The cardiomyocyte “redox rheostat”: Redox signalling via the AMPK-mTOR axis and regulation of gene and protein expression balancing survival and death

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1. Introduction

Heart failure, the end result of various progressive heart diseases, is the leading cause of cardiovascular mortality in the developing world [1]. The consequent inability of the heart to pump blood to the body is associated with loss of terminally-differentiated contractile cardiomyocytes, whether by necrosis (as occurs following myocardial infarction) or, if energy levels suffice, one of several forms of programmed cell death including apoptosis [2–4]. Enhancing cardiomyocyte survival and reducing rates of cardiomyocyte death would be therapeutically advantageous, but there are no clinical strategies yet available to achieve these aims.

Oxidative stress plays a pivotal role in modulating cardiomyocyte survival, growth and death, but the effects depend on the degree of stress [5]. High levels of reactive oxygen species (ROS) are clearly damaging and result in unregulated cell death. More moderate levels induce apoptosis through the mitochondrial death pathway with cleavage and activation of caspases 9 and 3, and regulated dismantling of cellular contents. In contrast, low ROS levels are associated with cardiomyocyte survival and may even promote hypertrophy. These are examples of...
cellular responses by redox stress induced signalling, in which ROS activate or inhibit intracellular redox-sensitive signal transduction pathways [6–8]. ROS are produced either as a by-product of normal cellular metabolism (e.g. mitochondrial leakage [9]) or by dedicated ROS-producing enzymes (e.g. NADPH oxidases [10,11]). In either case, H$_2$O$_2$, as a stable ROS moiety, is the predominant redox effector [7], and low-level H$_2$O$_2$ may be vital for upregulation of pro-survival and cytoprotective genes [12].

Failing cardiomyocytes are energetically challenged and generate less ATP [13,14]. This may be due in part to increased redox stress signals. The mammalian target of rapamycin (mTOR) and AMP-activated protein kinase (AMPK) signalling pathways play a central role in responding to ATP levels to modulate cardiomyocyte function [15,16]. mTOR, an evolutionarily conserved Thr/ser protein kinase, operates in one of two protein complexes, mTOR complex 1 (mTORC1) and mTORC2 [17,18]. Of these, mTORC1 controls protein synthesis and may particularly enhance expression of cytoprotective proteins, thereby contributing to cell survival [19]. In contrast, AMPK is viewed as the master regulator of energy homeostasis, being activated by nutrient-poor conditions and increases in AMP associated with concomitant loss of ATP [16]. AMPK inhibits mTORC1 via inhibitory phosphorylation of an essential mTORC1 protein, Raptor, thus inhibiting protein synthesis. Redox stress inhibits protein synthesis in cardiomyocytes [20], but the mechanism is not fully understood.

Clearly, in cardiomyocytes (as in other cells), redox stress induced signalling has a range of effects on the cellular response and this could be due to a number of factors including effects of different forms of ROS [21] and/or localised ROS production to elicit redox signalling (e.g. from NADPH oxidases or mitochondria [9–11]). Here, we revisited the more fundamental hypothesis that the level of ROS stress per se is a key factor in the cellular response. We applied different concentrations of H$_2$O$_2$ (as the most physiologically relevant form of ROS) globally to redox rheostat M compound C$_{119}$ and/or localised ROS production to elicit redox signalling to the same extent. We focused on the AMPK-mTOR signalling axis and assessed the impact on expression of immediate early genes (IEGs) and protein synthesis. We detected increased mTOR signalling and induction of cytoprotective proteins such as p21$^{Cip1/WAF1}$ with lower levels of oxidative stress, and inhibition of protein synthesis with higher concentrations associated with cell death. Thus, quite apart from considerations of ROS species and localisation, a “redox rheostat” effect operates in cells to elicit different responses according to the degree of stress.

2. Materials and methods

2.1. Cardiomyocyte isolation and culture conditions

Neonatal rat ventricular myocytes were dissociated from the ventricles of 2 to 4 day Sprague-Dawley rat hearts as described previously [22]. Cardiomyocytes were plated on Primaria culture dishes precoated with 1% (v/v) gelatin for 18 h in Dulbecco’s modified Eagle’s medium (DMEM)/M199 medium (4,1 ratio) containing 100 units/ml penicillin, 100 μg/ml streptomycin plus 15% (v/v) foetal calf serum (FCS) at 37 °C. Unattached cells were removed by gentle washing (10% (w/v) SDS, 300 mM Tris-HCl) trichloroacetic acid (6 ml), NaOH was added (10 μl, 10 M), and the pellets were dissolved in 1.8 ml Soluene (Perkin-Elmer, UK) before scintillation counting using Ultima Gold scintillation fluid (Perkin-Elmer, UK) before scintillation counting using Ultima Gold scintillation fluid (Perkin-Elmer, UK). Experiments were performed in duplicate, the mean values were taken and corrected according to total protein. The data are presented as means ± SEM of these values. IC$_{50}$ values for each experiment were calculated using GraphPad Prism 7 software and the mean of these values was taken.

2.2. Antisense oligodeoxycytucleotide transfection

Cardiomyocyte cell lysates were prepared as described previously [22]. Briefly, cardiomyocytes were washed in ice-cold PBS and scraped into Buffer A (20 mM β-glycerophosphate pH 7.5, 20 mM NaF, 2 mM EDTA, 0.2 mM Na$_3$VO$_4$, 10 mM benzamidine, 5 mM dithiotreitol, 300 μM phenylmethylsulfonyl fluoride, 200 μM leupeptin, 2 μM microcystin LR, 10 μM trans-epoxy-succinyl-L-leucylamido-(4-guanidino)butane) containing 1% (v/v) Triton X-100. Following centrifugation (10,000 × g, 5 min, 4 °C), the supernatants were boiled with 0.3 vol sample buffer (10% (w/v) SDS, 13% (w/v) glycerol, 300 mM Tris-HCl pH 6.8, 130 mM dithiothreitol, 0.2% (w/v) bromophenol blue). For isolation of the nuclear-enriched and cytosolic proteins, cells were processed as published [26]. Proteins were separated by SDS-polyacrylamide gel electrophoresis and transferred to nitrocellulose membranes. Proteins were detected with antibodies from Cell Signalling Technologies Inc. (phosphorylated AMPK (Thr$^{792}$) (cat. no.: 2535), total AMPK (cat. no.: 2603), phosphorylated Raptor (Ser$^{795}$) (cat. no.: 2083), total Raptor (cat. no.: 2280), phosphorylated mTOR (Ser$^{2448}$) (cat. no.: 2971), phosphorylated mTOR (Ser$^{2461}$) (cat. no.: 2974), total mTOR (cat. no.: 2983), phosphorylated PKB/Akt (Ser$^{473}$) (cat. no.: 4060), phosphorylated PKB/Akt (Thr$^{308}$) (cat. no.: 2965), total PKB/Akt (cat. no.: 2965).
were determined from the A260. For microarray analysis, total RNA values of 1.8 nuclease-free water and purity was assessed from the A260:A280 with according to the manufacturer's instructions. RNA was dissolved in LAS4000 system (GE Healthcare). ImageQuant 7.0 software (GE Healthcare) was used for densitometry.

2.6. RNA isolation, microarray analysis, ratiometric PCR and qPCR

Total RNA was prepared using RNA Bee (AMS Biotechnology Ltd) according to the manufacturer's instructions. RNA was dissolved in nuclease-free water and purity was assessed from the A260/A280 with values of 1.8–2.1 (being considered acceptable). RNA concentrations were determined from the A260. For microarray analysis, total RNA (4 × 10⁶ cells per sample) and polysomal RNA (16 × 10⁶ cells per sample) were prepared from control cardiomyocytes or cardiomyocytes exposed to 0.2 mM H₂O₂ (1 h) as described in [24]. RNAs were prepared from 12 separate preparations of cardiomyocytes and individual RNA samples were generated by combining equal amounts of RNA from three separate myocyte preparations. Four sets of samples were hybridised to individual Affymetrix rat genome 230 2.0 microarrays. cRNA preparations and microarray hybridizations were performed as previously described [27]. Data (as CEL files) are available from ArrayExpress (accession number: E-MTAB-6758).

The CEL files were imported into GeneSpring GX13 for analysis using MAS 5.0 summarisation. Data were normalised to the gene median and a confidence filter applied (> 50 raw value). Probesets were selected according to relative level of expression (> 1.5-fold increase induced by H₂O₂ in total or polysomal RNA pools relative to controls) followed by statistical testing (one-way ANOVA with SNK post-test) using the Benjamini and Hochberg correction for multiple controls or zero time.

First strand cDNA synthesis with oligo-dT priming and ratiometric RT-PCR were performed as previously described [28] using primers for p21cip1/WAF1 [F1, 5′-ACTTCTGACCTCGCAGAAGG-3′; F2, 5′-CTGCTACAGTGGCGCAGTTA-3′; F3, 5′-TCGGTGATGCGACTATGTA-3′; R1, 5′-ACAGCAGAAGGACGGACG-3′; R3, 5′-CAGAAGGAGGCTCCTCGA-3′; G3′, 83 bp product]; exogenous α subunit, a regulating subunit which binds adenine nucleotides, and detects increases in AMP and, to a lesser extent in ADP, AMPK binds adenine nucleotides, and detects increases in AMP and, to a lesser extent in ADP.

AMPK is a heterotrimer comprising a catalytic α subunit, a regulatory γ subunit which binds adenine nucleotides, and detects increases in AMP and, to a lesser extent....
H2O2 reduces ATP levels and inhibits protein synthesis in cardiomyocytes. Cardiomyocytes were exposed to the concentrations of H2O2 shown for the times indicated. (A) Concentrations of ATP were measured using a luciferase assay. Results are % of control value and are means ± SEM (n = 4 independent myocyte preparations). (B) Area under curve (AUC) analysis of cardiomyocyte ATP levels from the data in (A). ***p < .001 relative to control (one-way ANOVA with Tukey post-test). (C) Protein synthesis was measured by incorporation of [3H]Phe. Results are means ± SEM (n = 4 independent myocyte preparations). The IC50 was calculated using the 4-step parameter function in GraphPad Prism 7. **p < .01, ***p < .0001 relative to 0.1 mM H2O2 (one-way ANOVA with Tukey post-test).

extent, ADP [16]. It has been termed an ‘energy sensor’ or ‘intracellular fuel gauge’, becoming activated as ATP concentrations fall, and AMP (and ADP) concentrations rise. AMPK is activated by phosphorylation of AMPKα(Thr172), and decreases rates of anabolic processes (e.g. protein synthesis) whilst increasing rates of catabolic processes (e.g. lipolysis). Activation of AMPK by H2O2 in cardiomyocytes was assessed by immunoblotting of extracts for AMPKα(Thr172) phosphorylation. As in other cells [29], AMPKα(Thr172) was rapidly phosphorylated in response to 1 mM H2O2 (maximal within 3–5 min) (Fig. 2A) and the concentration-dependence was such that activation was detectable at 0.3 mM H2O2 and plateaued at 1 mM H2O2 (Fig. 2B).

mTORC1 regulates protein synthesis [17,18]. Raptor is a key regulatory subunit of mTORC1, and AMPK phosphorylates Raporter(Ser292), causing it to dissociate from mTORC1, thus inhibiting mTORC1 activity. Consistent with activation of AMPK, H2O2 increased phosphorylation of Raporter(Ser292) (Fig. 2A). This was delayed relative to AMPK activation, but the dependence on H2O2 concentration was similar (Fig. 2B). Compound C is an AMPK inhibitor, though it inhibits a number of other protein kinases [30]. SU6656 was originally identified as an inhibitor of the protein Tyr-kinase Src [31], but inhibits a number of other protein Ser/Thr- kinases including AMPK [30]. Both compound C (60 μM) and SU6656 (15 mM) inhibited phosphorylation of Raporter(Ser292) induced in cardiomyocytes by H2O2 (1 mM, 10 min) (Fig. 2C). We conclude that H2O2 reduces cardiomyocyte ATP concentrations and this activates AMPK leading to phosphorylation of Raporter(Ser292). This is consistent with inhibition of protein synthesis (Fig. 1C).

3.3. H2O2 induces PKB/Akt and mTOR phosphorylation

mTOR, the protein kinase component of mTORC1, is itself phosphorylated at several sites including mTOR(Ser2448) and mTOR(Ser2481). mTOR(Ser2448) phosphorylation probably represents a downstream ‘feedback’ phosphorylation whereas mTOR(Ser2481) phosphorylation is an autophosphorylation that occurs when mTOR is activated [32,33]. In cardiomyocytes, phosphorylation of both sites was increased by low concentrations of H2O2 (0.03–0.2 mM), whereas higher concentrations (1–10 mM) reduced mTOR phosphorylation (Fig. 3A and B). Canonical, mTOR is activated by PKB/Akt [17,18]. PKB/Akt is phosphorylated on Thr308 in its catalytic domain and this is required for mTOR activation. It is also phosphorylated on Ser473 in its C-terminal hydrophobic domain with phosphorylation of both residues probably necessary for maximal activation [34]. Concentrations of H2O2 > 0.3 mM resulted in phosphorylation of both PKB/Akt(Thr308) and PKB/Akt(Ser473) (Fig. 3C). This should ultimately induce phosphorylation of mTOR(Ser2448) and mTOR(Ser2481), but there was no correlation with these phosphorylations (Fig. 3A and B). This implies that a supervening intervention, presumably by phosphorylation of AMPK and Raptor (Fig. 2A–C), interferes with PKB/Akt-mediated phosphorylation of mTOR(Ser2448) and mTOR(Ser2481).

3.4. Redox signalling vs. stress and expression of IEGs

Expression of IEG mRNAs is driven by pre-existing transcription factors and de novo protein synthesis is not required [35]. This is characterised by an increase in mRNA expression in the presence of protein synthesis inhibitors such as cycloheximide. Indeed, because cycloheximide exerts an additional stress on the cell, IEG mRNAs are often superinduced. Many IEGs encode transcription factors which are required for expression of ‘later-phase’ genes and expression of these does require protein synthesis [36]. It may therefore be expected that high concentrations of H2O2 that inhibit protein synthesis do not affect IEG mRNAs but suppress expression of later-phase mRNAs. Jun, Atf3 and Egr1 are well-established IEGs. All were upregulated in cardiomyocytes exposed to 0.3 mM H2O2 (2 h) and this was enhanced by the protein synthesis inhibitor cycloheximide (Fig. 4A), confirming they are IEGs. As expected, these mRNAs were still upregulated by 1 mM H2O2, a concentration that substantially inhibits protein synthesis (Fig. 1C), although upregulation was delayed relative to 0.3 mM H2O2 (Fig. 4B). In contrast, upregulation of Nqo1 and Hmox1 by 0.3 mM H2O2 was inhibited by cycloheximide (Fig. 4C), confirming they are later phase genes. These mRNAs were not significantly upregulated by 1 mM H2O2 (Fig. 4D). Our previous work identified Mdm2 and Cdkn1a as genes which were significantly upregulated by low, sub-toxic concentrations of H2O2 (0.04 mM) [12] and we subsequently showed that Mdm2 is cytoprotective under conditions of oxidative stress [37]. Experiments with cycloheximide indicate that Mdm2 and Cdkn1a were both upregulated as IEGs (Fig. 4E). Consistent with this, they were both upregulated by a high concentration of H2O2 (1 mM), albeit with some delay relative to 0.3 mM H2O2 (Fig. 4F) as was seen with Jun, Atf3 and Egr1 (Fig. 4B).

3.5. Polysomal profiling of mRNA transcripts

Even though moderate concentrations of H2O2 (0.1–0.3 mM) did not suppress global protein synthesis to any significant extent (Fig. 1C), the substantial effect on ATP concentrations (Fig. 1A) could affect synthesis of specific proteins. We therefore examined recruitment of mRNAs to cardiomyocyte polysomes following exposure to 0.2 mM H2O2 (1 h)
using Affymetrix microarrays for global transcriptomic profiling. At this early time, 26 probesets (18 established protein-coding mRNAs) were significantly downregulated with 238 probesets (162 established protein-coding mRNAs) significantly upregulated (> 1.5-fold change, \( p < .05 \) FDR) in either the total or polysomal pool (Fig. 5A; Supplemental Spreadsheet 1). Of the upregulated mRNAs, 144 (e.g. \textit{Atf3}, \textit{Jun}, \textit{Hmox1}) were not differentially regulated in the total pool relative to the polysomes (Supplemental Spreadsheet 1) with a strong positive correlation between the relative upregulation in each of the mRNA pools (Fig. 5B). However, the profiles were not entirely overlapping (Fig. 5C) and 12 mRNA species (\textit{Anxa1}, \textit{Egr1}, \textit{Egr2}, \textit{Egr3}, \textit{Tp53inp1}, \textit{Ereg}, \textit{Hspa1}, \textit{Tacr2}, \textit{Mdm2}, \textit{Egr1}, \textit{Egr2}, \textit{Egr3}, \textit{Tp53inp1}, \textit{Ereg}, \textit{Hspa1}, \textit{Tacr2}, \textit{Mdm2}, \textit{Isg20}, and \textit{Cdkn1a}) were upregulated to a significantly greater extent (> 1.5-fold; FDR < 0.05) in the total pool relative to the polysomes suggesting that their polysomal recruitment was reduced. In contrast, there was preferential recruitment of four mRNA species (including \textit{Rasd1}, \textit{Clk1}, \textit{Nfil1} and \textit{Hist2h2aa3}) to the polysomes (Supplemental Spreadsheet 1). Others, such as \textit{Thbs1} were differentially regulated, but the difference was either not statistically significant or below our 1.5-fold threshold. Examples of genes with differential expression are shown in Fig. 5D. The data for \textit{Hmox1}, \textit{Atf3}, \textit{Nfil1}, \textit{Rasd1} and \textit{Mdm2} were validated by qPCR (Fig. 5E). Thus, even though ATP concentrations were substantially reduced (Fig. 1A),

polysomal recruitment of \( \sim 90\% \) of mRNA species was unaffected.

### 3.6. \textit{p21\textsuperscript{Cip1/WAF1}} (the protein product of the \textit{Cdkn1a} gene) induced by subtoxic \( \textit{H}_2\text{O}_2 \) levels is cytoprotective

\textit{p21\textsuperscript{Cip1/WAF1}} was identified as a cyclin-dependent kinase inhibitor [38], but has other roles according its subcellular localisation [39,40]. Our previous microarray studies identified \textit{Cdkn1a} as one of a small group of genes that was upregulated in cardiomyocytes by subtoxic concentrations of \( \textit{H}_2\text{O}_2 \) [12], whilst here we have confirmed it is an IEG (Fig. 4E and F). However, the functional role of \textit{p21\textsuperscript{Cip1/WAF1}} in cardiomyocytes is unknown. \textit{Cdkn1a} mRNA was similarly upregulated in total and polysomal RNA pools (Fig. 5D), indicating that it is likely to be translated. Consistent with this, \textit{p21\textsuperscript{Cip1/WAF1}} protein was rapidly increased in cardiomyocytes exposed to 0.2 mM \( \textit{H}_2\text{O}_2 \) with maximal expression from \( \sim 2 \) h that was sustained up to at least 24 h (Fig. 6A). \textit{p21\textsuperscript{Cip1/WAF1}} protein was detected in both nuclear and cytosolic extracts from \( \sim 90 \) min (Fig. 6B). Interestingly, the concentration-dependency of the response was bell-shaped and \textit{p21\textsuperscript{Cip1/WAF1}} was not induced by 0.5 mM \( \textit{H}_2\text{O}_2 \) at 2 h (Fig. 6C). This presumably reflects the reduced rate of protein synthesis (Fig. 1C).

To determine if \textit{p21\textsuperscript{Cip1/WAF1}} is cytoprotective in cardiomyocytes,
cardiomyocytes were transfected with Cdkn1a antisense oligonucleotides (Cdkn1a-AS-ODN) to suppress p21Cip1/WAF1 protein expression or a scrambled version of the Cdkn1a-AS-ODN (Cdkn1a-Scr-ODNs). As expected, Cdkn1a AS-ODN accumulated in the nucleus (not shown).

H2O2 (0.2 mM, 4 h) increased expression of p21Cip1/WAF1 protein in transfected cells (Fig. 6C). This was significantly inhibited by Cdkn1a-AS-ODN (52 ± 4.6% relative to H2O2 alone, p < .01) but not by Cdkn1a-Scr-ODN. We demonstrated that 0.2 mM H2O2 induces apoptosis in neonatal rat cardiomyocytes as assessed by loss of mitochondrial membrane potential, TUNEL analysis and immunoblotting for cleaved caspase 3 [37], with detection of cleaved caspase 3 being probably the most reliable marker of cell death for quantification purposes [44]. The reduction in p21Cip1/WAF1 by Cdkn1a-AS-ODN in the context of H2O2 stimulation enhanced the amount of cleaved caspase 3, indicative of increased apoptosis (Fig. 6C). The anthracyclin doxorubicin is an anti-cancer agent that is cardiotoxic and increases ROS generation and promotes cardiac oxidative stress [41]. Doxorubicin increased expression of p21Cip1/WAF1 protein over 3–4 h (Fig. 6D). As with H2O2, this was significantly inhibited by Cdkn1a-AS-ODN but not by Cdkn1a-Scr-ODN, and decreased expression of p21Cip1/WAF1 protein was associated with enhanced appearance of cleaved caspase 3 and, thus, apoptosis (Fig. 6E). Hence, p21Cip1/WAF1 is cytoprotective in the cardiomyocyte response to redox/anthracycline stress.

3.7. mTOR regulates expression of p21Cip1/WAF1

mTOR is phosphorylated in cardiomyocytes exposed to moderate levels of H2O2 (0.1–0.3 mM) (Fig. 3A and B), indicative of its activation. The pan-mTOR inhibitor KU63794 [42] and mTORC1 inhibitor rapamycin almost completely prevented p21Cip1/WAF1 expression in the nuclear fraction (Fig. 7A) but had no effect on its expression in the cytoplasmic fraction (Fig. 7B). This was associated with increased caspase-3 cleavage (5.76 ± 0.9 fold) (Fig. 7C). Thus, mTOR is required for cytoprotection in the context of low levels of redox stress, in part by increasing expression of cytoprotective proteins such as p21Cip1/WAF1.

4. Discussion

Redox levels exert pleiotropic effects on cellular responses, ranging from promotion of cell survival through to regulation of cell death. Perhaps unsurprisingly, therefore, redox stress underlies a plethora of disease states including heart failure. Understanding how ROS signalling can elicit such a panoply of responses is of crucial importance for...
the development of novel therapies for these diseases. Various hypotheses have been developed to explain the variation of responses, including effects of different forms of ROS [21] and localised ROS production for redox signalling (e.g. from NADPH oxidases or mitochondria [9–11]). Whilst these factors clearly play a role, we assessed a more fundamental hypothesis that the level of ROS per se is a key factor in the cellular response, focusing on the AMPK-mTOR signalling axis, regulation of protein synthesis and cell death. We demonstrated the presence of a "redox rheostat" in which lower levels of ROS activate mTOR with production of cytoprotective proteins such as p21Cip1/WAF1, whilst higher levels cause a reduction in ATP with activation of AMPK, inhibition of protein synthesis and cell death (Fig. 7D). We propose that a sliding scale operates between these extremes, with variation in production of antioxidants and cytoprotective proteins balanced against ATP levels. This accounts for whether cells survive or grow and, if the balance is in favour of cell death, the mode of cell death in which highly regulated apoptosis will proceed if ATP levels suffice, but necrotic cell death occurs if there is catastrophic loss of ATP [43].

The relationship between intracellular ATP concentrations, and AMPK-mTOR signalling in relation to protein synthesis is clearly
complex. Whilst it may seem obvious that declining ATP concentrations should be associated with inhibition of protein synthesis, the concentration-dependencies did not overlap fully, with substantial loss in global ATP at concentrations that did not appear to impinge on global protein synthesis (Fig. 1). Instead, significant inhibition of protein synthesis occurred at concentrations $\geq 1 \text{ mM H}_2\text{O}_2$, that are highly toxic to cardiomyocytes [44], and we suggest this represents complete shutdown of cellular processes whilst striving for survival. The mechanism most likely involves AMPK phosphorylation of Raptor(Ser792), a mechanism shown in other systems to inhibit global protein synthesis via inhibition of mTORC1 [15–18], since the concentrations of H$_2$O$_2$ required to promote phosphorylation of AMPK$\alpha$(Thr172) and Raptor

Fig. 5. Recruitment of mRNAs induced by H$_2$O$_2$ to polysomes for translation. Cardiomyocytes were unstimulated (Control) or exposed to 0.2 mM H$_2$O$_2$ (1 h) and total or polysomal RNA prepared for microarray analysis ([A] - [D]) or qPCR ([E]). (A) Heatmap (Log$_2$ scale) of all probesets with significantly decreased or increased expression (> 1.5-Fold change; FDR < 0.05) in total or polysomal RNA fractions. Expression values were normalised to the gene median. (B) Relative fold change of upregulated mRNAs in polysomal vs total RNA pools. Linear regression analysis indicates that most mRNAs are regulated similarly in total and polysomal fractions and are translated efficiently. (C) Overlay plot of mRNAs induced by H$_2$O$_2$ in total and polysomal RNA pools to show differential changes in some genes. (D) Heatmap (Log$_2$ scale) of specific genes relevant to this study is shown on the left, with fold change relative to controls on the right. (E) qPCR validation of microarray data showing similar changes in expression in total or polysomal RNA fractions for Hmox1 and Atf3, enhanced recruitment of Nfil3 and Rasd1 to polysomes for translation and less efficient recruitment of Mdm2 to polysomes. Results are means ± SEM ($n = 4$ independent myocyte preparations; these are different preparations from those used for microarray analysis). *p < .05, **p < .001 relative to unstimulated controls, #p < .05 relative to fold-change in total RNA pool (one-way ANOVA with Tukey post-test).
(Ser\textsuperscript{792}) (Fig. 2B) were those that caused inhibition of protein synthesis (Fig. 1C). Classically, mTOR (and therefore mTORC1) is activated by PKB/Akt \cite{17,18}, and we have shown previously that H\textsubscript{2}O\textsubscript{2} activates PKB/Akt, increasing phosphorylation of both Thr\textsuperscript{308} and Ser\textsuperscript{473} \cite{20}.

Here, as before \cite{20}, PKB/Akt was only significantly phosphorylated on both residues with > 1 mM H\textsubscript{2}O\textsubscript{2} (Fig. 1C), concentrations that appear incompatible with protein synthesis (Fig. 1C). Our previous work identified an over-riding phosphatase activity causing
dephosphorylation of 4E-BP1 to reduce availability of eIF4E for initiation of translation [20]. Here, the data suggest there is an additional mechanism with inhibition of mTOR via AMPK-dependent phosphorylation of Raptor(Ser792) (Fig. 2).

Whilst high concentrations of H2O2 inhibited mTORC1 and global protein synthesis, our data indicated that lower concentrations were associated with increased phosphorylation of mTOR(Ser2448) and mTOR(Ser2481) (Fig. 3A). The mechanism is unclear since we did not detect significant increases in PKB/Akt phosphorylation at these concentrations (Fig. 3C). This was not associated with a significant increase in global protein synthesis (Fig. 1C), but lower concentrations were associated with differential recruitment of some mRNAs to the polysomes of cardiomyocytes with enhanced recruitment (and therefore increased efficiency of translation) of some (e.g. Nfil3, Rasd1) and reduced efficiency of others (e.g. Mdm2) (Fig. 5). Indeed, these data are consistent with studies in brain in which focal ischaemia (associated with increased oxidative stress) results in selective recruitment of transcripts to the polysomes for translation [45]. As in the brain, and in
contrast to insulin treatment of cardiomyocytes [24], we did not detect selective recruitment of transcripts with 5’ terminal oligopyrimidine tracts (TOPs) that are classically recruited following activation of p70 ribosomal S6 kinase via mTORC1.

The AMPK-mTOR axis is intimately linked to regulation of protein synthesis. However, the rate of global protein synthesis has a significant impact on expression of certain transcripts, namely those which require de novo synthesis of the transcription factors that regulate their expression. The concept of IEGs derived from early work on viral gene expression, but was extended to mammalian genes in which IEGs were defined as those for which transcription requires only pre-existing transcription factors [35]. This means that protein synthesis is not required, and inhibiting protein synthesis with, for example, cycloheximide, or H2O2 did not abrogate upregulation of classic IEG mRNAs including Jun, Asf3 and Egr1 (Fig. 4A and B), although the rate of increase was delayed by 1 mM H2O2, possibly a reflection of the low energy status of the cells. These and many other IEGs encode transcription factors required for expression of later phase non-IEGs including Hmox1, and Nqo1, so if protein synthesis is inhibited and IEG mRNAs are not translated, these later phase genes are not upregulated even at the mRNA level. This was clearly apparent and upregulation of Hmox1 and Nqo1 mRNAs was abolished by cycloheximide or 1 mM H2O2 (Fig. 4C and D). These mRNAs along with other non-IEGs (e.g. Gclc, Txnrd1, Srm1) form part of the neutralising response to an oxidant load, so inhibition of expression of these genes is likely to compromise cellular defences further, exacerbating the effects of high levels of redox stress and hasten progression to cell death.

This study, together with our previous microarray studies [12], identified a number of genes that are classically regulated by p53 including Mdm2 and Cdkn1a (encoding p21Cip1/WAF1 protein). We have already reported that upregulation of Mdm2 mRNA by H2O2 did not appear to require de novo synthesis of p53, with it being regulated by AP-1 transcription factors [37]. Here, we show that both Mdm2 and Cdkn1a are upregulated by moderate concentrations of H2O2 (0.2 mM) in cardiomyocytes as IEGs (Fig. 4E and F), p21Cip1/WAF1 protein expression induced by 0.2 mM H2O2 was sustained over 2–24 h (Fig. 6A and B) and, as with Mdm2 [37], preventing protein expression with antisense ODNs enhanced the rate of apoptosis shown by caspase-3 cleavage [37,44] (Fig. 6C), indicating that it is also a cytoprotective protein. This is consistent with a recent report in which p21Cip1/WAF1 was shown to protect H9c2 cells (a cardiomyocyte-like cell line) in a simulated ischaemia-reperfusion injury model [46]. A role for p21Cip1/WAF1 in cardiomyocyte cytoprotection is also consistent with reports in other cells in which the protective effect is attributed to accumulation in the cytoplasm rather than the nucleus [47]. In lung adenocarcinoma cells [48,49], cytosolic p21Cip1/WAF1 suppresses mitochondrial cell death pathways, including caspase-3 activation by preserving anti-apoptotic Bcl-2 family members. Based on our findings and previous work, we rationalise that the role for cytosolic p21Cip1/WAF1 in myocytes is to inhibit mitochondrial death pathways given that oxidative stress negatively alters Bcl-2 signalling [44], leading to cardiac myocyte apoptosis. However, p21Cip1/WAF1 was detected in both myocyte compartments (Fig. 6B), suggesting that it has an additional role in the nucleus even in terminally-differentiated post-mitotic cells. Interestingly, inhibition of mTOR with Ku63794 or rapamycin partially inhibited the increase in p21Cip1/WAF1 protein induced by 0.2 mM H2O2, but inhibition was preferentially targeted to the nuclear compartment, with relative preservation of the protein in the cytoplasm (Fig. 7A and B). Nevertheless, both Ku63794 and rapamycin enhanced the rate of cardiomyocyte apoptosis induced by 0.2 mM H2O2.

Our data here indicate that p21Cip1/WAF1 is protective in cardiomyocytes exposed to 0.2 mM H2O2, and previously we have shown that Mdm2 also contributes to cytoprotection [37]. Nevertheless, cardiomyocytes still undergo apoptosis under these conditions as we have shown previously [44], indicating that the presence of these proteins is not sufficient for complete protection and raising the question of the importance of their upregulation. One consideration is that some degree of cytoprotection may be required to ensure that cell death proceeds via regulated programmed cell death and loss of protective elements such as expression of p21Cip1/WAF1 and Mdm2 may increase the probability of non-regulated cell death (i.e. necrosis with associated inflammation). Another consideration is that we all study an entire population of cells and, for this study, each sample was prepared from 4 million cardiomyocytes. There is undoubtedly a spectrum of response and we measure the average. We simply do not know (and do not have the ability to assess) if these proteins are expressed only in a sub-population of surviving cells. At higher concentrations of H2O2, protein synthesis is suppressed and, even though mRNAs increase, protein expression is compromised. Consistent with this, the concentration-dependency for expression of p21Cip1/WAF1 protein is bell-shaped with little induction of protein at 0.5 mM at 2 h (Fig. 6C). It remains to be established whether forced expression of proteins such as p21Cip1/WAF1 and Mdm2 would confer cytoprotection under conditions of high level ROS, when cellular metabolism is compromised.

In summary, we present data to support a novel concept of the cardiomyocyte “redox rheostat” in which different degrees of ROS stress influence cell energetics and intracellular signalling pathways to regulate mRNA and protein expression. This sliding scale of responses determines cell fate, modulating cell survival vs cell death.

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Author contributions

D.N.M., P.H.S. and A.C conceived and designed the experiments. D.N.M., R.P., G.Z., K.A.R., K.L., B.H., T.M., B.W. and A.C performed the experiments. D.N.M., R.P., G.Z., P.H.S and A.C. analyzed and interpreted the data. D.N.M., P.H.S. and A.C drafted the manuscript.

Conflict of interest

The authors declare that they have no conflict of interests.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.yjmcc.2019.02.006.

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