.1-K_v1.2 heteromultimers compared to homomultimeric K_v1.1 channels. Given the unexpected pharmacological profile of ShK-Dap²² for heteromultimeric K_v1.1-K_v1.2 channels and greatly reduced potency on K_v1.3, ShK-Dap²² is not predicted to have the efficacy or specificity that is needed for its development as an immunosuppressant. A preliminary report of these findings has been presented in abstract form (15).

EXPERIMENTAL PROCEDURES

Materials. Restriction enzymes and the pCI-neo vector were bought from Promega. The pEGFP-N1 vector was from Clontech, and *Pfu* DNA polymerase was from Stratagene. The TsA-201 cell line, a subclone of the human embryonic kidney cell line HEK293 that expresses the SV40 T antigen, was a gift of Dr. Robert DuBridge. All tissue culture media were from Gibco, serum was from Hyclone, and the FuGENE6 transfection reagent was from Boehringer Mannheim. ⁸⁶RbCl and [³H]thymidine (6.7 Ci/mmol) were purchased from NEN Life Science Products. CHO cells stably transfected with the human K_v1.3 channel were prepared as previously described (16). HEK293 cells stably transfected with homotetrameric human K_v1.1 and K_v1.3 channels were obtained from Professor Olaf Pongs (Zentrum für Molekulare Neurobiologie, Hamburg, Germany), whereas those transfected with homotetrameric human K_v1.2 channels were obtained as previously described (17). Human brain tissue was provided by Drs. H.-G. Knaus and H. Glossmann, University of Innsbruck, Innsbruck, Austria. ShK was purchased from Peptides International. Hongotoxin₁-A19Y/Y37F (HgTX₁A19Y/Y37F) was prepared and radioiodinated as described (18). CC2-DMPE and DiSBAC₂(3) were bought from Panvera (Madison, WI), and pluronic acid was from Molecular Probes (Eugene, OR). Human T cell conditioned medium was from Collaborative Research (Cambridge, MA). OKT3 (anti-CD3) mAb was obtained from Ortho Diagnostic Systems (Raritan, NJ). GF/C glass fiber filters were obtained from Whatman, and poly(ethylenimine) was from Sigma. All other reagents were obtained from commercial sources and were of the highest purity available.

K_v1.1-K_v1.2 Dimer and Tetramer Constructs. cDNA coding for a K_v1.1-K_v1.2 dimer was prepared as previously described (3). To obtain a K_v1.1-1.2-1.1-1.2 construct, the K_v1.1-1.2 dimer in pCI-neo served as starting material. The insert of the dimer plasmid was amplified by PCR (*Pfu* Turbo, Stratagene) with the following primer pair: K_v1.1Nhe-s, GCATGCTAGCAGCCACCATGACGGTGATGTCTGGGAG, and K_v1.2BspE-as, CGTATCCGGAGACATCAGTTAACATTTTGG. The resulting fragment was subcloned into pCI-neo and sequenced to ensure the correctness of the amplified dimer. The dimer was amplified with a second

primer pair: hK_v1.1Q10BspE, GCTATCCGGACAACAGC-AGCAACAACAGCAGCAACAACAGATGACGGTGATGTCTGGGGAG, and hK_v1.2op-Mlu-as, GCTAACGCGTTCAGACATCAGTTAACATTTTGG. The product of this PCR reaction was also subcloned in pCI-neo and sequenced.

The K_v1.1-1.2-1.1-1.2 tetramer was constructed by joining a dimer fragment with *NheI* and *BspEI* restriction sites at its 5' and 3' ends, respectively, from the first PCR reaction, with a dimer fragment from the second PCR reaction with *BspEI* and *MluI* sites at the 5' and 3' ends. The pCI expression vector (Promega) was prepared with the restriction enzymes *NheI* and *MluI*. The product of this ligation reaction was introduced into STBL2-competent cells (Invitrogen). A plasmid with the desired tetramer was chosen on the basis of the expected restriction pattern.

Synthesis of ShK-Dap²². ShK-Dap²² was prepared by solid-phase synthesis by Peptides International. The folded peptide was characterized by amino acid hydrolysis (Peptides International), HPLC, amino acid sequencing (Porton Instruments PI2090E), and mass spectroscopy. The mass contents of ShK and ShK-Dap²² solutions were determined by amino acid hydrolysis. Solutions of the peptides were made in 100 mM NaCl, 20 mM Tris-HCl, pH 7.4, and 0.1% bovine serum albumin. Aliquots were frozen in liquid N₂ and stored at -70 °C. Once thawed, the solutions were kept at 4 °C.

Human T Cell Preparation. Human peripheral blood mononuclear cells (PBMC) were isolated as previously indicated (13). Purified T cells were prepared by rosetting as described (13). Purity of human T cells was 95–97%, as determined by anti-CD3 staining in FACS analyses.

Electrophysiological Recordings from Human T Lymphocytes. Whole-cell recordings were made from purified human T lymphocytes as previously described using standard methods (19). Electrodes were pulled from Garner 7052 glass; their resistances were 1–3 MΩ when filled with standard pipet solution and immersed in bath solution. The pipet contained 120 mM KCl, 20 mM KF, 10 mM Hepes, and 10 mM K₂EGTA, pH 7.2, with KOH, and the bath solution contained 160 mM NaCl, 10 mM Hepes, 4.5 mM KCl, 2 mM CaCl₂, and 1 mM MgCl₂, pH 7.2, with NaOH. The amplifier inputs were connected to the experimental solutions via Ag/AgCl electrodes, and the bath electrode contacted the bath solution through an agar bridge containing 200 mM KCl. No corrections for junction potentials or series resistance were applied. Experiments were done under constant flow (1–2 mL/min) with a chamber volume of 0.2–0.4 mL at room temperature (22–24 °C).

Membrane currents were measured with Axopatch 1D (Axon Instruments) or EPC9 (HEKA Elektronik) amplifiers. Voltage control and data acquisition were done using ITC-16 interfaces (Instrutech Corp.) connected to Macintosh computers (Apple Computer) running Pulse software (HEKA Elektronik). Data analysis was done using PulseFit (HEKA Elektronik) and Igor Pro (Wavemetrics Inc.) software. Currents were filtered at 2–5 kHz and digitized at 5–10 kHz. Analogue capacity compensation was applied, and digital compensation of the leak and residual capacity currents was done using a P/4 protocol from the standard holding potential (-80 mV), with subtraction pulses applied 4–10 s after the test pulses. If peak current amplitudes were stable in the control for 10 min or more, peptides were applied until a steady-state level of block was reached. Mean

inhibition values (\pm SEM) at each peptide concentration were fit with Hill equations with the slope fixed to 1.

Electrophysiological Recordings from *Xenopus* Oocytes. *Xenopus* oocytes were injected with 50 nL of water containing 0.5–5 ng of RNA encoding human $K_v1.1$ or $K_v1.3$ channel proteins and stored at 18 °C. Membrane currents were recorded 1–5 days after injection using standard two-electrode voltage clamp methods. Currents were recorded with a Dagan CA-1 (Dagan Corp.) oocyte clamp. Data acquisition and analysis were done as described above for the experiments using T lymphocytes. Electrodes were filled with 2 M KCl, and current injection electrodes had resistances of 0.3–0.8 M Ω . Oocytes with peak current amplitudes in the range of 1–5 μ A were typically used. Recordings were made at room temperature (22–24 °C) in a 0.5 mL chamber with constant superfusion at 1–1.5 mL/min. Steady-state levels of channel block were calculated for each oocyte, and mean values (\pm SEM) at each peptide concentration were fit with Hill equations as described above.

$^{86}\text{Rb}^+$ Efflux Assay. The $^{86}\text{Rb}^+$ efflux assay is a modified form of a previously described technique (16, 19). CHO cells stably expressing human $K_v1.3$ are preincubated in 12-well plates overnight in the presence of trace amounts of $^{86}\text{Rb}^+$ in 1.5 mL of growth media. Triplicate samples of 2.5 mL peptide solutions in low K buffer (in mM: 135 NaCl, 4.6 KCl, 1 CaCl_2 , 20 Hepes, pH 7.4, with NaOH) with 2 mM glucose and 1% bovine serum albumin were added to each well. After at least 1 h incubation at 37 °C, each well was washed three times with 3.33 mL of low K buffer, and then 2 mL of high K buffer (in mM: 140 KCl, 1 CaCl_2 , 2 MgCl_2 , 10 Hepes-K, pH 7.4) was added. After 12 min, the high K buffer was removed and placed in a 20 mL vial containing 10 mL of scintillation fluid. Two milliliters of 1% sodium dodecyl sulfate was added to each well to rupture the cell membrane prior to counting the remaining intracellular $^{86}\text{Rb}^+$. After approximately 1 h, the 2 mL sodium dodecyl sulfate solution was removed, placed in a vial with 10 mL of scintillation fluid, and analyzed by liquid scintillation techniques. Efflux was defined as the percent of $^{86}\text{Rb}^+$ in each well that was present in the 2 mL high K buffer.

Transfection of TsA-201 Cells and Membrane Preparation. The procedures for handling TsA-201 cells, their transfection with FuGENE6 transfection reagent, and preparation of membrane vesicles have been previously described (17). The final membrane pellet was resuspended in 100 mM NaCl and 20 mM Hepes–NaOH, pH 7.4. Aliquots were frozen in liquid N_2 and stored at –70 °C.

^{125}I -HgTX₁A19Y/Y37F Binding. The interaction of ^{125}I -HgTX₁A19Y/Y37F with human $K_v1.x$ channels was determined in a medium consisting of 100 mM NaCl, 5 mM KCl, 20 mM Tris-HCl, pH 7.4, and 0.1% bovine serum albumin. A total volume of 12 mL was used in order to maintain the receptor concentration below the determined IC₅₀ values of inhibition. Incubations were carried out for 20 h at room temperature. Separation of bound from free ^{125}I -HgTX₁A19Y/Y37F was achieved using filtration protocols as described (18). Nonspecific binding was determined in the presence of 1 nM margatoxin (MgTX).

Membrane Potential Assay. CHO cells stably expressing $K_v1.3$ were plated in black-wall, clear-bottom 96-well plates and grown overnight in growth media to reach confluency prior to assay on VIPR (ca. 1×10^5 cells/well). Cells were

washed with 200 μ L of Dulbecco's phosphate-buffered saline supplemented to 10 mM glucose and 10 mM Hepes-Na, pH 7.2 (DPBS), and then incubated in 100 μ L of 5 μ M CC2-DMPE and 0.02% pluronic acid in DPBS for 30–60 min at room temperature. Wells were rinsed twice with 100 μ L of sodium gluconate (in mM: 150 sodium gluconate, 4 KCl, 1 CaCl_2 , 0.5 MgCl_2 , 11 glucose, 20 sodium phosphate, pH 7.2) and then incubated in 100 μ L of sodium gluconate supplemented with 10 μ M DiSBAC₂(3) and test sample at the indicated concentration for 30–60 min at room temperature. At the end of this incubation, the plate was placed in the VIPR reader, illuminated at 400 nm, and fluorescence emissions at 460 and 580 nm were recorded. After a 7 s baseline reading, 100 μ L of potassium gluconate solution was added (in mM: 150 potassium gluconate, 4 KCl, 1 CaCl_2 , 0.5 MgCl_2 , 11 glucose, 20 sodium phosphate, pH 7.2). The change in membrane potential was detected as the change in fluorescence resonance energy transfer, determined as the ratio, F/F_0 , or more explicitly as

$$F/F_0 = (M_{480}/M_{560})/(I_{480}/I_{560})$$

where M and I are maximal and initial fluorescence emission measurements at the indicated wavelengths.

Data Analysis. Data from saturation experiments were analyzed according to the equation $B_{\text{eq}} = (B_{\text{max}}L^*)/(K_d + L^*)$, where B_{eq} is the amount of ligand bound at equilibrium, B_{max} the maximum receptor concentration, K_d the ligand dissociation constant, and L^* the free ligand concentration. IC₅₀ values for inhibition of ^{125}I -HgTX₁A19Y/Y37F binding were determined using the equation $B_{\text{eq}} = (B_{\text{max}} - B_{\text{min}})/[1 + (I/\text{IC}_{50})^{nH}] + B_{\text{min}}$, where B_{max} is the binding with no inhibitors present, B_{min} is the minimum amount of ligand bound at the maximal inhibitor concentration, I is the inhibitor concentration, nH is the Hill coefficient, and IC₅₀ is the inhibition constant. For the data, B_{max} was usually around 100% and B_{min} was 0%. Inhibition of ^{125}I -HgTX₁A19Y/Y37F binding to $K_v1.1$ -1.2 dimer and $K_v1.1$ -1.2-1.1-1.2 membranes by ShK-Dap²² was analyzed according to the equation $B_{\text{eq}} = (B_{\text{max}} - B_{\text{min}})/[1 + (I/\text{IC}_{50(1)})^{nH1}] + B_{\text{min}}/[1 + (I/\text{IC}_{50(2)})^{nH2}]$, where the parameters corresponding to sites 1 and 2 are described above.

Proliferation Assays. Purified human T lymphocytes were cultured in 96-well microtiter plates (Costar, Cambridge, MA) as described (13). Compounds were added and incubated for 15–30 min at 37 °C. The cultures were stimulated with 0.3 ng/mL OKT3. Irradiated (1500 R) autologous PBMC cells were then added, and cultures were incubated for 3 days at 37 °C as described (13). T cell proliferation was measured by addition of 2 μ Ci/well [^3H]thymidine about 18 h before harvesting. Cultures were harvested, and radioactivity associated with filters was determined by liquid scintillation techniques. The data shown represent the means of triplicate wells.

RESULTS

ShK-Dap²² Blocks K_v Channels in Human T Cells Less Potently Than ShK. ShK has previously been characterized as a high-affinity blocker of $K_v1.1$ and $K_v1.3$ channels (6). $K_v1.3$ inhibitors have shown efficacy in suppressing immune responses in in vitro experiments (6, 13, 14, 19–23) and in in vivo models (11–14). Consistent with this, ShK inhibits

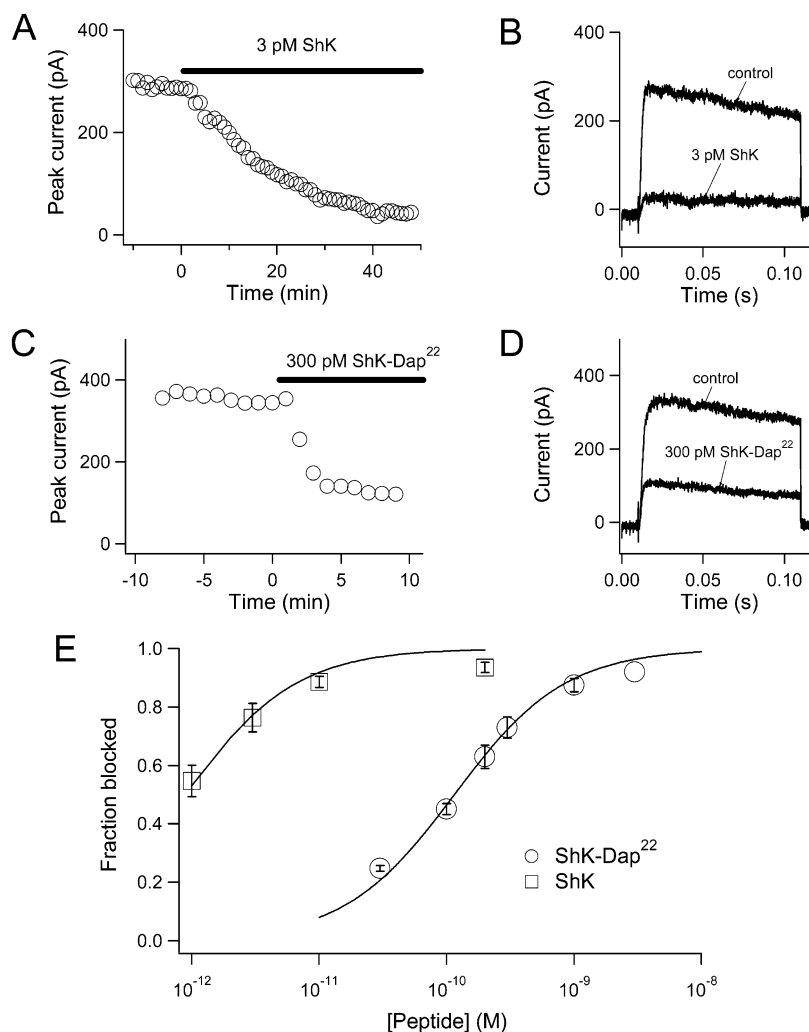


FIGURE 1: Block of $K_v1.3$ channels in human T lymphocytes by ShK and ShK-Dap²². The time course of channel block by 3 pM ShK is shown in (A), and membrane currents recorded in control and after 45 min in ShK are shown in (B). (C) shows the time course of block after 300 pM ShK-Dap²², and (D) shows currents recorded in control and after 9 min in 300 pM ShK-Dap²². The steady-state fraction of channels blocked was estimated for each experiment, and mean values are plotted against peptide concentration in (E). Mean values were calculated from three to ten determinations at each peptide concentration, except one determination was made at 3000 pM ShK-Dap²² and two determinations were made at 1 pM ShK.

human T cell proliferation (6, 10) and can prevent and ameliorate experimental autoimmune encephalomyelitis (11, 12). Thus, a selective $K_v1.3$ inhibitor could provide a potential immunosuppressive therapy. Toward this end, it was reported that substitution of diaminopropionic acid at the critical Lys²² residue generates a peptide, ShK-Dap²², that retains the same affinity for $K_v1.3$ as ShK but with 100-fold reduced potency against the $K_v1.1$ channel (6). To evaluate the efficacy of these peptides, ShK and ShK-Dap²² peptides were synthesized by solid-phase synthesis and folded, and their structures were confirmed by a number of analytical techniques.

Inhibition of $K_v1.3$ channels in human T lymphocytes by ShK and ShK-Dap²² was investigated using whole-cell, voltage clamp recording methods (Figure 1). T cells were held at a membrane potential of -80 mV, and the peak outward potassium current was measured during 100 ms voltage steps to $+20$ mV, delivered once per minute. Currents were blocked by both peptides. Figure 1A shows the time course of channel block by 3 pM ShK. Block equilibrated along an exponential time course with a time constant of 20 min, and a steady-state level of block (fraction

blocked = 0.75) was reached after 45 min. The prolonged time course of channel block seen in Figure 1A is simply due to the low toxin concentration applied. The rate constant for channel block (ca. $7 \times 10^7 \text{ M}^{-1} \text{ s}^{-1}$) was estimated from the slope of the inverse time constant for onset of block. In fact, this on-rate was somewhat higher than typical values reported for peptide-channel interactions (24–30). Due to the time required to reach steady-state block at low peptide concentration, we did not attempt to use ShK at concentrations below 1 pM (equilibration time ≥ 1 h). A fit of the titration of $K_v1.3$ channel block by ShK concentrations greater than 1 pM gives an estimated IC_{50} value of ~ 0.9 pM (Figure 1E).

In contrast to ShK, ShK-Dap²² blocked T lymphocyte potassium currents at 100-fold higher concentrations. Application of 300 pM ShK-Dap²² (Figure 1C,D) caused a similar level of channel block (fraction blocked = 0.65) as 3 pM ShK. The onset of channel block by 300 pM ShK-Dap²² equilibrated in 3–4 min, as expected at a higher peptide concentration. The observed rates for channel block at 30 and 100 pM suggest that the binding rate for ShK-Dap²² is slower (data not shown). Titration of T cell

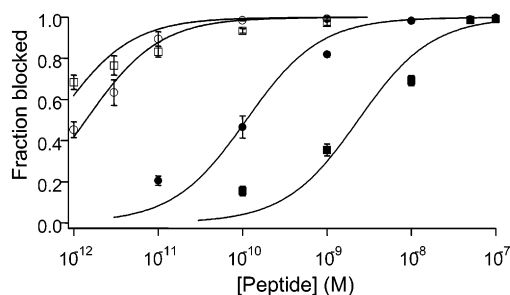


FIGURE 2: Block of $K_v1.1$ and $K_v1.3$ channels expressed in *Xenopus* oocytes by ShK and ShK-Dap²². Block of $K_v1.1$ currents (\square , \blacksquare) and $K_v1.3$ currents (\circ , \bullet) by ShK (\square , \circ) and ShK-Dap²² (\blacksquare , \bullet) is shown as a function of peptide concentration. The solid lines show fits to data with Hill equations. The IC_{50} 's determined for block of $K_v1.3$ by ShK and ShK-Dap²² were 1.4 and 110 pM, respectively, and for block of $K_v1.1$ by ShK and ShK-Dap²² 0.6 and 2300 pM, respectively. Mean values were calculated from four to eight determinations except for the value at 10 nM ShK-Dap²² applied to $K_v1.3$ channels, which was based on two determinations.

potassium channel block by ShK-Dap²² gave an IC_{50} of 115 pM (Figure 1E), indicating that ShK-Dap²² is at least 100-fold less potent than the parent ShK peptide. Given the technical difficulties associated with accurate measurements of steady-state block at concentrations <1 pM, the difference in potencies between both peptides could be >100 -fold.

Expression of $K_v1.1$ and $K_v1.3$ Channels in *Xenopus* Oocytes: Sensitivity to ShK and ShK-Dap²². To examine the selectivity of ShK and ShK-Dap²² for blocking $K_v1.3$ channels compared with block of related voltage-gated potassium channels, voltage clamp recordings were made with *Xenopus* oocytes expressing human $K_v1.3$ and $K_v1.1$ channels. Figure 2 shows titrations of steady-state block of $K_v1.3$ and $K_v1.1$ channels by ShK and ShK-Dap²². In harmony with the results obtained using human T lymphocytes (Figure 1), $K_v1.3$ channels expressed in *Xenopus* oocytes were blocked by ShK with an IC_{50} of 1.4 pM and by ShK-Dap²² at 100-fold higher concentrations ($IC_{50} = 110$ pM). $K_v1.1$ channels were blocked by ShK ($IC_{50} = 0.6$ pM) with similar potency, although these measurements were at the limit of determination in electrophysiological experiments. In contrast to the nearly 100-fold decrease in affinity observed for $K_v1.3$ channels, modification of ShK to ShK-Dap²² caused a nearly 4000-fold decrease in affinity for $K_v1.1$ channels. Therefore, ShK-Dap²² is less potent than ShK toxin on both channels but displays a 20-fold selectivity for block of human $K_v1.3$ over $K_v1.1$ channels, while native ShK peptide shows little selectivity.

$^{86}Rb^+$ Flux through $K_v1.3$ Channels: Effect of ShK and ShK-Dap²². An alternative method for evaluating the activity of $K_v1.3$ channels is to measure depolarization-induced $^{86}Rb^+$ efflux from cells stably expressing the channel (16, 19). For this purpose, CHO cells stably expressing the human $K_v1.3$ channel are loaded with $^{86}Rb^+$, and a high potassium solution is used to cause depolarization and open the channels. MgTX inhibits $^{86}Rb^+$ efflux through $K_v1.3$ channels with an $IC_{50} = 25$ pM (Figure 3). ShK displays a similar high potency in this assay, $IC_{50} = 10$ pM. In contrast, ShK-Dap²² is a less potent inhibitor of $K_v1.3$ channels with an $IC_{50} = 4500$ pM, which is ca. 500-fold weaker than that of ShK. Although the apparent potency of the peptides in the $^{86}Rb^+$ efflux assay is lower than in electrophysiological assays (see Discussion), a similar difference in rank order of potency between ShK

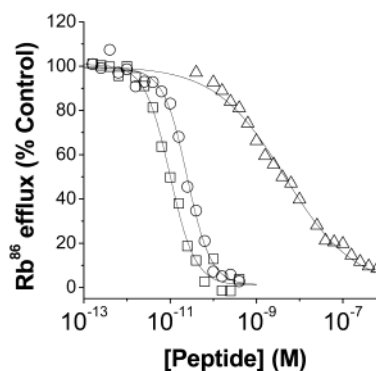


FIGURE 3: $^{86}Rb^+$ flux through $K_v1.3$: effect of ShK and ShK-Dap²². HEK293 cells that stably express $K_v1.3$ were incubated overnight in the presence of trace amounts of $^{86}Rb^+$. The cells were then preincubated with the indicated concentration of peptide for 1 h with $^{86}Rb^+$. Depolarization-induced efflux was initiated by addition of 140 mM KCl, and incubation was carried out at room temperature. After 12 min, efflux was measured as the ratio of the $^{86}Rb^+$ in the bath divided by the total $^{86}Rb^+$. Percent inhibition was defined according to the maximal produced by 10 nM MgTX. The data were fit to IC_{50} values of 24.7, 9.9, and 4530 pM for MgTX (\circ), ShK (\square), and ShK-Dap²² (\triangle), respectively.

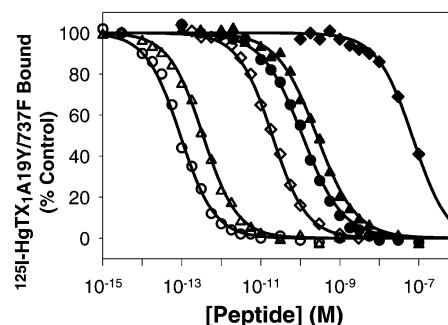


FIGURE 4: Binding of ^{125}I -HgTX_{1A19Y/Y37F} to $K_v1.1$, $K_v1.2$ or $K_v1.3$: effect of ShK and ShK-Dap²². Membranes prepared from HEK293 cells stably expressing human $K_v1.1$ (\circ , \bullet), $K_v1.2$ (\diamond , \blacklozenge), or $K_v1.3$ (\triangle , \blacktriangle) channels were incubated with ~ 0.1 pM ^{125}I -HgTX_{1A19Y/Y37F}, in the absence or presence of increasing concentrations of either ShK (open symbols) or ShK-Dap²² (closed symbols), for 20 h at room temperature. The incubation medium consisted of 100 mM NaCl, 5 mM KCl, 20 mM Tris-HCl, pH 7.4, and 0.1% bovine serum albumin. Nonspecific binding was determined in the presence of 1 nM MgTX. Specific binding data are presented relative to an untreated control. It was critical to maintain a receptor site density below 0.1 pM to ensure accurate determinations of K_i values.

and ShK-Dap²² is present in both protocols.

Binding of ^{125}I -HgTX_{1A19Y/Y37F} to $K_v1.1$, $K_v1.2$, and $K_v1.3$ Channels: Effect of ShK and ShK-Dap²². Under equilibrium conditions, ^{125}I -HgTX_{1A19Y/Y37F} binds with high affinity to membranes derived from HEK293 cells stably transfected with human $K_v1.1$, $K_v1.2$, or $K_v1.3$ channels. The equilibrium dissociation constants, K_d 's, determined in the presence of 100 mM NaCl, 5 mM KCl, and 20 mM Tris-HCl, pH 7.4, are 0.10 ± 0.005 , 0.046 ± 0.002 , and 0.3 ± 0.02 pM for $K_v1.1$, $K_v1.2$, and $K_v1.3$, respectively. Under the same experimental conditions, ShK and ShK-Dap²² cause concentration-dependent inhibition of ^{125}I -HgTX_{1A19Y/Y37F} binding to each of these membrane preparations (Figure 4). In all cases, inhibition is monophasic, and Hill coefficients are close to 1. The calculated K_i values for inhibition are presented in Table 1. ShK is a very potent inhibitor of ^{125}I -HgTX_{1A19Y/Y37F} binding to both $K_v1.1$ and $K_v1.3$ mem-

Table 1^a

	<i>K_i</i> (pM)		
	K _v 1.1	K _v 1.2	K _v 1.3
ShK	0.041 ± 0.001	5.03 ± 0.28	0.25 ± 0.005
ShK-Dap ²²	59 ± 2.5	20750 ± 1850	198 ± 5.5

^a ¹²⁵I-HgTX₁A19Y/Y37F binding to K_v1.1, K_v1.2, or K_v1.3 channels, in the absence or presence of either ShK or ShK-Dap²², was determined as described in the text. *K_i* values for inhibition were calculated as described under Experimental Procedures. Values represent the average ± SEM of three independent determinations, each one carried out in triplicate.

branes, with *K_i*'s of 0.041 and 0.25 pM, respectively, whereas it displays lower affinity, 5 pM, for K_v1.2. Substitution of diaminopropionic acid at Lys²², ShK-Dap²², decreases the potency of the peptide as an inhibitor of ¹²⁵I-HgTX₁A19Y/Y37F binding to all three channels. The shift in affinity caused by this substitution is 1438-, 4122-, and 792-fold for K_v1.1, K_v1.2, and K_v1.3, respectively. Thus, it appears that K_v1.3 is the least affected by mutating Lys²² in ShK, whereas the largest effects are observed with K_v1.2 channels.

Although electrophysiological experiments indicate that ShK-Dap²² is ca. 20-fold more potent as an inhibitor of K_v1.3 than K_v1.1 channels (Figure 2), these differences are not observed in ¹²⁵I-HgTX₁A19Y/Y37F equilibrium binding studies (Table 1). Although the ionic strength conditions of the binding assay, 100 mM NaCl and 5 mM KCl, can be considered similar to those of electrophysiological recordings, there are other differences between these assays that could contribute to the above results. For example, the occupancy by potassium of a binding site in the selectivity filter has been shown to cause destabilization of bound peptide in the outer vestibule (28, 31). Because of the low potassium concentration, 5 mM, used in the above binding studies, ¹²⁵I-HgTX₁A19Y/Y37F binding was carried out in the presence of 100 mM KCl, a condition that would be expected to lead to higher occupancy of ion binding sites in the selectivity filter. However, no difference in ShK-Dap²² potency was found for either K_v1.1 or K_v1.3 under these conditions (data not shown). In addition, K_v1.1 was transiently expressed in TsA-201 cells with the same DNA construct used to transcribe mRNA for oocyte expression. Again, the potency of ShK-Dap²² as an inhibitor of ¹²⁵I-HgTX₁A19Y/Y37F binding was identical to that determined from stably transfected HEK cells (data not shown and Figure 4). Thus, in equilibrium binding studies with ¹²⁵I-HgTX₁A19Y/Y37F, ShK-Dap²² does not display specificity between K_v1.1 and K_v1.3 channels, and its affinity for K_v1.1 is higher than that determined in electrophysiological measurements.

Binding of ¹²⁵I-HgTX₁A19Y/Y37F to Heteromultimeric Channels: Effect of ShK and ShK-Dap²². Native brain K_v1 channels are mostly formed as heteromultimers. These channels contain mainly K_v1.2 subunit(s), with K_v1.1 co-associated in about 75% of the complexes (3, 16, 18, 32, 33). The stoichiometry and relative orientation of the K_v1.x subunits in the tetramers are not known. ¹²⁵I-HgTX₁A19Y/Y37F binds to human brain membranes with high affinity and with a Hill coefficient of 1 (18). When binding of ¹²⁵I-HgTX₁A19Y/Y37F is monitored in the presence of increasing concentrations of either ShK or ShK-Dap²², a complex pattern of inhibition is observed (Figure 5A). Inhibition curves display Hill coefficients <<1 and most likely reflect

the presence of subtypes of ¹²⁵I-HgTX₁A19Y/Y37F receptors with different sensitivities to the peptides. The actual composition of the brain tetramers (i.e., the relative amounts of K_v1.1-sensitive to other insensitive subunits), and the spatial organization of the subunits (i.e., adjacent versus diagonal orientations), could be responsible for the observed complex inhibition patterns.

To study this in further detail, a K_v1.1-K_v1.2 dimer and a tetramer with all four subunits aligned in a single polypeptide, K_v1.1-K_v1.2-K_v1.1-K_v1.2, were transiently expressed in TsA-201 cells. ¹²⁵I-HgTX₁A19Y/Y37F binds with high affinity to membranes derived from these cells with *K_d*'s of 0.10 ± 0.0046 and 0.039 ± 0.0012 pM for the K_v1.1-K_v1.2 dimer and the K_v1.1-K_v1.2-K_v1.1-K_v1.2 construct, respectively (data not shown). ShK and ShK-Dap²² inhibit ¹²⁵I-HgTX₁A19Y/Y37F binding to the K_v1.1-K_v1.2 dimer (Figure 5B) and to the K_v1.1-K_v1.2-K_v1.1-K_v1.2 tetrameric channel (Figure 5C), but the inhibition patterns are markedly different. For both types of heteromultimers, ShK displaces ¹²⁵I-HgTX₁A19Y/Y37F binding with high potency, *K_i*'s of 0.081 ± 0.0037 (Figure 5B) and 0.028 ± 0.0003 pM (Figure 5C), respectively, and with Hill coefficients close to 1. In contrast, inhibition curves in the presence of ShK-Dap²² are not monophasic and can be better fit by two binding components (Table 2). In the case of channels resulting from K_v1.1-K_v1.2 dimers, the high-affinity component of ShK-Dap²² inhibition corresponds to ~29% of ¹²⁵I-HgTX₁A19Y/Y37F binding sites, whereas for the K_v1.1-K_v1.2-K_v1.1-K_v1.2 channel, this component is close to 50% of the ¹²⁵I-HgTX₁A19Y/Y37F receptors. It is interesting to note that the high-affinity site, *K_i* of 0.35 pM (Table 2), corresponds to a receptor with >100-fold higher affinity for ShK-Dap²² than the homomeric K_v1.1 channel, the more sensitive subunit of the K_v1.1-K_v1.2 complex. Thus, assembly of two K_v1 subunits with a 350-fold difference in ShK-Dap²² sensitivity creates a new receptor site with much higher sensitivity than either channel alone. Under our experimental conditions, this effect can be observed with ShK-Dap²² but not with ShK.

Functional Consequences of Blocking K_v1.3 Channels: Membrane Potential Measurements. An alternative functional assay for K_v1.3 channel activity is to measure changes in membrane potential with voltage-sensitive dyes (34, 35). This voltage-sensitive dye system measures the change in fluorescence energy transfer between a coumarin dye anchored to the outside of the cell and a charged dye that is mobile within the membrane phase. Fluorescence emission from both dyes is measured, and a subsequent change in this ratio is proportional to the change that occurs in the membrane potential of the cells. A CHO cell line stably expressing the human K_v1.3 channel (ca. 10⁵ channels/cell) was used for the membrane potential assay. In this cell line, K_v1.3 sets the membrane potential, and block of this channel causes membrane depolarization (36). After addition of a K_v1.3 channel inhibitor to these cells, the membrane slowly depolarizes as monitored with the voltage-sensitive dye pair (data not shown). Activity of K_v1.3 can also be assayed after preincubation with an inhibitor by measuring the depolarization caused by addition of a high potassium solution (Figure 6). The decrease in potassium-induced depolarization reflects the degree to which the membrane had been previously depolarized by the K_v1.3 inhibitor. Preincubation for 1 h with increasing concentrations of MgTX causes a

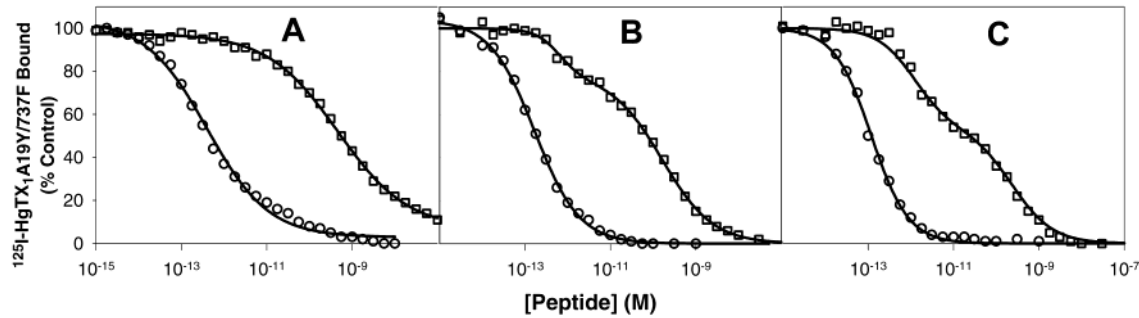


FIGURE 5: Binding of ^{125}I -HgTX $_1$ A19Y/Y37F to heteromultimeric Kv1.x channels: effect of ShK and ShK-Dap 22 . Membranes derived from human brain tissue (A) or TsA-201 cells transiently transfected with a Kv1.1-Kv1.2 dimer (B) or with a Kv1.1-Kv1.2-Kv1.1-Kv1.2 construct (C) were incubated with ~ 0.1 pM ^{125}I -HgTX $_1$ A19Y/Y37F, in the absence or presence of increasing concentrations of either ShK (○) or ShK-Dap 22 (□), for 20 h at room temperature. Specific binding data are presented relative to an untreated control. Data for ShK-Dap 22 in (B) and (C) were analyzed using a two binding site model as described under Experimental Procedures. Parameters derived from the curve fit are presented in Table 2.

Table 2^a

	ShK K_i (pM)	ShK-Dap 22		
		K_i (1) (pM)	no. of sites (1) (%)	K_i (2) (pM)
Kv1.1-Kv1.2 dimer	0.081 ± 0.003	0.35 ± 0.06	29 ± 1	85 ± 11.7
Kv1.1-Kv1.2- Kv1.1-Kv1.2	0.029 ± 0.0003	0.35 ± 0.06	48 ± 0.8	54 ± 5.7

^a ^{125}I -HgTX $_1$ A19Y/Y37F binding to Kv1.1-Kv1.2 dimer or Kv1.1-Kv1.2-Kv1.1-Kv1.2 channels, in the absence or presence of either ShK or ShK-Dap 22 , was determined as described in the text. K_i values for inhibition by ShK were calculated from the fit of the data to a one-site model. Binding parameters for inhibition by ShK-Dap 22 were calculated from the fit of the data to a two-site model as described under Experimental Procedures. Values represent the average \pm SEM of three independent determinations, each one carried out in triplicate.

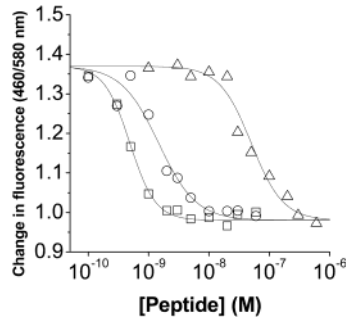


FIGURE 6: Membrane potential measurements in CHO cells stably transfected with Kv1.3. CHO cells stably expressing Kv1.3 were grown overnight in 96-well plates until confluent. The cells were stained with the CC2-DMPE dye for 30 min, washed, and incubated for 1 h with DiSBAC $_2$ (3) dye, in the absence or presence of the indicated concentrations of peptide. The amount of depolarization caused by inhibition of Kv1.3 was assessed by measuring the membrane potential change after addition of 90 mM KCl. The data were fit to IC_{50} values of 1.5, 0.51, and 50.4 nM for MgTX (○), ShK (□), and ShK-Dap 22 (Δ), respectively.

decrease in the potassium-induced depolarization with an IC_{50} of 3.8 ± 3.1 nM ($n = 2$). A similar potency, 0.56 ± 0.06 nM ($n = 2$), was determined for ShK (Figure 6). Under identical conditions, ShK-Dap 22 is 100-fold weaker as a channel inhibitor, with an IC_{50} of 71 ± 33 nM ($n = 2$). The apparent potency of all three peptides is ca. 1000-fold lower than that observed in equilibrium binding experiments (Table 1 and data not shown). One possible explanation is that

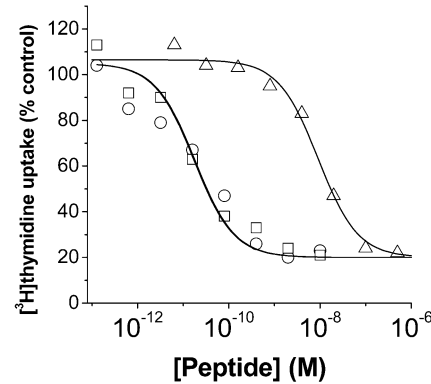


FIGURE 7: Inhibition of human T cell proliferation by ShK and ShK-Dap 22 . Purified human T cells were stimulated with anti-CD3 and mononuclear blood cells in the absence or presence of increasing concentrations of either MgTX (○), ShK (□), or ShK-Dap 22 (Δ). Inhibition of [^3H]thymidine uptake was assessed relative to an untreated control. (○) $\text{IC}_{50} = 0.018$ nM; (□) $\text{IC}_{50} = 0.017$ nM; (Δ) $\text{IC}_{50} = 9$ nM.

99.9% of the Kv1.3 channels need to be blocked before the cells depolarize, a consequence of the high channel density in this cell line. Since the mechanism for suppression of T-cell activation is presumably membrane depolarization due to Kv1.3 channel block, this assay indicates that ShK-Dap 22 is 100-fold less potent at depolarizing cells compared to ShK.

Inhibition of Human T Cell Proliferation in Vitro by ShK and ShK-Dap 22 . In human T cells, blockade of the Kv1.3 channel suppresses T cell activation. It is believed that Kv1.3 sets the resting potential of human T cells and that channel inhibition causes cell depolarization, leading to attenuation in the T cell receptor mediated elevation of intracellular calcium that is necessary for T cell proliferation (8, 13). When human T cells are stimulated with anti-CD3 and irradiated PBMC, there is a concentration-dependent inhibition of [^3H]thymidine uptake into human T cells by MgTX, ShK, and ShK-Dap 22 (Figure 7). Inhibition by all three peptides can be reversed by addition of conditioned medium from PHA-activated T cells, which contains a variety of cytokines. IC_{50} values for inhibition by MgTX, ShK, and ShK-Dap 22 are 0.018, 0.017, and 9 nM, respectively. Thus, under our experimental conditions, ShK-Dap 22 is about 500-fold weaker than ShK in inhibiting human T cell proliferation, a process that depends on the activity of the Kv1.3 channel.

DISCUSSION

The role that K_v1.3 channels play in the immune system has been the topic of many studies that have been prompted by the observation that K_v1.3 inhibitors attenuate the process of human T cell activation. On the basis of results from both *in vitro* and *in vivo* assays, K_v1.3 has been proposed to represent a therapeutic target for the prevention of graft rejection (13, 14). More recently, K_v1.3 channels have also been proposed to play a critical role in autoimmune diseases. Thus, activated, myelin-reactive T (T_{EM}) cells from patients with multiple sclerosis express significantly higher levels of K_v1.3 channels than naive or central memory T cells, and K_v1.3 inhibitors suppress proliferation of T_{EM} cells (10). To assess the therapeutic utility of modulating K_v1.3 channels in treatment of immune diseases, inhibitors with appropriate characteristics must be developed. In this context, ShK-Dap²² was characterized as a potent and selective K_v1.3 inhibitor. Although ShK blocks K_v1.1 and K_v1.3 channels with similar high affinity, substitution of diaminopropionic acid at the critical Lys²² residue was shown to have no effect on K_v1.3 inhibition but to significantly affect the peptide's potency on K_v1.1 channels (6). Thus, ShK-Dap²² might have potential for being developed as a therapeutic agent. However, the results of the present study reveal a different profile for ShK-Dap²² that suggests that its therapeutic utility may be compromised *in vivo* by the unexpected pharmacological properties of the peptide. In addition, a large body of evidence indicates that the potency of ShK-Dap²² is significantly reduced when compared to ShK.

Initially both ShK and ShK-Dap²² peptides were extensively characterized by analytical techniques, and the peptide content of the solutions was normalized by a number of techniques including amino acid sequencing, amino acid hydrolysis, and UV absorption. There are clear differences in the potency of these peptides against K_v1.1 and K_v1.3 channels, with ShK-Dap²² displaying significantly lower affinity under all experimental conditions. In electrophysiological recordings of either human T cells or oocytes injected with human K_v1.3 mRNA, ShK-Dap²² inhibits the K_v1.3 channel with a *K_i* value of ~100 pM (Figures 1 and 2). Previously published values for inhibition of mouse or human K_v1.3 by ShK-Dap²² range between 3.3 and 52 pM, with most values centered about 40 pM (6, 11, 37–40). Thus, the differences between our values and those of others could easily represent differences in the quantification of the mass of the peptides. It is also important to note that the *K_i* values of ShK-Dap²² for inhibition of K_v1.1 channels are not different between this (human) and previous (mouse) studies. The major discrepancy concerns the potency of the parent ShK peptide. In this study, we illustrate that ShK is a very potent, subpicomolar inhibitor of both K_v1.1 and K_v1.3 channels. Since development of steady-state block at low ShK concentrations requires incubation for long periods of time, we cannot exclude that the actual potency of ShK for these channels is even higher than reported in this study. We do not know for certain why the values in this study are different than those previously published (6, 11, 37, 38, 40, 41), but we suspect these differences could be related to the time allowed for ShK to reach maximal block. Thus, the features of ShK and ShK-Dap²² characterized in the present study are significantly different from those previously

reported and strongly indicate that the potency of ShK is significantly altered after substituting diaminopropionic acid at Lys²². It is interesting to note that the equivalent substitution in a related peptide, BgK, also leads to a marked loss in its potency against K_v1.1, K_v1.2, and K_v1.3 channels (7). There is, however, agreement in that ShK-Dap²² displays selectivity between human K_v1.1 and K_v1.3 channels in electrophysiological recordings, although the difference is only ~20-fold. In other assays (see below), the peptide does not appear to preferentially interact with human K_v1.1 or K_v1.3 channels.

Differences between ShK and ShK-Dap²² can also be observed in other types of assays that monitor the activity of K_v1.3 channels. ⁸⁶Rb⁺ flux assays monitoring K_v1.3 channels stably expressed in mammalian cells have been established and used to identify small molecule inhibitors of the channel (16, 19). In this assay, both ShK and ShK-Dap²² also display significant differences in their inhibitory activity. It is worth mentioning that the potencies of ShK and MgTX are most likely underestimated and limited by the actual concentration of K_v1.3 channels in the assay. To minimize this problem, the K_v1.3 concentration was decreased to a minimum that was technically acceptable for making accurate determinations. Even under these conditions, the potencies of ShK and MgTX may still reflect the concentration of K_v1.3 channels, and the peptides could be intrinsically more potent than what the assay indicates.

Members of the K_v1 channel family, such as K_v1.1, K_v1.2, and K_v1.3, are blocked by HgTX₁, and ¹²⁵I-HgTX₁A19Y/Y37F binds with very high affinity (i.e., *K_i*'s <1 pM) to these channels (18). In ¹²⁵I-HgTX₁A19Y/Y37F binding assays, ShK and ShK-Dap²² also display very large differences of ca. 1000-fold in potency as inhibitors of peptide binding. The potency of ShK for both K_v1.1 and K_v1.3 is <<1 pM, and in agreement with previous observations (6), the peptide is a weaker inhibitor of K_v1.2 channels. The present binding results do not agree with previously published data in which the potencies of ShK and ShK-Dap²² as inhibitors of ¹²⁵I-ChTX binding to K_v1.3 channels were evaluated and reported to be similar. It is most likely that the potency of ShK was underestimated in those studies because the receptor concentration that the authors used in the binding assay, 45 pM, is limiting (6). In the present binding assays, in which the incubation volume is 12 mL, the channel concentration is about 50 fM. This channel concentration could still limit the apparent observed potency, and ShK could have a higher intrinsic affinity for the K_v1.1 channel than that reported in this study. However, the data strongly indicate that the potency of ShK-Dap²² is much lower than that of the parent peptide in these experimental protocols. There are some differences in the specificity of ShK-Dap²² between electrophysiological and equilibrium binding experiments. In electrophysiology, the peptide is ~20-fold more potent in blocking K_v1.3 channels whereas such differences are not seen in the binding assays. These data suggest that the intrinsic affinity of ShK-Dap²² for both channels is indeed the same but that, during ion conduction, either voltage-dependent conformational changes or differences in ion occupancy in the channel (42, 43) affect the interaction of the peptide in the channel's outer vestibule.

The ability of K_v1.3 blockers to attenuate the Ca²⁺-dependent process of human T cell activation in *in vitro*

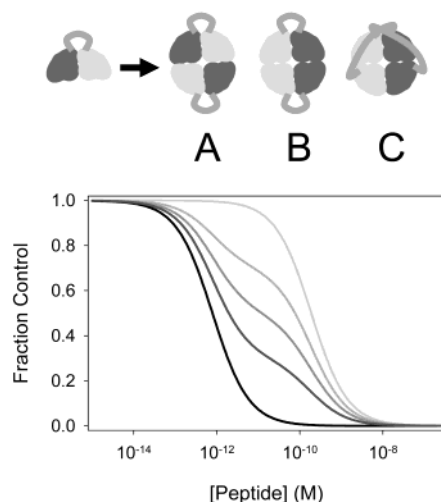


FIGURE 8: Heteromultimeric channels resulting from expression of a K_v1.1-K_v1.2 dimer. The predicted tetrameric subunit orientations A, B, and C after expression of a K_v1.1-K_v1.2 dimer construct are illustrated. The theoretical binding inhibition curves for a ligand that displays the same fold difference in affinity as ShK-Dap²² for a K_v1.1-K_v1.2 dimer (Table 2) are illustrated. From left to right: (1) high-affinity configuration; (2–4) increasing fraction (0.3, 0.5, and 0.7) of low-affinity configuration; (5) low-affinity configuration. Experimental data from Figure 5B approximate the inhibition curve with a 0.7 ratio of low-affinity configuration.

assays has been used as an indication of the therapeutic utility of these agents. In these assays, ShK and ShK-Dap²² also display markedly different potencies, although the concentrations that are needed to inhibit this process are higher than those predicted from electrophysiological experiments. The data are, however, consistent with the idea that a majority of channels must be blocked for cell depolarization to occur, which is necessary to prevent the rise in intracellular calcium that drives T cell activation (8, 13). The membrane potential measurement assays, which use cells with a much larger density of K_v1.3 channels than present in T cells, confirm this idea and provide further evidence for the difference in potencies between the two ShK peptides.

The therapeutic window of any drug candidate is determined by the separation between its efficacy and adverse side effects. The concentrations of ShK-Dap²² that are needed to prevent T cell activation also appear to affect other targets that would compromise the efficacy of the peptide as an immunosuppressant. For instance, the peptide displays an unexpected high affinity for some K_v1.1/K_v1.2 channel combinations that could be present in brain and peripheral tissues (3, 16, 18, 32, 33, 44), and preliminary data indicate that the neurotoxicity of ShK-Dap²² after ic injection in rats is only 2–3-fold lower than that of ShK (data not shown). This unexpected pharmacological behavior of ShK-Dap²² has been observed in channels formed after expression of either a K_v1.1-K_v1.2 dimer or a K_v1.1-K_v1.2-K_v1.1-K_v1.2 tetrameric construct. It is intriguing that the combination of K_v1.1-sensitive and K_v1.2-insensitive channels leads to channels that are more sensitive (~200-fold) to ShK-Dap²² than either K_v1.1 or K_v1.2. As previously observed for expression of cyclic nucleotide-gated dimer channel constructs (45), three possible dimer–dimer configurations can lead to the formation of tetrameric channels (Figure 8). First, dimers can associate with the K_v1.1 subunit of one dimer contacting the K_v1.2 subunit of the other (tetramer A). Second, K_v1.1 and

K_v1.2 subunits of each dimer can contact each other (tetramer B). Finally, the dimers could interlock to form channels, and the K_v1.1 and K_v1.2 subunits of each dimer, therefore, sit at opposite corners of the channel (tetramer C). The spatial orientation of the subunits in tetramers B and C is similar, and therefore two-thirds of the channels could have an identical pharmacological behavior. The present experimental data are consistent with the presence of one-third of high-affinity ShK-Dap²² receptors and two-thirds of receptors that display identical affinity to K_v1.1 channels. Thus, the structural arrangement of the K_v1.1 with the insensitive K_v1.2 subunit in tetramer A provides additional binding energy for the peptide and reveals an unexpected pharmacological profile. Preferential interaction of ShK-Dap²² with two adjacent subunits in K_v1.3 has been proposed from double-cycle mutant studies (37). However, our data appear to be more consistent with the peptide interacting with, at least, three of the channel subunits. Under the equilibrium binding conditions of our experiments, the two different ShK-Dap²² binding affinities could not be due to two different orientations of the peptide in a homogeneous population of receptors because the high-affinity site will always prevail. Lower affinity orientations similar to those of homomultimeric K_v1.2 channels may exist but would not be revealed in these experiments. The results with the tetrameric construct are consistent with the idea that, in ~50% of the channels, identical subunits are in a diagonally opposed orientation but they are adjacent to each other in the remaining 50% of the tetramers. It is interesting to note that ShK does not distinguish between the different K_v1.1-K_v1.2 channel combinations, as suggested by the monophasic inhibition curves that are observed with this peptide. However, we must emphasize that the experimental binding conditions do not allow the identification of inhibitors with *K_i* values <0.04 pM and that it is technically impossible to make those determinations with the experimental tools that are currently available.

Human brain membranes represent a system where heteromultimeric channels of many different compositions exist (16). As suggested by the inhibition patterns of ¹²⁵I-HgTX₁-A19Y/Y37F with ShK and ShK-Dap²², the complexity of these tetramers is large. However, the data also illustrate two additional features. One is the difference in potencies between ShK and ShK-Dap²² that has been observed consistently throughout this study. The other is that both peptides will be affecting native channels at much lower concentrations than those needed to inhibit T cell activation. Thus, these peptides do not appear to have the properties needed for therapeutic development. The search for K_v1.3 inhibitors with a good therapeutic window will be critical for their consideration as drug development candidates. Although some progress has been achieved in this area (16, 19), more work is needed to optimize these molecules in order to achieve that goal.

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