

Published in final edited form as:

Channels (Austin). 2009 ; 3(5): 308–310.

Transcriptional and electrophysiological consequences of KChIP2-mediated regulation of Ca_v1.2

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Keywords

L-type calcium current; mRNA; arrhythmia; knockout mouse; action potentials; potassium channel interacting protein

Potassium channel interacting proteins (KChIP) are Ca²⁺-binding proteins that originally were identified as auxiliary subunits for K_v4 channels. K_v4 channels encode the voltage gated A-current (*I_A*) in neuronal tissue and the fast, transient outward current (*I_{to,f}*) in cardiac tissue. Recently, we have reported that KChIP2 functionally modulates the cardiac Ca_v1.2-governed L-type Ca²⁺ current (*I_{Ca,L}*) through a direct interaction between KChIP2 and the amino-terminus of Ca_v1.2. Here, we show that KChIP2 and Ca_v1.2 co-immunoprecipitate enhancing the biochemical support for our previous finding. Using gene-chip and real-time PCR techniques, we find that KChIP2^{-/-} mice have an increased transcriptional activity of the calcium channel β₂ subunit, CACNB2, whereas the expression of Ca_v1.2 is preserved. Although *I_{to,f}* is absent and *I_{Ca,L}* is decreased in myocytes from KChIP2^{-/-} mice, the action potential morphology is not altered. Furthermore, we show that the ventricular effective refractory period (VERP) is comparable in wild-type (53 ± 5 ms) and KChIP2^{-/-} mice (48 ± 3 ms; *p* > 0.05). In summary, our findings document a novel function of KChIP2 and expand our insights into the in vivo modulation of cardiac ion currents.

The K⁺ channel interacting proteins (KChIPs) are small (216–270 amino acids) cytosolic, calcium-binding proteins that were initially identified as subunits for the voltage-gated A-type K⁺ current in neuronal tissue and the transient outward K⁺ current in cardiac tissue.¹ The pore-forming protein complex governing these K⁺ currents is K_v4. KChIPs, dipeptidyl aminopeptidase-like proteins² (DPP), K_vβ1,³ and potentially several other protein structures assemble in macromolecular structures with K_v4 to generate and regulate the native current.³

Four *KCHIP* genes have been identified in humans and mice.^{1,4,5} The proteins are characterized by a conserved Ca²⁺-binding region, which places the KChIPs in the family of small Ca²⁺-binding proteins, including Ca²⁺-binding protein 1,^{6,7} calmodulin^{8,9} and neuronal

Ca²⁺ sensor 1.¹⁰ The conserved Ca²⁺ binding domain of the KChIPs contains 4 EF hands, of which only the last 3 bind Ca²⁺.¹ A highly variable amino-terminal sequence preceding the Ca²⁺ binding domain distinguishes the KChIPs from other Ca²⁺-binding proteins and confers variability among the KChIPs themselves.⁶ The 4 *KCHIP* genes can, by use of alternative splicing or alternative use of transcription initiation sites, encode several protein isoforms.⁵ KChIP2 is the only KChIP expressed in the heart¹ where 4 and 5 transcript isoforms have been identified in mouse and man, respectively.⁵

Recently, we have shown that KChIP2, in addition to facilitating K_V4-mediated current in vivo,^{11,12} also modulates the cardiac L-type Ca²⁺ current (*I*_{Ca,L}).¹³ The hypothesis was triggered by the finding that KChIP2 immunoprecipitates with Ca_V1.2 α_{1C} from brain tissue (Fig. 1). We found that *I*_{Ca,L} density is significantly reduced in myocytes disaggregated from KChIP2^{-/-} mice compared to myocytes from wild-type (WT) mice. The decreased current density in the absence of KChIP2 did not result from reduced protein expression or trafficking of the pore-forming Ca_V1.2 α_{1C} subunit. Rather, we showed that the channel modulation results from a direct interaction between KChIP2 and the intracellular amino-terminus of the α_{1C} subunit. We were unable to show a direct association between Ca_V1.2 and KChIP2 in cardiac tissue, despite the demonstrated functional effects.¹³ Several reasons could underlie this, including antibodies with higher affinity for neuronal proteins and higher concentration of ion-channel proteins in brain. However, KChIP2 does copurify with the amino-terminus of Ca_V1.2 when co-expressed in a bacterial system.¹³ Moreover, co-expression of KChIP2 increased the current density governed by recombinant Ca_V1.2 in a transfected, mammalian cell line, further substantiating our finding that KChIP2 directly augments *I*_{Ca,L}.¹³ We proposed a model, in which KChIP2 indirectly increases the open probability of Ca_V1.2 by alleviating the inhibitory effects of the Ca_V1.2 amino-terminus, as previously characterized.¹⁴ Deleting the amino-terminus of Ca_V1.2 causes a large increase in the whole-cell current amplitude,^{13, 15} and studies have shown that the β₂ subunit of *I*_{Ca,L} in part increases Ca_V1.2 open probability by interacting with the amino-terminus.¹⁴ Additional studies showed that KChIP2 could not fully replace the β₂ subunit, likely due to the pivotal role of β₂ in Ca_V1.2 trafficking.^{16,17} Nevertheless, β₂ and possibly KChIP2 both increase the open probability of Ca_V1.2 via modulation of the aminoterminal inhibitory segment of Ca_V1.2. Single-channel recordings of Ca_V1.2 are required to determine the exact mechanism of KChIP2-induced augmentation of whole-cell Ca²⁺ current.

Microarray analysis with Mouse Genome 430A 2.0 array chips (Affymetrix) of cDNA from total RNA isolated from hearts of 4 KChIP2^{-/-} and 4 C57BL/6J mice revealed that transcription of several genes was comparatively altered in the KChIP2^{-/-} mice. We used quantitative, real-time PCR to verify the microarray results for the transcriptional activity of Ca_V1.2 and a number of associated subunits in KChIP2^{-/-} mice (Fig. 2). As anticipated, KChIP2 mRNA contents in KChIP2^{-/-} were below the detection levels of both assays, confirming the successful deletion of all KChIP2 isoforms (Fig. 2 and Table 1). Despite the increased protein levels of Ca_V1.2 that we observed in KChIP2^{-/-} ventricles,¹³ we found no increases in mRNA levels of Ca_V1.2 in either assay. This would be compatible with an increased protein stability or decreased protein degradation in the absence of KChIP2; however further experimental work is required to test this hypothesis and elucidate the mechanism. Transcriptional activity of the β₂ subunit was increased in KChIP2^{-/-} ventricles, compared to WT ventricles (*p* < 0.05 in both assays; Fig. 2).

In addition to a reduced *I*_{Ca,L}, the KChIP2^{-/-} mice had no residual K_V4.2-mediated *I*_{to,f}.^{11,12} however we were unable to identify any differences in action potential morphology in multicellular preparations.¹¹ This is in accordance with ECG analysis performed by Kuo et al.¹² and by us,¹³ showing a J-wave elevation in KChIP2^{-/-} mice, but no difference in QT intervals between WT and KChIP2^{-/-} mice. Furthermore, the ventricular effective refractory period

(VERP), established at a basic pacing rate of 100 ms is 53 ± 5 ms in anesthetized WT mice ($n = 5$) compared to 48 ± 3 ms in KChIP2^{-/-} mice ($n = 7$; $p > 0.05$). Hence, although the amplitudes of several depolarizing and repolarizing currents are altered, the overall repolarization reserve seems preserved.^{11,18}

It has been reported that KChIP2^{-/-} mice have an increased incidence of ventricular polymorphic tachyarrhythmias in response to programmed electrical stimulation.¹² Interestingly, K_v4.2^{-/-} mice have no arrhythmogenic phenotype,^{19,20} suggesting that the augmented susceptibility to arrhythmia in KChIP2^{-/-} mice does not result exclusively from the absence of a functional $I_{to,f}$. Given the prominent J-wave elevation, the KChIP2^{-/-} mice may serve as a model of the early repolarization syndrome, a familial disease characterized by ventricular ectopic activity and sudden death related to an accentuation of the J wave.²¹

Acknowledgments

We gratefully acknowledge Dr. Geoffrey S. Pitt (Duke University Medical Center, Durham, North Carolina, USA) and Dr. Michael R. Rosen (Columbia University, New York, New York, USA) for critical comments and discussions in the preparation of this manuscript. The present experimental work was performed during Dr. Thomsen's tenure as Research Fellow of the Heart Rhythm Society. This work was supported by US Public Health Service/National Heart, Lung and Blood Institute grants HL-67101 and HL-28958 (to Michael R. Rosen) and HL-088089 and HL-071165 (to Geoffrey S. Pitt).

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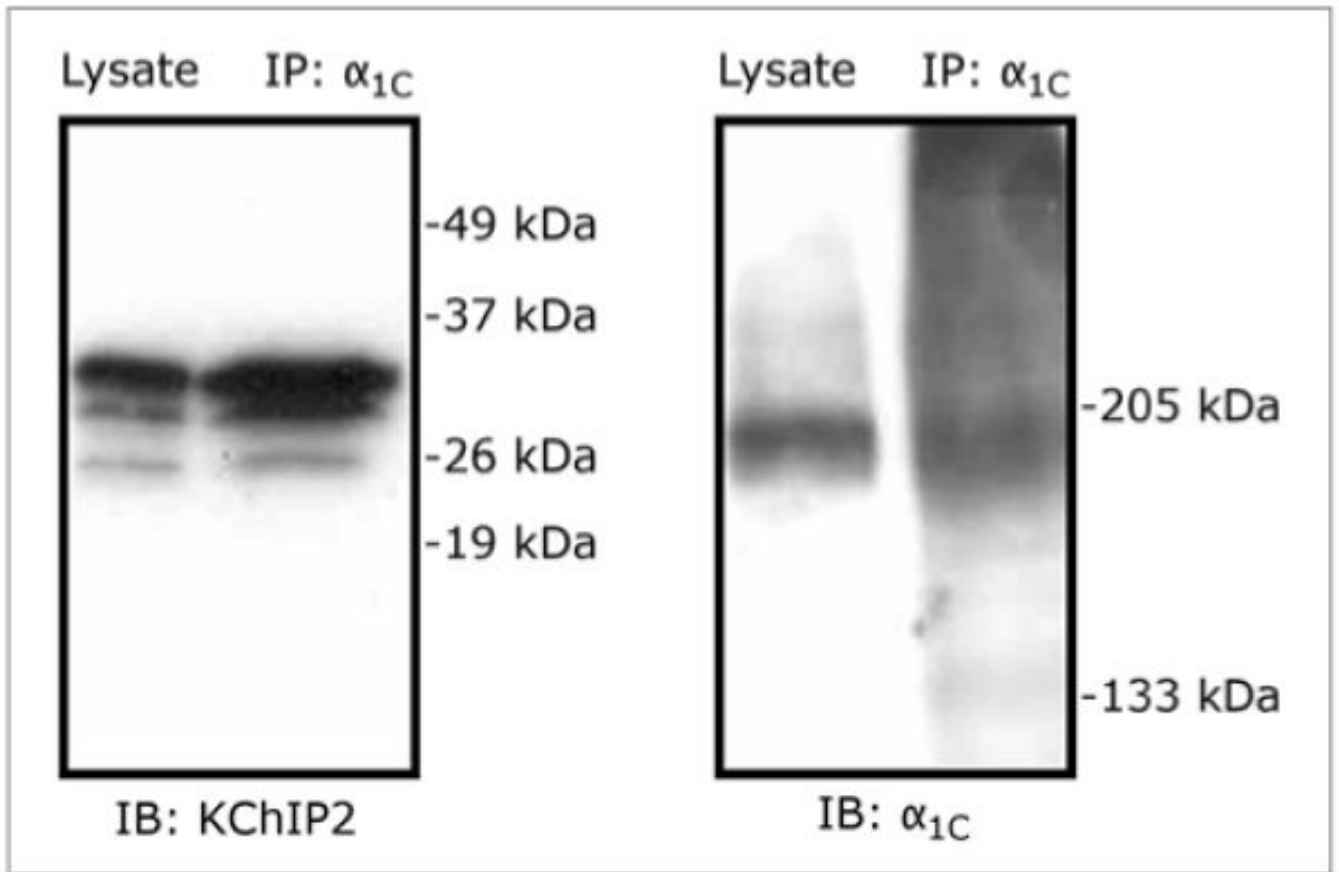


Figure 1. Co-immunoprecipitation showing a biochemical association between $\text{Ca}_v1.2 \alpha_{1C}$ and KChIP2. Tissue samples from adult rat brain were lysed and immunoprecipitated (IP) with anti- α_{1C} , according to methods described earlier.²² The lysate lanes represent total tissue lysates. The membranes are immunoblotted (IB) using anti-KChIP2 (left) and anti- α_{1C} (right).

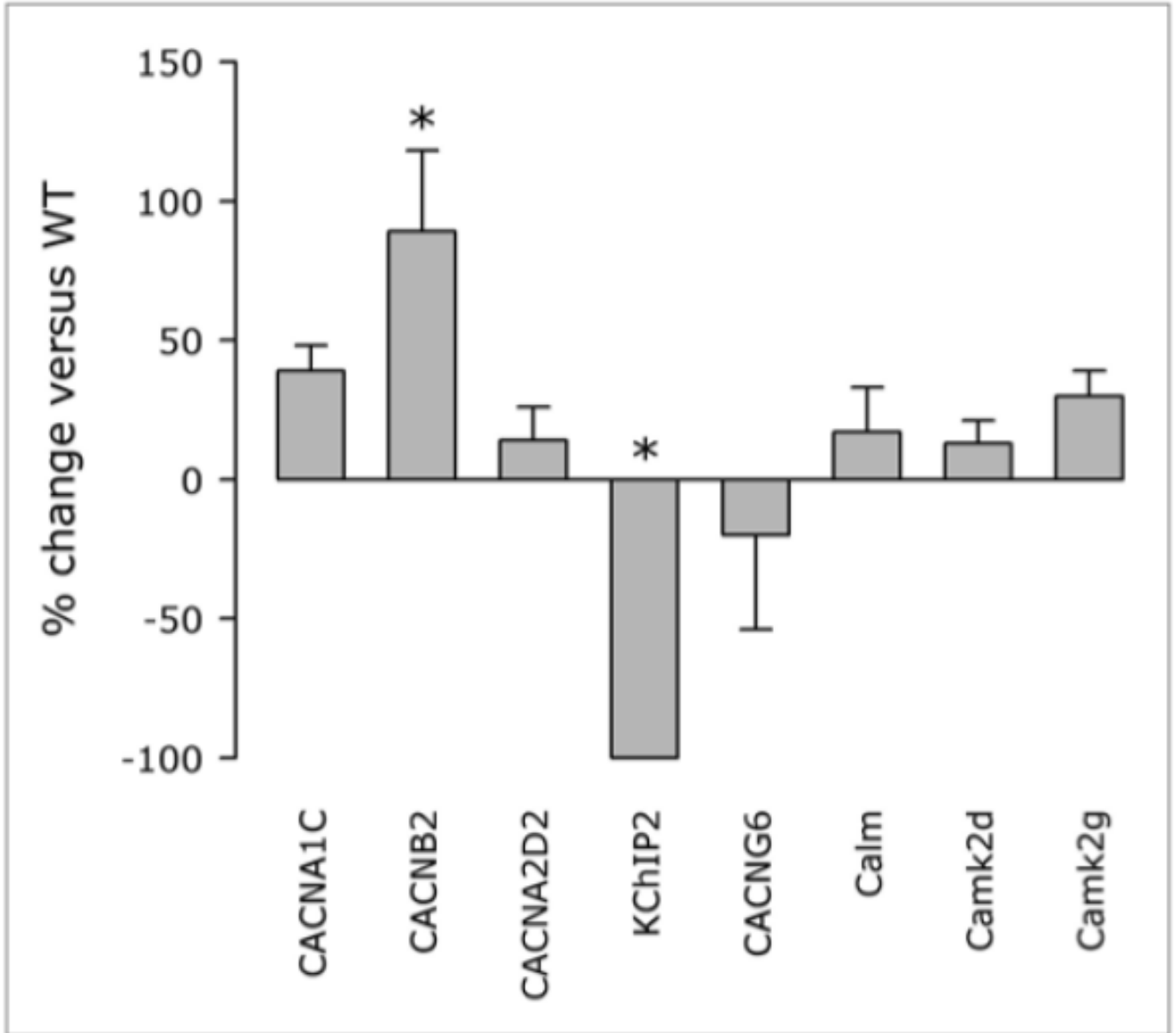


Figure 2.

Analysis of the molecular remodelling in $KChIP2^{-/-}$ ventricles reveals a significantly increased transcriptional activity of the β_2 subunit. The transcription levels of $I_{Ca,L}$ subunits and associated proteins in WT ($n = 6$) and $KChIP2^{-/-}$ ($n = 6$) ventricles were examined using quantitative real-time PCR, as previously described.¹¹ Values are normalized to cyclophilin A level; error bars represents SEM; * $p < 0.05$. All samples are tested in triplicate. Primers and abbreviations are provided in Table 1. These analyses revealed that β_2 expression is increased significantly, whereas $KChIP2$ mRNA could not be detected in $KChIP2^{-/-}$ ventricular tissue.

Table 1

Primers used for quantitative real-time PCR

| Gene | Forward primer | Reverse primer |
|----------------------------------|----------------------------|---------------------------|
| CACNA1C (Ca _v 1.2) | TGACTACCTGACTAGGGATTGGTCTA | TGCTCTAGGTTCCCTTCTGTTTTG |
| CACNB2 (β ₂) | TTGCAAGAACACTGCAATTGG | GGGCCAGTTTATCAGCTGCTA |
| CACNA2D2 (α _{2δ} 2) | TCCAAGACCAGCGCCTTAAG | ACGTTCCACTAACTGCTGTGTAATG |
| KChIP2 | AGCGTGGAGGATGAGTTTGAAC | TCCCCGAAGAATCACTGACA |
| CACNG6 (γ ₆) | AGCGAGAGGGCAAGATCAAG | TTGGTGGTTCGCTGGAAGAT |
| Calm | AGCCTTCTCCTCTTCGACAA | TAATCATGTCCTGCAGCTCCG |
| Camk2d | CAGACTTCGGCTTAGCCATAGAA | GGTGTGCCAGAAAACCAA |
| Camk2g | TTGAAGACATTGTGGCCAGAGA | GCCCAGATGTCCACAGGTTT |
| Cyclophilin A | TGGCGGCAGGTCCATCTA | TCCACAATGTTTCATGCCTTCTT |

Abbreviations: Calm, calmodulin; Camk2d and -g, Ca²⁺/calmodulin-dependent protein kinase II, subtype d and g, respectively.