

# Chronic $\beta_1$ -adrenergic blockade enhances myocardial $\beta_3$ -adrenergic coupling with nitric oxide-cGMP signaling in a canine model of chronic volume overload: new insight into mechanisms of cardiac benefit with selective $\beta_1$ -blocker therapy

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**Abstract** The  $\beta_1$ -adrenergic antagonist metoprolol improves cardiac function in animals and patients with chronic heart failure, isolated mitral regurgitation (MR), and ischemic heart disease, though the molecular mechanisms remain incompletely understood. Metoprolol has been reported to upregulate cardiac expression of  $\beta_3$ -adrenergic receptors ( $\beta_3$ AR) in animal models. Myocardial  $\beta_3$ AR signaling via neuronal nitric oxide synthase (nNOS) activation has recently emerged as a cardioprotective pathway. We tested whether chronic  $\beta_1$ -adrenergic blockade with metoprolol enhances myocardial  $\beta_3$ AR coupling with nitric oxide-stimulated cyclic guanosine monophosphate ( $\beta_3$ AR/NO-cGMP) signaling in the MR-induced, volume-overloaded heart. We compared the expression, distribution, and inducible activation of  $\beta_3$ AR/NO-cGMP signaling proteins within myocardial membrane microdomains in dogs (canines) with

surgically induced MR, those also treated with metoprolol succinate (MR+ $\beta$ B), and unoperated controls.  $\beta_3$ AR mRNA transcripts, normalized to housekeeping gene RPLP1, increased  $4.4 \times 10^3$ - and  $3.2 \times 10^2$ -fold in MR and MR+ $\beta$ B hearts, respectively, compared to Control. Cardiac  $\beta_3$ AR expression was increased 1.4- and nearly twofold in MR and MR+ $\beta$ B, respectively, compared to Control.  $\beta_3$ AR was detected within caveolae-enriched lipid rafts (Cav3<sup>+</sup>LR) and heavy density, non-lipid raft membrane (NLR) across all groups. However, in vitro selective  $\beta_3$ AR stimulation with BRL37344 (BRL) triggered cGMP production within only NLR of MR+ $\beta$ B. BRL induced *Ser*<sup>412</sup> phosphorylation of nNOS within NLR of MR+ $\beta$ B, but not Control or MR, consistent with detection of NLR-specific  $\beta_3$ AR/NO-cGMP coupling. Treatment with metoprolol prevented MR-associated oxidation of NO biosensor soluble guanylyl cyclase (sGC) within NLR. Metoprolol therapy also prevented MR-induced relocalization of sGC $\beta_1$  subunit away from

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caveolae, suggesting preserved NO-sGC-cGMP signaling, albeit without coupling to  $\beta_3$ AR, within MR+ $\beta$ B caveolae. Chronic  $\beta_1$ -blockade is associated with myocardial  $\beta_3$ AR/NO-cGMP coupling in a microdomain-specific fashion. Our canine study suggests that microdomain-targeted enhancement of myocardial  $\beta_3$ AR/NO-cGMP signaling may explain, in part,  $\beta_1$ -adrenergic antagonist-mediated preservation of cardiac function in the volume-overloaded heart.

**Keywords**  $\beta$ -Blockade · Nitric oxide · Cyclic guanosine monophosphate · Caveolae ·  $\beta_3$ -Adrenoceptor · Soluble guanylyl cyclase · Volume overload

## Introduction

$\beta$ -blockers ( $\beta$ Bs) confer cardiac benefit in disease through multiple mechanisms [4, 6, 16, 19, 27, 31, 38, 53], though many remain incompletely understood. In addition to disrupting the chronic adrenergic toxicity underlying heart failure (HF),  $\beta$ Bs improve  $\beta$ -adrenoceptor ( $\beta$ AR) function largely by reversing the downregulation of myocardial  $\beta_1$ - and  $\beta_2$ AR [18, 59] and by countering the upregulation of G protein-coupled receptor kinase 2 (GRK2) expression [21] otherwise induced by chronic sympathetic activation. Thus, chronic  $\beta$ B therapy recouples  $\beta$ AR and G protein activity and restores  $\beta$ AR responsiveness. While studies of the effect of  $\beta$ B on  $\beta$ AR signaling in the diseased heart focus predominantly on  $\beta_1$ - and  $\beta_2$ ARs, few have examined its effect on  $\beta_3$ AR. Myocardial  $\beta_2$ AR expression is reportedly increased in HF animal models and patients [8, 35] and, in limited studies, even more so with chronic  $\beta$ B therapy [51, 64]. Recently,  $\beta_3$ AR activation has been shown to induce nitric oxide (NO)-mediated cardioprotection in animal models of cardiac pressure overload, neurohormone-induced hypertrophy, myocardial ischemia/reperfusion injury, and acute myocardial infarction [1, 5, 14, 41, 60]. Chronic  $\beta_1$ -blockade ( $\beta_1$ B) might well amplify cardioprotective  $\beta_3$ AR signaling in the pathologically remodeled heart. Intriguing but little explored, such a mechanism would suggest novel approaches to enhancing innate cardioprotective signaling while assuring compatibility with current guideline-directed medical therapy.

$\beta$ AR signaling regulates cardiac myocyte contractility and hypertrophic signaling and, under normal physiological conditions, is modulated by NO via both direct [i.e., soluble guanylyl cyclase (sGC) activation] and indirect actions (e.g. S-nitrosylation, tyrosine nitration). NO activation of sGC, with its subsequent production of cyclic guanosine monophosphate (cGMP), blunts  $\beta_1$ - and  $\beta_2$ AR-stimulated cardiac contractility [55]. S-nitrosylation of GRK2 (also known as  $\beta$ -adrenergic receptor kinase 1 or  $\beta$ ARK1) inhibits the desensitization and downregulation of  $\beta_1$ - and  $\beta_2$ ARs [61].

Conversely,  $\beta_2$ - and  $\beta_3$ AR signaling can activate NO synthase (NOS), thereby coupling  $\beta$ AR signaling with NO signaling. Unlike  $\beta_1$ - and  $\beta_2$ ARs,  $\beta_3$ ARs are stimulated at high catecholamine levels and thus may contribute more significantly to  $\beta$ AR signaling in conditions of catecholamine excess such as HF and mitral regurgitation (MR) [17, 34]. In the healthy, non-failing heart,  $\beta_3$ AR activation inhibits cardiac myocyte contraction and induces cardiac myocyte relaxation [15]. However, the effect of  $\beta_3$ AR signaling on cardiac contractility remains incompletely understood, as both negative [40] and positive [7] inotropic effects have been demonstrated with  $\beta_3$ AR stimulation in diseased, failing hearts. Importantly, transgenic mice with cardiac-specific overexpression of human  $\beta_3$ AR show enhanced cardiac contractility [26] and attenuated neurohormone-induced hypertrophic remodeling [5].

Gene expression analysis of left ventricular (LV) tissue recently revealed that cardiac  $\beta$ AR and NO signaling pathways are markedly altered in patients with isolated MR compared to control subjects [66]. Yet how the interaction between  $\beta$ AR and NO signaling differs in the stressed and pathologically remodeled heart is not fully understood. We previously demonstrated that NO-sGC-cGMP signaling is dysregulated in animal models of concentric and eccentric cardiac hypertrophy with respect to myocardial expression, subcellular localization, and oxidation of sGC heterodimer subunits [29, 57].

In prior studies, chronic  $\beta_1$ B therapy preserved normal cardiac myocyte contractility and enhanced  $\beta$ AR responsiveness in the experimental chronic MR canine model after four months of treatment [43]. In the present study, we used a 4-week chronic MR canine model to investigate the early effects of chronic  $\beta_1$ B therapy on myocardial NO-sGC-cGMP signaling as well as  $\beta_3$ AR/NO-cGMP coupling. We hypothesized that chronic  $\beta_1$ B therapy preserves normal NO-sGC-cGMP signaling and enhances myocardial  $\beta_3$ AR/NO-cGMP coupling in a microdomain-specific fashion, thereby potentially mediating later cardiac myocyte functional benefits. We focused on signaling within and outside of myocardial caveolae—small, flask-shaped, lipid- and protein-rich invaginations of the plasma membrane (PM) that compartmentalize signal transduction. Importantly, all three  $\beta$ AR subtypes [2, 30, 45, 47, 49], eNOS [23], nNOS [9], sGC [57], and calcium channels [32, 33], reside within caveolae; some, exclusively.

## Methods

### Animal experiments

Mitral regurgitation (MR) was induced in conditioned mongrel dogs (19–26 kg) by rupturing a papillary chord

under fluoroscopy, as previously described [25, 29, 46]. Sixteen dogs underwent chordal rupture and ten unoperated dogs served as controls. At 24 h after MR induction, half of the MR dogs were started on metoprolol succinate 100 mg by mouth once daily (MR  $n = 8$ , MR+ $\beta$ B  $n = 8$ ). Two-dimensional and M-mode echocardiography (2.25-MHz transducer, ATL Ultramark VI) was performed at baseline and at the time of euthanasia (4 weeks after MR induction). Animals were maintained at a deep plane of general anesthesia using isoflurane and were mechanically ventilated. At the end of the *in vivo* experiments, the heart was arrested with intracardiac injection of KCl and quickly extirpated and placed in phosphate-buffered ice slush. The coronaries were flushed with oxygenated Krebs solution. A portion of the LV was cut and snap-frozen in liquid nitrogen for subsequent studies. We chose to study 4-week duration of therapy so as to identify early signaling changes that precede and thus underlie subsequent functional benefits already demonstrated with longer term treatment. Animal studies were approved by the Animal Services Committees at the University of Alabama at Birmingham and College of Veterinary Medicine, Auburn University and the Institutional Animal Care and Use Committee of Temple University School of Medicine. All animal protocols conformed to the Guide for the Care and Use of Laboratory Animals published by the National Institutes of Health (NIH publication No.85-23, revised 1996).

#### Quantitative reverse transcription polymerase chain reaction (qRT-PCR)

Total RNA was extracted from flash-frozen LV myocardium using a spin column chromatography method (Animal Tissue RNA Purification Kit, Norgen Biotek, Ontario, Canada), according to the manufacturer's instructions. Reverse transcription (RT) was performed using the SuperScript III First-Strand Synthesis System (Invitrogen, Life Technologies) and oligo-dt primers according to the manufacturer's instructions. Real-time PCR (qPCR) was performed using QuantiFast SYBR<sup>®</sup> Green PCR Kit (Qiagen). Data were normalized to large ribosomal protein P1 (RPLP1) RNA expression. The following primer sets were used (forward, reverse):  $\beta_3$ AR (5'-CGCCTCCAACATACCCTACG-3', 5'-CGCGTAGCCACGAGGAAAA-3'); RPLP1 (proprietary primer sequences, Qiagen). Individual samples were run in triplicate.

#### Isolation of caveolin-3-enriched lipid raft fraction by isopycnic ultracentrifugation

Caveolae-enriched lipid raft fractions (Cav3<sup>+</sup>LR) were prepared from snap-frozen LV tissue, using a discontinuous 35–5 % sucrose density gradient ultracentrifugation

method as previously described [29, 57]. LV tissue homogenization was carried out on ice, in detergent-free buffer (50 mmol/L Tris-HCl, pH 7.6, 1 mmol/L EDTA, 1 mmol/L DTT, 2 mmol/L PMSF, 50 mmol/L NaF, 1 mmol/L Na Vanadate) with protease inhibitors (Mammalian Cocktail, Sigma-Aldrich). Following 1-h incubation on ice with intermittent vortex, 0.6 mL of tissue homogenate was mixed with 1.4 mL of 60 % (w/w) sucrose in 20 mmol/L KCl, 0.5 mmol/L MgCl<sub>2</sub> and placed at the bottom of an ultracentrifuge tube. A discontinuous 35–5 % sucrose gradient was formed by overlaying each sample with 1.3 mL of 35 % sucrose and then with 1.3 mL of 5 % sucrose. The sucrose density gradient was topped off with 0.5 mL of 200 mmol/L KCl. Each sample was then centrifuged at >180,000g for 16–18 h at 4 °C in a swinging bucket rotor (Beckman Instruments, Palo Alto, CA) without any brake. The top KCl layer was discarded and fractions were collected every 400  $\mu$ l from the top sucrose layer corresponding to F1 (top, most buoyant) to F11 (bottom, least buoyant/heaviest).

A light-scattering band confined to the 35–5 % sucrose interface, typically F3–F5, corresponds to Cav3<sup>+</sup>LR fractions. Ponceau staining and protein concentrations determined by bicinchoninic acid (BCA) assay confirmed that total protein distribution was weighted toward heavier sucrose density gradient fractions (F7 through F11) lacking caveolin-3 (Cav3) in all hearts. Proteins were precipitated using 0.1 % w/v deoxycholic acid in 100 % w/v trichloroacetic acid. Protein concentrations were determined by BCA protein assay (Pierce). Non-lipid raft (NLR, F11) and Cav3<sup>+</sup>LR fractions (F3–F5) without TCA precipitation were also collected for BCA and subsequent cGMP assays. Cav3<sup>+</sup>LR fractions were selected based upon greatest enrichment of Cav3 as detected by Western.

#### Cardiomyocyte caveolae-immunoaffinity isolation

Cardiomyocyte caveolae organelles were isolated using an immunoaffinity protocol [42]. In brief, sheep anti-mouse IgG-coated magnetic beads (Dynabeads, Life Technologies, Carlsbad, CA) were pre-incubated with a monoclonal antibody specific for caveolin-3 (BD transduction) for 2 h at room temperature. Control beads were pre-incubated in PBS only. Both anti-Cav3 Dynabeads and control IgG Dynabeads were subsequently washed with PBS for 1 h at 4 °C on a rotator.

Plasmalemmal membrane rafts were fractionated from ventricular myocardial tissue as previously reported [44]. Canine LV (100 mg) was dounce homogenized in 1 mL ice cold, detergent-free Tricine buffer (20 mM Tricine, 1 mM EDTA, 250 mM sucrose, pH 7.4) and centrifuged at 1,000g for 10 min at 4 °C. Cell pellets were resuspended in 1 mL Tricine buffer, dounce homogenized, and centrifuged

again at 1,000g for 10 min at 4 °C. An aliquot of pooled supernatant (30 µl) was set aside as the homogenate (H) sample. The pooled supernatant was then mixed with 30 % Percoll (Sigma) in Tricine buffer and subjected to ultracentrifugation at >116,000g for 30 min at 4 °C (Beckman MLS50 rotor, 33,000 rpm, no break). The separated PM was collected, mixed with ice-cold MBS buffer (20 mM 2 N-morpholinoethane-sulfonic acid, 20 mM KCl, 135 mM NaCl), and microcentrifuged at approximately 21,000g for 30 min at 4 °C to pellet the membrane. The supernatant was discarded. The membrane pellet was resuspended in ice cold 1 mL PBS and sonicated on ice (30 s bursts × 3). An aliquot (30 µl) was set aside as the PM for subsequent Western blotting.

Remaining PM was incubated with the anti-Cav3-coated Dynabeads for 1 h at 4 °C, using a rotator. Bound material (B), representative of cardiomyocyte caveolae vesicles, was separated magnetically from unbound (U), non-caveolae membranes. An aliquot (30 µl) of the unbound fraction (U) was set aside for subsequent Western blotting. Using the magnetic rack, beads were washed five times with PBS, resuspended in 2× loading buffer (100 mM Tris, pH 6.8, 2 % SDS, 0.02 % bromophenol blue, 20 % glycerol, 100 mM DTT), and boiled at 95 °C for 5 min to dissociate the protein from the beads. Homogenate (H), PM, bound material representative of cardiomyocyte caveolae (B), and unbound material representative of non-caveolae plasmalemmal membrane (U) were subjected to SDS-PAGE and immunoblotted using the indicated antibodies.

#### Western analysis

Protein extracts were run on SDS-PAGE gels, transferred to nitrocellulose membranes, and immunoblotted using primary antibody probes as follows:  $\beta_3$ AR (1:1,000, Abnova); sGC $\alpha_1$  (1:1,000, Abcam); sGC $\beta_1$  (1:4,000, Cayman Chemicals); Cav3 (1:10,000, BD Transduction); total nNOS (1:1,000, BD Transduction); phospho-nNOS (*Ser*<sup>1412</sup> p-nNOS, 1:1,000, gifted by K.J. Hurt, University of Colorado) [20]; GAPDH (1:10,000, cell signaling). Specificity of anti-sGC $\alpha_1$  and - $\beta_1$  antibodies was confirmed using protein extracts from sGC $\alpha_1^{-/-}$  and sGC $\beta_1^{-/-}$  mouse hearts as previously published [57]. Primary antibody binding was visualized by either horseradish peroxidase-conjugated secondary antibodies with enhanced chemiluminescence (GE Healthcare) or Alexa Fluor 680 or 800-conjugated secondary antibodies (molecular probes) with an Odyssey infrared imager (LI-COR). Densitometry analysis of immunoblots was performed using Image J Software (NIH) or Image Studio Software (Odyssey CLx v2.1, LI-COR).

#### sGC activity assay and redox state determination

Baseline and agonist-stimulated cGMP levels of total LV, Cav3<sup>+</sup>LR, and NLR from Control, MR, and MR+ $\beta$ B hearts were measured by direct cGMP ELISA kit (New East Biosciences, Malvern, PA), as previously described [29, 57]. LV homogenates, Cav3<sup>+</sup>LR and NLR membrane fractions were pre-incubated at room temperature for 15 min in a solution for final concentrations of Tris 50 mM, pH 7.6, IBMX (3-isobutyl-1-methylxanthine) 0.75 mmol/L, creatine phosphate 3.5 mmol/L, creatinine phosphokinase 1 unit, GTP 1 mmol/L, and MgCl<sub>2</sub> 3 mmol/L. Samples were then incubated with or without DEA/NO (1 µmol/L) or BAY 60-2770 (0.01 µmol/L) at 37 °C for 10 min and subjected to diethyl ether extraction. cGMP levels of ether-extracted samples were measured by EIA according to kit manufacturer protocol. BAY60 compound was provided by J-P Stasch (Bayer AG, Wuppertal, Germany).

#### In vitro functional assays of $\beta_3$ AR/NO-cGMP coupling

Selective  $\beta_3$ AR agonist BRL 37344 (BRL, 0.1 and 1.0 µmol/L, Tocris Bioscience) was used to assess  $\beta_3$ AR induction of NO-sGC-cGMP signaling. cGMP levels were measured as above.

#### Statistical analysis

All values are expressed as mean ± SEM. Statistical analyses were performed using: two-way ANOVA when determining interaction of conditions or the source of variance; one-way ANOVA followed by Tukey or Holm-Sidak's multiple comparison test as appropriate; Brown-Forsythe test of variance, if relevant; and two-tailed paired, ratio paired, or one-tailed unpaired Student's *t* test, as appropriate. Statistical significance was defined as *P* < 0.05. GraphPad Prism 6.0 was used for statistical and graphical analysis.

## Results

MR-induced early eccentric remodeling persists and normal LV function remains preserved following 4 weeks of metoprolol therapy

As expected, dogs developed increased LV chamber dilation and decreased LV wall thickness to end-diastolic dimension, by 4 weeks post-MR induction, irrespective of metoprolol therapy (Table 1). LV fractional shortening remained normal in Control, MR, and MR+ $\beta$ B hearts at 4 weeks.

**Table 1** LV structure and function assessed by echocardiography in canine chronic MR model

	Control	MR	MR+βB
LVEDD (cm)	3.7 ± 0.1	4.5 ± 0.2*	4.9 ± 0.2*
LVESD (cm)	2.1 ± 0.1	2.5 ± 0.1*	2.8 ± 0.1*
LVWT/LVEDD	0.28 ± 0.03	0.19 ± 0.02*	0.18 ± 0.01*
FS (%)	43 ± 3	44 ± 3	43 ± 3

\*  $P < 0.05$  vs. control on two-tailed, unpaired Student's  $t$  test

### Chronic metoprolol therapy increases myocardial β<sub>3</sub>AR expression without altering membrane microdomain distribution

Although expressed at low levels in the normal adult heart, β<sub>3</sub>AR is upregulated in the concentric hypertrophied and failing heart [8, 35, 60, 65]. We induced early stage eccentric hypertrophy via MR-mediated chronic volume overload in dogs, as previously described [29], treated some MR dogs with β<sub>1</sub>B metoprolol succinate (MR+βB), and measured β<sub>3</sub>AR mRNA and protein expression as well as β<sub>3</sub>AR membrane microdomain distribution, comparing control, MR, and MR+βB animals. β<sub>3</sub>AR mRNA expression, normalized to housekeeping gene RPLP1, increased  $4.4 \times 10^3$ - and  $3.2 \times 10^2$ -fold in MR and MR+βB, respectively, relative to control (Fig. 1a). We detected β<sub>3</sub>AR by Western immunoblot at its predicted molecular weight of 43 kDa in both isolated adult canine cardiac myocytes and canine LV myocardium (Fig. 1b). Sensitivity and specificity of our β<sub>3</sub>AR antibody was demonstrated by immunoblotting various tissue and fractions known to have differential β<sub>3</sub>AR expression. As expected, β<sub>3</sub>AR expression was enriched in the PM fraction of murine LV relative to LV total protein. Our immunoblot likewise confirmed greater hepatic than myocardial β<sub>3</sub>AR expression [62]. β<sub>3</sub>AR expression was also greater in LV of human β<sub>3</sub>AR expressing transgenic mice than of wild type mice [5]. Chronic β<sub>1</sub>AR-blockade potentiated the increase in myocardial β<sub>3</sub>AR expression in MR, with  $1.4 \pm 0.1$ -fold and  $1.9 \pm 0.2$ -fold higher expression in MR and MR+βB, respectively, than in Control (Fig. 1c, d). We also examined the distribution of β<sub>3</sub>AR in myocardial membrane microdomains as resolved by isopycnic ultracentrifugation. β<sub>3</sub>AR was detected within caveolae microdomains (Cav3<sup>+</sup>LR, F4–F5) and heavy density, non-lipid raft membrane fractions (NLR, F11) of all hearts (Fig. 1e). While overall expression varied amongst the study groups, distribution of β<sub>3</sub>AR across myocardial membrane fractions was similar (Fig. 1f). Caveolae localization of β<sub>3</sub>AR within cardiomyocytes was further verified by plasmalemmal caveolae-immunoaffinity isolation and immunoblot analysis (Fig. 1g). Since only myocytes exclusively express Cav3, caveolae-immunoaffinity isolation

using anti-Cav3-antibody-coated magnetic beads ensured selection of only myocyte caveolae, and not that of endothelial cells, fibrocytes, or adipocytes.

Selective β<sub>3</sub>AR stimulation with BRL37344 (BRL) increases cGMP production within heavy density, NLR fractions

To assess β<sub>3</sub>AR/NO-cGMP coupling within membrane microdomains, we measured cGMP levels within Cav3<sup>+</sup>LR and NLR fractions at baseline and in response to the selective β<sub>3</sub>AR agonist BRL, all in the presence of non-selective phosphodiesterase inhibitor IBMX. While basal cGMP levels did not vary amongst Control, MR, and MR+βB within respective membrane microdomains, basal cGMP levels within Cav3<sup>+</sup>LR exceeded that within corresponding NLR of Control and MR+βB hearts (Fig. 2a). β<sub>3</sub>AR stimulation at increasing concentrations of BRL did not induce cGMP production within Cav3<sup>+</sup>LR of any study group (data not shown). Conversely, BRL did induce significant cGMP production within NLR of only MR+βB (Table 2; Fig. 2b). To verify that NO-inducible sGC cyclase activity was intact in NLR of all groups and not solely MR+βB, NO-donor DEA/NO-induced cGMP responses are shown for comparison. Thus, coupling of β<sub>3</sub>AR and NO-sGC-cGMP signaling was uniquely detected in NLR of MR+βB.

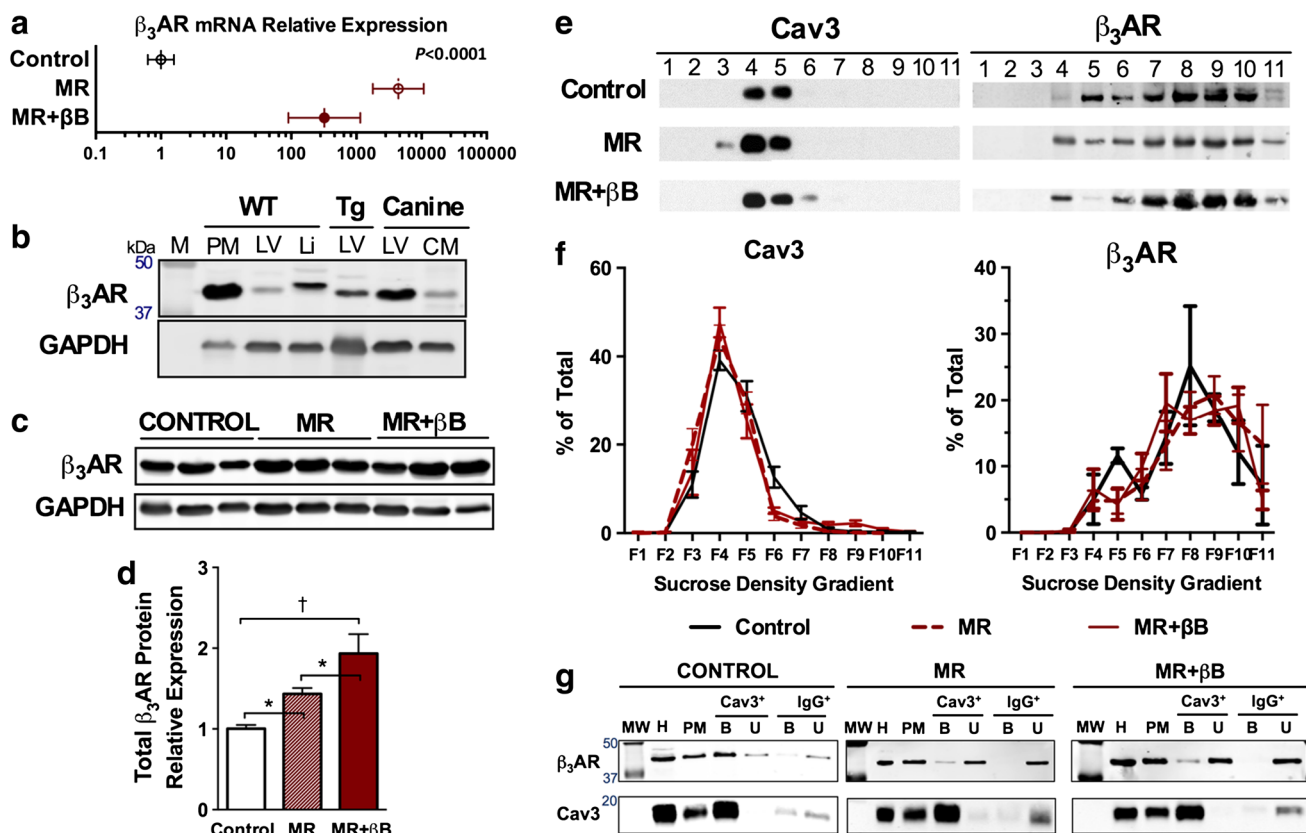
β<sub>3</sub>AR couples with NO-sGC-cGMP signaling via nNOS activation

β<sub>3</sub>AR stimulation has been demonstrated to modulate the phosphorylation and activity of NOS isoforms [1, 5, 41, 60]. While eNOS activation by β<sub>3</sub>AR is inconsistently reported amongst various animal and human models [1, 40, 41, 60], recent in vitro studies of isolated neonatal rat ventricular cardiac myocytes and in vivo mouse studies demonstrated cardioprotective β<sub>3</sub>AR signaling mediated via nNOS activation, specifically through Ser<sup>1412</sup> phosphorylation of nNOS [5, 41, 60]. To corroborate the role of this mechanism in BRL-induced cGMP production within MR+βB NLR, we assessed Ser<sup>1412</sup> p-nNOS and total nNOS by Western blot in BRL-stimulated NLR of Control, MR, and MR+βB hearts (Fig. 3a). Increased phosphorylation of nNOS upon BRL stimulation was detected in NLR of MR+βB but not MR or Control (Fig. 3b). These results are consistent with β<sub>3</sub>AR/NO-cGMP coupling in the NLR domain in a β<sub>1</sub>B therapy-dependent manner.

Effect of β<sub>1</sub>AR-blockade on myocardial membrane microdomain distribution of sGC subunits

As we have previously shown, α<sub>1</sub> and β<sub>1</sub> subunits of the sGC heterodimer localize to both Cav3<sup>+</sup>LR and NLR but





**Fig. 1** Volume-overload-induced  $\beta_3\text{AR}$  expression is potentiated by chronic  $\beta_1\text{AR}$ -blockade. **a** LV  $\beta_3\text{AR}$  mRNA levels normalized to RPLP1 mRNA levels (mean  $\pm$  SEM) were determined in Control, MR, and MR+ $\beta\text{B}$ .  $n = 5$  animals per group; one-way ANOVA  $P < 0.0001$  **b** Western of  $\beta_3\text{AR}$  in LV plasma membrane fraction (PM) and total protein from myocardium (LV), isolated cardiac myocytes (CM), and liver (Li) of C57Bl/6 mice (WT), human  $\beta_3\text{AR}$ -expressing transgenic mice (Tg), and dogs. **c** Representative Westerns of  $\beta_3\text{AR}$  in LV total protein extracts from study dogs. **d** Summary densitometry analysis of total  $\beta_3\text{AR}$  expression normalized to GAPDH and Control levels.  $n = 4$ –6 animals per study group. one-

way ANOVA  $P = 0.002$ . \* $P < 0.05$ ,  $\dagger P < 0.01$  on Holm–Sidak’s multiple comparison test. **e** Representative Westerns of Cav3 and  $\beta_3\text{AR}$  across sucrose density gradient fractions (F1–F11) of Control, MR, and MR+ $\beta\text{B}$ . **f** Cav3 and  $\beta_3\text{AR}$  distribution is presented for each fraction as a percentage of the sum signal across all fractions. For Cav3,  $n = 4$ –7 per study group. For  $\beta_3\text{AR}$ ,  $n = 3$ –6 per study group. **g** Cardiac myocyte plasmalemmal caveolae organelles were immunoprecipitated with anti-Cav3.  $\beta_3\text{AR}$  was detected in LV homogenate (H), LV plasmalemmal membrane fraction (PM), cardiomyocyte plasmalemmal caveolae (B bound fraction), and in LV plasmalemmal membrane depleted of caveolae (U unbound fraction)

differentially relocate in the hemodynamically stressed heart. Under pressure- and volume-overload cardiac stress, sGC $\beta_1$  relocates away from Cav3 $^+$ LR [29, 57]. Here, the distribution of sGC $\alpha_1$  was unperturbed by either volume overload or chronic  $\beta_1\text{AR}$ -blockade at this 4 week time point (Fig. 4a). Interestingly, chronic  $\beta_1\text{AR}$ -blockade prevented the shift of sGC $\beta_1$  towards NLR that was otherwise observed in MR hearts. In MR+ $\beta\text{B}$ , Cav3 $^+$ LR localization of sGC $\beta_1$  was preserved and relocation of sGC $\beta_1$  to heavy density, NLR was abated (Fig. 4b).

Chronic  $\beta_1\text{AR}$ -blockade is associated with less oxidized and more reduced sGC

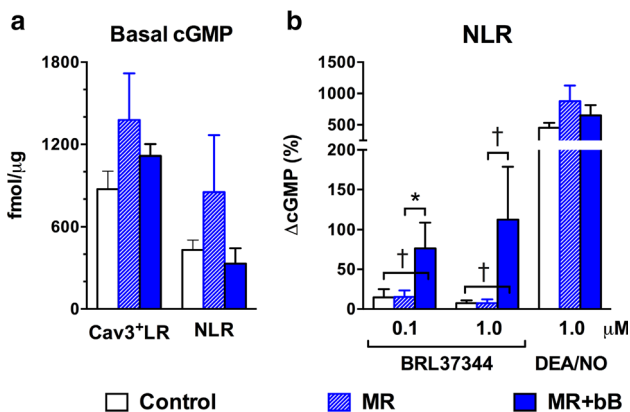
Given the observed membrane distribution of the sGC subunits and  $\beta_3\text{AR}$ , physical colocalization of these

proteins alone would not explain the functional coupling of  $\beta_3\text{AR}$  and NO-sGC-cGMP signaling detected exclusively within NLR of MR+ $\beta\text{B}$ . We hypothesized that chronic  $\beta_1\text{AR}$ -blockade may have impacted the redox state of sGC within the various membrane microdomains. Dependent upon its ferrous heme moiety, inducible cyclase activity of the sGC heterodimer varies with its redox state. Oxidized sGC does not respond normally to NO. Heme-free sGC is unresponsive to NO stimulation. sGC activators (e.g. BAY60) can stimulate sGC cyclase activity independent of NO or heme; oxidized sGC has a relatively potentiated response to sGC activators [24]. Thus, differential cyclase response of sGC to BAY60 versus NO-donor DEA/NO can reveal its redox state [48]. We previously showed that while NLR-localized sGC becomes oxidized in the volume-overloaded heart, caveolae-localized sGC does not

[29]. We measured cGMP levels of LV total protein extracts, Cav3<sup>+</sup>LR, and NLR at baseline and following stimulation with DEA/NO and BAY60, all in the presence of IBMX (Fig. 5). BAY60-induced cGMP production exceeded DEA/NO-induced cGMP production in MR and MR+βB, suggesting an overall predominance of oxidized sGC in the volume-overloaded heart. However, BAY60-induced cGMP production in MR+βB was similar to that in Control, both lower than in MR, suggesting that chronic β<sub>1</sub>AR-blockade blunts oxidation of sGC in the volume-overloaded heart (Fig. 5a). Alternatively, differential cyclase activity could reflect differential expression of sGC. Immunoblots of sGC subunits confirmed that sGCβ<sub>1</sub> expression did not vary amongst Control, MR, and MR+βB (Fig. 6). While sGCα<sub>1</sub> levels fell slightly in MR+βB compared to either Control or MR, there was no impact on either basal or NO-inducible sGC activity.

Baseline and DEA/NO-stimulated cGMP levels were similar for total protein extracts of all hearts.

We again found that caveolae localization protected sGC from oxidation in all hearts. In Cav3<sup>+</sup>LR, inducible sGC cyclase activity was similar for all study groups (Fig. 5b). Notably, the response to BAY60 was not potentiated within Cav3<sup>+</sup>LR, relative to control or DEA/NO. In fact, DEA/NO-induced cGMP production exceeded that of BAY60 within Cav3<sup>+</sup>LR, most significantly for MR and MR+βB, suggesting a predominance of reduced sGC within caveolae. As we previously reported oxidation of sGC within MR NLR, we hypothesized that chronic β<sub>1</sub>-blockade might prevent this stress-induced change in NLR-localized sGC. Indeed, we found that NLR-localized sGC was not oxidized in MR+βB (Fig. 5c). The BAY60 response of MR+βB NLR was markedly blunted compared to that of MR NLR and similar to that of Control NLR.



**Fig. 2** Coupling of β<sub>3</sub>AR and NO-sGC-cGMP signaling is detectable within NLR of MR+βB. cGMP levels of Control, MR, and MR+βB Cav3<sup>+</sup>LR and NLR membrane fractions were measured by EIA at **a** baseline and **b** upon stimulation with selective β<sub>3</sub>AR agonist BRL (0.1 and 1.0 μM) or NO-donor DEA/NO (1.0 μM). No significant BRL response was detected for Cav3<sup>+</sup>LR in any study group (not shown). All measurements were in the presence of IBMX. Averaged baseline cGMP levels included 10–12 measurements, including replicates, per study group. For summary analysis of BRL stimulated cGMP production, only paired baseline and BRL-induced cGMP levels were included, *n* = 4–6 per study group. For each BRL dose, one-way ANOVA *P* ≤ 0.1, \**P* < 0.05, and †*P* ≤ 0.1 on unpaired student *t* test. For BRL 0.1 μM dose, Brown-Forsythe *P* < 0.05

**Discussion**

We demonstrated that chronic β<sub>1</sub>B in MR is associated with enhanced myocardial NO-sGC-cGMP signaling and β<sub>3</sub>AR/NO-cGMP coupling in specific membrane microdomains. Although myocardial β<sub>3</sub>AR expression was slightly increased, β<sub>3</sub>AR/NO-cGMP coupling could not be detected in untreated MR hearts. Increased oxidation of sGC in MR may have accounted for the lack of β<sub>3</sub>AR/NO-cGMP coupling. In contrast, MR+βB hearts had greater upregulation of myocardial β<sub>3</sub>AR expression, improved sGC redox state, and detectable β<sub>3</sub>AR/NO-cGMP coupling, specifically in heavy-density membrane microdomains. These early changes in myocardial β<sub>3</sub>AR signaling at 4 weeks of metoprolol therapy in MR may contribute to the subsequent potentiated βAR responsiveness and improved cardiac myocyte and LV function seen after more prolonged 4-month metoprolol therapy [43].

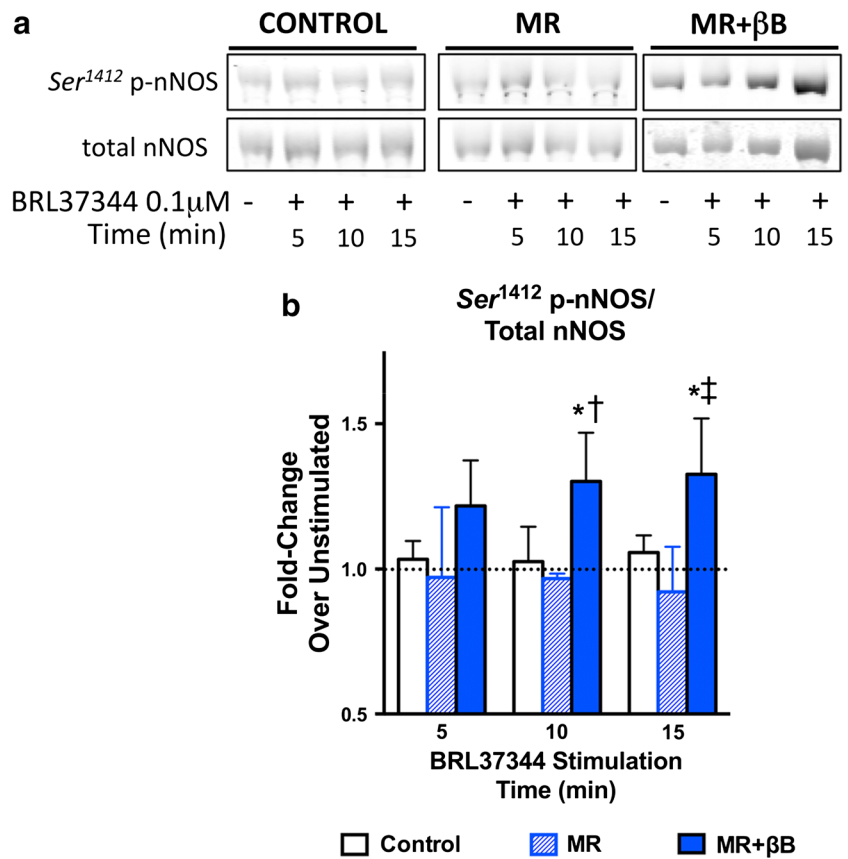
Although the functional role of β<sub>3</sub>AR upregulation in HF had been widely debated, several recent studies have clearly shown a cardioprotective role for cardiac β<sub>3</sub>AR signaling. Chronic BRL treatment blunted pathologic cardiac remodeling and improved cardiac function, via a proposed restoration of the nitroso-redox balance, in mice subjected to pressure-overload cardiac stress. [41]. Similarly, transgenic

**Table 2** cGMP levels at baseline and following BRL stimulation within NLR

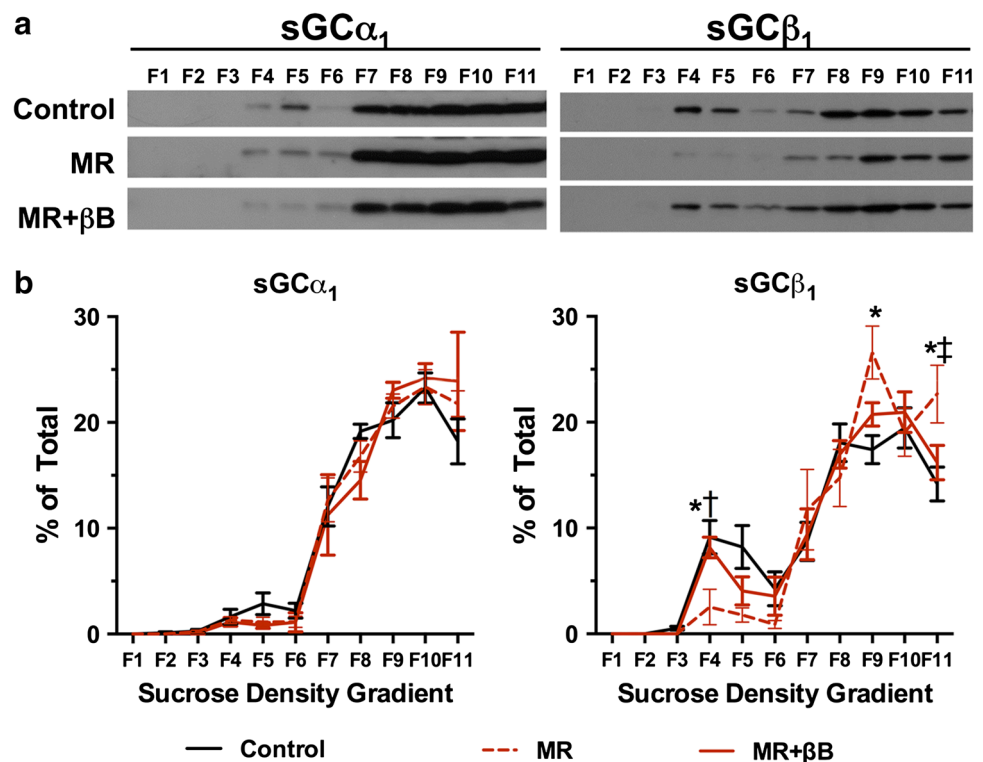
	<i>n</i>	Baseline	BRL-stimulated 0.1 μM	BRL-stimulated 1.0 μM
Control	4	418.8 ± 166.2	438.5 ± 193.3	445.9 ± 167.3
MR	6	1,191.0 ± 678.4	2,052.0 ± 1,595.0	3,345.0 ± 2,965.0
MR+βB	5	503.4 ± 256.8	622.3 ± 267.3*	753.4 ± 314.4†

\* *P* ≤ 0.10, † *P* < 0.05 on two-tailed, paired student *t* test

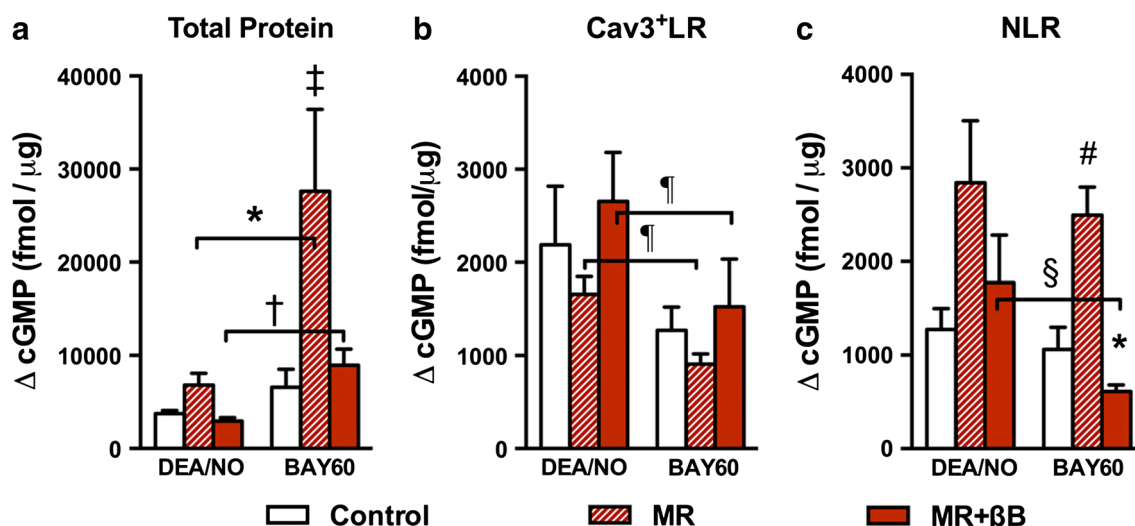
**Fig. 3** Selective  $\beta_3$ AR agonist BRL induces  $Ser^{1412}$ -phosphorylation of nNOS within MR+ $\beta$ B NLR. **a** Representative Westerns of  $Ser^{1412}$  p-nNOS and total nNOS in Control, MR, and MR+ $\beta$ B NLR. Samples were stimulated with BRL 0.1  $\mu$ M for 5, 10, and 15 min. **b** Summary densitometry analysis shows the ratio of  $Ser^{1412}$  p-nNOS to total nNOS as normalized to unstimulated levels of respective samples,  $n = 3-4$  per study group. Two-way ANOVA  $P < 0.01$  for study group. Tukey's multiple comparison testing  $*P < 0.05$  vs. control,  $^\dagger P < 0.05$  vs. MR,  $^\ddagger P < 0.01$  vs. MR



**Fig. 4** sGC $\beta_1$  relocates away from caveolae in MR whereas chronic  $\beta_1$ B therapy preserves Cav3<sup>+</sup>LR localization in MR+ $\beta$ B heart. **a** Representative Westerns of sucrose density gradient fractions of Control, MR, and MR+ $\beta$ B. sGC $\alpha_1$  and sGC $\beta_1$  are enriched in Cav3<sup>+</sup>LR of Control. sGC $\beta_1$  shifts away from F4-F5 in MR, with concomitant relocation to NLR (F11). sGC $\beta_1$  remains within in Cav3<sup>+</sup>LR in MR+ $\beta$ B. **b** Summary densitometry analysis of all hearts analyzed ( $n = 4-7$  per study group). One-way ANOVA for sGC $\beta_1$   $P = 0.012$  for F4,  $P = 0.007$  for F9,  $P = 0.031$  for F11. Unpaired student  $t$  test  $*P < 0.05$  for MR vs. control,  $^\dagger P < 0.05$  for MR+ $\beta$ B vs. MR,  $^\ddagger P < 0.10$  for MR+ $\beta$ B vs. MR

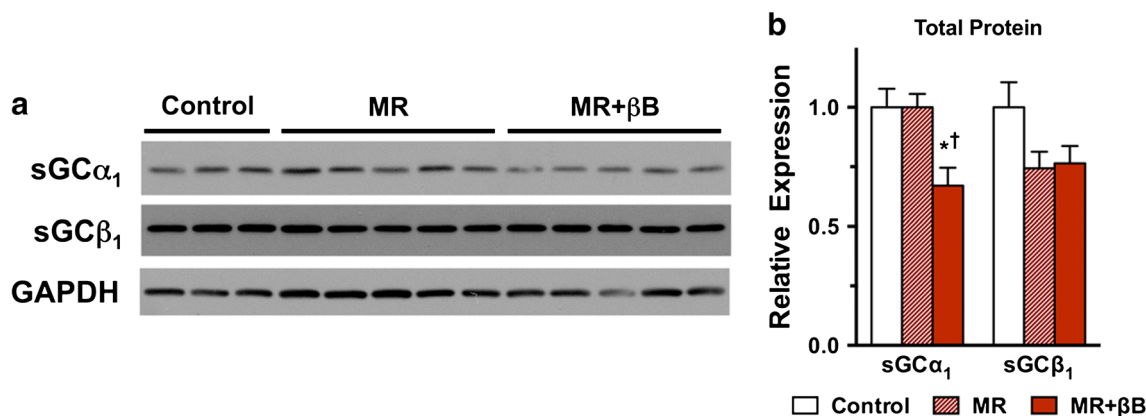






**Fig. 5** Chronic  $\beta_1$ AR blockade protects sGC from oxidation. **a** BAY60-induced cGMP production markedly exceeds NO-induced cGMP production of MR, indicating predominance of oxidized sGC in MR hearts. Levels of cGMP were measured at baseline and following stimulation with DEA/NO and BAY60 in the presence of IBMX in **a** LV total protein extract, **b** Cav3<sup>+</sup>LR and **c** NLR fractions.

Induced cGMP production is shown as the increment above baseline cGMP levels expressed in fmol cGMP/μg protein. \* $P < 0.01$ , † $P < 0.001$  on ratio paired  $t$  test; ‡ $P < 0.05$  vs. control and MR+βB on Tukey multiple comparison test; § $P < 0.1$  on ratio paired  $t$  test; § $P = 0.05$  on ratio paired  $t$  test; # $P < 0.01$  vs. control,  $P < 0.001$  vs. MR+βB on Tukey multiple comparison test



**Fig. 6** Chronic  $\beta_1$ AR-blockade differentially impacts sGC subunit expression. **a** Representative Western blot of total protein extracts from LV myocardium. **b** Summary densitometry analysis of all Westerns. Signals was standardized to respective GAPDH and then

normalized to Control. Mean of replicate measures was used for each heart sample. *Bar graph* represents group mean  $\pm$  SEM. Total dogs analyzed: Control  $n = 6$ , MR  $n = 5$ , and MR+βB  $n = 4$ . One-way ANOVA  $P = 0.007$  for sGC $\alpha_1$ ;  $P = 0.095$  for sGC $\beta_1$

mice with cardiac myocyte-specific expression of human  $\beta_3$ AR had attenuated hypertrophic response to chronic isoproterenol and angiotensin II stimulation [5]. Cardiac-specific  $\beta_3$ AR transgenic mice have also been shown to have enhanced cardiac contractility [26]. Furthermore, improved cardiac function and metabolism in a diabetic rat model was associated with metoprolol-induced upregulation of  $\beta_3$ AR signaling [50, 51].

In the studies reported here, we interrogated a presumed myocardial  $\beta_3$ AR/NO-cGMP signaling pathway to investigate this as a potential mechanism of cardiac benefit for metoprolol. We previously demonstrated that volume-

overload cardiac stress disturbs the nitroso-redox balance as reflected by increased oxidation of sGC in the myocardium [29]. Chronic  $\beta_1$ AR-blockade not only prevented the nitroso-redox imbalance in volume-overloaded hearts, as reflected by decreased oxidation of sGC in MR+βB hearts, but also induced coupling of  $\beta_3$ AR and NO-sGC-cGMP signaling in a membrane microdomain specific fashion.

Using the selective  $\beta_3$ AR agonist BRL, we tested the capacity for  $\beta_3$ AR triggered cGMP production within LV myocardium, caveolae, and heavy-density, NLR. We compared the BRL response to the DEA/NO response to assess the relative coupling between  $\beta_3$ AR and NO-sGC-cGMP

signaling. Given reports of caveolae localization of a  $\beta_3$ AR isoform in mice and of human  $\beta_3$ AR in a cardiac-specific transgenic mouse [5, 47], along with overall upregulation of  $\beta_3$ AR in metoprolol-treated diseased hearts [50–52], we expected to find enhanced  $\beta_3$ AR/NO-cGMP coupling specifically within caveolae of MR+ $\beta$ B hearts. Strikingly, chronic metoprolol therapy enhanced  $\beta_3$ AR/NO-cGMP coupling within NLR, not Cav3<sup>+</sup>LR, of the eccentric hypertrophied heart. In MR hearts,  $\beta_3$ AR did not increase cGMP production in any myocardial microdomain despite upregulation of  $\beta_3$ AR. This discrepancy between  $\beta_3$ AR upregulation and coupling with NO-sGC-cGMP may be explained by the relocalization of sGC $\beta_1$  away from caveolae and the oxidation of sGC within NLR of MR hearts. While the potential signaling partners may be within a shared membrane microdomain, it appears that inducible sGC cyclase activity was compromised by oxidation.

Alternatively, coupling of  $\beta_3$ AR and NO-sGC-cGMP within MR+ $\beta$ B NLR might reflect local coupling of  $\beta_3$ AR and nNOS. Recent studies in rodents demonstrated that  $\beta_3$ AR signaling activates nNOS, as the effects of  $\beta_3$ AR-mediated cardioprotection, NO production, and NOS signaling were blunted in mice with genetically deleted nNOS [41]. Moreover,  $\beta_3$ AR activation of nNOS was found to occur via phosphorylation of the nNOS positive regulatory site, Ser<sup>1412</sup> [5, 41, 60]. While levels of Ser<sup>1412</sup>-phosphorylated nNOS (p-nNOS) are low under physiological conditions, nNOS activation, as reflected by elevated Ser<sup>1412</sup> p-nNOS, may play a critical counter-regulatory role in stress induced, pathophysiological conditions. In our canine model, selective  $\beta_3$ AR agonist BRL induced an increase in Ser<sup>1412</sup> p-nNOS within NLR of MR+ $\beta$ B but not in MR or Control, which is consistent with our findings of BRL-induced cGMP production within NLR of MR+ $\beta$ B alone. These findings as a whole suggest that  $\beta_1$ AR-blockade within the volume-overloaded heart induces  $\beta_3$ AR/NO-cGMP coupling via enhanced  $\beta_3$ AR activation of nNOS.

Our findings regarding  $\beta_3$ AR and NO-sGC-cGMP signaling are novel and significant on several fronts. We are the first to demonstrate active and inducible coupling of  $\beta_3$ AR and NO-sGC-cGMP signaling within the heart, notably in the  $\beta_1$ B-treated, volume-overloaded heart and in a microdomain specific fashion. Recent studies of a double transgenic mouse with cardiac myocyte-specific expression of both the human  $\beta_3$ AR and a cGMP-specific FRET sensor revealed increased basal sGC activity [5]. However, inducible or active coupling between  $\beta_3$ AR and NO-sGC-cGMP was not interrogated. Our findings suggest that chronic  $\beta_1$ B therapy is associated with a beneficial inducible and active  $\beta_3$ AR/NO-cGMP coupling outside of myocardial caveolae. This is consistent with reports of

(a) differential subcellular localization and G protein coupling of murine  $\beta_3$ AR isoforms [47]; and (b) G<sub>i</sub> mediation of GPCR activation of NOS [3, 10]. Moreover, previously reported nuclear  $\beta_3$ AR regulation of gene transcription depends upon local downstream NO-sGC-cGMP activation [58]. While more studies are warranted to elucidate the mechanistic details, such reports of nuclear  $\beta_3$ AR activation of NO-sGC-cGMP signaling raise the possibility that the NLR microdomain may encompass nuclear envelope.

Interestingly, chronic metoprolol treatment was associated with the retention of sGC $\beta_1$  within caveolae. As the exact mechanism of caveolae localization of sGC $\beta_1$  remains to be determined, we can only hypothesize at this time that chronic  $\beta_1$ AR-blockade either directly or indirectly impacts upon protein–protein interactions or reversible post-translational modifications (e.g. S-palmitoylation) that are generally believed to mediate caveolae localization [11, 22, 63]. Such studies are beyond the scope of this manuscript.

Myocardial  $\beta_3$ AR expression is challenging to assess given the low expression of  $\beta_3$ AR relative to  $\beta_1$ AR and  $\beta_2$ AR in the heart [36]. While radioligand binding assays are commonly used to determine receptor expression, high-affinity and high-specificity radiolabeled  $\beta$ AR subtype antagonists are necessary to differentiate the relative expression of the three  $\beta$ AR subtypes. In adipose tissue, which predominantly expresses  $\beta_3$ AR over either  $\beta_1$ AR or  $\beta_2$ AR, radioligand binding assays are feasible for determining  $\beta_3$ AR expression. However, the lack of high-affinity, selective  $\beta_3$ AR antagonists precludes the use of radioligand binding assays for determining  $\beta_3$ AR expression and distribution in the heart [12, 37, 39]. The exceedingly high concentration of radioligand  $\beta_3$ AR antagonist needed would lead to high non-specific binding and inaccurate characterization of  $\beta_3$ AR expression. Hence, in lieu of radioligand binding assay, we selected a highly sensitive and specific  $\beta_3$ AR antibody that recognizes an epitope conserved within both canine and human  $\beta_3$ AR amino acid sequences and has only 60–80 % identity, at high E values, with  $\beta_1$ AR or  $\beta_2$ AR amino acid sequences. We confirmed our Western analysis with qRT-PCR. Most importantly, we successfully demonstrated functional coupling of  $\beta_3$ AR/NO-cGMP signaling with our in vitro BRL stimulation studies.

Our assessment of myocardial microdomain signaling is, by necessity, synthetic in nature, in that cyclase activity assays are performed on myocardial membrane fractions, as opposed to live, intact cardiac myocytes. Ideally, subcellular cGMP signaling within caveolae- and heavy-density NLR microdomains could be visualized in live cells with a FRET-based cGMP sensor. While transgenic mice with cardiac myocyte-specific expression of FRET-based cGMP sensors have recently been reported [5, 56], none

are microdomain-targeted cGMP sensors. Thus, our combinatorial approach of cGMP enzyme immunoassays and Western analyses effectively allow us to interrogate microdomain signaling.

This study shows for the first time that chronic  $\beta_1$ B with metoprolol therapy preserves and even enhances NO-cGMP signaling within specific myocardial microdomains in the volume-overloaded heart, in particular inducing coupling of  $\beta_3$ AR/NO-cGMP signaling in the heavy-density non-lipid raft fraction. The present analysis raises the possibility that the antioxidant action shared by  $\beta$ Bs may be an indirect restoration of nitroso-redox balance in myocardial NLR membrane microdomain, mediated by enhanced  $\beta_3$ AR signaling coupled with nNOS activation and sGC stimulation (Fig. 7). This indirect antioxidant mechanism may be particular to selective  $\beta_1$ -blockers, or even metoprolol succinate for that matter. Whereas metoprolol upregulates myocardial  $\beta_3$ AR expression, the non-selective  $\beta$ -blocker carvedilol does not [64]. Whereas carvedilol can directly scavenge free radicals, selective  $\beta_1$ -blockers do not [54]. In fact, carvedilol has been shown to block oxidative stress-mediated signaling via various mechanisms [27]. Thus, the comparative cardioprotection and cardioprotective mechanism of  $\beta_1$ B metoprolol versus non-selective  $\beta$ Bs may depend upon the etiology of HF and thereby the effect of the specific cardiac injury upon myocardial NO and/or  $\beta_3$ AR signaling [28]. Regardless, the enhancement of myocardial  $\beta_3$ AR/NO-cGMP coupling with chronic  $\beta_1$ AR-blockade in the volume-overloaded heart suggests new approaches to  $\beta$ AR modulation to optimize cardiac function.  $\beta$ AR modulation, with initial chronic  $\beta_1$ AR antagonism followed by additional  $\beta_3$ AR agonism, may offer further functional and clinical benefit

to HF and MR patients. Moreover, direct stimulation of myocardial sGC on a background of neurohormonal blockade may similarly confer additional clinical benefit [13]. Such potential therapeutic implications warrant further mechanistic and eventual clinical studies.

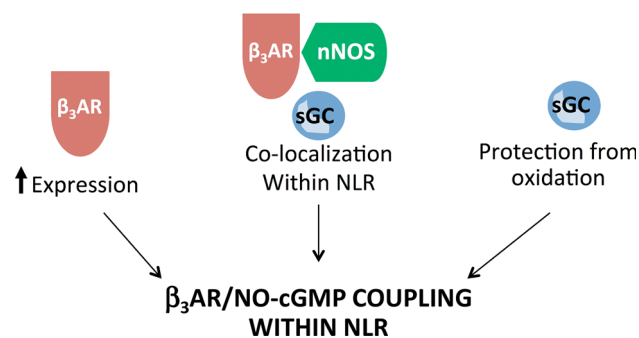
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**Conflict of interest** On behalf of all the authors, the corresponding author states that there is no conflict of interest.

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## CHRONIC $\beta_1$ AR BLOCKADE



**Fig. 7**  $\beta_1$ AR-blockade enhances coupling of  $\beta_3$ AR and NO-sGC-cGMP signaling within myocardial NLR. Increased myocardial  $\beta_3$ AR expression, colocalization of  $\beta_3$ AR, sGC, and nNOS, and protection of sGC from oxidation contribute to the enhanced  $\beta_3$ AR/NO-cGMP coupling in chronic  $\beta_1$ B treated, volume-overloaded hearts

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