Molecular distribution of volume-regulated chloride channels (ClC-2 and ClC-3) in cardiac tissues

FIONA C. BRITTON, WILLIAM J. HATTON, CHARLES F. ROSSOW, DAYUE DUAN, JOSEPH R. HUME, AND BURTON HOROWITZ

Department of Physiology and Cell Biology, University of Nevada School of Medicine, Reno, Nevada 89557-0046

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Britton, Fiona C., William J. Hatton, Charles F. Rossow, Dayue Duan, Joseph R. Hume, and Burton Horowitz. Molecular distribution of volume-regulated chloride channels (ClC-2 and ClC-3) in cardiac tissues. Am J Physiol Heart Circ Physiol 279: H2225–H2233, 2000.—The molecular identification of cardiac chloride channels has provided probes to investigate their distribution and abundance in heart. In this study, the molecular expression and distribution of volume-regulated chloride channels ClC-2 and ClC-3 in cardiac tissues were analyzed and quantified. Total RNA was isolated from atria and ventricles of several species (dog, guinea pig, and rat) and subjected to a quantitative RT-PCR strategy. ClC-2 and ClC-3 mRNA expression were calculated relative to ß-actin expression within these same tissues. The transcriptional levels of ClC-3 mRNA were between 1.8 and 10.2% of ß-actin expression in atria and between 3.4 and 8.6% of ß-actin in ventricles (n = 3 for each tissue). The levels of ClC-2 in both atria and ventricles were significantly less than those measured for ClC-3 (n = 3; P < 0.05). ClC-2 mRNA levels were between 0.04–0.08% and 0.03–0.18% of ß-actin expression in atria and ventricles, respectively (n = 3 for each tissue). Immunobots of atrial and ventricular wall protein extracts demonstrated ClC-2-and ClC-3-specific immunoreactivity at 97 and 85 kDa, respectively. Immunohistochemical localization in guinea pig cardiac muscle demonstrates a ubiquitous distribution of ClC-2 and ClC-3 channels in the atrial and ventricular wall. Confocal analysis detected colocalization of ClC-2 and ClC-3 in sarcosomal membranes and distinct ClC-3 immunoreactivity in cytoplasmic regions. The molecular expression of ClC-2 and ClC-3 in cardiac tissue is consistent with the proposed role of these chloride channels in the regulation of cardiac cell volume and the modulation of cardiac electrical activity.

CHLORIDE CONDUCTANCE may contribute to several important functions in cardiac myocytes (26, 29). In addition to a role in modulating action potential duration and resting membrane potential in these cells (5), these currents also participate in the regulation of cell volume (53), pH, and organic osmolyte transport (22).

Several types of Cl− currents have been recorded in cardiac myocytes from different regions of the heart and in different species (29). Among these Cl− currents are those that are activated by cAMP (ICl,cAMP) (1, 25), Ca2+ (ICl,Ca) (57), protein kinase C (ICl,PKC) (54), ATP (ICl,purinergic) (36), and cell volume (ICl,vol) (46, 49). In addition, a sustained Cl− conductance (ICl,basal), which may be active under unstimulated conditions, has been described in rabbit atrial myocytes (10). More recently, the molecular identification of these chloride channels has begun to be elucidated. ICl,cAMP is encoded by cystic fibrosis transmembrane conductance regulator (CFTR) (21, 28, 34), and there is mounting evidence that ICl,PKC (37, 56) and ICl,purinergic (14) are also mediated by CFTR. The outwardly rectifying volume-regulated Cl− current ICl,vol, including ICl,basal, may be encoded by ClC-3 (13), a member of a large family of chloride channels with similar topological structures and significant homologies (30).

ICl,vol undoubtedly contributes to myocyte volume regulation, as it does in most other cells, and may also play a role in action potential modulation in relation to its regulation by PKC (10) and membrane tension (49, 52). The classic ICl,vol recorded from cardiac myocytes is characterized by several common properties, including a halide selectivity of I− > Cl−, inactivation at positive membrane potentials, and unitary channels with outwardly rectifying, intermediate conductance (30–70 pS) (11, 12, 46, 49). Recently, we identified a novel volume-regulated inwardly rectifying Cl− current (ICl,in) in mouse and guinea pig atrial and ventricular myocytes with properties distinct from the outwardly rectifying ICl,vol but very similar to those of ClC-2 (14). ClC-2 was originally cloned from the rat heart and brain, and expression of ClC-2 in oocytes or mammalian cells resulted in a hyperpolarization-activated Cl− current that is sensitive to changes in cell volume (48). ClC-2 can also be activated by acidic extracellular pH, and deletion of amino acids at the amino terminus of protein removes regulation by both volume and pH, resulting in a constitutively open channel (31). An isoform of ClC-2 was identified in rabbit heart that was truncated at the amino terminus (19), but this cDNA may have been an artifact (20).

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With the molecular identification of CIC-2 and CIC-3 as volume-regulated Cl⁻ currents in cardiac myocytes, we now have molecular tools to determine the distribution and abundance of these channels in cardiac tissues. In this study, we used quantitative reverse transcription polymerase chain reaction (RT-PCR) in combination with immunohistochemistry and Western blotting to examine the RNA expression and protein distribution of CIC-2 and CIC-3 channels in cardiac atrial and ventricular tissues from various species. Our results indicate that both CIC-2 and CIC-3 are colocalized in the sarcolemmal membrane of both atrial and ventricular myocytes, consistent with their functional roles as sarcolemmal chloride channels that contribute to the regulation of electrical activity and other cellular functions. A preliminary report of these results has been published (3).

**MATERIALS AND METHODS**

**RNA isolation and cDNA synthesis.** Total RNA was isolated from atrial and ventricular tissues using the Trizol reagent (Life Technologies, Gaithersburg, MD), and following the manufacturer's instructions. Total RNA was incubated with RNase-free DNase (Promega, Madison, WI) for 20 min at 25°C, followed by heat inactivation at 90°C. Total RNA (1 µg) was reverse transcribed with 200 units of Superscript II reverse transcriptase (Life Technologies) in a 20-µl reaction containing 25 ng of oligo(dT)₁₂₋₁₈ primer, 500 µM each dNTP, 50 mM Tris·HCl, pH 8.3, 75 mM KCl, 3 mM MgCl₂, and 10 mM dithiothreitol (DTT). Competitive quantitative RT-PCR. Quantitative RT-PCR was performed using the PCR MIMIC construction kit (Clontech, Palo Alto, CA). MIMIC DNA fragments were constructed so that sequences specific for the target gene (CIC-2, CIC-3, or β-actin) were incorporated into the ends of each MIMIC construct. Competitive PCR was then performed with a pair of gene-specific primers that amplify efficiently both the MIMIC DNA and the target cDNA. Known concentrations of MIMIC DNA (10-fold serial dilutions) were titrated with constant amounts of target cDNA. PCR was performed in 25-µl reactions containing Taq buffer (50 mM KCl, 10 mM Tris·HCl, 1.5 mM MgCl₂, and 0.1% Triton X-100), 250 µM each dNTP, 20 µM each primer, 2.5 µl of cDNA, and 1 U of Taq polymerase (Promega). Amplifications were performed in a GeneAmp 2400 thermal cycler (Perkin Elmer, Hercules, CA) for 30 cycles at 94°C for 30 s, 50°C for 30 s, and 72°C for 1 min, followed by a final extension at 72°C for 7 min. Gene-specific primers were CIC-2 (GenBank accession no. X64139; forward 2,515–2,546 bp, reverse 2,803–2,824 bp); CIC-3 (GenBank accession no. U83464; forward 1,891–1,911 bp, reverse 2,130–2,150 bp); and β-actin (GenBank accession no. V01217; forward 2,282–2,400 bp, reverse 3,071–3,090 bp). RT-PCR products were resolved on 2% agarose gels alongside a molecular weight marker. The amount of target cDNA was determined from the MIMIC dilution in which MIMIC and target cDNA were equal. Gels were analyzed with Molecular Analyst software (Bio-Rad, Foster City, CA). Data were expressed as percentages of β-actin gene expression within the same tissue (n = 3 for each species). To confirm the correct amplification of either CIC-2 or CIC-3, PCR-generated fragments were sequenced with the use of the ABI Prism cycle sequencing kit (Perkin Elmer) and analyzed on a Genetic Analyzer (model 310; Perkin Elmer). There are a number of factors that can affect the relative efficiency of the different PCR reactions, such as primer specificity and unequal amplification of the standard and the target gene (17). However, this study controlled for primer specificity by using primers that had 100% cross-species homology. The amplicon generated from each species used was completely sequenced, and quantitative PCR primers were designed in a nested fashion such that there were no species differences in CIC-2 or CIC-3 sequence in the primer annealing regions.

**Northern blot analysis.** Total RNA (10–20 µg) from atrial and ventricular tissue was size fractionated on 1% agarose-formaldehyde gels alongside a 0.24- to 9.5-kb RNA ladder (Life Technologies) and transferred to nylon filters. Filters were baked and prehybridized in 50% formamide, 5× SSC (standard sodium citrate), 50 mM sodium phosphate, 5× Denhardt's solution, 50 µg/ml sonicated salmon sperm DNA, 0.1% SDS, and 10% dextran sulfate at 42°C overnight. A 420-bp CIC-2 cDNA fragment and a 500-bp CIC-3 cDNA fragment were radiolabeled with [³²P]CTP by random priming (15). The filters were washed at high stringency (3 times in 2× SSC at room temperature for 5 min and then twice in 0.2× SSC/0.1% SDS at 65°C for 30 min) to ensure specificity of labeling. Filters were exposed to film, and autoradiography was performed using a phosphorimag (Bio-Rad).

**Western blot analysis.** Crude protein lysate was prepared from atrial and ventricular tissue. Tissue (20–50 mg) was homogenized in buffer containing 10 mM HEPES, pH 7.4, 10% sucrose, and a cocktail of protease inhibitors (1 mM 4-(2-aminoethyl)benzenesulfonyl fluoride, 5 mM NaF, 1 µM leupeptin, 10 mM EGTA, and 1 mM NaN₃EDTA). The supernatant was cleared from cellular debris by centrifugation at 2,500 g for 15 min at 4°C. Protein concentration was assayed by the bicinchoninic acid method (44) with bovine serum albumin (BSA) as a standard. Protein (50–70 µg) from each tissue in 1× SDS buffer (0.06 M Tris·HCl, pH 6.8, 2% SDS, 10% glycerol, 1 mM DTT, and 0.03% bromphenol blue) was size fractionated on an 8% SDS polyacrylamide gel at 200 V for 50 min in electrode buffer (250 mM Tris, 2 M glycine, and 35 mM SDS). A broad-range protein standard marker (Bio-Rad) was included. Proteins were transferred onto nitrocellulose with the use of the Genie Electroblotter (IDEA Scientific) at 24 V at 4°C for 1 h in buffer containing 25 mM Tris, 192 mM Na₂SO₄, and 20% methanol. The blot was blocked in 5% nonfat milk in TNT buffer (100 mM Tris, 150 mM NaCl, and 0.05% Tween 20) for 1 h at room temperature. The blot was incubated at 4°C overnight with either CIC-2 or CIC-3 affinity-purified polyclonal antisera (1:200 dilution in TNT/0.1% gelatin; Alomone Labs, Jerusalem, Israel). Incubation was followed by washing in 10 ml of TNT (3 times for 5 min) and incubation for 90 min with anti-rabbit IgG alkaline phosphatase conjugate (1:5,500 dilution in TNT/0.1% gelatin; Promega). The blot was washed in TNT (3 times for 15 min), and specific CIC-2 or CIC-3 immunoreactivity was detected colorimetrically with the alkaline phosphatase substrates (50 mg/ml nitroblue tetrazolium and 50 mg/ml 5-bromo-4-chloro-3-indolyl phosphate p-toluidine) in 100 mM Tris, 100 mM NaCl, and 5 mM MgCl₂, pH 9.5. As a negative control, both antibodies were preabsorbed with the respective antigen-glutathione S-transferase (GST) fusion peptide used to generate that antibody.

**Immunohistochemistry.** Guinea pig hearts were perfused with 4% paraformaldehyde in phosphate-buffered saline (PBS), bisected coronally, further fixed with paraformaldehyde for 30 min, washed (4 times for 15 min) in PBS, and cryoprotected in a graded series of sucrose solutions (5, 10, 15, and 20% wt/vol made up in PBS, 1 h each). Both halves of the heart were then embedded in Tissue Tek embedding medium (Miles, IL) and 20% sucrose in PBS (1:2 vol/vol) and
rapidly frozen in isopentane precooled in liquid nitrogen. Cryosections were cut with a Leica CM 3500 cryostat at a thickness of 10 μm and were collected on Vectabond (Vector Laboratories, Burlingame, CA)-coated microscope slides. Sections were initially blocked with 10% BSA for 1 h and then incubated overnight with anti-CIC-2 or anti-CIC-3 antibodies were raised in rabbit (Alomone Labs, Jerusalem, Israel), washed with PBS, and incubated for 1 h with fluorescein isothiocyanate (FITC) or Texas Red anti-rabbit secondary antibodies at 5 μg/ml (Vector Laboratories), washed with PBS (3 times for 10 min), and mounted with Aquamount (Lerner Laboratories, Pittsburgh, PA). Colocalization studies were performed by first incubating sections with CIC-3 antibody and Texas Red anti-rabbit secondary antibody. Sections were then washed (4 times for 15 min) with PBS, incubated with CIC-2 antibody conjugated with FITC by incubating sections with biotinylated anti-rabbit secondary antibody at 5 μg/ml for 1 h, washed (2 times for 15 min) with PBS, incubated with FITC-avidin D at 5 μg/ml for 1 h (Vector Laboratories), washed (3 times for 10 min) with PBS, and then mounted. Sections incubated 1) without primary antibodies or 2) with preabsorbed primary antibodies (absorbed for 1 h with appropriate antigen) were used as negative controls. Sections were examined with the use of a Bio-Rad MRC 600 confocal microscope with excitation wavelengths appropriate for FITC and Texas Red. Confocal micrographs were obtained from digital composites of two-serial scans of 10 optical sections (Z) through a depth of 10 μm (10 × 1 μm), Z series were constructed with Bio-Rad Comos software, and final images were prepared using Adobe Photoshop software.

Statistical analysis. Experiments utilizing PCR to determine CIC-2 and CIC-3 expression were performed on tissue isolated from at least three different animals. For quantitative RT-PCR the concentration of the target DNA was normalized to β-actin expression. Data are expressed as means ± SE, n is the number of animals. One-way ANOVA was used to compare gene expression between the groups, and a Student-Newman-Keuls post hoc test was then used to identify differences among the groups. A two-tailed probability (P) of <0.05 indicates statistical significance.

RESULTS

Molecular expression of CIC-2 and CIC-3 transcripts in cardiac muscle. Northern blot analysis (Fig. 1, A and B) indicates that both CIC-2 and CIC-3 are expressed in the atria and ventricles of guinea pigs, dogs, and rats. The CIC-2 transcript yielded a band at 3.3 kb in all the species examined, which is similar to the transcript size reported by others (6, 48). The size of the CIC-3 transcript obtained by Northern analysis was 3.4 kb in guinea pig and rat and 4.0 kb in dog. Transcript sizes of 3.4 and 5.0 kb have been obtained for CIC-3 RNA expression in cardiac myocytes (13) and other tissues (32). The additional transcript size of 5.0 kb observed in our previous study (13) may be due to the use of poly(A+) RNA.

Quantitative analysis of CIC-2 and CIC-3 transcripts in cardiac muscle. Quantitative RT-PCR was used to quantify the expression of CIC-2 and CIC-3 transcripts relative to a housekeeping gene (β-actin). Specific primers were designed for CIC-2 and CIC-3 so that they did not cross-hybridize with other members of the CIC family. Qualitative RT-PCR indicated that CIC-2 and CIC-3 mRNA were present in cardiac tissue. The CIC-2 and CIC-3 PCR generated fragments (301 and 276 bp, respectively) were sequenced to confirm the correct amplification of either transcript. We used the competitive “mimic” approach of quantitative RT-PCR to determine the relative amounts of CIC-2 and CIC-3 transcripts in RNA isolated from atrial and ventricular tissues. In competitive RT-PCR, a dilution series of the standard RNA coamplified with equal amounts of total RNA (and therefore equal amounts of amounts of the native gene). The MIMIC standard competes with the native gene for primers and enzyme, thus reducing the signal for the native gene when the MIMIC standard is in excess. As the amount of native gene increases, the MIMIC standard signal decreases. A representative gel used for digital analysis and comparison of CIC-2 and CIC-3-specific amplification with “mimic DNA” amplification is shown in Figs. 2A and 3A, respectively. As the concentration of MIMIC was reduced from 100 to 0.1 amol/μl, the MIMIC band reduced in density, whereas the CIC-2 and CIC-3 bands increased in density. The amount of target cDNA was determined from the MIMIC dilution in which MIMIC and target cDNA were equal. Molecular Analyst software (Bio-Rad) was then used to accurately determine the ratio of density between the fluorescence of target cDNA and MIMIC bands. This ratio is included in the calculation of the concentration of target gene. The RT-PCR experiments were quantified by comparing CIC-2 and CIC-3 expression to the amount of β-actin gene expression (Figs. 2B and 3B, respectively). In the guinea pig, rat, and dog, quantitative RT-PCR experiments revealed significantly greater amounts of CIC-3 than CIC-2 transcripts in both atrial and ventricular tissue (P < 0.05; n = 3 for each species examined). The
normalized values for ClC-3 expression are much larger for the tissues examined (−10- to 40-fold) compared with those of ClC-2 expression within the same tissues. ClC-3 expression was between 1.8 and 10.2% of β-actin in atria and between 3.4 and 8.6% of β-actin in ventricles, whereas ClC-2 expression was 0.04–0.08% and 0.03–0.18% of β-actin expression in atrial and ventricular tissue, respectively. No significant difference in ClC-3 expression in atria and ventricles was observed for any of the species examined. ClC-2 expression was significantly higher in the ventricles than in atria of rat tissue (*P < 0.01; n = 3) and significantly higher in ventricles than in atria of rat tissue (*P < 0.01; n = 2).

Western analysis of ClC-2 and ClC-3 protein in cardiac muscle. Expression of ClC-2 and ClC-3 polypeptides in atrial and ventricular tissue was detected by immunoblotting with the use of affinity-purified polyclonal antibodies generated against GST fusion peptides corresponding to amino acid residues 888–906 of rat ClC-2 (Fig. 4A) and residues 592–661 of rat ClC-3 (Fig. 4B). ClC-2 and ClC-3 antibody specificity was confirmed in Western blots with the use of antibody that had been preabsorbed with purified ClC-2 or ClC-3 antigen that was used to generate the antibodies. The preabsorbed antibodies did not react with proteins isolated from the cardiac tissue. The ClC-2 antisera recognized a single band corresponding to a polypeptide of ~97 kDa, the expected size of the protein predicted from cDNA sequence analysis (48). ClC-3 protein migrated with a molecular mass of 85 kDa. This molecular mass is close to that predicted from the sequence of ClC-3 (32). Additional ClC-3-like immunoreactivity was observed in these homogenates at 65 and 70 kDa (Fig. 4B). These smaller molecular mass bands were also eliminated with the preabsorbed antibody and may represent different glycosylated ClC-3 forms (42) or ClC-3 proteolysis products. ClC-3 has considerable sequence homology with the chloride channels ClC-4 and ClC-5. The epitope fragment used to generate the ClC-3 polyclonal antibody (70 amino acids in the COOH terminus) has considerable homology with ClC-4 and ClC-5 proteins (46/70 and 49/70 identities in the carboxy terminus of rat ClC-4 and ClC-5, respectively). There is the possibility that there may be some degree of cross-reactivity with these related proteins in cardiac tissue. However, Schmieder et al. (42) observed no cross-reaction of the same ClC-3 antisera in immunoblots of _Xenopus laevis_ oocyte membrane preparations expressing exogenous rat ClC-4 or rat ClC-5.

**Immunohistochemical localization of ClC-2 and ClC-3 in cardiac muscle.** The localization of ClC-2 and ClC-3 channels in cardiac tissue was determined im-

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**Fig. 2.** Quantitative RT-PCR of ClC-2 gene expression in cardiac muscle. A: representative gel of quantitative RT-PCR for ClC-2 in canine ventricle. Known concentrations of MIMIC DNA (0.01–100 amol/μl) were coamplified with unknown concentrations of target cDNA. Competitive RT-PCR products were resolved on 2% agarose gels alongside a 100-bp marker. The MIMIC DNA band is visible at 574 bp and the ClC-2 band at 309 bp. The amount of ClC-2 cDNA can be determined from the MIMIC dilution in which the ClC-2 and MIMIC bands appear equal. Quantitative RT-PCR for β-actin expression was also performed from the same cDNA. B: concentrations of ClC-2 gene expression in various cardiac tissue were calculated and reported relative to β-actin gene expression within the same tissue (n = 3 for each species). ClC-2 expression was significantly higher in ventricles than in atria of rat tissue (P < 0.01; n = 3). Increasing our n values may have reduced the variability, and the difference in ClC-2 expression may be statistically significant.

**Fig. 3.** Quantitative RT-PCR of ClC-3 gene expression in cardiac muscle. A: representative gel of quantitative RT-PCR for ClC-3 in canine ventricle. Known concentrations of MIMIC DNA (0.1–100 amol/μl) were coamplified with unknown concentrations of cDNA. Competitive RT-PCR products were resolved on 2% agarose gels alongside a 100-bp marker. The MIMIC DNA band is visible at 650 bp and the ClC-3 band at 300 bp. The amount of target DNA can be determined from the MIMIC dilution in which the ClC-3 and MIMIC bands appear equal. Quantitative RT-PCR for β-actin expression was also performed from the same cDNA. B: concentrations of ClC-3 gene expression in various cardiac tissue were calculated and reported relative to β-actin gene expression within the same tissue (n = 3 for each species).
ClC-2 and ClC-3 Expression in Heart

DISCUSSION

Volume-regulated Cl⁻ currents are present in numerous cell types, including cardiac myocytes, and play important roles in the control of cell volume, pH, and membrane potential (16, 26, 27). However, the molecular identity of these anion channels has been a recent matter of debate (7, 39, 47). Many candidates have been proposed for the chloride conductance path that mediates regulatory volume decrease (RVD) (38). The molecular candidates include P-glycoprotein (pGp), the product of the multidrug resistance gene (51), and pICln (41), which, when expressed in fibroblasts, has been reported to be responsible for a Cl⁻ conductance activated by hypotonic solutions (24). Although it now appears that pGp and pICln may not actually be anion channels, their involvement in cell swelling raises the possibility that these proteins may modulate the volume-regulated Cl⁻ conductance in heart tissue.

ClC-2 and ClC-3, which certainly encode chloride channel proteins and are members of the ClC family of voltage-gated chloride channels, have been reported to be sensitive to changes in cell volume (13, 23). In addition, the ubiquitous expression of ClC-2 and ClC-3 in many cell types (32, 48) implies that ClC-2 and ClC-3 may play a role in a universal and necessary function in many types of cells.

ClC-2 and ClC-3 as candidates for volume regulation in cardiac myocytes. The functional expression of guinea pig cardiac ClC-3 (gpClC-3) in mammalian NIH/3T3 cells (9, 13) results in a large basally active Cl⁻ conductance, which is strongly modulated by cell volume and exhibits many of the same biophysical and pharmacological properties as the native I_{Cl,vol} present in cardiac myocytes (11, 53). Thus ClC-3 may be the gene responsible for I_{Cl,vol} found in cardiac myocytes of a variety of species (29). However, the identification of ClC-3 as the molecular counterpart responsible for native I_{Cl,vol} in some cells has certainly not been exempt from controversy (see Refs. 30, 39, and 50 for review).

ClC-2 currents are characterized by having inward rectification, time-dependent activation at hyperpolarizing voltages and a halide selectivity of Cl⁻ > I⁻. ClC-2 channels expressed in Xenopus oocytes have been shown to increase with large hyperpolarizing voltages as well as extracellular hypotonicity (23). A hyperpolarization-activated ClC-2-like current that is also modulated by cell volume has been characterized in the human T_84 adenocarcinoma cell line (2, 18) and in other noncardiac tissues (4, 8, 40). Recently, our group has demonstrated that similar volume-regulated inwardly rectifying currents (I_{Cl,ir}) can be recorded from native mouse and guinea pig cardiac myocytes (14). We have now found that ClC-2 is ubiquitously expressed in atria and in the ventricular wall including the epicardium and endocardium.
Localization of ClC-2 and ClC-3 channels to myocyte membranes. ClC-2-specific antibody predominantly stains cardiomyocyte sarcolemmal membranes. ClC-3-specific antibody stains both sarcolemmal and what appears to be intracellular membranes, which may indicate some cytoplasmic staining. However, it is possible that this apparent cytoplasmic staining may actually be due to the presence of ClC-3 in T-tubular membranes, which are known to have a complex reticular organization in cardiac myocytes (45). The presence or absence of ClC-3 in T tubules is important to investigate and may have implications for ClC-3 function. A followup study is required to evaluate the localization of ClC-3 in sarcolemmal and T-tubular membranes with the use of dual labeling with specific markers (e.g., di-8-ANEPPS; Ref. 43) on isolated atrial and ventricular cells. It is possible that the difference in staining pattern between ClC-2 and ClC-3 reflects functional differences of the two channels. However, the observed colocalization of the two channels at the sarcolemmal membrane suggests a role for both proteins as sarcolemmal chloride channels in myocytes and presents the intriguing possibility of ClC-2/ClC-3 heterodimer formation. The latter needs to be investigated by in vitro experiments.

CIC-2 versus ClC-3: a role in myocyte volume regulation. The role of CIC-2 in volume regulation may well depend on its expression level relative to other swelling activated chloride channels. T84 cells possess at least two distinct swelling-activated chloride conductance paths, one mediated by a ClC-2-like current (i.e., inwardly rectifying and Cd$^{2+}$ sensitive, tamoxifen insensitive), $I_{\text{Cl,ir}}$, and the other by a swelling-activated, tamoxifen-sensitive outwardly rectifying chloride current, $I_{\text{Cl,vol}}$, possibly encoded by ClC-3 (2). Bond and colleagues (2) suggested that $I_{\text{Cl,vol}}$ rather than $I_{\text{Cl,ir}}$ mediates RVD in T84 cells on the basis of the sensitivity of RVD to specific inhibitors of $I_{\text{Cl,vol}}$ or $I_{\text{Cl,ir}}$. Possibly, ClC-2 does not contribute significantly to RVD in T84 cells because it is not expressed at the same levels as the channel that mediates $I_{\text{Cl,vol}}$.

A similar conclusion can be made in cardiac myocytes. In a recent study, we observed that only a small population of mouse and guinea pig atrial and ventricular myocytes appear to exhibit hyperpolarization activated $I_{\text{Cl,ir}}$ (14). In this study, we used a competitive RT-PCR approach to quantify the level of ClC-2 and ClC-3 mRNA transcripts in cardiac tissue. Quantitatively, at the transcriptional level, we observed significantly lower levels of ClC-2 mRNA transcript expres-
sion compared with ClC-3 expression in both atrial and ventricular myocytes. This is consistent with a higher percentage of cells exhibiting functional outwardly rectifying ClC-3-like currents compared with inwardly rectifying ClC-2-like currents. Although this quantitative difference is not obvious in immunoblots or immunohistochemistry, these latter approaches are not quantitative in nature and may thus explain the apparent discrepancy between functional $I_{Cl,ir}$ and ubiquitous molecular ClC-2 expression. When the quantitative RT-PCR data are considered, it must be kept in mind that RNA was extracted from cardiac tissue rather than isolated myocytes, and thus the levels of ClC-2 and ClC-3 transcripts are from a mixed population of cells (see e.g., Ref. 33). Also the amount of mRNA detected by quantitative RT-PCR does not necessarily reflect a corresponding or equal measure of functional ClC-2 or ClC-3 protein. Of interest is the study by Wong and co-workers (55), who measured the density of ClC-3 mRNA levels across the left ventricular free wall of rabbit heart by in situ hybridization and who also measured the corresponding current density of swelling-activated chloride channels in myocytes isolated from various regions of the ventricular wall. They found that, although there was uniform expression of ClC-3 mRNA across the ventricular wall, the whole cell slope conductance of swelling-activated chloride channel activity was higher in myocytes isolated from the subepicardium than in myocytes isolated from the midmyocardium or subendocardium. They concluded that the control of gene expression might be less important for regulating the distribution of functional swelling-activated chloride channels in the heart.

Another possible explanation for the discrepancy between the apparent ubiquitous ClC-2 expression and the small population of mouse and guinea pig atrial and ventricular myocytes exhibiting a hyperpolarization activated $I_{Cl,ir}$ could be that many ClC-2 proteins may form heterodimeric channels with other ClC proteins (perhaps ClC-3) (35), resulting in channels with characteristics different from ClC-2 homodimers. It is also possible that ClC-2 is regulated in a way that renders the channel silent under basal conditions. Both of these possibilities are being studied.

In summary, we have demonstrated the molecular expression of two volume-regulated chloride channels in cardiac myocytes from several species. We have shown that ClC-3 transcriptional expression predominates in all species relative to a housekeeping gene. Finally, we have examined the cellular and subcellular localization of these channels in cardiac tissues and myocytes. Our findings indicate that both ClC-2 and ClC-3 are colocalized in the sarcolemmal membrane of both atrial and ventricular myocytes. This is consistent with their functional roles as sarcolemmal chloride channels that may regulate cardiac cell volume and electrical activity.

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