

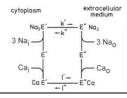
Fig. 5. Potassium ions in the selectivity filter as seen in the same simulation discussed in Fig. 4. Four snapshots from the simulation are superimposed, showing the filter regions of three of the four subunits, and the  $K^+$  ions (green spheres) that occupy (at different times) sites S0 to S4.

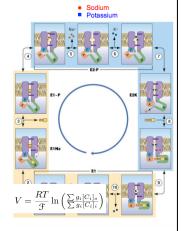
The structure of the KcsA channel is believed to be representative of all potassium channels because chimeras of full voltage-gated potassium channels S1-S4 segments with KcsA S5-P-S6 segments work Available from outside the cell normally (including gating). outside Water-filled pore, hydrophobic residue inside when the gate is closed Binding sites available from inside the cell, gate attract K+ to the om inside the cell, gate open only closed or open

The sequence of steps in the Na-K ATPase is complex, involving separate transport of Na out, K in, and ATP cleavage.

Note the gates (black) that occlude the Na and K during the transport

Motivated by this model Läuger and others have analyzed a slightly simpler transporter, the Na-Ca cotransporter with a similar scheme.





## 2. Ion Flux

$$\begin{split} J &= -uC \left[RT \frac{d \ln C}{dx} + z \mathcal{F} \frac{dV}{dx} \right] \\ I &= -z \mathcal{F} uC \left[RT \frac{d \ln C}{dx} + z \mathcal{F} \frac{dV}{dx} \right] \\ I_i &= \frac{\left(z \mathcal{F}\right)^2 u_i}{d} \Delta V \frac{C_i(d) e^{\frac{ia \mathcal{F} \Delta V}{4R}} - C_i(0)}{e^{\frac{ia \mathcal{F} \Delta V}{2R}} - 1} \\ \Delta V_{rest} &= \frac{RT}{\mathcal{F}} \ln \left( \frac{u_K K_o + u_{Na} Na_o + u_{Cl} Cl_o}{u_K K_i + u_{Na} Na_i + u_{Cl} Cl_o} \right) \end{split}$$
Nernst-Planck Equation **GHK** Equation  $k_i = (const)e^{\frac{-(G+\lambda_z \mathcal{F} \Delta V)}{RT}}$ Rate Constants  $J_{AB} = k_i A, J_{BA} = k_{-i} B,$ Flux Across Barrier  $J = J_{AB} - J_{BA}$  $J = (const)e^{\frac{-(G + \lambda z \mathcal{F} \Delta V)}{RT}} \left(A - Be^{\frac{z \mathcal{F} \Delta V}{RT}}\right)$ 

 $\frac{RT}{} = 26mV$ 

## 1. Equilibrium

 $\mu_i = \mu_i^o + RT \ln C_i + z_i \mathcal{F} V$ Free energy (equal at equil  $\Delta G = 0$  or  $\mu_s^1 = \mu_s^2$ Equilibrium is defined as  $E = \frac{RT}{z\mathcal{F}} \ln \frac{C_1}{C_2}$ Nernst Equation

## 2. Ion Flux

Nernst-Planck Equation  $J = -uC \left[RT \frac{d \ln}{dx} + z \mathcal{F} \frac{dV}{dx}\right]$  $I = -z \mathcal{F}uC \left[RT \frac{d \ln}{dx} + z \mathcal{F} \frac{dV}{dx}\right]$  $I_{i} = \frac{\left(z\mathcal{F}\right)^{2} u_{i}}{d} \Delta V \frac{C_{i}(d) e^{\frac{ze^{2}\Delta V}{RT}} - C_{i}(0)}{e^{\frac{ze^{2}\Delta V}{RT}} - 1}$ **GHK** Equation  $\Delta V_{rest} = \frac{RT}{\mathcal{F}} \ln \left( \frac{u_K K_o + u_{Na} N a_o + u_{Cl} C l_i}{u_K K_i + u_{Na} N a_i + u_{Cl} C l_o} \right)$  $k_i = (const)e^{\frac{-(G + \lambda_z \mathcal{F} \Delta V)}{RT}}$ Rate Constants Flux Across Barrier  $J_{AB} = k_i A, J_{BA} = k_{-i} B,$  $J = (const)e^{\frac{-(G+\lambda z^{\mathcal{H}\Delta V})}{RT}} \left(A - Be^{\frac{z^{\mathcal{H}\Delta V}}{RT}}\right)$  $\frac{RT}{\mathcal{F}} = 26mV$ 

The varieties of potassium channels (some of them):

- 1. Voltage gated  $K_V$  like the delayed rectifier of the HH model. Some of these also have inactivation gates. These repolarize action potentials and limit the spiking rate during excitation.

  2. Calcium dependent - K(Ca) There are two varieties of these:
- BK gated by both V and Ca. Important for repolarization and for activity-dependent sensing.

SK - gated by Ca only. Produce afterhyperpolarization (AHP) and help govern stability after bouts of activity (e.g. between bursts).

- 3. H channels non-specific channels that are related to K channels.
- These have only an inactivation gate.

  4. Inward rectifier Non-V-gated channels whose conductance is often controlled by intracellular second messengers.
- 5. Tandem pore domain contribute to the resting potential.

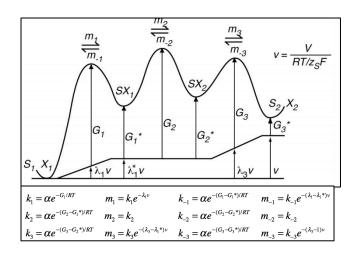
Varieties of calcium channels:

L-type - high threshold (>-30 mV), slow V inactivation, Ca++ inactivation.

P/Q, N, R - high threshold (>-20 mV), weak V inactivation, Ca++ inactivation.

T-type - low threshold (>-70 mV), strong V inactivation, no Ca++

These types were originally identified on voltage-clamp criteria, but have subsequently been associated with specific genes, with multiple genes for each type. They differ in pharmacology and in their localization.



$$\begin{aligned} \text{State Vector} & \dot{\vec{X}} = \begin{bmatrix} \dot{V} \\ \dot{\omega} \end{bmatrix} = \begin{bmatrix} F_1(\vec{x}) \\ F_2(\vec{x}) \end{bmatrix} = \vec{F}(\vec{X}) \\ \text{Nullclines for MLE case} & \dot{V} = 0 \rightarrow \omega = \frac{I_{ext} - \vec{G_{Ca}} m_{\infty} (V - E_{Ca}) - \vec{G_{L}} (V - E_{L})}{\vec{G_{K}} (V - E_{K})} \\ & \dot{\vec{G_{K}}} (V - E_{K}) \\ & \dot{\omega} = 0 \rightarrow \omega = \omega_{\infty}(V) \\ \end{bmatrix}_{q_{\ell}, p_{\ell}} & \vec{x}(t) = \sum_{i=1}^{N} a_{i} \vec{e_{i}} e^{\lambda_{i} t} \end{aligned}$$