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# Prevention of Protein Kinase G-1a Oxidation Suppresses Anti-Hypertrophic/Anti-fibrotic Effects from PDE5 Inhibition but not sGC Stimulation

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# Abstract

**Background**—Stimulation of soluble guanylate cyclase (sGC) or inhibition of phosphodiesterase type-5 (PDE5) activates protein kinase G-1a (PKG1a) to counteract cardiac hypertrophy and failure. PKG1a acts within localized intracellular domains; however, its oxidation at cysteine-42, linking homo-monomers, alters this localization, impairing suppression of pathological cardiac stress. Since PDE5 and sGC reside in separate micro-domains, we speculated that PKG1a oxidation might also differentially influence the effects from their pharmacological modulation.

**Methods and Results**—Knock-in mice expressing a redox-dead PKG1a (PKG1a<sup>C42S</sup>) or littermate controls (PKG1a<sup>WT</sup>) were subjected to trans-aortic constriction (TAC) to induce pressure-overload, and treated with a PDE5 inhibitor (sildenafil, SIL), sGC activator (BAY-602770, BAY), or vehicle. In PKG1a<sup>WT</sup> controls, SIL and BAY similarly enhanced PKG activity and reduced pathological hypertrophy/fibrosis and cardiac dysfunction after TAC. However, SIL failed to protect the heart in PKG1a<sup>C42S</sup>, unlike BAY, which activated PKG and thereby facilitated protective effects. This corresponded with minimal PDE5 activation in PKG1a<sup>C42S</sup> TAC versus higher activity in controls, and little colocalization of PDE5 with PKG1a<sup>C42S</sup> (versus co-localization with PKG1a<sup>WT</sup>) in stressed myocytes.

**Conclusions**—In the stressed heart and myocytes, PKG1a C42 disulfide formation contributes to PDE5 activation. This augments the pathological role of PDE5 and so in turn enhances the therapeutic impact from its inhibition. PKG1a oxidation does not change the benefits from sGC activation. This finding favors the use of sGC activators regardless of PKG1a oxidation, and may help guide precision therapy leveraging the cGMP/PKG pathway to treat heart disease.

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heart failure; cyclic GMP; protein kinase G; hypertrophy; pharmacology; oxidative stress

# Introduction

Despite many advances in therapy, heart failure (HF) continues to exact an enormous human, societal, and economic toll, and remains a leading cause of hospitalization, morbidity and mortality<sup>1</sup>. Among potential new therapies under active investigation are novel stimulators of the cyclic guanosine monophosphate (cGMP)-dependent protein kinase-1a (PKG1a) signaling system<sup>2-5</sup>. This pathway is long known for its vasodilatory role in pulmonary and systemic arterial beds, and has historically been leveraged to unload the right and/or left ventricles and reduce pulmonary congestion. PKG1a also confers direct myocardial effects<sup>6</sup>, where it serves as a counter-brake to blunt pathological hypertrophy and fibrotic pathways<sup>7-10</sup> while also improving calcium homeostasis and reducing myocyte stiffness<sup>11, 12</sup>. As methods to stimulate PKG1a have expanded, leveraging the therapeutic potential of these myocardial effects has become more feasible.

Cyclic GMP is generated by soluble guanylate cyclase (sGC) activated by nitric oxide (NO) and by particulate GC downstream of natriuretic peptides. Inhibition of selective phosphodiesterases such as PDE5 can also elevate cGMP levels<sup>13</sup> to engage PKG1a signaling. Acute studies in humans have employed both approaches and reported improvements in rest and exercise physiology in HF patients, including those with reduced (HFrEF) or preserved (HFpEF) ejection fraction<sup>5, 14, 15</sup>. Chronic PDE5 inhibition (PDE5-I) has benefited patients with dilated HF in some studies<sup>14</sup>, but not those with HFpEF<sup>4, 16</sup>. A Phase II trial with sGC stimulation by vericiguat yielded some potential results with HFrEF, less so in HFpEF<sup>2, 3</sup>. These findings motivated the current Phase III multicenter trial of this compound for HFrEF (NCT02861534).

A question raised by these variable responses to PDE5 inhibitors versus sGC stimulators is whether these methods of activating PKG1 $\alpha$  are interchangeable, or if one method may be particularly more useful in the context of a certain underlying heart disease.

A major factor that impacts both cGMP synthesis and PKG1a signaling is oxidative stress. Oxidation of NO synthase reduces NO generation to favor synthesis of superoxide, and contributes to pathological cardiac remodeling, dysfunction, and vascular disease<sup>17, 18</sup>. Oxidation of sGC lessens its NO response to compromise cGMP synthesis<sup>19</sup>. PKG1a can be oxidized at cysteine 42 to form a disulfide bond between homo-dimer subunits<sup>20</sup>. In resistance arteries, this provides a vasodilatory mechanism in response to  $H_2O_2^{21}$ . However, in myocardium, C42-oxidation reduces the capacity of PKG1a activation to counter hormone, hemodynamic<sup>22</sup>, and cardiotoxic stress<sup>23</sup>. We found this was related to a plasmamembrane localization of PKG1a when the kinase is activated in a reduced form as opposed to a diffuse distribution when it becomes oxidized. Such membrane localization favors PKG1a targeting of critical proteins at the plasma membrane that are coupled to HF pathophysiology, enhancing its ameliorative impact<sup>22</sup>.

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As the proteins synthesizing or hydrolyzing cGMP are also compartmentalized<sup>13, 24</sup>, redoxcontrolled relocalization of PKG1a might also alter its activation by different pharmacological methods to produce variable cardiac responses. The present study tests this hypothesis using intact mouse and cellular models, and compares the outcome and signaling of a selective PDE5 inhibitor versus sGC activator under each redox state of PKG1a. We reveal that the therapeutic impact of PDE5-I to block pathological stress is greatly hampered in myocytes and intact hearts expressing a redox-dead PKG1a<sup>C42S</sup>, whereas the efficacy of sGC stimulation is unaltered by the oxidative status of PKG1a.

# Methods

The data, analytic methods, and study materials will be made available to other researchers for purposes of reproducing the results or replicating the procedure. This would be accomplished upon reasonable and direct request with the corresponding author, and data transmitted via a secured server by email.

### **Experimental Models**

The study procedures were approved by the Johns Hopkins Animal Care and Use Committee in accordance with NIH guidelines. PKG1a<sup>C42S</sup> knock-in mice were generated on a C57BL6 background as previously reported<sup>21</sup>. Male mutant and littermate controls (WT) matched for body size were randomly assigned to experimental groups. Mice were subjected to 3-weeks of pressure overload from trans-aortic constriction (TAC, 7-0 prolene snare sized to a 27G needle)<sup>18</sup>. Surgical controls were subjected to a sham operation. Drug treatments were randomized between a PDE5-inhibitor (sildenafil; 200 mg/kg/day in Bio-Serv soft rodent chow), soluble guanylate cyclase activator (BAY602770; 0.3 mg/kg/day by oral gavage dissolved in Transcutol:Cremophor:water, 1:2:7 volume ratio), or to a corresponding vehicle. BAY602770 is an sGC heme-independent activator similar in action to cinaciguat<sup>25</sup> but different from riociguat or vericiguat that are heme-dependent sGC stimulators<sup>26</sup>. The dose of BAY602770 was selected as the highest that had no impact on arterial blood pressure in chronically treated mice (Supplemental Figure 1). The sildenafil dose has been shown to be appropriate to achieve therapeutic free plasma concentrations in mice<sup>8</sup>, and also has no impact on arterial pressure. Serial echocardiography performed in conscious mice (Acuson Sequoia C256, 13-MHz; Siemens) provided indexes of LV chamber size and function<sup>18</sup>. In our mice, resting LV morphometry and function are nearly identical between both PKG genotypes at the age studied (3-4 months, Supplemental Figure 2) and even at one year (Supplemental Figure 3)<sup>22</sup>. Data analysis was performed blinded to treatment and genotype.

# **Isolated Myocyte Studies**

Neonatal rat ventricular myocytes (NRVMs) were freshly isolated, and cultured for 24 hours before being infected with recombinant adenovirus (AdV) encoding human FLAG-tagged PKG1a<sup>WT</sup> or PKG1a<sup>C42S</sup> as described<sup>22</sup>. In other studies, NRVMs were co-infected with AdV expressing WT PDE5A, a PKG-phospho-mimetic PDE5 (S92D), or phospho-null PDE5 (S92A). These forms were generated from mouse lung cDNA subcloned into a pDsRed-C1 vector (Clontech)<sup>27</sup>. Twenty-four hours after infection, myocytes were

stimulated with ET1 (10 nM) in serum-free DMEM media supplemented with 0.1% Insulin-Transferrin-Selenium (Life Technologies) for 48 hours. Adult myocytes were also studied as previously described<sup>27</sup>, isolated from PKG1 $\alpha$ <sup>WT</sup> or PKG1 $\alpha$ <sup>C42S</sup> hearts and exposed to 8pCPT-cGMP (100  $\mu$ M) ± sildenafil (1  $\mu$ M) for 15 minutes with or without the selective PKG1 $\alpha$  inhibitor DT3 (1  $\mu$ M). Myocytes were washed in 1× PBS and flash-frozen as pellets. Lysates were probed by immunoblot for total or phosphorylated PDE5.

#### Myocardial Analysis

Details of tissue histological and molecular assays for gene and protein expression and phosphorylation are provided in an online supplement.

#### **Statistical Analysis**

Data in figures are presented as mean  $\pm$  SD unless otherwise noted. The *in vivo* treatment protocols, were performed in separate cohorts, and therefore the analysis was performed within each genotype using a mixed factorial ANOVA with cohort and intervention serving as grouping variables, followed by post-hoc hypothesis testing between interventions using a Tukey test for multiple comparisons. Additional pair-wise testing between gene groups was performed using a Mann-Whitney test with a multiple comparisons correction (Bonferroni). For isolated tissue and cell culture analysis, 1- or 2-way ANOVA, or t-tests were used, or if groups failed normality testing or had significantly different variances (Brown-Forsythe test), a non-parametric Kruskal Wallis or Mann Whitney test was used. Sample size and statistical methods and results are provided in each figure and associated legends. Statistical analysis was performed using Systat Version 10 or GraphPad Ver. 7 software.

### Results

#### PKG1a C42-oxidation is needed for PDE5-I but not sGC activation to counter TAC

PKG1a<sup>C42S</sup> and littermate PKG1a<sup>WT</sup> controls were subjected to trans-aortic constriction (TAC) and treated with the PDE5 inhibitor sildenafil (SIL), sGC activator (BAY), or vehicle. In PKG1a<sup>WT</sup> mice, 3-weeks of TAC doubled LV mass as measured by echocardiography and post-mortem analysis (Fig. 1A, 1B, Supplemental Table). Cardiac hypertrophy declined with either SIL or BAY treatment (e.g. for measured LV mass: -51% and -58% of the increase from TAC alone respectively, both p<0.0001, p=NS versus each other). TAC stimulated 45% less hypertrophy in PKG1a<sup>C42S</sup> mice (p<0.001), as previously observed<sup>22</sup>, though this still was significantly above sham control. In PKG1a<sup>C42S</sup> mice however, SIL did not reduce heart mass (+5%, p=NS), whereas it was diminished by BAY (-35%, p<0.03; red symbols, Fig 1A, 1B). The differential effects of the two drugs on LV mass between genotypes corresponded with molecular markers of pathological hypertrophy (B-type natriuretic peptide (Nppb), and regulator of calcineurin-1 (Rcan1), Supplemental Fig 4). We observed similar disparities on indexes of cardiac function (Fig 1C) and chamber dilation (Fig. 1D); SIL and BAY improved both in PKG1a<sup>WT</sup> after TAC, but only BAY did so in PKG1a<sup>C42S</sup>. TAC stimulated myocardial fibrosis significantly more in PKG1a<sup>WT</sup> than PKG1a<sup>C42S</sup> hearts, and here too, SIL suppressed fibrosis only in PKG1a<sup>WT</sup>, whereas BAY did so in both models (Fig. 1E, 1F, Supplemental Figure 5). Thus, PDE5-I counters cardiac

pathophysiology induced by TAC so long as PKG1a oxidation at C42 can occur. By contrast, sGC activation is effective independent of this oxidative modification.

#### Preventing PKG1a C42-oxidation blunts PDE5 and corresponding PKG activation

A potential mechanism to explain why SIL is only effective in TAC hearts expressing WT but not  $PKG1a^{C42S}$  relates to the impact of cGMP on the probability of forming the C42-dimer<sup>23</sup>. Binding of cyclic GMP to the regulatory domain of PKG1a leads to physical separation of the N-terminus monomers, reducing the probability of forming a disulfide between C42 residues<sup>28</sup>. As PDE5 inhibition increases cGMP by decreasing its hydrolysis, it could impede PKG1a oxidation and thereby benefit the heart against stress. However, this mechanism would not alter  $PKG1a^{C42S}$  hearts since dimerization is already prevented by the mutation. If true, then SIL treatment should reduce the PKG1a dimer/monomer ratio in WT after TAC. We examined this and found no change in dimer/monomer ratio from SIL in TAC hearts (Fig. 2A). As previously shown<sup>22</sup>, there was no dimer present in  $PKG1a^{C42S}$ .

An alternative explanation for why SIL is ineffective in PKG1a<sup>C42S</sup> mice is that it does not augment PKG1a activity so long as C42-dimerization is prevented. In vitro myocardial PKG1a activity was similarly elevated in both genotypes after TAC (Fig. 2B). However, whereas TAC+SIL increased PKG1a activity further in PKG1a<sup>WT</sup>, it had no impact in PKG1a<sup>C42S</sup> mice. By contrast, BAY treatment increased PKG1a activity similarly in both genotypes (Fig 2B). We tested if the disparity in SIL activation of PKG1a might be due to less PDE5 expression in PKG1a<sup>C42S</sup>-TAC hearts. However, while TAC increased PDE5 expression modestly, it did so similarly in both models (Fig. 2C, supplemental Figure 6), so this could not explain the disparities. PDE5 activity is also regulated post-translationally, and activity increased after TAC only in PKG1a<sup>WT</sup> mice (Fig. 2D). This lack of PDE5 activation in PKG1a<sup>C42S</sup> would be anticipated to blunt the impact of PDE5-I therapy.

#### PKG1a C42-disulfide enhances PDE5 phosphorylation and thus activation

To further probe mechanisms underlying the lack of SIL responsiveness in PKG1a<sup>C42S</sup>-TAC, we turned to a cell-based model. Neonatal rat ventricular myocytes (NRVMs) were infected with adenovirus that expressed WT or C42S mutant PKG1a, and then were exposed to 48-hours of endothelin-1 (ET-1). This hypertrophic stress stimulated *Nppb* and *Rcan1* gene expression (markers of pathological hypertrophy), but induction was less in PKG1a<sup>C42S</sup> versus PKG1a<sup>WT</sup> expressing cells (Fig. 3A, 3B). Both SIL and BAY suppressed gene expression when PKG1a<sup>WT</sup> was expressed, but only BAY did so when PKG1a<sup>C42S</sup> was expressed, recapitulating the *in vivo* disparities (Fig. 3C). Similar findings were obtained with phenylephrine as the hypertrophic agonist (Supplemental Figure 7). We then tested if SIL or BAY augmented cGMP to the same level independent of the form of PKG1a<sup>WT</sup>; however, SIL was somewhat less effective than BAY in PKG1a<sup>C42S</sup> (Fig. 3D).

Myocytes expressing either PKG1a<sup>WT</sup> or PKG1a<sup>C42S</sup> were next exposed to the cGMPanalog 8-p*CPT*-cGMP in combination with hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>, 10  $\mu$ M, for 20 minutes), the latter inducing C42-dimerization<sup>22</sup>. We again found PDE5 to be activated only in cells expressing PKG1a<sup>WT</sup> (Fig. 4A) despite similar PKG stimulation (Fig. 4B).

Administering cGMP alone without  $H_2O_2$  resulted in similar increases in PDE5 and PKG activity independent of the form of PKG1a expressed (Supplemental Figure 8). Thus, oxidation was required to observe the disparate response due to PKG1a redox genotype.

PDE5 activity is increased by cGMP binding to a regulatory domain in the N-terminus (GAF domains) and by PKG-dependent phosphorylation at serine-92<sup>29, 30</sup>. This provides a negative feedback loop whereby cGMP/PKG activation results in greater PDE5 activity to counter PKG. SIL stimulated slightly less cGMP in PKG1a<sup>C42S</sup> expressing cells, so this might contribute to reduced PDE5 activity. Serine-92 phosphorylation could also play a role, and this was tested in adult myocytes, where we indeed found SIL increased S92 phosphorylation only in cells that expressed PKG1a<sup>WT</sup> (Fig. 4C). This change was prevented by co-incubation with the PKG inhibitor DT3, supporting involvement of the kinase. To test the functional impact of S92 phosphorylation on hypertrophic modulation by SIL, cardiomyocytes expressing either normal PDE5<sup>WT</sup>, or a mutated phospho-silenced (PDE5<sup>S92A</sup>) or phospho-mimetic (PDE5<sup>S92D</sup>) form, were exposed to 48-hours of ET1 with or without SIL. When PDE5<sup>WT</sup> or PDE5<sup>S92A</sup> was expressed, SIL blocked the hypertrophic response. However, this did not happen if PDE5<sup>S92A</sup> was expressed (Fig. 4D). Thus, the lack of S92 phosphorylation of PDE5 in cells expressing PKG1a<sup>C42S</sup> would be anticipated to lessen PDE5 activity, and thus reduce the impact of SIL on blunting hypertrophy.

# PDE5 co-localizes with oxidized PKG1 $a^{WT}$ more than with PKG1 $a^{C42S}$

To determine if PDE5 and PKG1a interact physically in a manner that hinges on PKG1a oxidation state, we performed immunoprecipitation from NRVMs, pulling down FLAG-tagged PKG1a (WT or C42S) and probing for PDE5. PDE5 co-precipitated with PKG1a, particularly with the addition of  $H_2O_2$  or cGMP +  $H_2O_2$ . However, this increase was independent of C42-dimerization (i.e. oxidation; Fig. 4E, 4F), so changes in protein-protein interaction were unlikely to explain the results.

An alternative is a change in protein sub-cellular localization that can be missed in an immunoprecipitation assay. We previously reported that PKG1a<sup>C42S</sup> translocates to and remains primarily at the outer plasma membrane when cells or hearts are subjected to oxidant, hormone, or hemodynamic stress<sup>22</sup>. By contrast, oxidized WT PKG1a adapts a diffuse cytosolic distribution. Under normal conditions PDE5 is cytosolic, exhibiting a banding pattern coinciding with the Z-band protein a-actinin, but it becomes more diffuse when cells or hearts are stressed<sup>31</sup>. By contrast, sGC resides both in the cytosol and in the plasma membrane<sup>24, 32</sup>. Using confocal immunohistochemistry, we assessed the intracellular distribution of WT or C42S PKG1a with PDE5 (Fig. 5A). PDE5 was diffuse and remained so after ET-1 stimulation, and this corresponded to the distribution of PKG1a<sup>WT</sup> (Fig. 5B). However, PKG1a<sup>C42S</sup> was intensified at the outer plasma membrane upon exposure to ET1, and no longer localized with PDE5 (Fig. 5C). These findings support the notion that the spatial co-localization of PZE5 and PKG1a is diminished in myocytes subjected to stress so long as PKG1a oxidation at C42 is suppressed.

# Discussion

In addition to its role in regulating vasomotor tone, cGMP-PKG1a signaling regulates molecular pathways that counter pathological stress. These include its suppression of  $G_{q^-}$  coupled receptor signaling (e.g. angiotensin, endothelin) by activating regulator of G-protein coupled signaling RGS2 and RGS4<sup>9, 33</sup>, and inhibition of the non-selective cation channel - transient receptor potential canonical channel 6 (TRPC6)<sup>34, 35</sup>; both of which reduce cardiac hypertrophy and fibrosis. Functional cardiac improvement is linked to PKG phosphorylation of phospholamban and troponin I to enhance calcium cycling and relaxation, and of titin to increase muscle compliance<sup>11, 12</sup>. PKG1a also provides protection against ischemic injury by improving mitochondrial function<sup>36</sup>, and it enhances protein quality control by increasing activity of the proteasome<sup>37</sup>.

The capacity of PKG1a to counter maladaptive stress in cardiomyocytes and the intact heart is further determined by the redox state of an intermolecular disulfide bond formed at Cys42 between its monomers. As previously reported<sup>22, 23</sup>, oxidation of PKG1a at this site diminishes its protective impact, whereas preventing oxidation by expressing a C42S mutation, enhances it. We now demonstrate that this post-translational modification is also an important determinant of the therapeutic efficacy of PDE5 inhibition, a common therapy used to stimulate this pathway. Our results are summarized in Figure 6, which shows that preventing such C42 oxidation decreases stress-induced activation of PDE5 due in part to reduced phosphorylation of PDE5 by PKG at serine 92. This means that despite PDE5-I, cGMP-mediated activation of PKG1a is diminished, and the cardioprotective effects that ensue are blunted. This does not apply to activation of sGC, which augments PKG1a activity and suppresses pathological stress regardless of the redox state of PKG1a. These data show relevance of myocardial oxidative stress to the efficacy of pharmacological methods used to stimulate PKG1a, and they likely have implications for precision therapy.

PKG1a must interact with specific substrates to achieve its multiple effects, and this is largely regulated by colocalization with the various proteins that generate cGMP or degrade it. An unusual feature of the PKG1a signaling system is that these components are mobile, so interactions and localization can be altered by physiological and pathological signaling inputs. An early example of this mobility was the discovery that inactivation of endothelial NOS (NOS3) in cardiomyocytes leads to migration of PDE5 away from its normal distribution at the z-disk to a more diffuse cytosolic distribution<sup>31, 38</sup>. A similar redistribution was demonstrated in chronic heart disease models<sup>31, 39</sup>. Soluble GC shifts from cytosolic to plasma membrane compartments upon NO stimulation, and in the heart, the latter is further altered by chronic stress, leading to depressed sGC responsiveness to NO<sup>24, 32</sup>. PKG1a also translocates from the cytosol to the plasma membrane minutes after its stimulation by cGMP<sup>9</sup>, which is reversed upon its C42 oxidation<sup>22</sup>. Each of these studies has also shown how a change in location alters the function of a given component of the PKG1a signaling pathway to contribute to myocardial disease.

The current investigation supports the conclusion that the effective interaction between PDE5 and PKG1a, but not sGC and PKG1a, is sensitive to the latter's redox state. An alternative explanation might have been that by blocking PKG1a oxidation at C42, the

kinase became so effective at countering pathological stress that no further improvement was possible. However, TAC still stimulated pathophysiological changes in PKG1a<sup>C42S</sup> mice, and importantly these responses were diminished by sGC activation but not by SIL. Another alternative explanation is that SIL was not adequately dosed in PKG1a<sup>C42S</sup>-TAC. However, the doses we used were effective in cells and hearts expressing PKG1a<sup>WT</sup>. Moreover, even if a higher but still selective dose had more impact, this would still mean there is a substantial rightward shift in the dose response to SIL in PKG1a<sup>C42S</sup> versus WT controls, a finding with therapeutic implications. One prior study proposed that by elevating cGMP, SIL prevents C42 dimerization so as to mimic the protective effects from PKG1a<sup>C42S 23</sup>. However, we did not find evidence of such changes as the dimer/monomer ratio in WT-TAC hearts was increased similarly with or without SIL treatment. Furthermore, in the current study, we tested an alternative method to stimulate cGMP (sGC activation) and found it was effective, so the prior study's explanation could not apply.

The PKG1a<sup>C42S</sup> redox-dead mutant was first shown to suppress resistance artery dilation in response to an oxidant, supporting prior evidence that PKG1a oxidation activates the kinase independent of cGMP<sup>20</sup>. However, Kalyanaraman et al<sup>40</sup> have contested this, finding that PKG1a oxidation at C42 does not directly increase its activity but rather the C42S mutation reduces its activation by cGMP. In essence, they concluded that PKG1a<sup>C42S</sup> is a loss-of-function rather than oxidized PKG1a being a gain-of-function. This interpretation, however, cannot explain the behavior in myocardium, where PKG1a<sup>C42S</sup> is more protective under stress<sup>22, 23</sup>. We agree that PKG1a activity is probably not the primary altered property due to redox change, but believe its altered localization and consequent interactions are important factors. Kalyanaraman et al<sup>40</sup> did not test this, as they used recombinant proteins and *in vitro* lysates that eliminate subcellular localization effects.

The current findings may have implications for clinical studies involving PDE5 inhibitors. Oxidative stress is a component of most forms of HF, and PKG1a oxidation increases in human failing myocardium<sup>22</sup>. However, the extent of such oxidation likely varies among patients, and this could impact the efficacy of PDE5 inhibitor strategies. In HFpEF, PDE5-I trials have included many patients with relatively mild cardiac disease, and often without ventricular hypertrophy<sup>4</sup>. Yet, prior experimental studies found that the milder the cardiac disease induced by loading stress, the less the therapeutic impact from PDE5-I<sup>41</sup>. The present data provides a new explanation for this finding, as oxidative stress is often greater with more severe disease. Biomarkers of oxidative stress or even oxidation of PKG1a itself may ultimately prove useful to help target PDE5-I therapy. Alternatively, the present findings endorse sGC activation (stimulation) strategies as they are effective regardless of the redox state of PKG1a.

In conclusion, the redox state of PKG1a defined by C42-dimerization determines the therapeutic efficacy of PDE5-I in hearts and cardiomyocytes under pathological stress. By contrast, sGC stimulation is effective regardless of this redox change. The most likely mechanism is that preventing the oxidation of PKG1a depresses its interaction with PDE5, whereas coordinated signaling between proteins is assisted when the kinase is oxidized. This may be specific to PDE5, and further studies assessing other strategies such as natriuretic peptide stimulation, organic nitrite or nitrate<sup>42</sup>, and PDE9 inhibitors<sup>43</sup> are needed. Based on

the present results, consideration of oxidative stress and specifically PKG1a oxidation should be made when contemplating the therapeutic use of PDE5 inhibitors.

### Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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#### A) What is new

- Cyclic GMP-activated protein kinase G-1a conveys signaling linked to the nitric oxide and natriuretic peptide pathways. Its activation by phosphodiesterase type 5 (PDE5) inhibition or soluble guanylate cyclase (sGC) activation is being actively tested as a heart failure therapy.
- Oxidation of PKG1a at cysteine-42 reduces its efficacy to counter pathological myocardial stress due to changes in its intracellular localization and thus protein interactions.
- We now show that this oxidation is required in order for PDE5 inhibitors to protect against pathological hormone and mechanical stress, whereas sGC activation is protective independent of PKG1a redox state.

#### B) What are the clinical implications?

- Post-translational changes in proteins e.g. oxidation or phosphorylation are well recognized, but rarely do they alter the efficacy of pharmaceuticals targeting the protein in an almost binary manner. Oxidative stress is common to most cardiovascular diseases, and PKG1a oxidation is found in failing human hearts.
- In patients for whom activation of PKG1a is a desired therapy, those without sufficient myocardial stress to stimulate PKG1a-oxidation may be better served with sGC stimulators rather than PDE5 inhibitors.
- When using PDE5 inhibitors in trials or individual patients, the status of myocardial redox maybe an important factor underlying subject response variability.





**A, B)** Effect of sildenafil (SIL), BAY602770 (BAY), or vehicle (Veh) on cardiac hypertrophy induced by TAC in mice expressing WT or C42S mutant PKG1a. Dot plots (mean ± SD). LV mass from echocardiography shown in Panel A; post-mortem heart mass normalized to tibia length in Panel B. Sample size for each group is shown above the x-axis. Statistical results shown are from mixed factorial ANOVA, with experimental cohort and treatment group as categories, and using a Tukey multiple comparisons test for between group

significance testing (c.f. Supplemental Table): \* p<0.001 vs other WT TAC groups and SHAM; † p=0.009 vs BAY-KI and <0.001 vs SHAM; ‡ p=0.002 vs SIL-KI, ¶ p<0.005 vs Veh-WT; § p=0.004 vs SIL-KI and p=0.001 vs Veh-KI. **C**, **D**) Left ventricular fraction shortening and end-systolic diameter from echocardiography analysis. \* p<0.001 vs other WT groups; † p<0.001 vs SHAM, p=0.005 vs BAY-KI, p=0.31 vs SIL-KI, ¶ p<.001 vs Veh-WT; # p=0.001 vs SIL-KI; ‡ p<0.002 vs SHAM, BAY-WT, SIL-WT; § p<0.001 vs BAY-KI and vs SHAM, p=0.02 vs Veh-WT; \$ p=0.05 vs SIL-KI. **E**) Example myocardial histology stained with Masson trichrome. Scale bar = 200 µm. **F**) Summary of myocardial interstitial fibrosis assessed by Masson's trichrome staining. \*p<0.002 vs SHAM, SIL-WT and BAY-WT; ¶ p<0.001 vs Veh-WT and BAY-KI; ‡ p<0.001 vs SIL-KI.



Figure 2. SIL-induced PKG and TAC-stimulated PDE5 activation are suppressed in PKG1a  $^{\rm C42S}$  (KI) mice

A) TAC stimulates PKG oxidation (D - disulfide dimer, M - monomer) in WT myocardium, and this is not altered by SIL co-treatment. Summary data to the right (Box plot, min-max whiskers; sample size shown, \* p<0.0001 vs SHAM by one-way ANOVA. **B**) Myocardial PKG activity in both genotypes before and after TAC (mean  $\pm$  SD). SIL increases this further only in WT mice subjected to TAC (p<0.0001 for interaction of genotype with TAC vs TAC+SIL), whereas BAY increases activity similarly in both genotypes (p=0.76 for

interaction; p<0.0001 for BAY effect). Sample size provided in figure; results of Kruskal-Wallis analysis with multiple comparisons correction:  $\dagger p<0.001$  vs SHAM, SIL-WT and p=0.003 vs BAY-WT, \* p=0.01 vs BAY-KI, p<0.001 vs SHAM. C) PDE5 protein expression in myocardium in control and TAC hearts from PKG1a<sup>WT</sup> or PKG1a<sup>C42S</sup> mice; **top** - example immunoblot (m-marker), **bottom** – summary data. Two-way ANOVA results: p<0.001 for TAC response, p=0.57 for genotype effect, p=0.32 for interaction of TAC and genotype. \*p=0.01,  $\dagger p<0.001$  vs SHAM. D) PDE5 activation after TAC occurs in WT but not PKG1a<sup>C42S</sup>, p=0.021 for interaction of genotype and TAC. \*p=0.001 vs Sham. Data are shown as box and whisker plots.

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Figure 3. Disparity of drug response is observed in cells expressing PKG1a.<sup>C42S</sup> A, B) *Nppb* and *Rcan1* mRNA expression normalized to *Gapdh* in NRVMs stimulated with endothelin-1 (ET1)  $\pm$  SIL (1 µM) or BAY602770 (1 nM). N=6/group; \* p<0.001,  $\dagger$  p=0.003,  $\ddagger$  p=0.03. C) Percent reduction of *Nppb* or *Rcan1* expression induced by ET-1 due to each drug treatment. N=6/group; p values for Mann-Whitney-U test. D) Myocyte cGMP in NRVMs at rest, and with ET-1 exposure with or without SIL or BAY co-treatment. Analysis by 2 way ANOVA; Genotype p<0.0001; Drug Intervention p<0.0001; interaction p=0.043.

Post-hoc Sidak multiple comparisons: \* p<0.0001 vs CON and ET-1; † p=0.05 vs PDE5-I in C42S group.

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# Figure 4. PKG1a C42 oxidation determines PDE5 activation and SIL efficacy in isolated myocytes

All bar graphs are shown as mean  $\pm$  SD. **A**) PDE5 activity in NRVMs exposed to cGMP+ H<sub>2</sub>O<sub>2</sub>; p<0.001 for genotype effect; p=0.003 for interaction of cGMP+H<sub>2</sub>O<sub>2</sub> × genotype by 2-way ANOVA; \* p<0.001 vs CON. **B**) PKG activity before and after H<sub>2</sub>O<sub>2</sub>+cGMP; p<0.0001 for effect of cGMP+H<sub>2</sub>O<sub>2</sub>; p>0.5 for interaction of cGMP+H<sub>2</sub>O<sub>2</sub> × genotype by 2-way ANOVA. **C**) PDE5 Ser92 phosphorylation and total protein level in adult mouse cardiomyocytes from WT and KI hearts. Example gel and summary data are shown. Cells

were stimulated with cGMP+SIL with or without addition of PKG1a inhibitor DT3; \* p<0.001 vs other groups. **D**) *Nppb/Gapdh* expression in response to ET-1 in NRVMs expressing PDE5<sup>WT</sup>, PDE5<sup>S92D</sup> or PDE5<sup>S92A</sup>. \* P<0.001 vs WT and S92A responses, by 1way ANOVA. **E**) Non-reducing gel for PKG-PDE5 interaction in NRVMs expressing FLAG-PKG1a<sup>WT</sup> or FLAG-PKG1a<sup>C42S</sup>. Pull-down used mouse monoclonal anti-FLAG antibody and gels probed for PDE5A or FLAG to detect dimer/monomer ratio of PKG1a forms. **F**) Summary data for studies as in Panel E. *Upper*) The percentage of dimeric PKG increases after H<sub>2</sub>O<sub>2</sub> ± cGMP in WT expressing cells; \* p<0.0001 vs CON. *Lower*) Coprecipitation of PDE5 and PKG1a: p<0.001 for effect of H<sub>2</sub>O<sub>2</sub>±cGMP, p=0.54 for stimulus genotype interaction. † p=0.009, ‡ p=0.06 vs CON.



Figure 5. Oxidized WT but not C42S PKG1a co-localizes with PDE5 in NRVMs subjected to ET-1  $\,$ 

A) Representative confocal images showing subcellular localization of expressed PKG1 $\alpha^{WT}$  or PKG1 $\alpha^{C42S}$  (green), endogenous PDE5A (red), nuclei (DAPI, blue), and merged images (lower) in NRVMs with and without ET1 stimulation. Scale bar shows =50 µm. **B**, **C**) Densitometry line scan analysis shows correspondence of FLAG (PKG) and PDE5 in cells expressing PKG1 $\alpha^{WT}$  or PKG1 $\alpha^{C42S}$ . X-axis shows distance (µm) and Y-axis fluorescence

intensity. In ET-1 exposed cells, PDE5 coincides with  $PKG1a^{WT}$  but not  $PKG1a^{C42S}$  outside the nucleus. Neither is nuclear in localization.



# Figure 6. Summary scheme depicting impact of PKG1a oxidation on the efficacy of PDE5 inhibition or sGC stimulation to exert anti-hypertrophic regulation

**Left:** By preventing PKG1a oxidation at C42, protection against hormone or hemodynamic stress is enhanced, with less hypertrophy and fibrosis as a result (black arrow). This involves PKG1a<sup>C42S</sup> translocation to the plasma membrane where it better inhibits RGS proteins and the cation channel TRPC6 (see text for details). This translocation, however, also moves PKG1a<sup>C42S</sup> away from PDE5, reducing the impact of PDE5-I (sildenafil, SIL), whereas sGC activation remains capable of activating PKG1a<sup>C42S</sup> in this location (blue/purple arrows). **Right:** PKG1a oxidation blunts its anti-hypertrophic/anti-fibrotic effects (black arrow) as it becomes less effective at targeting TRPC6 (as previously reported<sup>22</sup> and depicted by a dashed line). However, the diffuse distribution of oxidized PKG1a means it can be impacted by cGMP enhanced following PDE5 inhibition, so now both BAY and SIL are effective as therapies to enhance anti-hypertrophic and fibrotic changes (blue/purple arrows). TRPC6, transient receptor potential canonical channel type 6; RGS, Regulator of G protein signaling; ROS, reactive oxygen species.