

# Structural basis for $K_v7.1$ – $KCNE_x$ interactions in the $I_{Ks}$ channel complex

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The cardiac  $I_{Ks}$  current is involved in action potential repolarization, where its primary function is to limit action potential prolongation during sympathetic stimulation. The  $I_{Ks}$  channel is mainly composed of  $K_v7.1$  ion channels associated with  $KCNE1$  auxiliary subunits. The availability of  $KCNE1$  solution structure by nuclear magnetic resonance spectroscopy in conjunction with biochemical assays addressing  $K_v7.1$ – $KCNE1$  residue interactions has provided new insights into the structural basis for  $K_v7.1$  modulation by  $KCNE1$ . Recent evidence further suggests that  $KCNE2$  may associate with the  $K_v7.1$ – $KCNE1$  channel complex and modulate its current amplitude. Here we review recent studies in this area and

discuss potential roles for multiple  $KCNE_x$  subunits in  $I_{Ks}$  generation and modulation as well as the clinical relevance of the new information.

**KEYWORDS**  $I_{Ks}$ ;  $KCNE1$ ;  $KCNE2$ ;  $KCNQ1$ ;  $K_v7.1$

**ABBREVIATIONS**  $I_{Kr}$  = cardiac rapid delayed rectifier current;  $I_{Ks}$  = cardiac slow delayed rectifier current;  $K_v$  = voltage-gated potassium channel; **NMR** = nuclear magnetic resonance; **PIP<sub>2</sub>** = phosphatidylinositol 4,5-bisphosphate

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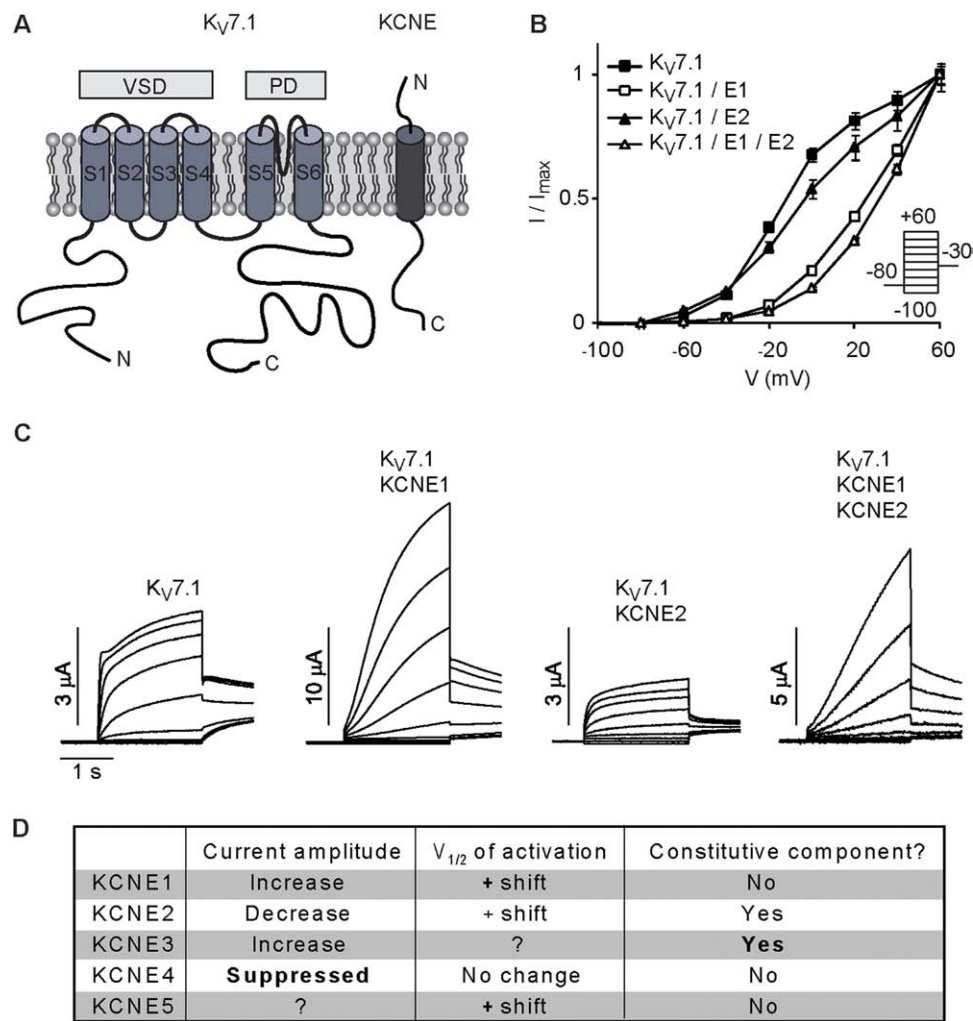
## Introduction

In human heart, the cardiac delayed rectifier current comprising  $I_{Ks}$  (cardiac slow delayed rectifier current) and  $I_{Kr}$  (cardiac rapid delayed rectifier current) is an important determinant of action potential duration. With its slow rate of activation,  $I_{Ks}$  primarily contributes to action potential repolarization during  $\beta$ -adrenergic stimulation, when its current amplitude is increased and rate of activation accelerated via the protein kinase A pathway. A number of studies have identified different signaling molecules, such as calmodulin and phosphatidylinositol 4,5-bisphosphate ( $PIP_2$ ), which contribute to regulation of  $I_{Ks}$  and  $I_{Kr}$  in the heart (for an excellent review on these topics, see Charpentier et al<sup>1</sup>). The  $\alpha$ -subunit that mediates  $I_{Ks}$  is  $K_v7.1$  (also known as  $KCNQ1$  or  $KvLQT1$ ; see “The  $I_{Ks}$  Babylon” in the Online Supplemental Data).  $K_v7.1$  channels are tetramers, with each subunit containing six transmembrane segments forming peripheral voltage-sensing domains (S1–S4) and a central pore domain (S5–S6) (Figure 1A). The significance of  $K_v7.1$  in normal heart function is highlighted

by more than 240 identified *KCNQ1* mutations associated with arrhythmias such as long QT syndrome, short QT syndrome, and atrial fibrillation (<http://www.fsm.it/cardmoc/>). In the majority of cases,  $K_v7.1$  mutations associated with loss of function of the  $I_{Ks}$  current appear to result in long QT syndrome, whereas gain-of-function mutations lead to short QT syndrome or atrial fibrillation. However,  $K_v7.1$  mutations simultaneously linked to long QT syndrome and atrial fibrillation have been reported.<sup>2</sup> As  $K_v7.1$  properties are differentially modulated by the  $KCNE$  accessory subunits (Figure 1), this complexity may be at least partially due to a heterogeneous pattern of  $K_v7.1$  association with different  $KCNE$  subunits in the heart.

Compelling evidence has established that  $KCNE1$  is the major accessory subunit of the  $I_{Ks}$  channel.  $KCNE1$  increases  $K_v7.1$  channel conductance, shifts its activation to a more positive voltage range, and, importantly, confers the unique slow activation rate of  $I_{Ks}$ . Computational work suggests that  $KCNE1$  resides in a cleft between voltage-sensing domains in the  $K_v7.1$  channel structure. In support of this model, three  $K_v7.1$  mutations associated with cardiac arrhythmia that reveal their phenotype only upon co-expression with  $KCNE1$  all localize to a voltage-sensing domain–pore domain interface that is part of the open-state cleft where  $KCNE1$  resides.<sup>3</sup> Since 1999, other members of the  $KCNE$  family have been cloned and characterized<sup>4</sup> (note that  $KCNE1$  is equivalent to minK, and  $KCNE2$ – $KCNE5$

This work was supported by the Danish National Research Foundation to Drs. Lundby and Schmitt and by the National Heart, Lung, and Blood Institute of the National Institutes of Health Grant RO1-HL67840 to Dr. Tseng. **Address reprint requests and correspondence:** Dr. Alicia Lundby, NNF Center for Protein Research, Blegdamsvej 3B 6.2.42, DK-2200 Copenhagen N, Denmark. E-mail address: [alicia.lundby@cpr.ku.dk](mailto:alicia.lundby@cpr.ku.dk). (Received September 28, 2009; accepted December 16, 2009.)



**Figure 1**  $K_V7.1$ -KCNE1-KCNE2 current characteristics. **A**: Topology of  $K_V7.1$  and KCNE subunits.  $K_V7.1$  subunits encompass six transmembrane segments with intracellular N- and C- termini, where S1–S4 encode the voltage-sensing domain (VSD) and S5–S6 encode the pore domain (PD). The KCNE proteins contain a single transmembrane segment flanked by an extracellular N-terminus and a cytosolic C-terminus. **B**: Normalized amplitudes of currents elicited from *Xenopus* oocytes upon stimulation with the indicated voltage clamp protocol 48 hours after injection of  $K_V7.1$  and KCNE1–KCNE2 cRNA as a function of clamp potential reveals that KCNE1 shifts the voltage-dependence of  $K_V7.1$  activation in the depolarizing direction to a much greater extent than does KCNE2. **C**: Representative current traces from the experiments analyzed in **B** illustrate the diverse effects of KCNE proteins on  $K_V7.1$  channel properties. Homomeric  $K_V7.1$  channels activate relatively rapidly, exhibit sustained currents at maintained depolarization, and slowly deactivate upon repolarization. Co-expression with KCNE1 greatly increases  $K_V7.1$  current amplitude and slows activation, in addition to its effect on channel voltage-dependency. Co-expression with KCNE2 reduces current amplitudes and induces a constitutively active current component. Activation of the time-dependent current component is slower than activation in the absence of KCNE2.<sup>28</sup> Co-expression with KCNE1 and KCNE2 generate currents with a mixture of the features, where KCNE1 dictates kinetics, whereas both KCNE1 and KCNE2 contribute to determination of current amplitude.<sup>2,29</sup> **D**: Effects exerted by KCNE subunits on  $K_V7.1$  currents. Strong effects are highlighted in bold.

corresponds to minK-related peptides or MiRP1-4 in previous nomenclature; see “The  $I_{Ks}$  Babylon” in the Online Supplemental Data). All KCNE genes are reportedly transcribed into mRNA in the human heart,<sup>5</sup> and expression of KCNE1–KCNE4 proteins has been detected. Emerging evidence suggests a role for KCNE2 in regulating  $I_{Ks}$  as well. KCNE2 reduces the  $K_V7.1$  current amplitude and confers a constitutively active current component (Figures 1B–1D).<sup>6</sup> If  $I_{Ks}$  in some cardiac myocytes is mediated by a  $K_V7.1$  channel complex encompassing KCNE2, it would have major functional consequences. Understanding the structural requirements for KCNE modulation of  $K_V7.1$  is important for delineating the role of KCNE subunits in  $I_{Ks}$  generation

and regulation. Here we review current knowledge of the structural basis for  $K_V7.1$ -KCNE1 interactions (with focus on the membrane-spanning regions), describe evidence for the presence of additional KCNE proteins in the channel complex (with focus on KCNE2), and discuss the clinical relevance of these recent findings.

**$K_V7.1$ -KCNE1 channel stoichiometry**

To resolve the structural basis for  $K_V7.1$ -KCNE<sub>x</sub> interactions, it is essential to know the stoichiometry of the channel complex. The number of KCNE subunits in the  $I_{Ks}$  complex has been a matter of debate. Recently, an elegant approach was used: iterative rounds of channel blocking/modification

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