Regulation of urocortin I and its related peptide urocortin II by inflammatory and oxidative stresses in HL-1 cardiomyocytes

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Abstract

Despite our knowledge on the regulation of urocortin (Ucn) I and its related peptides in the heart, the possible involvement of cardiovascular stress substances, such as cytokines or angiotensin II (Ang II), on this regulation remains to be fully elucidated. We therefore evaluated the potential role of cardiovascular stress substances on the regulation of the Ucn–corticotropin-releasing hormone (CRH) receptor system in HL-1 cardiomyocytes using a Ucn I-specific RIA, conventional reverse transcription-PCR (RT-PCR) and quantitative real-time RT-PCR. Ucn I mRNA levels were shown to be up-regulated by lipopolysaccarides (LPS), tumor necrosis factor- α (TNF- α), Ang II, H₂O₂, and pyrrolidinedithiocarbamate (PDTC). The LPS- and Ang II-induced increase in Ucn I mRNA levels was abolished by tempol. In addition, the secretion of Ucn I from HL-1 cardiomyocytes was stimulated by LPS and TNF- α . On the contrary, Ucn II mRNA was increased by TNF- α alone and Ang II with tempol, and the TNF- α -induced increase in Ucn II mRNA was abolished by erythromycin and PDTC. These results suggested that Ucn I mRNA may be up-regulated by oxidative stress, whereas Ucn II mRNA may be up-regulated by the activated nuclear factor- κ B, i.e. inflammatory stress. CRH-R2 mRNA may be negatively regulated by the increase in expression of Ucn I and/or Ucn II mRNA. In conclusion, the Ucn–CRH receptor system may be regulated by two major forms of cardiac stresses, i.e. oxidative and inflammatory stress, and may play a critical role in cardiac stress adaptation in heart diseases.

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Introduction

Urocortin (murine urocortin: Ucn, human urocortin: UCN) I, Ucn II, and Ucn III, the members of corticotropin-releasing hormone (CRH)-related peptides, have various actions on the cardiovascular system via cAMP-dependent pathways and the extracellularly regulated kinase 1/2 pathway (Ikeda et al. 1998, 2002, 2005a, Brar et al. 2004a, Honjo et al. 2006). We previously reported the pathophysiological involvement of UCN I in cardiomyopathies (Ikeda et al. 2003), in which a patient's plasma concentration of tumor necrosis factor (TNF)-a increased (Matsumori et al. 1994). TNF- α can produce various deleterious effects when expressed in large amounts and it is produced in the heart by both cardiomyocytes and resident macrophages under conditions of cardiac stress (Sarzi-Puttini et al. 2005). In addition, Ucn I was up-regulated by TNF- α in human umbilical vein endothelial cells (Honjo et al. 2006), and, in turn, CRH type 2 receptor (CRH-R2) was down-regulated by lipopolysaccarides

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(LPS) and TNF-a in the mouse heart (Ikeda et al. 1998, Coste et al. 2001). Because CRH-R2 was also downregulated by Ucn I in mouse cardiomyocytes (Heldwein et al. 1997, Coste et al. 2001) and in the mouse heart (Asaba et al. 2000), we hypothesize that LPS and TNF- α may stimulate the release of endogenous ligand(s) for CRH-R2, such as CRH, Ucn I, Ucn II, and/or Ucn III, from the heart. Also, we previously demonstrated that LPS and TNF- α stimulated the secretion of Ucn I, but not of CRH from neonatal rat cardiac myocytes and non-cardiac myocytes (Ikeda et al. 2001). These findings suggest that Ucn I and its related peptides may be regulated by inflammatory cytokines, such as LPS and TNF- α , and may play a pathophysiological role in the diseased heart because CRH-R2 signaling in the heart may be very important for adaptation to cardiac stress in pathological conditions (Coste et al. 2000). Ucn I may be regulated in response to oxidative stress, thereby exerting a vasoprotective role against the oxidative stress caused by angiotensin II (Ang II) in HUVECs (Honjo et al. 2006). We hypothesized that Ucn I and its

Journal of Molecular Endocrinology (2009) 42, 479–489

related peptides may be regulated by inflammatory and/or oxidative stress(es) in the diseased heart. Therefore, the present study aims to evaluate the regulation of Ucn I and Ucn II in relation to inflammatory and oxidative stress.

Materials and methods

Cell culture

HL-1 cardiomyocytes, an immortalized cardiomyocyte cell line derived from mouse atria (Claycomb et al. 1998), were cultured as previously described (Ikeda et al. 2005b) with slight modification. Briefly, cells were plated in 10 cm culture dishes pre-coated with 0.02%Bacto gelatin (Becton, Dickinson, and Company, Franklin Lakes, NJ, USA) and 5 µg/ml fibronectin (Sigma-Aldrich Inc., St Louis, MO, USA) or in fibronectin-pre-coated 10 cm culture dishes (BD Bio-Coat, Becton, Dickinson, and Company) and cultured until cells reached confluence in Claycomb Medium (SAFC Biosciences, Lenexa, KS, USA) supplemented with 10% fetal bovine serum (FBS, Sigma-Aldrich Inc.), 0.1 mM norepinephrine (Sigma-Aldrich Inc.), 1% L-GlutaMAX (Invitrogen Corp.), and antibiotics $(100 \text{ u/ml penicillin G and } 10 \mu\text{g/ml streptomycin}).$ The cells were then removed by trypsinization and passed into another 10 cm culture dish, 6 cm culture dish, 12-well plate $(3.0 \times 10^5 \text{ cells/well})$, or a 6-well plate $(6.0 \times 10^5 \text{ cells/well})$ pre-coated with fibronectin/ gelatin. Cells were cultured in FBS and norepinephrine-free Claycomb Medium supplemented with 1% L-GlutaMAX and antibiotics for 24 h prior to each experiment except when cells were used for conventional reverse transcription-PCR (RT-PCR).

cDNA preparation and conventional RT-PCR

Total RNA was extracted from HL-1 cardiomyocytes (at confluence in a 6 cm culture dish) by the acidguanidium-phenol-chloroform (AGPC) method with 1ml/dish TRIzol Reagent (Invitrogen Corp.) and treated with DNase I (Takara Bio Inc., Otsu, Japan). Three micrograms of total RNA were used to synthesize cDNA with SuperScript III First-Strand Synthesis System (Invitrogen Corp.) after contamination of genomic DNA was ruled out by 50 cycle PCR with β -actin primers (shown in Table 1, estimated amplicon size: 510 bp). PCR was performed using Takara taq hot start version (Takara Bio Inc.) and primers specific for CRH-R1, CRH-R2 (Brar et al. 2004a), Ucn I, Ucn II (Li et al. 2003), and Ucn III (GenBank accession No. AF361944, designed by the Primer3 software (Rozen & Skaletsky 2000), estimated amplicon size: 254 bp). PCR was performed on cDNA from

HL-1 cardiomyocytes, with conditions consisting of initial denaturation at 94 °C for 4 min, 3-step PCR cycles (CRH-R1, CRH-R2, Ucn I, and Ucn II, 35 cycles; Ucn III, 36 cycles; β-actin, 25 cycles: denaturation at 94 °C for 1 min, annealing at the temperatures shown in Table 1 for 1 min, and extension at 72 °C for 1 min), with a final extension at 72 °C for 7 min. As a positive control, cDNA from mouse brain (mouse brain QUICK-Clone cDNA, Clontech Laboratories, Inc., Mountain View, CA, USA) was used. In addition, expression of CRH-R1/R2 and Ucn mRNA in the mouse heart was also evaluated using 0.1 ng cDNA/ reaction (Mouse Heart QUICK-Clone cDNA, Clontech Laboratories, Inc.). Primer sequences and annealing temperatures are summarized in Table 1.

Measurement of Ucn I levels secreted from HL-1 cardiomyocytes

To evaluate secretion of Ucn I from HL-1 cardiomyocytes, cells were cultured in 6-well plates and stimulated with LPS (1 ng/ml, Sigma-Aldrich Inc.), TNF-a (10 ng/ml, Sigma-Aldrich Inc.) or Ang II (10^{-7}) mol/l, Peptide Institute, Inc., Osaka, Japan) for 3, 6,

Table 1 Primers for conventional reverse transcription-PCR

	Primer sequences and annealing temperatures
CRH-R1	
Annealing temperature	62·9 °C
Forward	5'-GGTGTGCCTTTCCCCATCATT-3'
Reverse	5'-CAACATGTAGGTGATGCCCAG-3'
CRH-R2	
Annealing	60 °C
temperature	
Forward	5'-GGCAAGGAAGCTGGTGATTTG-3'
Reverse	5'-GGCGTGGTGGTCCTGCCAGCG-3'
Ucn I	
Annealing	68 °C
temperature	
Forward	5'-CTTCGCCCGGAGAGCAGCCAGTG-3'
Reverse	5'-GCGTTCCAGCCCCGGGGTAGGTAA-3'
Ucn II	
Annealing	66·5 °C
temperature	
Forward	5'-GGCCGCCGCTGAGACTGAA-3'
Reverse	5'-GGCCTGTGGACCTTAGATGGACTT-3'
Ucn III	
Annealing	55∙5 °C
temperature	
Forward	5'-CAAGCCTCTCCCACAAGTTC-3'
Reverse	5'-TGCCTGGGATTGGTATCTGT-3'
β-actin	
Annealing temperature	54·4 °C
Forward	5'-GACTACCTCATGAAGATCCT-3'
Reverse	5'-CCACATCTGCTGGAAGGTGG-3'

 Table 2
 Primers for quantitative real-time reverse transcription-PCR

Primer sequences

CRH-R2	
Forward	5'-CTTCAACTCTTTCCTGCAGTCCTTC-3'
Reverse	5'-GCTGTGGAAGCTGATCCTGGT-3'
Ucn I	
Forward	5'-CGCGCTCCTCTTGCTGTTAG-3'
Reverse	5'-ATGGACAGTGGAGGGTCGTC-3'
Ucn II	
Forward	5'-CCCTTACCTAGACACCCGTG-3'
Reverse	5'-CGAGCCTGTTCCAGTAAGATCC-3'
GAPDH	
Forward	5'-CAAACGGGTCATCATCTCCG-3'
Deverse	
neverse	5-CICGIGGIICACACCCATCAC-3

12, and 24 h. The culture medium was collected and stored at -80 °C until measurement of Ucn I by Ucn I-specific RIA kit (Pheonix Pharmaceutical, Inc., Belmont, CA, USA). The total amount of protein from the HL-1 cardiomyocytes in each well was extracted by the M-PER Mammalian Protein Extraction Reagent (Pierce Biotechnology, Inc., Rockford, IL, USA) and measured using a bicinchoninic acid Protein Assay Reagent Kit (Pierce Biotechnology, Inc.) according to the manufacturer's protocol (Smith *et al.* 1985). Secreted Ucn I was normalized against the total cellular protein of the HL-1 cardiomyocytes in each well. Data are presented as pmol/mg protein.



cDNA preparation and quantitative real-time RT-PCR

HL-1 cardiomyocytes cultured in 6-well plates were stimulated with or without LPS (1 ng/ml) and TNF- α (10 ng/ml) for 3, 6, 12, and 24 h. The HL-1



Figure 1 Expression of CRH-R1, CRH-R2, Ucn I, Ucn II, Ucn III, and β -actin mRNA in HL-1 cardiomyoyctes by RT-PCR. CRH-R2, Ucn I, and Ucn II mRNAs, but not CRH-R1 and Ucn III mRNAs, were expressed in HL-1 cardiomyocytes. HL, HL-1 cardiomyo-cytes cDNA, MH, mouse heart QUICK-clone cDNA, MB, mouse brain QUICK-clone cDNA.

Figure 2 The influence on the secretion of Ucn I from HL-1 cardiomyocytes by cytokines LPS (A) and TNF- α (B) and Ang II (C). Secretion of Ucn I was significantly increased by LPS, TNF- α , and Ang II. Data were represented as mean \pm s.p. **P*<0.01 versus vehicle, ***P*<0.05 versus vehicle.



Figure 3 Time-dependent expression of Ucn I mRNA stimulated by LPS (A), TNF- α (B), Ang II (C), and H₂O₂ (D). Ucn I mRNA was significantly increased by LPS, TNF- α , Ang II, and H₂O₂ at 3 h. And, thereafter, Ang II significantly suppressed Ucn I mRNA. **P*<0.01 versus vehicle, ***P*<0.05 versus vehicle. Data are presented as the mean \pm s.p.

cardiomyocytes were then stimulated by LPS (0.01-10 ng/ml), TNF- α (0·1–100 ng/ml), and Ang II (10⁻¹¹, 10^{-9} , 10^{-7} , and 10^{-6} mol/l) for 3 h with or without a nuclear factor (NF)- κ B inhibitor (erythromycin (10⁻⁵) mol/l, Sigma-Aldrich Inc.; Desaki et al. 2004) or ammonium pyrrolidinedithiocarbamate (PDTC, 10^{-4} mol/l, Sigma-Aldrich Inc.; Sherman et al. 1993, Boyd et al. 2006). To evaluate the involvement of oxidative stress on the expression of Ucn I and Ucn II mRNAs, we used H₂O₂ (Nakalai Tesque, Inc., Kyoto, Japan) at 0.5, 0.75 (Saito *et al.* 2001), and 1 mmol/l and the superoxide dismutase mimetic, 4-hydroxy-2, 2, 6, 6-tetramethylpiperidine-1-oxyl (tempol, 10^{-4} mol/l, Merck KGaA (Calbiochem), Darmstadt, Germany; Sakai et al. 2007). After washing twice with cold PBS, the cells were lysed by TRIzol reagent (1 ml/well) and stored at -80 °C until RNA extraction. Total RNA was extracted by the AGPC method and treated with DNase I until genomic DNA was no longer detected by 50 cycle PCR as described. Then cDNA was synthesized by primescript RT reagent kit (Takara Bio, Inc.) with oligo dT primers. Real-time PCR was performed on a Thermal Cycler Dice (Takara Bio, Inc) with SYBR premix Ex Taq/Taq II (Takara Bio, Inc.) according to the manufacturer's protocols. The specific primers against mouse CRH-R2, Ucn I, Ucn II, and glyceraldehyde-3-phosphate-dehydrogenase (GAPDH) are summarized in Table 2. The real-time PCR was performed with conditions consisting of initial denaturation at 94 °C for 10 s, 2-step PCR cycles (50 cycles, denaturation at 95 °C for 5 s, annealing and detection step at 60 °C for 30 s), and the confirmation step of quality of PCR products by the dissociation curve (denaturation at 95 °C for 15 s followed by step-up elevation of temperature from 60 to 95 °C by 0.5 °C for every 30 s). Quantitative data were analyzed by the $2^{-\Delta\Delta C_t}$ method (Livak & Schmittgen 2001), using the 2nd derivative curve of the amplification plots (Thermal Cycler Dice Real Time System TP800 software version 2.00B, Takara Bio, Inc.) and normalized against GAPDH cycle thresholds.

Statistical analysis

Statistical analysis was performed using ANOVA followed by a *post hoc* test for between-group comparison (StatView 5.0, SAS Institute, Inc., Cary, NC, USA).



Figure 4 Time-dependent expression of Ucn II mRNA stimulated by LPS and TNF- α (A) and Ang II (B). **P*<0.01 versus vehicle. TNF- α significantly increased Ucn II mRNA at 3 h but LPS and Ang II did not exert significant actions on expression of Ucn II mRNA. Data are presented as the mean±s.p.

P values <0.05 were considered to indicate statistical significance, and all data were expressed as the means \pm s.D.

Results

Expression of mouse Ucn I and its related peptides in HL-1 cardiomyocytes

RT-PCR revealed that CRH-R2, Ucn I, and Ucn II mRNA were expressed in both HL-1 cardiomyocytes and the mouse heart (Fig. 1). However, CRH-R1 and Ucn III mRNA were not expressed in this cardiomyocyte cell line and the mouse heart (Fig. 1).

Secretion of Ucn I by HL-1 cardiomyocytes stimulated with LPS, TNF- α , and Ang II

Ucn I-like immunoreactivity (Ucn I-LI) increased in the culture medium of HL-1 cardiomyocytes in a timedependent manner. The secretion of Ucn I, as detected by RIA, significantly increased in response to LPS (3, 6, 12 h: P < 0.01 versus vehicle, Fig. 2A) and to TNF- α (24 h: P < 0.05 versus vehicle, Fig. 2B). In addition, secretion of Ucn I-LI from HL-1 cardiomyocytes was also significantly increased by Ang II (3, 6, 12 h: P < 0.01 versus vehicle, Fig. 2C).

Real-time RT-PCR detection of mouse Ucn I, Ucn II, and CRH-R2 mRNA

Real-time RT-PCR demonstrated that both LPS and TNF-α significantly increased Ucn I mRNA expression at 3 h (Fig. 3A and B). At 3 h, expression of Ucn II mRNA was significantly increased by TNF- α , but not by LPS (Fig. 4A). Expression of Ucn I mRNA increased in a dose-dependent manner in response to LPS at 3 h (Fig. 5A). On the contrary, expression of Ucn II mRNA was not significantly affected by LPS at 3 h (Fig. 5E). TNF- α , on the other hand, increased expression of both Ucn I and Ucn II mRNA dose dependently (Fig. 5B and F). Furthermore, Ang II and H₂O₂ significantly stimulate the expression of Ucn I mRNA compared with vehicle at 3 h (Fig. 3C and D). This increase in Ucn I mRNA occurs in a dose-dependent manner at 3 h (Fig. 5C and D). But Ang II suppressed the expression of Ucn I mRNA at 6 and 12 h (Fig. 3C). On the contrary, Ang II did not affect expression of Ucn II mRNA (Fig. 4B). Expression of CRH-R2 mRNA seemed to be decreased by the combined effects of the Ucn I and Ucn II induced by LPS and TNF- α at 3 and 12 h (Fig. 6A and B). Erythromycin ameliorated the LPS-induced increase in Ucn I mRNA. However, erythromycin did not affect the TNF-α-induced increase in Ucn I mRNA (Fig. 7A and B). PDTC alone significantly increased Ucn I mRNA but exerted no significant effects on TNFα-induced increase in Ucn I mRNA (Fig. 7C and D). And the increase in the expression of Ucn I mRNA by PDTC and LPS seemed to be additive to that of LPS but the difference did not reach statistical significance (Fig. 7C). The TNF- α -induced increase in Ucn II mRNA was abolished by erythromycin and PDTC (Fig. 7E). Tempol, an antioxidant, abolished the LPS-induced increase in Ucn I mRNA, whereas tempol significantly potentiated the action of the TNF-a-induced increase in Ucn I mRNA (Fig. 8A and B). Furthermore, the Ang II-induced increase in Ucn I mRNA was abolished by tempol, whereas Ucn II mRNA was inversely regulated by Ang II and tempol (Fig. 8C and E). In addition, tempol abolished the PDTC-induced increase in Ucn I mRNA (Fig. 8D).

Discussion

In the present study, we demonstrate that HL-1 cardiomyocytes express Ucn I, Ucn II, and CRH-R2, indicating that this cardiomyocyte cell line is a useful



Figure 5 Dose-dependent expression of Ucn I and Ucn II mRNA by LPS (Ucn I (A), Ucn II (E)) and by TNF- α (Ucn I (B), Ucn II (F)) and expression of Ucn I mRNA by Ang II (C) and H₂O₂ (D) in HL-1 cardiomyocytes at 3 h. Expression of Ucn I mRNA following stimulation by LPS, TNF- α , Ang II, and H₂O₂, and Ucn II mRNA by TNF- α were generally increased in a dose-dependent manner. Data are presented as the mean±s.p. **P*<0.01 versus vehicle.

model for investigating the Ucn–CRH receptor system (Ikeda et al. 2005a). Although CRH-R1 is involved in anxiety and neuroendocrine stress and CRH-R1 and Ucn III were reported to be expressed in the human heart (Kimura et al. 2002, Takahashi et al. 2004), neither CRH-R1 nor Ucn III mRNA was expressed in the HL-1 mouse atrial cardiomyocyte cell line. These data are supported by previous studies using rat and mouse cardiomyocytes (Brar et al. 2004b, Ikeda et al. 2005a). Therefore, Ucns act through CRH-R2, the main mediator of the stress response in cardiomyocytes (Coste et al. 2000, Pañeda et al. 2005), rather than through CRH-R1. This suggests that the autocrine stress adaptation system is mediated by endogenous Ucn I, Ucn II, and CRH-R2 in HL-1 cardiomyocytes and by exogenous CRH-R2 ligands.

Previous studies demonstrated an increase in the expression of Ucn I in target regions of inflammation in diseases involving TNF- α (Uzuki *et al.* 2001, Ikeda *et al.* 2003, Saruta *et al.* 2004). In addition, a recent study showed that the expression of Ucn II mRNA was increased in mucosal samples of patients with inflammatory bowel disease, and in human intestinal xenografts following exposure to *Clostridium difficile* toxin A (Moss *et al.* 2007), an activator of NF- κ B (Jefferson *et al.* 1999), indicating that the regulation of Ucn II may be involved in the NF- κ B pathway. Our present results showed that LPS, Ang II, and H₂O₂



Figure 6 Time-dependent expression of CRH-R2 mRNA stimulated by LPS (A) and TNF- α (B). LPS and TNF- α significantly suppressed the expression of CRH-R2 mRNA at 3 h and at 12 h. LPS and TNF- α also tended to suppressed CRH-R2 mRNA at 6 h and 24 h, but differences to vehicle did not reach statistical significance. **P*<0.01 versus vehicle, ***P*<0.05 versus vehicle. Data are presented as the mean \pm s.p.

individually enhanced the expression of Ucn I mRNA in as well as the secretion of Ucn I from HL-1 cardiomyocytes, and that these effects were abolished by tempol. This increase in Ucn I mRNA by LPS and Ang II was abolished by antioxidants such as erythromycin (Miyachi et al. 1986) and tempol. Although HL-1 cardiomyocytes expressed toll-like receptor (TLR; Boyd et al. 2006), the present results showed that the actions of LPS may not be the action via the TLR signaling because of the absence of LPS-binding protein, which enhances biological action of LPS (Hailman et al. 1994), in stimulation medium and abolishment of the action of LPS on expression of Ucn I mRNA by antioxidant. These results, taken in combination with the demonstration that LPS and Ang II cause oxidative stress (Honjo et al. 2006, Yuan et al. 2009), strongly suggests that Ucn I may be positively regulated by oxidative stress. Ang II markedly increased the secretion of Ucn I up to 12 h, with a temporal increase of Ucn I mRNA followed by

suppression. The increase in Ucn I levels in the culture medium may result in an increase in intracellular cAMP (Ikeda et al. 1998), leading to the induction of a family of cAMP-responsive nuclear factors, including inducible cAMP early repressor (Sassone-Corsi 1998). Consequently, due to the presence of a cAMP responsive element (CRE) in the Ucn I promoter region (Zhao et al. 1998), the decrease in the expression of Ucn I mRNA may be attributed to the binding of inducible cAMP early repressor to the CRE after an initial increase in the expression of Ucn I mRNA. A return to basal Ucn I levels in the culture medium with LPS and Ang II may be, at least in part, due to the endocytosis of Ucn I (Tu et al. 2007). But further studies are required to clarify these results. In addition, PDTC alone enhanced the expression of Ucn I mRNA. PDTC is known as an inhibitor of nitric oxide synthase (NOS; Sherman et al. 1993), suggesting that up-regulation of Ucn I mRNA may be caused by increased oxidative stress secondary to inhibition of NOS by PDTC. A demonstration of an inhibition of PDTC-induced increase in Ucn I mRNA by tempol will support this hypothesis. But the precise mechanism of the regulation of Ucn I mRNA by TNF- α is not known. The expression of Ucn II mRNA was enhanced by Ang II with tempol and TNF- α , suggesting that a possible regulatory mechanism of Ucn II may involve the NF-KB pathway, i.e. inflammatory stress, because Ang II stimulates both oxidative stress and inflammatory stress (Luft 2002). A search for transcription factor binding motifs (Akiyama 1995) within the Ucn II promoter, using the UCSC Genome browser (Chen et al. 2003, Kent et al 2002, Karolchik et al. 2003), also supported the potential involvement of activated NF- κ B in the transcription of Ucn II mRNA. The NF-kB binding motif, however, has not been shown in the mouse Ucn I promoter region (Zhao et al. 1998). Furthermore, our results on the expression of Ucn II mRNA by co-incubation with TNF- α and potential inhibitors, such as erythromycin and PDTC (Sherman et al. 1993), supports our hypothesis that the regulation of Ucn II mRNA by TNF- α may be mediated by the NF-KB pathway, i.e. Ucn II mRNA expression may be induced by inflammatory stress rather than by oxidative stress. Although erythromycin has miscellaneous actions, such as antibiotic and anti-oxidative actions, it is reported that erythromycin also has the inhibitory properties of NF-kB signaling in addition to such actions (Desaki et al. 2004, Yasutomi et al. 2005), therefore, suppression of TNF-a-induced increase in Ucn II mRNA by erythromycin may be, at least in part, attributed to the inhibition of NF-KB signaling. The results on the expression pattern of Ucn I and Ucn II mRNA by Ang II may also indicate that the expression of Ucn I mRNA may be relatively dominant in HL-1 cardiomyocytes and these peptides may



Figure 7 The effects of erythromycin (EM) and ammonium pyrrolidinedithiocarbamate (PDTC) on LPS- or TNF- α -induced expression of Ucn I (A–D) and Ucn II (E) mRNAs at 3 h. Erythromycin abolished increase in Ucn I mRNA, but not by TNF- α (A and B), but PDTC increased expression of Ucn I mRNA (C and D). Ucn II mRNA was regulated by TNF- α , but not by LPS, and TNF- α -induced increase in Ucn II mRNA was suppressed by erythromycin and PDTC, indicating that Ucn II mRNA may be regulated by nuclear factor- κ B. Data are presented as the mean ±s.p. LPS, LPS 1 ng/ml, TNF, TNF- α 10 ng/ml, EM, erythromycin 10⁻⁵ mol/l, PDTC, PDTC 10⁻⁴ mol/l, **P*<0.01 versus vehicle, ***P*<0.05 versus vehicle, #*P*<0.01 versus LPS, \$*P*<0.01 versus TNF.

negatively regulate in each other. Taken together, the present results suggest that Ucn I mRNA and Ucn II mRNA are differentially regulated, i.e. NF-κB may, at least in part, be involved in the regulation of Ucn II mRNA, while oxidative stress may up-regulate Ucn I mRNA in HL-1 cardiomyocytes. These data also suggest that Ucn I and Ucn II may play a pathophysiological role in cardiac disease, especially in heart failure, in which the levels of vasoactive substances such as cytokines and Ang II (Matsumori *et al.* 1994, Ikeda *et al.* 2008) are increased.

In conclusion, the present results demonstrate that HL-1 cardiomyocytes contain the Ucn–CRH receptor system, which may be regulated by two major forms of cardiac stress, oxidative and inflammatory stress. In heart disease, such differential regulation of Ucn I and Ucn II could play a critical role in stress adaptation via the Ucn–CRH receptor system.



Figure 8 The effects of tempol on the regulation of Ucn I mRNA induced by LPS (A), TNF- α (B), Ang II (C), and ammonium pyrrolidinedithiocarbamate (PDTC) (D) and on Ucn II mRNA induced by Ang II (E) at 3 h. Tempol abolished the LPS- and Ang II-induced expression of Ucn I mRNA, indicating that Ucn I mRNA may be dominantly regulated by oxidative stress. On the contrary, co-incubation with Ang II and tempol resulted in an increase in Ucn II mRNA expression. Data are represented as the mean \pm s.D. LPS, LPS 1 ng/ml, TNF, TNF- α 10 ng/ml, Ang II, Ang II 10⁻⁷ mol/l, PDTC, PDTC 10⁻⁴ mol/l, Tem, Tempol 10⁻⁴ mol/l, (A) **P*<0.01 versus vehicle, ***P*<0.01 versus LPS, (B) **P*<0.01 versus vehicle, ***P*<0.05 versus Versus TNF, \$*P*<0.01 versus tem, (C) **P*<0.05 versus vehicle, ***P*<0.01 versus vehicle, ***P*<0.01 versus vehicle, ***P*<0.01 versus vehicle, ***P*<0.05 versus vehicle, ***P*<0.01 versus vehicle, ***P*<0.05 versus Vehicle, ***P*<0.01 versus vehicle, ***P*<0.05 ver

Declaration of interest

The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

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