Almost a decade ago, a standardized nomenclature for the six-transmembrane domain (TM), voltage-gated K⁺ channel genes—the Kᵥ naming system—was widely adopted (Chandy et al., 1991; Gutman and Chandy, 1993). This nomenclature was based on deduced phylogenetic relationships; channels that shared 65% sequence identity being assigned to one subfamily. A parallel nomenclature—KCN—was developed by the Human Genome Organisation (HUGO) (White et al., 1997). Since then, the K⁺ channel superfamily of genes has greatly expanded, requiring an update of the naming system.

Structural Characteristics

Several structural classes of the potassium channels are now known, as illustrated by the transmembrane folding diagrams for this section of the Compendium, and most of these classes have multiple members.
The 6TM proteins include the $K_V$ channels, and the related small-conductance and intermediate-conductance $Ca^{2+}$-activated $K^+$ channels ($K_Ca$). Both the N and C termini of these proteins are located intracellularly, and the region between the fifth and sixth transmembrane domains (the P region) forms the ion conduction pathway. The functional channel is formed by the tetrameric association of these 6TM/1P subunits.

The second class of 2TM proteins includes the inward rectifiers, the $K_{ATP}$ channels and the G protein-coupled channels (Doupnik et al., 1995). The N and C termini of these channels are also located cytoplasmically, the P region between the two transmembrane domains forms the pore, and the functional channel is a tetramer of these 2TM/1P subunits.

A third class has 7TM and encodes the large-conductance channel, Slo. There is a P region between TMVI and TMVII, and the channel functions as a tetramer, but unlike the other channels, Slo has its N terminus located extracellularly.

A fourth class of proteins has a 6TM/1P segment linked in tandem to a 2TM/1P segment, and the functional channel in this case is formed from the dimeric association of the 8TM/2P subunits.

Yet another class of channels, the $K_{2P}$ family, contains a P region between the fifth and sixth transmembrane domains, and the functional channel is a tetramer of these 2TM/1P subunits.

Human Gene Nomenclature Committee System

The $KCN$ system established by the Human Gene Nomenclature Committee (HGNC) of HUGO (Table 1) suffers from a lack of any rational basis for nomenclature and, in particular, ignores the structural and phylogenetic relationships of these proteins. For example, the $KCN$ subfamilies of $K_v$–$K_v$6 have not been assigned HGNC names. Similarly, the small-conductance (SKCa1–SKCa3) and intermediate-conductance (IKCa1) $Ca^{2+}$-activated $K^+$ channels are grouped together in the $KCN$ subfamily even though they share only ~45% amino acid sequence identity and therefore are best considered as belonging to distinct subfamilies.

The Standardized $K^+$ Channel Nomenclature System

The original $K_V$ nomenclature that created subfamilies $K_V$1–$K_V$6 has not been updated for several years. As new genes were discovered the name $K_V$7 was skipped, and these new genes were instead assigned to subfamilies $K_V$8 and $K_V$9. Also, the more recently discovered $KCNH$ (Eag, Erg, Elk) and $KCNQ$ ($K_V$-LQT) subfamilies have not been included in the $K_V$ classification. A standardized nomenclature has been adopted in the case of the 2TM/1P channels, and subfamilies defined in this $K_{ir}$ family determined by the degree of sequence relatedness.

Formulation of a Rational Classification

With the completion of the mapping of the human genome, the time may be ripe for a re-evaluation of these issues, and the development of a uniform and rational nomenclature for all $K^+$-selective channels. Such a naming system could incorporate the architectural similarities between different channel families, as well as their phylogenetic relationships. For example, the numerous 6TM/1P proteins and the sole 7TM/1P channel listed in Table 1 could be grouped into a single large family comprising multiple subfamilies defined according to their phylogenetic relatedness. Similarly, the 2TM/1P channels and the 2P channels could each be clustered into a separate family containing multiple subfamilies.

The standardized nomenclature for potassium channels presented in this compendium is shown in the phylogenetic trees of Figs. 1 through 4. The 6TM/1P channels have been organized into two distinct groups based on their structural relatedness and predominant functional characteristics, namely the voltage-gated ($K_V$) and calcium-activated ($K_{Ca}$) channels. The two-pore ($K_{2P}$) and inward rectifier ($K_{ir}$) channels likewise form two additional groups. Figure 1a shows the voltage-gated $K^+$ channels of families $K_V$1–$K_V$6 and $K_V$8–$K_V$9.

<table>
<thead>
<tr>
<th>Name</th>
<th>Protein</th>
</tr>
</thead>
<tbody>
<tr>
<td>KCNA1–KCNA7</td>
<td>6TM1P $K_v$ channel (Shaker-related)</td>
</tr>
<tr>
<td>KCNB1, KCNB2</td>
<td>6TM1P $K_v$ channel (Shah-related)</td>
</tr>
<tr>
<td>KCNC1–KCNC4</td>
<td>6TM1P $K_v$ channel (Shaw-related)</td>
</tr>
<tr>
<td>KCND1–KCND3</td>
<td>6TM1P $K_v$ channel (Shal-related)</td>
</tr>
<tr>
<td>KCNE1–KCNE3</td>
<td>1TM/5K accessory subunit</td>
</tr>
<tr>
<td>KCNFI</td>
<td>6TM1P $K_v$ channel (modulatory)</td>
</tr>
<tr>
<td>KCNG1–KCNG2</td>
<td>6TM1P $K_v$ channel (modulatory)</td>
</tr>
<tr>
<td>KCNH1–KCNH5</td>
<td>6TM1P $K_v$ channel (EAG, ERG, ELK)</td>
</tr>
<tr>
<td>KCNII</td>
<td>2TM1P $K_v$ channel</td>
</tr>
<tr>
<td>KCNJ1–KCNJ15</td>
<td>4TM2P (TWIK, TASK, TREK)</td>
</tr>
<tr>
<td>KCN1L</td>
<td>7TM1P maxi-$K_{Ca}$ channel</td>
</tr>
<tr>
<td>KCNB1</td>
<td>$\beta$ subunit of maxi-$K_{Ca}$ channel</td>
</tr>
<tr>
<td>KCNN1–KCNN4</td>
<td>6TM1P $SK_{Ca}$ and $IK_{Ca}$ channel</td>
</tr>
<tr>
<td>KCNO</td>
<td></td>
</tr>
<tr>
<td>KCNP</td>
<td></td>
</tr>
<tr>
<td>KCNQ1–KCNQ4</td>
<td>6TM1P $K_v$ channel</td>
</tr>
<tr>
<td>KCNR</td>
<td></td>
</tr>
<tr>
<td>KCNS1–KCNS3</td>
<td>6TM1P $K_v$ channel (modulatory)</td>
</tr>
</tbody>
</table>
in a phylogenetic reconstruction using maximum parsimony based on an amino acid sequence alignment. Among this group, only KV1.8 currently lacks an HGNC name. The five members of a second KV group, the KV7 family (KCNQ1–KCNQ5), cannot readily be aligned with other KV channel proteins and are therefore shown in a separate tree in Fig. 1b. The three remaining KV families, KV10, KV11 and KV12, are closely enough related to each other to be shown in the single tree of Fig. 1c.

The five families comprising the calcium-sensitive potassium channels, KCa1–KCa5, numbered according...
to the order of their discovery, are shown in the two
trees of Fig. 2. The phylogenetic relationship between
the KCa1, KCa4, KCa5 group on the one hand, and the
KCa2, KCa3 group on the other, is insufficiently clear
at this time to readily connect them into a single tree.
The two-pore or K2P potassium channels are shown
in the tree of Fig. 3. The numbers have been taken
from the HGNC “KCNK” numbering, without resequencing around the missing numbers (namely 8, 11,
and 14), and without consolidating clearly related
channels into subfamilies. A consensus among re-
searchers in the field will hopefully establish a more
rational nomenclature in the future.
The last remaining group of potassium channels, the
inward rectifier or Kir channels, is represented in the
tree of Fig. 4, using the previously established nomen-
clature and subfamily groupings.

References
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Fig. 2. Two phylogenetic trees showing the KCa1–KCa5 families. See
Fig. 1 for details of analysis.

Fig. 3. Phylogenetic tree showing the K2P families. See Fig. 1 for
details of analysis.

Fig. 4. Phylogenetic tree showing the Kir families. See Fig. 1 for
details of analysis.