Background—Abnormal Ca\(^{2+}\) handling may contribute to impaired atrial contractility and arrhythmogenesis in human chronic atrial fibrillation (cAF). Here, we assessed the phosphorylation levels of key proteins involved in altered Ca\(^{2+}\) handling and contractility in cAF patients.

Methods and Results—Total and phosphorylation levels of Ca\(^{2+}\)-handling and myofilament proteins were analyzed by Western blotting in right atrial appendages of 49 patients in sinus rhythm and 52 cAF patients. We found a higher total activity of type 1 (PP1) and type 2A phosphatases in cAF, which was associated with inhomogeneous changes of protein phosphorylation in the cellular compartments, ie, lower protein kinase A (PKA) phosphorylation of myosin binding protein-C (Ser-282 site) at the thick myofilaments and enhanced PKA phosphorylation of troponin I at the thin myofilaments and enhanced PKA (Ser-16 site) and Ca\(^{2+}\)-calmodulin protein kinase (Thr-17 site) phosphorylation of phospholamban. PP1 activity at sarcoplasmic reticulum is controlled by inhibitor-1 (I-1), which blocks PP1 in its PKA-phosphorylated form only. In cAF, the ratio of Thr-35–phosphorylated to total I-1 was 10-fold higher, which suggests that the enhanced phosphorylation of phospholamban may result from a stronger PP1 inhibition by PKA-hyperphosphorylated (activated) I-1.

Conclusions—Altered Ca\(^{2+}\) handling in cAF is associated with impaired phosphorylation of myosin binding protein-C, which may contribute to the contractile dysfunction after cardioversion. The hyperphosphorylation of phospholamban probably results from enhanced inhibition of sarcoplasmic PP1 by hyperphosphorylated I-1 and may reinforce the leakiness of ryanodine channels in cAF. Restoration of sarcoplasmic reticulum–associated PP1 function may represent a new therapeutic option for treatment of atrial fibrillation. (Circulation. 2006;114:670-680.)

Key Words: atrial fibrillation ■ calcium ■ myosin binding protein C, cardiac, human ■ phospholamban protein, human ■ protein phosphatase-1 ■ protein phosphatase-2A

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Functional regulation of ion channels and modulator proteins of Ca\(^{2+}\) homeostasis and contractility relies on phosphorylation processes. Protein kinase A (PKA) and calmodulin-dependent protein kinase II (CAMKII) phosphorylation of L-type Ca\(^{2+}\) channel (\(I_{\text{Ca,L}}\)) subunits increases current amplitude. Phosphorylation of ryanodine receptor channels (RyR2) at the Ser-2809 (PKA site) and Ser-2815 (CAMKII site), respectively, enhances Ca\(^{2+}\) release. PKA and CAMKII phosphorylation of phospholamban (PLB) at Ser-16 and Thr-17, respectively, relieves sarcoplasmic reticulum Ca\(^{2+}\)–adenosine triphosphatase (Serca2a) inhibition and enhances relaxation rate and contractility. PKA phosphorylation of inhibitory troponin subunit (Tn-I) at Ser-23/24 and of myosin binding protein-C (MyBP-C) at Ser-282 decreases myofibrillar Ca\(^{2+}\) sensitivity, thereby accelerating the relaxation rate.

The phosphorylation level of Ca\(^{2+}\)-handling proteins is controlled by serine/threonine protein phosphatases (PPs) in a highly regulated manner. We have recently shown that reduced \(I_{\text{Ca,L}}\) amplitude in human cAF is associated with increased activity of type 1 (PP1) and type 2 (PP2A) phosphatases. Although increased PP activity is expected...
to dephosphorylate regulatory Ca\(^{2+}\)-handling proteins, phosphatase activity may be differently regulated in distinct cellular microdomains. For instance, PP1 is anchored to sarcoplasmic reticular RyR2 and PLB by the noncatalytic targeting subunits spinophilin and RGL, respectively. Targeting to the close vicinity of these proteins enhances PP1 specificity and availability.\(^6\) Furthermore, PP1 is regulated by 2 cytosolic heat- and acid-stable proteins, inhibitor-1 (I-1) and inhibitor-2 (I-2).\(^7\) I-1 becomes active upon phosphorylation on Thr-35 by PKA. This results in inhibition of PP1 and enhanced PKA-mediated protein phosphorylation.\(^8\)–\(^10\) However, PKC or mitogen-activated protein kinase–mediated phosphorylation of I-1 at Ser-67 converts I-1 in a less efficient substrate for PKA, which suggests an antithetic regulation of I-1 by PKA and other kinases, respectively.\(^11\)\(^,\)\(^12\) Thus, abnormalities in local signaling, ie, altered kinase/phosphatase balance in the cellular microdomains, may contribute to impaired atrial Ca\(^{2+}\) handling and contractility in AF.

The mRNA and protein levels of \(I_{\text{cL}}\), RyR2, calsequestrin (CSQ), Serca2a, PLB, and Tn-I were stable in human cAF.\(^5\),\(^13\)–\(^19\) However, PKA phosphorylation of RyR2 was higher in cAF than in patients in sinus rhythm (SR),\(^20\) which is consistent with the larger spontaneous Ca\(^{2+}\) release from sarcoplasmic reticulum.\(^21\) This, together with an enhanced Ca\(^{2+}\) extrusion through the Na\(^+/\)Ca\(^{2+}\) exchanger (NCX1),\(^17\),\(^21\) is expected to reduce the Ca\(^{2+}\) load of sarcoplasmic reticulum that contributes to the blunted atrial force of contraction in cAF patients.\(^17\),\(^22\),\(^23\) In addition, abnormal Ca\(^{2+}\) dissociation from cardiac myofilaments may promote arrhythmogenic Ca\(^{2+}\) release from the sarcoplasmic reticulum.\(^24\) Thus, impaired phosphorylation-dependent regulation of Tn-I and MyBP-C may contribute to both contractile dysfunction and arrhythmogenesis in cAF. Although it is obvious that impaired Ca\(^{2+}\) homeostasis contributes to initiation and perpetuation of AF, its precise role in cAF and the underlying molecular mechanisms are currently unknown. In the present study, we assessed the phosphorylation-dependent regulation of key proteins involved in Ca\(^{2+}\) handling and contractility in patients with cAF.

**Methods**

**Patients**

The study was approved by the local ethics committee (No. EK114082202). Each patient gave written informed consent. Right atrial appendages were obtained from 49 patients with SR and 52 patients with cAF (AF >6 months; Table).

**Reverse-Transcription Polymerase Chain Reaction Analysis**

Total RNA was isolated from atrial tissue, and reverse-transcription polymerase chain reactions were performed as described previously.\(^9\) Primers were constructed according to published sequences (online-only Data Supplement, Table I).

**Enrichment of I-1**

I-1 was enriched from atrial tissue of SR (844±67 mg, n=6) and cAF patients (782±82 mg, n=7) by an optimized trichloroacetic acid (TCA) extraction procedure.\(^25\) This procedure yielded 0.12 μg/mg tissue (n=13), with no significant difference between the

**Patient Characteristics**

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**CAD** indicates coronary artery disease; **MVD**, mitral valve disease requiring valve replacement; **AVD**, aortic valve disease requiring valve replacement; **LVEF**, left ventricular ejection fraction; **LVEDP**, left ventricular end-diastolic pressure; **LAD**, left atrial diameter; **LVEDD**, left ventricular end-diastolic diameter; **IVS**, interventricular septum thickness; **LVPW**, left ventricular posterior wall thickness; **ACE**, angiotensin-converting enzyme; and **AT**, angiotensin receptor.

*P<0.05, nonpaired Student t test for continuous variables and χ\(^2\) test for categorical variables.

**Recombinant I-1 Protein**

Recombinant I-1 protein was generated by cloning the complete cDNA of rat I-1 into the pGEX-AT expression vector (Stratagene, La Jolla, Calif). The plasmid was transformed into competent Escherichia coli BL21 (Novagen, Madison, Wis) to express I-1/glutathione-S-transferase. I-1/glutathione-S-transferase was purified from clarified bacterial lysate by affinity purification with glutathione-agarose beads. Loaded beads were washed 3 times, and recombinant I-1 was released by thrombin cleavage. Recombinant human I-2 was purchased from Calbiochem (EMD Biosciences, Inc, Darmstadt, Germany).

**Adenovirus Infection of Neonatal Rat Cardiomyocytes**

For testing specificity of antibodies, neonatal rat cardiac myocytes were isolated and cultured, and for the I-1 studies, they were infected with an adenovirus encoding the full-length rat I-1 (Ad-I-1) as described previously.\(^9\)

**Western Blot Analysis**

Total and phosphorylation levels of human I-1 at Thr-35 or Ser-67 (total protein 1:1000 and phospho-Ser-67 1:200, custom-made purified polyclonal antibodies [Eurogentec, Brussels, Belgium]; and
phospho-Thr-35, 1:2000 (Cell Signaling Technology Danvers, Mass.) and I-2 (1:2000; Calbiochem) were analyzed by immunoblotting as described previously. For testing specificity of total I-1, TCA extracts were preincubated with recombinant I-1 protein or preimmune serum. The specific signal at Thr-35 was verified by increasing PKA phosphorylation with isoproterenol (0.001 to 1 μmol/L) in Ad-I-1–infected neonatal rat ventricular myocytes. The latter were also incubated with shrimp alkaline phosphatase (Roche Diagnostics GmbH, Mannheim, Germany) for dephosphorylation of the Ser-67 site.

The protein levels of CSQ (1:2500; Dianova, Hamburg, Germany), Tn-I (1:30000; Chemicon International, Temecula, Calif), phospho-Thr-I (1:30000; HyTest Ltd., Turku, Finland), Serca2a (1:2000; Santa Cruz Biotecnhology, Santa Cruz, Calif), total PLB, Ser-16 and Thr-17 phosphorylated PLB (all 1:5000; Badrilla Ltd., Leeds, United Kingdom), PP1α (1:500; Biomol, Plymouth Meeting, Pa), total PP2A (1:1000), affinity purified; Upstate Biotechnology, Lake Placid, NY), and methylated and demethylated PP2A (1:100 and 1:1000, respectively; Upstate), NCX1 (1:1000; Affinity BioReagents, Neshanic Station, NJ, and Golden, CO), total MyBP-C (1:5000; kind gift from Wolfgang Linke, University of Münster, Germany), and Ser-282 phosphorylated MyBP-C (1:100; Eurogentec) were quantified by Western blotting as described previously. The phospho-MyBP-C antibody (GAGRTPsDSHDEDA) was raised in rabbits with a mouse-specific peptidic and purified by affinity chromatography. Specificity at Ser-282 was verified by increasing PKA phosphorylation with isoproterenol (0.001 to 1 μmol/L) in cultured neonatal rat cardiomyocytes.

Phosphatase Assay
Phosphatase activity was measured in atrial homogenates, and okadaic acid (3 nmol/L) was used to differentiate between PP1 and PP2A activities as described previously.

Statistical Analysis
One-way ANOVAs were applied to determine the sources of protein level and phosphatase activity variation (SPSS version 12.0; SPSS, Inc., Chicago, Ill). Independent variables were cAF, selected clinical variables, and medication (Table). Differences between group means for continuous data were compared by unpaired Student t test or, when patients with SR or cAF were stratified by underlying disease or valve disease, hypertension, hyperlipidemia, left atrial diameter, and left ventricular end-diastolic pressure. cAF patients more often received digitalis and diuretics (Table). Total and phosphorylation levels of proteins were related to selected clinical variables and patients’ medication. With 1-way ANOVAs, PP1 was the only predictor of total and phosphorylation levels of proteins (data not shown).

Results
Significant differences between the SR and cAF groups were found for gender, incidence of coronary artery disease or valve disease, hypertension, hyperlipidemia, left atrial diameter, and left ventricular end-diastolic pressure. cAF patients more often received digitalis and diuretics (Table). Total and phosphorylation levels of proteins were related to selected clinical variables and patients’ medication. With 1-way ANOVAs, PP1 was the only predictor of total and phosphorylation levels of proteins (data not shown).

Protein Levels of Serca2a and PLB in cAF Patients
Levels of proteins were normalized to the tissue amount of CSQ, which was similar in SR and cAF patients (Figure 1A). Serca2a levels were ~25% lower in cAF than in patients with SR (P=0.055). Although protein levels of PLB were not significantly different (P=0.3291; Figure 1A), the ratio of total PLB to Serca2a was higher in cAF than in SR patients (Figure 1A).

Phosphorylation Levels of PLB in cAF Patients
The cAF samples showed a higher Ser-16 (PKA site) and a nonsignificantly enhanced Thr-17 (CAMKII site) phosphorylation of PLB in cAF compared with SR (Figure 1B). The ratio of phosphorylated PLB to Serca2a was significantly higher for both phosphorylation sites in cAF.

Phosphorylation Levels of Tn-I and MyBP-C in cAF Patients
Total and PKA phosphorylation levels of Tn-I did not differ between the groups (Figure 2A). In contrast, total MyBP-C was higher, whereas phosphorylation level at Ser-282 was smaller in cAF than in SR, which resulted in an ~40% lower ratio of phosphorylated to total MyBP-C (Figure 2B).

Protein Levels of NCX1 in cAF Patients
Consistent with previous results, we found higher protein abundance of NCX1 in cAF than in SR patients (Figure 3).

PP1 and PP2A Activity in SR and cAF Patients
Because PLB is dephosphorylated mainly by PP1,28,29 the higher PLB phosphorylation suggests lower PP1 activity in cAF than in SR. We found, however, that the PP1- and PP2A-related activities were both significantly higher in cAF than in SR (Figure 4A). The stronger PP1 and PP2A activities in cAF were associated with increased protein levels of the corresponding catalytic subunits (Figure 4B).

PP1- and PP2A-Anchoring Proteins in cAF Patients
Reduced PP targeting to the RyR2 and PLB/Serca2a complexes may underlie altered PP function in cAF. However, the mRNA abundance of spinophilin and RGL, which target PP1 to RyR2 and PLB, respectively, was comparable in SR and cAF (Figure 5A). The same holds true for the mRNA level of the PP2A-anchoring protein PR130 (Figure 5B). Methylation of PP2A by methyltransferases alters its subcellular targeting and substrate specificity. Immunoblotting with methylation-specific antibodies revealed comparable abundance of methylated and demethylated PP2A in SR and cAF (Figure 5C).

PP1 Inhibitors in cAF Patients
Because increased PLB phosphorylation in cAF may result from reduced microdomain PP1 activity, we analyzed the phosphatase inhibitors I-1 and I-2. Their transcript levels were similar in SR and cAF (Figure 6A).

To quantify the protein level of I-1 in human atrium, a dilution of recombinant rat I-1 was probed with the I-1 antibody in parallel with a dilution of TCA extracts (Figure 6B). Under the assumption that the antibody detects human I-1 with similar affinity as rat I-1, we calculated a I-1 concentration of 92 fmol/mg protein (92 nmol/L). The latter is similar to the I-1 levels in human left ventricle (126 nmol/L) and is ~100-fold higher than the I-1 concentration required to inhibit PP1 by 50% (~1 nmol/L). Although the physical properties of I-1 and I-2 are similar, I-2 proteins...
were not detectable in either standard homogenates (not shown) or TCA extracts of atrial tissue (Figure 6B).

With the exception of larger left atria in cAF versus SR, the clinical characteristics of the patients used for determination of I-1 proteins were comparable in both groups (online Data Supplement, Table II). Total I-1 proteins tended to be lower in cAF than in SR (Figure 7A). Interestingly, the levels of Thr-35–phosphorylated to total I-1 were ~10-fold higher in cAF than in SR (Figure 7A). The latter was associated with lower phosphorylation at Ser-67 (Figure 7A); the ratio of Ser-67–phosphorylated to total I-1, however, was unaltered in cAF. Figure 7B demonstrates specificity of the antibodies recognizing total, Thr-35–phosphorylated, or Ser-67–phosphorylated I-1.

Discussion

In the present study, we demonstrate that increased total activity of PP1 and PP2A in cAF is associated with lower PKA phosphorylation of MyBP-C but with hyperphosphorylation of PLB. Thus, the changes in phosphorylation-dependent regulation in cAF are not homogeneous and point toward local regulation of kinase/phosphatase balance in cAF, ie, lower phosphorylation of MyBP-C at the thick myofilaments but preserved Tn-I phosphorylation at the thin myofilaments and enhanced PLB phosphorylation at the sarcoplasmic reticulum (Figure 8). These changes were accompanied by higher protein levels of NCX1. The different phosphorylation levels in the distinct compartments do not involve modified expression of PP1- and PP2A-anchoring proteins or impaired PP2A regulation through carboxymethylation.30 The decrease in MyBP-C phosphorylation is in agreement with the higher PP activity and may contribute to contractile dysfunction in cAF. The higher PLB phosphorylation appears to result from a stronger PP1 inhibition by PKA hyperphosphorylated (activated) I-1. This is predicted to render Serca2a more active and to increase Ca\(^{2+}\) loading of sarcoplasmic reticulum, leading to larger spontaneous Ca\(^{2+}\) release that may promote the occurrence of late after-depolarizations that trigger AF.
Comparison With Previous Studies
Although altered atrial Ca\(^{2+}\) homeostasis contributes to electrical and contractile remodeling in AF,\(^1\) the underlying cellular mechanisms are poorly understood. Current concepts propose that disturbed function of Ca\(^{2+}\) handling and myofilament proteins may result from changes in their phosphorylation levels. The higher PKA phosphorylation of RyR2 in cAF than in SR\(^{20}\) is associated with enhanced single RyR2 activity and larger spontaneous Ca\(^{2+}\) release from sarcoplasmic reticulum.\(^{21}\) This together with the larger influx of Ca\(^{2+}\) via \(I_{\text{Ca,L}}\) (less influx of Ca\(^{2+}\) per beat but more beats per time unit) is consistent with the Ca\(^{2+}\)-overload hypothesis in AF (Figure 8).\(^1\) Because cAF is associated with enhanced phosphorylation of PLB and reduced expression of sarcocin,\(^32\) another endogenous Serca2a inhibitor, Serca2a function is probably increased, compensating for the diastolic Ca\(^{2+}\) “leak” through RyR2 channels.\(^20\)

The greater phosphorylation of PLB at Thr-17 in cAF compared with SR despite increased total PP activity\(^5\) is consistent with the stronger stimulation of CAMKII at increased heart rates\(^3,33\) and the higher CAMKII\(\theta\) protein levels in cAF.\(^34\) The PKA hyperphosphorylation of PLB, however, was unexpected, because the increase in stimulation frequency does not affect the level of PKA phosphorylation at Ser-16.\(^3,33\) In addition, \(\beta\)-adrenoceptor density, G\(_{\alpha}\)-protein abundance, and adenylyl cyclase activity were not different between SR and cAF patients,\(^17,22,35\) which indicates similar PKA activity in SR and cAF.
Although modified phosphatase anchoring and reduced activity of cAMP-degrading phosphodiesterases may be involved,\textsuperscript{36,37} we suggest that the hyperphosphorylation of PLB and RyR2\textsuperscript{20} may result from diminished local PP1 function due to enhanced I-1 activity, because the atrial concentration of I-1 and the 10-fold higher PKA phosphorylation levels reflecting its enzymatic activity are sufficient to shut down PP1 activity at the PLB/Serca2a complex. These results support the notion of compartmentation of protein kinase/phosphatase signaling in the atrium and that sarcoplasmic reticulum–associated PP1 activity is lower in cAF than in SR patients.

In contrast to the situation at sarcoplasmic reticulum, PKA phosphorylation of MyBP-C at thick myofilaments was lower in cAF than in SR, whereas phosphorylation levels of Tn-I were similar in both groups. The 2 PKA sites of Tn-I are not phosphorylated exclusively by PKA but also by protein kinases C and G.\textsuperscript{38} Thus, increased activity of these kinases in cAF may counteract the higher PP activity at the thin myofilaments. Phosphorylation of MyBP-C by PKA increases the number of myosin heads simultaneously attaching to actin, enhances the maximum force development, and decreases myofibrillar Ca\textsuperscript{2+} sensitivity, accelerating relaxation.\textsuperscript{39} The lower PKA phosphorylation of MyBP-C in cAF may increase myofibrillar Ca\textsuperscript{2+} sensitivity\textsuperscript{4} and thus muscle stiffness, resulting in reduced force of contraction\textsuperscript{17,22,23} and slowed relaxation kinetics. Hence, the impaired myofilament function may contribute to the contractile dysfunction in cAF and mask the effect of increased Serca2a and NCX1 activity on relaxation kinetics.\textsuperscript{17} Further studies are needed to verify this hypothesis.

The increased total PP1 and PP2A activity in cAF appears to be the consequence of higher protein levels of the catalytic subunits, but it is unlike our previous finding of unaltered PP1\textsubscript{α} proteins in cAF.\textsuperscript{5} The reason for these inconsistent observations is currently unknown but may be due in part to an uncontrolled state of the cardiac diseases and/or patients’ medication.

Study Limitations

The present study did not address the signaling pathways that lead to higher PKA phosphorylation of I-1. Phosphorylation of I-1 at Ser-67 was unaltered in cAF, which renders a reduced contribution of this countervailing mechanism unlikely.\textsuperscript{12} One possible explanation could be related to the renin-angiotensin system. During AF, the atrial levels of angiotensin II increase,\textsuperscript{40} which may result in stronger activation of presynaptic AT\textsubscript{1}-receptors, with the concomitant release of norepinephrine from cardiac sympathetic nerve endings.\textsuperscript{41,42} Thus, the PKA hyperphosphorylation of I-1 may involve increased \(\beta\)-adrenoceptor signaling, with a concomitant increase in PKA activity.\textsuperscript{43}
However, the cAF patients in the present study had no indices of increased sympathetic tone and were not in clinical heart failure, which is consistent with the normal blood levels of catecholamines in AF patients. Further studies are required to identify the molecular mechanisms of higher PKA phosphorylation of I-1 in cAF.

The determination of I-1 proteins was limited by the small sample size, which does not allow for a direct extrapolation of the results to the general AF population. Finally, we cannot exclude that human atria in vivo express I-2 proteins that contribute to modified phosphorylation-dependent regulation in cAF.

Potential Clinical Implications

PP1 inactivates transcription factors and is a repressor of protein translation. Thus, the increased total PP1 and PP2A activity may contribute to modified protein expression in cAF. Consistently, the overexpression of PP1 and PP2A in mice resulted in ventricular hypertrophy, dilatation, and increased interstitial fibrosis, which were associated with reduced contractility.

To the best of our knowledge, the present study is the first study demonstrating expression and function (phosphorylation) of PP inhibitors in the atrium. Overexpression of constitutively active I-1 in mice reduced ventricular hypertrophy and fibrosis in heart failure models, which suggests that increased I-1 function could be protective. However, mice overexpressing the PKA catalytic subunit exhibit hyperphosphorylation of PLB and RyR2 and develop AF, and high basal PKA-dependent phosphorylation of PLB and RyR2 in rabbits drives rhythmic sarcoplasmic reticulum Ca\(^{2+}\) oscillations and spontaneous beating of cardiac pacemaker cells, which was attributable to activation of NCX1. Thus, restoration of sarcoplasmic reticulum–associated PP1 function may normalize leaky RyR2 channels.

The results of the present study point toward compartmentation of kinase/phosphatase signaling in the atrium (Figure 8). In cAF, increased total PP1 and PP2A activity is not translated into globally enhanced dephosphorylation of Ca\(^{2+}\)-handling and myofilament proteins. Although phosphorylation-dependent regulation of I\(_{Ca,L}\) and!
MyBP-C was impaired, Tn-I phosphorylation at thin myofilaments is apparently preserved. In contrast, phosphorylation of sarcoplasmic RyR2 and PLB is higher in cAF than in SR. This is most likely due to enhanced PKA phosphorylation and therefore activity of inhibitor-1 of PP1, which prevents their dephosphorylation. Although the higher PLB phosphorylation may prevent sarcoplasmic reticulum Ca\(^{2+}\) depletion, it could reinforce the leakiness of RyR2, promoting AF. Thus, the higher phosphorylation of RyR2 and PLB together with the upregulation of NCX1 (present study)\(^{17,21}\) may represent the molecular correlate of triggered activity mediated by late afterdepolarizations.\(^{49}\)

Figure 6. mRNA levels of I-1 and I-2 and detection/quantification of corresponding proteins in SR and cAF patients. A, Representative ethidium bromide–stained agarose gels and statistical analysis of I-1 and I-2 normalized to α-actin. Number in columns indicates number of patients. B, Top, Immunoblot to detect and quantify human I-1 protein (26 kDa) in TCA extracts from an SR patient (range of 1 to 8 μg) and increasing amounts of recombinant rat I-1 (30 kDa) for calibration. Note the species-dependent differences in size of I-1. Bottom, Immunoblot of I-2 (30 kDa) in TCA extracts with recombinant human I-2 as control. Recomb indicates recombinant.

Figure 7. Total and phosphorylation levels of I-1 at Thr-35 and Ser-67 in SR and cAF patients. A, Representative immunoblots and densitometric analysis of total, Thr-35–phosphorylated, and Ser-67–phosphorylated I-1 in TCA extracts (8 μg/lane). Same format as in Figure 1. *P<0.05 vs SR. B, Specificity of total, Thr35-, and Ser67-phosphorylated I-1 is shown. CSQ was internal control. HA indicates human atrium from cAF; ISO, isoproterenol; andCtl, recombinant I-1.

We identified impaired MyBP-C phosphorylation as a potential novel molecular mechanism for contractile dysfunction, which is one major contributor to atrial thrombogenesis. Because positive inotropic drugs exhibit low efficacy and cause arrhythmias, restoration of MyBP-C
phosphorylation may be a promising therapeutic target to improve atrial contractility in the postcardioversion period.

The clinical consequences of hyperphosphorylated PLB are difficult to predict. Although disruption of the PLB gene (equivalent to hyperphosphorylation of PLB) results in improved cardiac function in mice,^5^ increased Serca2a function may be associated with higher vulnerability to arrhythmias. Thus, the hyperphosphorylation of PLB and the putative increase in Serca2a function probably compensate in part for the reduced contractility but at the expense of an increased propensity for atrial arrhythmias. Further study in clinically relevant animal models will be needed to address this issue.

**Conclusions**

We provide evidence that the fine-tuning of kinases and phosphatases is disturbed in cAF, resulting in impaired phosphorylation of MyBP-C but hyperphosphorylation of PLB. The former appears to involve increased PP1 and PP2A activity and may contribute to contractile dysfunction; the latter probably results from reduced sarcoplasmic reticulum–associated PP1 activity due to increased function of its endogenous inhibitor I-1. This may also contribute to the reported hyperphosphorylation of RyR2 that results in leaky RyR2 channels in cAF. The results of the present study provide new insights into the phosphorylation-dependent regulation of sarcoplasmic reticulum and myofilament function in cAF, which may help to design new therapeutic options for AF treatment.

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**Disclosures**

None.

**References**


In chronic atrial fibrillation (cAF), abnormal Ca\(^{2+}\) handling contributes to the pathophysiology underlying both arrhythmogenesis and contractile dysfunction. The molecular mechanisms, however, are poorly understood. We hypothesize that cAF may be associated with altered expression levels or phosphorylation status of key regulatory proteins. Despite increased total activity of phosphatases, protein phosphorylation status was inhomogeneous in various cellular compartments. For instance, in the sarcoplasmic reticulum, phosphorylation of phospholamban was increased at the protein kinase A and Ca\(^{2+}\)-calmodulin protein kinase sites. Phospholamban phosphorylation increases Ca\(^{2+}\)-adenosine triphosphatase activity and causes Ca\(^{2+}\) overload of the sarcoplasmic reticulum, which results in spontaneous Ca\(^{2+}\) release that induces late afterdepolarizations that may trigger cAF. Thus, a reduction of phospholamban phosphorylation and the subsequent normalization of Ca\(^{2+}\)-adenosine triphosphatase function may represent a new therapeutic option for cAF treatment. In the myofilament compartment, on the other hand, we found reduced protein kinase A phosphorylation of myosin binding protein-C (MyBP-C). This regulatory protein is involved in the actin-myosin interaction, and reduced phosphorylation of MyBP-C is suggested to be a potential molecular mechanism for contractile dysfunction. Therefore, restoration of MyBP-C phosphorylation may be a promising therapeutic target for improvement of contractile function. Because reduced atrial contractility facilitates atrial thrombus formation, the associated risk of stroke in the postcardioversion period is expected to decline with this putative therapeutic concept.
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Ali El-Armouche, Peter Boknik, Thomas Eschenhagen, Lucie Carrier, Michael Knaut, Ursula Ravens and Dobromir Dobrev

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