Prevention of PKG1α oxidation augments cardioprotection in the stressed heart

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The cGMP-dependent protein kinase-1α (PKG1α) transduces NO and natriuretic peptide signaling; therefore, PKG1α activation can benefit the failing heart. Disease modifiers such as oxidative stress may depress the efficacy of PKG1α pathway activation and underlie variable clinical results. PKG1α can also be directly oxidized, forming a disulfide bond between homodimer subunits at cysteine 42 to enhance oxidant-stimulated vasorelaxation; however, the impact of PKG1α oxidation on myocardial regulation is unknown. Here, we demonstrated that PKG1α is oxidized in both patients with heart disease and in rodent disease models. Moreover, this oxidation contributed to adverse heart remodeling following sustained pressure overload or Gq agonist stimulation. Compared with control hearts and myocytes, those expressing a redox-dead protein (PKG1αC42S) better adapted to cardiac stresses at functional, histological, and molecular levels. Redox-dependent changes in PKG1α altered intracellular translocation, with the activated, oxidized form solely located in the cytosol, whereas reduced PKG1αC42S translocated to and remained at the outer plasma membrane. This altered PKG1α localization enhanced suppression of transient receptor potential channel 6 (TRPC6), thereby potentiating antihypertrophic signaling. Together, these results demonstrate that myocardial PKG1α oxidation prevents a beneficial response to pathological stress, may explain variable responses to PKG1α pathway stimulation in heart disease, and indicate that maintaining PKG1α in its reduced form may optimize its intrinsic cardioprotective properties.

Introduction

Cyclic GMP (cGMP) and its principal effector PKG transduce NO and natriuretic peptide signaling to regulate cardiac and vascular function (1). In the heart, PKG activation suppresses adverse responses to a broad range of pathological cardiac stresses (2–4). These benefits have driven efforts to leverage PKG signaling for the treatment of heart failure, activating the kinase by stimulating cGMP synthesis, reducing natriuretic peptide proteolysis, and/or blocking cGMP hydrolysis (5, 6).

Despite enthusiasm for the therapeutic potential of PKG enhancement strategies, their impact has been somewhat variable, raising concerns that cGMP/PKG signaling may become blunted by disease modifiers such as oxidative stress (7), which depresses NO (7) and cGMP synthesis (8, 9). Studies have also shown that oxidative stress impacts PKG1α, the primary cardiovascular isoform. PKG1α is a homodimeric serine/threonine kinase containing protein interactive (leucine zipper), autoinhibitory, and cGMP-binding domains in the N terminus and a catalytic domain in the C terminus (10). Classical activation occurs upon cGMP binding to regulatory sites, releasing autoinhibition; however, the kinase can also be stimulated by oxidation at cysteine 42 (C42), forming an intermolecular disulfide bond (11). As this cysteine lies at the proximal end of the leucine zipper, it may also influence protein interactions and localization. In resistance arteries, PKG1α oxidation transduces endothelium-derived hyperpolarizing factor to induce vasorelaxation (11, 12), and mice harboring a knockin redox-dead mutation (PKG1αC42S, abbreviated herein as KI) develop modest hypertension (12). Here, we reveal that in the heart, PKG1α oxidation impairs its cardioprotective effects against pathological stress. This is linked to redox-sensitive changes in intracellular localization and protein targeting of the kinase, diminishing the ability of PKG1α to counter prohypertrophic and profibrotic pathways.

Results and Discussion

PKG1α C42 oxidation occurs in heart disease and worsens the cardiac response to pressure overload. PKG1α oxidation increased in human ischemic heart failure (Figure 1A and see patient characteristics in Supplemental Table 1; supplemental material available online with this article; doi:10.1172/JCI80275S1), and similar increases were observed in mouse hearts exposed to sustained pressure overload (Supplemental Figure 1A) and in canine dilated cardiomyopathy (Supplemental Figure 1B). Hearts expressing PKG1αC42S only formed the monomer (Supplemental Figure 1A), confirming that its appearance in nonreducing gels indeed reflects C42 dimerization. To test whether PKG1α oxidation alters the cardiac response to stress, KI and littermate control mice were subjected to chronic transaortic constriction (TAC). TAC induced chamber dilation, contractile depression, ventricular hypertrophy, interstitial fibrosis, and lung edema, and all were blunted in PKG1αC42S-KI mice (Figure 1, B and C, and Supplemental Figures 2 and 3). The blunted organ-level structural and functional disease was accompanied by suppressed fetal gene reexpression (Supplemental Figure 4) and blunted pathological signaling cascades, including calcineurin/nuclear factor of activated T cells (Cn/NFAT), calcium/calmodulin-activated kinase II (CaMKII) activation, and natriuretic peptide proteolysis, and/or blocking cGMP hydrolysis (5, 6).
baseline. However, after a 10-minute exposure to H$_2$O$_2$, both forms of PKG1$\alpha$ translocated to the sarcolemmal membrane (Figure 3A), whereas after 1 to 2 hours of exposure, WT PKG1$\alpha$ was again cytosolic, while PKG1$\alpha$C42S remained predominantly at the membrane. This disparity was also observed in myocytes isolated from 3-week-old TAC hearts (Figure 3B). PKG1$\alpha$ relocalization was confirmed by subfractionation immunoblots (Supplemental Figure 7), in which the H2O$_2$-induced (60 minutes) PKG1$\alpha$ dimer appeared only in the cytosol, whereas the reduced monomer appeared in both the cytosol and membrane. This disparity was unaltered by blocking PKG1$\alpha$ activity with DT3, so it was independent of kinase activity.

**Coupling of differential localization of PKG1$\alpha$ to antihypertrophic molecular targeting.** Plasma membrane–localized PKG1$\alpha$C42S could potentially augment antihypertrophic signaling by enhancing its targeting of disease-related proteins at this location. We tested this in neonatal rat cardiomyocytes (NRCMs) expressing WT or C42S-mutant PKG1$\alpha$ (adenoviral infection) that were then exposed to 48 hours of endothelin 1 (ET1) or phenylephrine (PE). The dominant form of PKG1$\alpha$ was provided by the transgene, and this cellular model recapitulated the in vivo findings, including lack of dimer formation (Supplemental Figure 8), sustained plasma membrane localization, and suppression of myocyte hypertrophic

(CaMKII), AKT, and ERK1/2 (Figure 2, A–D). Cardioprotection occurred without an overall decline in oxidative stress, as the myocardial ratio of reduced glutathione/oxidized glutathione and lipid peroxidation (malondialdehyde [MDA] and 4-hydroxyalkenals [4-HAE]) were similar in both genotypes (Figure 2E).

**Myocyte PKG1$\alpha$ oxidation controls its sarcolemmal membrane translocation.** While previous studies predicted that PKG1$\alpha$ oxidation would increase activity (12), an in vitro kinase assay analysis yielded similar increases in activity in both WT and KI TAC myocardium (Supplemental Figure 5A). The lack of apparent enhanced activity despite PKG1$\alpha$ oxidation may be due in part to assay limitations (see Supplemental Methods) but most likely relates to higher cGMP levels (Supplemental Figure 5B) that blunt oxidative activity change (11, 13). This effect was confirmed in isolated myocytes exposed to 10 minutes of H$_2$O$_2$ (10 mM, dose response in Supplemental Figure 6A), where increased in vitro activity was detected if cGMP levels were low, but not when they became elevated (Supplemental Figure 6B). Expression of PKG1$\alpha$C42S prevented H$_2$O$_2$-stimulated activation (Supplemental Figure 6, B and C).

An alternative mechanism for altering PKG1$\alpha$ functionality is a change in intracellular localization. IHC showed that both WT and C42S PKG1$\alpha$ proteins were diffusely distributed in adult myocytes at baseline. However, after a 10-minute exposure to H$_2$O$_2$, both forms of PKG1$\alpha$ translocated to the sarcolemmal membrane (Figure 3A), whereas after 1 to 2 hours of exposure, WT PKG1$\alpha$ was again cytosolic, while PKG1$\alpha$C42S remained predominantly at the membrane. This disparity was also observed in myocytes isolated from 3-week-old TAC hearts (Figure 3B). PKG1$\alpha$ relocalization was confirmed by subfractionation immunoblots (Supplemental Figure 7), in which the H2O$_2$-induced (60 minutes) PKG1$\alpha$ dimer appeared only in the cytosol, whereas the reduced monomer appeared in both the cytosol and membrane. This disparity was unaltered by blocking PKG1$\alpha$ activity with DT3, so it was independent of kinase activity.

Coupling of differential localization of PKG1$\alpha$ to antihypertrophic molecular targeting. Plasma membrane–localized PKG1$\alpha$C42S could potentially augment antihypertrophic signaling by enhancing its targeting of disease-related proteins at this location. We tested this in neonatal rat cardiomyocytes (NRCMs) expressing WT or C42S-mutant PKG1$\alpha$ (adenoviral infection) that were then exposed to 48 hours of endothelin 1 (ET1) or phenylephrine (PE). The dominant form of PKG1$\alpha$ was provided by the transgene, and this cellular model recapitulated the in vivo findings, including lack of dimer formation (Supplemental Figure 8), sustained plasma membrane localization, and suppression of myocyte hypertrophic

**Figure 1. PKG1$\alpha$ oxidation at C42 increases in failing and hypertrophied myocardium, and its prevention protects the heart against pressure overload.**

(A) PKG1$\alpha$ disulfide dimer formation was increased in human heart failure ($n = 7$–8/group, *$P < 0.001$). D, PKG1$\alpha$ dimer; HF, heart failure; M, PKG1$\alpha$ monomer; NF, nonfailing. (B) An example of M-mode echocardiograms from PKG1$\alpha$C42S and littermate controls subjected to TAC and summary data for fractional shortening ($n = 9$–10, WT sham; $n = 17$–19, WT TAC; $n = 9$–10, KI sham; $n = 20$–23, KI TAC). Sham data were superimposable and thus combined for 2-way ANOVA interaction between TAC and genotype; ANOVA results: *$P < 0.005$ versus sham and KI TAC; †$P < 0.01$ versus sham. (C) Histopathology (wheat germ agglutinin [WGA] and Masson’s trichrome) shows larger heart and myocyte size and fibrosis in WT versus PKG1$\alpha$C42S after TAC. Left ventricular cross-sectional myocyte area and interstitial fibrosis ($n = 6$, sham; $n = 8$, TAC). *$P < 0.001$ versus baseline; †$P < 0.01$ versus baseline. $P$ values show 2-way ANOVA interaction between TAC and genotype. CSA, cross-sectional area.
signaling in PKG1αC42S-expressing cells (Supplemental Figures 9 and 10). Enhanced cytoprotection was lost by adding DT3, confirming the need for PKG activation. As in the myocardium, cellular PKG1α activity measured in vitro was similar in cells expressing WT or PKG1αC42S protein (Supplemental Figure 11).

We next tested whether membrane-localized PKG1α-targeted proteins were preferentially impacted by PKG1αC42S, focusing on 3 known candidates. Regulator of G protein signaling (RGS) RGS2 and RGS4 bind to and are activated by PKG1α, blunting the hypertrophy and dilation otherwise induced by Gq activation and mechanical stress (14, 15). To test whether reduced PKG1α favored RGS2/4 activation, one or both RGS genes were suppressed by siRNA (Supplemental Figure 12A). However, the relative protective response from C42S PKG1α persisted, regardless of RGS2 or RGS4 suppression (Supplemental Figure 12B), and the PKG1α redox state did not impact protein PKG1α-RGS2 binding (Supplemental Figure 12C); thus, this was not the mechanism. A third major candidate is the transient receptor potential canonical channel type 6 (TRPC6), which is activated by Gq-coupled stimuli to trigger Cn/NFAT signaling (16). TRPC6 is also phosphorylated by PKG, blunting its conductance and stimulation of hypertrophy and fibrosis (17, 18). To test its role, NRCMs were incubated with a selective TRPC3/6 antagonist (GSK503A). ET1-stimulated hypertrophic signaling was substantially blocked by GSK503A (Figure 3C and Supplemental Figure 13A) in controls, whereas cells expressing PKG1αC42S had a blunted ET1 response that was not further altered by adding GSK503A (P < 0.001 for interaction between GSK503A treatment and the PKG1α genotype). TRPC6 inhibition also reduced Cn, CaMKII, and ERK1/2 activation (Figure 3D and Supplemental Figure 13B) in WT PKG1α-expressing cells, but had less effect in cells expressing PKG1αC42S (P < 0.01 for interaction). These results indicated that TRPC6-dependent signaling was blunted more if PKG1α oxidation was prevented.

PKG1α phosphorylates TRPC6 at T70 and S322 (for human; T69 and S321 for mouse) (18). Accurate detection of either modification in myocardium or myocytes remains difficult because of assay limitations. As an alternative, myocytes were coinfected with either WT TRPC6 or a phosphosilenced mutant (TRPC6 T70A,S322Q), the latter preventing TRPC6 modulation by PKG (18). Cells expressing either form of PKG1α were then exposed to ET1. Baseline hypertrophic gene expression was similar in all groups (Figure 3E), and ET1 induced similar increases in cells expressing WT PKG1α, regardless of the form of TRPC6. However, TRPC6T70A,S322Q selectively increased ET1 responses in PKG1αC42S-expressing cells, returning them toward WT PKG levels (P < 0.01, PKG1α and TRPC6 genotype interaction). Thus, PKG1αC42 oxidation blunts its targeting and suppression of TRPC6 and associated signaling, whereas keeping PKG1α reduced more effectively blocks the pathway.

Figure 2. Prevention of PKG1α C42 oxidation blocks maladaptive signaling due to pressure overload, without altering global myocardial oxidative stress. (A) Gene expression of regulator of calcineurin 1 (Rcan1) and (B) protein levels of Cn. (C) Representative gels for phosphorylated and total proteins for CaMKII, AKT, and ERK1/2 in sham and 3-week-old TAC hearts and (D) summary data (n = 6/group). (E) Ratio of reduced glutathione/oxidized glutathione (GSH/GSSG) (n = 6, WT; n = 8, KI) and MDA and 4-HAE (n = 6, WT; n = 12, KI). *P < 0.001, †P < 0.01, ‡P < 0.001, and §P < 0.05 versus respective controls. P values shown relate to the genotype interaction effect on the TAC-stimulated response. p-, phosphorylated; t-, total; TAC × genotype, interaction between TAC and genotype.
This study reveals what we believe to be a novel mechanism for oxidative stress--mediated dysfunction in the stressed heart and myocytes involving PKG1α oxidation and consequent changes in its intracellular targeting. This differs from a net gain of function from the PKG1α oxidation observed in resistance vessels (12, 13) that has been attributed to cGMP-independent kinase activity (11) revealing increased substrate-binding affinity from oxidation. However, oxidative activation was reduced when cGMP was increased (11, 13), likely due to physical separation of N terminus domains following the binding of cGMP to its regulatory sites (19).

Here, we reveal an alternative mechanism for PKG1α functionality, namely a change in intracellular targeting that is likely due to modification of leucine zipper domain interactions (20). This concept is supported by results in KI mice expressing a PKG1α leucine zipper–deficient protein, which display worsened stress cardiomyopathy (21) despite unaltered in vitro PKG kinase activity (22).

Membrane translocation of PKG1α occurs in smooth muscle (23) and cardiomyocytes (14), where it facilitates suppression of Gq-coupled signaling by RGS2 and RGS4. However, this relocalization and protection is transient (14), and the current results show how PKG1α oxidation could explain this time course. Though we did not find favored interactions between PKG1αC42S and RGS2 or RGS4, results supporting enhanced targeting of TRPC6 were obtained. In addition to Gq-coupled (17, 18) and mechanical stimulation (24), TRPC6 is indirectly stimulated by cGMP (19, 25, 26). This study reveals what we believe to be a novel mechanism for oxidative stress–mediated dysfunction in the stressed heart and myocytes involving PKG1α oxidation and consequent changes in its intracellular targeting. This differs from a net gain of function from the PKG1α oxidation observed in resistance vessels (12, 13) that has been attributed to cGMP-independent kinase activity (11) revealing increased substrate-binding affinity from oxidation. However, oxidative activation was reduced when cGMP was increased (11, 13), likely due to physical separation of N terminus domains following the binding of cGMP to its regulatory sites (19).

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oxidative stress that involves oxidation of another previously unidentified intracellular protein (25). Reduced channel suppression by PKGII α oxidation fits this observation. Redox sensitivity of PKGII α suppression of TRPC6 may also have therapeutic implications beyond the heart, including in dystrophinopathies (24) and glomerulosclerosis (26, 27), where ROS and TRPC6 play a pathophysiological role. Future studies are needed to identify the protein partners that control PKGII α translocation and develop strategies to selectively sustain its reduced state to maximize the efficacy of its activation against myocardial disease.

Methods

Mice expressing the PKGII α C42S mutant as a global Ki were generated on a C57BL/6 background as previously described (12) and compared with littermate controls. Pressure overload was induced by TAC (3), with serial echocardiography used to assess intact heart function. Postmortem tissue was analyzed for molecular signaling and histology. A cell-based model was also used, involving isolated NRMCs infected with adenovirus expressing either WT or C42S-mutant PKGII α.

Statistics

Statistical analysis included 1- or 2-way ANOVA, analysis of covariance, and paired tests with nonparametric analysis when required. Complete experimental and statistical methods are provided in the supplemental materials.

Study approval.

All procedures were performed in accordance with institutional and NIH guidelines for the care and use of animals in biomedical research and were approved by the IACUC of the Johns Hopkins Medical Institutions.

Acknowledgments

This work was supported by NIH grants HL-119012, HL-093432, HL-114910, HHSN268201000032C, and HL-107153; the Fonda- tion Leducq Transatlantic Network of Excellence, Abraham and Virginia Weiss and Michael and Janet Huff Endowments (to D.A. Kass); National Heart, Lung, and Blood Institute (NHLBI) grant RO1-GM090161 (to C. Kim); an American Heart Association Mid-Atlantic Fellowship Grant (to T. Nakamura and D.I. Lee); a Japan Heart Foundation/Bayer Yakuhin Research Grant Abroad (to T. Nakamura), NHLBI grant T32-HL-07227 (to M.J. Ranek); the Sarnoff Foundation (to V. Shalkey Hahn); and British Heart Foundation grant RG/12/12/29872 (to P. Eaton). The authors thank Kenneth Margulies for providing the human myocardial samples.

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